DETECTION OF DIFFERENTIALLY EXPRESSED GENES UPON COMPATIBLE AND INCOMPATIBLE INOCULATION OF WHEAT WITH YELLOW RUST USING SUPPRESSION SUBTRACTIVE HYBRIDIZATION (SSH)

A THESIS SUBMITTED TO
THE GRADUATE SCHOOL OF NATURAL AND APPLIED SCIENCES
OF
MIDDLE EAST TECHNICAL UNIVERSITY

BY

İLAY ÇELİK

IN PARTIAL FULFILLMENT OF THE REQUIREMENTS
FOR
THE DEGREE OF MASTER OF SCIENCE
IN
BIOTECHNOLOGY

NOVEMBER 2007

Approval of the thesis:

DETECTION OF DIFFERENTIALLY EXPRESSED GENES UPON COMPATIBLE AND INCOMPATIBLE INOCULATION OF WHEAT WITH YELLOW RUST USING SUPPRESSION SUBTRACTIVE HYBRIDIZATION (SSH)

submitted by **İLAY ÇELİK** in partial fullfillment of the requirements for the degree of **Master of Science in Biotechnology Department, Middle East Technical University** by,

Prof. Dr. Canan Özgen _____
Dean, Graduate School of **Natural and Applied Sciences**

Prof. Dr. Gülay Özcengiz _____
Head of Department, **Biotechnology**

Prof. Dr. Mahinur S. Akkaya _____
Supervisor, **Chemistry Dept., METU**

Assist. Prof. Dr. Şenay Vural Korkut _____
Co-Supervisor, **Biology Dept., YTU**

Examining Committee Members:

Prof. Dr. Gülay Özcengiz _____
Biology Dept., METU

Prof. Dr. Mahinur S. Akkaya _____
Chemistry Dept., METU

Prof. Dr. Fatih İzgü _____
Biology Dept., METU

Assoc. Prof. Dr. Candan Gürakan _____
Food Engineering Dept., METU

Dr. Semra Hasançebi _____
Plant Biotech. Unit, TÜBİTAK GEBI

Date: 30.11.2007

I here by declare that all information in this document has been obtained and presented in accordance with academic rules and ethical conduct. I also declare that, as required by these rules and conduct, I have fully cited and referenced all materials and results that are not original to this work.

Name, Last name: İlay Çelik

Signature :

ABSTRACT

DETECTION OF DIFFERENTIALLY EXPRESSED GENES UPON COMPATIBLE AND INCOMPATIBLE INOCULATION OF WHEAT WITH YELLOW RUST USING SUPPRESSION SUBTRACTIVE HYBRIDIZATION (SSH)

Çelik, İlay

M.S., Department of Biotechnology

Supervisor: Prof. Dr. Mahinur S. Akkaya

Co-Supervisor: Assist. Prof. Dr. Şenay Vural Korkut

November 2007, 200 pages

Yellow rust disease is one of the most important problems in wheat production. It causes substantial yield losses throughout the world. There are resistant and susceptible wheat varieties to various yellow rust pathotypes. In this thesis genes that are induced in wheat, in virulence and avirulence conditions upon yellow rust inoculations were investigated. Consequently, it was aimed to identify genes that may be playing critical roles in the disease resistance mechanism. The strategy was to construct subtracted cDNA libraries from resistant and susceptible plants and analyse the sequences obtained from these libraries. The subtraction approach in this study differs from the common subtraction designs implicated in plant-pathogen interactions; instead of comparing a compatible or an incompatible interaction with a control, one of the subtractions in this study is done taking a compatible interaction as the tester and an incompatible one as the driver, and the second subtraction, vice versa. Therefore, it was intended to compare the transcriptomes from compatible and incompatible plant-pathogen interactions directly.

Suppression Subtractive Hybridization method was used to construct subtracted cDNA libraries. Two subtractions were performed; SSH1 (D-R), taking a compatible interaction as the tester sample

and an incompatible one as the driver sample, and SSH2 (R-D), taking an incompatible interaction as the tester sample and a compatible one as the driver. In the end, two subtracted cDNA libraries, SSH1 (D-R) library (1536 clones) and SSH2 (R-D) library (1152 clones) were obtained and the libraries were sequenced.

Sequence results were subjected to BlastN and BlastX analysis. We looked for a group of genes that were frequently emphasized in plant disease related studies when we searched within the Blast N homology results of the two libraries. We found out that 19 such genes are present in our libraries. We discussed supposed induction of these genes in the interactions investigated in our study. The fact that these genes were found to be present in our libraries enhances the reliability of our results suggesting that the gene sequences we found indeed belong to genes differentially expressed in the respective comparisons investigated in our study. As such, it also implies that other sequences that were found similar to genes of known functions may represent candidate genes as subjects of further studies investigating wheat-yellow rust interactions.

Key words**:** Wheat, yellow rust, suppression subtractive hybridization (SSH), cDNA library, differential gene expression.

ÖZ

HASSAS VE DAYANIKLI BUĞDAYLARDA SARI PAS ENFEKSİYONU ÜZERİNE FARKLI ANLATIM YAPAN GENLERİN BASKILAYICI ÇIKARIM HİBRİDİZASYONU (SSH) YÖNTEMİ İLE BELİRLENMESİ

Çelik, İlay

Yüksek Lisans, Biyoteknoloji Bölümü

Tez Yöneticisi: Prof. Dr. Mahinur S. Akkaya

Yardımcı Danışman: Yrd. Doç. Dr Şenay Vural Korkut

Ağustos 2007, 200 sayfa

Sarı pas hastalığı buğday üretimindeki en önemli sorunlardan biridir. Tüm dünyada oldukça fazla ürün kaybına neden olmaktadır. Çeşitli sarı pas patotiplerine karşı direnç ve hassasiyet gösteren buğday çeşitleri mevcuttur.

Bu çalışmada, buğdayda hastalık ve direnç durumlarında anlatımı artan genler tespit edilmeye çalışılmıştır Sonuç olarak hastalık mekanizmasında hayati rol oynayan genlerin belirlenmesi amaçlanmıştır. Bu çalışmada benimsenen yaklaşım, bitki-patojen etkileşimi çalışmalarında yaygın olarak uygulanan stratejiden farklıdır; patojenle etkileşim üzerine hastalık ya da direnç gösteren bitkileri hiçbir etkileşime sokulmayan kontrol bitkileriyle karşılaştırmak yerine, bu çalışmada yapılan çıkarımlardan birisinde hastalık geliştiren bitki Tester, direnç gösteren bitki Driver olarak alınmış, diğer çıkarımda ise tam tersi bir karşılaştırma yapılmıştır. Böylece bitki-patojen etkileşiminde hastalık ve direnç durumlarındaki transkriptomların doğrudan karşılaştırılması amaçlanmıştır.

Baskılayıcı Çıkarım Hibridizasyonu yöntemi kullanılarak çıkarımlı cDNA kütüphaneleri kurulmuştur. Biri, uyumlu bir etkileşimi tester örneği, uyumsuz bir etkileşimi ise driver örneği olarak alan SSH1 (D-R) ve diğeri, uyumsuz bir etkileşimi tester örneği, uyumlu bir etkileşimi driver örneği olarak alan SSH2 (R-D) olmak üzere iki çıkarım gerçekleştirilmiştir. Sonuçta SSH1 (D-R) (1536 klon) ve SSH2 (R-D) (1152 klon) kütüphaneleri elde edilmiş ve bu kütüphaneler için dizin analizi yapılmıştır.

Dizin analizi sonuçları Blast N ve Blast X analizlerine tabi tutulmuştur. Bitki hastalıklarıyla ilgili daha önce yapılan çalışmalarda sıklıkla vurgulanan bir grup geni kütüphanelerimizin Blast N benzerlik sonuçları içerisinde aradık. Bu genlerden 19 tanesinin kütüphanelerimizde de bulunduğunu gördük. Bu genlerin bu çalışmada araştırılan etkileşimlerdeki öne sürülen anlatım artışını tartıştık. Bu genlerin kütüphanelerimizde bulunması, bulduğumuz dizinlerin gerçekten de çalışmamızda yapılan karşılaştırmalarda anlatımı artan genlere ait olduğunu önererek sonuçlarımızın güvenilirliğini artırmaktadır. Böylece işlevi bilinen genlere benzerlik gösteren diğer dizinlerin de ilerideki çalışmalara konu olabilecek aday genleri temsil edebileceğini düşündürmektedir.

Anahtar Kelimeler: Buğday, sarı pas, baskılayıcı çıkarım hibridizasyonu (SSH), cDNA kütüphanesi, farklı gen ifadesi.

To Nevin Çelik;
mother, teacher, intellectual

ACKNOWLEDGEMENTS

I would like to thank my supervisor *Prof. Dr. Mahinur S. Akkaya*, not only for her encouragement, motivation, friendship, guiding supervision and limitless support but also for her motherly affection.

I would also like to thank my co-supervisor *Assist.Prof.Dr. Şenay Vural Korkut* for the guidance, encouragement and the support she provided.

I am grateful to *Assist.Prof.Dr. Tolga Can* and *Mr. Alper Söyler* for their support and guidance in bioinformatics analyses.

My thanks also go to *Dr. Semra Hasançebi*, *Assist.Prof. Dr. Aslıhan Günel* and *Ms. Banu Avcıoğlu* for their support, guidance and friendship.

I have benefited enormously from *Akkaya Lab. Members*, I give many thanks to them all.

I must especially acknowledge my first teacher in METU, *Claire Özel*, who later became a friend, a sister, a mother and beyond all a real reminder of the value of life for me.

I owe thanks to my teacher *Dr. Cenk Güray* for his support and encouragement.

I also send may sincerest thanks to *Dr. Şebnem Düzgün*, who always motivated me by not only standing as a model science woman herself but also encouraging and guiding me with a sisterly affection throughout my studies.

I am also sincerely grateful to my friends *Şule Şehirli*, *Şule Çivi*, *Berrin Tığlı*, *Mustafa Göçer*, *Ekin Özman*, *Yiğit Ozan Aydın*, *Muhammet Ali Karaduman*, *Tolga Tezcan* and *Hamza Sucu* for their sensibility, encouragement and support.

I would like to thank *TEV* and *TÜBİTAK* for supporting my graduate study with scholarships.

I would also like to acknowledge and thank to my employer *TÜBİTAK* for providing me the time to carry out a thesis work.

Finally, special thanks to my mother *Nevin Çelik* and brothers *Afşar* and *Bilge Çelik* for their sensibility, support and encouragement.

TABLE OF CONTENTS

ABSTRACT..... iv
ÖZ..... vi
ACKNOWLEDGEMENTS..... ix
TABLE OF CONTENTS..... xi
LIST OF ABBREVIATIONS..... xiv
CHAPTER
1. INTRODUCTION.....1
1.1 Wheat.....1
1.2 Rust Diseases of Wheat.....1
1.3 Yellow Rust Disease of Wheat.....2
1.4 Resistance and Pathogenicity Mechanisms in Plant Diseases.....5
1.5 Suppression Subtractive Hybridization.....11
1.6 Aim of the Study.....14
2. MATERIALS AND METHODS.....17
2.1 Preparation of Plant Material and Infections.....17
2.1.1 Growth of Plant Material.....17
2.1.2 Inoculation of Plants with Yellow Rust Spores.....17
2.1.3 Collection of Leaf Sample.....17
2.2 Suppression Subtractive Hybridization.....18
2.2.1 Total RNA Isolation.....18
2.2.1.1 Precautions for RNA Handling.....18
2.2.1.2 Isolation of Total RNA.....18
2.2.1.3 Gel Analyses and Concentration Determination of Total RNA Samples.....19
2.2.2 Isolation of mRNA.....19
2.2.2.1 Isolation of mRNA from Total RNA Sample.....19
2.2.2.2 Preparation of Gel Spots for Determination of mRNA Concentrations.....20
2.2.3 cDNA Synthesis.....21
2.2.3.1 First Strand cDNA Synthesis.....21
2.2.3.2 Second Strand cDNA Synthesis.....22
2.2.3.3 Rsa I Digestion.....23
2.2.3.4 Gel Analyses of *Rsa* I Digestion Products..... 24

2.2.4 Adaptor Ligation....24
2.2.5 First Hybridization....26
2.2.6 Second Hybridization....28
2.2.7 Primary PCR Amplifications....30
2.2.8 Secondary PCR Amplifications....31
2.3 Cloning of Subtraction Products to Cloning Vectors and Preparation of SSH Libraries....32
2.3.1 Ligation of cDNA Libraries to pGEM®-T Easy Vector....32
2.3.2 Transformation of cDNA Libraries Ligated to pGEM®-T Easy Vector....33
2.3.3 Growth of Transformed Libraries in 96-Well Plates....34
2.3.4 Sequencing of SSH Libraries....34
2.3.5 Analyses of Resulting EST Libraries....34
2.4 Preparation of Buffers and Growth Media for Cloning....35
2.4.1 Preparation of LB and SOC Growth Media....35
2.4.2 Preparation of TB....36
2.5 Preparation of Haugland Plant Growth Medium....36
2.5.1 Preparation of Macronutrient Solution....36
2.5.2 Preparation of Micronutrient, Fe-EDTA and Zinc Solutions....36
2.6 Preparation of Electrophoresis Gels and Buffers....36
2.6.1 Preparation of RNA Gels....36
2.6.2 Preparation of DNA Gels....37
2.6.3 Preparation of Phosphate Buffer and TBE Buffer....37
3. RESULTS AND DISCUSSION....38
3.1 Infection of Plants with Yellow Rust Pathogen....38
3.2 Gel Analyses and Concentration Determination of Total RNA Samples....38
3.3 Isolation of mRNA from Total RNA Samples....39
3.4 Gel Analyses of Rsa I Digestion Products....42
3.5 Primary and Secondary PCR Amplifications....44
3.6 Analyses of Sequence Results of SSH Libraries....45
3.7 Transcripts with Homologies to Significant Genes/Gene Families....47
4. CONCLUSION....68
REFERENCES....70
Appendix A....76
Appendix B....77
Appendix C....78
Appendix D....82
Appendix E....84
Appendix F....111

Appendix G.....127
Appendix H.....159

LIST OF ABBREVIATIONS

ATP	: adenosine triphosphate
BA	: benzoic acid
CC	: coiled coil
cDNA	: complementer DNA
cm	: centimetre
DDBJ	: DNA Data Bank of Japan
DEPC	: diethylpyrocarbonate
DMF	: dimethyl formamide
DMSO	: dimethyl sulfoxide
DNA	: deoxyribonucleic acid
dNTP	: deoxyribonucleoside triphosphate
DTT	: dithiothreitol
EDTA	: ethylenediamine tetraacetic acid
EMBL	: European Molecular Biology Laboratory
EST	: expressed sequence tag
EtBr	: ethidium bromide
g	: gram
GSS	: genome survey sequence
GTP	: guanoside 5'-triphosphate
HEPES	: N(2-hydroxyethyl)piperazine-N'-(2-ethanesulphonic acid)
HR	: hypersensitive response
hr	: hour
HTGS	: high throughput genome sequence
IPTG	: isopropyl β-D-thiogalactoside
LB	: Luria broth
LRR	: leucine rich repeat
LTP	: lipid transfer protein
LZ	: leucine zipper
M	: molar
MAPK	: mitogen-activated protein kinase
MAPKKK	: mitogen-activated protein kinase kinase kinase
mg	: milligram
min	: minute
MJ	: methyl jasmonate

mL	: millilitre
mM	: millimolar
mRNA	: messenger RNA
NADPH	: nicotinamide adenine dinucleotide
ng	: nanogram
nm	: nanometre
PAMP	: pathogen associated molecular pattern
PCR	: polymerase chain reaction
PDB	: Protein Data Bank
PIG	: in-planta induced gene
PIPES	: piperazine-N,N'-bis(2-ethanesulfonic acid)
PK	: protein kinase
PPIase	: peptidyl-prolyl *cis*/*trans* isomerase
PR	: pathogenesis related proteins
RLK	: receptor-like kinase
RNA	: ribonucleic acid
RNAse	: ribonuclease
ROS	: reactive oxygen species
rpm	: revolutions per minute
RT	: reverse transcriptase
RT-PCR	: real-time PCR
RubisCo	: ribulose-1-5-biphosphote carboxylase
SA	: salicylic acid
SAR	: systemic acquired resistance
SCF	: Skp, Cul1 and F-box-containing
SOD	: superoxide dismutase
SSH	: suppression subtractive hybridization
STS	: sequence tagged site
TBE	: tris, boric acid, EDTA
TM	: transmembrane
TMV	: tobacco mosaic virus
UV	: ultra violet
X-gal	: 5-bromo-4-chloro-3-indolyl β-D-galactoside
ZEP	: zeaxanthin epoxidase
°C	: degree Celcius
µL	: microlitre
µg	: microgram

CHAPTER I

INTRODUCTION

1.1 Wheat

Wheat is one of the most important cereal crops. It is mostly consumed as human food, and in fact, it is the basic human food in Turkey. In total world production ranking, wheat comes second after maize (IGC, 2007). Turkey is among the main wheat producers, ranking ninth in total wheat production in the world (IGEME, 2007).

The species name for bread wheat is *Triticum aestivum*. *T. aestivum* belongs to the order *Poales* (*Glumiflorae*), family *Poaceae* (*Gramineae*), tribe *Triticeae*, genus *Triticum* (OECD, 1999).

Wheat is known to have originated in the Fertile Crescent, in Middle East. The genetic relationships between wild and domesticated einkorn and emmer indicate that wheat was first cultivated at a site near Diyarbakır in Turkey (reviewed in Dubcovsky and Dvorak, 2007), as part of the first agricultural practices dating back to between 10.500 and 9500 yr B.P. and taking place in the region of south-eastern Turkey and northern Syria (reviewed in Tanno and Willcox, 2006).

1.2 Rust Diseases of Wheat

Rust diseases of wheat are caused by fungal wheat pathogens. These diseases can be found in most places where wheat is cultivated. The pathogenic rust fungi are spread in the form of clonally produced dikaryotic urediniospores. Since these spores can be easily blown and transported by wind to far distances, the extent of epidemics can reach continental scale and the disease may even disseminate overseas. Rust fungi of wheat are obligate parasites. They are highly specific to their host plant, depending on a gene-for-gene interaction which, makes it difficult to develop durable resistance in wheat cultivars (Kolmer, 2005; Marsalis and Goldberg, 2006). In addition, their dynamic genetic structure enables them to overcome plant resistance and to persist as significant disease factors (Marsalis and Goldberg, 2006).

The three rust diseases that occur on wheat are stem rust, leaf rust and stripe rust. Wheat stem rust is caused by *Puccinia graminis* f. sp. *tritici*, wheat leaf rust by *Puccinia triticina*, and wheat stripe rust by *Puccinia striiformis*. The symptoms of these rusts and their requirements for infection are similar (Marsalis and Goldberg, 2006).

There are more than 40 pathogenic organisms that cause yield losses in wheat production under various conditions. However, the biggest threat to wheat production worldwide comes from regional rust epidemics caused by these rust fungi (Singh and Huerto-Espino, 2001).

1.3 Yellow Rust Disease of Wheat

Yellow rust is the common name for the pathogenic rust fungus *Puccinia striiformis*, which is also called the stripe rust. Yellow rust requires living green plant material in order to survive. The fungus survives the winter as dormant mycelium or active sporulating lesions on volunteers or early autumn-sown crops. Set-aside provides an excellent source of yellow rust over-wintering inoculum. Yellow rust within plant tissue can survive very low temperatures. Only if the wheat is killed by frost will the yellow rust fungus within the plant tissues die. In the spring, particularly in cool moist weather, the fungus starts to grow and produces active sporulating lesions. Temperatures of 10-15°C and a relative humidity of 100% are optimal for spore germination, penetration and production of new, wind-dispersed spores. The fungus is inhibited by temperatures over 20°C.

Yellow rust is one of the most frequent and significant cereal diseases in Turkey. Stripe rust can cause 100% yield losses if infection occurs very early and the disease continues developing during the growing season. In most places of wheat production, yield losses have ranged between 10% and 70%. The proportion of yield loss depends on susceptibility of the cultivar, earliness of the initial infection, rate of disease development, and duration of disease (Chen, 2005).

Yellow rust is characterized by the presence of light yellow, straight sided, powdery pustules arranged in stripes parallel to the veins in the leaf or on head. These elongate pustules are thin and vary in length. Yellow-orange spores, which give the name “yellow rust”, become visible as the pustule matures. As the disease progresses tissues around the pustules get brownish yellow and dry, and a scorched appearance develops. Besides, the leaves lose colour because of chlorosis. (Marsalis and Goldberg, 2006).

According to present knowledge, some characteristic properties for biotrophic fungi can be described as: (1) highly developed infection structures; (2) limited secretory activity, especially of lytic enzymes; (3) carbohydrate-rich and protein-containing interfacial layers that separate fungal and plant plasma membranes; (4) long-term suppression of host defence; (5) haustoria, which are specialized hyphae for nutrient absorption and metabolism (Mendgen and Hahn, 2002).

Rust fungi form an obligately parasitic relationship in which the host plant becomes a source for sugars, amino acids and other nutrients. These parasites develop a specialized organ called “haustorium” (Figure 1.2.a). The infection of rust fungi (Figure 1.2.b) typically begins with the germination of a spore on the leaf surface, followed by the development of appressorium. An

infection peg formed by the appressorium enters the leaf through a pore (stoma), followed by the development of a substomatal vesicle, an infection hypha, a haustorial mother cell, penetration of a photosynthetic mesophyll cell by a peg and the establishment of haustorium (Szabo and Bushnell, 2001). Figure 1.3 depicts the infection cycle on the plant at tissue level.

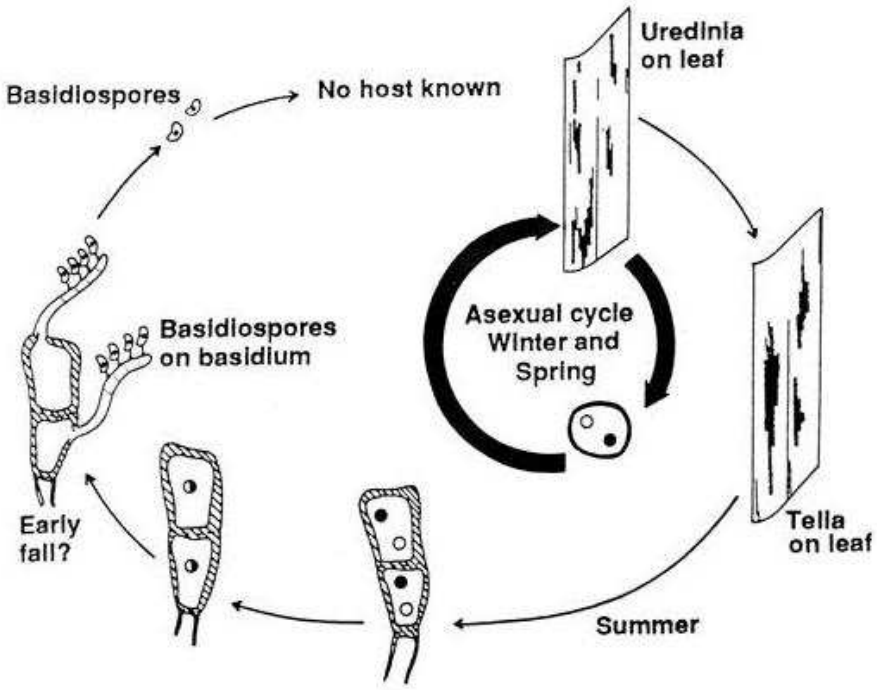


Fig. 1.1 Life and disease cycle of yellow rust (USDA, 2007).

The complete cycle (Figure 1.1) from infection to the production of new spores can take as little as 7 days during ideal conditions. The disease cycle may therefore be repeated many times in one season. During late summer, the dark teliospores may be produced. These can germinate to produce yet another spore type, the basidiospore, but no aecial alternate host has been identified up to now. Its dicaryotic spores are thus produced by mitotic cycle during infection of wheat (HGCA, 2007; Enjalbert *et al.*, 2005).

At present, it is known that haustorium functions in uptake of nutrients from host plant cell, although the mechanisms are not fully understood. The haustorium contains a normal complement of organelles and its own set of nuclear genes. Mendgen and his co-workers have shown that there are at least 31 *in planta*-induced genes (*PIGs*), single or low-copy number genomic genes that code for a variety of proteins involved in amino acid transport, thiamine biosynthesis, metallothioneins, cytochrome P-450 mono-oxygenases and short-chain dehydrogenases. An additional *in planta*-

induced gene, *HXT1*, was indentified and shown to encode a glucose transporter localized in the haustorial plasma membrane (reviewed in Staples, 2001).

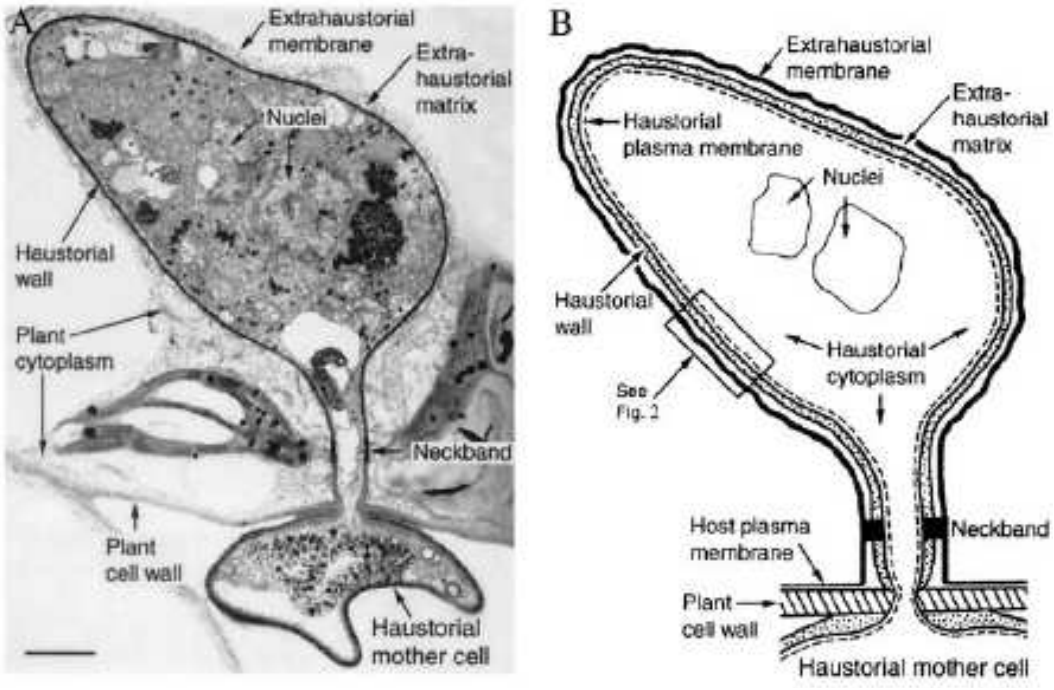


Fig. 1.2.a Haustorial complex, a specialized feeding organ of biotrophic fungal parasites of plants. To move from host cell to fungus, nutrients must traverse the extrahaustorial membrane, the extrahaustorial matrix, the haustorial wall, and the haustorial plasma membrane. A neckband seals the extrahaustorial matrix from the plant cell wall region so that the matrix becomes a unique, isolated, apoplast-like compartment. The haustorium connects to intercellular fungal hyphae by way of a haustorial mother cell. **A:** Transmission electron micrograph of a flax rust haustorium. **B:** Drawing showing key features of the fungal haustorium (Szabo and Bushnell, 2001).

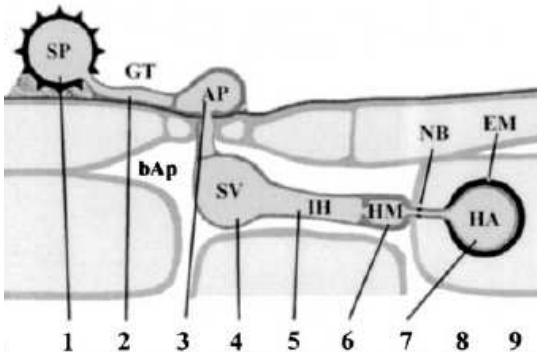


Fig. 1.2.b Schematic representation of rust infection structures. **1:** uredospore (SP), **2:** germtube (GT), **3:** appressorium (AP) stage, **4:** substomatal vesicle (SV) stage, **5:** infection hyphae (IH) stage **6:** haustorial mother cell (HM) stage **7:** haustoria (HA); **bAp:** bulk apoplast, **NB:** neckband, **EM:** extrahaustorial matrix (Voegele *et al.*, 2001).

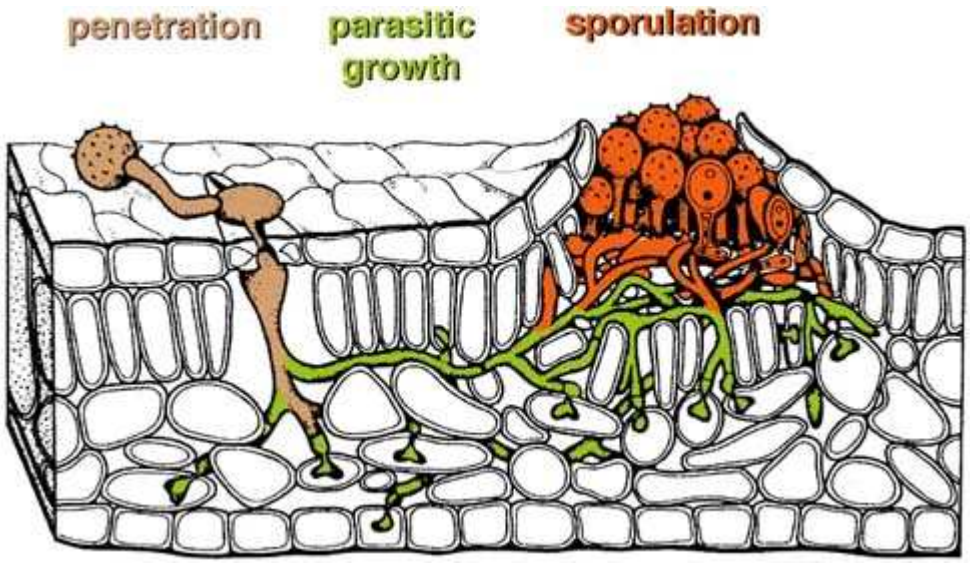


Fig. 1.3 Schematic representation of rust infection cycle on plant leaf tissue (Hahn, 2000).

1.4 Resistance and Pathogenicity Mechanisms in Plant Diseases

In nature, plants are continuously being challenged by a variety of pathogens, but disease rarely realizes. The reason is that plants have an innate ability to recognize potential invading pathogens and to initiate successful defence mechanisms (Staskawicz, 2001). In their review in 1996, Hammond-Kosack and Jones define three broad categories of reasons why most pathogens are unable to cause disease on plants: (1) the plant is unable to support the niche requirements of a

potential pathogen and is thus a non-host; (2) the plant possesses preformed structural barriers or toxic compounds that confine successful infections to specialized pathogen species; or (3) upon recognition of the attacking pathogen, defence mechanisms are elaborated and the invasion remains localized (Hammond-Kosack and Jones, 1996).

Specific recognition of pathogens by plants is mostly explained by gene-for-gene model. According to this model, resistance mechanisms are induced in the plant when proteins encoded by pathogen *Avr* ("Avr" for avirulence) genes are recognized (in molecular sense) by products of corresponding *R* ("R" for resistance) genes of the host plant. When this specific recognition cannot be realized, in other words, if the pathogen is able to escape the recognition by the plant, disease occurs. The former case is referred to as the incompatibility and the latter, as the compatibility.

Rust fungi are host specific and will develop compatible or incompatible associations with their host plants in a gene-for-gene manner, depending on the presence or absence of avirulence (*Avr*) genes in the pathogen and corresponding resistance (*R*) genes in the host (Eckardt, 2006).

When the recognition by *R* gene products occurs, a defence response is triggered in the host plant. This response is characterized by rapid calcium and ion fluxes, an extracellular oxidative burst, transcriptional reprogramming within and around the infection sites and, in most cases, a localized programmed cell death, which is termed as the hypersensitive response (HR). It is thought that the sum of these events leads to a halt in pathogen growth. In the absence of specific recognition, a basal defence response also occurs, which is apparently driven by pathogen-associated molecular patterns (PAMPS) such as flagellin and lipopolysaccharides. The basal defence response overlaps significantly with R-protein-mediated defence, but is temporally slower and of lower amplitude. Basal defence does not prohibit pathogen colonization but does limit the extent of its spread. Thus, R-protein action apparently accelerates and amplifies innate basal defence responses (Belkhadir *et al.*, 2004).

There is a great diversity in the lifestyles and pathogenic mechanisms of disease causing organisms and surprisingly *R* genes were found to encode proteins with certain common motifs (Martin, 1999).

They mainly include a nucleotide-blinding site (NBS), leucine-rich repeat (LRR), a motif with homology to the cytoplasmic domains of the *Drosophila* Toll protein and the mammalian interleukin-1 receptor (TIR), a coiled-coil (CC) or leucine zipper (LZ) structure, transmembrane domain (TM), and protein kinase domain (PK). According to these features, at least four classes are distinguished among most *R* genes as follows: NBS-LRR, Receptor-like kinase (RLK), LRR-TM and TM-CC. The NBS-containing *R* genes are highly homologous to the NBS region of cell death-related genes such as *CED4* from *Caenorhabditis elegans* and *Apaf-1*, *FLASH*, *CARD4*, and *Nod1*

from humans, which mainly function in nucleotide triphosphate binding. The NBS domain plays a significant role in plant defence signalling. The conserved LRR domain is also present in many *R* genes (e.g., NBS-LRR, LRR-TM and LRR-PK genes). Related evidence showed that the LRR domains are involved in the interaction with effector proteins and are the major determinant of resistance specificity. The TIR and CC domains play an important role in R-Avr specific recognition to activate the downstream defence signalling. In plant-microbe systems, plants RLKs mainly play an important role in perception and transmition of external signals from pathogens (Liu *et al.*, 2007).

For the mechanism by which R proteins recognize *Avr* gene products, two models have been proposed. One suggests the direct physical interaction of the two molecules resulting in downstream signalling events and initiation of defence responses. However, there were only two cases where a direct interaction was shown between the gene products; one, the interaction of rice *R* gene *Pi-ta* with *AVR-Pita* from *Magnaporthe grisea* and the other, that between the flax *L* alleles and corresponding flax rust *Avr* genes (reviewed in Liu *et al.*, 2007). The absence of evidence for direct interaction in many other systems examined, led to the formulation of the "guard" hypothesis, which proposes that the interaction between an R protein and its cognate Avr determinant is mediated by a host protein that is the target for the effector function of the Avr determinant on the one hand, and under R-protein surveillance or check for such interference on the other (Jones and Takemoto, 2004). One example to this model is the AvrPto / AvrPtoB- Pto- Prf mediated defence signalling in tomato against *Pseudomonas syringae*. According to this model, *Prf* is likely the real *R* gene which encodes a typical LZ-NBS-LRR protein and it guards Pto, which is a component of R-Avr complex as a target of AvrPto (reviewed in Liu *et al.*, 2007).

Plants try to restrict pathogen infections to the site of attempted ingress by inducing local defences (Maleck and Lawton, 1998). The plant resistance response that is associated with most gene-for-gene interactions is the hypersensitive response (HR), a localized reaction in which the invaded cells and perhaps adjacent cells quickly die, presumably limiting fungal nutrient uptake and further growth. HR is thought to be initiated by an elicitor molecule binding to a receptor molecule. Elicitors of HR can be non-specific or specific. Non-specific elicitors can be of fungal or plant origin and are often cell wall degradation products arising in the initial infection. Although non-specific elicitors can play a role in host recognition and response, specific elicitors that mediate gene-for-gene interactions are the primary or, perhaps sometimes, secondary products of fungal avirulence genes. The host receptor is most likely the protein encoded by R genes (Funnel and Schardll, 2001).

The production of reactive oxygen species (ROS) probably plays a key role in plant defence. Often the first response activated in many incompatible reactions, it may be the trigger for initiation of the HR. Several roles for ROS in plant defence have been proposed. H_2O_2 could be directly toxic to

microbes at levels known to be produced in plants. It may contribute to reinforcement of plant cell walls since it is essential for the formation of lignin polymer precursors via peroxidase activity. A signalling role for some ROS is also probable. H_2O_2 activates some protection mechanisms such as glutathion-S-transferase gene expression in neighbouring cells. There is a strong likelihood that the generation of ROS will alter the redox balance within the cell. Redox balance may regulate the specific defence-related mRNA transcripts (Hammon-Kosack and Jones, 1996).

Fortifying the plant cell wall can be another defence strategy and increase resistance in various ways. For sophisticated haustorial biotrophs, preventing entry into the plant cell inhibits parasitism. Rapid callose deposition in cell walls is frequently associated with sites of pathogen incompatibility. Basic hydroxyproline-rich glycoproteins are thought to play a key role in the organization of primary cell wall architecture and may act as the foci for the initiation of lignin polymerization. An additional but probably slower mechanism that renders cell walls impermeable is the local elevation of their lignin content (Hammon-Kosack and Jones, 1996).

Incompatible pathogens, whether fungi, viruses, or bacteria, frequently provoke the accumulation of both free benzoic acid (BA) and salicylic acid (SA) and their respective glucoside conjugates, with the highest concentrations forming in the immediate vicinity of the infection site. The induction of these compounds is commonly associated with the HR. Several other roles for SA and/or BA in plant defence have been proposed. Both compounds may be directly antimicrobial. Furthermore, exogenous SA application induces the coordinated expression of a subset of PR (pathogenesis related) genes in numerous plant species (Hammond-Kosack and Jones, 1996). SA appears to be a common signalling molecule in both the HR and SAR (Systemic Acquired Resistance) responses. Thus, SA may play multiple roles in the initial plant defence response including potentiation of H_2O_2 production, HR induction (Maleck and Lawton, 1998).

Defence responses also involve expression of genes encoding PR proteins. A group of plant-coded proteins induced by different stress stimuli, named “pathogenesis related proteins” (PRs) is assigned an important role in plant defence against pathogenic constraints and in general adaptation to stressful environment (Edreva, 2005). Several PR proteins possess either antifungal or antibacterial activity in vitro and are now known to be chitinases, or glucanases, or to bind chitin. Studies suggest that coordinated activity of several PR genes is necessary for resistance (Hammond-Kosack and Jones, 1996).

Rapid increases in lipoxygenase (LOX) enzyme activity and/or mRNA and protein levels are frequently found to be specifically associated with *R-Avr* gene-mediated incompatibility**.** Increased LOX activity may contribute to resistance in a number of ways. For example, LOX may generate signal molecules such as JA, methyl-JA, or lipid peroxides, which co-ordinately amplify specific

responses. LOX activity may also cause irreversible membrane damage (Hammon-Kosack and Jones, 1996).

Phytoalexins are low molecular weight, lipophilic, antimicrobial compounds that accumulate rapidly around sites of incompatible pathogen infections and in response to an extensive array of biotic and abiotic elicitors (Hammond-Kosack and Jones, 1996).

Although highly localized defences such as HR are crucial, local infections can also induce defences throughout a plant. Systemic acquired resistance (SAR) is a phenomenon in which plant parts at a distance from the initial infection site are more resistant or even immune to further infection. Exogenous application of SA can induce SAR, suggesting that SA is a signal in SAR. When SA accumulation is prevented (using transgenic plants that degrade it) PR protein accumulation following infection is low and plants are more susceptible to disease (Funnell and Schardll, 2001).

It is evident that the specific and non-specific defence responses involve downstream signal transduction events. In some plant–bacterium interactions, it was shown that resistance gene-encoded proteins bind the direct or indirect products of avirulence genes and trigger signal transduction pathways that induce genes for various defences. Proton (H^+) influx coupled to K^+ (potassium ion) efflux may be an early event in signal transduction. Other possible primary signals are similar to those in many mammalian cells, including influx or intracellular release of calcium ions (Ca^{2+}), generation of lipid-derived signals and inositol phosphates, and the generation of active oxygen species. As in the mammalian systems, plasma membrane NADPH oxidase is involved in generating active oxygen species, though other enzymes may also contribute to this oxidative burst. G Protein activities, cyclic nucleotide mono-phosphates and protein phosphorylation cascades are also implicated. The essential role of the phenolic signal, salicylic acid (SA), in many defence responses has been investigated intensively. The lipid signal, methyl jasmonate (MJ), plays a role in the wound response against insect herbivores, but may also trigger defences against some fungi (Funnell and Schardll, 2001). Some mitogen-activated protein kinases, MAPKs in plants were shown to be activated upon pathogen and elicitor treatments. Findings suggest that MAPK cascade could be a convergence point for signal transduction pathways leading to both host-specific and non-host resistance (Jones and Takemoto, 2004).

Protein degradation also seems to play a significant role in resistance signalling. Two important proteins RAR1 and SGT1, and their interactions were associated with pathways leading to ubiquitination and requirement of many R proteins for them was reported. An obvious role for protein degradation might be the removal of defective, and perhaps dangerous, R proteins capable of causing inappropriate cell death. An alternative, and highly favoured hypothesis, is that controlled degradation of R proteins or their negative regulators may be an integral part of

resistance signalling. Recent discoveries suggest that ubiquitination may play an important role in plant disease resistance. In 2003 it became clear that another molecule, heat-shock protein 90 (HSP90) was also involved in R protein function (Jones and Takemoto, 2004; Devoto *et al.*, 2003).

The activation of specific cellular protection mechanisms is likely to accompany the defence response. These mechanisms include up-regulation of the cytoplasmic Halliwell-Asada cycle that minimizes the consequences of oxidative stress. Furthermore, increased transcription of specific SOD and catalase genes may occur to ensure that maximal enzymatic activity is maintained within the appropriate cellular compartments. For example, the expression of glutathione peroxidase, glutathione S-transferase, and polyubiquitin genes has been detected in incompatible interactions (Hammond-Kosack and Jones, 1996).

Overall, precise temporal and spatial coordination of induced defence responses is required to successfully kill or contain the invading microbe while simultaneously minimizing the damage to host tissue. In the initially attacked cell(s), rapid responses may ultimately lead to cell death, whereas in the surrounding cells, induced defence may be more transcription dependent (Hammond-Kosack and Jones, 1996).

A successful colonization of the host plant by the pathogen is not simply the result of failure of the plant to recognize the pathogen and activate its defence responses but depends on similarly complex mechanisms by which the pathogen interacts with the host. Accumulating evidence from cytological, pharmacological, phytopathological and molecular studies indicates that pathogens mediate the suppression of host defences in a range of plant-biotic interactions (Panstruga, 2003).

Lack of host cell death in plant–biotroph interactions might be accomplished by the pathogen's ability to avoid or durably suppress preformed and induced host defences. It is plausible that specific host genes and/or proteins are targeted by biotrophs to achieve these goals, and as such may be considered compatibility factors that are essential for successful pathogenesis (Panstruga, 2003).

Haustoria, which is formed by biotrophic pathogens, is known to function in nutrient uptake from the host cell. Findings demonstrate that deactivation of host defences appear to correlate with haustorium formation, suggesting that haustoria might play a key role not only in nutrient absorption but also in mediating defence suppression (Panstruga, 2003).

The programmed cell death called the HR is a common defence response that inhibits host colonization. Therefore, it should be avoided by successful pathogens in some way, such as by elicitors released during cell wall penetration. The "green island" effect is a phenomenon that

provides evidence for cell death suppression by successful pathogens. In this effect, leaf areas surrounding the successful infection site display delayed senescence (Panstruga, 2003).

Loss of function of host genes that are required for a compatible plant– pathogen interaction is generally predicted to result in incompatibility. Thus, recessively inherited resistance to single or closely related pathogen species without constitutive activation of defence responses, indicate the lack of a pathogen-specific host compatibility factor. Genetic analysis of resistant lines in natural plant populations and of induced mutations, have revealed single recessive resistance loci that confer resistance to a wide range of pathogens in a range of plant species (Panstruga, 2003).

1.5 Suppression Subtractive Hybridization

Suppression Subtractive Hybridization (SSH) is a PCR based method, which is used to construct subtracted cDNA libraries. Subtracted cDNA libraries can enable scientists to identify and subsequently clone and study differentially expressed genes. The method was first developed by Diatchenko *et al.* in 1996 (Diatchenko *et al*., 1996). The method employs subtraction and suppression PCR techniques together. The subtraction excludes the sequences common to both samples and the suppression PCR achieves selective amplification of target sequences while suppressing non-target cDNA amplification. Besides, the method comprises a normalization step, which means equalization of abundantly and rarely expressed sequences. This feature makes SSH superior over traditional subtraction methods and enables identification of differentially but rarely expressed sequences (Clontech, 2002).

First, mRNA isolated from each sample to be compared is separately converted to cDNA. The sample that contains the differentially expressed target sequences is designated as the “Tester” and the reference sample is referred to as the “Driver”. Both ds cDNAs are digested with the four-base-cutting restriction enzyme *Rsa* I, which yields blunt ends. The tester cDNA is then divided into two portions and each portion of the tester cDNA is ligated with a different cDNA adaptor, one with Adaptor 1 and the other with Adaptor 2R. Since the ends of the adaptors do not possess phosphate groups, only one strand of each adaptor molecule is ligated to the 5’ end of a cDNA. Later when the ends are filled in, the common sequence within the two adaptors enables annealing of the primer during the consequent PCR amplification. Two hybridizations are performed. In the first hybridization an excess of driver is added to both tester cDNA samples, the samples are heat denatured and allowed to anneal. This annealing yields four different types of molecules, **a**, **b, c,** and **d** (Figure 1.4). Self annealed sequences yield **b** type molecules. Non-differentially expressed sequences are eliminated through formation of **c** type molecules. Since abundant sequences of type **a** re-anneal faster than rare sequences do, the concentration of abundant and rare clones are equalized. Single stranded **a** type molecules are highly enriched for differentially expressed sequences since common, i.e. non-differentially expressed sequences form **c** type molecules by

hybridizing to excess driver molecules. In the second hybridization the two products from the first hybridization are mixed together without heat denaturation but with addition of excess fresh denatured driver. The types of molecules formed are the same with those of the first hybridization products separately, except the new hybrid **e** type of molecules. These molecules are formed by hybridization of the same differentially expressed sequences from the two tester populations. These molecules, unlike **b** and **c** type molecules, possess two different adaptors on their two ends. The purpose of adding fresh denatured driver in the second hybridization is to further enrich the **e** type hybrid molecules by eliminating non-differentially expressed fragments. Then the ends of molecules are filled by DNA polymerase and consequently the two ends of the hybrid **e** type molecules possess different annealing sites for nested primers (Clontech, 2002).

The product of the second hybridization is subjected to PCR using primer 1. Only **e** type molecules are exponentially amplified in this reaction. Both adaptor 1 and adaptor 2R have, on their ends, an inverted sequence that enables primer 1 to anneal to both strands of **e** type molecules. **a** and **d** type molecules cannot be amplified since they do not possess necessary annealing sites. **c** type molecules are linearly amplified as they have an annealing site only on one end. Most **b** type molecules form a pan-like structure and cannot be amplified, which exerts the suppression effect. SSH also introduces a slight suppression effect to very short (under 200 nucleotides) differentially expressed sequences because formation of pan structures for shorter molecules is more efficient than annealing of the primer. The suppression PCR is illustrated in Figure 1.5. Thus, the differentially expressed and equalized **e** type molecules are exponentially amplified. In order to enrich differentially expressed sequences and to reduce any background, the secondary PCR amplification is performed with nested primers, which anneal to the two different inner annealing sites of the two adaptors (designated with white and grey colours on blocks that represent adaptors, in Figure 1.4) (Clontech, 2002). The sequences of the adaptors and primers are given in Appendix A.

After the subtraction by SSH, the differentially expressed RNAs can be identified by sequence and hybridization analysis.

Once a subtracted cDNA library is obtained, it is important to confirm the differential expression of individual clones. Differential screening of the library before performing individual clone analysis helps eliminate false positives.

Since its development, SSH method was successfully used in hundreds of studies and is very popular as a high throughput method that produces data at expression level.

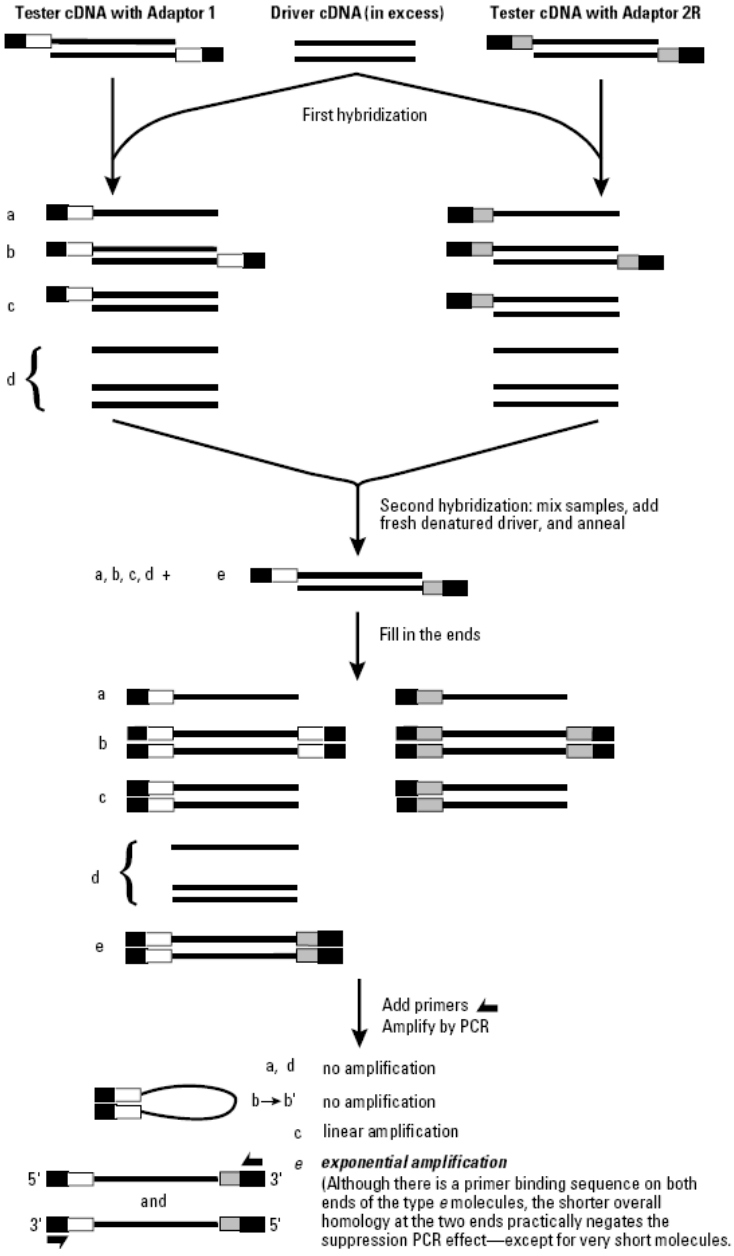


Figure 1.4 Schematic representations of molecular events taking place during SSH. The lines represent cDNA strands and the blocks at the ends of the lines represent adaptors. The two different adaptors are distinguished by white and grey colours (Clontech, 2002).

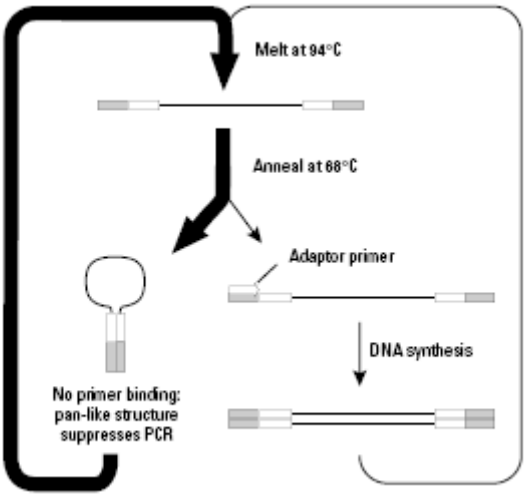


Figure 1.5 Schematic representation of suppression PCR. The adaptor primer is the PCR primer 1. (Clontech, 2002).

1.6 Aim of the Study

In this study, two subtraction experiments were conducted using SSH method: SSH1, in order to identify genes that are differentially expressed in a compatible interaction as compared to an incompatible one, and SSH2, in order to identify genes that are differentially expressed in an incompatible interaction as compared to a compatible one.

Yellow rust pathotype 169E136 is virulent on Yr 1/ Avocet S wheat line but avirulent on Yr 10/ Avocet S line. On the other hand, yellow rust pathotype 232E137 is avirulent on both Yr 1/ Avocet S and Yr 10/ Avocet S wheat lines.

In the first strategy, cDNA from Yr 1/ Avocet S plants inoculated with yellow rust pathotype 169E136 was assigned as the tester and cDNA from Yr 1/ Avocet S plants inoculated with yellow rust pathotype 232E137, as the driver. Therefore, genes that were differentially or more abundantly expressed in a compatible interaction, as compared to an incompatible one, were intended to be identified. This subtraction experiment was entitled SSH1 and referred to by this name throughout the thesis. In order to recall that the tester sample comes from a compatible interaction and the driver sample from an incompatible one, the initials of the words “disease” (D) and “resistance” (R) were used to represent the subtraction performed, as SSH1 (D-R), the “-“ sign representing the subtraction.

It is appropriate here, to associate the specific strategy in this study with the molecular principles of SSH, described in Section 1.5. Depending on the representations in Figure 1.4, Figure 1.6A schematically depicts the tester and driver cDNA molecules at the beginning of the subtraction experiment SSH1 (D-R); similarly Figure 1.7A displays the cDNA molecules to be exponentially amplified at the end of SSH1 (D-R).

In the second strategy, cDNA from Yr 10/ Avocet S plants inoculated with yellow rust pathotype 169E136 was assigned as the tester and cDNA from Yr 1/ Avocet S plants inoculated with yellow rust pathotype 169E136, as the driver. Conversely to the first one, this second approach intended to identify genes that were differentially or more abundantly expressed in an incompatible interaction, as compared to a compatible one. This second subtraction experiment was entitled SSH2 and referred to by this name throughout the thesis. Similar to the nomenclature used for SSH1 (D-R), this second subtraction was named as SSH2 (R-D), to recall that the tester sample comes from an incompatible interaction and the driver sample from a compatible one. Figure 1.6B schematizes the tester and driver molecules in SSH2 (R-D) and Figure 1.7B displays the cDNA molecules to be exponentially amplified at the end of SSH2 (R-D).

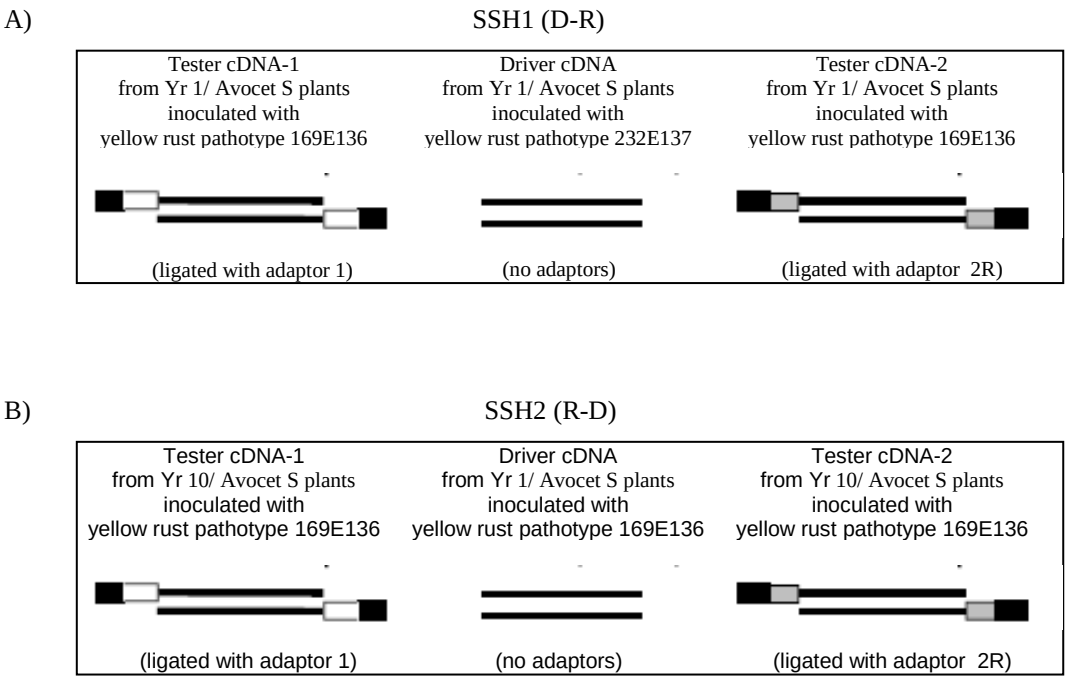
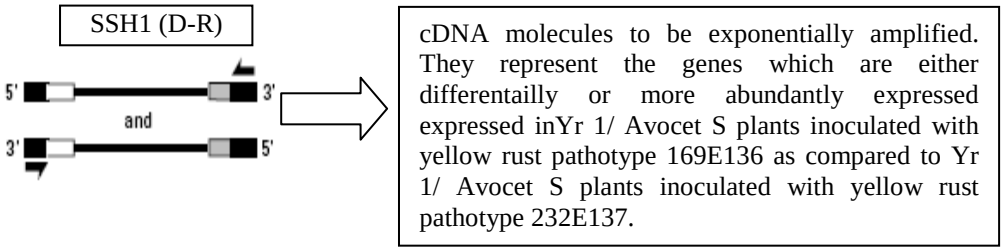


Figure 1.6 Schematic representations of tester and driver molecules at the beginning of SSH1 (D-R) (A) and SSH2 (R-D) (B). The representations depend on Figure 1.4.

A)



B)

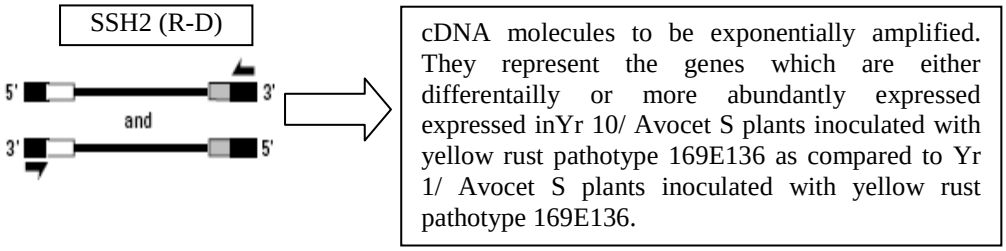


Figure 1.7 Schematic representations of cDNA molecules to be exponentially amplified at the end of SSH1 (D-R) (A) and SSH2 (R-D) (B). The representations depend on Figure 1.4.

Reverse subtractions for both SSH1 (D-R) and SSH2 (R-D) were performed as it was described in Clontech PCR-Select^{TM} cDNA Subtraction Kit User Manual so that differential screening analysis could have been done using Clontech PCR-Select Differential Screening Kit. Because differential screening would have been more costly, it was preferred to have the cDNA libraries directly sequenced after subtraction, in a high throughput manner.

High throughput identification of genes that are up-regulated specifically in compatible and incompatible interactions of wheat with yellow rust may provide important clues about the defence and pathogenicity mechanisms of this rust fungus on wheat. It may be useful in elucidation of mechanisms that are similar to those of other plant-pathogen interactions, but it may also help suggest candidate genes that have not yet been assigned known functions in disease.

CHAPTER II

MATERIALS AND METHODS

2.1 Preparation of Plant Material and Infections

2.1.1 Growth of Plant Material

Yr 10/ Avocet S and Yr 1/ Avocet S seeds were aerated by a small air pump in pure water for 12 hours. Seeds were sown in perlite saturated with water in 5 x 7 x 12 cm plastic boxes. Seeds were germinated in dark until they reached a length of 3-4 cm. Germinated seedlings were covered with sponge pieces near the bottom of the seedling, at the beginning of roots and transferred to Haugland medium. Seedlings were placed on the containers leaving the roots in the medium solution. The containers were specially prepared such that they had holes on the lid to place the seedlings. The medium was refreshed for every 3 days. Seedlings were grown under photoperiod conditions of 16 hr light and 18 hr dark, at 22°C under light and 18°C in dark.

2.1.2 Inoculation of Plants with Yellow Rust Spores

To prepare SSH1 (D-R) tester sample plants, Yr 1/ Avocet S plants were inoculated with spores of yellow rust pathotype 169E136 and to prepare SSH1 (D-R) driver sample plants Yr 1/ Avocet S plants were inoculated with yellow rust pathotype 232E137. On the other hand, SSH2 (R-D) tester sample plants were prepared by inoculating Yr 10/ Avocet S plants with yellow rust pathotype 169E136 and SSH2 (R-D) driver sample plants were prepared by inoculating Yr 1/ Avocet S plants with yellow rust pathotype 169E136.

Plants were treated with cold vapour for 3-4 hr prior to infection in order to facilitate opening of stomata and attachment of spores on leaf surfaces. Rust spores to be inoculated were diluted by mixing with odourless talk powder in a one to one ratio. Leaves were inoculated with rust spores by applying with a clean brush. Inoculated plants were incubated at 11°C under cold vapour treatment with 16 hr light 8 hr dark photoperiod for 24 hr. Control plants were mock-inoculated by applying talk powder with a brush and incubated under the same conditions.

2.1.3 Collection of Leaf Samples

At 12th, 24th, and 48th hr post-infection, leaf samples were collected from Yr 10/ Avocet S wheat plants inoculated with yellow rust of pathoype 169E136 and Yr 1/ Avocet S wheat plants

inoculated with yellow rust of pathoype 169E136 (for SSH2 (R-D)). Samples were collected at third, 6th, and 9th days post-infection from Yr 1/ Avocet S wheat plants infected with 169E136 and Yr 1/ Avocet S wheat plants infected with yellow rust of pathoype 232E137 (for SSH1 (D-R)). Plant leaves were cut by clean scissors, excluding the stem, immediately wrapped in aluminium foil, quick-frozen in liquid nitrogen and stored at -80°C in a deep freezer. A few inoculated leaves were left on plants in order to confirm the disease formation on susceptible plants.

2.2 Suppression Subtractive Hybridization

Subtractions were performed using the Clontech PCR-Select™ cDNA Subtraction Kit (Catalogue #: K1804-1), according to Clontech PCR-Select™ cDNA Subtraction Kit User Manual.

2.2.1 Total RNA Isolation

2.2.1.1 Precautions for RNA Handling

Before total RNA isolation, workbench was cleaned with a detergent and then with Applichem Rnase-OFF solution in order to get rid of any possible RNAse contamination. Micropipette tips, tubes, mortars and pestles and any material to be in contact with the samples were immersed in 0.1% active diethylpyrocarbonate (DEPC) overnight and then autoclaved. All solutions except Tris were added DEPC to 0.1%, left overnight and then autoclaved. Tris was prepared with DEPC treated autoclaved deionized water.

2.2.1.2 Isolation of Total RNA

Total RNA, for each tester and driver sample was isolated from 500-700 mg plant leaf material using Invitrogen Trizol reagent. Leaves were crushed into powder using a pre-cooled mortar and pestle. The powder was suspended in Trizol reagent in 2 mL tubes; 1 mL of Trizol reagent was used for each 100 mg of leaf material. Tubes were briefly vortexed. The homogenate was incubated at room temperature. Two hundred µL of chloroform was added for each mL of homogenate in order to dissociate nucleoprotein complexes. After 3-4 min incubation at room temperature, tubes were centrifuged at 12000xg for 20 min at 4°C. The upper phases were removed to separate tubes, added 500 µL of isopropanol and incubated at room temperature for 10 min after gentle inversion (2-3 times). Tubes were centrifuged at 12000xg for 20 min at 4°C and 1 mL of 75% cold ethanol was added to each tube. RNA to be used immediately were centrifuged under the same conditions, ethanol portions were discarded. Pellets were air dried for a short time until a transparent appearance was observed and then dissolved in 50-100 µL of nuclease free sterile water by immersing the tubes in a 65°C water bath. Besides, RNA to be used in future was stored in 75% ethanol at -80°C.

2.2.1.3 Gel Analyses and Concentration Determination of Total RNA Samples

RNA samples were analysed in 1% agarose gels run in 1X (10 mM) phosphate buffer (pH 6.8) containing ethidium bromide (0.5 µg/mL final concentration). RNA concentrations were determined by UV spectrophotometer using the formula A_{260} x the dilution x 40 µg/mL.

2.2.2 Isolation of mRNA

2.2.2.1 Isolation of mRNA from Total RNA Samples

mRNA was isolated using DYNAL Biotech. Dynabeads Oligo$(dT)_{25}$ magnetic particles on Promega magnetic stand. Equal amounts of total RNA from each three time points of tester and driver samples were mixed and diluted such that 75 µg RNA was dissolved in 100 µL final volume. When this was not possible due to relatively low total RNA concentrations, 75 µg of RNA, with equal contribution from three time-points, was prepared in higher volumes. This solution was used for mRNA isolation. 200 µL of magnetic particles suspended in storage buffer (250 mM Tris-HCl (pH 7.5), 20 mM EDTA 0.1% Tween-20 and 0.02% Sodium azide) was taken into a sterile eppendorf tube. The tube was placed on the magnetic stand in order for the particles to be separated from the suspension, the storage buffer was discarded, and the tube was removed from the stand. The particles were washed once with 2x binding buffer (20 mM Tris-HCl pH 7.5, 1.0 M LiCl, 2 mM EDTA) by suspending the particles in 100 µL of 2x binding buffer, placing the tube on the magnetic stand and discarding the separated buffer. The particles were then re-suspended in 100 µL 2x binding buffer. In cases when the volume of 75 µg of RNA exceeded 100 µL, equal volume of 2x binding buffer was used. Total RNA was incubated for 2 min in a 65°C water bath to eliminate secondary structures. Total RNA was transferred into the magnetic particle suspension and the mixture was incubated at room temperature with gentle shaking in order to facilitate binding of mRNA to magnetic particles. The tube was placed on the magnetic stand and kept there for about 1 min until the solution was clear, the supernatant was discarded. The particles were washed twice with 2x Washing Buffer B (10 mM Tris-HCl (pH 7.5) 0.15 M LiCl, 1 mM EDTA). Washing was achieved by adding 200 µL of Washing Buffer B to magnetic particles, suspending the particles, placing the tube on the magnetic stand and then discarding the supernatant. For eluting mRNA, 10 µL of elution buffer (10 mM HCl pH 7.5) was added, the suspension was incubated in an 80°C water bath for 2 min, the tube was quickly placed on the magnetic stand and after sufficient time for separation of particles from the suspension, the supernatant was immediately removed to a separate tube. mRNA samples were stored at -80°C.

2.2.2.2. Preparation of Gel Spots for Determination of mRNA Concentrations

mRNA concentrations were determined by a method that employs agarose gels (Sambrook, Fritsch and Maniatis 1989). 1% agarose gel was prepared. 0.5 g of Agarose (Applichem) was dissolved in 50 mL of 10 mM sodium phosphate buffer by boiling in a microwave oven and the solution was allowed to cool. When it was around 60°C, ethidium bromide was added to a final concentration of 0.5 µg/mL and the gel was poured into a tray and left to solidify. Meanwhile dilution series of control mRNA (1 µg/µL; from human skeletal muscle) from Clontech PCR-Select^{TM} cDNA Subtraction Kit were prepared as indicated in Table 2.1, Table 2.2 and Table 2.3. Dilution series were also prepared for tester and driver mRNA samples of each SSH experiment. Dilution series were prepared by diluting the mRNA samples in nuclease free water. When the gel was polymerised, 0.5 or 1.0 µL spots (as indicated in table 2.1, 2.2 and 2.3) of dilution series of control mRNA and samples were formed by gently releasing from the pipette tip at once as a drop. After the spots penetrated into the gel, the gel was visualized and photographed under UV transilluminator.

Table 2.1 Dilution series prepared from SSH1 (D-R) and control mRNA samples.

Sample/Control Name	Dilution Series	Spot Volume (µL)
SSH1 Tester mRNA Sample	5x, 10x, 20x, 40x	1
SSH1 Driver mRNA Sample	5x, 10x, 20x, 40x	1
Control mRNA (1 µg/µL)	20x, 25x, 40x, 50x, 100x	1

Table 2.2 Dilution series prepared from SSH2 (R-D) Tester mRNA sample.

Sample/Control Name	Dilution Series	Spot Volume (µL)
SSH2 Tester mRNA Sample	5x, 10x	0.5
Control mRNA (1 µg/µL)	12.5x, 25x, 50x	0.5

Table 2.3 Dilution series prepared from SSH2 (R-D) Driver mRNA sample.

Sample/Control Name	Dilution Series	Spot Volume (µL)
SSH2 Tester mRNA Sample	5x, 10x	0.5
Control mRNA (1 µg/µL)	25x, 50x, 100x	0.5

2.2.3 cDNA Synthesis

2.2.3.1 First Strand cDNA Synthesis

cDNA synthesis was performed using approximately 2 µg of mRNA as recommended in the Clontech PCR-Select cDNA Subtraction Kit's manual (Clontech, 2002). The synthesis reactions were performed also with the "Control mRNA" (from human skeletal muscle) provided with the kit. The components shown in Table 2.4 were combined in 0.5 mL microcentrifuge tubes; contents were mixed and spinned briefly in a microcentrifuge.

Table 2.4 Reaction mixtures for binding of cDNA synthesis primer.

	SSH1 Tester	**SSH1 Driver**	**SSH2 Tester**	**SSH2 Driver**	**Control**
mRNA volume (~2 µg) (µL)	17.5	20.5	6	9	2
cDNA synthesis primer (10 µM) (µL)	1	1	1	1	1
Sterile H_2O (µL)	-	-	3	-	2
Total (µL)	18.5	21.5	10	10	5

The volumes of mRNA samples were adjusted according to their concentrations calculated in Section 3.2 to supply approximately 2 µg of mRNA. The calculation results are presented in Table 2.5. The reaction volumes were adjusted regarding these volumes.

Table 2.5 mRNA volumes and quantities used in cDNA synthesis.

	SSH1 Tester	**SSH1 Driver**	**SSH2 Tester**	**SSH2 Driver**
Concentration of mRNA (ng/µL)	~125	~100	~400	~200
Volume of mRNA used in cDNA synthesis (µL)	17.5	20.5	6	9
Amount of mRNA used in cDNA synthesis (ng)	~2187.5	~2050	~2400	~1800

The tubes prepared were incubated at 70 °C in a thermal cycler (Eppendorf Mastercycler gradient) for 2 min and then cooled on ice for 2 min. The tubes were briefly centrifuged and the reaction mixtures shown in Table 2.6 were prepared.

Table 2.6 Reaction mixtures for first strand cDNA synthesis.

	SSH1 Tester	SSH1 Driver	SSH2 Tester	SSH2 Driver	Control
Primer binding reaction mix (µL)	18.5	21.5	10	10	5
5X First Strand Buffer (µL)	5.2	6	3	3	2
dNTP mix (10mM) (µL)	1.3	1.5	1	1	1
Sterile H_2O (µL)	0.3	0.5	-	-	1
RT Enzyme (AMV 20 u/µL) (µL)	1	1	1	1	1
Total (µL)	26.3	30.5	15	15	10

cDNA synthesis primer (10 µM), 5X First-Strand Buffer (250 mM Tris-HCl (pH 8.5), 40 mM $MgCl_2$, 150 mM KCl, 5 mM Dithiothreitol) and RT Enzyme (AMV Reverse Transcriptase (20 units/µl) were supplied by the kit. Necessary modifications in volumes of reagents were made according to ratios of total reactions volumes. The tubes were gently vortexed, briefly centrifuged and then incubated at 42 °C in a thermal cycler (Eppendorf Mastercycler gradient) for 1.5 h. The tubes were placed on ice to terminate reactions. The second strand synthesis reactions were prepared immediately.

2.2.3.2 Second Strand cDNA Synthesis

The reaction mixtures shown in Table 2.7 were prepared in the first strand cDNA synthesis reaction tubes. 5X Second Strand Buffer (500 mM KCl, 50 mM Ammonium sulfate, 25 mM $MgCl_2$, 0.75 mM β-NAD, 100 mM Tris-HCl (pH 7.5), 0.25 mg/ml BSA), dNTP mix (10mM) and 20X second strand enzyme cocktail (DNA polymerase I, 6 units/µL; RNase H, 0.25 units/µL; E. Coli DNA ligase, 1.2 units/µL) were supplied by Clontech PCR-Select cDNA Subtraction Kit.

Table 2.7 Reaction mixtures for second strand cDNA synthesis.

	SSH1 Tester	SSH1 Driver	SSH2 Tester	SSH2 Driver	Control
First strand cDNA synthesis reaction mix (µL)	26.3	30.5	15	15	10
5X second strand buffer (µL)	16	16	16	16	16
dNTP mix (10mM) (µL)	2	2	1.6	1.6	1.6
Sterile H_2O (µL)	32	28	43.4	43.4	48.4
20X second strand enzyme cocktail (µL)	4	4	4	4	4
Total (µL)	80.3	80.5	80	80	80

The contents were mixed and briefly spinned. The final volumes varied according to the first strand synthesis reaction volumes. The tubes were incubated at 16°C in a thermal cycler (Eppendorf Mastercycler gradient) for 2 hr. 2 µL (6 units) of T_4 DNA polymerase (3 units/µl), supplied by the kit, was added to each tube and the tubes were mixed well. The tubes were incubated at 16°C for 30 min in a thermal cycler (Eppendorf Mastercycler gradient). 4 µL 20X EDTA/Glycogen Mix was added to each tube to terminate the second-strand synthesis. The volume was completed to 100 µL by adding sterile H_2O. 100 µL phenol: chloroform: isoamyl alcohol (25:24:1) was added to each tube. The tubes were thoroughly vortexed and centrifuged at 14000 rpm for 10 min at room temperature. The top aqeous phase was carefully taken and removed to a clean (sterile) 0.5-mL microcentrifuge tube. The interphase and the lower phase were discarded. 100 µL chloroform: isoamyl alcohol (24:1) was added to each tube. Tubes were vortexed and centrifuged and the top aqeous layer was removed as described for the preceding extraction. Forty microlitres of 4M NH_4OAc and 300 0f 95% ethanol was added to each tube. The tubes were vortexed thoroughly and centrifuged at 14000 rpm at room temperature. The supernatant was removed carefully and discarded. The pellet was overlaid with 500 µL 80% ethanol. The tubes were centrifuged at 14000 rpm for 10 min. The pellets were air dried for about 10 min to evaporate the ethanol. The precipitate was dissolved in 50 µL deionized water.

2.2.3.3 *Rsa* I Digestion

The components shown in Table 2.8 were combined in each ds cDNA obtained in Section 2.2.3.2. 10X Rsa I Restriction Buffer (100 mM Bis Tris Propane-HCl (pH 7.0), 100 mM $MgCl_2$, 1 mM DTT) and *Rsa* I enzyme (10 units/µl) were supplied by the kit. 6.5 µL of each ds cDNA was removed and reserved for control of digestion reaction beforehand. The remaining 43.5 µL was used in the digestion mixture. Control reaction refers to the digestion of cDNA synthesized from the Control mRNA (from human skeletal muscle) provided with the kit.

Table 2.8 Reaction mixtures for *Rsa* I digestion.

	SSH1 Tester	**SSH1 Driver**	**SSH2 Tester**	**SSH2 Driver**	**Control**
ds cDNA (µL)	43.5	43.5	43.5	43.5	43.5
10X *Rsa* I Restriction Buffer (µL)	5	5	5	5	5
***Rsa* I (10 units/ µL) (µL)**	1.5	1.5	1.5	1.5	1.5
Total (µL)	50	50	50	50	50

After addition of reagents, tubes were vortexed, briefly centrifuged and incubated at 37°C for 1.5 hr. 5µL of the digest mixture was taken and reserved fort the efficiency analyses of *Rsa* I digestion. 2.5 µL 20X EDTA/Glycogen Mix was added to terminate the reaction. 50 µL phenol: chloroform:

isoamyl alcohol (25:24:1) was added to the tubes. Tubes were vortexed thoroughly and centrifuged at 14000 rpm for 10 min to separate phases. The top aqeous layer was taken and placed in a clean 0.5-mL tube. 50 µL of chloroform: isoamyl alcohol (24:1) was added to each tube; the tubes were vortexed thoroughly and centrifuged at 14000 rpm for 10 min. The top aqeous layer was removed and placed in a clean 0.5-mL tube. 25 µL of 4 M NH_4OAc and 187.5µL 95% ethanol was added to each tube. Mixtures were vortexed thoroughly and centrifuged for at 14000 rpm for 30 min at room temperature. Supernatant was removed carefully from each tube. The pellets were overlaid with 200 µL of 80% ethanol. Tubes were centrifuged at 14000 rpm for 5 min. Pellets were air dried for about 10 min, dissolved in 5.5 µL of H_2O and stored at -20 °C.

2.2.3.4 Gel Analyses of *Rsa* I Digestion Products

In order to control the efficiency of *Rsa* I Digestion, 2.5 µL of undigested and 5 µL of digested cDNAs from *Rsa* I digestion, were electrophoresed on a 1% agarose/EtBr gel in 1X TBE buffer.

2.2.4 Adaptor Ligation

One µL of each *Rsa* I digested experimental cDNA was diluted with 5µL sterile water. These diluted cDNA samples were used in ligation reaction. A ligation master mix (for 8 + 1 reactions) was prepared in a 0.5-µL microcentrifuge tube by combining the reagents given in table 2.9.

Ligation mixtures were prepared with each digested experimental cDNA (diluted), as shown in Tables 2.10 and 2.11. 5X ligation buffer (250 mM Tris-HCl (pH 7.8), 50 mM $MgCl_2$, 10 mM DTT, 0.25 mg/mL BSA), T4 DNA ligase (400 units/ µL, contains 3 mM ATP), Adaptor 1 (10 µM) and Adaptor 2R (10 µM) were supplied by Clontech PCR-Select cDNA Subtraction Kit.

Table 2.9 Master mix for adaptor ligation.

	Per Reaction (µL)	**Master Mix (µL)**
Sterile H_2O	3	27
5X Ligation Buffer	2	18
T4 DNA Ligase	1	9

Table 2.10 Ligation mixes for SSH1 (D-R).

	SSH1 Tester (1-1)	**SSH1 Tester (1-2)**	**SSH1 Tester (2-1)**	**SSH1 Tester (2-2)**
SSH1 Tester cDNA (µL)	2	2	-	-
SSH1 Driver cDNA (µL)	-	-	2	2
Adaptor 1 (10 µM) (µL)	2	-	2	-
Adaptor 2R (10 µM) (µL)	-	2	-	2
Master Mix (µL)	6	6	6	6
Total (µL)	10	10	10	10

Table 2.11 Ligation mixes for SSH1 (D-R).

	SSH2 Tester (1-1)	**SSH2 Tester (1-2)**	**SSH2 Tester (2-1)**	**SSH2 Tester (2-2)**
SSH2 Tester cDNA (µL)	2	2	-	-
SSH2 Driver cDNA (µL)	-	-	2	2
Adaptor 1 (10 µM) (µL)	2	-	2	-
Adaptor 2R (10 µM) (µL)	-	2	-	2
Master Mix (µL)	6	6	6	6
Total (µL)	10	10	10	10

After ligation mixes were prepared, 2 µL of the ligation mix for Tester 1-1 and 2 µL of the ligation mix for Tester 1-2 of each of two SSH experiments were combined in fresh microcentrifuge tubes. These were the Unsubtracted Tester Controls. The same was done for Tester 2-1 and 2-2 of each SSH, in order to prepare the unsubtracted tester controls for the reverse subtractions of SSH-1 and SSH-2. The operation is summarized in table 2.12 and 1.13. Tubes containing the ligation mixtures and unsubtracted tester controls were centrifuged briefly and incubated at 16°C overnight. 1 µL of EDTA/Glycogen mix was added to stop the ligation. The tubes were incubated at 72°C for 5 min to inactivate the ligase. Tubes were centrifuged briefly. Samples were stored at -20°C.

Table 2.12 Preparation of unsubtracted tester controls of forward and reverse subtractions for SSH1 (D-R).

	Ligation Mix for SSH1 Tester (1-1) (µL)	**Ligation Mix for SSH1 Tester (1-2) (µL)**	**Ligation Mix for SSH1 Tester (2-1) (µL)**	**Ligation Mix for SSH1 Tester (2-2) (µL)**
Unsubtracted Tester Control for Forward Subtraction of SSH1	2	2	-	-
Unsubtracted Tester Control for Reverse Subtraction of SSH1	-	-	2	2

Table 2.13 Preparation of unsubtracted tester controls of forward and reverse subtractions for SSH2 (R-D).

	Ligation Mix for SSH2 Tester (1-1) (µL)	**Ligation Mix for SSH2 Tester (1-2) (µL)**	**Ligation Mix for SSH2 Tester (2-1) (µL)**	**Ligation Mix for SSH2 Tester (2-2) (µL)**
Unsubtracted Tester Control for Forward Subtraction of SSH2	2	2	-	-
Unsubtracted Tester Control for Reverse Subtraction of SSH2	-	-	2	2

2.2.5 First Hybridization

The reagents in Tables 2.14, 2.15, 2.16 and 2.17 were combined in 0.5-mL tubes for each experimental subtraction. 4X Hybridization Buffer was supplied by the kit. Samples were overlaid with one drop of mineral oil and centrifuged briefly. Tubes were incubated in a thermal cycler (Eppendorf Mastercycler gradient) at 98°C for 1.5 min and then incubated at 68°C for 12 hr. Second hybridization followed immediately.

Table 2.14 First hybridization of forward subtraction for SSH1 (D-R).

	Hybridization Sample 1	**Hybridization Sample 2**
***Rsa* I-digested driver cDNA of SSH1 (µL)**	1.5	1.5
Adaptor I ligated Tester 1-1 of SSH1 (µL)	1.5	-
Adaptor 2R ligated Tester 1-2 of SSH1 (µL)	-	1.5
4X Hybridization Buffer (µL)	1	1
Total (µL)	4	4

Table 2.15 First hybridization of reverse subtraction for SSH1 (D-R).

	Hybridization Sample 1	**Hybridization Sample 2**
***Rsa* I-digested Tester cDNA of SSH1* (µL)**	1.5	1.5
Adaptor I ligated Tester 2-1 of SSH1 (µL)	1.5	-
Adaptor 2R ligated Tester 2-2 of SSH1 (µL)	-	1.5
4X Hybridization Buffer (µL)	1	1
Total (µL)	4	4

* It serves as the driver for this reverse subtraction.

Table 2.16 First hybridization of forward subtraction for SSH2 (R-D).

	Hybridization Sample 1	**Hybridization Sample 2**
***Rsa* I-digested driver cDNA of SSH1 (µL)**	1.5	1.5
Adaptor I ligated Tester 1-1 of SSH2 (µL)	1.5	-
Adaptor 2R ligated Tester 1-2 of SSH2 (µL)	-	1.5
4X Hybridization Buffer (µL)	1	1
Total (µL)	4	4

Table 2.17 First hybridization of reverse subtraction for SSH2 (R-D).

	Hybridization Sample 1	**Hybridization Sample 2**
***Rsa* I-digested Tester cDNA of SSH2* (µL)**	1.5	1.5
Adaptor I ligated Tester 2-1 of SSH2 (µL)	1.5	-
Adaptor 2R ligated Tester 2-2 of SSH2 (µL)	-	1.5
4X Hybridization Buffer (µL)	1	1
Total (µL)	4	4

* It serves as the driver for this reverse subtraction.

2.2.6 Second Hybridization

One µL of driver cDNA, 1 µL of 4X Hybridization Buffer and 2 µL of sterile H_2O were combined in sterile tubes for each four subtractions, as presented in Tables 2.18, 2.19, 2.20 and 2.21.

Table 2.18 Driver denaturation for second hybridization of forward subtraction for SSH1 (D-R).

	Driver Denaturation Mix (µL)
***Rsa* I-digested Driver cDNA of SSH1**	1
4X Hybridization Buffer	1
Sterile H_2O	2
Total	4

Table 2.19 Driver denaturation for second hybridization of reverse subtraction for SSH1 (D-R).

	Driver Denaturation Mix (µL)
Rsa* I-digested Tester cDNA of SSH1	1
4X Hybridization Buffer	1
Sterile H_2O	2
Total	4

* It serves as the driver for this reverse subtraction.

Table 2.20 Driver denaturation for second hybridization of forward subtraction for SSH2 (R-D).

	Driver Denaturation Mix (µL)
***Rsa* I-digested Driver cDNA of SSH2**	1
4X Hybridization Buffer	1
Sterile H_2O	2
Total	4

Table 2.21 Driver denaturation for second hybridization of reverse subtraction for SSH2 (R-D).

	Driver Denaturation Mix (µL)
Rsa* I-digested Tester cDNA of SSH2	1
4X Hybridization Buffer	1
Sterile H_2O	2
Total	4

* It serves as the driver for this reverse subtraction.

One µL of this mixture was placed in a 0.5-mL microcentrifuge tube and overlaid with 1 drop of mineral oil. The tube was incubated at 98°C for 1.5 min. Denatured drivers were combined with hybridization samples as indicated in Tables 2.22, 2.23, 2.24 and 2.25. In order to ensure that the two First hybridization samples mix only in the presence of freshly denatured driver a special procedure recommended in the Clontech PCR-Select™ cDNA Subtraction Kit's manual was used.

Table 2.22 Second hybridization of forward subtraction for SSH1 (D-R).

	Second Hybridization Mix (µL)
Freshly denatured *Rsa* I-digested Driver cDNA of SSH1	4
Hybridization Sample 1 of Forward Subtraction for SSH1	4
Hybridization Sample 2 of Forward Subtraction for SSH1	4
Total	12

Table 2.23 Second hybridization of reverse subtraction for SSH1 (D-R).

	Second Hybridization Mix (µL)
Freshly denatured *Rsa* I-digested Tester cDNA of SSH1*	4
Hybridization Sample 1 of Reverse Subtraction for SSH1	4
Hybridization Sample 2 of Reverse Subtraction for SSH1	4
Total	12

* It serves as the driver for this reverse subtraction.

Table 2.24 Second hybridization of forward subtraction for SSH2 (R-D).

	Second Hybridization Mix (µL)
Freshly denatured *Rsa* I-digested Driver cDNA of SSH2	4
Hybridization Sample 1 of Forward Subtraction for SSH2	4
Hybridization Sample 2 of Forward Subtraction for SSH2	4
Total	12

Table 2.25 Second hybridization of reverse subtraction for SSH1 (D-R).

	Second Hybridization Mix (µL)
Freshly denatured *Rsa* I-digested Tester cDNA of SSH2*	4
Hybridization Sample 1 of Reverse Subtraction for SSH1	4
Hybridization Sample 2 of Reverse Subtraction for SSH1	4
Total	12

* It serves as the driver for this reverse subtraction.

A micropipettor was set at 15 µL. The entire Hybridization sample 2 was taken into the pipette by gently touching the pipette to the mineral oil/sample interface. The pipette tip was removed from the sample tube, a small amount of air was drawn into the tube, and a slight air space was formed below the sample. The freshly denatured driver was drawn into the tube and again an air space was formed. The entire mixture was transferred to the tube containing Hybridization sample 1. During this operation, Hybridization samples were not removed from a thermal cycler (Eppendorf Mastercycler gradient) for longer than necessary for addition of fresh driver. The content of the tube was mixed by pipetting up and down. The tube was centrifuged briefly and incubated at 68°C overnight. 200 µL of Dilution buffer (pH 8.3, 20 mM HEPES (pH 6.6), 20 mM NaCl 0.2 mM EDTA (pH 8.0)), supplied by the kit, was added and the content was mixed by pipetting. The tube was incubated in thermal cycler at 68°C for 7 min and stored at -20°C. The procedure was repeated for both reverse and forward subtractions of SSH-1 and SSH-2.

2.2.7 Primary PCR Amplifications

One µL of each diluted cDNA (i.e., subtraction products obtained in section 2.4.7 and the corresponding diluted Unsubtracted tester control from section 2.2.4) were taken into labelled tubes and prepared as PCR templates as indicated in Table 2.26. A master mix was prepared for (8+1) reactions by mixing the reagents indicated in Table 2.27. PCR Primer 1 (10 µM) and dNTP Mix (10mM each) were supplied by Clontech PCR-Select cDNA Subtraction Kit. 10X PCR Reaction Buffer and 50X Advantage cDNA Polymerase Mix were provided in Clontech Advantage® cDNA Polymerase Mix. The master mix was vortexed and centrifuged briefly. 24 µL of Master Mix was aliquoted in the tubes containing the templates. These PCR reaction mixtures were overlaid with mineral oil and incubated in a thermal cycler (Eppendorf Mastercycler gradient) at 75ºC for 5 min for extension of the adaptors. The PCR program shown in Table 2.28 was immediately started. After the reactions were completed, 8 µL from each primary PCR tube was aliquoted to be analyzed on an agarose gel with the secondary PCR products.

Table 2.26 Templates for primary PCR reactions.

	Template Volume (µL)
Product of Forward Subtraction for SSH1	1
Product of Forward Subtraction for SSH2	1
Unsubtracted Tester Control for Forward Subtraction of SSH1	1
Unsubtracted Tester Control for Forward Subtraction of SSH2	1
Product of Reverse Subtraction for SSH1	1
Product of Reverse Subtraction for SSH2	1
Unsubtracted Tester Control for Reverse Subtraction of SSH1	1
Unsubtracted Tester Control for Reverse Subtraction of SSH2	1

Table 2.27 Preparation of master mix for primary PCR amplifications.

	Per Reaction (µL)	**Master Mix (µL)**
Sterile H_2O	19.5	175.5
10X PCR Reaction Buffer	2.5	22.5
dNTP Mix (10mM)	0.5	4.5
PCR Primer 1 (10 µM)	1	9
50X Advantage cDNA Polymerase Mix	0.5	4.5
Total	24	216

Table 2.28 Primary PCR conditions.

Temperature (ºC)	**Time (sec)**	**Cycle(s)**
94	10	1
94	25	30
66	3	
72	90	

2.2.8 Secondary PCR Amplifications

1 µL of each primary PCR mixture was aliquoted in labelled tubes as templates for secondary PCR reactions. A master mix for (8+1) reactions was prepared for the secondary PCRs as indicated in Table 2.29.

Table 2.29 Preparation of master mix for secondary PCR amplifications.

	Per Reaction (µL)	Master Mix (µL)
Sterile H_2O	18.5	166.5
10X PCR Reaction Buffer	2.5	22.5
Nested PCR primer 1 (10µM)	1	9
Nested PCR primer 2R (10µM)	1	9
dNTP Mix (10mM)	0.5	4.5
50X Advantage cDNA Polymerase Mix	0.5	4.5
Total	24	216

Nested primers were provided within Clontech PCR-Select™ cDNA Subtraction Kit. 10X PCR Reaction Buffer and 50X Advantage cDNA Polymerase Mix were provided in Clontech Advantage® cDNA Polymerase Mix. The mix was vortexed and centrifuged briefly. 24 µL of Master Mix was aliquoted in the tubes containing 1 µL aliquots of primary PCR mixtures. Each reaction mixture was overlaid with mineral oil. Thermal cycling was started with the conditions indicated in Table 2.30 preset. Eight µL aliquots of primary PCR products and 8 µL of each secondary PCR product were analysed in a 1% agarose/EtBr gel run in 1X TBE buffer.

Table 2.30 Secondary PCR conditions.

Temperature (ºC)	Time (sec)	Cycle(s)
94	30	12
66	30	
72	90	

2.3 Cloning of Subtraction Products to Cloning Vectors and Preparation of SSH Libraries

2.3.1 Ligation of cDNA Libraries to pGEM®-T Easy Vector

Resulting cDNA libraries from both subtraction experiments were ligated to a TA cloning vector, Promega pGEM®-T Easy Vector. The map and the sequence of the vector are provided in Appendix B. Ligation mixtures shown in Table 2.31 were prepared for subtracted cDNA libraries (i.e. products of secondary PCR reactions) from the two subtraction experiments, SSH1 (D-R) and SSH2 (R-D). Each content was added in the order indicated in the table. 2X Rapid Ligation Buffer, PGEM-T Easy Vector and T4 DNA Ligase were included in the Promega pGEM®-T Easy Vector System I product. Ligation mixtures were incubated at 4°C for 2 days.

Table 2.31 Ligation mixtures for ligation of cDNA libraries to PGEM-T Easy Vector.

	Ligation Mix for SSH1 Products (µL)	**Ligation Mix for SSH2 Products (µL)**
2X Rapid Ligation Buffer	5	5
PGEM-T Easy Vector (50ng/µL)	1	1
Secondary PCR Product of Forward Subtraction of SSH1	3	-
Secondary PCR Product of Forward Subtraction of SSH2	-	3
T4 DNA Ligase (3u/µL)	1	1
Total	10	10

2.3.2 Transformation of cDNA Libraries Ligated to pGEM®-T Easy Vector

Transformation was achieved using two procedures. One was a procedure, which included preparation of laboratory-made competent cells (Tu *et al.*, 2005). The other procedure was given by the manual of Invitrogen UltraMAXTM DH5α-FTTM Competent Cells.

The first procedure was as follows. E. coli DH5α FT+ cells were grown overnight in 5 mL LB medium. 100 µL of fresh overnight culture was inoculated in 50 mL of SOC medium and grown until A_{600} reached 0.4. A_{600} was measured measured using a Shimadzu UV-1601 spectrophotometer. The cells were pelleted by centrifuging in 20 mL polypropylene tubes at 8000 rpm at 4°C for 1 min. Supernatant was discarded and the pellet was re-suspended in 20 mL of TB (pre-cooled at 4°C) and incubated on ice for 30 min. Cells were centrifuged again at 8000 rpm at 4°C for 1 min and the pellet was re-suspended in 4 mL TB and 280 µL 7% DMSO was added. Suspension was aliquoted to eppendorf tubes (100 µL each). Aliquots not to be used immediately were quick frozen in liquid nitrogen and stored at -80°C.

5 µL of the ligation mixture obtained in section 2.4.10 was added to 100 µL competent cell suspension. 1 µL of DMSO was added to this mixture and the mixture was incubated on ice for 30 min. The mixture was heat shocked at 42°C for 90 seconds and added 900 µL of liquid SOC immediately. The mixture was incubated in a shaker incubator at 37 °C for 1 hr. 100 µL of 10X, 100X and 500X diluted transformation mixture was plated on pre-warmed LB-agar plates containing Ampicillin (100 µg/mL), IPTG (20 µg/mL) and X-Gal (45 µg/mL). 50 pg of PUC plasmid was transformed simultaneously in order to calculate the transformation efficiency. The transformation efficiency was calculated as 7×10^7.

For transformation using Invitrogen UltraMAX™ DH5α-FT™ Competent Cells, first, competent cells were thawed on wet ice. Three 20 mL polypropylene tubes were placed on ice. Cells were gently mixed immediately after thawing and 100 µL competent cells were aliquoted into the polypropylene tubes. Five µL (50 pg) of control DNA was added to one of the polypropylene tubes containing 100 µL competent cells. The pipette was moved through the cells while releasing the DNA. 5 µL of the ligation mixture obtained in section 2.4.10 was added to the two polypropylene tubes containing 100 µL competent cells, by moving the pipette through the cells while releasing. Tubes were gently tapped in order to mix. Cells were incubated on ice for 30 min and then heat-shocked in a 42 °C water bath for 45 sec without shaking. Cells were placed on ice for 2 min. 0.9 mL of room temperature SOC medium was added to each tube and tubes were shaken at 225 rpm, 37 °C for 1 hr. 100 µL of 10X, 100X and 500X diluted transformation mixture was plated on pre-warmed LB-agar plates containing Ampicillin (100 µg/mL), IPTG (20 µg/mL) and X-Gal (45 µg/mL). The transformation efficiency was calculated as 5 X 10^6.

2.3.3 Growth of Transformed Libraries in 96-Well Plates

Only white colonies were chosen from transformation plates and grown in Greiner 96-well plates with 100 µL LB (100 µg/mL Ampicillin) in each well. 1536 white colonies from transformation plates for SSH1 (D-R) and 1152 white colonies from transformation plates for SSH2 (R-D) were picked and inoculated in LB (100 µg/mL Ampicillin) in 96-well plates. Cultures were grown overnight at 37°C, added equivalent volume of 50% sterile glycerol and stocked at -80°C.

2.3.4 Sequencing of SSH Libraries

Clones of both SSH libraries were sequenced at a facility of Genome Sequencing Centre in Washington University School of Medicine. The facility accepted clones in glycerol stocks and made sequencing. All 1536 clones resulting from SSH1 (D-R) and 1152 clones resulting from SSH2 (R-D) were sequenced by this facility.

2.3.5 Analyses of Resulting EST Libraries

cDNA sequences were subjected to Blast N analyses (in All GenBank + EMBL + DDBJ + PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)) and Blast X analyses (in nr database). The vector sequences were removed before these analyses.

cDNA sequences, from which vector sequences were removed, were also subjected to cluster analysis using the Cap3 program. Default parameters were used when operating the program. A trial account for a web interface of the program was temporarily provided by Husar Bionfirmatics

Lab, Germany. Up to 1000 sequences could be analysed at once for contig assembly using the trial account. The numbers of read sequences from both SSH1 (D-R) and SSH2 (R-D) libraries were above this limit. Therefore, at first about 1000 sequences were clustered from each library and the rest were clustered separately. The libraries contained large numbers of clones that belonged to some constitutively expressed genes such as those belonging to rubisco and chlorophyll A/B binding, and to vector sequences. Most of these were assembled into contigs by Cap3 analysis. In order to analyse the remaining clones together in the same cluster analysis, these abundant clones were excluded from both portion of the library, which were analysed separately at first. The number of remaining sequences were under 1000, thus could be clustered by Cap3 at once. The clones excluded from both portions were then brought together and analysed in Cap3. Therefore, contig assemblies were done for whole libraries.

Blast N results were examined and representative homology hit(s) for each sequence were recorded and organized into tables.

2.4 Preparation of Buffers and Growth Media for Cloning

2.4.1 Preparation of LB and SOC Growth Media

In order to prepare LB growth medium, 5 g of yeast extract, 10 g of tryptone and 10 g of NaCl were dissolved in 1 L distilled water. The solution was autoclaved at 121 °C for 30 minutes. 1.5 % LB agar was prepared by adding 15 g of agar to the LB solution before autoclave. Ampicillin, IPTG and X-Gal were added after autoclave. Ampicillin stock solution was prepared as 100 mg/mL by dissolving 5 g of Ampicillin in 50 mL deionized sterile water. The solution was filter sterilized, aliquoted in sterile eppendorf tubes and labelled. IPTG stock solution (200mg/mL) was prepared by dissolving 2 g of IPTG in 10 mL sterile deionized water and filter sterilizing. The stock solution was aliquoted to sterile 1.5 mL Eppendorf tubes. X-Gal stock solution (30mg/mL) was prepared by dissolving 30 mg of X-Gal in 1 mL of DMF (Dimethyl formamide) and then filter sterilizing the solution. 1 mL of Ampicillin was added to 1 L LB to obtain a 100 µg/mL final concentration. Ampicillin was added after the temperature of the autoclaved medium dropped below 60 °C. A hundred µL of 200mg/mL IPTG stock solution and 1.5 mL of 30mg/mL X-Gal stock solution were also added.

10 g of tryptone (2% final concentration), 2.5 g of yeast extract (0.5 final concentration), 0.292 g of NaCl (10 mM final concentration), 0.932 g of KCl (25 mM final concentration) were dissolved in mL of deionized water and autoclaved for preparing SOC. 1M stock solutions $MgCl_2$, $MgSO_4$ and glucose were prepared and filter sterilized. 5 µL of 1 M $MgCl_2$ stock solution (10 mM final concentration), 5 µL of 1 M of MgSO4 stock solution (10 mM final concentration) and 10 of

glucose solution (20 mM final concentration) were added to autoclaved solution. Five hundred µL of 100mg/mL Ampicillin stock solution was added for a final concentration of 100 µg/ mL.

2.4.2 Preparation of TB

In order to prepare 50 mL of TB, 0.151 g of PIPES (10 mM final concentration), 0.083 g of $CaCl_2$ (15 mM final concentration), 0.931 g of KCl (250 mM final concentration) were dissolved in 45 mL sterile deionized water. pH of the solution was adjusted to 6.7 using KOH. Finally, 0.346 g of $MnCl_2$ (55 mM final concentration) was dissolved in the solution.

2.5 Preparation of Haugland Plant Growth Medium

695.5 mL of macronutrient solution, 1.75 mL of micronutrient solution, 15 mL of 50 mM Fe-EDTA stock solution and 350 µL of 20 mM $ZnSO_4.7H_2O$ solution were dissolved in 2 L of distilled water. The volume was completed to 7 L adding distilled water.

2.5.1 Preparation of Macronutrient Solution

In order to prepare macronutrient solution, 31.4 g of K_2SO_4, 5.4 g of KH_2PO_4, 48 g of $MgSO_4.7$ H_2O and 94.46 g of $Ca(NO_3)_2.4$ H_2O were dissolved in 2 L of distilled water by stirring by a magnetic stirrer. The volume was completed to 10 L and the macronutrient solution was stored at room temperature.

2.5.2 Preparation of Micronutrient, Fe-EDTA and Zinc Solutions

0.124 g of H_3BO_3, 0.066 g of $MnSO_4$, 0.1 g of $CuSO_4$ and 0.048 g of $(NH_4)_6Mo_7.O_{24}.4H_2O$ were dissolved in 1 L of distilled water by stirring the solution using a magnetic stirrer and the micronutrient solution was stored at room temperature.

Fe-EDTA stock solution was prepared as 50 mM and $ZnSO_4.7H_2O$ stock solution was prepared as 20 mM. These stock solutions were stored at room temperature. Fe-EDTA solution was protected from light by wrapping the bottle with aluminium foil and storing in dark.

2.6 Preparation of Electrophoresis Gels and Buffers

2.6.1 Preparation of RNA Gels

All surfaces of gel apparatus, combs and trays were washed with DEPC treated deionized water and cleaned with RNAse-OFF (Applichem) solution. Appropriate amount of agarose (1%) was

weighed and added into corresponding volume of 1X (10 mM) phosphate buffer (pH6.8), adjusted according to the gel apparatus used. Containers were formerly treated with DEPC and autoclaved. Agarose was dissolved by heating in a microwave oven and allowed to cool. When the temperature of the solution dropped to around 60 °C, EtBr (0.5 µg/mL final concentration) was added, the gel solution was poured off into a tray, a comb was placed appropriately and the gel was left to polymerize. After the polymerization was completed, the comb was removed carefully and the gel was embedded in phosphate buffer in the electrophoresis tank.

2.6.2 Preparation of DNA Gels

Appropriate amount of agarose (1%) was weighed and added into corresponding volume of 0.5 X TBE buffer, adjusted according to the gel apparatus used. Agarose was dissolved by heating in a microwave oven and allowed to cool. When the temperature of the solution dropped to around 60 °C, EtBr (0.5 µg/mL final concentration) was added, the gel solution was poured off into a tray, a comb was placed appropriately and the gel was left to polymerize. After the polymerization was completed, the comb was removed carefully and the gel was embedded in 0.5 X TBE buffer in the electrophoresis tank.

2.6.3 Preparation of Phosphate Buffer and TBE Buffer

In order to prepare 10 X (0.1 M) phosphate buffer 13.4 g of $Na_2HPO_4.7H_2O$ and 6.899 g of $NaH_2PO_4.2H_2O$ were dissolved in 980 mL DEPC treated autoclaved deionized water. The pH of the buffer was adjusted to 6.8. The volume was completed to 1 L with DEPC treated autoclaved deionized water.

10 X TBE buffer (pH 8.3) was prepared by dissolving 107.78 g Tris, 7.44 gr EDTA-Na_2 salt and and 55 g boric acid in 1L deionized water.

CHAPTER III

RESULTS AND DISCUSSION

3.1 Infection of Plants with Yellow Rust Pathogen

Wheat plants were inoculated with yellow rust spores as described in section 2.1.2. About 15 days after inoculations, yellow rust was observed on susceptible plants, therefore efficiency of infection was confirmed. Control plants mock inoculated with talk powder and resistant experimental plants showed no disease symptoms.

3.2 Gel Analyses and Concentration Determination of Total RNA Samples

Integrity of RNA samples were analysed in 1% agarose gels as described in Section 2.2.1.3 (Figures 3.1 and 3.2). RNA samples appeared intact and concentrations were found satisfactory (Table 3.1). RNA concentrations were determined by UV spectrophotometer using the formula A_{260} x dilution factor x 40 µg/mL.

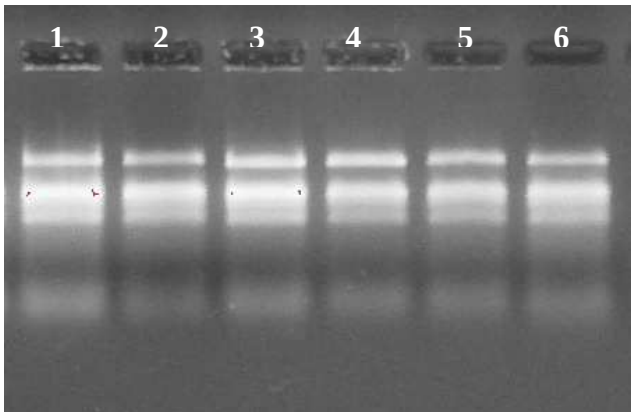


Figure 3.1 Total RNA samples for SSH1 (D-R), visualized on 1% agarose gel. **Lanes 1, 2, 3:** Tester RNA from leaf tissue, 3, 6, 9 days post-infection (dpi), respectively, **Lanes 4, 5, 6:** Driver RNA from leaf tissue, 3, 6, 9 dpi.

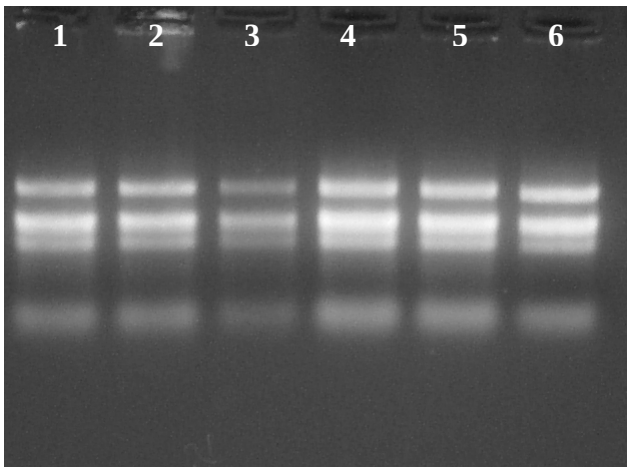


Figure 3.2 Total RNA samples for SSH2 (R-D), visualized on 1% agarose gel. **Lanes 1, 2, 3:** Tester RNA from leaf tissue, 12, 24, 48 hr post-infection (hpi), respectively, **Lanes 4, 5, 6:** Driver RNA from leaf tissue, 12, 24, 48 hpi.

Table 3.1 Concentrations of total RNA samples isolated from leaf samples.

Total RNA Sample	Concentration (µg / µL)
SSH1 Tester 3 days	0.59
SSH1 Tester 6 days	1.22
SSH1 Tester 9 days	1.74
SSH1 Driver 3 days	0.94
SSH1 Driver 6 days	1.15
SSH1 Driver 9 days	1.36
SSH2 Tester 12 hr	1.15
SSH2 Tester 24 hr	1.00
SSH2 Tester 48 hr	0.62
SSH1 Driver 12 hr	0.75
SSH1 Driver 24 hr	0.51
SSH1 Driver 48 hr	0.43

3.3 Isolation of mRNA from Total RNA Samples

mRNA from each tester and driver samples was isolated as described in section 2.2.2.1. The concentrations of mRNA samples were determined using agarose gels as described in section 2.2.2.2. Gels prepared for concentration determination were visualized and photographed under UV transilluminator (Figures 3.3, 3.4 and 3.5).

According to comparisons of gel spots of mRNA samples with spots of control mRNA; the spot for 5x dilution of SSH1 (D-R) Tester mRNA (spot 9 in Figure 3.3) is at approximately equal intensity with the spot for 25 ng/μL control dilution (spot 3 in Figure 3.3). Since the spot was formed by dropping 1 μL of sample, the concentration of SSH1 (D-R) Tester mRNA sample is calculated as:

(25 ng/μL) x (5 dilution factor) ≈ 125 ng/μL

Similarly, the spot for 5x dilution of SSH1 (D-R) Driver mRNA (spot 11 in Figure 3.3) is at approximately equal intensity with the spot for 20 ng/μL control dilution (spot 2 in Figure 3.3). Since the spot was formed by dropping 1 μL of sample, the concentration of SSH1 (D-R) Tester mRNA sample is calculated as:

(20 ng/μL) x (5 dilution factor) ≈ 100 ng/μL

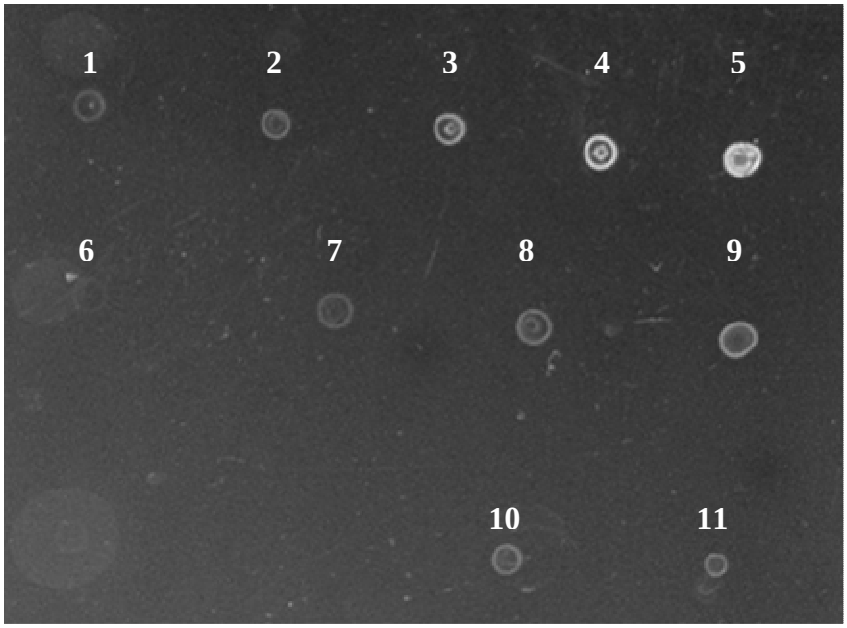


Figure 3.3 mRNA from SSH1 (D-R) Tester and Driver samples visualized on 1% agarose gel. **Spots 1, 2, 3, 4, 5:** Dilutions of control mRNA, 10 ng/μL, 20ng/μL, 25 ng/μL, 40 ng/μL and 50 ng/μL respectively, **Spots 6, 7, 8, 9:** 40x, 20x, 10x and 5x dilutions of Tester mRNA of SSH1 (D-R), **Spots 10, 11:** 10x and 20 x dilutions of Driver mRNA of SSH1 (D-R).

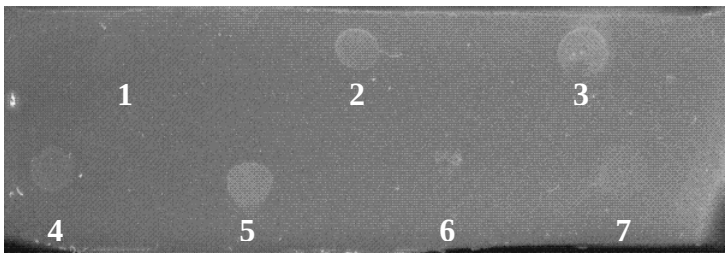


Figure 3.4 mRNA from SSH2 (R-D) Tester sample visualized on 1% agarose gel. **Spots 1, 2, 3:** Dilutions of control mRNA, 10 ng/μL, 20 ng/μL, 40 ng/μL respectively, **Spot 4:** 10x dilution of Tester mRNA of SSH2 (R-D), **Spot 5:** 5x dilution of Tester mRNA of SSH2 (R-D), **Spots 6, 7:** These spots belong to second elution of mRNA from magnetic particles (They were not used in the subtraction experiments.).

The spot for 5x dilution of SSH2 (R-D) Tester mRNA (spot 5 in Figure 3.4) is at approximately equal intensity with the spot for 80 ng/μL control dilution(spot 3 in Figure 3.4). Since the spots were formed by dropping 0.5 μL of sample, the control spot 3 contained 40 ng control mRNA and the concentration of SSH1 (D-R) Tester mRNA sample was calculated as:
(40 ng) x (1 μL / 0.5 μL) x (5 dilution factor) ≈ 400 ng in 1 μL
Concentration ≈ 400 ng/ μL

The spot for 2x dilution of SSH2 (R-D) Driver mRNA (spot 5 in Figure 3.5) is at approximately equal intensity with the spot for 100 ng/μL control dilution (spot 1 in Figure 3.5). Since the spot was formed by dropping 1 μL of sample, the concentration of SSH1 (D-R) Tester mRNA sample is calculated as:
(100 ng/μL) x (2 dilution factor) ≈ 200 ng/μL

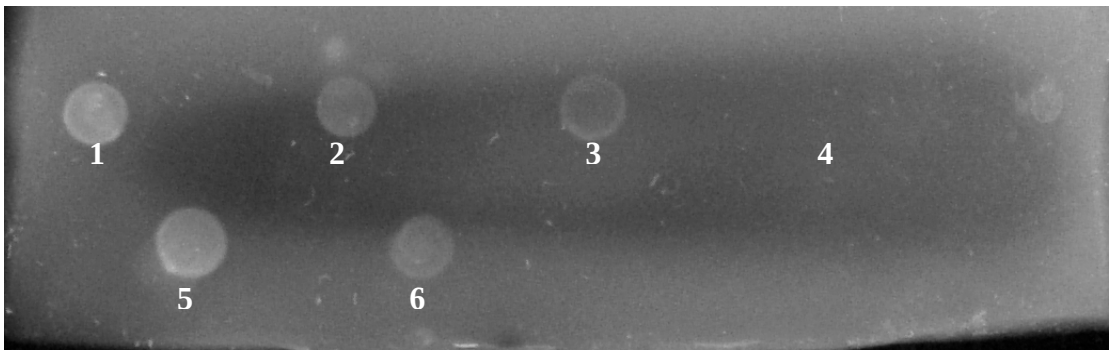


Figure 3.5 mRNA from SSH2 (R-D) Driver sample visualized on 1% agarose gel. **Spots 1, 2, 3, 4:** Dilutions of control mRNA, 100 ng/µL, 50 ng/µL, 20 ng/µL and 10 ng/µL respectively, **Spot 5:** 2x dilution of Driver mRNA of SSH2 (R-D), **Spot 6:** 4x dilution of Driver mRNA of SSH2 (R-D).

3.4 Gel Analyses of *Rsa* I Digestion Products

2.5 µL of undigested and 5 µL of digested cDNAs from *Rsa* I digestion, were electrophoresed on 1% agarose/EtBr gels run in 1X TBE buffer. The electrophoresis gels were visualized under UV transilluminator (Figures 3.6 and 3.7).

The digestions for tester and driver samples were observed to be efficient (Figure 3.6 and 3.7). As can be seen in Figures 3.6 and 3.7, digested cDNA samples (Lanes 2, 4 in Figure 3.6; Lanes 2, 4, 6 in Figure 3.7) seem lower on the gel as compared to the corresponding undigested cDNA samples (Lanes 1, 3 in Figure 3.6; Lanes 1, 3, 5, in Figure 3.7 respectively). This is reasonable because the digestion would result in decrease in sizes of cDNA molecules. The appearance of the samples on gels resembles the sample pictures shown in the Clontech PCR-Select™ cDNA Subtraction Kit' manual, which makes this result more reliable.

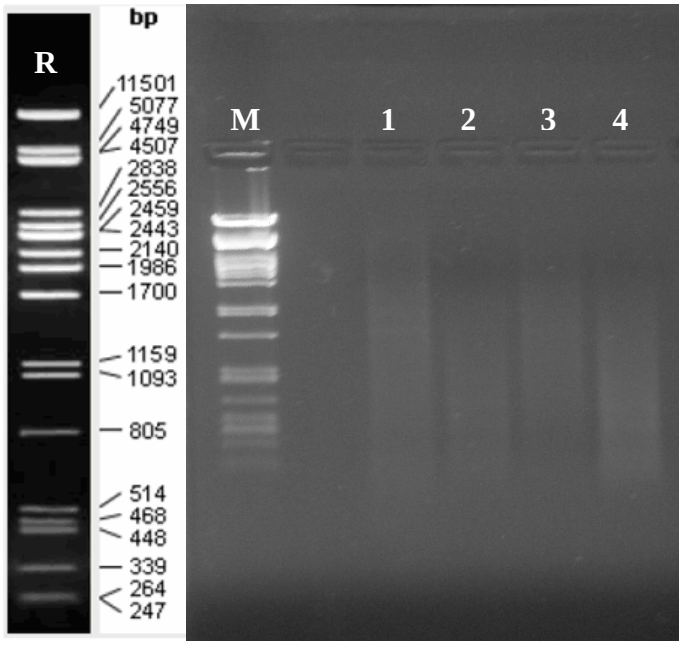


Figure 3.6 Products of *Rsa* I Digestion of SSH1 (D-R) Tester and Driver cDNA samples visualized on 1% agarose gel. **R:** Size ruler for *Pst* I digested λ DNA marker. **Lane M:** *Pst* I digested λ DNA as marker. **Lane 1:** Undigested SSH1 (D-R) Tester cDNA sample. **Lane 2:** *Rsa* I digested SSH1 (D-R) Tester cDNA sample. **Lane 3:** Undigested SSH1 (D-R) Driver cDNA sample. **Lane 2:** *Rsa* I digested SSH1 (D-R) Driver cDNA sample.

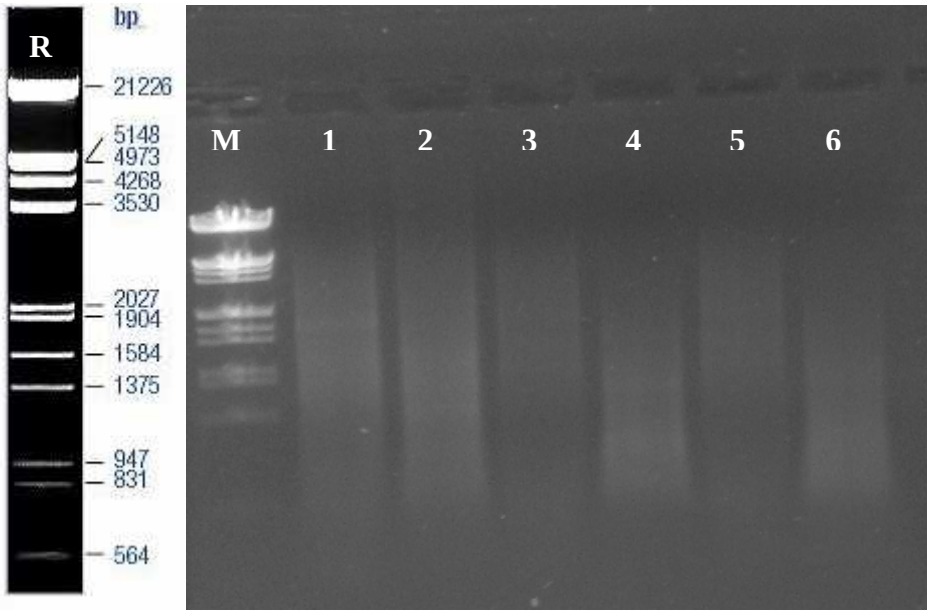


Figure 3.7 Products of *Rsa* I Digestion of SSH2 (R-D) Tester and Driver cDNA samples visualized on 1% agarose gel. **R:** Size ruler for *Hind* III/*Eco*R I digested λ DNA marker. **Lane M:** *Hind* III/*Eco*R I digested λ DNA as marker. **Lane 1:** Undigested control skeletal muscle cDNA. **Lane 2:** *Rsa* I digested control skeletal muscle cDNA. **Lane 3:** Undigested SSH2 (R-D) Tester cDNA sample. **Lane 4:** *Rsa* I digested SSH2 (R-D) Tester cDNA sample. **Lane 5:** Undigested SSH2 (R-D) Driver cDNA sample. **Lane 6:** *Rsa* I digested SSH2 (R-D) Driver cDNA sample.

3.5 Primary and Secondary PCR Amplifications

Primary and secondary PCR product were analysed in a 1% agarose/EtBr gel run in 1X TBE buffer as described in section 2.2.8. Figure 3.8 displays primary and secondary PCR products visualized on 1% agarose gel. Since the templates for these PCR reactions were clones of cDNA populations of various sizes, the smeary appearance was quite expectable. The secondary PCR amplifications resulted in much more intense smears (Lanes 1-7 in Figure 3.8) on the gel than corresponding primary PCR amplifications did (Lanes 8-14 in Figure 3.8), as expected because products of the first PCR amplification were further amplified in this secondary PCR amplification. There a large number of different-sized fragments, since the subtractions were done between whole transcriptomes. The amplification results demonstrated that the resulting fragments covered a reasonable size range to continue with the subsequent cloning steps.

Lanes 3, 4, 7, 8, 11, 12, 15, 16 in Figure 3.8 represent unsubtracted tester controls that were prepared for possible subsequent screening analysis, but screening analysis was not performed, therefore this data is of no use in this study.

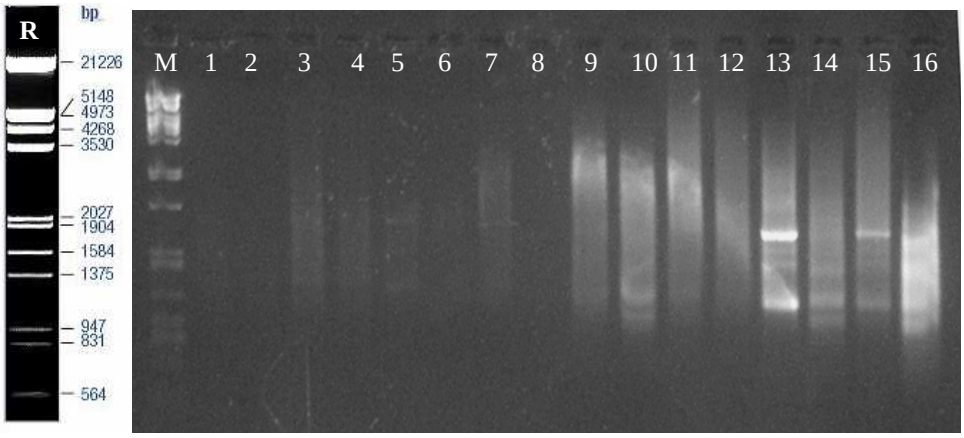


Figure 3.8 Primary and secondary PCR products visualized on 1% agarose gel. **R:** Size ruler for *Hind* III/*Eco*R I digested λ DNA marker. **Lanes M:** *Hind* III/*Eco*R I digested λ DNA as marker. **Lane 1:** Primary PCR of Forward Subtraction product of SSH2 (R-D). **Lane 2:** Primary PCR of Forward Subtraction product of SSH1 (D-R). **Lane 3:** Primary PCR of Unsubtracted Tester Control for Forward Subtraction of SSH2 (R-D). **Lane 4:** Primary PCR of Unsubtracted Tester Control for Forward Subtraction of SSH1 (D-R). **Lane 5:** Primary PCR of Reverse Subtraction product of SSH2 (R-D). **Lane 6:** Primary PCR of Reverse Subtraction product of SSH1 (D-R). **Lane 7:** Primary PCR of Unsubtracted Tester Control for Reverse Subtraction of SSH2 (R-D). **Lane 8 :** Primary PCR of Unsubtracted Tester Control for Reverse Subtraction of SSH1 (D-R). **Lane 9:** Secondary PCR of Forward Subtraction product of SSH2 (R-D). **Lane 10:** Secondary PCR of Forward Subtraction product of SSH1 (D-R). **Lane 11:** Secondary PCR of Unsubtracted Tester Control for Forward Subtraction of SSH2 (R-D). **Lane 12:** Secondary PCR of Unsubtracted Tester Control for Forward Subtraction of SSH1 (D-R). **Lane 13:** Secondary PCR of Reverse Subtraction product of SSH2 (R-D). **Lane 14:** Secondary PCR of Reverse Subtraction product of SSH1 (D-R). **Lane 15:** Secondary PCR of Unsubtracted Tester Control for Reverse Subtraction of SSH2 (R-D). **Lane 16:** Secondary PCR of Unsubtracted Tester Control for Reverse Subtraction of SSH1 (D-R).

3.6 Analyses of Sequence Results of SSH Libraries

A high proportion of clones, 46.92 % of SSH1 (D-R) library and 10.36 % of SSH2 (R-D) library, showed similarity to small and large subunits of RubisCo (Ribulose-1,5-bisphosphate carboxylase/oxygenase), which were considered to be back ground. RubisCo mRNA is highly abundant in plant cells; therefore it can interfere with the specificity of the method as reported in other studies (Neu *et al.*, 2003). Subtractions with low or no RubisCo hit results can be considered more efficient (Thara *et al.*, 2003). Another gene which appear as background in plant SSH libraries is chlorophyll A/B binding gene, which constituted 4.53 % of SSH1 (D-R) and 1.89 % of SSH2 (R-D) library. The total RubisCo and chlorophyll A/B binding gene hit proportions in our

libraries are high. Nevertheless, there are still a significant number of clones that show homology to genes of assigned functions, which can be considered with putative roles in plant-pathogen interactions. Some of these were reported to be biotic stress responsive genes and were associated with plant disease resistance and/or pathogenicity in previous studies; a collection of these genes is discussed in this study. Detailed tables displaying the Blast N results of all clones of SSH1 (D-R) and SSH2 (R-D) libraries classified according to functional categories are provided in Appendix G (for SSH1 (D-R)) and Appendix H (SSH2 (R-D)).

Contig assemblies were performed using Cap3 contig assembly program as described in Section 2.3.5. Each contig generated is assumed to represent transcripts of the same gene and they are referred to as "unigenes" throughout the thesis. Clones that were not assembled into any contigs are referred as "singletons". Table 3.2 displays overall numbers of unigenes, numbers of clones that these unigenes represent (given in parentheses near the numbers of unigenes) and numbers of singletons. The contig assemblies are presented in Appendix C and Appendix D, for SSH1 (D-R) and SSH2 (R-D) respectively. The alignments performed by Cap3 during generation of contig assemblies are presented in Appendix E (for SSH1 (D-R) and Appendix F (for SSH2 (R-D)).

Table 3.2 Numbers and proportions of clones, which were classified according to their Blast N homology results.

	SSH1	**SSH2**
Metabolism and Energy	Singleton: 70 Unigene: 12 (48 Total) Total: 118 8.35 %	Singleton: 93 Unigene: 12 (47 Total) Total: 165 14.88 %
Signal Transduction	Singleton: 35 Unigene: 3 (7 Total) Total: 42 2.97 %	Singleton: 93 Unigene: 5 (20 Total) Total: 81 7.30 %
Apoptosis	Singleton: 2 Unigene: NO Total: 2 0.14 %	NO
Defence Related	Singleton: 6 Unigene: 1 (5 Total) Total: 11 0.78 %	Singleton: 8 Unigene: 1 (2 Total) Total: 10 0.90 %
Stress Related	Singleton: NO Unigene: 2 (5 Total) Total: 5 0.35 %	Singleton: 10 Unigene: 1 (2 Total) Total: 12 1.08 %
Protein Degradation and Ubiquitinylation	Singleton: 3 Unigene: 1 (3 Total) Total: 6 0.42 %	Singleton: 13 Unigene: 6 (26 Total) Total: 38 3.43 %

Table 3.2 *(Continued)*

	SSH1	**SSH2**
Transcription and Translation	Singleton: 8 Unigene: 1 (2 Total) Total: 10 0.71 %	Singleton: 18 Unigene: 1 (3 Total) Total: 21 1.89 %
Cellular Organization	Singleton: 3 Unigene: 1 (2 Total) Total: 5 0.35 %	Singleton: 21 Unigene: NO Total: 22 1.98 %
Other	Singleton: 67 Unigene: 7 (21 Total) Total: 88 6.23 %	Singleton: 250 Unigene: 10 (29 Total) Total: 283 25.52 %
Unknown	Singleton: 273 Unigene: 8 (27 Total) Total: 300 21.23 %	Singleton: 220 Unigene: 6 (17 Total) Total: 231 20.83 %
Rubisco	Singleton: 145 Unigene: 16 (518 Total) Total: 663 46.92 %	Singleton: 36 Unigene: 6 (79 Total) Total: 115 10.36 %
Chlorophyll A/B Binding Protein	Singleton: 21 Unigene: 7 (43 Total) Total: 64 4.53 %	Singleton: 13 Unigene: 2 (8 Total) Total: 21 1.89 %
Ribosomal RNA	Singleton: 4 Unigene: NO Total: 4 0.28 %	Singleton: 17 Unigene: 3 (27 Total) Total: 44 3.97 %
SSH Adaptors	Singleton: 68 Unigene: 6 (17 Total) Total: 85 6.02 %	Singleton: 42 Unigene: 1 (2 Total) Total: 46 4.15 %
Vector	Singleton: 6 Unigene: 2 (4 Total) Total: 10 0.71 %	Singleton: 4 Unigene: 2 (9 Total) Total: 13 1.17 %
TOTAL	**Singleton: 711** **Unigene: 67 (702 Total)** **Total: 1413**	**Singleton: 838** **Unigene: 56 (271 Total)** **Total: 1109**

3.7 Transcripts with Homologies to Significant Genes/Gene Families

Here is discussed the supposed induction of clones that were found to show homology, in Blast N and Blast X analysis, to genes that were commonly emphasized in plant-pathogen interaction studies. Similar induction results or functional assignments associated with plant diseases may exist

for clones not discussed here, but this discussion focuses on those clones that displayed similarity to genes that were implicated in plant disease for long or commonly.

One unigene (3 clones) and 2 singletons in SSH1 (D-R) suggested induction of a plant aconitate hydratase gene (Table 3.3). Aconitate hydratase (aconitase) is the enzyme from the TCA cycle that catalyzes the reversible isomerization of citrate and isocitrate. Cytoplasmic aconitate hydratase (aconitase) was shown to be induced during HR response (Kaneda *et al.*, 2007). Moeder *et al.*, in 2006, showed that aconitase-silenced *N. Benthamiana* plants inoculated with avirulent *Pseudomonas syringae* pv. *tabaci* displayed delayed HR and allowed higher levels of bacterial growth and that disease-associated cell death was also reduced in these plants. They commented that, aconitase played a role in regulating cell death. It seems from these findings that aconitate hydratase (aconitase), has a function in HR response. In our study, this gene was found to be induced in SSH1 (D-R), i.e. in a compatible interaction as compared to an incompatible one. In the compatible interaction, the plant is unable to limit pathogen growth by showing HR response. It can be hypothesized that molecular events/signalling leading to HR is suppressed by the pathogen, and the plant somehow induces HR activators, such as aconitase as counteract.

Proton-inorganic pyrophosphatase was represented by one unigene (5 clones) in SSH1 (D-R) library (Table 3.4). Vacuolar proton-inorganic pyrophosphatase was found to be induced upon overexpression of the disease resistance gene *Pto* in tomato (Mysore *et al.*, 2003) and was shown to be differentially expressed in *Xanthomonas axonopodis* pv. manihotis infected cassava (Lopez *et al.*, 2005). Supposed induction in SSH1 (D-R), can be explained as that the gene is induced upon pathogen attack in both tester (compatible interaction) and driver (incompatible interaction); however since an efficient defence against pathogen cannot be achieved in the former one, the induction of this disease associated gene may be higher in an effort to compensate.

One unigene (4 clones) from SSH1 (D-R) and one (4 clones) from SSH2 (R-D) showed homology to two different FtsH genes (Table 3.5). FtsH1, together with FtsH2, FtsH5 and FtsH8, comprise the thylakoid membrane-bound ATP-dependent FtsH complex, which is thought to degrade misfolded or damaged membrane proteins in chloroplast thylakoid membranes. The steady-state level of FtsH1 was reduced in plants over-expressing the Arabidopsis E3 ligase *AtCHIP* under high-intensity light conditions, and these plants displayed a cell-death phenotype under high-intensity light conditions. It was previously reported that reduced levels of FtsH protease in tobacco mosaic virus-infected tobacco leaves accelerate the hypersensitive reaction. Shen *et al.* showed that cell-death observed in *AtCHIP*-over-expressing plants was associated with increased production of reactive oxygen species. Thus, they hypothesize that high-intensity light-induced cell death is probably due to decreased capacity, by Ftsh complex, to remove photo-damaged D1 protein in the PSII of *AtCHIP*-over-expressing plants (Shen *et al.* 2007). Another support for involvement of Ftsh in HR comes from Lam and his co-workers, who report that the plastid-localized protein DS9 was

found to regulate the rate of HR cell death in the *N* gene/TMV system. The level of DS9 was suppressed during the onset of the HR, concomitant with a decrease in photosynthetic electron flow. Overexpression of DS9 led to a delay of cell-death activation by TMV, along with increased systemic movement of the virus, even though markers of the HR were still induced. Conversely, suppression of DS9 led to hyperactivation of HR cell death, resulting in smaller lesions that are indicative of more efficient restriction of the virus. Because *DS9* encodes a homologue of the bacterial protease FtsH, which is involved in quality maintenance of cellular proteins, Lam and his co-workers suggest that accumulation of damaged proteins in the plastids might act as a signal for HR induction (Lam *et al.*, 2001). Supposed induction in SSH2 (R-D) may be associated with the defence response. Since it was suggested that reduced Ftsh1 level seemed to be linked to cell death response, an increased expression of this gene in SSH1 (D-R) could be associated with suppression of cell death (i.e. HR) by the pathogen.

Table 3.3 Sequence analysis results for clones with homology to aconitate hydratase gene.

SSH 1 Contig 3	3 clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-10 e05	593	Expect = 4e-039 128/142 (90%)	Sorghum propinquum putative aconitate hydratase 1 gene, exons 16, 17 and partial cds gi|94961050|gb|DQ463100.1|
		Expect = e-113 417/482 (86%)	Oryza sativa (japonica cultivar-group) Os03g0136900 (Os03g0136900) mRNA, complete cds
SSH1-10 f09 In SSH1-10 e05	429	Expect = 2e-074 241/273 (88%)	Oryza sativa (japonica cultivar-group) Os03g0136900 (Os03g0136900)mRNA, complete cds
		Expect = 2e-039 125/138 (90%)	Sorghum propinquum putative aconitate hydratase 1 gene, exons 16,17 and partial cds
SSH1-5 e06 In SSH1-10 e05	640	Expect = e-149 514/590 (87%)	Oryza sativa (japonica cultivar-group) Os03g0136900 (Os03g0136900) mRNA, complete cds
		Expect = 2e-041 129/142 (90%)	Sorghum propinquum putative aconitate hydratase 1 gene, exons 16,17 and partial cds
Blast X Results			
Clone #	Blast X Homology Result		
SSH1-10 e05	gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [Sorghum bicolor] Length = 991 Score = 236 bits (603), Expect(3) = 3e-76 Identities = 111/135 (82%), Positives = 121/135 (89%), Gaps = 2/135 (1%) Frame = +2		
SSH1 Singletons	1 Clone		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-10 d06	658	Expect = e-144 458/522 (87%)	Oryza sativa (japonica cultivar-group) Os03g0136900 (Os03g0136900) mRNA, complete cds
		Expect = 2e-034 111/122 (90%)	Sorghum propinquum putative aconitate hydratase 1 gene, exons 16,17 and partial cds
Blast X Results			
Clone #	Blast X Homology Result		
SSH1-10 d06	>gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [Sorghum bicolor] Length = 991 Score = 342 bits (877), Expect = 9e-93 Identities = 163/198 (82%), Positives = 176/198 (88%) Frame = +2		

Table 3.4 Sequence analysis results for clones with homology to proton-inorganic pyrophosphatase genes.

SSH1 Contig 4	(5 clones)		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-10 h10	363	Expect = e-118 295/318 (92%)	Triticum aestivum vacuolar proton-inorganic pyrophosphatase RNA,complete cds gi|31580800|gb|AY296911.1|
SSH1-11 h04	838	Expect = 0.0 432/445 (97%)	Cloning vector pGEM-WIZ, complete sequence
SSH1-9 a08 In SSH1-11 h04	371	Expect = 7e-058 232/273 (84%)	Hordeum vulgare mRNA for vacuolar membrane proton-translocating inorganic pyrophosphatase, complete cds
SSH1-2 a09 In SSH1-11 h04	559	Expect = e-115 292/317 (92%)	Hordeum brevisubulatum vacuolar proton-inorganic pyrophosphatase(AVP1) mRNA, complete cds
SSH1-4 d03 In SSH1-11 h04	359	Expect = e-159 320/331 (96%)	Hordeum brevisubulatum vacuolar proton-inorganic pyrophosphatase (AVP1) mRNA, complete cds
Blast X Results			
Clone #	Blast X Homology Result		
SSH1-10 h10	gi|11527561|dbj|BAB18681.1| vacuolar proton-inorganic pyrophosphatase [Hordeum vulgare subsp. vulgare] Length = 771 Score = 206 bits (524), Expect = 3e-52 Identities = 104/110 (94%), Positives = 105/110 (95%) Frame = +3		

Table 3.5 Sequence analysis results for clones with homology to FtsH protease genes.

SSH1 Contig 6	(4 clones)		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-11 c07	620	Expect = 2e-028 152/180 (84%)	Arabidopsis thaliana mRNA for putative chloroplast FtsH protease,clone: RAFL08-16-K08 gi|110742013|dbj|AK226853.1|
		Expect = 2e-028 152/180 (84%)	Arabidopsis thaliana FTSH1; ATP-dependent peptidase/ ATPase/ metallopeptidase (FTSH1) mRNA, complete cds
SSH1-2 c01 In SSH1-11 07	691	Expect = 2e-028 152/180 (84%)	Arabidopsis thaliana putative chloroplast FtsH protease (At1g50250) mRNA, complete cds
		Expect = 6e-026 148/176 (84%)	Arabidopsis thaliana VAR1 (VARIEGATED 1); ATP-dependent peptidase/ ATPase/ metallopeptidase (VAR1) mRNA, complete cds
SSH1-14 e01	803	Expect = 0.0 552/556 (99%)	Triticum aestivum clone wl1n.pk0059.g7:fis, full insert mRNA sequence
		Expect = 5e-045 149/160 (93%)	Photobacterium damselae subsp. piscicida partial coi genes for putative cytochrome C oxidase proteins, clone pRDA19
SSH1-14 g01 In SSH1-14 01	707	Expect = 0.0 527/548 (96%)	Triticum aestivum clone wl1n.pk0059.g7:fis, full insert mRNA sequence
		Expect = 5e-017 142/173 (82%)	Arabidopsis thaliana FTSH1; ATP-dependent peptidase/ ATPase/metallopeptidase (FTSH1) mRNA, complete cds
Blast X Results			
Clone #	Blast X Homology Result		
SSH1-11 c07	gi|115470052|ref|NP_001058625.1| Os06g0725900 [Oryza sativa (japonica cultivar-group)] Cell division protease ftsH homolog, chloroplast precursor putative chloroplast FtsH protease [Oryza sativa (japonica cultivar-group)] Os06g0725900 [Oryza sativa (japonica cultivar-group)] Length = 686 Score = 264 bits (674), Expect = 3e-69 Identities = 135/147 (91%), Positives = 142/147 (96%) Frame = +3		
SSH2 Contig 53	(4 clones)		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result

Table 3.5 *(Continued)*			
SSH2-4 e10	399	Expect = 4e-041 190/226 (84%)	Oryza sativa (japonica cultivar-group) Os05g0458400 (Os05g0458400) mRNA, complete cds
		Expect = 0.006 55/65 (84%)	Arabidopsis thaliana mRNA for AAA-type like ATPase, partial cds, clone: RAFL05-07-P08
		Expect = 1.4 Identities = 21/21 (100%)	Acholeplasma laidlawii ChpAl (chpAl) and 25 kDa protein genes, complete cds; dnaK operon gene, complete sequence; lipoate protein ligase A (lplA), and 50S ribosomal protein L32 (L32) genes, complete cds
		Expect = 1.4 36/41 (87%)	Pisum sativum AAA-metalloprotease FtsH (FTSH) mRNA, complete cds; nuclear gene for mitochondrial product
SSH2-4 f10 In SSH2-4 e10	470	Expect = 3e-036 188/226 (83%)	Oryza sativa (japonica cultivar-group) Os05g0458400 (Os05g0458400)mRNA, complete cds
		Expect = 3e-005 38/41 (92%)	Arabidopsis thaliana FTSH3; ATP-dependent peptidase/ ATPase (FTSH3) mRNA, complete cds
		Expect = 1e-004 58/68 (85%)	Medicago sativa clone C43 putative splicing factor Prp8 mRNA, partial cds
		Expect = 0.007 37/41 (90%)	Pisum sativum AAA-metalloprotease FtsH (FTSH) mRNA, complete cds; nuclear gene for mitochondrial product
SSH2-4 h11 In SSH2-4 e10	395	Expect = 6e-086 269/304 (88%)	Zea mays PCO146144 mRNA sequence
		Expect = 7e-018 104/122 (85%)	Pisum sativum AAA-metalloprotease FtsH (FTSH) mRNA, complete cds; nuclear gene for mitochondrial product
SSH2-4 g11	555	Expect = 8e-040 193/227 (85%)	Oryza sativa (japonica cultivar-group) Os05g0458400 (Os05g0458400) mRNA, complete cds
		Expect = 1e-010 68/78 (87%)	Arabidopsis thaliana FTSH3; ATP-dependent peptidase/ ATPase (FTSH3) mRNA, complete cds
		Expect = 2e-006 46/51 (90%)	Arabidopsis thaliana FTSH10; ATP binding / ATPase/ metalloendopeptidase/ nucleoside-triphosphatase/ nucleotide binding (FTSH10) mRNA, complete cds
Blast X Results			
Clone #	Blast X Homology Result		
SSH2-4 e10	>gi|52353449|gb|AAU44017.1| putative AAA-metalloprotease FtsH (fragment) [Oryza sativa (japonica cultivar-group)] Length = 475 Score = 140 bits (354), Expect = 2e-32 Identities = 69/94 (73%), Positives = 78/94 (82%) Frame = +3		

In SSH1 (D-R), one unigene (2 clones) was found homologous to a wheat zeaxanthin epoxidase gene (Table 3.6). Zeaxanthin epoxidase (ZEP) is an important enzyme involved in abscisic acid (ABA) biosynthesis as well as in xanthophyll cycle. ABA plays very important roles in responses to environmental stress such as drought and high salt, inducing many osmotic stress-responsive genes. Transgenic plants over-expressing arabidopsis zeaxanthin epoxidase were found to promote osmotic-stress tolerance (Hye-Yeon *et al.* 2007). Strzalka *et al.* stated that the rise in production of zeaxanthin protected the photosynthetic apparatus against the over-excitation (Strzalka *et al.*, 2003). In a compatible interaction, pathogen invasion progresses and the plant is under stress. It is also known that reactive oxygen species (ROS) are produced upon pathogen attack. Since the pathogen cannot be stopped and the stress condition persists, ROS production may be higher in a compatible interaction than in an incompatible one. The induction of zeaxanthin epoxidase, in SSH1 (D-R), may be related with radical scavenging function induced in order to protect plant against the oxidative burst associated with the stress caused by pathogen invasion.

Table 3.6 Sequence analysis results for clones with homology to zeaxanthin epoxidase genes.

SSH1 Contig 8	(2 clones)		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-11 h09	692	Expect = 0.0 626/653 (95%)	Triticum aestivum zeaxanthin epoxidase (WZE) mRNA, partial cds gi|69054056|gb|AF384103.2|
SSH1-3 g08 In SSH1-11 h09	393	Expect = e-155 315/325 (96%),	Triticum aestivum zeaxanthin epoxidase (WZE) mRNA, partial cds
Blast X Results			
Clone #	Blast X Homology Result		
SSH1-11 h09	gi|69054057|gb|AAN63502.2|AF384103_1 zeaxanthin epoxidase [Triticum aestivum] Length = 363 Score = 393 bits (1010), Expect = e-108 Identities = 196/212 (92%), Positives = 201/212 (94%) Frame = +1		

A wheat phosphoribulokinase homolog was found to be induced in SSH1 (D-R), represented by one unigene (4 clones) (Table 3.7). Phosphoribulokinase is an enzyme that, in the presence of ATP, catalyzes the phosphorylation of d-ribulose-5-phosphate to d-ribulose 1,5-bisphosphate and ADP, a reaction important in the carbon dioxide fixation cycle of photosynthesis. TMV induced expression of a gene that encodes phosphoribulokinase in tomato plants (Itaya *et al*., 2002). Phosphoribulokinase was shown to be more abundantly transcribed in resistant soybean plants compared with susceptible plants, in response to *Pseudomonas syringae* (Zou *et al.*, 2005). In our

Table 3.7 Sequence analysis results for clones with homology to phosphoribulokinase genes.

SSH1 Contig 9	(4 clones)		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-14 a04	511	Expect = 0.0 473/485 (97%)	Triticum aestivum RNA for phosphoribulokinase gi|21840|emb|X51608.1|TAPRKGEN
SSH1-2 f07 In SSH1-14 a04	513	Expect = 6e-053 149/161 (92%)	Triticum aestivum RNA for phosphoribulokinase
		Expect = 3e-030 77/79 (97%)	T.aestivum PRK gene for ribulose-5-phosphate kinase
SSH1-3 h08 In SSH1-14 a04	432	Expect = 0.0 400/410 (97%)	Triticum aestivum RNA for **phosphoribulokinase**
SSH1-11 e04	797	Expect = 0.0 693/712 (97%)	Triticum aestivum RNA for phosphoribulokinase
Blast X Results			
Clone #	Blast X Homology Result		
SSH1-14 a04	gi|125580|sp|P26302|KPPR_WHEAT Phosphoribulokinase, chloroplast precursor (Phosphopentokinase) (PRKase) (PRK) phosphoribulokinase (EC 2.7.1.19) - wheat phosphoribulokinase [Triticum aestivum] Length = 404 Score = 324 bits (830), Expect = 1e-87 Identities = 157/165 (95%), Positives = 160/165 (96%) Frame = +3		

study, this gene seems to be induced in the compatible interaction as compared to the incompatible one. The disease related regulation of the gene may be different in wheat-yellow rust interaction from those observed in tobacco and tomato plants. The gene may still be induced as part of a

defence response but the regulation may be such that the pathogen is unable to suppress. Therefore, although it cannot confer resistance, this gene may be more up-regulated in the compatible interaction since pathogen invasion continues.

One singleton in SSH1 (D-R) show homology to a plant β-1,3-glucanase (Table 3.8). Recognized and proposed families of pathogenesis-related proteins include β-1,3-glucanases. PR-2 gene, coding for β-1,3-glucanase, confer resistance of carrot to several fungal pathogens (Edreva, 2005). Sorghum genotypes that differ in their resistance to the fungus, *Fusarium moniliforme* or aphids were analyzed for their response to stress induced by infection with the fungus, by feeding injury due to insect pests, or by mechanical wounding. The pathogenesis-related (PR) proteins, chitinases and β -1,3-glucanases, were induced in the plant tissues in all inbreds under all three stress conditions (Krishnaveni *et al.*, 1999). The supposed induction of β-1,3-glucanase in our case, is probably the result of the stress condition associated with colonization of the pathogen yellow rust.

Table 3.8 Sequence analysis results for clones with homology to beta-1,3-glucanase genes.

SSH1 Singletons	1 Clone		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-12 a05	356	Expect = 1e-031 221/270 (81%)	Triticum aestivum beta-1,3-glucanase precursor (Glb3) mRNA, complete cds gi|4741845|gb|AF112965.1|
Blast X Results			
Clone #	Blast X Homology Result		
SSH1-12 a05	gi|115442157|ref|NP_001045358.1| Os01g0941200 [Oryza sativa(japonica cultivar-group)] putative endo-1,3-beta-glucanase [Oryza sativa (japonica cultivar-group)] Os01g0941200 [Oryza sativa (japonica cultivar-group)] Length = 334 Score = 169 bits (428), Expect = 5e-41 Identities = 79/106 > (74%), Positives = 89/106 (83%) Frame = +2		

One unigene in SSH2 showed high homology to a wheat cyclophilin (Table 3.9). Cyclophilins are general folding catalysts and possess peptidyl-prolyl *cis/trans* isomerase (PPIase) activity, and they are conserved throughout eukaryotes. In their investigations about the role of *CYP1* (a cyclophilin-encoding gene in the phytopathogenic fungus *Magnaporthe grisea*, which is the causal agent of rice blast disease), Viaud *et al.* showed by targeted gene replacement that *CYP1* acted as a virulence determinant in rice blast. Cyp1 mutants show reduced virulence and are impaired in associated functions (Viaud *et al.*, 2002). More recently cyclophilin was identified as the *Arabidopsis* eukaryotic activator of AvrRpt2, a *P. syringae* effector that is a cysteine protease (Coaker *et al.*, 2005) and the mechanism of AvrRpt2 activation by the *Arabidopsis* cyclophilin ROC1 was demonstrated (Coaker *et al.*, 2006). It seems from these findings that cyclophilins may be necessary for either or resistance in different organisms. In our subtractions, cyclophilin seems to be induced in SSH2 (R-D). Induction of cyclophilin in the incompatible interaction may be related to a defence

response, in which a cyclophilin may be necessary to activate some R genes to trigger defence responses or may function in activating an *avr* gene product to render it recognizable by a corresponding R protein.

Table 3.9 Sequence analysis results for clones with homology to cyclophilin genes.

SSH2 Contig 25	2 clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH2-5 h12	471	Expect = 0.0 384/400 (96%)	Triticum aestivum cyclophilin mRNA, partial cds
SSH2-11 a07	546	Expect = 3e-079 310/360 (86%)	Triticum aestivum cyclophilin mRNA, partial cds
Blast X Results			
Clone #	Blast X Homology Result		
SSH2-5 h12	>gi|32351008|gb|AAP76508.1| cyclophilin [Triticum aestivum] cyclophilin [Triticum aestivum] Length = 233 Score = 195 bits (496), Expect = 6e-49 Identities = 98/112 (87%), Positives = 98/112 (87%) Frame = +1		

Two unigenes (2 and 3 clones) from SSH1 (D-R) were found to show homology to a wheat lipid transfer protein gene (Table 3.10). A lipid transfer protein (LTP) was shown to be up-regulated in tobacco in response to an avirulent tobacco blue mold. Additionally, the constitutive expression of a lipid transfer protein (a defensin) in susceptible tobacco plants yielded clones which were highly resistant to tobacco blue mold and black shank (Borrás *et al.*, 2007). In Arabidopsis, in a mutant screen *dir1-1* was shown to exhibit wild type local resistance to avirulent and virulent *Pseudomonas syringae*, but pathogenesis-related gene expression in uninoculated distant leaves was abolished and these mutants failed to develop SAR to virulent *Pseudomonas* and *Peronospora parasitica*; and *DIR1* encodes a putative lipid transfer protein. Maldonado *et al*. proposed that DIR1 interacted with a lipid-derived molecule to promote long distance travelling (Maldonado, 2002) Constitutive high level expression of barley lipid transfer protein 2 was shown confer resistance to bacterial pathogens in Arabidopsis (reviewed in Maleck and Lawton, 1998). Also transient over-expression of lipid transfer protein (LTP1) gene of wheat was shown to reduce the penetration efficiency (PE) of powdery mildew in a susceptible wheat cultivar (Ai-li *et al*., 2006). Apparently, lipid transfer proteins play a significant role in plant disease resistance. The induction of a lipid transfer protein homolog in SSH1 (D-R), may be related to SAR response. Maldonado had associated a lipid transfer protein with SAR in Arabidopsis. The gene is probably induced in both the tester (compatible interaction) and the driver (incompatible interaction) as compared to the basal level expression. However, in the compatible interaction, in order to enhance activation of SAR response in distant tissues, presumably by promoting long distance travelling of some signals as Maldonado *et al*. proposed, this protein may be more up-regulated.

Table 3.10 Sequence analysis results for clones with homology to lipid transfer protein genes.

SSH1 Singletons	2 Clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-7 b10	420	Expect = 3e-060 181/201 (90%)	Triticum aestivum lipid transfer protein 3 (LTP3) mRNA, complete cds gi|30385243|gb|AY226580.1|
		Expect = 0.096 23/23 (100%)	EST from a gravity versus microgravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions
Blast X Results			
Clone #	Blast X Homology Result		
SSH1-7 b10	gi|30385244|gb|AAP23941.1| lipid transfer protein 3 [Triticum aestivum] Length = 122 Score = 120 bits (302), Expect = 2e-26 Identities = 60/76 (78%), Positives = 62/76 (81%) Frame = -2		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-7 c10	739	Expect = 8e-050 161/180 (89%)	Triticum aestivum ltp9.4b gene for type 1 non specific lipid transfer protein precursor, exons 1-2
		Expect = 5e-020 82/90 (91%)	Elymus sibiricus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) mRNA, complete cds; chloroplast
Blast X Results			
Clone #	Blast X Homology Result		
SSH1-7 c10	>gi|30385244|gb|AAP23941.1| lipid transfer protein 3 [Triticum aestivum] Length = 122 Score = 101 bits (251), Expect = 4e-20 Identities = 50/74 (67%), Positives = 54/74 (72%) Frame = -2		
SSH1 Contig 20	3 clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-4 d11	345	Expect = 1e-080 245/275 (89%)	Triticum aestivum lipid transfer protein 3 (LTP3) mRNA, complete cds gi|30385243|gb|AY226580.1|
SSH1-7 b09	455	Expect = e-138 309/328 (94%)	Triticum aestivum lipid transfer protein 3 (LTP3) mRNA, complete cds
		Expect = 1.6 21/21 (100%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries
SSH1-7 b11 In SSH1-7 b09	341	Expect = e-147 273/275 (99%)	Triticum aestivum lipid transfer protein 3 (LTP3) mRNA, complete cds
Blast X Results			
Clone #	Blast X Homology Result		
SSH1-4 d11	gi|30385244|gb|AAP23941.1| lipid transfer protein 3 [Triticum aestivum] Length = 122 Score = 92.8 bits (229), Expect = 5e-18 Identities = 45/55 (81%), Positives = 47/55 (85%) Frame = -2		

One singleton in SSH2 (R-D) was homologous to a wheat peroxidase (Table 3.11). Peroxidases are among pathogenesis-related proteins (Edreva, 2005). The oxidative burst is an early response to pathogen attack leading to the production of reactive oxygen species (ROS) including hydrogen peroxide. Peroxidases function in production of ROS in plants. Bindschedler *et al.*, identified an Arabidopsis thaliana azide-sensitive but diphenylene iodonium-insensitive apoplastic oxidative burst that generates H_2O_2 in response to a *Fusarium oxysporum* cell-wall preparation. Transgenic Arabidopsis plants expressing an anti-sense cDNA encoding a type III peroxidase, exhibited an impaired oxidative burst and were more susceptible than wild-type plants to both fungal and

bacterial pathogens. Transcriptional profiling and RT-PCR analysis showed that the anti-sense (FBP1) transgenic plants had reduced levels of specific peroxidase-encoding mRNAs. These data were interpreted to indicate that peroxidases play a significant role in generating H_2O_2 during the Arabidopsis defence response and in conferring resistance to a wide range of pathogens (Bindschedler *et al.*, 2006). Seeming induction of a peroxidase gene in SSH2 (R-D) may be a contribution to HR response by ROS production, since it was induced in the incompatible interaction, in which effective HR response achieved to stop pathogen growth.

Table 3.11 Sequence analysis results for clones with homology to peroxidase genes.

SSH1 Singletons	2 Clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH2-12 a06	266	Expect = e-103 202/205 (98%)	Triticum monococcum peroxidase 6 (POX6) mRNA, complete cds gi|57635156|gb|AY857760.1|
Blast X Results			
Clone #	Blast X Homology Result		
SSH2-12 a06	gi|57635157|gb|AAW52720.1| peroxidase 6 [Triticum monococcum] Length = 322 Score = 85.9 bits (211), Expect = 7e-16 Identities = 41/42 (97%), Positives = 42/42 (100%) Frame = +3		

In SSH2 (R-D), one clone showed found highly homologous to a wheat cytochrome P450 reductase (Table 3.12). Cytochrome P450s are heme-containing enzymes that catalyze many, but not all, of the hydroxylation reactions of plant natural product biosynthesis, as well as more 'exotic' reactions, such as phenol coupling and oxidative ring closure (Dixon, 1999). Takemoto *et al.* identified *CYP82E1*, a cytochrome P450 homolog in tobacco, differentially expressed upon treatment with pathogen elicitiors. They also showed that *CYP82E1* was strongly induced in tobacco by the soybean pathogen *Pseudomonas syringae* pv. *glycinea* (avirulent on tobacco), but it was activated only slightly and in a delayed fashion by the tobacco pathogen *P. syringae* pv. *tabaci* (virulent on tobacco), which implied that the product of *CYP82E1* may be involved in disease resistance in tobacco (Takemoto *et al.*, 1999). In TMV-inoculated tobacco plants, activity of BA2H, a soluble Cyt P450 monooxygenase, was found to be induced strongly in the inoculated leaf prior to the appearance of the HR (reviewed in León *et al.*, 1995). These results suggest that these enzymes may play a role in plant defence. As SSH2 (R-D) had an incompatible interaction, i.e. resistance situation, as the tester, it can be hypothesized that a cytochrome P450 reductase was induced in the incompatible interaction with the pathogen, as a part of defence responses.

Table 3.12 Sequence analysis results for clones with homology to cytochrome P450 enzyme genes.

SSH1 Singletons	1 Clone		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH2-9 f05	551	Expect = 0.0 501/522 (95%)	Triticum aestivum mRNA for cytochrome P450 reductase (r2 gene) gi|18103932|emb|AJ303373.1|TAE303373
Blast X Results			
Clone #	Blast X Homology Result		
SSH2-9 f05	gi|18103933|emb|CAC83301.1| cytochrome P450 reductase [Triticum aestivum] Length = 703 Score = 332 bits (851), Expect = 6e-90 Identities = 165/174 (94%), Positives = 167/174 (95%) Frame = +3		
SSH2-9 f05	gi|115480641|ref|NP_001063914.1| Os09g0558900 [Oryza sativa (japonica cultivar-group)] putative NADPH-cytochrome P450 oxydoreductase isoform 3 [Oryza sativa (japonica cultivar-group)] Os09g0558900 [Oryza sativa (japonica cultivar-group)] Length = 714 Score = 306 bits (783), Expect = 5e-82 Identities = 147/170 (86%), Positives = 159/170 (93%) Frame = +3		

A unigene (2 clones) in SSH1 (D-R) library showed high homology to a plant hexose transporter (Table 1.13). An important role proposed for haustoria is uptake of nutrients from host cell. In fact, sugars were shown to pass into the haustorium from the host via a sugar transporter, a hexose-proton symport located exclusively in the haustorial plasma membrane (reviewed in Staples, 2001). Although the homology was found for a plant gene, the induced transcripts in SSH1 (D-R) may still belong to a fungal hexose transporter gene. Since a compatible interaction occurred and presumably haustoria was formed in the tester plants of SSH1 (D-R), related hexose transporter gene may have been differentially expressed in the tester plants.

Table 3.13 Sequence analysis results for clones with homology to hexose transporter genes.

SSH1 Contig 22	3 clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-5 a05	522	Expect = 2e-046 170/194 (87%)	Zea mays hexose transporter (pGlcT) mRNA, partial cds; nuclear gene for chloroplast product gi|8347247|gb|AF215854.1|AF215854
SSH1-10 a08	435	Expect = 4e-041 167/193 (86%)	Zea mays hexose transporter (pGlcT) mRNA, partial cds; nuclear gene for chloroplast product
Blast X Results			
Clone #	Blast X Homology Result		
SSH1-5 a05	>gi|53792164|dbj|BAD52797.1| putative hexose transporter [Oryzasativa (japonica cultivar-group)] Length = 513 Score = 216 bits (550), Expect = 4e-55 Identities = 106/132 (80%), Positives = 114/132 (86%) Frame = +1		

Three singletons and 1 unigene (11 clones) in SSH2 (R-D) represented clones that showed high similarity to plant H^+ transporting ATPases (Table 3.14). NIP1 is an avirulence protein secreted by

the fungal barley pathogen *Rhynchosporium secalis*. The defence-activating activity of NIP1 is mediated by barley resistance gene *Rrs1*. In addition, NIP1 has a virulence-associated function; independent of the plant genotype, it stimulates the formation of necrotic lesions, a process that appears to be based on an indirect stimulation of the plant plasma membrane H^+-ATPase activity (reviewed in Slot *et al*., 2003). Fusicoccin, the major phytotoxin from the peach and almond pathogen *Fusicoccum amygdali*, also stimulates H^+-ATPase (reviewed in Yang, 1997). Apparently, fungal elicitors or avirulence proteins have a stimulatory affect on H^+-ATPase activity. Struck *et al.* isolated the gene (*Uf-PMA1*) encoding the plasma membrane H^+-ATPase from *Uromyces fabae*, in order to investigate its role in nutrient uptake of the fungus from host cell. Unexpectedly, the *PMA1*-encoded rust protein is more similar to H^+-ATPases from plants (55% identity) than from ascomycetous fungi (36% identity) (Struck *et al*., 1998). As evident from these studies H^+-ATPases can be functional in either disease or resistance. Since pH of compartments is critical in signalling events, H+ transporting ATPases may be regulated to adjust compartment pH to direct signalling events. The induced transcripts in this case may belong to genes that function in regulating pH of cytoplasm or other compartments to direct necessary defence signalling pathways.

Table 3.14 Sequence analysis results for clones with homology to hydrogen-transporting ATPase genes.

SSH1 Singletons	4 Clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH2-7 b09	479	Expect = 1.7 70/85 (82%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28710) mRNA, complete cds gi|30689308|ref|NM_113791.2|
		Expect = 1.7 70/85 (82%)	Arabidopsis thaliana putative adenosine triphosphatase (At3g28710) mRNA, complete cds
Blast X Results			
Clone #	Blast X Homology Result		
	>gi|124360985|gb|ABN08957.1| H+-transporting two-sector ATPase, C (AC39) subunit [Medicago truncatula] Length = 351 Score = 77.0 bits (188), Expect(2) = 4e-14 Identities = 39/62 (62%), Positives = 44/62 (70%) Frame = -1		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH2-8 f11	385	Expect = e-129 295/313 (94%),	Triticum aestivum plasma membrane H+-ATPase (ha1) mRNA, complete cds
Blast X Results			
Clone #	Blast X Homology Result		
SSH2-8 f11	>gi|56112362|gb|AAV71150.1| plasma membrane H+-ATPase [Triticum aestivum] Length = 951 Score = 155 bits (391), Expect(2) = 2e-44 Identities = 78/80 (97%), Positives = 78/80 (97%) Frame = -3		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result

Table 3.14 *(Continued)*

SSH2-11 b04	473	Expect = 0.43 25/26 (96%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28715) mRNA, complete cds
		Expect = 1.7 21/21 (100%)	PREDICTED: Pan troglodytes similar to RNA binding motif protein, Y-linked, family 1, member F (LOC736159), mRNA
Blast X Results			
Clone #	Blast X Homology Result		
SSH2-11 b04	>gi|124360985|gb|ABN08957.1| H+-transporting two-sector ATPase, C (AC39) subunit [Medicago truncatula] Length = 351 Score = 42.4 bits (98), Expect(2) = 0.003 Identities = 17/23 (73%), Positives = 23/23 (100%) Frame = -1		
SSH2 Contig 44	11 clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH2-11 b02	439	Expect = 1e-010 74/86 (86%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28710) mRNA, complete cds
		Expect = 1e-010 74/86 (86%)	Arabidopsis thaliana putative adenosine triphosphatase (At3g28710)mRNA, complete cds
SSH2-11 d01 In SSH2-11 b02	642	Expect = 3e-018 162/199 (81%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28715) mRNA, complete cds
SSH2-11 c02	600	Expect = 4e-011 157/199 (78%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28715) mRNA, complete cds
SSH2-11 c03 In SSH2-11 c02	457	Expect = 0.007 61/73 (83%)	Oryza sativa (japonica cultivar-group) Os01g0587000 (Os01g0587000) mRNA, complete cds
		Expect = 6.5 23/24 (95%)	Canis familiaris masticatory myosin heavy chain 2M gene, complete cds
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH2-11 b03 In SSH2-11 c02	207	Expect = 0.70 24/25 (96%)	Homo sapiens BAC clone CTD-2507I16 from 2, complete sequence
		Expect = 2.8 20/20 (100%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6895 genomic sequence
SSH2-11 a02 In SSH2-11 c02	467	Expect = 3e-011 72/83 (86%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28715) mRNA, complete cds
		Expect = 2e-006 Identities = 70/83 (84%)	Arabidopsis thaliana putative protein kinase (At3g23310) mRNA,complete cds
SSH2-11 e02	444	Expect = 3e-017 106/125 (84%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28710) mRNA, complete cds
SSH2-11 d02 In SSH2-11 c02	636	Expect = 4e-008 73/86 (84%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28715) mRNA, complete cds
SSH2-11 c01 In SSH2-11 c02	474	Expect = 1e-010 74/86 (86%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28715) mRNA, complete cds
SSH2-11 e01	833	Expect = 0.77 28/30 (93%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28710) mRNA, complete cds
SSH2-11 a03 In SSH2-11 e01	605	Expect = 0.002 44/50 (88%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28715) mRNA, complete cds
Blast X Results			
Clone #	Blast X Homology Result		
SSH2-11 b02	>gi|124360985|gb|ABN08957.1| H+-transporting two-sector ATPase, C (AC39) subunit [Medicago truncatula] Length = 351 Score = 125 bits (315), Expect = 6e-28 Identities = 63/75 (84%), Positives = 68/75 (90%) Frame = -2		

A singleton transcript homologous to a putative NBS-LRR protein from Triticum aestivum seems to be induced in SSH1 (D-R) (Table 3.15). As explained in Section 1.4 plant resistance genes confer resistance to pathogens by triggering downstream defence signalling and consequently defence responses. In an incompatible interaction, R protein successfully recognizes the corresponding *Avr* gene product of the pathogen and defence responses are thus activated. R genes are usually constitutively expressed but there are cases of induction in incompatible interactions. A sunflower CC-NBS-LRR resistance gene analogue was shown to be induced during incompatible interaction with *Plasmopara halstedii* (Radwan *et al.*, 2005). The *Xa1* gene of rice, which confers resistance to Japanese race 1 of *Xanthomonas oryzae* pv. *oryzae*, the causal pathogen of bacterial blight (BB), was found to be induced upon inoculation with a bacterial pathogen and wound (Yoshimura, 1998). As there is no a general rule for induction of R genes specifically in incompatible interactions, assuming that the induced transcript in SSH1 (D-R) belongs to an *R* gene, it can be hypothesized that since the plant is unable to activate effective defence responses, it may be inducing the R gene as a reaction to the stress condition caused by the progressing pathogen invasion.

Table 3.15 Sequence analysis results for clones with homology to NBS-LRR genes.

SSH1 Singletons	1 Clone		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-5 b07	568	Expect = 0.008 34/37 (91%)	Triticum aestivum partial mRNA for Putative NBS-LRR protein
Blast X Results			
Clone #	Blast X Homology Result		
SSH1-5 b07	>gi|28555909|emb|CAD45034.1| NBS-LRR disease resistance protein homologue [Hordeum vulgare] Length = 909 Score = 102 bits (253), Expect = 1e-20 Identities = 59/112 (52%), Positives = 68/112 (60%), Gaps = 2/112 (1%) Frame = +1		

In SSH2 (R-D), a singleton transcript and one unigene (2 clones) were found homologous to ubiquitin protein ligases (Table 3.16). The homology of the unigene was for Arabidopsis ubiquitin protein ligase. There was also one unigene (4 clones) in SSH2 (R-D) library, which showed high homology to a ubiquitin-conjugating enzyme E2 (Table 3.16). In ubiquitin degradation system, ubiquitin-conjugating enzyme (E2) catalyzes the attachment of ubiquitin to the substrate protein. E3 ligases specifically recognize target proteins and promote their degradation. Different roles for ubiquitin pathway in plant-pathogen interactions were reported. Several putative ubiquitin ligases were identified as defence regulators. In addition, a combination of genetic screens and gene-silencing technologies has identified subunits and proposed regulators of SCF ubiquitin ligases as

essential components of resistance (R)-gene-mediated resistance (reviewed in Devoto *et al*., 2003). AvrPtoB is a type III effector expressed by the plant pathogen *Pseudomonas syringae* pv. *tomato*

Table 3.16 Sequence analysis results for clones with homology to ubiquitin protein ligase and ubiquitin-conjugating enzyme genes.

SSH1 Singletons	1 Clone		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH2-7 c07	597	Expect = 0.55 22/22 (100%)	Human DNA sequence from clone RP3-468O1 on chromosome 20 Contains the 3' end of the ITCH gene for itchy homolog E3 ubiquitin protein ligase (mouse), a ferredoxin 1 (FDX1) pseudogene, the 5' end of the DNCL2A gene for cytoplasmic dynein light polypeptide 2A, two novel genes and two CpG islands, complete sequence
Blast X Results			
Clone #	Blast X Homology Result		
	>gi|110224438|ref|YP_443846.2| ubiquitin E3 ligase ICP0 [Cercopithecine herpesvirus 16] ubiquitin E3 ligase ICP0 [Cercopithecine herpesvirus 16] Length = 713 Score = 35.0 bits (79), Expect = 2.5 Identities = 25/56 (44%), Positives = 25/56 (44%), Gaps = 5/56 (8%) Frame = +2		
SSH2 Contig 24	2 clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH2-5 f04	401	Expect = 2e-005 68/81 (83%)	Arabidopsis thaliana ZTL (ZEITLUPE); ubiquitin-protein ligase (ZTL) mRNA, complete cds
SSH2-5 g03	362	Expect = 2e-005 68/81 (83%)	Arabidopsis thaliana ZTL (ZEITLUPE); ubiquitin-protein ligase (ZTL) mRNA, complete cds
Blast X Results			
Clone #	Blast X Homology Result		
SSH2-5 f04	>gi|18423971|ref|NP_568855.1| ZTL (ZEITLUPE); ubiquitin-protein ligase [Arabidopsis thaliana] Adagio protein 1 (Protein ZEITLUPE) (LOV kelch protein 1) (Flavin-binding kelch repeat F-box protein 1-like protein 2) (FKF1-like protein 2) (F-box only protein 2b) (FBX2b) (Clock-associated PAS protein ZTL) FKF1-like protein 2 [Arabidopsis thaliana] clock-associated PAS protein ZTL; ZEITLUPE [Arabidopsis thaliana] Adagio 1 [Arabidopsis thaliana] FKF1-like protein 2 [Arabidopsis thaliana] LOV kelch protein 1 [Arabidopsis thaliana] At5g57360/MSF19_2 [Arabidopsis thaliana] Length = 609 Score = 191 bits (484), Expect = 1e-47 Identities = 88/125 (70%), Positives = 103/125 (82%) Frame = +1		
SSH2 Contig 50	4 clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH2-3 c05		Expect = e-102 222/232 (95%)	Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds
		Expect = 4e-065 171/185 (92%)	Oryza sativa (japonica cultivar-group) OsRad6 mRNA for Rad6,complete cds
		Expect = 4e-031 159/188 (84%)	partial cDNA sequence from a Lambda ZAP II normalized full-length cDNA library of differentiating xylem from Eucalyptus gunnii
SSH2-9 d04	279	Expect = e-130 241/242 (99%)	Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds
SSH2-9 c04	279	Expect = e-132 242/242 (100%)	Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds
SSH2-8 h07	267	Expect = e-132 242/242 (100%)	Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds
Blast X Results			
Clone #	Blast X Homology Result		
SSH2-3 c05	>gi|136640|sp|P25866|UBC2_WHEAT Ubiquitin-conjugating enzyme E2-17kDa (Ubiquitin-protein ligase) (Ubiquitin carrier protein) ubiquitin carrier protein Length = 152 Score = 158 bits (399), Expect = 1e-37 Identities = 76/79 (96%), Positives = 76/79 (96%) Frame = -3		

and has a carboxy-terminal domain that is an E3 ubiquitin ligase. Deletion of this domain allows an amino-terminal region of AvrPtoB ($AvrPtoB_{1–387}$) to be detected by certain tomato varieties leading to immunity-associated programmed cell death. Rosebrock *et al.* showed that a host kinase, Fen, physically interacted with $AvrPtoB_{1–387}$ and is responsible for activating the plant immune response. The AvrPtoB E3 ligase specifically ubiquitinates Fen and promotes its degradation in a proteasome-dependent manner. This degradation leads to disease susceptibility in Fen-expressing tomato lines (Rosebrock *et al.*, 2007). E3 ubiquitin ligases also function in disease resistance. Many R genes require SGT1 and RAR1 for their function. SGT1 associates with RAR1 and SKP1, a component of the SCF-type of E3 complexes. Suppression of the tobacco (*Nicotiana benthamiana*) SKP1 gene leads to the loss of N-mediated resistance to Tobacco mosaic virus (reviewed in Wang *et al*., 2006). As these examples suggest, ubiquitin pathway can be functional either in resistance or in pathogenicity. This mechanism exerts its effect by promoting degradation of target proteins, and the final effect depends on the function of the degraded protein. Ubiquitin pathway may be functional at some stage of the defence response of wheat against yellow rust and related genes may have been upregulated upon recognition of the pathogen in the incompatible interaction, i.e. the tester sample of SSH2 (R-D). Therefore, the clones that were homologous to ubiquitin-conjugating and ubiquitin-protein ligase enzymes may represent ubiquitin pathway proteins may be components of a ubiquitin degradation pathway that functions in resistance of wheat to yellow rust. In this case, ubiquitin pathway may be promoting degradation of effector molecules from the pathogen or it may assist in degradation of host proteins, which may need to be degraded for their function in defence.

In SSH2 (R-D) library, one unigene (2 clones) showed homology to a wheat glutathione S-transferase gene (Table 3.17). Glutathione S-transferase detoxifies the products of lipid membrane peroxidation and other products of cellular oxidative stress. The expression of glutathione S-transferase has been detected in incompatible interactions (reviewed in Hammond-Kosack, 1996). Dean *et al*. showed induction of two glutathione S-transferase genes in tobacco upon infection by *Colletotrichum destructivum* and *Colletotrichum orbiculare*, and found a statistically significant increase in susceptibility of tobacco to *C. orbiculare* infection when one of these genes was silenced by virus-induced gene silencing (Dean *et al*., 2005). Seeming induction of a glutathione S-transferase homolog in SSH2 (R-D) is reasonable because previous studies associated induction of this gene with plant disease resistance. The gene that is represented by the clone from SSH2 (R-D) library may have been induced due to the resistance response in the tester plants, which are resistant.

Table 3.16 Sequence analysis results for clones with homology to glutathione-S-transferase genes.

SSH2 Contig 4	2 clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH2-11 f03	470	Expect = 5e-013 60/66 (90%)	Wheat gstA1 gene for glutathione-S-transferase
SSH2-5 c11 In SSH2-11 f03	151	Expect = 1e-010 70/81 (86%)	Triticum aestivum mRNA for glutathione transferase (gstf6b gene)
Blast X Results			
Clone #	Blast X Homology Result		
SSH2-11 f03	>gi|232200|sp|P30111|GSTF2_WHEAT Glutathione S-transferase 2 (GST class-phi) glutathione transferase [Triticum aestivum] Length = 291 Score = 39.7 bits (91), Expect = 0.054 Identities = 19/29 (65%), Positives = 20/29 (68%) Frame = -2		

Two singleton transcripts from SSH1 (D-R) and one unigene (7 clones) from SSH2 (R-D) were found to have high homology to GTP-binding proteins (Table 3.17). Small GTP-binding proteins exist in eukaryotes from yeast to animals to plants and constitute a superfamily whose members function as molecular switches that cycle between ‘‘active’’ and ‘‘inactive’’ states (Ma, 2007). The results of a study by Kawasaki *et al*. indicated that the small GTP-binding protein Rac was a regulator of reactive oxygen species production and cell death in rice (Kawasaki *et al*., 1999). Legendre *et al*. found results that supported involvement of GTP- binding proteins in elicitor signal transduction in soybean cells (Legendre, 1992). Depending on their results Sano and Ohashi suggested that the defence signal-transduction system consists of a complicated and finely tuned network of several regulatory factors, including cytokinins, salicylic acid, and small GTP-binding proteins (Sano and Ohashi, 1995). Unpublished data by Gao *et al*., report that a small Ras-related GTP-binding protein gene Ta-Ran1, was up-regulated in wheat (*Triticum aestivum*, L.) roots in response to inorganic phosphate starvation stress. In living systems, many processes are controlled or regulated by signal transduction pathways and there are many conserved mechanisms or components even in between distantly related organisms. Previous studies about GTP-binding proteins in plant-pathogen interactions indicate they are important components of plant defence against pathogens. The clones induced in SSH2 (R-D) may belong to a GTP-binding protein gene that is involved in defence signalling in wheat against yellow rust. On the other hand the clones induced in SSH1 (D-R), which also gave homology to a wheat GTP-binding protein, may belong to a GTP-binding protein gene that is functional in signalling in pathogenesis. It is known that virulent rust fungi are able to manipulate host metabolism or processes for their proliferation. This gene may be functional in some signalling leading to shift(s) in host metabolic events for pathogen growth or in suppression of host defences.

Table 3.17 Sequence analysis results for clones with homology to GTP-binding protein genes.

SSH1 Singletons	2 Clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-15 g07	390	Expect = 0.0 356/362 (98%)	Triticum aestivum GTP-binding protein mRNA, complete cds
SSH1-15 g07	>gi|37548544|gb|AAP43929.1| GTP-binding protein [Triticum aestivum] Length = 232 Score = 243 bits (619), Expect = 3e-63 Identities = 116/120 (96%), Positives = 119/120 (99%) Frame = +2		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-15 h06	543	Expect = 2e-022 153/181 (84%)	Triticum aestivum GTP-binding protein mRNA, complete cds
Blast X Results			
Clone #	Blast X Homology Result		
	>gi|37548544|gb|AAP43929.1| GTP-binding protein [Triticum aestivum] Length = 232 Score = 89.0 bits (219), Expect(2) = 4e-25 Identities = 47/80 (58%), Positives = 54/80 (67%) Frame = +1		
SSH2 Contig 60	7 clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH2-9 c12	378	Expect = e-136 310/333 (93%)	Triticum aestivum small Ras-related GTP-binding protein mRNA,complete cds
SSH2-3 f03 In SSH2-9 c12	373	Expect = e-158 322/334 (96%)	Triticum aestivum small Ras-related GTP-binding protein mRNA, complete cds
SSH2-7 f10	383	Expect = e-165 330/341 (96%)	Triticum aestivum small Ras-related GTP-binding protein mRNA, complete cds
SSH2-9 a12 In SSH2-7 f10	396	Expect = 5e-065 284/333 (85%)	Triticum aestivum small Ras-related GTP-binding protein mRNA,complete cds
SSH2-9 b12	519	Expect = e-139 313/333 (93%)	Triticum aestivum small Ras-related GTP-binding protein mRNA,complete cds
SSH2-9 c11	557	Expect = e-145 318/336 (94%)	Triticum aestivum small Ras-related GTP-binding protein mRNA, complete cds
SSH2-9 a11 In SSH2-9 c11	267	Expect = 1e-021 150/180 (83%)	Triticum aestivum small Ras-related GTP-binding protein mRNA, complete cds
Blast X Results			
Clone #	Blast X Homology Result		
SSH2-9 c12	>gi|16903082|gb|AAL30396.1|AF433653_1 small Ras-related GTP-binding protein [Triticum aestivum] small Ran-related GTP-binding protein [Triticum aestivum] Length = 221 Score = 228 bits (581), Expect = 8e-59 Identities = 103/110 (93%), Positives = 105/110 (95%) Frame = -2		

One unigene (5 clones) from SSH2 (R-D), represented clones showing high similarity to a putative MAPKKK (Table 3.18). Previously it was shown that knockout of Arabidopsis MAP kinase 4 (mpk4) lead to accumulation of SA and activation of SA-dependent resistance, and hypersusceptibility to herbivore feeding and infection by an ET/JA pathway-inducing fungus (reviewed in Andreasson *et al*., 2005). Yang *et al*. showed that NtMEK2, a MAPK kinase, was upstream of salicylic acid-induced protein kinase (SIPK) and wounding-induced protein kinase (WIPK), which are two tobacco MAPKs that are activated by various pathogens or pathogen-derived elicitors, and their studies demonstrated that a plant MAPK cascade controls multiple defence responses against pathogen invasion (Yang *et al*., 2001). Negative regulation of defence responses by two different MAPK cascades in *Arabidopsis* was also suggested. MAPKs are

thought to be to be one of the converging points in the defence-signalling network (Zhang and Klessig, 2001). The induction of a putative MAPKKK in SSH2 (R-D) is probably related with the defence response of the tester plants. MAPKKKs are kinases that are upstream of MAPKs in signal transduction cascades. Therefore, this clone may belong to a MAPKKK gene that functions in a MAPK cascade to trigger defence responses.

Two singleton transcripts from SSH1 (D-R) displayed homology to a wheat glutamine synthetase (Table 3.19). Glutamine synthetase is the primary enzyme for assimilation of ammonia in plants; it catalyzes the formation of glutamine from glutamate, ammonia, and ATP. Viral and bacterial infection of tobacco leaves and oxidative stress was shown to induce GS1 (cytosolic glutamine synthetase) expression (Pageau *et al*., 2006) Glutamine synthetase of plants is the physiological target of tabtoxinine-β -lactam, a toxin produced by several disease-causing pathovars of *Pseudomonas syringae* (Langston *et al*., 1987). These findings imply that Glutamine synthetases may play an important role in defence responses. In SSH1 (D-R) tester plants were unable to stop pathogen infection, which causes a continuous stress condition. Not all defence responses are inactive during a compatible interaction, but rather induced responses are insufficient to achieve full resistance. A glutamine synthetase gene may have been upregulated at a higher degree in the compatible interaction than in the incompatible one as a response to continuing stress status.

Table 3.18 Sequence analysis results for clones with homology to MAPK cascade related genes.

SSH2 Contig 22	5 clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH2-5 e03	282	Expect = 5e-089 232/253 (91%)	Oryza sativa (japonica cultivar-group) Os04g0660500 (Os04g0660500) mRNA, complete cds
SSH2-10 g10	582	Expect = 6e-016 158/195 (81%)	Arabidopsis thaliana MAPKKK6; ATP binding / kinase/ protein kinase/protein serine/threonine kinase/ protein-tyrosine kinase (MAPKKK6) mRNA, complete cds
SSH2-12 a10 In SSH2-10 g10	580	Expect = e-111 453/532 (85%)	Oryza sativa (japonica cultivar-group) Os04g0660500 (Os04g0660500)mRNA, complete cds
		Expect = 9e-006 51/58 (87%)	Arabidopsis thaliana MAPKKK6; ATP binding / kinase/ protein kinase/protein serine/threonine kinase/ protein-tyrosine kinase(MAPKKK6) mRNA, complete cds
SSH2-5 g05 In SSH2-10 g10	517	Expect = 6e-016 158/195 (81%)	Arabidopsis thaliana MAPKKK6; ATP binding / kinase/ protein kinase/protein serine/threonine kinase/ protein-tyrosine kinase (MAPKKK6) mRNA, complete cds
SSH2-10 f11	734	Expect = 5e-011 78/91 (85%)	Zea mays clone EL01N0524D03.d mRNA sequence
Blast X Results			
Clone #	Blast X Homology Result		
SSH2-10 g10	>gi|19387284|gb|AAL87195.1|AF480497_23 putative MAP3K epsilon protein kinase [Oryza sativa (japonica cultivar-group)] Length = 1264 Score = 334 bits (857), Expect = 1e-90 Identities = 171/176 (97%), Positives = 172/176 (97%) Frame = +1		

Table 3.19 Sequence analysis results for clones with homology to glutamine synthetase genes.

SSH1 Singletons	2 Clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-1 a05	420	Expect = 0.0 388/399 (97%)	Triticum aestivum plastid glutamine synthetase isoform GS2c (GS2) mRNA, complete cds; nuclear gene for plastid product
Blast X Results			
Clone #	Blast X Homology Result		
	>gi|71362640|gb|AAZ30062.1| plastid glutamine synthetase isoform GS2c [Triticum aestivum] Length = 427 Score = 269 bits (688), Expect = 3e-71 Identities = 130/132 (98%), Positives = 131/132 (99%) Frame = +3		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-2 b05		Expect = e-166 323/331 (97%)	Triticum aestivum plastid glutamine synthetase isoform GS2c GS2)mRNA, complete cds; nuclear gene for plastid product
Blast X Results			
Clone #	Blast X Homology Result		
	>gi|71362640|gb|AAZ30062.1| plastid glutamine synthetase isoform GS2c [Triticum aestivum] Length = 427 Score = 233 bits (595), Expect = 6e-60 Identities = 109/110 (99%), Positives = 110/110 (100%) Frame = +3		

Two singletons and one unigene (4 clones) were found homologous to *S*-adenosylmethionine decarboxylase, the homologies of the unigene and one of the singletons and were for wheat in SSH1 (D-R) *S*-adenosylmethionine decarboxylase (Table 3.20). A homolog of *S*-adenosylmethionine decarboxylase proenzyme (potato) was found to be induced upon overexpression of the disease resistance gene *Pto* in Tomato, and also in human and/or fruit fly immune response (Mysore *et al*., 2003). *S*-adenosylmethionine decarboxylase is a key enzyme in polyamine metabolism. Increased levels of polyamines accompanied by increased activity of this biosynthetic enzyme were shown in barley reacting hypersensitively to the powdery mildew fungus *B. graminis* f. sp. *hordei*. Polyamine metabolism has also long been known to be altered in plants responding to abiotic environmental stress (reviewed in Walters, 2003). The enzyme was found to be upregulated in SSH1 (D-R). Although previous studies associated induction of activity of this enzyme with resistance, since a compatible interaction results in a continuous stress condition, this enzyme may have been up-regulated to a greater extent in the compatible than in the incompatible wheat-yellow rust interaction. The upregulation of this enzyme may be controlled by some signalling that is not completely inactive during disease progress in susceptible plants.

Table 3.20 Sequence analysis results for clones with homology to S-adenosylmethionine decarboxylase genes.

SSH1 Singletons	2 Clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-8 a01	506	Expect = 3e-036 147/169 (86%)	H.chilense x T.turgidum conv. durum (Tritordeum) mRNA for S-adenosylmethionine decarboxylase
Blast X Results			
Clone #	Blast X Homology Result		
	>gi|28566347|gb|AAO43185.1| S-adenosylmethionine decarboxylase leader [Narcissus pseudonarcissus] Length = 51 Score = 46.2 bits (108), Expect = 7e-04 Identities = 23/35 (65%), Positives = 26/35 (74%), Gaps = 1/35 (2%) Frame = -3		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-11 a05	872	Expect = 1e-027 293/367 (79%)	Triticum aestivum S-adenosylmethionine decarboxylase precursor, mRNA, complete cds
		Expect = 5e-005 32/33 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions
Blast X Results			
Clone #	Blast X Homology Result		

Table 3.20 *(continued)*

	>gi|4325045|gb|AAD17232.1| S-adenosylmethionine decarboxylase precursor [Triticum aestivum] Length = 392 Score = 109 bits (272), Expect = 2e-22 Identities = 59/88 (67%), Positives = 68/88 (77%) Frame = -1		
SSH1 Contig 24	4 clones		
Blast N Results			
Clone #	Length of Read Sequence	E-Value and identities	Blast N Homology Result
SSH1-5 e11	359	Expect = e-163 321/330 (97%)	Triticum aestivum S-adenosylmethionine decarboxylase precursor,mRNA, complete cds
SSH1-4 a10	439	Expect = 0.0 384/402 (95%)	Triticum aestivum S-adenosylmethionine decarboxylase precursor, mRNA, complete cds
SSH1-4 g05	516	Expect = e-119 281/300 (93%)	H.chilense x T.turgidum conv. durum (Tritordeum) mRNA for S-adenosylmethionine decarboxylase
SSH1-8 a02	520	Expect = e-145 418/468 (89%)	H.chilense x T.turgidum conv. Durum (Tritordeum) mRNA for S-adenosylmethionine decarboxylase
Blast X Results			
Clone #	Blast X Homology Result		
SSH1-5 e11	>gi|4325045|gb|AAD17232.1| S-adenosylmethionine decarboxylase precursor [Triticum aestivum] Length = 392 Score = 204 bits (520), Expect = 1e-51 Identities = 106/113 (93%), Positives = 107/113 (94%) Frame = -3		

CHAPTER IV

CONCLUSION

Studies of plant-pathogen interactions are gaining importance especially because the agricultural production of the plants that constitute the main human food and animal feed is becoming insufficient to supply rapidly growing world human and live-stock populations. The production is mainly limited by the shortage of fertile agricultural land. Classical breeding practices to grow more productive plants bring no absolute solution. Genetic engineering for improving crop plants seems to be indispensable in the future. However, genetics and molecular biology of these crop plants, especially in terms of biotic and abiotic stresses need to be well understood in order for genetic intervention to be a useful tool.

In this study, it was aimed to identify genes that were differentially expressed in compatible and incompatible interactions of yellow rust pathogen, *Puccinia striiformis* f. sp. *tritici*, with its host plant, wheat, *Triticum aestivum*. However, unlike common strategies, which compare either compatible or incompatible interactions with controls that involve no interactions, the comparison was done between a compatible and an incompatible interaction, and vice versa.

In order to obtain the differential expression profile in a compatible interaction as compared to an incompatible one, we generated SSH1 (D-R) subtracted library; and in order to obtain the differential expression profile in an incompatible interaction as compared to a compatible one, we generated SSH2 (R-D) subtracted library.

In SSH1 (D-R) library, 8.35 % of clones showed homology to genes related to metabolism and energy; 2.97 %, to genes related to signal transduction; 0.14 %, of clones, to apoptosis related genes; 0.78 %, to defence related genes; 0.35 % stress related genes; 0.42 %, to genes associated with protein degradation and ubiquitinylation; 0.71 %, to genes related with transcription and translation; 0.35 %, to genes related with cellular organization; 6.23 %, to genes of other functions; 21.23 % to genes of unknown function; 46.92 % to RubisCo genes; 4.53 % to chlorophyll A/B binding protein genes; 0.28 % ribosomal RNA genes; 6.02 % to sequences homologous to adaptor used in SSH; and 0.71 % to vector sequences.

On the other hand in SSH2 (R-D) library, 14.88 % of clones showed homology to genes related to metabolism and energy; 7.30 %, to genes related to signal transduction; 0.90 %, to defence related genes; 1.08 % to stress related genes; 3.43 %, to genes associated with protein degradation and ubiquitinylation; 1.89 %, to genes related with transcription and translation; 1.98 %, to genes

related with cellular organization; 25.52 %, to genes of other functions; 20.83 % to genes of unknown function; 10.36 %, to RubisCo genes; 1.89 %, to chlorophyll A/B binding protein genes; 3.97 %, to ribosomal RNA genes; 4.15 %, to sequences homologous to adaptor used in SSH; and 1.17 %, to vector sequences.

The libraries constructed in this study contain sequences that show significant similarity to a variety of genes that were associated with plant-pathogen interactions in previous studies. Some of these genes/gene families are well characterized in terms of structure and function, or significant amount of data about the roles they play in related mechanisms. However, for most of them, mechanisms or modes of action remain to be elucidated. The differential expression of homologs of these genes was discussed in Chapter III. Supposed induction of these homologs in this study is important first because it suggests that the subtraction strategy worked in mining differential expression profile. Second, these homologs present potential starting points for further studies; taking the functions of the original genes, to which they show homology, as reference, investigations can be designed to elucidate mechanisms of these homologs. Loss of function experiments, for instance, could be conducted using these clones in order to investigate their function, or, experiments to identify interactors of the products of these genes could be designed.

Clones, which showed homology to genes, for which no function in plant-pathogen interaction was suggested in previous studies, may still be important. They may belong to yet unidentified genes that play role in plant-pathogen interactions, or specifically in wheat-yellow rust interactions. Together with supporting data from other differential expression profiling studies (e.g. microarray, two dimensional protein gel electrophoresis etc.), these clones may be candidate novel genes, for which further studies can be done to elucidate their functions in plant disease.

REFERENCES

Ai-li L, Cheng-Sheng M, Rong-Hua Z, Zhi-Ying M, Ji-Zeng J **(2006)** Assessment of Lipid Transfer Protein (LTP1) Gene in Wheat Powdery Mildew Resistance *Agricultural Sciences in China* 4:241.

Andreasson E, Jenkins T, Brodersen P, Thorgrimsen S, Petersen NHT Zhu S, Qiu J, Micheelsen P, Rocher A, Petersen M, Newman MA, Nielsen HB, Hirt H, Somssich I, Mattsson O, Mundy J **(2005)** The MAP kinase substrate MKS1 is a regulator of plant defence responses *The EMBO Journal* 24:2579–2589.

Belkhadir Y, Subramaniam R, Dangl JL **(2004)** Plant disease resistance protein signalling: NBS–LRR proteins and their partners *Current Opinion in Plant Biology* 7:391–399.

Bindschedler LV, Dewdney J, Blee KA, Stone JM, Asai T, Plotnikov J, Denoux C, Hayes T, Gerrish C, Davies DR, Ausubel FM, Bolwell GP **(2006)** Peroxidase-dependent apoplastic oxidative burst in Arabidopsis required for pathogen resistance *The Plant Journal* 47:851–863.

Borrás O, Chacón O, Portieles R, Collazo C, López Y, Borroto CJ, Ayra C, Pujol M, Rodríguez R, Sunchís M, Simón M, Oliva O, Crespo JA, García H, Andino V **(2007)** Identification of new disease resistance genes in tobacco via functional genomics *Biotecnología Aplicada* 24:76-78.

Chen XM. **(2005)** Epidemiology and control of stripe rust [*Puccinia striiformis* f. sp. *tritici*] on wheat *Can. J. Plant Pathol*. 27: 314–337.

Clontech **(2002)** Clontech PCR-Select^{TM} cDNA Subtraction Kit User Manual PT1117-1 (PR22926).

Coaker G, Falick A, Staskawicz B **(2005)** Activation of a Phytopathogenic Bacterial Effector Protein by a Eukaryotic Cyclophilin *Science* 308: 548-550.

Coaker G, Zhu G, Ding Z, Van Doren SR, Staskawicz B **(2006)** Eukaryotic cyclophilin as a molecular switch for effector activation *Molecular Microbiology* 61:1485–1496.

Dean JD, Goodwin PH, Hsiang T **(2005)** Induction of glutathione S-transferase genes of Nicotiana benthamiana following infection by Colletotrichum destructivum and *C. orbiculare* and involvement of one in resistance *Journal of Experimental Botany* 56:1525–1533.

Devoto A, Muskett PR, Shirasu K **(2003)** Role of ubiquitination in the regulation of plant defence against pathogens *Current Opinion in Plant Biology* 6: 307-311.

Diatchenko L, Lau YC, Campbell AP, Chenchik A, Moqadam F, Huang B, Lukyanov S, Lukyanov K, Gurskaya N, Sverdlov ED, Siebert PD **(1996)** Suppression subtractive hybridization: A method for generating differentially regulated or tissue-specific cDNA probes and libraries *Proc. Natl. Acad. Sci. USA*. 93:6025–6030.
Dixon RA **(1999)** Plant natural products: the molecular genetic basis of biosynthetic diversity *Current Opinion in Biotechnology* 10:192–197.

Dubcovsky J, Dvorak J **(2007)** Genome Plasticity a Key Factor in the Success of Polyploid Wheat Under Domestication *Science* 316:1862-1866.

Eckardt **(2006)** Identification of Rust Fungi Avirulence Elicitors *The Plant Cell* 18:1-3.

Edreva A **(2005)** Pathogenesis-related proteins: research progress in the last 15 years *Gen. Appl. Plant Physiology*. 31:105-124.

Enjalbert J, Duan X, Leconte M, Hovmøller MS, De vallavieille-pope C **(2005)** Evidence of local adaptation of wheat yellow rust (*Puccinia striiformis* f. sp. *tritici*) within France *Molecular Ecology* 14:2065–2073.

Funnell DL, Schardl CL **(2001**) Plant Defences against Fungal Attack: Recognition and Signal Transduction *Encyclopedia of Life Sciences* 1-4.

Hammond-Kosack KE, Jones JDG **(1996)** Resistance Gene-Dependent Plant Defense Responses *The Plant Cell* 8:1773-1791.

HGCA (Home-Grown Cereals Authority) **(2007)**
http://www.hgca.com/hgca/wde/diseases/Yellow%20rust/Yrcyc.html
[cited 24 October 2007].

Hye-Yeon S, Hee-Yeon P, Dong-Hyouk W, Choon-Hwan L, Young-Hwan M **(2007)** Transgenic Plants Overexpressing Arabidopsis *Zeaxanthin Epoxidase* Promote Osmotic-Stress Tolerance *Botany&Plant Biology 2007 Joint Congress* Abstract ID:1624.

IGC (International Grains Council) **(2007)** Grain Market Report Summary GMR No. 372.

Itaya A, Matsuda Y, Gonzales RA, Nelson RS, Ding B **(2002)** *Potato spindle tuber viroid* Strains of Different Pathogenicity Induces and Suppresses Expression of Common and Unique Genes in Infected Tomato *MPMI* 15:990–999.

İGEME (Undersecretariat of the Prime Ministry for Foreign Trade) **(2007)** Cereals.

Jones DA, Takemoto D **(2004)** Plant innate immunity – direct and indirect recognition of general and specific pathogen-associated molecules *Current Opinion in Immunology* 16:48–62.

Kanedal T, Fujiwaral S, Takail R, Takayamal S, Isogail A, Che F **(2007)** Identification of genes involved in induction of plant hypersensitive cell death *Plant Biotechnology* 24, pp.191–200.

Kawasaki T, Henmi K, Ono E, Hatakeyama S, Iwano M, Satoh H, Shimamoto K **(1999)** The small GTP-binding protein Rac is a regulator of cell death in plants *Plant Biology* 96:10922–10926.

Kolmer JA **(2005)** Tracking wheat rust on a continental scale *Current Opinion in Plant Biology* 8:441–449.

Kong L, Anderson JM, Ohm HW **(2005)** Induction of wheat defense and stress-related genes in response to *Fusarium graminearum. Genome* 48: 29–40.

Krishnaveni S, Muthukrishnan S, Liang GH, Wilde G, Manickam A **(1999)** Induction of chitinases and β-1,3-glucanases in resistant and susceptible cultivars of sorghum in response to insect attack, fungal infection and wounding *Plant Science* 144:9–16.

Lam E, Kato N, Lawton M **(2001)** Programmed cell death, mitochondria and the plant hypersensitive response *Nature* 411:848-853.

Langston-Unkefer PJ, Robinson AC, Knight TJ, Durbin RD **(1987)** Inactivation of Pea Seed Glutamine Synthetase by the Toxin, Tabtoxinine-β-lactam *The Journal of Biological Chemistry* 262:1608-1613.

Legendre L, Heinstein PF, Low PS **(1992)** Evidence for Participation of GTP-binding Proteins in Elicitation of the Rapid Oxidative Burst in Cultured SoybeaCne lls *The Journal of Biolohical Chemistry* 267:20140-20147.

León J, Lawton MA, Raskin I **(1995)** Hydrogen Peroxide Stimulates Salicylic Acid Biosynthesis in Tobacco *Plant Physiol.* 108: 1673-1 678.

Liu J, Liu X, Dai L, Wang G **(2007)** Recent Progress in Elucidating the Structure, Function and Evolution of Disease Resistance Genes in Plants *Journal of Genetics and Genomics* 34:765-776.

Lopez C, Soto M, Restrepo S, Pie'gul B, Cooke R, Delseny M, Tohme J, Verdier V **(2005)** Gene expression profile in response to Xanthomonas axonopodis pv. manihotis infection in cassava using a cDNA microarray *Plant Molecular Biology* 57:393–410.

Ma, Q **(2007)** Small GTP-binding Proteins and their Functions in Plants *J Plant Growth Regul.* DOI 10.1007/s00344-007-9022-7.

Maldonado AM, Doerner P, Dixon RA, Lamb CJ, Cameron RK **(2002)** A putative lipid transfer protein involved in systemic resistance signalling in *Arabidopsis. Nature.* 419:399-403

Maleck K, Lawton K **(1998)** Plant strategies for resistance to pathogens *Current Opinion in Biotechnology* 9:208-213.

Marsalis MA, Natalie NP **(2006)** Leaf, Stem and Stripe Rust Diseases of Wheat *University of Nebraska–Lincoln Extension Publications* G1245.

Martin GB **(1999)** Functional analysis of plant disease resistance genes and their downstream effectors *Current Opinion in Plant Biology* 2:273-279.

Mendgen K, Hahn M **(2002)** Plant infection and the establishment of fungal biotrophy Review *Trends in Plant Science* 7:352-356.

Mitchell HJ, Ayliffe MA, Rashid KY, Pryor AJ **(2006)** A rust-inducible gene from flax (fis1) is involved in proline catabolism *Planta* 223: 213–222.

Moeder W, Pozo O, Navarre AD, Martin GB, Klessig DF **(2006)** Aconitase plays a role in regulating resistance to oxidative stress and cell death in Arabidopsis and *Nicotiana benthamiana Plant. Mol Biol*. 63:273–287.

Mysore KS, D'Ascenzo MD, He X, Martin GB **(2003)** Overexpression of the Disease Resistance Gene *Pto* in Tomato Induces Gene Expression Changes Similar to Immune Responses in Human and Fruitfly1[w]. *Plant Physiology*132:1901–1912.

Neu C, Keller B, Feuillet C **(2003)** Cytological and Molecular Analysis of the Hordeum vulgare–Puccinia triticina Nonhost Interaction *MPMI* 16:626–633.

OECD (Organisation for Economic Co-operation and Development) **(1999)** Consensus Document on the Biology of *Triticum aesticum* (Bread Wheat). Serious on Harmonization of Regulatory Oversight in Biotechnology 9:11.

Ohashis Y, Sano H **(1995)** Involvement of small GTP-binding proteins in defense signal-transduction pathways of higher plants *Proc. Natl. Acad. Sci. USA.* 92: 4138-4144.

Pageau K, Reisdorf-Cren M, Morot-Gaudry JF, Masclaux-Daubresse1 C **(2006)** The two senescence-related markers, GS1 (cytosolic glutamine synthetase) and GDH (glutamate dehydrogenase), involved in nitrogen mobilization, are differentially regulated during pathogen attack and by stress hormones and reactive oxygen species in *Nicotiana tabacum* L. leaves. *Journal of Experimental Botany* 57:547–557.

Panstruga R **(2003)** Establishing compatibility between plants and obligate biotrophic pathogens *Current Opinion in Plant Biology* 6:320–326.

Perez-Garcia A, Canovas M, Gallardo F, Hirel B, Vicente A **(1995)** Differential Expression of Glutamine Synthetase Isoforms in Tomato Detached Leaflets Infected with *Pseudomonas syringae* pv. *tomato*. *The American Phytopathological Society MPMI* 8:96-103.

Radwan O, Mouzeyar S, Nicolas P, Bouzidi MF **(2005)** Induction of a sunflower CC-NBS-LRR resistance gene analogue during incompatible interaction with Plasmopara halstedii *Journal of Experimental Botany* 56:567–575.

Rosebrock TR, Zeng L, Brady JJ, Abramovitch RB, Xiao F, Martin GB **(2007)** A bacterial E3 ubiquitin ligase targets a host protein kinase to disrupt plant immunity *Nature* 448:370-374.

Sambrook J, Fritsch EF, Maniatis T **(1989)** Molecular Cloning 2nd edn. New York, NY: Cold Spring Harbor Laboratory Press.

Shen G, Adam Z, Zhang H **(2007)** The E3 ligase AtCHIP ubiquitylates FtsH1, a component of the chloroplast FtsH protease, and affects protein degradation in chloroplasts *The Plant Journal* 52:309–321.

Singh RP, Huerta-Espino J **(2001)** *Research Highlights of the CIMMYT Wheat Program, 1999-2000* CIMMYT. Mexico, D.F. pp:38-40.

Slot KAE, Burg HA, Kloks CPAM, Hilbers CW, Knogge W, Papavoine CHM **(2003)** Solution Structure of the Plant Disease Resistance-triggering Protein NIP1 from the Fungus *Rhynchosporium secalis* Shows a Novel _-Sheet Fold *The Journal of Biological Chemistry* 278:45730-45736.

Staples RC **(2001)** Nutrients for a rust fungus: the role of haustoria *Trends in Plant Science* Research Update 6:496-498.

Staskawicz BJ **(2001)** Genetics of Plant-Pathogen Interactions Specifying Plant Disease Resistance *Plant Physiology* 125:73–76.

Struck C, Siebels C, Wernitz ORM, Hahn M **(1998)** The Plasma Membrane H+-ATPase from the Biotrophic Rust Fungus Uromyces fabae: Molecular Characterization of the Gene (PMA1) and Functional Expression of the Enzyme in Yeast *Molecular Plant-Microbe Interaction* 6:458-465.

Strza K, Kostecha-Guga A, Latowski D **(2003)** Carotenoids and Environmental Stress in Plants: Significance of Carotenoid-Mediated Modulation of Membrane Physical Properties *Russian Journal of Plant Physiology* 50:168–172.

Szabo LJ, Bushnell WR **(2001)** Hidden robbers: The role of fungal haustoria in parasitism of plants *PNAS* Commentary 98:7654–7655.

Takemotol D, Hayashi M, Dokel N, Nishimura M, Kawakita K **(1999)** Molecular Cloning of a Defense-Response-Related Cytochrome P450 Gene from Tobacco Plant Cell Physiol. 40:1232-1242.

Tanno K, Willcox G **(2006)** How Fast Was Wild Wheat Domesticated? Brevia *Science* 311:1886.

Thara VK, Fellers JP, Zhou J **(2003)** In planta induced genes of Puccinia triticina *Molecular Plant Pathology* 4:51–56.

USDA (United States Department of Agriculture) **(2007)**
http://www.ars.usda.gov/SP2UserFiles/ad_hoc/36400500Cerealrusts/pst-lcyc.gif
[cited 4 October 2007].

Tu Z, He G, Li KX, Chen MJ, Chang J, Chen L, Yao Q, Liu DP, Ye H, Shi J, Wu X **(2005)** An improved system for competent cell preparation and high efficiency plasmid transformation using different *Escherichia coli* strains. *Electronic Journal of Biotechnology* [online] 15 April 2005, vol. 8 no.1
[cited 22 October 2007]. Available at:
http://www.ejbiotechnology.info/content/vol8/issue1/full/8/index.html ISSN: 0717-3458.

Viaud MC, Balhadère PV, Talbot NJ **(2002)** A *Magnaporthe grisea* Cyclophilin Acts as a Virulence Determinant during Plant Infection *The Plant Cell* 14:917–930.

Voegele RT, Struck C, Hahn M, Mendgen K **(2001)** The role of haustoria in sugar supply during infection of broad bean by the rust fungus Uromyces fabae *Proc. Natl. Acad. Sci. USA*. 98:8133–8138.

Walters DR **(2003)** Polyamines and plant disease *Phytochemistry* 64 97–107.

Wanga Y, Pi L, Chen X, Chakrabarty PK, Jiang J, De Leon AL, Liu G, Li L, Benny U, Oard J, Ronal PC, Songa W **(2006)** Rice XA21 Binding Protein 3 Is a Ubiquitin Ligase Required for Full Xa21-Mediated Disease Resistance W OA *The Plant Cell* 18:3635–3646.

Yang K, Liu Y, Zhang S **(2001)** Activation of a mitogen-activated protein kinase pathway is involved in disease resistance in tobacco *Proc. Natl. Acad. Sci. USA* 98:741–746.

Yang Y, Shah J, Klessig DF **(1997)** Signal perception and transduction in plant defense responses *Genes & Development* 11:1621-1639.

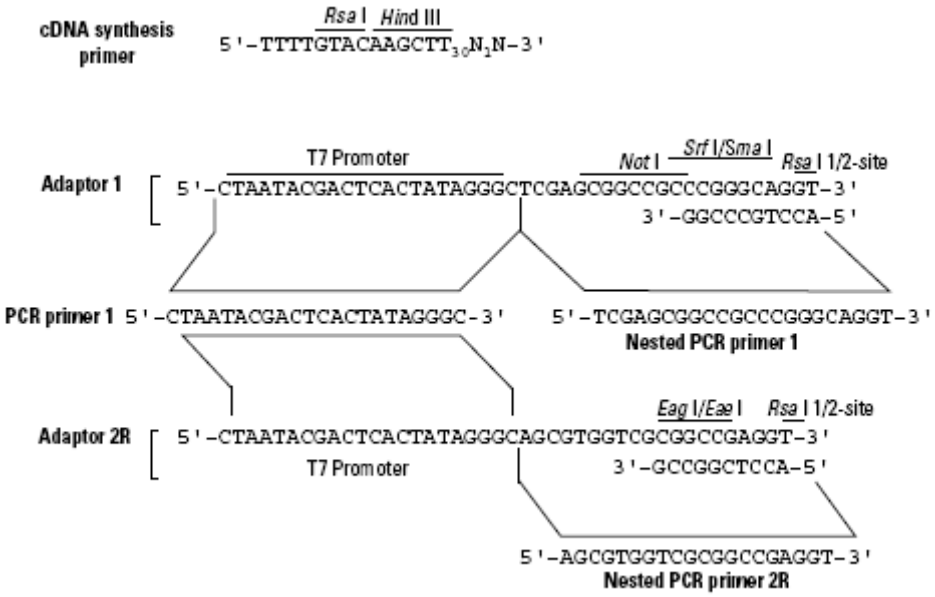
Zhang S, Klessing DF **(2001)** MAPK cascades in plant defense signalling *TRENDS in Plant Science* 6:520-527.

Yoshimura S, Yamanouchi U, Katayose Y, Toki S, Wang Z, Kono I, Kurata N, Yano M, Iwata N, Sasaki T **(1998)** Expression of Xa1, a bacterial blight-resistance gene in rice, is induced by bacterial inoculation *Proc. Natl. Acad. Sci. USA*.95:1663–1668.

Zou J, Rodriguez-Zas S, Aldea M, Li M, Zhu J, Gonzales DO, Vodkin LO, DeLucia E, Clough SJ **(2005)** Expression Profiling Soybean Response to *Pseudomonas syringae* Reveals New Defense-Related Genes and Rapid HR-Specific Downregulation of Photosynthesis *MPMI* 18:1161–1174.

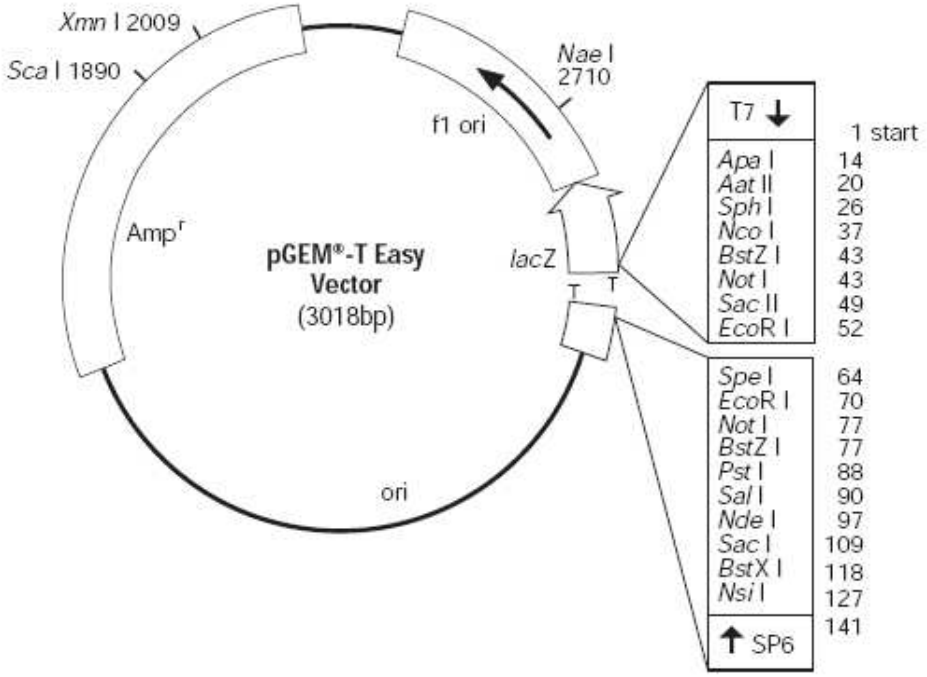
APPENDIX A

Sequences of cDNA synthesis primer , Adaptor 1, Adaptor 2R, PCR primer 1 and nested PCR primer 2R.

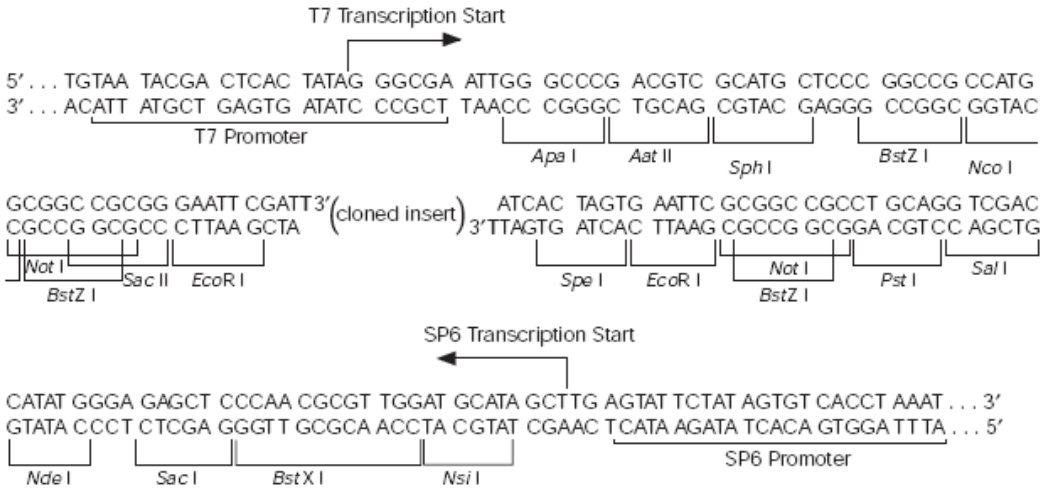


APPENDIX B

The circle map of pGEM®-T Easy Vector (pGEM®-T and pGEM®-T Easy Vector Systems Technical Manual).



The promoter and multiple cloning sequence of pGEM®-T Easy Vector (pGEM®-T and pGEM®-T Easy Vector Systems Technical Manual).



APPENDIX C

Contig assemblies of SSH1 (D-R) library generated by Cap3 contig assembly program.

•

Number of segment pairs = 979110; number of pairwise comparisons = 939
'+' means given segment; '-' means reverse complement

Overlaps Containments No. of Constraints Supporting Overlap

```
******************** Contig 1 ********************
U_HW-SSH1_10a12.b1.seq+
        U_HW-SSH1_10a06.b1.seq+ is in U_HW-SSH1_10a12.b1.seq+
U_HW-SSH1_10b06.b1.seq+
        U_HW-SSH1_10c06.b1.seq+ is in U_HW-SSH1_10b06.b1.seq+
******************** Contig 2 ********************
U_HW-SSH1_10d10.b1.seq+
        U_HW-SSH1_12e06.b1.seq- is in U_HW-SSH1_10d10.b1.seq+
        U_HW-SSH1_10d09.b1.seq+ is in U_HW-SSH1_10d10.b1.seq+
******************** Contig 3 ********************
U_HW-SSH1_10e05.b1.seq+
        U_HW-SSH1_10f09.b1.seq+ is in U_HW-SSH1_10e05.b1.seq+
        U_HW-SSH1_5e06.b1.seq+ is in U_HW-SSH1_10e05.b1.seq+
******************** Contig 4 ********************
U_HW-SSH1_10h10.b1.seq+
U_HW-SSH1_11h04.b1.seq+
        U_HW-SSH1_9a08.b1.seq+ is in U_HW-SSH1_11h04.b1.seq+
        U_HW-SSH1_2a09.b1.seq+ is in U_HW-SSH1_11h04.b1.seq+
        U_HW-SSH1_4d03.b1.seq+ is in U_HW-SSH1_11h04.b1.seq+
******************** Contig 5 ********************
U_HW-SSH1_11b04.b1.seq+
        U_HW-SSH1_4c09.b1.seq+ is in U_HW-SSH1_11b04.b1.seq+
******************** Contig 6 ********************
U_HW-SSH1_11c07.b1.seq+
        U_HW-SSH1_2c01.b1.seq+ is in U_HW-SSH1_11c07.b1.seq+
U_HW-SSH1_14e01.b1.seq+
        U_HW-SSH1_14g01.b1.seq+ is in U_HW-SSH1_14e01.b1.seq+
******************** Contig 7 ********************
U_HW-SSH1_11e05.b1.seq+
        U_HW-SSH1_11e09.b1.seq+ is in U_HW-SSH1_11e05.b1.seq+
        U_HW-SSH1_11f09.b1.seq+ is in U_HW-SSH1_11e05.b1.seq+
******************** Contig 8 ********************
U_HW-SSH1_11h09.b1.seq+
        U_HW-SSH1_3g08.b1.seq+ is in U_HW-SSH1_11h09.b1.seq+
******************** Contig 9 ********************
U_HW-SSH1_14a04.b1.seq+
        U_HW-SSH1_2f07.b1.seq+ is in U_HW-SSH1_14a04.b1.seq+
        U_HW-SSH1_3h08.b1.seq+ is in U_HW-SSH1_14a04.b1.seq+
U_HW-SSH1_11e04.b1.seq-
******************** Contig 10 ********************
U_HW-SSH1_14d01.b1.seq+
U_HW-SSH1_10b02.b1.seq+
******************** Contig 11 ********************
U_HW-SSH1_16b12.b1.seq+
        U_HW-SSH1_1a09.b1.seq+ is in U_HW-SSH1_16b12.b1.seq+
U_HW-SSH1_13c09.b1.seq+
U_HW-SSH1_13b07.b1.seq+
******************** Contig 12 ********************
U_HW-SSH1_16c04.b1.seq+
U_HW-SSH1_16c03.b1.seq+

******************** Contig 13 ********************
U_HW-SSH1_16g05.b1.seq+
        U_HW-SSH1_16g06.b1.seq+ is in U_HW-SSH1_16g05.b1.seq+
U_HW-SSH1_16h05.b1.seq+
        U_HW-SSH1_16h06.b1.seq+ is in U_HW-SSH1_16h05.b1.seq+
******************** Contig 14 ********************
U_HW-SSH1_16g09.b1.seq+
U_HW-SSH1_16f09.b1.seq+
        U_HW-SSH1_11b03.b1.seq+ is in U_HW-SSH1_16f09.b1.seq+
******************** Contig 15 ********************
U_HW-SSH1_2f05.b1.seq+
        U_HW-SSH1_2f06.b1.seq+ is in U_HW-SSH1_2f05.b1.seq+
U_HW-SSH1_16h09.b1.seq+
        U_HW-SSH1_2h02.b1.seq+ is in U_HW-SSH1_16h09.b1.seq+
U_HW-SSH1_14a02.b1.seq+
******************** Contig 16 ********************
U_HW-SSH1_3d09.b1.seq+
        U_HW-SSH1_3d10.b1.seq+ is in U_HW-SSH1_3d09.b1.seq+
******************** Contig 17 ********************
U_HW-SSH1_3h05.b1.seq+
        U_HW-SSH1_4a02.b1.seq+ is in U_HW-SSH1_3h05.b1.seq+
******************** Contig 18 ********************
U_HW-SSH1_4b09.b1.seq+
        U_HW-SSH1_4a09.b1.seq+ is in U_HW-SSH1_4b09.b1.seq+
******************** Contig 19 ********************
U_HW-SSH1_4c04.b1.seq+
        U_HW-SSH1_15f09.b1.seq+ is in U_HW-SSH1_4c04.b1.seq+
        U_HW-SSH1_12a09.b1.seq+ is in U_HW-SSH1_4c04.b1.seq+
U_HW-SSH1_15h12.b1.seq+
        U_HW-SSH1_11h03.b1.seq+ is in U_HW-SSH1_15h12.b1.seq+
U_HW-SSH1_2g01.b1.seq+
******************** Contig 20 ********************
U_HW-SSH1_4d11.b1.seq+
U_HW-SSH1_7b09.b1.seq+
        U_HW-SSH1_7b11.b1.seq+ is in U_HW-SSH1_7b09.b1.seq+
******************** Contig 21 ********************
U_HW-SSH1_4e11.b1.seq+
        U_HW-SSH1_11e01.b1.seq+ is in U_HW-SSH1_4e11.b1.seq+
U_HW-SSH1_1e08.b1.seq+
U_HW-SSH1_9g10.b1.seq+
        U_HW-SSH1_4g10.b1.seq+ is in U_HW-SSH1_9g10.b1.seq+
******************** Contig 22 ********************
U_HW-SSH1_5a05.b1.seq+
U_HW-SSH1_10a08.b1.seq+
******************** Contig 23 ********************
U_HW-SSH1_5a07.b1.seq+
U_HW-SSH1_14h08.b1.seq+
******************** Contig 24 ********************
U_HW-SSH1_5e11.b1.seq+
U_HW-SSH1_4a10.b1.seq+
U_HW-SSH1_4g05.b1.seq+
        U_HW-SSH1_8a02.b1.seq+ is in U_HW-SSH1_4g05.b1.seq+
******************** Contig 25 ********************
U_HW-SSH1_5f09.b1.seq+
        U_HW-SSH1_5g09.b1.seq+ is in U_HW-SSH1_5f09.b1.seq+
******************** Contig 26 ********************
U_HW-SSH1_6e09.b1.seq-
        U_HW-SSH1_5g12.b1.seq+ is in U_HW-SSH1_6e09.b1.seq-
        U_HW-SSH1_14b01.b1.seq+ is in U_HW-SSH1_6e09.b1.seq-
        U_HW-SSH1_5g05.b1.seq- is in U_HW-SSH1_14b01.b1.seq+
        U_HW-SSH1_15c06.b1.seq- is in U_HW-SSH1_14b01.b1.seq+
        U_HW-SSH1_14c02.b1.seq+ is in U_HW-SSH1_14b01.b1.seq+
        U_HW-SSH1_14c01.b1.seq+ is in U_HW-SSH1_14b01.b1.seq+
U_HW-SSH1_9d11.b1.seq+
        U_HW-SSH1_9c10.b1.seq+ is in U_HW-SSH1_9d11.b1.seq+
******************** Contig 27 ********************
U_HW-SSH1_7a02.b1.seq+
U_HW-SSH1_8g09.b1.seq+
******************** Contig 28 ********************
U_HW-SSH1_7d09.b1.seq+
U_HW-SSH1_7e09.b1.seq+
******************** Contig 29 ********************
U_HW-SSH1_7g05.b1.seq+
        U_HW-SSH1_7f05.b1.seq+ is in U_HW-SSH1_7g05.b1.seq+
        U_HW-SSH1_7e04.b1.seq+ is in U_HW-SSH1_7f05.b1.seq+
        U_HW-SSH1_7h05.b1.seq+ is in U_HW-SSH1_7g05.b1.seq+
        U_HW-SSH1_7g06.b1.seq+ is in U_HW-SSH1_7g05.b1.seq+
        U_HW-SSH1_7f06.b1.seq+ is in U_HW-SSH1_7g06.b1.seq+
U_HW-SSH1_7g08.b1.seq+
        U_HW-SSH1_7f07.b1.seq+ is in U_HW-SSH1_7g08.b1.seq+
        U_HW-SSH1_7g07.b1.seq+ is in U_HW-SSH1_7g08.b1.seq+
******************** Contig 30 ********************
U_HW-SSH1_7h01.b1.seq+
U_HW-SSH1_7h02.b1.seq+
        U_HW-SSH1_7g01.b1.seq+ is in U_HW-SSH1_7h02.b1.seq+
        U_HW-SSH1_7g03.b1.seq+ is in U_HW-SSH1_7h02.b1.seq+
        U_HW-SSH1_7g02.b1.seq+ is in U_HW-SSH1_7h02.b1.seq+
U_HW-SSH1_7f02.b1.seq+
U_HW-SSH1_7h03.b1.seq+
******************** Contig 31 ********************
U_HW-SSH1_8b02.b1.seq+
        U_HW-SSH1_9h04.b1.seq+ is in U_HW-SSH1_8b02.b1.seq+
        U_HW-SSH1_12b09.b1.seq+ is in U_HW-SSH1_9h04.b1.seq+
******************** Contig 32 ********************
U_HW-SSH1_8d07.b1.seq+
        U_HW-SSH1_8e07.b1.seq+ is in U_HW-SSH1_8d07.b1.seq+
******************** Contig 33 ********************
U_HW-SSH1_8f06.b1.seq+
        U_HW-SSH1_9h09.b1.seq+ is in U_HW-SSH1_8f06.b1.seq+
******************** Contig 34 ********************
U_HW-SSH1_9f03.b1.seq+
        U_HW-SSH1_9h03.b1.seq+ is in U_HW-SSH1_9f03.b1.seq+
******************** Contig 35 ********************
U_HW-SSH1_9h08.b1.seq+
U_HW-SSH1_9g05.b1.seq+
******************** Contig 36 ********************
U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_7h07.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_8e05.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_12b01.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_10d01.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_12f03.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_7e08.b1.seq+ is in U_HW-SSH1_12f03.b1.seq+
        U_HW-SSH1_10f08.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_10b12.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_12b10.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_10g07.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_10a01.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_10e12.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_6c10.b1.seq+ is in U_HW-SSH1_10e12.b1.seq+
        U_HW-SSH1_11g09.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_4c07.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_8f05.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_8g01.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_8h04.b1.seq+ is in U_HW-SSH1_8g01.b1.seq+
        U_HW-SSH1_6c03.b1.seq+ is in U_HW-SSH1_10e11.b1.seq+
        U_HW-SSH1_6c06.b1.seq+ is in U_HW-SSH1_6c03.b1.seq+
U_HW-SSH1_11d04.b1.seq+
        U_HW-SSH1_12c04.b1.seq+ is in U_HW-SSH1_11d04.b1.seq+
        U_HW-SSH1_1d04.b1.seq+ is in U_HW-SSH1_11d04.b1.seq+
        U_HW-SSH1_4a12.b1.seq+ is in U_HW-SSH1_11d04.b1.seq+
U_HW-SSH1_11e08.b1.seq+
        U_HW-SSH1_13g05.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
        U_HW-SSH1_13g12.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
        U_HW-SSH1_12c11.b1.seq- is in U_HW-SSH1_11e08.b1.seq+
        U_HW-SSH1_10d11.b1.seq+ is in U_HW-SSH1_12c11.b1.seq-
        U_HW-SSH1_12b03.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
        U_HW-SSH1_14c10.b1.seq- is in U_HW-SSH1_11e08.b1.seq+
        U_HW-SSH1_10e07.b1.seq- is in U_HW-SSH1_11e08.b1.seq+
        U_HW-SSH1_10b11.b1.seq- is in U_HW-SSH1_11e08.b1.seq+
        U_HW-SSH1_10h08.b1.seq- is in U_HW-SSH1_11e08.b1.seq+
        U_HW-SSH1_12c02.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
        U_HW-SSH1_13f09.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
        U_HW-SSH1_8f10.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
        U_HW-SSH1_12c10.b1.seq- is in U_HW-SSH1_11e08.b1.seq+
        U_HW-SSH1_10d12.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
        U_HW-SSH1_13d06.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
        U_HW-SSH1_3b03.b1.seq+ is in U_HW-SSH1_13d06.b1.seq+
```

U_HW-SSH1_15h10.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_14c09.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_16f11.b1.seq- is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_13g10.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_13g11.b1.seq+ is in U_HW-SSH1_13g10.b1.seq+
U_HW-SSH1_13h11.b1.seq+ is in U_HW-SSH1_13g11.b1.seq+
U_HW-SSH1_11d08.b1.seq- is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_10e10.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_15h11.b1.seq+ is in U_HW-SSH1_10e10.b1.seq+
U_HW-SSH1_3h12.b1.seq+ is in U_HW-SSH1_10e10.b1.seq+
U_HW-SSH1_3h07.b1.seq+ is in U_HW-SSH1_10e10.b1.seq+
U_HW-SSH1_9b12.b1.seq+ is in U_HW-SSH1_10e10.b1.seq+
U_HW-SSH1_15g10.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_10e09.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_13g06.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_3g07.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_13f06.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_3h11.b1.seq+ is in U_HW-SSH1_13f06.b1.seq+
U_HW-SSH1_13g08.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_5g03.b1.seq+ is in U_HW-SSH1_13g08.b1.seq+
U_HW-SSH1_10h11.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_13e06.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_13h06.b1.seq+ is in U_HW-SSH1_13e06.b1.seq+
U_HW-SSH1_3e08.b1.seq+ is in U_HW-SSH1_13h06.b1.seq+
U_HW-SSH1_13e08.b1.seq+ is in U_HW-SSH1_13e06.b1.seq+
U_HW-SSH1_3d01.b1.seq- is in U_HW-SSH1_13e08.b1.seq+
U_HW-SSH1_9f05.b1.seq+ is in U_HW-SSH1_13e08.b1.seq+
U_HW-SSH1_4d05.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_11h01.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_5e09.b1.seq+ is in U_HW-SSH1_11h01.b1.seq+
U_HW-SSH1_11f02.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_5h11.b1.seq+ is in U_HW-SSH1_11f02.b1.seq+
U_HW-SSH1_3g11.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_11d02.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_13h09.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_11f08.b1.seq- is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_3d12.b1.seq- is in U_HW-SSH1_11f08.b1.seq-
U_HW-SSH1_8h09.b1.seq- is in U_HW-SSH1_11f08.b1.seq-
U_HW-SSH1_5f04.b1.seq- is in U_HW-SSH1_11f08.b1.seq-
U_HW-SSH1_14a11.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_4a04.b1.seq+ is in U_HW-SSH1_14a11.b1.seq+
U_HW-SSH1_13f02.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_13g09.b1.seq+ is in U_HW-SSH1_13f02.b1.seq+
U_HW-SSH1_11f01.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_11g10.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_13f08.b1.seq+ is in U_HW-SSH1_11g10.b1.seq+
U_HW-SSH1_5f05.b1.seq+ is in U_HW-SSH1_11g10.b1.seq+
U_HW-SSH1_5g04.b1.seq+ is in U_HW-SSH1_5f05.b1.seq+
U_HW-SSH1_8e12.b1.seq+ is in U_HW-SSH1_11g10.b1.seq+
U_HW-SSH1_13g07.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_1f06.b1.seq+ is in U_HW-SSH1_13g07.b1.seq+
U_HW-SSH1_2h09.b1.seq+ is in U_HW-SSH1_13g07.b1.seq+
U_HW-SSH1_9d12.b1.seq- is in U_HW-SSH1_2h09.b1.seq+
U_HW-SSH1_3a03.b1.seq+ is in U_HW-SSH1_9d12.b1.seq-
U_HW-SSH1_3f09.b1.seq+ is in U_HW-SSH1_13g07.b1.seq+
U_HW-SSH1_16a08.b1.seq+ is in U_HW-SSH1_11e08.b1.seq+
U_HW-SSH1_10a10.b1.seq+ is in U_HW-SSH1_16a08.b1.seq+
U_HW-SSH1_10a09.b1.seq+ is in U_HW-SSH1_10a10.b1.seq+
********** Contig 37 **********
U_HW-SSH1_10h09.b1.seq-
U_HW-SSH1_13e04.b1.seq+ is in U_HW-SSH1_10h09.b1.seq-
********** Contig 38 **********
U_HW-SSH1_11b01.b1.seq-
U_HW-SSH1_2b06.b1.seq+ is in U_HW-SSH1_11b01.b1.seq-
U_HW-SSH1_4h10.b1.seq+ is in U_HW-SSH1_11b01.b1.seq-
U_HW-SSH1_5a01.b1.seq+ is in U_HW-SSH1_11b01.b1.seq-
U_HW-SSH1_14g03.b1.seq+ is in U_HW-SSH1_11b01.b1.seq-
U_HW-SSH1_16e06.b1.seq- is in U_HW-SSH1_11b01.b1.seq-
U_HW-SSH1_11d07.b1.seq+ is in U_HW-SSH1_11b01.b1.seq-
U_HW-SSH1_2g09.b1.seq+ is in U_HW-SSH1_11b01.b1.seq-
U_HW-SSH1_10a02.b1.seq+ is in U_HW-SSH1_11b01.b1.seq-
U_HW-SSH1_10d03.b1.seq+ is in U_HW-SSH1_11b01.b1.seq-
U_HW-SSH1_5b12.b1.seq+ is in U_HW-SSH1_11b01.b1.seq-
U_HW-SSH1_12e02.b1.seq+ is in U_HW-SSH1_11b01.b1.seq-
U_HW-SSH1_12h02.b1.seq+ is in U_HW-SSH1_12e02.b1.seq+
U_HW-SSH1_12f06.b1.seq+ is in U_HW-SSH1_12e02.b1.seq+
U_HW-SSH1_6e07.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_9a07.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_5a02.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_5a06.b1.seq+ is in U_HW-SSH1_5a02.b1.seq+
U_HW-SSH1_4c02.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_10c11.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_15h07.b1.seq+ is in U_HW-SSH1_10c11.b1.seq+
U_HW-SSH1_5c04.b1.seq+ is in U_HW-SSH1_15h07.b1.seq+
U_HW-SSH1_14e04.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_14f12.b1.seq+ is in U_HW-SSH1_14e04.b1.seq+
U_HW-SSH1_12g09.b1.seq+ is in U_HW-SSH1_14e04.b1.seq+
U_HW-SSH1_3a04.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_9c07.b1.seq+ is in U_HW-SSH1_3a04.b1.seq+
U_HW-SSH1_9b07.b1.seq+ is in U_HW-SSH1_3a04.b1.seq+
U_HW-SSH1_15h08.b1.seq+ is in U_HW-SSH1_9b07.b1.seq+
U_HW-SSH1_15h09.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_5e04.b1.seq+ is in U_HW-SSH1_15h09.b1.seq+
U_HW-SSH1_4h06.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_4h05.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_4a08.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_2d08.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_5b06.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_14h01.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_12g07.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_9h11.b1.seq+ is in U_HW-SSH1_12g07.b1.seq+
U_HW-SSH1_7b08.b1.seq+ is in U_HW-SSH1_12g07.b1.seq+
U_HW-SSH1_2c08.b1.seq+ is in U_HW-SSH1_12f06.b1.seq+
U_HW-SSH1_7b12.b1.seq+ is in U_HW-SSH1_2c08.b1.seq+
U_HW-SSH1_11d11.b1.seq- is in U_HW-SSH1_2c08.b1.seq+
U_HW-SSH1_5e12.b1.seq+ is in U_HW-SSH1_2c08.b1.seq+
U_HW-SSH1_4f10.b1.seq+ is in U_HW-SSH1_2c08.b1.seq+
U_HW-SSH1_5b02.b1.seq+ is in U_HW-SSH1_2c08.b1.seq+
U_HW-SSH1_10g12.b1.seq+
U_HW-SSH1_11a07.b1.seq+ is in U_HW-SSH1_10g12.b1.seq+
U_HW-SSH1_11c06.b1.seq+ is in U_HW-SSH1_10g12.b1.seq+
U_HW-SSH1_11e07.b1.seq- is in U_HW-SSH1_10g12.b1.seq+
U_HW-SSH1_10e03.b1.seq+ is in U_HW-SSH1_10g12.b1.seq+
U_HW-SSH1_13c04.b1.seq+ is in U_HW-SSH1_10g12.b1.seq+
U_HW-SSH1_4g09.b1.seq+ is in U_HW-SSH1_10g12.b1.seq+
U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_2c12.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_4e01.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_8c06.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_8d06.b1.seq+ is in U_HW-SSH1_8c06.b1.seq+
U_HW-SSH1_4g08.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_2g04.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_8f04.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_7b03.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_2d06.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_9e07.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_8d04.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_8c04.b1.seq+ is in U_HW-SSH1_8d04.b1.seq+
U_HW-SSH1_12e04.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_2c06.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_2a04.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_2a06.b1.seq+ is in U_HW-SSH1_2a04.b1.seq+
U_HW-SSH1_2b04.b1.seq+ is in U_HW-SSH1_2a04.b1.seq+
U_HW-SSH1_7b04.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_11c09.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_16h12.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_12e03.b1.seq+ is in U_HW-SSH1_16h12.b1.seq+
U_HW-SSH1_2g05.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_2c11.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_2g06.b1.seq+ is in U_HW-SSH1_2c11.b1.seq+
U_HW-SSH1_7b07.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_8h06.b1.seq+ is in U_HW-SSH1_7b07.b1.seq+
U_HW-SSH1_7c07.b1.seq+ is in U_HW-SSH1_7b07.b1.seq+
U_HW-SSH1_13a07.b1.seq- is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_9g01.b1.seq+ is in U_HW-SSH1_13a07.b1.seq-
U_HW-SSH1_15g11.b1.seq+ is in U_HW-SSH1_9g01.b1.seq+
U_HW-SSH1_12g10.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_7c04.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_11g06.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_4c03.b1.seq+ is in U_HW-SSH1_11g06.b1.seq+
U_HW-SSH1_7d11.b1.seq+ is in U_HW-SSH1_11g06.b1.seq+
U_HW-SSH1_7a08.b1.seq+ is in U_HW-SSH1_11g06.b1.seq+
U_HW-SSH1_15g09.b1.seq+ is in U_HW-SSH1_7a08.b1.seq+
U_HW-SSH1_13e02.b1.seq- is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_13g01.b1.seq- is in U_HW-SSH1_13e02.b1.seq-
U_HW-SSH1_16d07.b1.seq- is in U_HW-SSH1_13e02.b1.seq-
U_HW-SSH1_13f03.b1.seq- is in U_HW-SSH1_13e02.b1.seq-
U_HW-SSH1_4d12.b1.seq+ is in U_HW-SSH1_13e02.b1.seq-
U_HW-SSH1_5b04.b1.seq+ is in U_HW-SSH1_13e02.b1.seq-
U_HW-SSH1_5e03.b1.seq+ is in U_HW-SSH1_5b04.b1.seq+
U_HW-SSH1_2g08.b1.seq+ is in U_HW-SSH1_13e02.b1.seq-
U_HW-SSH1_3h02.b1.seq+ is in U_HW-SSH1_2g08.b1.seq+
U_HW-SSH1_5c11.b1.seq+ is in U_HW-SSH1_2g08.b1.seq+
U_HW-SSH1_9a06.b1.seq+ is in U_HW-SSH1_5c11.b1.seq+
U_HW-SSH1_7c11.b1.seq+ is in U_HW-SSH1_2g08.b1.seq+
U_HW-SSH1_4f12.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_5f11.b1.seq+ is in U_HW-SSH1_4f12.b1.seq+
U_HW-SSH1_7d01.b1.seq+ is in U_HW-SSH1_5f11.b1.seq+
U_HW-SSH1_5g06.b1.seq+ is in U_HW-SSH1_5f11.b1.seq+
U_HW-SSH1_4a07.b1.seq+ is in U_HW-SSH1_5f11.b1.seq+
U_HW-SSH1_7a10.b1.seq+ is in U_HW-SSH1_4f12.b1.seq+
U_HW-SSH1_8h11.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_2e06.b1.seq+ is in U_HW-SSH1_11d06.b1.seq+
U_HW-SSH1_11f10.b1.seq+
U_HW-SSH1_5e01.b1.seq+ is in U_HW-SSH1_11f10.b1.seq+
U_HW-SSH1_5d03.b1.seq+ is in U_HW-SSH1_11f10.b1.seq+
U_HW-SSH1_3e06.b1.seq+ is in U_HW-SSH1_11f10.b1.seq+
U_HW-SSH1_12e05.b1.seq+ is in U_HW-SSH1_11f10.b1.seq+
U_HW-SSH1_12g05.b1.seq+ is in U_HW-SSH1_11f10.b1.seq+
U_HW-SSH1_7b01.b1.seq+ is in U_HW-SSH1_11f10.b1.seq+
U_HW-SSH1_6h08.b1.seq+ is in U_HW-SSH1_7b01.b1.seq+
U_HW-SSH1_15d01.b1.seq+ is in U_HW-SSH1_7b01.b1.seq+
U_HW-SSH1_10g11.b1.seq+
U_HW-SSH1_1e04.b1.seq+ is in U_HW-SSH1_10g11.b1.seq+
U_HW-SSH1_1e03.b1.seq+ is in U_HW-SSH1_1e04.b1.seq+
U_HW-SSH1_6b11.b1.seq+ is in U_HW-SSH1_10g11.b1.seq+
U_HW-SSH1_13a05.b1.seq+ is in U_HW-SSH1_10g11.b1.seq+
U_HW-SSH1_13b05.b1.seq+ is in U_HW-SSH1_10g11.b1.seq+
U_HW-SSH1_3e03.b1.seq+ is in U_HW-SSH1_10g11.b1.seq+
U_HW-SSH1_13h05.b1.seq+ is in U_HW-SSH1_10g11.b1.seq+
U_HW-SSH1_13h01.b1.seq+ is in U_HW-SSH1_10g11.b1.seq+
U_HW-SSH1_13f04.b1.seq+ is in U_HW-SSH1_13h01.b1.seq+
U_HW-SSH1_13d05.b1.seq+ is in U_HW-SSH1_10g11.b1.seq+
U_HW-SSH1_13f01.b1.seq- is in U_HW-SSH1_13d05.b1.seq+
U_HW-SSH1_3b04.b1.seq+ is in U_HW-SSH1_13d05.b1.seq+
U_HW-SSH1_13g02.b1.seq+ is in U_HW-SSH1_10g11.b1.seq+
U_HW-SSH1_4f08.b1.seq+ is in U_HW-SSH1_13g02.b1.seq+
U_HW-SSH1_9g07.b1.seq+ is in U_HW-SSH1_13g02.b1.seq+
U_HW-SSH1_14f04.b1.seq+ is in U_HW-SSH1_10g11.b1.seq+
U_HW-SSH1_15g04.b1.seq+ is in U_HW-SSH1_14f04.b1.seq+
U_HW-SSH1_7a09.b1.seq+ is in U_HW-SSH1_14f04.b1.seq+
U_HW-SSH1_1d08.b1.seq+ is in U_HW-SSH1_10g11.b1.seq+
U_HW-SSH1_14b07.b1.seq+
U_HW-SSH1_1b07.b1.seq+ is in U_HW-SSH1_14b07.b1.seq+
U_HW-SSH1_13c05.b1.seq+ is in U_HW-SSH1_14b07.b1.seq+
U_HW-SSH1_1e05.b1.seq+ is in U_HW-SSH1_14b07.b1.seq+
U_HW-SSH1_3f07.b1.seq+ is in U_HW-SSH1_14b07.b1.seq+
U_HW-SSH1_10a04.b1.seq+ is in U_HW-SSH1_3f07.b1.seq+
U_HW-SSH1_3h04.b1.seq+ is in U_HW-SSH1_10a04.b1.seq+
U_HW-SSH1_8e06.b1.seq+ is in U_HW-SSH1_14b07.b1.seq+
********** Contig 39 **********
U_HW-SSH1_11b12.b1.seq+
U_HW-SSH1_2h11.b1.seq+ is in U_HW-SSH1_11b12.b1.seq+
U_HW-SSH1_11h12.b1.seq+ is in U_HW-SSH1_11b12.b1.seq+
U_HW-SSH1_8g04.b1.seq+
U_HW-SSH1_2e05.b1.seq+ is in U_HW-SSH1_8g04.b1.seq+
U_HW-SSH1_11b11.b1.seq+ is in U_HW-SSH1_8g04.b1.seq+
U_HW-SSH1_9e08.b1.seq+ is in U_HW-SSH1_8g04.b1.seq+
U_HW-SSH1_13e05.b1.seq+ is in U_HW-SSH1_8g04.b1.seq+
U_HW-SSH1_3a09.b1.seq+ is in U_HW-SSH1_13e05.b1.seq+
U_HW-SSH1_16a06.b1.seq+
U_HW-SSH1_11a10.b1.seq+ is in U_HW-SSH1_16a06.b1.seq+
U_HW-SSH1_16d10.b1.seq+ is in U_HW-SSH1_11a10.b1.seq+
U_HW-SSH1_16c09.b1.seq+ is in U_HW-SSH1_11a10.b1.seq+
U_HW-SSH1_4d10.b1.seq+ is in U_HW-SSH1_11a10.b1.seq+
U_HW-SSH1_11b10.b1.seq+ is in U_HW-SSH1_11a10.b1.seq+
U_HW-SSH1_16b06.b1.seq+ is in U_HW-SSH1_16a06.b1.seq+
U_HW-SSH1_16c06.b1.seq+ is in U_HW-SSH1_16b06.b1.seq+
********** Contig 40 **********
U_HW-SSH1_11c12.b1.seq-
U_HW-SSH1_7c06.b1.seq+ is in U_HW-SSH1_11c12.b1.seq-
********** Contig 41 **********

U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_12h05.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_15f12.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_5d05.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_9c03.b1.seq+ is in U_HW-SSH1_5d05.b1.seq+
U_HW-SSH1_9h02.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_3e11.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_6h04.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_5e02.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_4b06.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_3f12.b1.seq+ is in U_HW-SSH1_4b06.b1.seq+
U_HW-SSH1_9b03.b1.seq+ is in U_HW-SSH1_4b06.b1.seq+
U_HW-SSH1_3f08.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_9h01.b1.seq+ is in U_HW-SSH1_3f08.b1.seq+
U_HW-SSH1_12h06.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_8g11.b1.seq- is in U_HW-SSH1_12h06.b1.seq+
U_HW-SSH1_9d04.b1.seq+ is in U_HW-SSH1_12h06.b1.seq+
U_HW-SSH1_9c04.b1.seq+ is in U_HW-SSH1_12h06.b1.seq+
U_HW-SSH1_9b04.b1.seq+ is in U_HW-SSH1_9c04.b1.seq+
U_HW-SSH1_12g06.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_11g02.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_4c06.b1.seq+ is in U_HW-SSH1_11g02.b1.seq+
U_HW-SSH1_14a10.b1.seq+ is in U_HW-SSH1_11g02.b1.seq+
U_HW-SSH1_15c07.b1.seq+ is in U_HW-SSH1_11g02.b1.seq+
U_HW-SSH1_15a05.b1.seq+ is in U_HW-SSH1_15c07.b1.seq+
U_HW-SSH1_12f11.b1.seq+ is in U_HW-SSH1_11g02.b1.seq+
U_HW-SSH1_2g10.b1.seq+ is in U_HW-SSH1_12f11.b1.seq+
U_HW-SSH1_2a10.b1.seq+ is in U_HW-SSH1_11g02.b1.seq+
U_HW-SSH1_4e02.b1.seq+ is in U_HW-SSH1_2a10.b1.seq+
U_HW-SSH1_5g02.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_7d08.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_4d02.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_4d04.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_11h02.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_4d08.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_11g03.b1.seq+ is in U_HW-SSH1_11d05.b1.seq+
U_HW-SSH1_11h08.b1.seq+
U_HW-SSH1_15b01.b1.seq+ is in U_HW-SSH1_11h08.b1.seq+
U_HW-SSH1_12e10.b1.seq+ is in U_HW-SSH1_11h08.b1.seq+
U_HW-SSH1_12e11.b1.seq+ is in U_HW-SSH1_12e10.b1.seq+
U_HW-SSH1_8g10.b1.seq+ is in U_HW-SSH1_12e11.b1.seq+
U_HW-SSH1_14h12.b1.seq+ is in U_HW-SSH1_11h08.b1.seq+
U_HW-SSH1_14b12.b1.seq+ is in U_HW-SSH1_11h08.b1.seq+
U_HW-SSH1_7c03.b1.seq+ is in U_HW-SSH1_11h08.b1.seq+
U_HW-SSH1_11g08.b1.seq+ is in U_HW-SSH1_11h08.b1.seq+
U_HW-SSH1_5f02.b1.seq+ is in U_HW-SSH1_11g08.b1.seq+
U_HW-SSH1_13b06.b1.seq+ is in U_HW-SSH1_11h08.b1.seq+
U_HW-SSH1_14f07.b1.seq+ is in U_HW-SSH1_13b06.b1.seq+
U_HW-SSH1_4h09.b1.seq+ is in U_HW-SSH1_11h08.b1.seq+
U_HW-SSH1_11f04.b1.seq+ is in U_HW-SSH1_4h09.b1.seq+
U_HW-SSH1_16h11.b1.seq+ is in U_HW-SSH1_11h08.b1.seq+
U_HW-SSH1_5c05.b1.seq+ is in U_HW-SSH1_16h11.b1.seq+
U_HW-SSH1_2h04.b1.seq+ is in U_HW-SSH1_16h11.b1.seq+
U_HW-SSH1_4f06.b1.seq+ is in U_HW-SSH1_16h11.b1.seq+
U_HW-SSH1_4f05.b1.seq+ is in U_HW-SSH1_4f06.b1.seq+
U_HW-SSH1_9f11.b1.seq+ is in U_HW-SSH1_4f06.b1.seq+
U_HW-SSH1_2h05.b1.seq+ is in U_HW-SSH1_4f06.b1.seq+
U_HW-SSH1_4f07.b1.seq+ is in U_HW-SSH1_4f06.b1.seq+
U_HW-SSH1_11b09.b1.seq+
U_HW-SSH1_8d02.b1.seq+ is in U_HW-SSH1_11b09.b1.seq+
U_HW-SSH1_12f12.b1.seq+ is in U_HW-SSH1_11b09.b1.seq+
U_HW-SSH1_13d12.b1.seq+ is in U_HW-SSH1_11b09.b1.seq+
U_HW-SSH1_2h07.b1.seq+ is in U_HW-SSH1_11b09.b1.seq+
U_HW-SSH1_2h08.b1.seq+ is in U_HW-SSH1_2h07.b1.seq+
U_HW-SSH1_7a06.b1.seq+ is in U_HW-SSH1_2h07.b1.seq+
U_HW-SSH1_2c09.b1.seq+ is in U_HW-SSH1_11b09.b1.seq+
U_HW-SSH1_12d02.b1.seq+ is in U_HW-SSH1_11b09.b1.seq+
U_HW-SSH1_2d05.b1.seq- is in U_HW-SSH1_12d02.b1.seq+
U_HW-SSH1_3h09.b1.seq+ is in U_HW-SSH1_12d02.b1.seq+
U_HW-SSH1_9c09.b1.seq+ is in U_HW-SSH1_12d02.b1.seq+
U_HW-SSH1_6d11.b1.seq+ is in U_HW-SSH1_9c09.b1.seq+
U_HW-SSH1_3a08.b1.seq+ is in U_HW-SSH1_12d02.b1.seq+
U_HW-SSH1_9b09.b1.seq+ is in U_HW-SSH1_12d02.b1.seq+
U_HW-SSH1_2c04.b1.seq- is in U_HW-SSH1_12d02.b1.seq+
U_HW-SSH1_15f11.b1.seq+ is in U_HW-SSH1_12d02.b1.seq+
U_HW-SSH1_3c11.b1.seq+ is in U_HW-SSH1_15f11.b1.seq+
U_HW-SSH1_2d12.b1.seq- is in U_HW-SSH1_12d02.b1.seq+
U_HW-SSH1_16d09.b1.seq+
U_HW-SSH1_16e10.b1.seq+
U_HW-SSH1_16b10.b1.seq+ is in U_HW-SSH1_16e10.b1.seq+
********** Contig 42 **********
U_HW-SSH1_11d10.b1.seq+
U_HW-SSH1_3f11.b1.seq+ is in U_HW-SSH1_11d10.b1.seq+
U_HW-SSH1_2e04.b1.seq+ is in U_HW-SSH1_11d10.b1.seq+
U_HW-SSH1_11e06.b1.seq+ is in U_HW-SSH1_11d10.b1.seq+
********** Contig 43 **********
U_HW-SSH1_11e11.b1.seq+
U_HW-SSH1_12h09.b1.seq+ is in U_HW-SSH1_11e11.b1.seq+
U_HW-SSH1_14d09.b1.seq+ is in U_HW-SSH1_11e11.b1.seq+
U_HW-SSH1_11b02.b1.seq+ is in U_HW-SSH1_11e11.b1.seq+
U_HW-SSH1_14a06.b1.seq+ is in U_HW-SSH1_11e11.b1.seq+
U_HW-SSH1_12d08.b1.seq+ is in U_HW-SSH1_11e11.b1.seq+
U_HW-SSH1_15b06.b1.seq+ is in U_HW-SSH1_11e11.b1.seq+
U_HW-SSH1_15b04.b1.seq+ is in U_HW-SSH1_15b06.b1.seq+
U_HW-SSH1_11g07.b1.seq+ is in U_HW-SSH1_11e11.b1.seq+
U_HW-SSH1_11g12.b1.seq+ is in U_HW-SSH1_11e11.b1.seq+
U_HW-SSH1_12d09.b1.seq+ is in U_HW-SSH1_11e11.b1.seq+
U_HW-SSH1_4f11.b1.seq+ is in U_HW-SSH1_12d09.b1.seq+
U_HW-SSH1_1b03.b1.seq+ is in U_HW-SSH1_12d09.b1.seq+
U_HW-SSH1_1a03.b1.seq+ is in U_HW-SSH1_12d09.b1.seq+
U_HW-SSH1_3e10.b1.seq+ is in U_HW-SSH1_12d09.b1.seq+
U_HW-SSH1_4b11.b1.seq+ is in U_HW-SSH1_12d09.b1.seq+
U_HW-SSH1_11e12.b1.seq+ is in U_HW-SSH1_4b11.b1.seq+
U_HW-SSH1_4g07.b1.seq+ is in U_HW-SSH1_12d09.b1.seq+
U_HW-SSH1_7e11.b1.seq+ is in U_HW-SSH1_4g07.b1.seq+
U_HW-SSH1_5h06.b1.seq+ is in U_HW-SSH1_4g07.b1.seq+
U_HW-SSH1_5h09.b1.seq+ is in U_HW-SSH1_4g07.b1.seq+
U_HW-SSH1_5e05.b1.seq+ is in U_HW-SSH1_4g07.b1.seq+
U_HW-SSH1_13e10.b1.seq+
U_HW-SSH1_16a07.b1.seq+ is in U_HW-SSH1_13e10.b1.seq+
U_HW-SSH1_3b12.b1.seq+ is in U_HW-SSH1_16a07.b1.seq+
U_HW-SSH1_13b11.b1.seq+ is in U_HW-SSH1_13e10.b1.seq+
U_HW-SSH1_11d12.b1.seq+ is in U_HW-SSH1_13e10.b1.seq+
U_HW-SSH1_7c01.b1.seq+ is in U_HW-SSH1_11d12.b1.seq+
U_HW-SSH1_14b04.b1.seq+
U_HW-SSH1_2g02.b1.seq+ is in U_HW-SSH1_14b04.b1.seq+
U_HW-SSH1_2g12.b1.seq+ is in U_HW-SSH1_14b04.b1.seq+
U_HW-SSH1_4a06.b1.seq+ is in U_HW-SSH1_14b04.b1.seq+
U_HW-SSH1_4b12.b1.seq+ is in U_HW-SSH1_14b04.b1.seq+
U_HW-SSH1_4c12.b1.seq+ is in U_HW-SSH1_4b12.b1.seq+
U_HW-SSH1_1d09.b1.seq+ is in U_HW-SSH1_4b12.b1.seq+
U_HW-SSH1_11f05.b1.seq+ is in U_HW-SSH1_4b12.b1.seq+
U_HW-SSH1_11h10.b1.seq+ is in U_HW-SSH1_4b12.b1.seq+
U_HW-SSH1_1a07.b1.seq+ is in U_HW-SSH1_11h10.b1.seq+
U_HW-SSH1_2e08.b1.seq+ is in U_HW-SSH1_11h10.b1.seq+
U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_14b05.b1.seq- is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_12c08.b1.seq- is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_3e02.b1.seq+ is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_11a04.b1.seq+ is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_4h07.b1.seq+ is in U_HW-SSH1_11a04.b1.seq+
U_HW-SSH1_9a04.b1.seq+ is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_3c02.b1.seq+ is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_8f07.b1.seq- is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_5h12.b1.seq- is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_10b03.b1.seq+ is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_16f12.b1.seq- is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_1c04.b1.seq+ is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_1d12.b1.seq- is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_1b08.b1.seq- is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_1d02.b1.seq+ is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_8g08.b1.seq- is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_8f09.b1.seq- is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_8g07.b1.seq- is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_8h02.b1.seq- is in U_HW-SSH1_8g07.b1.seq-
U_HW-SSH1_9a05.b1.seq+ is in U_HW-SSH1_8h05.b1.seq+
U_HW-SSH1_9b06.b1.seq+ is in U_HW-SSH1_9a05.b1.seq+
U_HW-SSH1_9b05.b1.seq+ is in U_HW-SSH1_9a05.b1.seq+
U_HW-SSH1_9d01.b1.seq+ is in U_HW-SSH1_9b05.b1.seq+
U_HW-SSH1_13e09.b1.seq+
U_HW-SSH1_1b05.b1.seq+ is in U_HW-SSH1_13e09.b1.seq+
U_HW-SSH1_10d07.b1.seq+ is in U_HW-SSH1_13e09.b1.seq+
U_HW-SSH1_10e02.b1.seq+ is in U_HW-SSH1_10d07.b1.seq+
U_HW-SSH1_10h02.b1.seq+ is in U_HW-SSH1_10d07.b1.seq+
U_HW-SSH1_1d01.b1.seq+ is in U_HW-SSH1_13e09.b1.seq+
U_HW-SSH1_1c01.b1.seq+ is in U_HW-SSH1_1d01.b1.seq+
U_HW-SSH1_3a05.b1.seq+ is in U_HW-SSH1_13e09.b1.seq+
U_HW-SSH1_3a06.b1.seq+ is in U_HW-SSH1_3a05.b1.seq+
U_HW-SSH1_9c05.b1.seq+ is in U_HW-SSH1_3a05.b1.seq+
U_HW-SSH1_12g11.b1.seq+ is in U_HW-SSH1_13e09.b1.seq+
U_HW-SSH1_6b08.b1.seq+ is in U_HW-SSH1_12g11.b1.seq+
U_HW-SSH1_3e01.b1.seq+ is in U_HW-SSH1_12g11.b1.seq+
U_HW-SSH1_15a04.b1.seq+ is in U_HW-SSH1_13e09.b1.seq+
U_HW-SSH1_3b11.b1.seq+ is in U_HW-SSH1_15a04.b1.seq+
U_HW-SSH1_3e07.b1.seq+ is in U_HW-SSH1_15a04.b1.seq+
U_HW-SSH1_1b01.b1.seq+ is in U_HW-SSH1_3e07.b1.seq+
U_HW-SSH1_14a05.b1.seq+ is in U_HW-SSH1_13e09.b1.seq+
********** Contig 44 **********
U_HW-SSH1_12a04.b1.seq+
U_HW-SSH1_3c09.b1.seq+ is in U_HW-SSH1_12a04.b1.seq+
U_HW-SSH1_8h08.b1.seq+ is in U_HW-SSH1_12a04.b1.seq+
U_HW-SSH1_11f12.b1.seq+
********** Contig 45 **********
U_HW-SSH1_12b12.b1.seq+
U_HW-SSH1_11f06.b1.seq+ is in U_HW-SSH1_12b12.b1.seq+
********** Contig 46 **********
U_HW-SSH1_12d06.b1.seq+
U_HW-SSH1_7a05.b1.seq+ is in U_HW-SSH1_12d06.b1.seq+
U_HW-SSH1_7a12.b1.seq+ is in U_HW-SSH1_12d06.b1.seq+
U_HW-SSH1_12d07.b1.seq+
U_HW-SSH1_8c07.b1.seq+ is in U_HW-SSH1_12d07.b1.seq+
U_HW-SSH1_6f10.b1.seq+ is in U_HW-SSH1_12d07.b1.seq+
U_HW-SSH1_12f07.b1.seq+ is in U_HW-SSH1_12d07.b1.seq+
U_HW-SSH1_12g08.b1.seq+ is in U_HW-SSH1_12f07.b1.seq+
U_HW-SSH1_9g04.b1.seq+ is in U_HW-SSH1_12d07.b1.seq+
U_HW-SSH1_8e04.b1.seq+ is in U_HW-SSH1_9g04.b1.seq+
U_HW-SSH1_6h09.b1.seq+ is in U_HW-SSH1_9g04.b1.seq+
********** Contig 47 **********
U_HW-SSH1_12g04.b1.seq+
U_HW-SSH1_8h07.b1.seq+
U_HW-SSH1_12c09.b1.seq- is in U_HW-SSH1_8h07.b1.seq+
********** Contig 48 **********
U_HW-SSH1_13f10.b1.seq+
U_HW-SSH1_3g01.b1.seq+ is in U_HW-SSH1_13f10.b1.seq+
U_HW-SSH1_14g04.b1.seq+
********** Contig 49 **********
U_HW-SSH1_14f06.b1.seq-
U_HW-SSH1_1d10.b1.seq+
U_HW-SSH1_13c02.b1.seq+
U_HW-SSH1_16e09.b1.seq+ is in U_HW-SSH1_13c02.b1.seq+
U_HW-SSH1_5d08.b1.seq- is in U_HW-SSH1_13c02.b1.seq+
U_HW-SSH1_14e06.b1.seq- is in U_HW-SSH1_5d08.b1.seq-
U_HW-SSH1_1d06.b1.seq+ is in U_HW-SSH1_13c02.b1.seq+
U_HW-SSH1_7c12.b1.seq+ is in U_HW-SSH1_1d06.b1.seq+
U_HW-SSH1_1a02.b1.seq+ is in U_HW-SSH1_13c02.b1.seq+
U_HW-SSH1_11b06.b1.seq-
U_HW-SSH1_11b07.b1.seq- is in U_HW-SSH1_11b06.b1.seq-
U_HW-SSH1_4e10.b1.seq+
********** Contig 50 **********
U_HW-SSH1_16e05.b1.seq+
U_HW-SSH1_16b05.b1.seq+ is in U_HW-SSH1_16e05.b1.seq+
U_HW-SSH1_16c05.b1.seq+ is in U_HW-SSH1_16e05.b1.seq+
U_HW-SSH1_16b03.b1.seq+ is in U_HW-SSH1_16c05.b1.seq+
U_HW-SSH1_16d04.b1.seq+ is in U_HW-SSH1_16e05.b1.seq+
U_HW-SSH1_16d05.b1.seq+ is in U_HW-SSH1_16d04.b1.seq+
U_HW-SSH1_16f04.b1.seq+ is in U_HW-SSH1_16d04.b1.seq+
U_HW-SSH1_16g04.b1.seq+ is in U_HW-SSH1_16e05.b1.seq+
U_HW-SSH1_16e04.b1.seq+
********** Contig 51 **********
U_HW-SSH1_16f03.b1.seq+
U_HW-SSH1_16e02.b1.seq+ is in U_HW-SSH1_16f03.b1.seq+
********** Contig 52 **********
U_HW-SSH1_16f08.b1.seq-
U_HW-SSH1_13a01.b1.seq+ is in U_HW-SSH1_16f08.b1.seq-
U_HW-SSH1_9e06.b1.seq+ is in U_HW-SSH1_16f08.b1.seq-
U_HW-SSH1_3a10.b1.seq+ is in U_HW-SSH1_16f08.b1.seq-
U_HW-SSH1_11d03.b1.seq- is in U_HW-SSH1_3a10.b1.seq+
U_HW-SSH1_2f04.b1.seq+ is in U_HW-SSH1_16f08.b1.seq-
U_HW-SSH1_11e10.b1.seq+ is in U_HW-SSH1_2f04.b1.seq+
U_HW-SSH1_16a09.b1.seq+ is in U_HW-SSH1_16f08.b1.seq-
U_HW-SSH1_9e03.b1.seq+ is in U_HW-SSH1_16f08.b1.seq-
U_HW-SSH1_16a11.b1.seq+ is in U_HW-SSH1_9e03.b1.seq+

U_HW-SSH1_7e05.b1.seq+
********** Contig 53 **********
U_HW-SSH1_16h08.b1.seq+
	U_HW-SSH1_2b01.b1.seq+ is in U_HW-SSH1_16h08.b1.seq+
	U_HW-SSH1_2c07.b1.seq+ is in U_HW-SSH1_2b01.b1.seq+
U_HW-SSH1_15c08.b1.seq+
	U_HW-SSH1_2e03.b1.seq+ is in U_HW-SSH1_15c08.b1.seq+
	U_HW-SSH1_16g08.b1.seq+ is in U_HW-SSH1_15c08.b1.seq+
	U_HW-SSH1_9d05.b1.seq+ is in U_HW-SSH1_15c08.b1.seq+
	U_HW-SSH1_1e09.b1.seq+ is in U_HW-SSH1_15c08.b1.seq+
	U_HW-SSH1_2a07.b1.seq+ is in U_HW-SSH1_15c08.b1.seq+
	U_HW-SSH1_2b07.b1.seq+ is in U_HW-SSH1_2a07.b1.seq+
U_HW-SSH1_11a09.b1.seq-
	U_HW-SSH1_12a06.b1.seq- is in U_HW-SSH1_11a09.b1.seq-
	U_HW-SSH1_14b02.b1.seq- is in U_HW-SSH1_11a09.b1.seq-
********** Contig 54 **********
U_HW-SSH1_2b03.b1.seq+
U_HW-SSH1_2a01.b1.seq+
	U_HW-SSH1_2c03.b1.seq+ is in U_HW-SSH1_2a01.b1.seq+
********** Contig 55 **********
U_HW-SSH1_2e12.b1.seq+
	U_HW-SSH1_16f02.b1.seq+ is in U_HW-SSH1_2e12.b1.seq+
	U_HW-SSH1_16g02.b1.seq+ is in U_HW-SSH1_2e12.b1.seq+
U_HW-SSH1_1b09.b1.seq+
	U_HW-SSH1_2f10.b1.seq+ is in U_HW-SSH1_1b09.b1.seq+
	U_HW-SSH1_13c03.b1.seq- is in U_HW-SSH1_2f10.b1.seq+
	U_HW-SSH1_5b01.b1.seq+ is in U_HW-SSH1_2f10.b1.seq+
********** Contig 56 **********
U_HW-SSH1_2h10.b1.seq+
U_HW-SSH1_2d11.b1.seq+
********** Contig 57 **********
U_HW-SSH1_4b02.b1.seq+
	U_HW-SSH1_4b03.b1.seq+ is in U_HW-SSH1_4b02.b1.seq+
	U_HW-SSH1_4b08.b1.seq+ is in U_HW-SSH1_4b03.b1.seq+
U_HW-SSH1_4b01.b1.seq+
********** Contig 58 **********
U_HW-SSH1_5d04.b1.seq+
U_HW-SSH1_1a06.b1.seq+
	U_HW-SSH1_1c09.b1.seq+ is in U_HW-SSH1_1a06.b1.seq+
	U_HW-SSH1_5a12.b1.seq+ is in U_HW-SSH1_1a06.b1.seq+
	U_HW-SSH1_11g11.b1.seq+ is in U_HW-SSH1_1a06.b1.seq+
	U_HW-SSH1_8g06.b1.seq+ is in U_HW-SSH1_1a06.b1.seq+
	U_HW-SSH1_4g11.b1.seq+ is in U_HW-SSH1_8g06.b1.seq+
U_HW-SSH1_8h12.b1.seq+
	U_HW-SSH1_5h07.b1.seq+ is in U_HW-SSH1_8h12.b1.seq+
U_HW-SSH1_11b05.b1.seq+
********** Contig 59 **********
U_HW-SSH1_7d05.b1.seq+
U_HW-SSH1_7f09.b1.seq+
U_HW-SSH1_7g09.b1.seq+
	U_HW-SSH1_7d07.b1.seq+ is in U_HW-SSH1_7g09.b1.seq+
	U_HW-SSH1_7a07.b1.seq+ is in U_HW-SSH1_7d07.b1.seq+
U_HW-SSH1_7h09.b1.seq+
	U_HW-SSH1_7e07.b1.seq+ is in U_HW-SSH1_7h09.b1.seq+
	U_HW-SSH1_7c09.b1.seq+ is in U_HW-SSH1_7e07.b1.seq+
********** Contig 60 **********
U_HW-SSH1_7f10.b1.seq+
U_HW-SSH1_7e10.b1.seq+
********** Contig 61 **********
U_HW-SSH1_7h12.b1.seq+
U_HW-SSH1_6c09.b1.seq+
U_HW-SSH1_10a03.b1.seq+
U_HW-SSH1_9e10.b1.seq+
U_HW-SSH1_14c04.b1.seq+
	U_HW-SSH1_10c01.b1.seq+ is in U_HW-SSH1_14c04.b1.seq+
	U_HW-SSH1_2e07.b1.seq+ is in U_HW-SSH1_10c01.b1.seq+
	U_HW-SSH1_10c03.b1.seq+ is in U_HW-SSH1_14c04.b1.seq+
	U_HW-SSH1_1a08.b1.seq+ is in U_HW-SSH1_10c03.b1.seq+
********** Contig 62 **********
U_HW-SSH1_8a04.b1.seq+
	U_HW-SSH1_8a06.b1.seq+ is in U_HW-SSH1_8a04.b1.seq+
U_HW-SSH1_8a05.b1.seq+
********** Contig 63 **********
U_HW-SSH1_8b07.b1.seq+
U_HW-SSH1_8b08.b1.seq+
********** Contig 64 **********
U_HW-SSH1_8c08.b1.seq-
U_HW-SSH1_12b02.b1.seq-
	U_HW-SSH1_6e08.b1.seq- is in U_HW-SSH1_12b02.b1.seq-
	U_HW-SSH1_4b10.b1.seq- is in U_HW-SSH1_12b02.b1.seq-
	U_HW-SSH1_9e11.b1.seq- is in U_HW-SSH1_12b02.b1.seq-
	U_HW-SSH1_1d05.b1.seq+ is in U_HW-SSH1_12b02.b1.seq-
U_HW-SSH1_11h11.b1.seq-
U_HW-SSH1_9f02.b1.seq-
	U_HW-SSH1_2b02.b1.seq- is in U_HW-SSH1_9f02.b1.seq-
	U_HW-SSH1_2c02.b1.seq- is in U_HW-SSH1_9f02.b1.seq-
	U_HW-SSH1_2d01.b1.seq- is in U_HW-SSH1_2c02.b1.seq-
	U_HW-SSH1_8a09.b1.seq+ is in U_HW-SSH1_9f02.b1.seq-
	U_HW-SSH1_8a10.b1.seq+ is in U_HW-SSH1_9f02.b1.seq-
	U_HW-SSH1_8b11.b1.seq+ is in U_HW-SSH1_9f02.b1.seq-
	U_HW-SSH1_8b12.b1.seq+ is in U_HW-SSH1_8b11.b1.seq+
	U_HW-SSH1_1b06.b1.seq- is in U_HW-SSH1_9f02.b1.seq-
	U_HW-SSH1_2e01.b1.seq- is in U_HW-SSH1_1b06.b1.seq-
	U_HW-SSH1_8a08.b1.seq+ is in U_HW-SSH1_1b06.b1.seq-
	U_HW-SSH1_10g10.b1.seq- is in U_HW-SSH1_9f02.b1.seq-
	U_HW-SSH1_10f10.b1.seq- is in U_HW-SSH1_10g10.b1.seq-
	U_HW-SSH1_9g02.b1.seq- is in U_HW-SSH1_9f02.b1.seq-
	U_HW-SSH1_11a11.b1.seq+ is in U_HW-SSH1_9f02.b1.seq-
	U_HW-SSH1_12b11.b1.seq+ is in U_HW-SSH1_11a11.b1.seq+
	U_HW-SSH1_11c02.b1.seq+ is in U_HW-SSH1_11a11.b1.seq+
	U_HW-SSH1_1d11.b1.seq+ is in U_HW-SSH1_11c02.b1.seq+
	U_HW-SSH1_11c04.b1.seq+ is in U_HW-SSH1_11a11.b1.seq+
	U_HW-SSH1_4f02.b1.seq+ is in U_HW-SSH1_11c04.b1.seq+
	U_HW-SSH1_16a12.b1.seq+ is in U_HW-SSH1_11c04.b1.seq+
	U_HW-SSH1_4e09.b1.seq+ is in U_HW-SSH1_16a12.b1.seq+
	U_HW-SSH1_2c10.b1.seq+ is in U_HW-SSH1_11c04.b1.seq+
	U_HW-SSH1_2g07.b1.seq- is in U_HW-SSH1_11a11.b1.seq+
U_HW-SSH1_11a12.b1.seq+
********** Contig 65 **********
U_HW-SSH1_9b02.b1.seq+
U_HW-SSH1_3f10.b1.seq+
********** Contig 66 **********
U_HW-SSH1_9g09.b1.seq+
U_HW-SSH1_4e08.b1.seq+

APPENDIX D

Contig assemblies of SSH2 (R-D) library generated by Cap3 contig assembly program.

Number of segment pairs = 997002; number of pairwise comparisons = 421
'+' means given segment; '-' means reverse complement

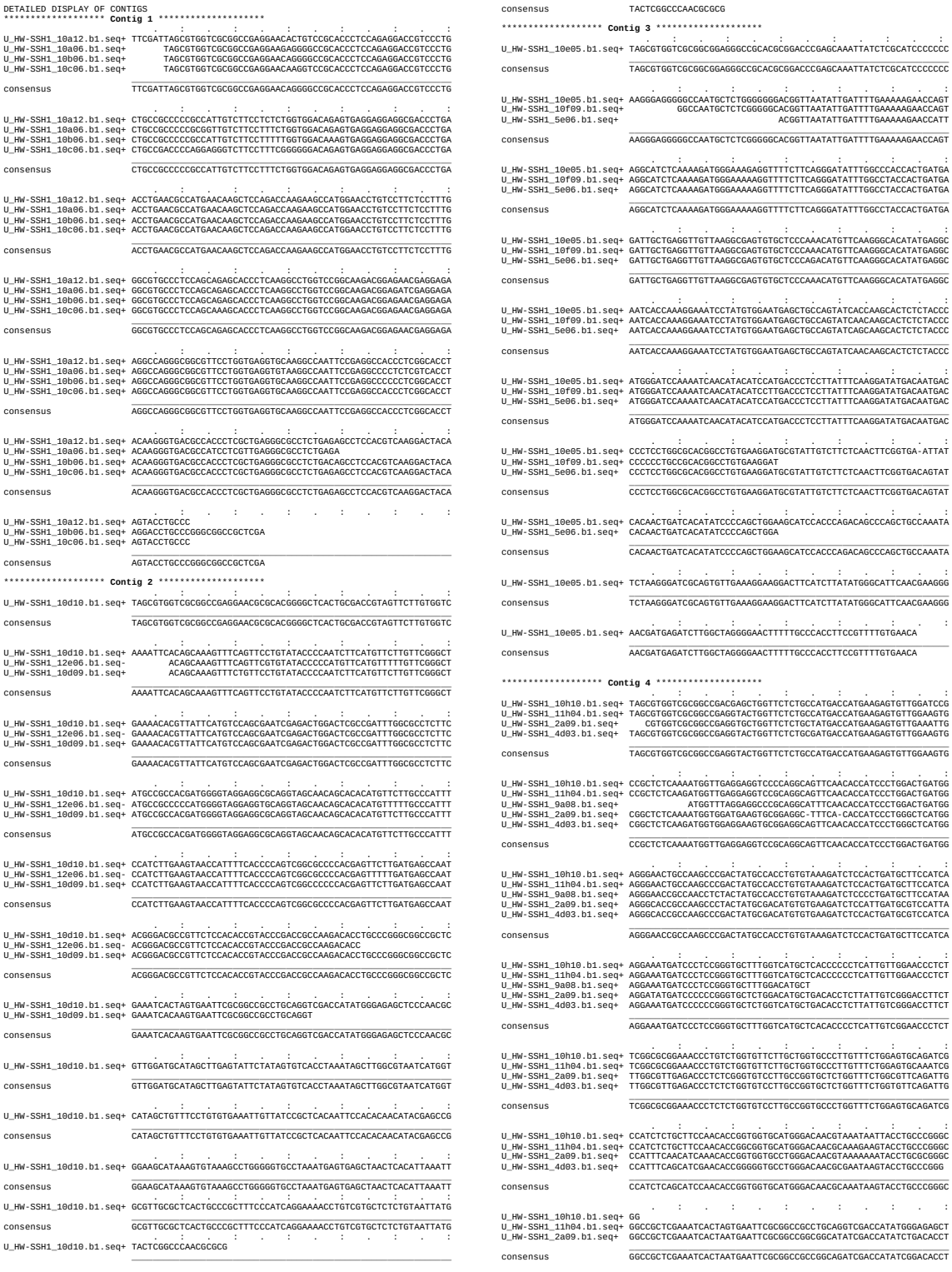
Overlaps Containments No. of Constraints Supporting Overlap

```
******************** Contig 1 **********************
U_HW-SSH2_10f06.b1.seq+
U_HW-SSH2_12e12.b1.seq+
******************** Contig 2 **********************
U_HW-SSH2_10g12.b1.seq+
        U_HW-SSH2_10h01.b1.seq+ is in U_HW-SSH2_10g12.b1.seq+
******************** Contig 3 **********************
U_HW-SSH2_11b01.b1.seq+
        U_HW-SSH2_6f07.b1.seq+ is in U_HW-SSH2_11b01.b1.seq+
******************** Contig 4 **********************
U_HW-SSH2_11f03.b1.seq-
        U_HW-SSH2_5c11.b1.seq+ is in U_HW-SSH2_11f03.b1.seq-
******************** Contig 5 **********************
U_HW-SSH2_11g02.b1.seq+
        U_HW-SSH2_11h04.b1.seq+ is in U_HW-SSH2_11g02.b1.seq+
        U_HW-SSH2_11h01.b1.seq+ is in U_HW-SSH2_11g02.b1.seq+
******************** Contig 6 **********************
U_HW-SSH2_11h07.b1.seq+
        U_HW-SSH2_5e02.b1.seq+ is in U_HW-SSH2_11h07.b1.seq+
        U_HW-SSH2_5c01.b1.seq+ is in U_HW-SSH2_11h07.b1.seq+
        U_HW-SSH2_11h08.b1.seq+ is in U_HW-SSH2_11h07.b1.seq+
        U_HW-SSH2_1g12.b1.seq+ is in U_HW-SSH2_11h08.b1.seq+
        U_HW-SSH2_1f11.b1.seq+ is in U_HW-SSH2_11h08.b1.seq+
******************** Contig 7 **********************
U_HW-SSH2_11h12.b1.seq+
        U_HW-SSH2_11h10.b1.seq+ is in U_HW-SSH2_11h12.b1.seq+
U_HW-SSH2_5b12.b1.seq+
******************** Contig 8 **********************
U_HW-SSH2_12a04.b1.seq+
U_HW-SSH2_12a05.b1.seq+
******************** Contig 9 **********************
U_HW-SSH2_12a07.b1.seq+
        U_HW-SSH2_12b06.b1.seq+ is in U_HW-SSH2_12a07.b1.seq+
        U_HW-SSH2_12b07.b1.seq+ is in U_HW-SSH2_12a07.b1.seq+
******************** Contig 10 *********************
U_HW-SSH2_12c05.b1.seq+
        U_HW-SSH2_5b11.b1.seq+ is in U_HW-SSH2_12c05.b1.seq+
U_HW-SSH2_12b04.b1.seq+
******************** Contig 11 *********************
U_HW-SSH2_1a02.b1.seq+
        U_HW-SSH2_1h08.b1.seq+ is in U_HW-SSH2_1a02.b1.seq+
******************** Contig 12 *********************
U_HW-SSH2_1h07.b1.seq+
        U_HW-SSH2_1a01.b1.seq+ is in U_HW-SSH2_1h07.b1.seq+
U_HW-SSH2_9c08.b1.seq-
******************** Contig 13 *********************
U_HW-SSH2_2c07.b1.seq+
U_HW-SSH2_1d01.b1.seq+
******************** Contig 14 *********************
U_HW-SSH2_2g06.b1.seq+
        U_HW-SSH2_2h06.b1.seq+ is in U_HW-SSH2_2g06.b1.seq+
******************** Contig 15 *********************
U_HW-SSH2_3a08.b1.seq+
U_HW-SSH2_3e06.b1.seq+
        U_HW-SSH2_9d05.b1.seq+ is in U_HW-SSH2_3e06.b1.seq+
U_HW-SSH2_3a07.b1.seq+
******************** Contig 16 *********************
U_HW-SSH2_3f04.b1.seq+
        U_HW-SSH2_9b04.b1.seq+ is in U_HW-SSH2_3f04.b1.seq+
        U_HW-SSH2_3g01.b1.seq+ is in U_HW-SSH2_3f04.b1.seq+
U_HW-SSH2_3f02.b1.seq+
******************** Contig 17 *********************
U_HW-SSH2_3f08.b1.seq+
        U_HW-SSH2_3e07.b1.seq+ is in U_HW-SSH2_3f08.b1.seq+
        U_HW-SSH2_3f07.b1.seq+ is in U_HW-SSH2_3f08.b1.seq+
        U_HW-SSH2_3g07.b1.seq+ is in U_HW-SSH2_3f07.b1.seq+
        U_HW-SSH2_3g02.b1.seq+ is in U_HW-SSH2_3f08.b1.seq+
U_HW-SSH2_3e08.b1.seq+
******************** Contig 18 *********************
U_HW-SSH2_5a09.b1.seq+
U_HW-SSH2_5a10.b1.seq+
******************** Contig 19 *********************
U_HW-SSH2_5a11.b1.seq+
        U_HW-SSH2_11h05.b1.seq+ is in U_HW-SSH2_5a11.b1.seq+
******************** Contig 20 *********************
U_HW-SSH2_5c08.b1.seq+
        U_HW-SSH2_5c09.b1.seq+ is in U_HW-SSH2_5c08.b1.seq+
******************** Contig 21 *********************
U_HW-SSH2_5c10.b1.seq+
U_HW-SSH2_5c05.b1.seq+
******************** Contig 22 *********************
U_HW-SSH2_5e03.b1.seq+
U_HW-SSH2_10g10.b1.seq+
        U_HW-SSH2_12a10.b1.seq+ is in U_HW-SSH2_10g10.b1.seq+
        U_HW-SSH2_5g05.b1.seq- is in U_HW-SSH2_10g10.b1.seq+
U_HW-SSH2_10f11.b1.seq+
******************** Contig 23 *********************
U_HW-SSH2_5e07.b1.seq+
        U_HW-SSH2_3h10.b1.seq+ is in U_HW-SSH2_5e07.b1.seq+
U_HW-SSH2_11a11.b1.seq+
******************** Contig 24 *********************
U_HW-SSH2_5f04.b1.seq+
        U_HW-SSH2_5g03.b1.seq+ is in U_HW-SSH2_5f04.b1.seq+
******************** Contig 25 *********************
U_HW-SSH2_5h12.b1.seq+
U_HW-SSH2_11a07.b1.seq+
******************** Contig 26 *********************
U_HW-SSH2_6b08.b1.seq+
        U_HW-SSH2_2b07.b1.seq+ is in U_HW-SSH2_6b08.b1.seq+
******************** Contig 27 *********************
U_HW-SSH2_6c06.b1.seq+
        U_HW-SSH2_10c03.b1.seq+ is in U_HW-SSH2_6c06.b1.seq+
U_HW-SSH2_6c07.b1.seq+
        U_HW-SSH2_5h06.b1.seq+ is in U_HW-SSH2_6c07.b1.seq+
        U_HW-SSH2_12g07.b1.seq+ is in U_HW-SSH2_6c07.b1.seq+
        U_HW-SSH2_3a05.b1.seq- is in U_HW-SSH2_6c07.b1.seq+
******************** Contig 28 *********************
U_HW-SSH2_6c11.b1.seq-
U_HW-SSH2_12h05.b1.seq+
        U_HW-SSH2_9f08.b1.seq- is in U_HW-SSH2_12h05.b1.seq+
        U_HW-SSH2_3h12.b1.seq- is in U_HW-SSH2_12h05.b1.seq+
        U_HW-SSH2_12g05.b1.seq+ is in U_HW-SSH2_12h05.b1.seq+
U_HW-SSH2_12g04.b1.seq+
******************** Contig 29 *********************
U_HW-SSH2_6e07.b1.seq+
        U_HW-SSH2_6e09.b1.seq+ is in U_HW-SSH2_6e07.b1.seq+
        U_HW-SSH2_3h02.b1.seq+ is in U_HW-SSH2_6e09.b1.seq+
        U_HW-SSH2_6b10.b1.seq+ is in U_HW-SSH2_6e09.b1.seq+
******************** Contig 30 *********************
U_HW-SSH2_6f08.b1.seq+
        U_HW-SSH2_6g05.b1.seq+ is in U_HW-SSH2_6f08.b1.seq+
U_HW-SSH2_6g06.b1.seq+
******************** Contig 31 *********************
U_HW-SSH2_6f10.b1.seq+
U_HW-SSH2_1b02.b1.seq+
        U_HW-SSH2_1d12.b1.seq+ is in U_HW-SSH2_1b02.b1.seq+
        U_HW-SSH2_1g08.b1.seq+ is in U_HW-SSH2_1b02.b1.seq+
******************** Contig 32 *********************
U_HW-SSH2_6g01.b1.seq+
        U_HW-SSH2_6g02.b1.seq+ is in U_HW-SSH2_6g01.b1.seq+
******************** Contig 33 *********************
U_HW-SSH2_6g03.b1.seq-
U_HW-SSH2_1g04.b1.seq+
******************** Contig 34 *********************
U_HW-SSH2_7a12.b1.seq+
U_HW-SSH2_10a08.b1.seq+
******************** Contig 35 *********************
U_HW-SSH2_7b02.b1.seq+
U_HW-SSH2_7b03.b1.seq+
******************** Contig 36 *********************
U_HW-SSH2_7d10.b1.seq+
U_HW-SSH2_10e02.b1.seq+
U_HW-SSH2_10e05.b1.seq+
******************** Contig 37 *********************
U_HW-SSH2_7d11.b1.seq+
U_HW-SSH2_10a12.b1.seq+
U_HW-SSH2_10a10.b1.seq+
******************** Contig 38 *********************
U_HW-SSH2_8h09.b1.seq+
U_HW-SSH2_7h04.b1.seq+
******************** Contig 39 *********************
U_HW-SSH2_9b05.b1.seq+
U_HW-SSH2_9a04.b1.seq+
        U_HW-SSH2_9a05.b1.seq+ is in U_HW-SSH2_9a04.b1.seq+
******************** Contig 40 *********************
U_HW-SSH2_9c03.b1.seq+
        U_HW-SSH2_9d08.b1.seq+ is in U_HW-SSH2_9c03.b1.seq+
******************** Contig 41 *********************
U_HW-SSH2_9h10.b1.seq+
U_HW-SSH2_9h09.b1.seq+
******************** Contig 42 *********************
U_HW-SSH2_10d05.b1.seq+
U_HW-SSH2_5b10.b1.seq+
U_HW-SSH2_4b09.b1.seq-
        U_HW-SSH2_12g10.b1.seq+ is in U_HW-SSH2_4b09.b1.seq-
        U_HW-SSH2_12g11.b1.seq+ is in U_HW-SSH2_12g10.b1.seq+
        U_HW-SSH2_4a12.b1.seq+ is in U_HW-SSH2_4b09.b1.seq-
        U_HW-SSH2_10e01.b1.seq- is in U_HW-SSH2_4b09.b1.seq-
        U_HW-SSH2_3d11.b1.seq+ is in U_HW-SSH2_10e01.b1.seq-
        U_HW-SSH2_6c05.b1.seq+ is in U_HW-SSH2_10e01.b1.seq-
        U_HW-SSH2_12h12.b1.seq+ is in U_HW-SSH2_4b09.b1.seq-
        U_HW-SSH2_10d02.b1.seq+ is in U_HW-SSH2_12h12.b1.seq+
        U_HW-SSH2_10g06.b1.seq+ is in U_HW-SSH2_4b09.b1.seq-
        U_HW-SSH2_9h12.b1.seq+ is in U_HW-SSH2_10g06.b1.seq+
        U_HW-SSH2_6g10.b1.seq+ is in U_HW-SSH2_10g06.b1.seq+
        U_HW-SSH2_8e11.b1.seq+ is in U_HW-SSH2_10g06.b1.seq+
U_HW-SSH2_5e10.b1.seq-
        U_HW-SSH2_5f11.b1.seq+ is in U_HW-SSH2_5e10.b1.seq-
        U_HW-SSH2_12h02.b1.seq+ is in U_HW-SSH2_5e10.b1.seq-
        U_HW-SSH2_10d12.b1.seq- is in U_HW-SSH2_12h02.b1.seq+
        U_HW-SSH2_5a01.b1.seq+ is in U_HW-SSH2_12h02.b1.seq+
        U_HW-SSH2_5f10.b1.seq+ is in U_HW-SSH2_5e10.b1.seq-
        U_HW-SSH2_6f06.b1.seq- is in U_HW-SSH2_5e10.b1.seq-
******************** Contig 43 *********************
U_HW-SSH2_10h08.b1.seq+
        U_HW-SSH2_10h11.b1.seq+ is in U_HW-SSH2_10h08.b1.seq+
******************** Contig 44 *********************
U_HW-SSH2_11b02.b1.seq+
        U_HW-SSH2_11d01.b1.seq+ is in U_HW-SSH2_11b02.b1.seq+
U_HW-SSH2_11c02.b1.seq+
        U_HW-SSH2_11c03.b1.seq+ is in U_HW-SSH2_11c02.b1.seq+
        U_HW-SSH2_11b03.b1.seq+ is in U_HW-SSH2_11c02.b1.seq+
        U_HW-SSH2_11a02.b1.seq+ is in U_HW-SSH2_11c02.b1.seq+
        U_HW-SSH2_11e02.b1.seq+ is in U_HW-SSH2_11c02.b1.seq+
        U_HW-SSH2_11d02.b1.seq+ is in U_HW-SSH2_11c02.b1.seq+
        U_HW-SSH2_11c01.b1.seq+ is in U_HW-SSH2_11c02.b1.seq+
U_HW-SSH2_11e01.b1.seq+
```

U_HW-SSH2_11a03.b1.seq+ is in U_HW-SSH2_11e01.b1.seq+
********** Contig 45 **********
U_HW-SSH2_12c07.b1.seq+
U_HW-SSH2_12c08.b1.seq+ is in U_HW-SSH2_12c07.b1.seq+
U_HW-SSH2_5c03.b1.seq+ is in U_HW-SSH2_12c07.b1.seq+
U_HW-SSH2_4c09.b1.seq+ is in U_HW-SSH2_5c03.b1.seq+
U_HW-SSH2_5d03.b1.seq+ is in U_HW-SSH2_5c03.b1.seq+
U_HW-SSH2_5e01.b1.seq+ is in U_HW-SSH2_5c03.b1.seq+
U_HW-SSH2_5d02.b1.seq+ is in U_HW-SSH2_5c03.b1.seq+
********** Contig 46 **********
U_HW-SSH2_12d04.b1.seq+
U_HW-SSH2_12d09.b1.seq+ is in U_HW-SSH2_12d04.b1.seq+
U_HW-SSH2_12d08.b1.seq+
U_HW-SSH2_12e04.b1.seq+ is in U_HW-SSH2_12d08.b1.seq+
U_HW-SSH2_12c11.b1.seq+ is in U_HW-SSH2_12d08.b1.seq+
U_HW-SSH2_12d11.b1.seq+ is in U_HW-SSH2_12d08.b1.seq+
U_HW-SSH2_12d10.b1.seq+ is in U_HW-SSH2_12d08.b1.seq+
********** Contig 47 **********
U_HW-SSH2_12e02.b1.seq+
U_HW-SSH2_12e01.b1.seq+ is in U_HW-SSH2_12e02.b1.seq+
********** Contig 48 **********
U_HW-SSH2_1f04.b1.seq-
U_HW-SSH2_1h06.b1.seq- is in U_HW-SSH2_1f04.b1.seq-
U_HW-SSH2_12a11.b1.seq-
U_HW-SSH2_11h09.b1.seq+ is in U_HW-SSH2_12a11.b1.seq-
U_HW-SSH2_3g05.b1.seq+ is in U_HW-SSH2_12a11.b1.seq-
U_HW-SSH2_9h07.b1.seq- is in U_HW-SSH2_12a11.b1.seq-
U_HW-SSH2_1e04.b1.seq+ is in U_HW-SSH2_9h07.b1.seq-
U_HW-SSH2_3h04.b1.seq+ is in U_HW-SSH2_12a11.b1.seq-
U_HW-SSH2_5g09.b1.seq+ is in U_HW-SSH2_3h04.b1.seq+
U_HW-SSH2_5d09.b1.seq-
U_HW-SSH2_10a05.b1.seq+
********** Contig 49 **********
U_HW-SSH2_3a06.b1.seq+
U_HW-SSH2_7h05.b1.seq+ is in U_HW-SSH2_3a06.b1.seq+
********** Contig 50 **********
U_HW-SSH2_3c05.b1.seq-
U_HW-SSH2_9d04.b1.seq+
U_HW-SSH2_9c04.b1.seq+
U_HW-SSH2_8h07.b1.seq+
********** Contig 51 **********
U_HW-SSH2_3e04.b1.seq+
U_HW-SSH2_3g06.b1.seq+
U_HW-SSH2_3e03.b1.seq+
U_HW-SSH2_3f06.b1.seq+
U_HW-SSH2_3f05.b1.seq+
********** Contig 52 **********
U_HW-SSH2_3g08.b1.seq+
U_HW-SSH2_9h05.b1.seq+ is in U_HW-SSH2_3g08.b1.seq+
U_HW-SSH2_7g02.b1.seq+ is in U_HW-SSH2_9h05.b1.seq+
U_HW-SSH2_8h06.b1.seq+ is in U_HW-SSH2_3g08.b1.seq+
U_HW-SSH2_9e06.b1.seq+ is in U_HW-SSH2_3g08.b1.seq+
U_HW-SSH2_7f02.b1.seq+ is in U_HW-SSH2_3g08.b1.seq+
U_HW-SSH2_9d03.b1.seq+ is in U_HW-SSH2_7f02.b1.seq+
U_HW-SSH2_10d06.b1.seq+
U_HW-SSH2_10c07.b1.seq+ is in U_HW-SSH2_10d06.b1.seq+
U_HW-SSH2_10d07.b1.seq+ is in U_HW-SSH2_10d06.b1.seq+
U_HW-SSH2_10h05.b1.seq+ is in U_HW-SSH2_10d06.b1.seq+
U_HW-SSH2_10f04.b1.seq+ is in U_HW-SSH2_10d06.b1.seq+
U_HW-SSH2_9f09.b1.seq+ is in U_HW-SSH2_10d06.b1.seq+
U_HW-SSH2_5h05.b1.seq- is in U_HW-SSH2_10d06.b1.seq+
U_HW-SSH2_10e06.b1.seq+
U_HW-SSH2_9h04.b1.seq+ is in U_HW-SSH2_10e06.b1.seq+
U_HW-SSH2_9e10.b1.seq+ is in U_HW-SSH2_10e06.b1.seq+
********** Contig 53 **********
U_HW-SSH2_4e10.b1.seq+
U_HW-SSH2_4f10.b1.seq+ is in U_HW-SSH2_4e10.b1.seq+
U_HW-SSH2_4h11.b1.seq+ is in U_HW-SSH2_4e10.b1.seq+
U_HW-SSH2_4g11.b1.seq+
********** Contig 54 **********
U_HW-SSH2_5b08.b1.seq+
U_HW-SSH2_5d08.b1.seq+ is in U_HW-SSH2_5b08.b1.seq+
U_HW-SSH2_5e08.b1.seq+
U_HW-SSH2_6h08.b1.seq+ is in U_HW-SSH2_5e08.b1.seq+
U_HW-SSH2_7a10.b1.seq+ is in U_HW-SSH2_6h08.b1.seq+
U_HW-SSH2_6h09.b1.seq+ is in U_HW-SSH2_6h08.b1.seq+
U_HW-SSH2_5h03.b1.seq+ is in U_HW-SSH2_6h09.b1.seq+
U_HW-SSH2_5f03.b1.seq+ is in U_HW-SSH2_5e08.b1.seq+
U_HW-SSH2_1h12.b1.seq+ is in U_HW-SSH2_5f03.b1.seq+
U_HW-SSH2_1a06.b1.seq+ is in U_HW-SSH2_5f03.b1.seq+
U_HW-SSH2_5f07.b1.seq+ is in U_HW-SSH2_5f03.b1.seq+
U_HW-SSH2_3h07.b1.seq+
********** Contig 55 **********
U_HW-SSH2_5d01.b1.seq-
U_HW-SSH2_11c12.b1.seq+ is in U_HW-SSH2_5d01.b1.seq-
U_HW-SSH2_9g11.b1.seq+ is in U_HW-SSH2_5d01.b1.seq-
U_HW-SSH2_12h03.b1.seq+ is in U_HW-SSH2_5d01.b1.seq-
U_HW-SSH2_9f11.b1.seq+
********** Contig 56 **********
U_HW-SSH2_6h04.b1.seq-
U_HW-SSH2_3e11.b1.seq+ is in U_HW-SSH2_6h04.b1.seq-
U_HW-SSH2_3a11.b1.seq+ is in U_HW-SSH2_6h04.b1.seq-
U_HW-SSH2_11f02.b1.seq+ is in U_HW-SSH2_6h04.b1.seq-
U_HW-SSH2_3f11.b1.seq+ is in U_HW-SSH2_11f02.b1.seq+
U_HW-SSH2_12h11.b1.seq+ is in U_HW-SSH2_6h04.b1.seq-
U_HW-SSH2_8h11.b1.seq- is in U_HW-SSH2_6h04.b1.seq-
********** Contig 57 **********
U_HW-SSH2_7f11.b1.seq+
U_HW-SSH2_7f12.b1.seq+ is in U_HW-SSH2_7f11.b1.seq+
U_HW-SSH2_7e12.b1.seq+ is in U_HW-SSH2_7f11.b1.seq+
U_HW-SSH2_5c12.b1.seq+ is in U_HW-SSH2_7e12.b1.seq+
U_HW-SSH2_5f05.b1.seq+ is in U_HW-SSH2_7e12.b1.seq+
U_HW-SSH2_5g12.b1.seq+ is in U_HW-SSH2_7e12.b1.seq+
********** Contig 58 **********
U_HW-SSH2_7h09.b1.seq+
U_HW-SSH2_10c01.b1.seq+
U_HW-SSH2_6c08.b1.seq+ is in U_HW-SSH2_10c01.b1.seq+
U_HW-SSH2_3a10.b1.seq+ is in U_HW-SSH2_10c01.b1.seq+
U_HW-SSH2_6g08.b1.seq+ is in U_HW-SSH2_10c01.b1.seq+
U_HW-SSH2_3f10.b1.seq+ is in U_HW-SSH2_10c01.b1.seq+
U_HW-SSH2_3g11.b1.seq+ is in U_HW-SSH2_10c01.b1.seq+
U_HW-SSH2_7g09.b1.seq+ is in U_HW-SSH2_3g11.b1.seq+
U_HW-SSH2_6d12.b1.seq+ is in U_HW-SSH2_3g11.b1.seq+
U_HW-SSH2_6a08.b1.seq+ is in U_HW-SSH2_10c01.b1.seq+
U_HW-SSH2_7h07.b1.seq+ is in U_HW-SSH2_10c01.b1.seq+
U_HW-SSH2_5f02.b1.seq+ is in U_HW-SSH2_7h07.b1.seq+
U_HW-SSH2_12f06.b1.seq- is in U_HW-SSH2_7h07.b1.seq+
U_HW-SSH2_6a05.b1.seq+ is in U_HW-SSH2_10c01.b1.seq+
U_HW-SSH2_7b06.b1.seq+
********** Contig 59 **********
U_HW-SSH2_8g11.b1.seq+
U_HW-SSH2_9e07.b1.seq+ is in U_HW-SSH2_8g11.b1.seq+
U_HW-SSH2_9e12.b1.seq+ is in U_HW-SSH2_9e07.b1.seq+
U_HW-SSH2_10g07.b1.seq+ is in U_HW-SSH2_9e07.b1.seq+
U_HW-SSH2_9f04.b1.seq+ is in U_HW-SSH2_9e07.b1.seq+
U_HW-SSH2_6g07.b1.seq+
U_HW-SSH2_12g06.b1.seq- is in U_HW-SSH2_6g07.b1.seq+
U_HW-SSH2_4g12.b1.seq- is in U_HW-SSH2_12g06.b1.seq-
U_HW-SSH2_7g12.b1.seq- is in U_HW-SSH2_12g06.b1.seq-
U_HW-SSH2_5d10.b1.seq- is in U_HW-SSH2_12g06.b1.seq-
********** Contig 60 **********
U_HW-SSH2_9c12.b1.seq+
U_HW-SSH2_3f03.b1.seq+ is in U_HW-SSH2_9c12.b1.seq+
U_HW-SSH2_7f10.b1.seq+
U_HW-SSH2_9a12.b1.seq+ is in U_HW-SSH2_7f10.b1.seq+
U_HW-SSH2_9b12.b1.seq+
U_HW-SSH2_9c11.b1.seq+
U_HW-SSH2_9a11.b1.seq+ is in U_HW-SSH2_9c11.b1.seq+
********** Contig 61 **********
U_HW-SSH2_9g05.b1.seq+
U_HW-SSH2_9g04.b1.seq+ is in U_HW-SSH2_9g05.b1.seq+
U_HW-SSH2_5h01.b1.seq+
U_HW-SSH2_7b11.b1.seq+ is in U_HW-SSH2_5h01.b1.seq+
U_HW-SSH2_5g01.b1.seq+
U_HW-SSH2_10c02.b1.seq+
U_HW-SSH2_9f06.b1.seq+ is in U_HW-SSH2_10c02.b1.seq+
U_HW-SSH2_3d05.b1.seq+ is in U_HW-SSH2_10c02.b1.seq+
U_HW-SSH2_6b06.b1.seq+ is in U_HW-SSH2_10c02.b1.seq+
U_HW-SSH2_6a04.b1.seq+ is in U_HW-SSH2_10c02.b1.seq+
U_HW-SSH2_9e11.b1.seq+ is in U_HW-SSH2_10c02.b1.seq+
U_HW-SSH2_11a09.b1.seq+ is in U_HW-SSH2_10c02.b1.seq+
U_HW-SSH2_1a03.b1.seq+ is in U_HW-SSH2_11a09.b1.seq+
U_HW-SSH2_3h08.b1.seq+ is in U_HW-SSH2_10c02.b1.seq+
U_HW-SSH2_3c01.b1.seq+ is in U_HW-SSH2_3h08.b1.seq+
U_HW-SSH2_5h02.b1.seq+
U_HW-SSH2_7h02.b1.seq+

APPENDIX E

Detailed display of contig alignments, performed by Cap3 contig assembly program, for contig assemblies of SSH1 (D-R) sequence data.



```
                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11h04.b1.seq+ CCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGTCACCTAAATAGCTTGGCGTA
U_HW-SSH1_2a09.b1.seq+  CC-AACGCGATAGATGCATAGATTGACTATTCTATAGTGT

consensus               CCCAACGCGATAGATGCATAGATTGACTATTCTATAGTGTCACCTAAATAGCTTGGCGTA

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11h04.b1.seq+ ATCATGGTCATAGCTGTTTCCTGTGTAAAATTGTTATCCGCTCACAATTCCACACAACAT

consensus               ATCATGGTCATAGCTGTTTCCTGTGTAAAATTGTTATCCGCTCACAATTCCACACAACAT

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11h04.b1.seq+ ACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACAT

consensus               ACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACAT

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11h04.b1.seq+ TAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATT

consensus               TAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATT

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11h04.b1.seq+ AATGACTCGGCCAACGCGCGGGGAAGAGGCGGTTTGCGTATTGGCGCTCTTCCGCTTCCT

consensus               AATGACTCGGCCAACGCGCGGGGAAGAGGCGGTTTGCGTATTGGCGCTCTTCCGCTTCCT

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11h04.b1.seq+ CGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGCGAGCGTATCAGCTCACTCAAAG

consensus               CGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGCGAGCGTATCAGCTCACTCAAAG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11h04.b1.seq+ GCGGTAATACGTTATCCCACAGATCGGGGGGATAACGCAGGAAAGAAACTGTGGACCA

consensus               GCGGTAATACGTTATCCCACAGATCGGGGGGATAACGCAGGAAAGAAACTGTGGACCA
```

****************** **Contig 5** *******************

```
                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11b04.b1.seq+ TTCGATTACCGTGGTCCCGGCCGACGTACAAGGGCCCCCTTGATGACATATATGCAAATG
U_HW-SSH1_4c09.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACTAGGGCCCCCTTGATGACATATATGCAAATG

consensus               TTCGATTACCGTGGTCCCGGCCGACGTACAAGGGCCCCCTTGATGACATATATGCAAATG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11b04.b1.seq+ CCATCACAAACTGTGACCCTGAAGGTCCTCTTATGCTGTATGTCTCCAAAATGATTCCAC
U_HW-SSH1_4c09.b1.seq+  CCATCAGAAACTGTGACCCTGAAGGTCCTCTTATGCTGTATGTCTCCAAAATGATTCCAG

consensus               CCATCACAAACTGTGACCCTGAAGGTCCTCTTATGCTGTATGTCTCCAAAATGATTCCAC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11b04.b1.seq+ CATCTGACAAGGGTAAATTCTTTGCCTTTGGACGTGTTTTCGCCGGGAGGGTCGCAACTG
U_HW-SSH1_4c09.b1.seq+  CATCTGACAAGGGTACATTCTTTGCCTTTGGACGTGTTTTCGCCGGGAGGGTCGCAACTG

consensus               CATCTGACAAGGGTAAATTCTTTGCCTTTGGACGTGTTTTCGCCGGGAGGGTCGCAACTG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11b04.b1.seq+ GCATGAAGGTCCGTATCATGGGTCCCAACTTTGTTCCTGGCCAAAAAAAGGATCTATATG
U_HW-SSH1_4c09.b1.seq+  GCATGAAGGTCCGTATCATGGGTCCCAACTTTGTTCCTGGCAAAAAAAAAGATCTATATG

consensus               GCATGAAGGTCCGTATCATGGGTCCCAACTTTGTTCCTGGCAAAAAAAAAGATCTATATG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11b04.b1.seq+ TGAAGAGTGTCCAGCGGACTGTTATCTGGATGGGAAAGAAGCAAGAGTCTGTTGAGGATG
U_HW-SSH1_4c09.b1.seq+  TGAAGAGTGTCCAGCGGACTGTTATCTGGATGGGAAAGAAGCAAGAGTCTGTTGAGGATG

consensus               TGAAGAGTGTCCAGCGGACTGTTATCTGGATGGGAAAGAAGCAAGAGTCTGTTGAGGATG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11b04.b1.seq+ TTCCCTGTGGTAACACCGTTGTTTTGGTTGGTTTGGATCAGTTCATCACCAAAAATGCAA
U_HW-SSH1_4c09.b1.seq+  TTCCCTGTGGAAACACCGTTGCTTTGGTTGGTTTGAATCAGTTCATCACCAAGAATGCGA

consensus               TTCCCTGTGGAAACACCGTTGCTTTGGTTGGTTTGAATCAGTTCATCACCAAAAATGCAA

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11b04.b1.seq+ CCCTGACAAACGAAAAGGAAGTTGATGCCTGCCCAATCAGGGCAATGAAGTTCTCTGTGT
U_HW-SSH1_4c09.b1.seq+  ACTTGAAAAACGAGAAGGAATTTGATGCCTGCCCAACCAGGGCAATGA

consensus               ACCTGAAAAACGAAAAGGAAGTTGATGCCTGCCCAACCAGGGCAATGAAGTTCTCTGTGT

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11b04.b1.seq+ CCCCTGTTGTACCTGCCAGGGCGACAAATCGAAATCCCTACGGAATTCCCGGCCGCACTG

consensus               CCCCTGTTGTACCTGCCAGGGCGACAAATCGAAATCCCTACGGAATTCCCGGCCGCACTG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11b04.b1.seq+ AATGAATACGCTCCCGCCTGCTCTCCCT

consensus               AATGAATACGCTCCCGCCTGCTCTCCCT
```

****************** **Contig 6** *******************

```
                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11c07.b1.seq+ TTCGATTAGCGTGGTCGCGGCCGAGGTACAGCAGGAGCTACCTAAAGAACCAAATGGCTG
U_HW-SSH1_2c01.b1.seq+        TAGCGTGGTCGCGGCCGAGGTACAGCAGGAGCTACCTAGAGAACCAAATGGCTG
U_HW-SSH1_14e01.b1.seq+       TAGCGTGGTCGCGGCCGAGGTACAGCAGGAGCTACCTAAAGAACCAAATGGCTG
U_HW-SSH1_14g01.b1.seq+       TAGCGTGGTCCCGGCCGAGGTGCACGAGGAGCTACCTAAAAAACCAAATGGCTG

consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACAGCAGGAGCTACCTAAAGAACCAAATGGCTG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11c07.b1.seq+ TGGCACTTGGTGGCAGGGTTGCCGAGGAGGTGATCTTTGGGCAAGACAATGTGACAACCG
U_HW-SSH1_2c01.b1.seq+  TGGCACTTGGTGGCAGGGTTGCCGAGGAGGTGATCTTTGGGCAAGACAATGTGACAACCG
U_HW-SSH1_14e01.b1.seq+ TGGCACTTGGTGGCAGGGTTGCCGAGGAGGTGATCTTTGGGCAAGACAATGTGACAACCG
U_HW-SSH1_14g01.b1.seq+ TGGCACTTGGGGGCAGGGTTGCCGAGGAGGTGATCTTTGGGCAAAACAATGTGACAACCG

consensus               TGGCACTTGGTGGCAGGGTTGCCGAGGAGGTGATCTTTGGGCAAGACAATGTGACAACCG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11c07.b1.seq+ GGGCATCCAGCGACTTCATGCAGGTCTCACGTGTCGCCAGACAAATGGTTGAAAGGTTTG
U_HW-SSH1_2c01.b1.seq+  GGGCATCCAGCGACTTCATGCAGGTCTCACGTGTCGCCAGACAAATGGTTGAAAGGTTTG
U_HW-SSH1_14e01.b1.seq+ GGGCATCCAGCGACTTCATGCAGGTCTCACGTGTCGCCAGACAAATGGTTGAAAGGTTTG
U_HW-SSH1_14g01.b1.seq+ GGGCATCCATCGACTTCATGCAGGTCTCACGTGTCCCCAGACAAATGGTTGAAAGGTTTG

consensus               GGGCATCCAGCGACTTCATGCAGGTCTCACGTGTCGCCAGACAAATGGTTGAAAGGTTTG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11c07.b1.seq+ GGTTCAGCAAAAAGATTGGGCAAGTCGCCATCGGGTCATCTGGTGGAAACCCTTTCTTGG
U_HW-SSH1_2c01.b1.seq+  GGTTCAGCAAGAAGATTGGGCAAGTCGCCATCGGGTCATCTGGTGGAAACCCTTTCTTGG
U_HW-SSH1_14e01.b1.seq+ GGTTCAGCAAGAAGATTGGGCAAGTCGCCATCGGGTCATCTGGTGGAAACCCTTTCTTGG
U_HW-SSH1_14g01.b1.seq+ GGTTCAGCAAGAAGATTGGGCAAGTCCCCTTCGGGTCATCTGGTGGAAACCCTTTCTTGG

consensus               GGTTCAGCAAGAAGATTGGGCAAGTCGCCATCGGGTCATCTGGTGGAAACCCTTTCTTGG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11c07.b1.seq+ GCCAGCAGATGTCGAGCCAAAAGGACTACTCGATGGCCACGGCGGACATCGTAAACGCCG
U_HW-SSH1_2c01.b1.seq+  GCCAGCAGATGTCGAGCCAGAAGGACTACTCGATGGCCACGGCGGACATCGTAAACGCCG
U_HW-SSH1_14e01.b1.seq+ GCCAGCAGATGTCGAGCCAGAAGGACTACTCGATGGCCACGGCGGACATCGTAAACGCCG
U_HW-SSH1_14g01.b1.seq+ GCCAGCAGATGTCGAGCCACAAGGACTACTCGATGGCCACGGCGGACATCGTAAACGCCG

consensus               GCCAGCAGATGTCGAGCCAGAAGGACTACTCGATGGCCACGGCGGACATCGTAAACGCCG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11c07.b1.seq+ AGGTCAGGGAACTCGTGGAGACGGCCTACTCGCGCGCGACGCAAATCATCAACACCCACA
U_HW-SSH1_2c01.b1.seq+  AGGTCAGGGAACTCGTGGAGACGGCCTACTCGCGCGCGACGCAAATCATCAACACCCACA
U_HW-SSH1_14e01.b1.seq+ AGGTCAGGGAACTCGTGGAGACGGCCTACTCGCGCGCGACGCAGATCATCAACACCCACA
U_HW-SSH1_14g01.b1.seq+ AGGTCAGGGAACTCGTGGAGACGGCCTACTCGCGCGCGACGCAGATCATCAACACCCACA

consensus               AGGTCAGGGAACTCGTGGAGACGGCCTACTCGCGCGCGACGCAAATCATCAACACCCACA

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11c07.b1.seq+ TCGACATCCTCCACAGGCTCGCCAACCTCCTCATCGAGAAGGAGACCGTGGACGGGGAGG
U_HW-SSH1_2c01.b1.seq+  TCGACATCCTCCACAGGCTCGCCAACCTCCTCATCGAGAAGGAGACCGTGGACGGGGAGG
U_HW-SSH1_14e01.b1.seq+ TCGACATCCTCCACAGGCTCGCCAACCTCCTCATCGAGAAGGAGACCGTGGACGGGGAGG
U_HW-SSH1_14g01.b1.seq+ TCAACATCCTCCACAGGCTCGCCAACCTCCTCATCAAGAAGGAGACCGTGGACGGGGAGG

consensus               TCGACATCCTCCACAGGCTCGCCAACCTCCTCATCGAGAAGGAGACCGTGGACGGGGAGG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11c07.b1.seq+ AGTTCATGAGCCTCTTCATCGACGGGCAGGCAGAGCTGTTCGTTGCATAAGTCGACTCGC
U_HW-SSH1_2c01.b1.seq+  AGTTCATGAGCCTCTTCATCGACGGGCAGGCAGAGCTGTTCGTTGCATAAGTCGACTCGC
U_HW-SSH1_14e01.b1.seq+ AGTTCATGAGCCTCTTCATCGACGGGCAGGCAGAGCTGTTCGTTGCATAAGTCGACTCGC
U_HW-SSH1_14g01.b1.seq+ AGTTCATGAGCCTCTTCATCGACGGGCAGGCAGAGCTGTTCGTTGCATAAGTCGACTCGC

consensus               AGTTCATGAGCCTCTTCATCGACGGGCAGGCAGAGCTGTTCGTTGCATAAGTCGACTCGC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11c07.b1.seq+ CTGTATGTTTTTCGGTGATTACACGAGGGTCCAACTTGTAGGAACCACATTGATCTAGTA
U_HW-SSH1_2c01.b1.seq+  CTGTATGTTTTTCGGTGATTACACGAGGGTCCAACTTGTAGGAACCACATTGATCTAGTA
U_HW-SSH1_14e01.b1.seq+ CTGTATGTTTTTCGGTGATTACACGAGGGTCCAACTTGTAGGAACCACATTGATCTAGTA
U_HW-SSH1_14g01.b1.seq+ CTGTATGTTTTTCGGTGATTACACGAGGGTCCAACTTGTA

consensus               CTGTATGTTTTTCGGTGATTACACGAGGGTCCAACTTGTAGGAACCACATTGATCTAGTA

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11c07.b1.seq+ AAAATGTTCTTTTCGCAAACATGTTTGTATAGTTTCCTTGTAAAAAAATGCCTGTACCTG
U_HW-SSH1_2c01.b1.seq+  AAAATGTTCTTTTCGCAAACATGTTTGTATAGTTTCCTTGTAAAAAAATGCCTGTACCTG
U_HW-SSH1_14e01.b1.seq+ AAAATGTTCTTTTCGCAAACATGTTTGTATAGTTTCCTTGTAAAAAAATGCCTGTACCTG

consensus               AAAATGTTCTTTTCGCAAACATGTTTGTATAGTTTCCTTGTAAAAAAATGCCTGTACCTG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11c07.b1.seq+ GCCCGG
U_HW-SSH1_14e01.b1.seq+ CCCGGGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAGGTCGACCATATGG

consensus               CCCCGGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAGGTCGACCATATGG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14e01.b1.seq+ GAAGAGCTCCCAACGCGTTGGGATGCATAGCTTGAGTATTCTATAGTGTCACTAAAATAG

consensus               GAAGAGCTCCCAACGCGTTGGGATGCATAGCTTGAGTATTCTATAGTGTCACTAAAATAG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14e01.b1.seq+ CTGACGTAATCATGATCATAGCTGCTTGCTGTGTGAATTGTTATCGCTCACAATCCACAC

consensus               CTGACGTAATCATGATCATAGCTGCTTGCTGTGTGAATTGTTATCGCTCACAATCCACAC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14e01.b1.seq+ ACATACGAGGCTGGAAGCTATAAGTGTCA

consensus               ACATACGAGGCTGGAAGCTATAAGTGTCA
```

****************** **Contig 7** *******************

```
                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11e05.b1.seq+ TTCAATTTCGAGCGGCCGCCCGGGCAGGTGCCAATACGTGCTGATCCAGCTGGGAATGTA
U_HW-SSH1_11e09.b1.seq+     ATTTCGAGCGGCCGCCCGGGCAGGTGCCAGTACGTGCTGATCCAGCTGGGAATGAA
U_HW-SSH1_11f09.b1.seq+     ATTTCGAGGGGCCGCCCGGGCGGGTGCCAATACGTGCTGATCCAGCTGGGAATGTA

consensus               TTCAATTTCGAGCGGCCGCCCGGGCAGGTGCCAATACGTGCTGATCCAGCTGGGAATGTA

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11e05.b1.seq+ TGTAGTTTTGGTCTACTCATGCTGGAAATCATATCAGGAAAGCCTCCAAATTCTGAACAC
U_HW-SSH1_11e09.b1.seq+ TGTAGTTTTGGTCTACTCATGCTGGAAATCATATCAGGAAAGCCTCAAGATTCTGAACAG
U_HW-SSH1_11f09.b1.seq+ TGTATTTTTGGTCTACTCATGCTGGAAATCATATCGGGAAAGCCTCCAGATTCTGAACAC

consensus               TGTAGTTTTGGTCTACTCATGCTGGAAATCATATCAGGAAAGCCTCCAGATTCTGAACAC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11e05.b1.seq+ GAGGGCTCTCTTGCGAACTTAGCTATGGAGTGCATTAAGGATGACCGGAGTATATCCTGT
U_HW-SSH1_11e09.b1.seq+ GAGGGCTCTCTTGCTAACTTATCTATGGAGTGCATTAAGGATGACCGGAGTATATCCTGT
U_HW-SSH1_11f09.b1.seq+ GAGGGCTCTCTTGCTAACTTAGCTATGGAGTGCATTAAGGATGACCGGAGTATATCCTGT

consensus               GAGGGCTCTCTTGCTAACTTAGCTATGGAGTGCATTAAGGATGACCGGAGTATATCCTGT

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11e05.b1.seq+ TTGCTTGACCCTACCTTGACGACTCACAAAAAAAACGATCTAGATATCATTTGCGAGTTG
U_HW-SSH1_11e09.b1.seq+ TTGCTTGACCCTACCTTGACGACTCACAAAGAAAACGATCTAT-TATCATTTGCGAGTTG
U_HW-SSH1_11f09.b1.seq+ TTGCTTGACCCTACCTTGACGACTCAAAAAAAAAACAATCTATTTATCTTTTGCGAGTTG

consensus               TTGCTTGACCCTACCTTGACGACTCACAAAAAAAACGATCTATATATCATTTGCGAGTTG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11e05.b1.seq+ ATCGAGGACTGCATCCAGAGTGATCCGAAAAAGAGACCAAGTATGAGAGAGGTCACCGCT
U_HW-SSH1_11e09.b1.seq+ ATCGAGGACTGCATCCAGAGTGATCCGAGAAAGACACCAAGTATGAGACAGGTCACCGCT
U_HW-SSH1_11f09.b1.seq+ ATCGAGGACTGCATCCAGAGTGATCCAAAAAAGAGACCAAGTATGAGAGAGGTCACCGCT

consensus               ATCGAGGACTGCATCCAGAGTGATCCGAAAAAGAGACCAAGTATGAGAGAGGTCACCGCT

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11e05.b1.seq+ AAATTGCGAGAAGTGCTATCGATTTCACCAGAGGCAGCAACGCCGAGGTTATCTCCGCTT
U_HW-SSH1_11e09.b1.seq+ AAATTGCGAGAAGTGCTATCGATTTCACCAGAGGCACCAACGCCAAGATTATCTCCGCTT
U_HW-SSH1_11f09.b1.seq+ AAATTGCGAGAAGTGCTACCGATTTCACCAGAGGCACCAACGCCGAGGTTATCTCCGCTT

consensus               AAATTGCGAGAAGTGCTATCGATTTCACCAGAGGCACCAACGCCGAGGTTATCTCCGCTT

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11e05.b1.seq+ TGGTGGGCAGAGCTTGAGATACTTTCAGTTGAATCCTAG-GAAGAAA-CATGTTGATATG
U_HW-SSH1_11e09.b1.seq+ TGGTGGGCAGAGCTTGAGATACTTTCAGCTGAATCCTAGAGAAGAAAACATGTTGATATG
U_HW-SSH1_11f09.b1.seq+ TGGGGGGCAGAGCTTGAGATACTTTCAGTTGAATCCTAG-GAAGAAA-CATGTTGATATG

consensus               TGGTGGGCAGAGCTTGAGATACTTTCAGTTGAATCCTAG-GAAGAAA-CATGTTGATATG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11e05.b1.seq+ G-TATGGTTCTTGCAGCAACACTGAGGTCCTGTGCGTACCTCGGCCGCGACCACGCTA
U_HW-SSH1_11e09.b1.seq+ GGTATGGCTCTTGCA-CAACACTGAGGTCGTGAGCGTACCTCGGCCGCTACCATGCTA
U_HW-SSH1_11f09.b1.seq+ G-TATGGTTCTTGCAGCAACACTGAGGTCCTGTGCGTACCTCGGCCGCGACCACGCTA

consensus               G-TATGGTTCTTGCAGCAACACTGAGGTCCTGTGCGTACCTCGGCCGCGACCACGCTA
```

****************** **Contig 8** *******************

```
                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11h09.b1.seq+ TTCGATTAGCGTGGTCGCGGCCGAGGTACTGATCCTGATAATGGCAAAAACAAAATACTG
U_HW-SSH1_3g08.b1.seq+        TAGCGTGGTCGCGGCCGAGGAACGGATCCTGAGAATGGCAAAAAGAAAAGACTG

consensus               TTCGATTAGCGTGGTCGCGGCCGAGGAACGGATCCTGAGAATGGCAAAAACAAAAGACTG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11h09.b1.seq+ CTCGAAATATTTAGCGGTTGGAGGGAGAATGTCATATATCTGCTAAATGCAACTGAGGAC
U_HW-SSH1_3g08.b1.seq+  CTCAAAAAAAAAAGGGGTTGGTGTGATAATGTCATAGATCTGCTAAATGCAACTGAGGAG

consensus               CTCAAAAAAAAAAGCGGTTGGAGGGAGAATGTCATAGATCTGCTAAATGCAACTGAGGAC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11h09.b1.seq+ GAATTTTTTCTTCGCCGGGATATATACGACCGGCCACCTACTATCAACTGGGGGAAAGGT
U_HW-SSH1_3g08.b1.seq+  GAAGCAATTCTTCGCCGGGATATATACGACCGGCCACCTACTATCAACTGGGGGAAAGGT

consensus               GAAGCAATTCTTCGCCGGGATATATACGACCGGCCACCTACTATCAACTGGGGGAAAGGT

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11h09.b1.seq+ CGTGTCACCTTGCTTGGTGACTCTGTCCATGCTATGCACCCAAATCTGGGACAGGGTGGC
U_HW-SSH1_3g08.b1.seq+  CGTGTCACCTTGCTTGGTGACTCTGTCCATGCTATGCAGCCAAATCTGGGACAGGGGGGC

consensus               CGTGTCACCTTGCTTGGTGACTCTGTCCATGCTATGCACCCAAATCTGGGACAGGGGGGC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11h09.b1.seq+ TGCATGGCTATTGAGGATGGTTACCAGCTGGCTGTAGAGCTTGAGAAGGCCTGGGAAGAG
U_HW-SSH1_3g08.b1.seq+  TGCATGGCTATTGAGGATGGTTACCAGCTGGCTGTAGAGCTTGAGCAGGCCTGGGAAGAG

consensus               TGCATGGCTATTGAGGATGGTTACCAGCTGGCTGTAGAGCTTGAGAAGGCCTGGGAAGAG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11h09.b1.seq+ AGTGTCAAGTCTAGAACTCCTGTGGACGTTATTTCCTCCTTGAGGAGTTATGAGAAGGAG
U_HW-SSH1_3g08.b1.seq+  AGTGTCAAGTCAAGAACTCCGGTGGACGTTATTTCCTCCTTGAGGAGTTATGATAAGGAG

consensus               AGTGTCAAGTCAAGAACTCCGGTGGACGTTATTTCCTCCTTGAGGAGTTATGAGAAGGAG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11h09.b1.seq+ AGAAAGCTACGTGTTGCTATCATACATGGATTGGCAAGAATGGCGGCAATCATGGCTACC
U_HW-SSH1_3g08.b1.seq+  AGAAAGCTACGTGTTGCTATC-TCCATGGATTGGCAAGAA

consensus               AGAAAGCTACGTGTTGCTATCATACATGGATTGGCAAGAATGGCGGCAATCATGGCTACC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_11h09.b1.seq+ ACTTACAGACCATATCTAGGTGTGGGTCTGGGACCTTTGTCGTTTTTGACAAAGTTGAGG
```

```
consensus               ACTTACAGACCATATCTAGGTGTGGGTCTGGGACCTTTGTCGTTTTTGACAAAGTTGAGG

U_HW-SSH1_11h09.b1.seq+ ATACCGCATCCTGAAAGAGTTGGCGGCAGATTTTTCATCAAGGTTGGAATGCCTTTGATG

consensus               ATACCGCATCCTGAAAGAGTTGGCGGCAGATTTTTCATCAAGGTTGGAATGCCTTTGATG

U_HW-SSH1_11h09.b1.seq+ CTGAGCTGGATTTTAGGTGGCAACAGTTCAAAGCTAGAAGGAAGACCGTTAAGTTGCCGG

consensus               CTGAGCTGGATTTTAGGTGGCAACAGTTCAAAGCTAGAAGGAAGACCGTTAAGTTGCCGG

U_HW-SSH1_11h09.b1.seq+ CTTTCTGACAAGGCAAGCAACCAGCTTGGTCGATGGTTTCAGGATGACGATGCATTGGAA

consensus               CTTTCTGACAAGGCAAGCAACCAGCTTGGTCGATGGTTTCAGGATGACGATGCATTGGAA

U_HW-SSH1_11h09.b1.seq+ CAAGCTATGGGTGGAGAGTGGCCACCTGCCCG

consensus               CAAGCTATGGGTGGAGAGTGGCCACCTGCCCG


****************** Contig 9 ********************

U_HW-SSH1_14a04.b1.seq+ TAGCGTGGTCCCGGCCGAGGTACAAGGAACGTGTGAGGGAGCTCCTTGATTTCAGCATCT

consensus               TAGCGTGGTCCCGGCCGAGGTACAAGGAACGTGTGAGGGAGCTCCTTGATTTCAGCATCT

U_HW-SSH1_14a04.b1.seq+ ACTTAGACATCAGCAATGAGGTTAAGTTCCCATGGAAAATTCAAAAAGACATGGCAAAGC
U_HW-SSH1_3h08.b1.seq+          CATCAGCAATGAGGTTAAGTTCGCATGGAAAATTCAGAGAGACATGGCAGAGC

consensus               ACTTAGACATCAGCAATGAGGTTAAGTTCCCATGGAAAATTCAAAAAGACATGGCAAAGC

U_HW-SSH1_14a04.b1.seq+ GTGGGCACTGTCTTGAAAGCATCAAGGCTAGCATCGAAGCCAGGAAACCTGATTTTGATG
U_HW-SSH1_2f07.b1.seq+                                                GAAACCTGATTTTGATG
U_HW-SSH1_3h08.b1.seq+  GTGGGCACAGTCTTGAAAGCATCAAGGCTAGCATCGAAGCCAGGAAACCTGATTTTGATG
U_HW-SSH1_11e04.b1.seq-                                               GAAACCTGATTTTGATG

consensus               GTGGGCACAGTCTTGAAAGCATCAAGGCTAGCATCGAAGCCAGGAAACCTGATTTTGATG

U_HW-SSH1_14a04.b1.seq+ CCTTTATTGATCCGCAAAAGCAATACGCTGATGCTGTGATTGAAGTTCTGCCAA-CCCGG
U_HW-SSH1_2f07.b1.seq+  GCTTTATTGATCCGCGGAT-CAATACGCTGATGCTGTGATTGAGGGCCTGCCAA-CCCAG
U_HW-SSH1_3h08.b1.seq+  CCTTTATTGATCCGCAAAAGCAATACGCTGATGCTGTGATTGAAGTTCTGCCAA-CCCAG
U_HW-SSH1_11e04.b1.seq- CCCTTATT-ATCCGCAGAAGCAATACGCTGATGCTGTGATTGAAGTTCTGCCAAACCCAG

consensus               CCTTTATTGATCCGCAGAAGCAATACGCTGATGCTGTGATTGAAGTTCTGCCAA-CCCAG

U_HW-SSH1_14a04.b1.seq+ CTGATTCCTGATGACAACGAAGGAAAGGTGCTGCGTGTTAAATTGATCATGAAAGAAGGC
U_HW-SSH1_2f07.b1.seq+  CTGATTCCTGATGACAACGGTCGAAAGGTGCTGGATGTTAAATTGATCCTGAAAGAAGGG
U_HW-SSH1_3h08.b1.seq+  CTGATTCCTGATGACAACAAAGGAAAGGTGCTGCGTGTTAAATTGATCATGAAAGAAGGC
U_HW-SSH1_11e04.b1.seq- CTGATTCCTGATGACAACGAAGGAAAGGTGCTGCGTGTTAAATTGATCATGAAAGAAGGC

consensus               CTGATTCCTGATGACAACGAAGGAAAGGTGCTGCGTGTTAAATTGATCATGAAAGAAGGC

U_HW-SSH1_14a04.b1.seq+ ATTAAGTTCTTCAACCCAGTTTACCTCTTCGATGAAGGATCAACCATCAACTGGATCCCT
U_HW-SSH1_2f07.b1.seq+  TTCTGTTCCTTC--CCCCGTTTACCACTTTGATGAGGGATCCGCCATTGGATGGATCCCT
U_HW-SSH1_3h08.b1.seq+  ATTAAGTTCTTCAACCCAGTTTACCTCTTCGATGAAGGATCAACCATCAACTGGATCCCT
U_HW-SSH1_11e04.b1.seq- ATTAAGTTCTTCAACCCAGTTTACCTCTTCGATGAAGGATCAACCATCAACTGGATCCCT

consensus               ATTAAGTTCTTCAACCCAGTTTACCTCTTCGATGAAGGATCAACCATCAACTGGATCCCT

U_HW-SSH1_14a04.b1.seq+ TGTGGAAGAAAGCTTACATGCTCTTATCCTGGCATCAAATTTTCCTATGGCCCAGACACT
U_HW-SSH1_2f07.b1.seq+  GGTGGAAAAGCCCTTACATGCTCTTATCCTGTGATCAAATTTTCCTATGGCCCACG-ACT
U_HW-SSH1_3h08.b1.seq+  TGTGGAAGAAAGCTTACATGCTCTTCTCCTGGCATCAAATTTTCCTATGGCCCATACTTT
U_HW-SSH1_11e04.b1.seq- TGTGGAAGAAAGCTTACATGCTCTTATCCTGGCATCAAATTTTCTTATGGCCCAGACACT

consensus               TGTGGAAGAAAGCTTACATGCTCTTATCCTGGCATCAAATTTTCCTATGGCCCAGACACT

U_HW-SSH1_14a04.b1.seq+ TACTTTGGCCAAGAGGTATCGGTGCTGGAGATGGATGGGCAATTTGACAGACTGGATGAA
U_HW-SSH1_2f07.b1.seq+  TACTTTGGCCAAGAGGTATCGGTGCTGGACAGGGATGGGCAATTTGACAGACTAGATGAA
U_HW-SSH1_3h08.b1.seq+  TACTTTGGCCAA
U_HW-SSH1_11e04.b1.seq- TACTTTGGCCAAGAGGTATCGGTGCTGGAGATGGATGGGCAATTTGACAGACTAGATGAA

consensus               TACTTTGGCCAAGAGGTATCGGTGCTGGAGATGGATGGGCAATTTGACAGACTAGATGAA

U_HW-SSH1_14a04.b1.seq+ CTCTTCTATGTTGAGAGCCACCTAAGCAACCT
U_HW-SSH1_2f07.b1.seq+  CTCATCTATGTTGAGAGCCACCTAAGCAACCT
U_HW-SSH1_11e04.b1.seq- CTCATTTATGTTGAGAGCCACCTAAGCAACCTCTCAACCAAGTTTTACGGGGAGGTGACA

consensus               CTCATCTATGTTGAGAGCCACCTAAGCAACCTCTCAACCAAGTTTTACGGGGAGGTGACA

U_HW-SSH1_11e04.b1.seq- CAGCAAATGCTAAAGCATGCAGACTTCCCAGGCAGCAACAATGGAACAGGTCTCTTCCAG

consensus               CAGCAAATGCTAAAGCATGCAGACTTCCCAGGCAGCAACAATGGAACAGGTCTCTTCCAG

U_HW-SSH1_11e04.b1.seq- ACCATCGTAGGACTGAAGATTAGAGATCTCTATGAACAGATCATCGCTGAGAGGGCCGGC

consensus               ACCATCGTAGGACTGAAGATTAGAGATCTCTATGAACAGATCATCGCTGAGAGGGCCGGC

U_HW-SSH1_11e04.b1.seq- GTTCCTGCTGAAGCAGCAAAAGTTTGATCAGCCCCAAATTCAAGTCCACGAATCGTTTCA

consensus               GTTCCTGCTGAAGCAGCAAAAGTTTGATCAGCCCCAAATTCAAGTCCACGAATCGTTTCA

U_HW-SSH1_11e04.b1.seq- TCACCAACTCTATGAGAATGAGCATCCTCGCATTTCCTGTACCCGCCCGGGCGGCCGCTC

consensus               TCACCAACTCTATGAGAATGAGCATCCTCGCATTTCCTGTACCCGCCCGGGCGGCCGCTC

U_HW-SSH1_11e04.b1.seq- GAAATCGAA

consensus               GAAATCGAA


****************** Contig 10 *******************

U_HW-SSH1_14d01.b1.seq+ TAGCGTGGTCCCGGCCGAGGTGCATGATTGAAGGATACCTTAAACGGTTCAACCGTGTGG

consensus               TAGCGTGGTCCCGGCCGAGGTGCATGATTGAAGGATACCTTAAACGGTTCAACCGTGTGG

U_HW-SSH1_14d01.b1.seq+ CGATTGAAAGGATGAAGGAGATCCGGTGCTACAAGGGCATCCGGCACAAGCTCGGCCTCC
U_HW-SSH1_10b02.b1.seq+         AGGATGAAGGAGATCCGGGGCTACAAGGGCATCCGGAACAAGCTCGGCCTCC

consensus               CGATTGAAAGGATGAAGGAGATCCGGGGCTACAAGGGCATCCGGAACAAGCTCGGCCTCC

U_HW-SSH1_14d01.b1.seq+ CGGTCCGTGGCCAGAGGACAAAGAACAACTGCAGGACGCTCAAGGGAAGAGGGCTTCCG
U_HW-SSH1_10b02.b1.seq+ CGGTCCGTGGCCAGAAGACAAAGAACAACTGCAGGACGCTCAAGGGAAGAGGGCTTCCG

consensus               CGGTCCGTGGCCAGAAGACAAAGAACAACTGCAGGACGCTCAAGGGAAGAGGGCTTCCG

U_HW-SSH1_14d01.b1.seq+ TCGCCAAGAAGAAGTCGGCTTCGTCCTCCTACAAATAAGTGACACTGCCATGTGTATTTG
U_HW-SSH1_10b02.b1.seq+ TCCCCAAAAAGAAGTCGGCTTCGTCCTCCAACAAATAAGTGACACTGCCATGTGTATTTG

consensus               TCCCCAAAAAGAAGTCGGCTTCGTCCTCCAACAAATAAGTGACACTGCCATGTGTATTTG

U_HW-SSH1_14d01.b1.seq+ CCTCCTGTTTGGTTTTTGTTTGCTGCATCACGGCGCTACCACAATTCGGTACCTGCCCGG
U_HW-SSH1_10b02.b1.seq+ CCTCCTGTTTGGTTTTTGTTTGCTGCCTCACGGCGCTACCACCATTCGGTACCTGCCCGG

consensus               CCTCCTGTTTGGTTTTTGTTTGCTGCATCACGGCGCTACCACAATTCGGTACCTGCCCGG

U_HW-SSH1_14d01.b1.seq+ GCGGACGCTCGAAATCACTGTTGAATTCGCGGCCCCCTGCTGGTCGACCATATGGGATAC
U_HW-SSH1_10b02.b1.seq+ GCGGACGCTCTAAATCACTACTGAATGGCCGGCCCCTTGGAGATCTACCGTGTGGCAGAC

consensus               GCGGACGCTCGAAATCACTACTGAATGCCCGGCCCCCTGCAGATCGACCATATGGCAGAC

U_HW-SSH1_14d01.b1.seq+ CTCCCAACGGGTTGGATGCATACCCTGAGTAT
U_HW-SSH1_10b02.b1.seq+ CACCCAGCCAGTTGAATGAATAGCTTTAGTATTCTGTTGTGTCACATACATGGCGTGATG

consensus               CACCCAACCAGTTGAATGAATACCCTGAGTATTCTGTTGTGTCACATACATGGCGTGATG

U_HW-SSH1_10b02.b1.seq+ TTAATCAAGGTCAAGCTCTGTTTCCTGGGCGAAATTGACAGCCCCGGGAATTCCAGAAAA

consensus               TTAATCAAGGTCAAGCTCTGTTTCCTGGGCGAAATTGACAGCCCCGGGAATTCCAGAAAA

U_HW-SSH1_10b02.b1.seq+ CCTATGAGCCACTTTTTAACGCGTAAAGCCTGAGGTCCCTAACGATAAAGCAACTCTCAT

consensus               CCTATGAGCCACTTTTTAACGCGTAAAGCCTGAGGTCCCTAACGATAAAGCAACTCTCAT

U_HW-SSH1_10b02.b1.seq+ AACCTGCATCTAACTGTGTTAAGACTTTTGAGCCTGATGCTTGTCATGCCCGTTTAATTA

consensus               AACCTGCATCTAACTGTGTTAAGACTTTTGAGCCTGATGCTTGTCATGCCCGTTTAATTA

U_HW-SSH1_10b02.b1.seq+ TCGACCGGGCAGCGAGCGGTGTAGAGTGATTCGCCGATTGGCGACTGTTGACTTTTTCAT

consensus               TCGACCGGGCAGCGAGCGGTGTAGAGTGATTCGCCGATTGGCGACTGTTGACTTTTTCAT

U_HW-SSH1_10b02.b1.seq+ AGCTGCCTCCCGGGTTAACGCTTTCGATGCTGTCAGCAGGTCCCTCACTGATTGGGGGAA

consensus               AGCTGCCTCCCGGGTTAACGCTTTCGATGCTGTCAGCAGGTCCCTCACTGATTGGGGGAA

U_HW-SSH1_10b02.b1.seq+ TCCGGGCTTCCGCCGGTGTCCGGGGGGTATAATTCTGGACCGCCTCCCCTAACGAATAGGC

consensus               TCCGGGCTTCCGCCGGTGTCCGGGGGGTATAATTCTGGACCGCCTCCCCTAACGAATAGGC

U_HW-SSH1_10b02.b1.seq+ CACAAAAGCGCAGTAATCTGTGTATAGGGGCCCGAGATAATTGCTCGTCATCATAAATGA

consensus               CACAAAAGCGCAGTAATCTGTGTATAGGGGCCCGAGATAATTGCTCGTCATCATAAATGA

U_HW-SSH1_10b02.b1.seq+ ACTACTCCA

consensus               ACTACTCCA


****************** Contig 11 *******************

U_HW-SSH1_16b12.b1.seq+ TTCGATTTCGAGCGGCCGCCCGGGCATGTACGCGCCGTTCCCGCCCGGGGGCATGTTCCA

consensus               TTCGATTTCGAGCGGCCGCCCGGGCATGTACGCGCCGTTCCCGCCCGGGGGCATGTTCCA

U_HW-SSH1_16b12.b1.seq+ CAGCCAGGGCGGGCTCAAAAGCTTCGAGCACCCCATGAACCGGCTCAAGGCGTTCCCGCG
U_HW-SSH1_1a09.b1.seq+                                CACCCCATGAACCGGCTCAAGGCGTTCCCGCG
U_HW-SSH1_13c09.b1.seq+                               CACCCCATGAACTTGCTCAAGGCGTTCCCACG
U_HW-SSH1_13b07.b1.seq+                                        GCTCAAGGCCTCCCCACG

consensus               CAGCCAGGGCGGGCTCAAAAGCTTCGAGCACCCCATGAACCGGCTCAAGGCGTTCCCACG

U_HW-SSH1_16b12.b1.seq+ CGTGGACAGCGAGGGCTTCATGTGCGGCGCCAACTTCAAGGTCA-ACGCTTTCGCCAAGA
U_HW-SSH1_1a09.b1.seq+  CGTGGACAGCGAGGGCGTCATGTGCGGCGCCAACTTCAAGGTCG-ACGCATTCACCAAGA
U_HW-SSH1_13c09.b1.seq+ CGTGCACAGCTAGGGCGCCATGTGCGCCCCCAACTTCCAGGTCG-AAGCATTCTCTACTA
U_HW-SSH1_13b07.b1.seq+ CGAGGACAGCTAGGGCGCCATGTGCGCCCCATACTTCCAGGTTTTAATCATTCTCCACAA

consensus               CGTGGACAGCGAGGGCGCCATGTGCGCCCCCAACTTCAAGGTCG-AAGCATTCTCCAAGA

U_HW-SSH1_16b12.b1.seq+ TCAACTCCATGCCCCGCGTCGGCAGCGCCACCAACTGGCCCGCCACCTGGGACAACGCCG
U_HW-SSH1_1a09.b1.seq+  TCAACTCCATGCCCCGCGTCGGCAGCGCCACCAACTGGGCCGCCACCTGGGACGACGCCG
U_HW-SSH1_13c09.b1.seq+ TCATCTCCCTGCCCCGTTTCGGCAGCGCCACCAACTGGGCAGCCACCTGGAACAACCCCC
U_HW-SSH1_13b07.b1.seq+ TCCTTTCCATGCCCCGGGTAAGAAACCCAGCCAACTGGACCGCCACCTGGAACAACTCCC

consensus               TCAACTCCATGCCCCGCGTCGGCAGCGCCACCAACTGGGCCGCCACCTGGAACAACGCCC

U_HW-SSH1_16b12.b1.seq+ CCATCTAGCTGGGCTGGTGTGCATCACCTCGCCGGCGCCGCTCGCCTAGGTCGTCGGACT
U_HW-SSH1_1a09.b1.seq+  CCATCTAGCTGGGCTGGTGTGCATCACCTCGCCGGCGCCGCTCGCCTAGCTCGTCGGACT
U_HW-SSH1_13c09.b1.seq+ CCATGTAGCTGGGCTGGTGTGCATAAACTCCCCGGCGCCGATCGCCTTGGTGGTCGAACT
U_HW-SSH1_13b07.b1.seq+ CCATGTAGCTGGCCAGGCCCGCAAAAACTCACTTGCACCAATCGCCTTGGTGGTTGAACT

consensus               CCATCTAGCTGGGCTGGTGTGCATAAACTCCCGGCGCCGATCGCCTAGGTCGTCGAACT

U_HW-SSH1_16b12.b1.seq+ TCTGAATTTGGGCTTACCGCATTTTACTTACCTTTTTTCTTTGGCAATGTACCTCGGCCG
U_HW-SSH1_1a09.b1.seq+  TCTGAATTTGGGCTTACCGCATTTTACTTACCTTTTTTCTTTGGCAATGTACCTCGGCCG
U_HW-SSH1_13c09.b1.seq+ TCTGAATTTGGGTTTACCGCATTTTACTTTCTTTTTTTCTTTGGCAATGTACCTCGGCCG
U_HW-SSH1_13b07.b1.seq+ GATCAATTTGGGCGCACCGCCTTCTCCTTTCCTTTTTGCATTGGCGATGTCCCTCGGCTC

consensus               TCTGAATTTGGGCTTACCGCATTTTACTTACCTTTTTTCTTTGGCAATGTACCTCGGCCG

U_HW-SSH1_16b12.b1.seq+ CAACCACGCTA
U_HW-SSH1_1a09.b1.seq+  CGACCACGCTA
U_HW-SSH1_13c09.b1.seq+ CAACCACGCTA
U_HW-SSH1_13b07.b1.seq+ CAACAACGGGAAGAGCTTTGATTTTTTTGGATGCCTGCAG

consensus               CAACCACGCTAAGAGCTTTGATTTTTTTGGATGCCTGCAG


****************** Contig 12 *******************

U_HW-SSH1_16c04.b1.seq+ TTCGATTTCGTGGTCCCGCCGGGGGTACACGGGCAAGTATGTTACAAAGAGCTCTGTTT

consensus               TTCGATTTCGTGGTCCCGCCGGGGGTACACGGGCAAGTATGTTACAAAGAGCTCTGTTT

U_HW-SSH1_16c04.b1.seq+ GCGCCATTTTTTGGGTTCGTCTATTGTGTGTGCCACCATATGGCGGGAGGATGCACCCGG

consensus               GCGCCATTTTTTGGGTTCGTCTATTGTGTGTGCCACCATATGGCGGGAGGATGCACCCGG

U_HW-SSH1_16c04.b1.seq+ TAGGATCGGGCTCTCGATCGCGCCTAGAAGGTGCCATACCTTCCCTCCTTTGCAAGTTTT

consensus               TAGGATCGGGCTCTCGATCGCGCCTAGAAGGTGCCATACCTTCCCTCCTTTGCAAGTTTT

U_HW-SSH1_16c04.b1.seq+ TTTACTTTGTTTTAATTAGAAATTTCCTTTTCTATTTACCATGGGGACTGCGTCGGTGAA
U_HW-SSH1_16c03.b1.seq+                        TCCTTTTCTAGCC-CCATGGGGACTGCGTTGGTGAA

consensus               TTTACTTTGTTTTAATTAGAAATTTCCTTTTCTAGCCACCATGGGGACTGCGTCGGTGAA

U_HW-SSH1_16c04.b1.seq+ ATGGGCT-GGGGGGGAGAGACTAAATTCTGTTGAGGCGGCCGGGGGCGGGCAGTCGAATT
U_HW-SSH1_16c03.b1.seq+ ATGGGCCAGGGGGGGAGAGACGCAATTCTCTGAAGGCGGCCGGGGGCGGGCTTTCGAATT

consensus               ATGGGCCAGGGGGGGAGAGACGAAATTCTCTGAAGGCGGCCGGGGGCGGGCAGTCGAATT

U_HW-SSH1_16c04.b1.seq+ TGTATTA
U_HW-SSH1_16c03.b1.seq+ TGTATTA

consensus               TGTATTA


****************** Contig 13 *******************

U_HW-SSH1_16g05.b1.seq+ TTCGATTTCCAGCGGCCCGCCGGGCGGGCACCGGTAAATATGTGATAAAAAGATCTGTTT
U_HW-SSH1_16h05.b1.seq+ TTCGATTTCCAGCGGCCCCCCCGGCGTGCACTTGTAAATATGATATAAAAAGATCACTTA
U_HW-SSH1_16h06.b1.seq+ TTCGATTACCAGCGGCCCCCCGGGCGTGCACTTGTAATTATGTTATTAAAAAGATCAGTTA

consensus               TTCGATTTCCAGCGGCCCCCCGGGCGTGCACTTGTAAATATGTTATAAAAAGATCAGTTA
```

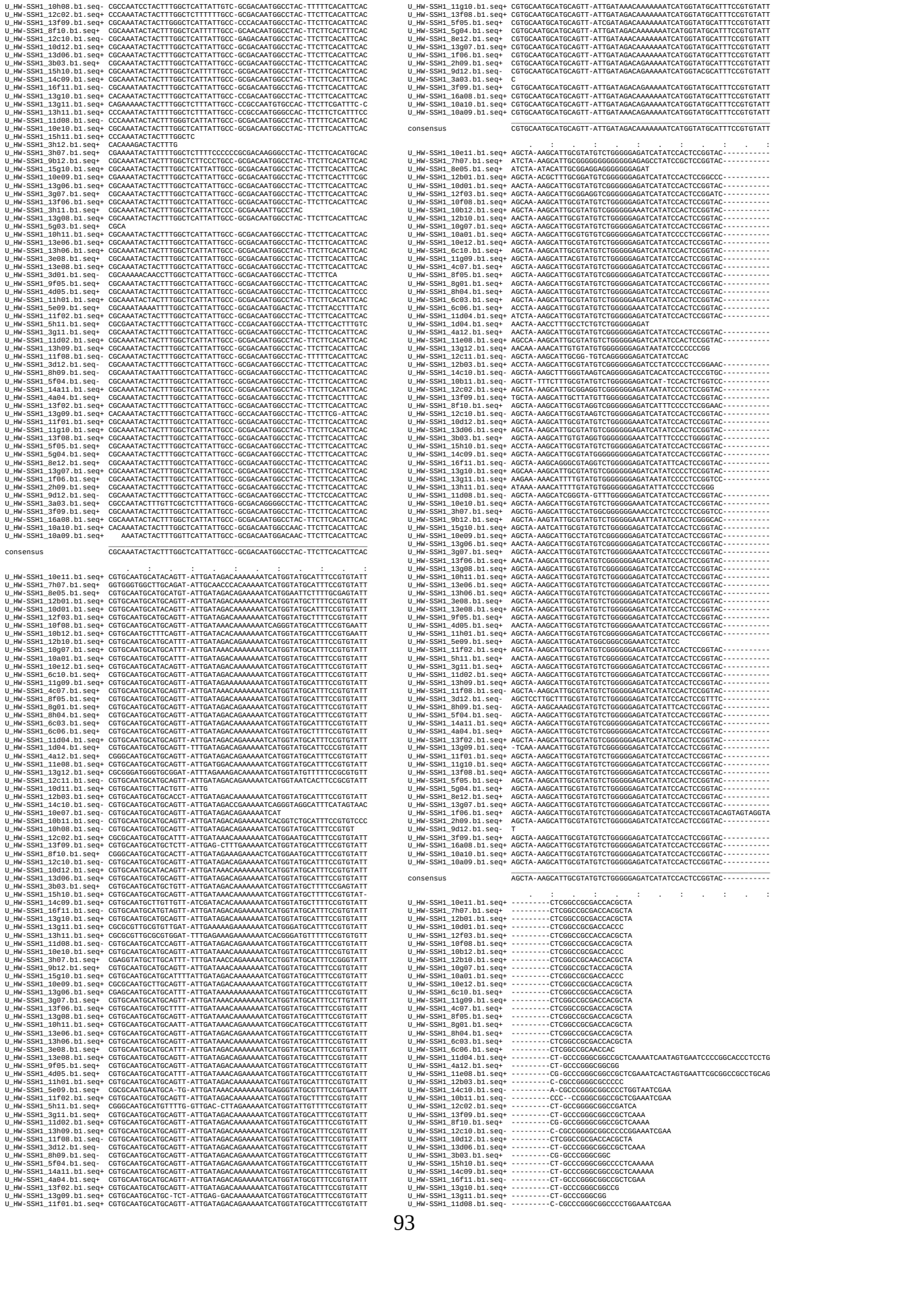
```
U_HW-SSH1_16g05.b1.seq+ TTGCCTTTTGGTTTTTTGTTTTTTTTGTGTGCATGACCATTTGGGGGGAGGATGCAGGGC
U_HW-SSH1_16h05.b1.seq+ ACGCCTTTTGGTTTTTTGTTTTTTTTGTGTGTATGACCATTTTTGGGGAGGATGCAGGGC
U_HW-SSH1_16h06.b1.seq+ ATGCCTTTAGGTTTTTTGTTTTTTATTGTGTGCATGACCATTTAGGGGGAGGATGCAGGGG
                        ___________________________________________________________
consensus               ATGCCTTTTGGTTTTTTGTTTTTTTTGTGTGCATGACCATTTAGGGGGAGGATGCAGGGC

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16g05.b1.seq+ AAATACAACGGGGGCTCATTATTGCCGAG-ACCTGGCATACTTCTTCATTTTCTCCTCGG
U_HW-SSH1_16g06.b1.seq+                                      GGCATACTTCTTCATTTTCTCCTCGG
U_HW-SSH1_16h05.b1.seq+ AGATTTT-CGGGCTCTCATTTTTGCCTACTACCCCTTTGTGCTTTCCACTTTCTCCTCGG
U_HW-SSH1_16h06.b1.seq+ AGAACCAACTGTGGCTCATTTTTCCTATGACCCCCTTTGTAATCTTCACTTTCTCCTCGG
                        ___________________________________________________________
consensus               AGATACAACGGGGGCTCATTTTGCCAAGAACCCGCAGACTTCTTCACTTTCTCCTCGG

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16g05.b1.seq+ GGGGTTCTTATGTGTCAGGTCCCACCCCTCTCTTGGTATGTTTTTCAGTATATTATGTAA
U_HW-SSH1_16g06.b1.seq+ GGGGTTTGCATTTGTC-GATGACCCCCCTCTCTTGGTTTTTTTTTCAGTTTATTATGTAA
U_HW-SSH1_16h05.b1.seq+ GGGGTTCTTATGTGTCAAATTCCCTCCCTCTTTTGGAATTTTTTTCAAAATATTATGTTA
U_HW-SSH1_16h06.b1.seq+ GGGGTTCTTGTGTGTCAGATTCGCCCCCTCTCTTGGAATGCTTTTCAAAATATTATGTAA
                        ___________________________________________________________
consensus               GGGGTTCTTATGTGTCAGATTCCCCCCCTCTCTTGGAATGTTTTTCAAAATATTATGTAA

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16g05.b1.seq+ TATTTTGCGTGGGGGGGGGAGAGATAATTTCCTGGGGAGGACCCCGGGGGCGAGAATACT
U_HW-SSH1_16g06.b1.seq+ TACTTTGCGTGTGGGGGGGAGAGATTATTTGCAGTCGAGGACCCCGGGGCCGAGAATACT
U_HW-SSH1_16h05.b1.seq+ TATTTTGCATGGGGGGGGGAGAAACAAATTCCTGGGGAGGGGCCCGGGGCCCAGAATACT
U_HW-SSH1_16h06.b1.seq+ TAGTTTGCGTGGGGGGGGGAGAGACCATTTGCAGGGGAGGACCCCGGGGCCCAGACTACT
                        ___________________________________________________________
consensus               TATTTTGCGTGGGGGGGGGAGAGACAATTTCCAGGGGAGGACCCCGGGGCCCAGAATACT

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16g05.b1.seq+ AATAA
U_HW-SSH1_16g06.b1.seq+ AATAA
U_HW-SSH1_16h05.b1.seq+ AATAAATAGTAAAGTACCCGCCGCCTGGAGGGCCACCATATGGTAGAGCTCCCAGGCCCT
U_HW-SSH1_16h06.b1.seq+ AATAAATAGAAAAGTA
                        ________________________________________________________
consensus               AATAAATAGAAAAGTACCCGCCGCCTGGAGGGCCACCATATGGTAGAGCTCCCAGGCCCT

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16h05.b1.seq+ CGGATGCATAGGTTGTGTATTCTAAAGTGTCGCCCCTCGAGCTTGACAGATACAGGGTCA
                        ___________________________________________________________
consensus               CGGATGCATAGGTTGTGTATTCTAAAGTGTCGCCCCTCGAGCTTGACAGATACAGGGTCA

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16h05.b1.seq+ TATCTGATTGCCGATAGAAAATCTGAGGCGCTCACTGGGCGACCCGGCTTGCGAACTGGA
                        ___________________________________________________________
consensus               TATCTGATTGCCGATAGAAAATCTGAGGCGCTCACTGGGCGACCCGGCTTGCGAACTGGA

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16h05.b1.seq+ TGACCTCAGTTACCACCCCGGTGTGCCTAATGGAAATCCCTGCCCACAGTAAATGCGTCG
                        ___________________________________________________________
consensus               TGACCTCAGTTACCACCCCGGTGTGCCTAATGGAAATCCCTGCCCACAGTAAATGCGTCG

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16h05.b1.seq+ CGTTCGATGCCCCCTTTCGAGTCGGCAAACCTGTTGGGTGAGCTGCTTTGCCCACTCGGC
                        ___________________________________________________________
consensus               CGTTCGATGCCCCCTTTCGAGTCGGCAAACCTGTTGGGTGAGCTGCTTTGCCCACTCGGC

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16h05.b1.seq+ CACCGCGCGGGGAATCGGGGCTTGCATTTTTGTTGCTGAACCTGTCCCCCCGCCAAGAAT
                        ___________________________________________________________
consensus               CACCGCGCGGGGAATCGGGGCTTGCATTTTTGTTGCTGAACCTGTCCCCCCGCCAAGAAT

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16h05.b1.seq+ TCTCTGCGCTGAGTCGGTCGATTTAGTGATCGCAAACAAGTGAGGCGAGGCGAGTAATAC
                        ___________________________________________________________
consensus               TCTCTGCGCTGAGTCGGTCGATTTAGTGATCGCAAACAAGTGAGGCGAGGCGAGTAATAC

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16h05.b1.seq+ GTTAGCAAAATGGCGGCTAACAAATGGGCAAGATCGGGTAGGGAAACGCCGACAGCCGAC
                        ___________________________________________________________
consensus               GTTAGCAAAATGGCGGCTAACAAATGGGCAAGATCGGGTAGGGAAACGCCGACAGCCGAC

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16h05.b1.seq+ TGCAATACGGAACAAGGCCACTGTGAGGAGTATGTATCTGGGCTCCGCCCACCCTAAAGA
                        ___________________________________________________________
consensus               TGCAATACGGAACAAGGCCACTGTGAGGAGTATGTATCTGGGCTCCGCCCACCCTAAAGA

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16h05.b1.seq+ CAATCCCTAAT
                        ___________________________________________________________
consensus               CAATCCCTAAT

****************** Contig 14 ******************
                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16g09.b1.seq+ TTCGATTAGCGTGGTCGCGGCCGAGGTACAACCTGCCGCTGGTGGGGAACAAAGCACCGG
                        ___________________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACAACCTGCCGCTGGTGGGGAACAAAGCACCGG

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16g09.b1.seq+ ACTTCGCCGCGGAGGCCGTGTTCGACCAGGAGTTCATCAACGTCAAGCTATCTGATTACA
                        ___________________________________________________________
consensus               ACTTCGCCGCGGAGGCCGTGTTCGACCAGGAGTTCATCAACGTCAAGCTATCTGATTACA

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16g09.b1.seq+ TTGGGAAGAAGTATGTGATTCTTTTCTTCTACCCTCTGGACTTCACCTTCGTCTGCCCAA
                        ___________________________________________________________
consensus               TTGGGAAGAAGTATGTGATTCTTTTCTTCTACCCTCTGGACTTCACCTTCGTCTGCCCAA

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16g09.b1.seq+ CTGAAATTACGGCTTTCAGCGACAGACATGAGGAGTTCGAGAAGATAAACACTGAAATTC
U_HW-SSH1_16f09.b1.seq+                                                         TTC
U_HW-SSH1_11b03.b1.seq+                                                         TTC
                        ___________________________________________________________
consensus               CTGAAATTACGGCTTTCAGCGACAGACATGAGGAGTTCGAGAAGATAAACACTGAAATTC

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16g09.b1.seq+ TTGGTGTTTCAGTTGATAGTGTGTTTTCCCATCTTGCATGGGTGCAGACAGAAAGGAAAT
U_HW-SSH1_16f09.b1.seq+ TTGGTGTTTCAGTTGATAGTGTGTTTTCCCATCTTGCATGGGTGCAGACAGAAAGGAAAT
U_HW-SSH1_11b03.b1.seq+ TTGGGGTTCCAGTGGATAGTGTGTTTTCCCATCTTGAATGGGGGCGGAGGGAAAGAAGTT
                        ___________________________________________________________
consensus               TTGGTGTTTCAGTTGATAGTGTGTTTTCCCATCTTGCATGGGTGCAGACAGAAAGGAAAT

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16g09.b1.seq+ CTGGTGGACTTGGTGATCTGAAATATCCGCTGGTTTCTGACGTCACCAAATCAATCTCAA
U_HW-SSH1_16f09.b1.seq+ CTGGTGGACTTGGTGATCTGAAATATCCGCTGGTTTCTGACCTCACCAAATCAATCTCAA
U_HW-SSH1_11b03.b1.seq+ CTGGGGGACTTGGAGATCTTAAGGATCGGGTGGTTTCTGATGTCCCCAAATCAATCTCAC
                        ___________________________________________________________
consensus               CTGGTGGACTTGGTGATCTGAAATATCCGCTGGTTTCTGACGTCACCAAATCAATCTCAA

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16g09.b1.seq+ AGTCTTTTGGTGTATTGATCCCTGATCAGGGAATTGCTCTGAGAGGATTATTCATCATTG
U_HW-SSH1_16f09.b1.seq+ AGTCTTTTGGTGTATTGATCCCTGATCAGGGAATTGCTCTGAGAGGATTATTCATCATTG
U_HW-SSH1_11b03.b1.seq+ ATTCTTTTGGTGAATTGATCCCTGATCTGGGAATTGCTCGGATGAGATTATTCTTCATTC
                        ___________________________________________________________
consensus               AGTCTTTTGGTGTATTGATCCCTGATCAGGGAATTGCTCTGAGAGGATTATTCATCATTG

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16g09.b1.seq+ ACAAGGAGGGTGTGATTCACCATTCCACTATTAACAACCTTGGTATTGGCCGTAGTGTGG
U_HW-SSH1_16f09.b1.seq+ ACAAGGAGGGTGTGATTCACCATTCCACTATTAACAACCTTGGTATTGGCCGTAGTGTGG
U_HW-SSH1_11b03.b1.seq+ ACAAGGAGGGTGTGAGGCAGCATTCGACTATTAACATCCTTGGTATTGGCCGTAGTGTGG
                        ___________________________________________________________
consensus               ACAAGGAGGGTGTGATTCACCATTCCACTATTAACAACCTTGGTATTGGCCGTAGTGTGG

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16g09.b1.seq+ ATAGAGACCTTGAGAACCCTTCAGGCTCTGCAATACGTCCAAGAAACCCAAACGAGGTCT
U_HW-SSH1_16f09.b1.seq+ ATAGAGACCTTGAGAACCCTTCAGGCTCTGCAATACGTCCAATAAAACCCAGACGACGTCT
U_HW-SSH1_11b03.b1.seq+ ATAGAGACCTTGACATCCCTTCCGGCTCTGCAATACACCCC-TAAAACCCAGACAAGGTCT
                        ___________________________________________________________
consensus               ATGAGACCTTGAGAACCCTTCAGGCTCTGCAATACGTCCAATAAAACCCAGACGAGGTCT

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16g09.b1.seq+ GCCCGGCGGGATGGAAACCTGGGGAAAAGTCA-ATGACCCCTGACCCCAAGGGCAGCAAG
U_HW-SSH1_16f09.b1.seq+ GCCCGGCGGGATGGAAACCTGGGGAAAAGTCAGATGAAGCCTGACCCCACGGGCAGCAAG
U_HW-SSH1_11b03.b1.seq+ GCGCGGCGGGATGGAAATCTGGGGAAAA
                        ____________________________________________________________
consensus               GCCCGGCGGGATGGAAACCTGGGGAAAAGTCAGATGAACCCTGACCCCAAGGGCAGCAAG

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16g09.b1.seq+ GAGTACCTG
U_HW-SSH1_16f09.b1.seq+ GAGTACCTGCCCAGGCGTCCGCTCATAACGCTAGAGAAATCGCGCGCGTATACGACACGA
                        _________________________________________________________
consensus               GAGTACCTGCCCAGGCGTCCGCTCATAACGCTAGAGAAATCGCGCGCGTATACGACACGA

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f09.b1.seq+ CATATCGGAAACCGCAGAAGGCTTGGATGCTGCGTTATTCTTC
                        ___________________________________________________________
consensus               CATATCGGAAACCGCAGAAGGCTTGGATGCTGCGTTATTCTTC

****************** Contig 15 ******************
                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_2f05.b1.seq+  TTCGATTTCCAGGGGCCGCCCGGGCGGGTACTACTGGTGTCA-CTACATACAAAGCTTAT
U_HW-SSH1_2f06.b1.seq+         TTCGAGCGGCCGCCCGGGCGGGTACTACTGGTGTCAACTAAAGACAAAGCTTAT
U_HW-SSH1_16h09.b1.seq+              GGCCGCCCGGGCAGGTACTACTGGTGTCAACTAGAGACAAAGCTTAT
U_HW-SSH1_2h02.b1.seq+               GGCCGCCCGGGCGGGTACTACTGGTGTCAACTACAGACAAAGCTTAT
U_HW-SSH1_14a02.b1.seq+                                        AGACAAAGCTTAT
                        ___________________________________________________________
consensus               TTCGATTTCCAGCGGCCGCCCGGGCGGGTACTACTGGTGTCAACTACAGACAAAGCTTAT

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_2f05.b1.seq+  ATTGCCTTGCCAGTGGTGACCAATGCTGCTGTTCATGCTATTGTTGAAAAACAGGGACTG
U_HW-SSH1_2f06.b1.seq+  ATTGGCATGCCAGTGGTGACCAATGCTGCTGTTCATGCAATTGTTGAAGAACAGGGACTG
U_HW-SSH1_16h09.b1.seq+ ATTGGCATGCCAGTGGTGACCAATGCTGCTGTTCATGCAATTGTTGAAGAACAGGGACTG
U_HW-SSH1_2h02.b1.seq+  ATTGGCATGCCAGTGGTGACCAATGCTGCTGTTCATGCAATTGTTGAAAAACAGGGACTG
U_HW-SSH1_14a02.b1.seq+ ATTGGCATGCCAGTGGTGACCCTTGCTGCTGTTCATGCAATTGTTAAAAAACTGGGACTG
                        ___________________________________________________________
consensus               ATTGGCATGCCAGTGGTGACCAATGCTGCTGTTCATGCAATTGTTGAAAAACAGGGACTG

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_2f05.b1.seq+  GATGATAAAGTGATTGTTTTCAAGTTCAAAAAGAAGAAAAAGTACCTCGGCCGCTACCAC
U_HW-SSH1_2f06.b1.seq+  GACAATAAAGTGATTGTTTTCAAGTTCAAAAAGAAGAAAAAGTACCTCGGCCGCGACCAC
U_HW-SSH1_16h09.b1.seq+ GACGATAAAGTGATTGTTTTCAAGTTCAAAAAAAAAAAAAAGTACCTCGGCCGCGACCAC
U_HW-SSH1_2h02.b1.seq+  GACGATAAAGTGATTGTTTTCAAGTTCAAGAAAAAAAAAAAAGTACCTCGGCCGCGACCAC
U_HW-SSH1_14a02.b1.seq+ GACGATAAAGTGATTGTTTTCTT-TACAAGAAGAAAAAAAATTACCGCGGCCGCGACCAC
                        ___________________________________________________________
consensus               GACGATAAAGTGATTGTTTTCAAGTTCAAAAAGAAAAAAAAGTACCTCGGCCGCGACCAC

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_2f05.b1.seq+  GCTA
U_HW-SSH1_2f06.b1.seq+  GCTA
U_HW-SSH1_16h09.b1.seq+ GCTA
U_HW-SSH1_2h02.b1.seq+  GCTA
U_HW-SSH1_14a02.b1.seq+ GCTAATTT
                        ________
consensus               GCTAATTT

****************** Contig 16 ******************
                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_3d09.b1.seq+  TAGCGTGGTCGCGGGGAG-AAACACCAAACGACCGAGACCAAGGGCACCGCCGTCGACCG
U_HW-SSH1_3d10.b1.seq+  TAGCGTGGTCGCGGCGAGGAAACACCAAAGACCGAGACCAAGGGCACCGCCGTCGACCG
                        ___________________________________________________________
consensus               TAGCGTGGTCGCGGCGAGGAAACACCAAAGACCGAGACCAAGGGCACCGCCGTCGACCG

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_3d09.b1.seq+  CGCAATCCACATAACCCATTGGAGGGGGGAGGGACCCCCTGCAGCGAGCACTGCGATCTC
U_HW-SSH1_3d10.b1.seq+  CAGCATCCTCCACGCCCTTTGGGGGGGGGAGGGACCCCCTGCAGCGAGCACTGCGATCTC
                        ___________________________________________________________
consensus               CACAATCCACAAAACCCATTGGAGGGGGGAGGGACCCCCTGCAGCGAGCACTGCGATCTC

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_3d09.b1.seq+  TTCTTCACCTTCGTTCTCTGACGAGCTTCTCCGACGATTGCCGTCCCTCTACTGCTCCTA
U_HW-SSH1_3d10.b1.seq+  TTCTTCACCTTCGG-CTCTGACGAGCTTCTCCGACGATTGCCGTCGCTCTACTGCTCCTA
                        ___________________________________________________________
consensus               TTCTTCACCTTCGGTCTCTGACGAGCTTCTCCGACGATTGCCGTCCCTCTACTGCTCCTA

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_3d09.b1.seq+  AGCAAACACCGAGCCTCCATGTGCTCCTCTGATGGTGGATCCTTGGAGCCAGATGCCACC
U_HW-SSH1_3d10.b1.seq+  AGCAAACACCGAGCCTCCATGTGCTCCTCTGATGGGGGATCCTTGGAGCCAGATGCCACC
                        ___________________________________________________________
consensus               AGCAAACACCGAGCCTCCATGTGCTCCTCTGATGGGGGATCCTTGGAGCCAGATGCCACC

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_3d09.b1.seq+  GCCGATGGATGCTGGGAGGTGGAGGCCGTCGACGACCAAGAGTAGTTAGGGGGTCCCAGG
U_HW-SSH1_3d10.b1.seq+  GCCGATGGATGCTACTATGTGGAGGCCGTCAACAACCACGAGTAGTTAGGAGGTCCCAGG
                        ___________________________________________________________
consensus               GCCGATGGATGCTACGAGGTGGAGGCCGTCAACAACCAAGAGTAGTTAGGAGGTCCCAGG

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_3d09.b1.seq+  CAGGAGGCCTTGCCTCTTCGATTGGGTTGCTTTTGTGCTAGCCTTCTTATGGCACCCTTG
U_HW-SSH1_3d10.b1.seq+  GGGGAGGCCTTGCCTCTTCCATTGTGGGGCTTTTGTGCTAGCCTTCTTAAGGCACCTTG
                        ___________________________________________________________
consensus               CAGGAGGCCTTGCCTCTTCCATTGGGGGGCTTTTGTGCTAGCCTTCTTAAGGCACCCTTG

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_3d09.b1.seq+  CTTAATTTTTGTCTGTACCTGCCGGGGCGGCCGCTCGA
U_HW-SSH1_3d10.b1.seq+  TTTAATTTT
                        _____________________________________________________________
consensus               CTTAATTTTTGTCTGTACCTGCCGGGGCGGCCGCTCGA

****************** Contig 17 ******************
                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_3h05.b1.seq+  TTCGAGCGGCCGCCCGGGAAGGAAGGGGCGAACAACTACTACCGTGCAGATGGCCAGAAC
U_HW-SSH1_4a02.b1.seq+  TTCGAGCGGCCGCCCGGGCAGGTCGGG-CGAACAACTACTACCGTGCAGATGGCCAGAAC
                        ___________________________________________________________
consensus               TTCGAGCGGCCGCCCGGGAAGGAAGGGGCGAACAACTACTACCGTGCAGATGGCCAGAAC

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_3h05.b1.seq+  AAGGGCAACTTCCTTACGGACCGTCCTTCAACCAAGGTTCATGCTGCTCCCGGCGGTGGC
U_HW-SSH1_4a02.b1.seq+  ACGGGCAACTTCCTTACGGACCGTCCTTCAACCAAGGTTCATGCTGCTCCCGGCGGTGGC
                        ___________________________________________________________
consensus               AAGGGCAACTTCCTTACGGACCGTCCTTCAACCAAGGTTCATGCTGCTCCCGGCGGTGGC

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_3h05.b1.seq+  TCGTCCCTGGGCTACTTGTTTGGCGGGAAGTGATCTCTGTTAATGATGCTGCGATGAATT
U_HW-SSH1_4a02.b1.seq+  TCGTCCCTGGGCTACTTGTTTGGCGGGAAGTGATCTCTGTTAATGATGCTGCGATGAATT
                        ___________________________________________________________
consensus               TCGTCCCTGGGCTACTTGTTTGGCGGGAAGTGATCTCTGTTAATGATGCTGCGATGAATT

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_3h05.b1.seq+  GGCCTGTATCTCTGTTATCCATGTGGAGAAAACTGGAAGTGTTTGGTTTCAGCAGTTTAC
U_HW-SSH1_4a02.b1.seq+  GGCCTGTATCTCTGTTATCCATGTGGTGAAAACTGGAAGTGTTTGGTTTCAGCAGTTTAC
                        ___________________________________________________________
consensus               GGCCTGTATCTCTGTTATCCATGTGGAGAAAACTGGAAGTGTTTGGTTTCAGCAGTTTAC

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_3h05.b1.seq+  CACCTGCGTCGATGTACCTCGGCCGCGACCACGCTA
U_HW-SSH1_4a02.b1.seq+  CACCTGCGTCGATGTACCTCGGCCGCGACCACGCTA
                        ___________________________________________________________
consensus               CACCTGCGTCGATGTACCTCGGCCGCGACCACGCTA

****************** Contig 18 ******************
                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_4b09.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGAACTGGACAAGCTTTGTGCTGCTCTAAACATCAA
U_HW-SSH1_4a09.b1.seq+        TAGCGTGGTCGCGGCCGAGGAACTGGACAAGCTTTGTGCTGCTCTAAACATCAA
                        ___________________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGAACTGGACAAGCTTTGTGCTGCTCTAAACATCAA

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_4b09.b1.seq+  TAAAAAGAGCGTGGATAGAGACCTTGACGTTTACCGCAACTTACTCTCGAAACTGGTTCA
U_HW-SSH1_4a09.b1.seq+  TAAAAAGAGCGTGGATAGAGACCTTGACGTTTACCGCAACTTACTCTCGAAACTGGTTCA
                        ___________________________________________________________
consensus               TAAAAAGAGCGTGGATAGAGACCTTGACGTTTACCGCAACTTACTCTCGAAACTGGTTCA

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_4b09.b1.seq+  AGCCAAGGAACTTCTCAAGGAATACATCGAGAGGGAAAAGAAAAAGAGAGAGGAGAGATT
U_HW-SSH1_4a09.b1.seq+  AGCCAAGGAACTTCTCAAGGAATACATCGAGAGGGAAAAGAAGAAGAGAGAGGAGAGATT
                        ___________________________________________________________
consensus               AGCCAAGGAACTTCTCAAGGAATACATCGAGAGGGAAAAGAAAAAGAGAGAGGAGAGATT

                              .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_4b09.b1.seq+  GGAGACGCCCAAGCCGAATGAGGCTGTTGCAAAATTCGATGGAAGCGCTTATCCCTTGAA
U_HW-SSH1_4a09.b1.seq+  GGAGACGCCCAAGCCGAATGAGGCTGTTGCAAAATTCGATGGAAGCGCTTATCCCTTGAA
```

```
consensus                GGAGACGCCCAAGCCGAATGAGGCTGTTGCAAAATTCGATGGAAGCGCTTATCCCTTGAA

U_HW-SSH1_4b09.b1.seq+  GCATTAACTCAACCTTTCCCCAAAGGACAGCTTGTCCGGATAACAGATATTAACAGTTAT
U_HW-SSH1_4a09.b1.seq+  GCATTAACTCAACCTTTCCCCAGAGGACAGCCTGTCCGGATAACAGATATTAACAGTTAT
consensus                GCATTAACTCAACCTTTCCCCAAAGGACAGCCTGTCCGGATAACAGATATTAACAGTTAT

U_HW-SSH1_4b09.b1.seq+  ACACATCTGGATAGCGTTGAGAACTATTGGGGGCATCTTTGGCTGCTCTTCGCCCGAGTG
U_HW-SSH1_4a09.b1.seq+  ACACATCTGGATAGCGTTGAGAACTATTGGGGGCATCTTTGGCCGCTCTTCGCCCGAGTG
consensus                ACACATCTGGATAGCGTTGAGAACTATTGGGGGCATCTTTGGCCGCTCTTCGCCCGAGTG

U_HW-SSH1_4b09.b1.seq+  TAGTACCTGCCCGGGCGGCCTCACAAACCCACTCCCCAATTCACGACCGCCGGAGGTGGC
U_HW-SSH1_4a09.b1.seq+  TAGTACCTGCCCGG
consensus                TAGTACCTGCCCGGGCGGCCTCACAAACCCACTCCCCAATTCACGACCGCCGGAGGTGGC

U_HW-SSH1_4b09.b1.seq+  CAAATATGGCATCAGGGCGGGGGCATTGGATGCACATGGCTTGAGTATACTAAAAGTGTC
consensus                CAAATATGGCATCAGGGCGGGGGCATTGGATGCACATGGCTTGAGTATACTAAAAGTGTC

U_HW-SSH1_4b09.b1.seq+  ACCAAAATAGCTGGATAAAACCTGGAACTTAGCTGTAGGCGGGGGGGAAAAGGTTATCCG
consensus                ACCAAAATAGCTGGATAAAACCTGGAACTTAGCTGTAGGCGGGGGGGAAAAGGTTATCCG

U_HW-SSH1_4b09.b1.seq+  TTTTGTTTTCCCGCGCGTCATTCAAGTCGGAATCAAAAATTGCATGGGCGTGGGGGTGCC
consensus                TTTTGTTTTCCCGCGCGTCATTCAAGTCGGAATCAAAAATTGCATGGGCGTGGGGGTGCC

U_HW-SSH1_4b09.b1.seq+  AGACGAATCATATCAAATGCAATAACTAGGGGTGGCGTCTCA
consensus                AGACGAATCATATCAAATGCAATAACTAGGGGTGGCGTCTCA

****************** Contig 19 ******************
U_HW-SSH1_4c04.b1.seq+  TTCGAGCGGCCGCCCGGGCAGGTACCAGGACAAGCTTTCCGGCGACGAGCTTCTGTCGGA
U_HW-SSH1_15f09.b1.seq+ TACCAGGGGCCCCCCCGACAGGAACGAGAACAAGTTTTCCGGCGACAAGCTACTGTCCCA
consensus                TACCAGCGGCCCCCCCGACAGGAACCAGAACAAGCTTTCCGGCGACAAGCTACTGTCCCA

U_HW-SSH1_4c04.b1.seq+  TTCGTTCCCTTACAGGGAGCTGGAGAACGGCGTGCTCTGGGAAGTCGATGGCCATTGGGT
U_HW-SSH1_15f09.b1.seq+ ACCAAACCCTTACAGGGAGCTGGAGAACGGCTTGCTCTGGGAAGTCAATGGCCCTTGGGT
U_HW-SSH1_12a09.b1.seq+                                                  TTGGGT
consensus                ACCAAACCCTTACAGGGAGCTGGAGAACGGCGTGCTCTGGGAAGTCAATGGCCATTGGGT

U_HW-SSH1_4c04.b1.seq+  CGTTCAAGGAGCAGTTGATGTGGACATTGGAGCCAATCCCTCTGCTGAGGGTGGTGGTGA
U_HW-SSH1_15f09.b1.seq+ CTTTCCAGGAGCATTTGATGTGGACATTGGACCCAATCCCTCTGCTGAGGGGGGTGGTGT
U_HW-SSH1_12a09.b1.seq+ CGTTCAAGGAGCACTTGATGTGGACATTGCACCCAATCCCTCTGCTGAGGGTGGTGGTGA
U_HW-SSH1_15h12.b1.seq+ CGTTCAAGGAGCAGTTGATGTGGACATTGGAAAAAAGCCCACTGCTGAGGGTGGTGGTGA
U_HW-SSH1_11h03.b1.seq+                          ATTGGAGCCAATCCCTCTGCTGAGGGTGGTGGTGA
U_HW-SSH1_2g01.b1.seq+                           ATTGGAGCCAGTCCCTCTGCTGAGGGTGGTGGTGA
consensus                CGTTCAAGGAGCAGTTGATGTGGACATTGGAGCCAATCCCTCTGCTGAGGGTGGTGGTGA

U_HW-SSH1_4c04.b1.seq+  TGATGAGGGTGTTGATGACCAGGCCGTGAAGGGGGTTGACTTTGTTGACCCCTTCCGTCT
U_HW-SSH1_15f09.b1.seq+ TGATGAGGGGGTCCAAGACCAGTCAGGGAAAGGGGTTGAAATTGTTGAGACCTTCCTTCT
U_HW-SSH1_12a09.b1.seq+ TGATGAGGGTGTCGATGACCAGGCCGGGAAGGTGGTTGACTTTGTTGACACCTTCCGTCT
U_HW-SSH1_15h12.b1.seq+ TGATGAGGGTGTCGATGACCAGGCCGTGAAGGTGGTTGACATTGTTGACACCTTCCGTCT
U_HW-SSH1_11h03.b1.seq+ TGATGAGGGTGTCGATGACCAGGCCGTGAAGGTGGTTGACATTGTTGACCCTTCCGTCT
U_HW-SSH1_2g01.b1.seq+  TGATGAGGGTGTCGATGACCATTCCGTGAAGGTGGTTGACATTGTTAACACCTTCCGTCT
consensus                TGATGAGGGTGTCGATGACCAGGCCGTGAAGGTGGTTGACATTGTTGACACCTTCCGTCT

U_HW-SSH1_4c04.b1.seq+  TCAGGAGCAACCTGCTTTTGACAAAAACCAGTTTATCTCTCACATGAAGCGCTACATCAA
U_HW-SSH1_15f09.b1.seq+ CCAGGAG
U_HW-SSH1_12a09.b1.seq+ TCAGGAGCAACCTGCTTTTGACAAAAAGCATTTTATCTCTCACATGAAGCGCTACATCAA
U_HW-SSH1_15h12.b1.seq+ TCAGGAGCAACCTGCTTTTGACAAGAAGCAGTTTATCTCTCACATGAAGCGCTACATCAA
U_HW-SSH1_11h03.b1.seq+ TCAGGAGCACCCTGCTTTTGACAAAAAGCAGTTTATCTCTCACATGAAGCGCTACATCAA
U_HW-SSH1_2g01.b1.seq+  TCAGGAGCAACCTGCTTTTGACAAAAAGCAGTTTATCTCTCACATGAAGCGCTACATCAA
consensus                TCAGGAGCAACCTGCTTTTGACAAAAAGCAGTTTATCTCTCACATGAAGCGCTACATCAA

U_HW-SSH1_4c04.b1.seq+  GAACCTCTCTGCCAAGCTGGAGGGGGGTGACCTAGATGCTTTCAAAAAGAATGTTGAGTC
U_HW-SSH1_12a09.b1.seq+ GAACCTCTCTGCCAAGCTTGAAGGGGATGACCTATATGTTTTCAAGAAAAATGTTGAGTC
U_HW-SSH1_15h12.b1.seq+ GAACCTCTCTGCCAAGCTTGAAGGGGATGACCTAGATGTTTTCAAGAAGAATGTTGAGTC
U_HW-SSH1_11h03.b1.seq+ GAACCTCTCTGCCAAGCTTGAAGGGGATGACCTATATGTTTTCAAAAAAAATGTTGAGTC
U_HW-SSH1_2g01.b1.seq+  GAACCTCTCTGCCAAGCTTGAAGGGGATGACCTATATGTTTTCAAAAAAAATGTTGAGTC
consensus                GAACCTCTCTGCCAAGCTTGAAGGGGATGACCTATATGTTTTCAAAAAAAATGTTGAGTC

U_HW-SSH1_4c04.b1.seq+  CGCCACAAAGTATCTTCTTACCAAGCTCAAGGACCTTCAGTT
U_HW-SSH1_12a09.b1.seq+ TGCCACAAAGTATCTTCTTAGCAAGCTCAAGGACCTTCA
U_HW-SSH1_15h12.b1.seq+ TGCCACAAAGTATCTTCTTAGCAAGCTCAAGGACCTTCAGTT-TCTTTGTTGGCGAGAAC
U_HW-SSH1_11h03.b1.seq+ TGCCACAAAGTATCTTCTTAGCAAGCTCAAGGACCTTCAGTT
U_HW-SSH1_2g01.b1.seq+  TGCCACAAAGTATCTTCTTAGCAAGCTCAAGGACCTTCAGTTGTAAGTTCTCTCTTTGCC
consensus                TGCCACAAAGTATCTTCTTAGCAAGCTCAAGGACCTTCAGTTGTAAGTGCTCGCGAGAAC

U_HW-SSH1_15h12.b1.seq+ ATGCATGATGATGGGGGCGTGGTGTTCGCCTACTACAAGGAGGGAGCTGCTGATCCA
U_HW-SSH1_2g01.b1.seq+  TTGCTCGAAAGTGCAGGCACTGTTTATCATTGGTCCGTCCAGACACGTTAGTACCTGCCC
consensus                ATGCACGAAAATGCAGGCACGGTGTACCACTACTACAACCAGACACCTGAGGACCCACCC

U_HW-SSH1_2g01.b1.seq+  GGGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAGGTCGACCATATGGGAG
consensus                GGGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAGGTCGACCATATGGGAG

U_HW-SSH1_2g01.b1.seq+  AGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGTCACCTAAATAGCTTGG
consensus                AGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGTCACCTAAATAGCTTGG

U_HW-SSH1_2g01.b1.seq+  CGTACTCATGGTCATACCTGTTTCCTGTGAGAAATTGTTATCCGCTCACAATTCCCCACA
consensus                CGTACTCATGGTCATACCTGTTTCCTGTGAGAAATTGTTATCCGCTCACAATTCCCCACA

U_HW-SSH1_2g01.b1.seq+  CCATCCACCTCGGAAACATATTGTGTAAAGTCTGGGGTGACTAATGAGTGAGCCACTCAA
consensus                CCATCCACCTCGGAAACATATTGTGTAAAGTCTGGGGTGACTAATGAGTGAGCCACTCAA

U_HW-SSH1_2g01.b1.seq+  ATTATTTGCGTTGCGCTCACTGCCCGCATCCAACC
consensus                ATTATTTGCGTTGCGCTCACTGCCCGCATCCAACC

****************** Contig 20 ******************
U_HW-SSH1_4d11.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACATACATATCCACGTACTGAGAGAACGACACA
consensus                TTCGATTAGCGTGGTCGCGGCCGAGGTACATACATATCCACGTACTGAGAGAACGACACA

U_HW-SSH1_4d11.b1.seq+  GGTCTTTTGGTTTTATTTTTTAATAGCGCAACATCTTATGAGAAATCAATCAAGGTAGAA
U_HW-SSH1_7b09.b1.seq+           TTTTATTTTTTTATTAGCTCAACATCTTATGAGCACTCCATCAAGGTAGAA
U_HW-SSH1_7b11.b1.seq+           TTTTATTTTTTAGTAGCTCAACATCGTATGAGCACTCCATCAACGTAAAA
consensus                GGTCTTTTGGTTTTATTTTTTAATAGCTCAACATCTTATGAGCACTCCATCAAGGTAGAA

U_HW-SSH1_4d11.b1.seq+  ATTAATCTCCCCCTCAGCGCGTCGATGCATGCACGTAGGAAGGATTATATATTGAACTGG
U_HW-SSH1_7b09.b1.seq+  ATTTCTCTCCACCCCAGCGCGTCCATGCCTGCCCGTAGGAAGGATTATATATTGAACTAG
U_HW-SSH1_7b11.b1.seq+  ATTAAGCTCCACGCAAGCGCGTCCATGCATGCACGTAGGAAGGATTATATATTGAACTAG
consensus                ATTAATCTCCACCCCAGCGCGTCCATGCATGCACGTAGGAAGGATTATATATTGAACTAG

U_HW-SSH1_4d11.b1.seq+  TTGACCTTGTTGCATTTGGTGGACATGCTGATGGGAAAGGGGACCCTGACTCCGCACTTG
U_HW-SSH1_7b09.b1.seq+  TTGACTTTGTTGCAGTTGGGGGACATGCTGATGGGGAAGGGCACGCTGACACCGCATTTG
U_HW-SSH1_7b11.b1.seq+  TTGACATTGTTGCAGTTGGTGGACATGCTGATGGGGAAGGGCACGCTGACGCCGCACTTG
consensus                TTGACATTGTTGCAGTTGGTGGACATGCTGATGGGGAAGGGCACGCTGACACCGCACTTG

U_HW-SSH1_4d11.b1.seq+  CCGGGCACGCCGGAAACCTTGCCCATGTTGATGGACTTGATGCTGGTGGCGAGGCTCTTG
U_HW-SSH1_7b09.b1.seq+  CCGGGCACGCCGGAAACCTTGCCCATGTTGATGGACTTGATGCTGGGGGCGAGGCTCTTG
U_HW-SSH1_7b11.b1.seq+  CCGGGCACGCCGGAGACCTTGCCCATGTTGATGGACTTGATGCTGGTGGCGAGGCTCTTG
consensus                CCGGGCACGCCGGAAACCTTGCCCATGTTGATGGACTTGATGCTGGTGGCGAGGCTCTTG

U_HW-SSH1_4d11.b1.seq+  ACGTGCCTGCACACTATCGTGTGGCCCGGGGTGCTGCGGGCCAGG
U_HW-SSH1_7b09.b1.seq+  AGGCACCTGCACACTATCTTGCGGTCCGGGGGGCTGCGGGCCAGGCCGTTCAGCCCCTGC
U_HW-SSH1_7b11.b1.seq+  AGGCACCTGCACGCTATCTTGCGGTCCGGGCTGCTGCGGGCCAGG
consensus                AGGCACCTGCACACTATCTTGCGGTCCGGGGTGCTGCGGGCCAGGCCGTTCAGCCCCTGC

U_HW-SSH1_7b09.b1.seq+  ACGCCGGAGCACCACTCCTTGCTGATCGAGGACGCCCTCCCCGTCACGTACCTGCCCGGG
consensus                ACGCCGGAGCACCACTCCTTGCTGATCGAGGACGCCCTCCCCGTCACGTACCTGCCCGGG

U_HW-SSH1_7b09.b1.seq+  CTATTGTACATAGTCACCTATGTATCTGAGACTTATTTCC
consensus                CTATTGTACATAGTCACCTATGTATCTGAGACTTATTTCC

****************** Contig 21 ******************
U_HW-SSH1_4e11.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTGCCTCCATTCCCACCATCAACAGCAACAACAAC
U_HW-SSH1_1e08.b1.seq+         TAGCGTGGTCGCGGCCGAGGACCCGGGAGTCCCAGCAGCAGCAGCAACAACAAC
consensus                TTCGATTAGCGTGGTCGCGGCCGAGGACCCGCCAGTCCCACCAGCAACAGCAACAACAAC

U_HW-SSH1_4e11.b1.seq+  CACCTTCCCTTGTTTGCGATCATCATCGGGGGCCGCTCCTGCGCGAGGCCTTGT-GACGC
U_HW-SSH1_1e08.b1.seq+  CACCTTCCCAGGCCGGCGATCAGCAGCGGGGGCCGCTCCTGCGCGAGGCCATGTCGACGC
U_HW-SSH1_9g10.b1.seq+                                                    GACGC
consensus                CACCTTCCCAGGCCGGCGATCAGCAGCGGGGGCCGCTCCTGCGCGAGGCCATGTCGACGC

U_HW-SSH1_4e11.b1.seq+  CCGTGCTGATGGTCACAACGGAGCAGGCGCTGGTGGAGGTTGAAGGCCACTTTCAGCTCG
U_HW-SSH1_11e01.b1.seq+                GCGGAGCAGGCGCGGGTGGAGGTTAAAGGCCTTTTCAGCTCG
U_HW-SSH1_1e08.b1.seq+  CCGTGCTGATGGTCACAGCGGAGCAGGTGCTGGTGGAGGTTGAAGGCCACTTTCAGCTCG
U_HW-SSH1_9g10.b1.seq+  CCGTGCTGATGGTCACGGCGGAGCAGGGGCTGGTGGAGGTTGAAGGCCCTTTCAGCTCG
consensus                CCGTGCTGATGGTCACAGCGGAGCAGGCGCTGGTGGAGGTTGAAGGCCACTTTCAGCTCG

U_HW-SSH1_4e11.b1.seq+  TGTCAAGCCTCCCGGTTGTCGACCCCGTTCGAATATGCATCGGGGTCCTCATCAAGAACT
U_HW-SSH1_11e01.b1.seq+ TGTCAGGCCTCCCGGTTGTCGAC
U_HW-SSH1_1e08.b1.seq+  TGTCAGGCCTCCCGGTTGTCGACAGCGCTCGCAGATGCATCGGGGTCGTCGTCAAGAGCG
U_HW-SSH1_9g10.b1.seq+  GGTCAGGCCTCCCGGTTGTCGACAGCGCTCGCAGATGCGTCGGGGTCGTCATGAAGAGCG
consensus                TGTCAGGCCTCCCGGTTGTCGACAGCGCTCGCAAATGCATCGGGGTCGTCATCAAGAGCG

U_HW-SSH1_4e11.b1.seq+  ATCGTGTGAGGGCTG-AAATGGCTCGAACACAAACATAGCAGATGCTGTGACCTCTCCAC
U_HW-SSH1_1e08.b1.seq+  ATCGTGTGAGGGCTTCACATGGGTCGAAAACAAAGATTGCAGATGTGATGACATCTCCAG
U_HW-SSH1_9g10.b1.seq+  ATTGCGCGAGGGCTTCACATGGTCCAAAGACTAAAATTGCAAATGTGATGACATCTCCAG
U_HW-SSH1_4g10.b1.seq+                        ACAAAGATTGCAGATGTGAAGACATCTCCAG
consensus                ATCGTGTGAGGGCTTCACATGGCTCGAAAACAAAGATTGCAGATGTGATGACATCTCCAG

U_HW-SSH1_4e11.b1.seq+  CTATCGCGCTATCATGCGATAGTGCGCTGACGGATGCCGCAGCTCTGATGCTCAAGAAAA
U_HW-SSH1_1e08.b1.seq+  CAATCACGCTATCATGCGATAAAACAGTGACCGATGCCGCAGCTCTGATGCTCAAGAAGA
U_HW-SSH1_9g10.b1.seq+  CGGTCACCCTATCATGTGATAAAACAGTGACCGATGCCCCATCTCTGATGCTCAAAAAAA
U_HW-SSH1_4g10.b1.seq+  CAATCACGCTATCATGCGATAAAACAGTGACCGATGCCGCAGCTCTGATGCTCAAGAAAA
consensus                CAATCACGCTATCATGCGATAAAACAGTGACCGATGCCGCAGCTCTGATGCTCAAGAAAA

U_HW-SSH1_4e11.b1.seq+  TGATCCCCAGATTACCGATTTAAACCAGGACAATCAAGTATTAGGTATAGTTACCCGCC
U_HW-SSH1_1e08.b1.seq+  AGATCCACAGATTACCGATAGTAAACCAGGACAATCAAGTAATAGGTATAGTTACCCGCG
U_HW-SSH1_9g10.b1.seq+  AGATCCGCACATTACCGATAGGAAACGAGGACAATCAATTAATAGGTATAGTTACCCGCA
U_HW-SSH1_4g10.b1.seq+  ATATCCACAGATTACCGATAGTAAACCAGGACAATCAAGTAATAGGTATAGTTACCCGCG
consensus                AGATCCACAGATTACCGATAGTAAACCAGGACAATCAAGTAATAGGTATAGTTACCCGCG

U_HW-SSH1_4e11.b1.seq+  ATGACGTTCTTCGCGCGTTGGAGGCCATGCTGAATTT
U_HW-SSH1_1e08.b1.seq+  ATGACGTTCTTCGCGCGTTGGAGGCCATGCTGAATTTTTTAGTGATGCAGGAGTCCATGCC
U_HW-SSH1_9g10.b1.seq+  ACGACCTTCTTCGCGCGTGGGAGGCCATGCTGAATTTTTTTAGATGCAGGAGTCCATGCC
U_HW-SSH1_4g10.b1.seq+  ACGACGTTCTTCGCGCGTTGGAGGCCTTGCTGAATTTTTAGAGATGCAGGAGTCCGTGCC
consensus                ACGACGTTCTTCGCGCGTTGGAGGCCATGCTGAATTTTTAGAGATGCAGGAGTCCATGCC

U_HW-SSH1_1e08.b1.seq+  CGGTACCTGCCCG
U_HW-SSH1_9g10.b1.seq+  CGGTACCTGCCCGGGCGGCCCCTTGAAAACAA
U_HW-SSH1_4g10.b1.seq+  CGGTCCCTGCCCGGG
consensus                CGGTACCTGCCCGGGCGGCCCCTTGAAAACAA

****************** Contig 22 ******************
U_HW-SSH1_5a05.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACAATTAATCAGCTGTTTATCTGCATTGGAATT
U_HW-SSH1_10a08.b1.seq+        TAGCGTGGTCGCGGCCGAGGGACAGGTAATCAGCTGTTTATCTGCATTGGAATT
consensus                TTCGATTAGCGTGGTCGCGGCCGAGGGACAAGTAATCAGCTGTTTATCTGCATTGGAATT

U_HW-SSH1_5a05.b1.seq+  CTTGCAGCTTTGGTAGCTGGATTGCCATTACCACAAAATCCTGCATGGTGGAGGACAATG
U_HW-SSH1_10a08.b1.seq+ CTTGCACCAGTGGTAGCTGGATTGCCATTAGCACAAAATCCTGCATGGTGGAGGACAATG
consensus                CTTGCACCAGTGGTAGCTGGATTGCCATTACCACAAAATCCTGCATGGTGGAGGACAATG

U_HW-SSH1_5a05.b1.seq+  TTTGGAATTTCAATAGTTCCATCTATTTTGTTGGCTCTAGGAATGGCTGTTTCACCTGAA
U_HW-SSH1_10a08.b1.seq+ TTTGGAATTTCAATAGTTCCATCTATTTTGTTGGCTCTAGGAATGGCTGTTTCACCTGAA
consensus                TTTGGAATTTCAATAGTTCCATCTATTTTGTTGGCTCTAGGAATGGCTGTTTCACCTGAA

U_HW-SSH1_5a05.b1.seq+  AGCCCTCGCTGGCTATTCCAGCAAGGAAAGATTTCTCAAGCAGAAGCAGCTATAAAAAAA
U_HW-SSH1_10a08.b1.seq+ AGCCCTCGCTGGCTATTCCAGCAAGGAAAGATTTCTCAAGCAGAAGCAGCTATAAAAAAA
consensus                AGCCCTCGCTGGCTATTCCAGCAAGGAAAGATTTCTCAAGCAGAAGCAGCTATAAAAAAA

U_HW-SSH1_5a05.b1.seq+  TTGTATGAAAAAAAGAAGGTTACTGAAGTCATGTATGACCTGAAGGCTAGTGGGCAAGGA
U_HW-SSH1_10a08.b1.seq+ TTGTATGGAAAAGAAGAAGGTTACTGAAGTCATGTATGACCTGAAGGCTAGTGGGCAAGGA
consensus                TTGTATGAAAAAAAGAAGGTTACTGAAGTCATGTATGACCTGAAGGCTAGTGGGCAAGGA

U_HW-SSH1_5a05.b1.seq+  TCTAATGAGCCAAATGCCAACTGGTTTGATCTATTCAGCAAACGCTATTGGAAAGTTGTG
U_HW-SSH1_10a08.b1.seq+ TCTAATGAGCCAAATGCCAACTGGTTTGATCTATTCACCAAACGCTATTGGAAAGTTGTG
consensus                TCTAATGAGCCAAATGCCAACTGGTTTGATCTATTCACCAAACGCTATTGGAAAGTTGTG

U_HW-SSH1_5a05.b1.seq+  AGCGTGGGAGCGGCACTGTTTTTGTTGCAGCAACTTGCTGGCATAAATGCTGTTGTGTAC
U_HW-SSH1_10a08.b1.seq+ AGCGTGGGAGCGGCCCTGTTTTTGTTGCAGCAACTTGCTGGCATAAATGCTGTTGTGTAC
```

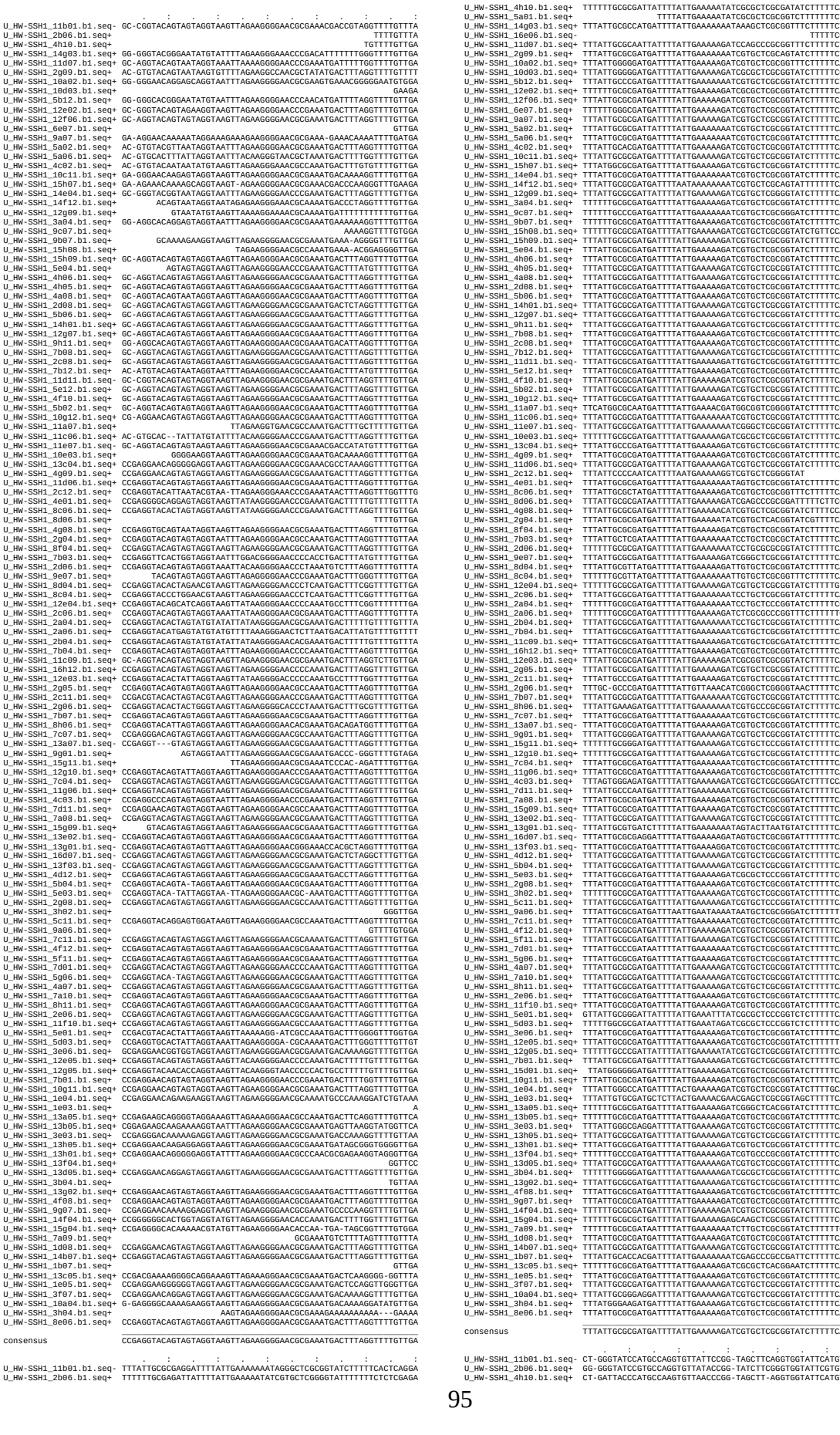
```
consensus               AGCGTGGGAGCGGCACTGTTTTTGTTGCAGCAACTTGCTGGCATAAATGCTGTTGTGTAC

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5a05.b1.seq+  CTGCCCGGGCGG
U_HW-SSH1_10a08.b1.seq+ CTGCCCGGGCGGCCCCTCCAA
                        ____________________________________________________________
consensus               CTGCCCGGGCGGCCCCTCCAA

****************** Contig 23 ********************
                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5a07.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACCTCGAGAAGAGCAAGCTCAACAAGGAGCTGA
U_HW-SSH1_14h08.b1.seq+       TAGCGTGGTCGCGGCCGAGGTACCTCGAGAAGAGCAAGCTCAACAAGGAGCTGA
                        ____________________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACCTCGAGAAGAGCAAGCTCAACAAGGAGCTGA

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5a07.b1.seq+  ACGACAAGAAGAGGGCGGCGACGAGCGGCGCCAACTTCGCGCGCGCGCCTACACCGTCCAGT
U_HW-SSH1_14h08.b1.seq+ ACGACAAGAAGAGGGCGGCGACGAGCGGCGCCAACTTCGCGCGCGCCTACACCGTCCAGT
                        ____________________________________________________________
consensus               ACGACAAGAAGAGGGCGGCGACGAGCGGCGCCAACTTCGCGCGCGCCTACACCGTCCAGT

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5a07.b1.seq+  TCGGCAGCTGCAAGTTCCCCTACAACTTCACCGGCTGCCAGGACCTCGCCAAGCAAAAGA
U_HW-SSH1_14h08.b1.seq+ TCGGCAGCTGCAAGTTCCCCTACAACTTCACCGGCTGCCAGGACCTCGCCAAGCAGAAGA
                        ____________________________________________________________
consensus               TCGGCAGCTGCAAGTTCCCCTACAACTTCACCGGCTGCCAGGACCTCGCCAAGCAAAAGA

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5a07.b1.seq+  AAGTCCCGTTCATCACCGACGACCTGGAGATCGAGTGCGAGGGGAAGGAGAAGTTCAAGT
U_HW-SSH1_14h08.b1.seq+ AAGTCCCGTTCATCACCGACGACCTGGAGATCGAGTGCGAGGGGAAGGAGAAGTTCAAGT
                        ____________________________________________________________
consensus               AAGTCCCGTTCATCACCGACGACCTGGAGATCGAGTGCGAGGGGAAGGAGAAGTTCAAGT

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5a07.b1.seq+  GCGGATCCAACGTCTTCTGGAAATGGTGAAGCTGGTCGATCTGCCAGGCAATATGGCGAG
U_HW-SSH1_14h08.b1.seq+ GCGGATCCAACGTCTTCTGGAAATGGTGAAGCTGGTCGATCTGCCAGGCAATATGGCGAG
                        ____________________________________________________________
consensus               GCGGATCCAACGTCTTCTGGAAATGGTGAAGCTGGTCGATCTGCCAGGCAATATGGCGAG

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5a07.b1.seq+  TGCTGATGTATGTCAGCGCACCGCGTGTACCTGCCCGGGCGGC
U_HW-SSH1_14h08.b1.seq+ TGCTGATGTATGTCAGCGCACCGCGTGTACCTGCCCGGGCGGCCGCTCGAAATCACTAGT
                        ____________________________________________________________
consensus               TGCTGATGTATGTCAGCGCACCGCGTGTACCTGCCCGGGCGGCCGCTCGAAATCACTAGT

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14h08.b1.seq+ GAATTCGCGCCCGCCTGCAGGTCCACCATATGGGAGAGCTCCCCACGAGGTGATTGCATA
                        ____________________________________________________________
consensus               GAATTCGCGCCCGCCTGCAGGTCCACCATATGGGAGAGCTCCCCACGAGGTGATTGCATA

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14h08.b1.seq+ CCATGACTATTCCATAGCGTCACATAAGCAGGGTGGCATACTCATGGTCATAGCTGTTTC
                        ____________________________________________________________
consensus               CCATGACTATTCCATAGCGTCACATAAGCAGGGTGGCATACTCATGGTCATAGCTGTTTC

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14h08.b1.seq+ GTGTGTAAAACTGTTACCCGCTCTAATTCCACACAACATCAAGCCGGAAGCATAAAGTGT
                        ____________________________________________________________
consensus               GTGTGTAAAACTGTTACCCGCTCTAATTCCACACAACATCAAGCCGGAAGCATAAAGTGT

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14h08.b1.seq+ AAAGCCTGGGAAAATAAAAAGGGAGCGCAACTCACATTAATTGGGTGGCGTTCACTGCCC
                        ____________________________________________________________
consensus               AAAGCCTGGGAAAATAAAAAGGGAGCGCAACTCACATTAATTGGGTGGCGTTCACTGCCC

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14h08.b1.seq+ GCTTTCCGGGGGGAAATCTGGACGGCATCTGATTATATCAATCGCCCACGGGCGGGGAGA
                        ____________________________________________________________
consensus               GCTTTCCGGGGGGAAATCTGGACGGCATCTGATTATATCAATCGCCCACGGGCGGGGAGA

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14h08.b1.seq+ GCCGGTCCCCATATGGGGTGTTTTTCCGGTTTCTCTTCCTACCTGACCTCTCCAGCTCGG
                        ____________________________________________________________
consensus               GCCGGTCCCCATATGGGGTGTTTTTCCGGTTTCTCTTCCTACCTGACCTCTCCAGCTCGG

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14h08.b1.seq+ ATAGGCCGGTGGGGGTAGAGGAGGTTTCTAGCTC
                        ____________________________________________________________
consensus               ATAGGCCGGTGGGGGTAGAGGAGGTTTCTAGCTC


****************** Contig 24 ********************
                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5e11.b1.seq+  TTCGATTTCGAGCGGCCGCCCGGGCAGGTACTTCACGGCAGCAAGCGGCATGCACAGCTC
U_HW-SSH1_4a10.b1.seq+       ATTTCGAGCGGCCGCCCGGTCAGGTCCTTCACGGCAGCAAGCGGCATGCACAGCTC
                        ____________________________________________________________
consensus               TTCGATTTCGAGCGGCCGCCCGGGCAGGTACTTCACGGCAGCAAGCGGCATGCACAGCTC

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5e11.b1.seq+  TTCAGCAAGCTCAAGAATCCTAGG-AATGGTGAGCAGGAGCATGGTAGTCCCACAGGTCT
U_HW-SSH1_4a10.b1.seq+  TCCAGAAAGCTCAAGAATCCTATTTAATGGGGAGCAGGAGCATGGTAGTCCCACAGGTCT
                        ____________________________________________________________
consensus               TCCAGAAAGCTCAAGAATCCTAGGTAATGGGGAGCAGGAGCATGGTAGTCCCACAGGTCT

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5e11.b1.seq+  TGATCACAATCTTCTGAGAGTAGATGAACAGGCTCAACTCAGATAGCACATAGGAGTCGA
U_HW-SSH1_4a10.b1.seq+  TGATCACAATCTTCTGAGAGTTGATGAACAGGCTCGACTCAAATAGCACATAGGAGTCGA
U_HW-SSH1_4g05.b1.seq+                                                      GAGTCAA
U_HW-SSH1_8a02.b1.seq+                                                      GAGTCAA
                        ____________________________________________________________
consensus               TGATCACAATCTTCTGAGAGTAGATGAACAGGCTCAACTCAAATAGCACATAGGAGTCAA

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5e11.b1.seq+  AGTCCTTGTTGGAGAGCTCGGACACAATGGTGCACCGTGCAAGATCAAGAACAGAGTCAA
U_HW-SSH1_4a10.b1.seq+  AGTCCTTGTTGGAGAGCTCGGACACAATGGTGCACCGTGCAAGATCAAGAACAGAGTCAA
U_HW-SSH1_4g05.b1.seq+  AGTCCTTGTTGGAGAGCTCGGACACAATGGTGCACCGTGCAAGATCAAGAACAGAGTCAA
U_HW-SSH1_8a02.b1.seq+  AGTCTTTGTTGGAGACCTCGCACTCACTGGTGCACCGTGCAACATCAAGAACAGAGTCAA
                        ____________________________________________________________
consensus               AGTCCTTGTTGGAGAGCTCGGACACAATGGTGCACCGTGCAAGATCAAGAACAGAGTCAA

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5e11.b1.seq+  TCTGGGCCCTGGAGAGGGCGCGCAGGCCACGACCATGAGGGTCGGCAAAGATTGATGCCT
U_HW-SSH1_4a10.b1.seq+  TCTGGGCCCTGGAGAGGGCGCGCAGGCCACGACCATGAGGGTCGGCAAAGATTGATGCCT
U_HW-SSH1_4g05.b1.seq+  TCTGGGCCCTGGAGAGGGCGCGCAGGCCACGACCATGAGGGTCAGCAAAGATTGATGCCT
U_HW-SSH1_8a02.b1.seq+  TCTGGGCCCTGGAGAGGGCGCGCAGGCCACAACCTTGAGGGTCAGCAAAAATTGATGCCT
                        ____________________________________________________________
consensus               TCTGGGCCCTGGAGAGGGCGCGCAGGCCACGACCATGAGGGTCAGCAAAGATTGATGCCT

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5e11.b1.seq+  CAAAGAAGGTGATCTCTAGGCGCTTCTCATATCCCTCAAACCCGATCGCATAGGTCGG
U_HW-SSH1_4a10.b1.seq+  CGGAGAAGGTGATCTCGAGGCGCTTCTCGTAGCCCTCAAACCCGATCGCAAAGGTCGGGG
U_HW-SSH1_4g05.b1.seq+  CAAAGAAGGTGATATCAAGGCGCTTCTCGTAGCCCTCAAATCCGATCGCAGAGGTCGGGG
U_HW-SSH1_8a02.b1.seq+  CAGAGAAGGGGATATCGAGGCGCTTCTCTTAGCCCTCAAATCCGATCGCAGAGGTCGGGG
                        ____________________________________________________________
consensus               CAAAGAAGGTGATATCGAGGCGCTTCTCGTAGCCCTCAAACCCGATCGCAGAGGTCGGGG

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_4a10.b1.seq+  CACCCATTGTTGCA
U_HW-SSH1_4g05.b1.seq+  CAGCCATTGTTGCAGTTTTGAGTCAGAAAGTAGAGCAAAGAGGAACAGAGGGAGAAAGAC
U_HW-SSH1_8a02.b1.seq+  CACCCTTTGTTGCATTTTTGAGTCAGAAATTAGAGCGGAGAGGAACAAAGGGAGAAAGAC
                        ____________________________________________________________
consensus               CACCCATTGTTGCAGTTTTGAGTCAGAAAGTAGAGCAAAGAGGAACAAAGGGAGAAAGAC

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_4g05.b1.seq+  TAGAGAACTGGTCGATTATCGTGAAGCAGCAAGCCAGAGAGATTGGTGGGAAAAAAGAGT
U_HW-SSH1_8a02.b1.seq+  TAGAGACCTGGCCAATTATCGTGAATCAGCAAGCCAAAGAGATTGGGGGGAGAAAAAGAGA
                        ____________________________________________________________
consensus               TAGAGAACTGGCCAATTATCGTGAAGCAGCAAGCCAAAGAGATTGGGGGGAAAAAAGAGA

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_4g05.b1.seq+  CAAAATAAAATTGCATAAAAATCCTAAACTACGGGAAGGGGATGCCAAAAACGATATCAG
U_HW-SSH1_8a02.b1.seq+  CAGAATAAAATTGCATAAAAATCCTAAACTACGGGAAGGGGATGCCAAAAACGATATCGG
                        ____________________________________________________________
consensus               CAAAATAAAATTGCATAAAAATCCTAAACTACGGGAAGGGGATGCCAAAAACGATATCAG

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_4g05.b1.seq+  GATGGCTTCTTCGCGCAGTTCGAGTATGCAACAAAGAACTTCTTGGCGCCTCCAGCAGGT
U_HW-SSH1_8a02.b1.seq+  GATGGGTTCTTCGCGCATTTCGAGTATGCAGCATAGAACTTCTTGGCGCCTCCGGCAGGT
                        ____________________________________________________________
consensus               GATGGCTTCTTCGCGCAGTTCGAGTATGCAACAAAGAACTTCTTGGCGCCTCCAGCAGGT

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_4g05.b1.seq+  CAAACGTCTTCAATGCTGTAGCCGAGGGGAGCTTCTTACCTCGGCCGCGACCACCCTA
U_HW-SSH1_8a02.b1.seq+  CAAACGTCTTCAATGCTGTAGCCGAGGGGAGCTTCGTACCTCGGCCGCGACCAC
                        ____________________________________________________________
consensus               CAAACGTCTTCAATGCTGTAGCCGAGGGGAGCTTCGTACCTCGGCCGCGACCACCCTA

****************** Contig 25 ********************
                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5f09.b1.seq+  TTCGATTACGTGGTCCCGCCCGAGGTGCACGTGTAGGTTTGTTTGAAGGGCTCCCCCAC
U_HW-SSH1_5g09.b1.seq+  TTCGATTACCGTGGTCCGGCCCGAGGTGCACGTGTAGGTATTTTTGCACGGATCCCCCAC
                        ____________________________________________________________
consensus               TTCGATTACCGTGGTCCGGCCCGAGGTGCACGTGTAGGTATGTTTGAACGGATCCCCCAC

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5f09.b1.seq+  CTTTTTTTTTTTTGTGCTTATTTTCCTAGGACTTTTTTTTTGGTTAACCAAAAAAAAAGA
U_HW-SSH1_5g09.b1.seq+  CGTTTTT
                        ____________________________________________________________
consensus               CGTTTTTTTTTTTGTGCTTATTTTCCTAGGACTTTTTTTTTGGTTAACCAAAAAAAAAGA

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5f09.b1.seq+  TTCTTTCTGCTCTGTAAATTTTATCCCTGGACTTGTTAAAACCTTTGTATTGCAATATTT
                        ____________________________________________________________
consensus               TTCTTTCTGCTCTGTAAATTTTATCCCTGGACTTGTTAAAACCTTTGTATTGCAATATTT

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5f09.b1.seq+  TTTTCTCTTACGGGGCCAACTTTGAGAGTTAACGTTGGCGTGAATTAGGGAAAGCAGTGT
                        ____________________________________________________________
consensus               TTTTCTCTTACGGGGCCAACTTTGAGAGTTAACGTTGGCGTGAATTAGGGAAAGCAGTGT

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5f09.b1.seq+  ATCGGCGGGGGGCTCGAATTCCCCGTGGGGTACGGGCCCGGCCATGTCCATGAATTGAAA
                        ____________________________________________________________
consensus               ATCGGCGGGGGGCTCGAATTCCCCGTGGGGTACGGGCCCGGCCATGTCCATGAATTGAAA

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5f09.b1.seq+  ATAAAAAACCGACATCGTTGGGGGGCCCTCTTTAGTGATCTGCACCGCAGCCCCCCCCCC
                        ____________________________________________________________
consensus               ATAAAAAACCGACATCGTTGGGGGGCCCTCTTTAGTGATCTGCACCGCAGCCCCCCCCC

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5f09.b1.seq+  TGGCCGCACAATGGAATTACCAGCCTCCTGTCGTCGTCTATTCTCGGATAGTTCTTATCG
                        ____________________________________________________________
consensus               TGGCCGCACAATGGAATTACCAGCCTCCTGTCGTCGTCTATTCTCGGATAGTTCTTATCG

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5f09.b1.seq+  AGCTCGACAATCGCGAGGAGTACCCTGGCCTGACATGTATCTAGTGGGGATTATCATGCG
                        ____________________________________________________________
consensus               AGCTCGACAATCGCGAGGAGTACCCTGGCCTGACATGTATCTAGTGGGGATTATCATGCG

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5f09.b1.seq+  TCACACCTGTGTCGTGAGAATGTGCCAACCTCAAGGAATCAAACAGGATGTGAATACTAA
                        ____________________________________________________________
consensus               TCACACCTGTGTCGTGAGAATGTGCCAACCTCAAGGAATCAAACAGGATGTGAATACTAA

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_5f09.b1.seq+  TAGCTAAA
                        ____________________________________________________________
consensus               TAGCTAAA

****************** Contig 26 ********************
                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_6e09.b1.seq-  TTATAGGTTGGCCAGCCAGGCGGGCCGCGGAATTCATTAGGGATTTTTAAGCGGCCCCCC
U_HW-SSH1_5g12.b1.seq+                                                  TTCGAGCGGCCGCCC
U_HW-SSH1_14b01.b1.seq+                                                 TTCGAGCGGCCGCCC
U_HW-SSH1_15c06.b1.seq-                                                    GAGCGGCCGCCC
U_HW-SSH1_14c02.b1.seq+                                                   AGCGGCCGCCC
U_HW-SSH1_14c01.b1.seq+                                                 TTCGAGCGGCCGCCC
                        ____________________________________________________________
consensus               TTATAGGTTGGCCAGCCAGGCGGGCCGCGGAATTCATTAGGGATTTTCGAGCGGCCGCCC

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_6e09.b1.seq-  CCGGCCAGGGTAGGGGTTTGCATTTTGCCAATGAAAAAATAGGAAGTTAACCGCTGGGGA
U_HW-SSH1_5g12.b1.seq+  --GGGCAGG-TACGCGTTTGTATT---CGCATGTATATATAGGA-GTTAACCGGTGGGGA
U_HW-SSH1_14b01.b1.seq+ --GGGCAGG-TACGCGTTTGTATT---CGCATGTATATATAGGA-GTTAACCGGTGGGGA
U_HW-SSH1_5g05.b1.seq-     AGG-TACGCGTTTGTATT---CGCATGTATATATAGGA-GTTAACCGGTGGGGA
U_HW-SSH1_15c06.b1.seq- --GGGCAGG-TACGCGTTTGCATT---CGCATGTATATATAGGA-GTTAACCGCTGGGGA
U_HW-SSH1_14c02.b1.seq+ --GGGCAGG-TACGCGTTTGTATT---CGCATGTATATATAGGA-GTTAACCGGTGGGGA
U_HW-SSH1_14c01.b1.seq+ --GGGCAGG-TACGCGTTTGTATT---CGCATGTATATATAGGA-GTTAACCGGTGGGGA
U_HW-SSH1_9d11.b1.seq+                 TTTGTATT---CGCATGTATATATAGGA-GTTAACCGGGGGGGA
                        ____________________________________________________________
consensus               --GGGCAGG-TACGCGTTTGTATT---CGCATGTATATATAGGA-GTTAACCGGTGGGGA

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_6e09.b1.seq-  AAGATTTCATTCTCCCAATGTCTCGAAACTTGCCGGAAGACGAAAGTTGTAGTGACCCCC
U_HW-SSH1_5g12.b1.seq+  A-GATTTACTGCTCCCA-TGTCTCGAA-CTTGCTGGA-GACGAA-GTCGTAGTGGCCGCC
U_HW-SSH1_14b01.b1.seq+ A-GATTTACTGCTCCCA-TGTCTCGAA-CTTGCTGGA-GACGAA-GTCGTAGTGGCCGCC
U_HW-SSH1_5g05.b1.seq-  A-GATTTACTGCTCCCA-TGTCTCGAA-CTTGCCGGA-GACGAA-GTCGTAGTGGCCGCC
U_HW-SSH1_15c06.b1.seq- A-GATTTACTGCTCCCA-TGTCTCGAA-CTTGCCGGA-GACGAA-GTCGTAATGGCCGCC
U_HW-SSH1_14c02.b1.seq+ A-GATTTACTGCTCCCT-TGTCTCGAA-CTTGCTGGA-GACAAA-GTCGTAGTGGCCGCC
U_HW-SSH1_14c01.b1.seq+ A-GATTTACTGCTCCCA-TGTCTCGAA-CTTGCTGGA-GACGAA-GTCGTAGTGGCCGCC
U_HW-SSH1_9d11.b1.seq+  A-GATTTACTGCTCCCA-TGGCTCGAA-CTTGCCGGA-GACGAA-GTCGTAGTGGCCGCC
U_HW-SSH1_9c10.b1.seq+                                                     TGGCCGCC
                        ____________________________________________________________
consensus               A-GATTTACTGCTCCCA-TGTCTCGAA-CTTGCCGGA-GACGAA-GTCGTAGTGGCCGCC

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_6e09.b1.seq-  CGACCCACCTTGAGGGTTCCGTTTGGCCCCCCCCCTCCCTTACGAAACGGGGTAGGTCAG
U_HW-SSH1_5g12.b1.seq+  --AACGAGCTTGAGGGTTCCGTTGGACACACCC--TCCTTGACGAAC--GGGTAGGTCAA
U_HW-SSH1_14b01.b1.seq+ --AACGAGCTTGAGGGTTCCGTTGGACACACCC--TCCTTGACGAAC--GGGTAGGTCAA
U_HW-SSH1_5g05.b1.seq-  --AACGAGCTTGAGGGTTCCGTTGGACACACCC--TCCTTGACGAAC--GGGTAGGTCAA
U_HW-SSH1_15c06.b1.seq- --GACGAGCTTGAGGGTTCCGTTGGACACACCC--TCCTTGACGAAC--GGGTAGGTCAG
U_HW-SSH1_14c02.b1.seq+ --AACGAGCTTGAGGGTTCCGTTGGACACACCC--TCCTTGACGAAC--GGGTAGGTCAA
U_HW-SSH1_14c01.b1.seq+ --AACGAGCTTGAGGGTTCCGTTGGACACACCC--TCCTTGACGAAC--GGGTAGGTCAA
U_HW-SSH1_9d11.b1.seq+  --AACGAGCTTGAGGGTTCCGTTGGACACACCC--TCCTTGACGAAC--GGGTAGGTCAA
U_HW-SSH1_9c10.b1.seq+  --AACAATCTTGACGGTTCTTTGGACACACCC--TCCTTGACGATT--TTGTAGGTCAA
                        ____________________________________________________________
consensus               --AACGAGCTTGAGGGTTCCGTTGGACACACCC--TCCTTGACGAAC--GGGTAGGTCAA

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_6e09.b1.seq-  GAGGTTTTGGAGGGACACGTTCACTGCCTCCTTTTCGAGGACGGTGCACTGG-TCATCGA
U_HW-SSH1_5g12.b1.seq+  GAGGTTCTGGAGGGACACGTTCACGGCCTCCTTTTCGAGGACGGTGCACTGG-TCATCGA
U_HW-SSH1_14b01.b1.seq+ GAGGTTCTGGAGGGACACGTTCACGGCCTCCTTTTCGAGGACGGTGCACTGG-TCATCGA
U_HW-SSH1_5g05.b1.seq-  GAGGTTCTGGCGGGGCAGGTTCACGGCCTCCTTTTATATGACCCTACCCTGG-TCAATGA
U_HW-SSH1_15c06.b1.seq- GAGGTTCTGCAGGGACACGTTCACTGCCTCCTTTTCGAGGACGGTGCACTGG-TCATCGA
U_HW-SSH1_14c02.b1.seq+ GAGGTTCTGGAGGGACACGTTCCCGGCCTCCTTTTCGAGGACGGTGCACTGG-TCATCGA
U_HW-SSH1_14c01.b1.seq+ GAGGTTCTGGAGGGACACGTTCACGGCCTCCTTTTCGAGGACGGTGCACTGG-TCATCGA
U_HW-SSH1_9d11.b1.seq+  GAGGTTCTGGAGGGACACGTTCACGGCCTCCTTTTCAAGGACGGTGCACTGG-TCATCGA
U_HW-SSH1_9c10.b1.seq+  GAGTTTCTGAATGGACACGTTCAACCCCTCCTTTTCAAGGACGGTGCTTTGAATCATCAA
                        ____________________________________________________________
consensus               GAGGTTCTGGAGGGACACGTTCACGGCCTCCTTTTCGAGGACGGTGCACTGG-TCATCGA

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_6e09.b1.seq-  AAGGCATGGAGGCGCACTCAGTCTGCCCCTCTTTTTGGCCGGGAAGCCGATCCTGACCC
U_HW-SSH1_5g12.b1.seq+  AAGGCATTGAGGCGCACTCAGTCTGCACCTTCTTCTTGGCCGGGAAGCCGATCCTGACCC
U_HW-SSH1_14b01.b1.seq+ AAGGCATTGAGGCGCACTCAGTCTGCACCTTCTTCTTGGCCGGGAAGCCGATCCTGACCC
U_HW-SSH1_5g05.b1.seq-  AAGGCATAATGGAGCAAACAGTATGCACAATTATTTTTGGCCGGGAAGCCGATCCTGACCC
U_HW-SSH1_15c06.b1.seq- AAGGCATGGAGGCGCACTCAGTCTGCCCCTTTTTTTTGGCCGGGAAGCCGATCATGACCC
U_HW-SSH1_14c02.b1.seq+ AAGGCATTGAGGCGCACTCATTCTGCACCTTCTTCTTGGCCGGGAAGCCGATCCTGACCC
U_HW-SSH1_14c01.b1.seq+ AAGGCATTGAGGCGCACTCAGTCTGCACCTTCTTCTTGGCCGGGAAGCCGATCCTGACCC
U_HW-SSH1_9d11.b1.seq+  AAGGCATTGAGGCGCACTCAGTCTGCACCTTCTTCTTGGCCGGGAAGCCGATCCTGACCC
U_HW-SSH1_9c10.b1.seq+  AAGGGGTTCCGGCCCAGTCGGCCTGCACCTTTTTCTTGGGCGGGAAGCCCATCCTGACCC
                        ____________________________________________________________
consensus               AAGGCATTGAGGCGCACTCAGTCTGCACCTTCTTCTTGGCCGGGAAGCCGATCCTGACCC

                          .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_6e09.b1.seq-  AGTCCTCGACGAAGTGGAAGGAGTCGTTTGCGCCATCCTTGAGTGAGAGCAGAGCCTTGA
U_HW-SSH1_5g12.b1.seq+  TTTCCTCGACAAAGTGGAAGGATTCGTCTGCGCCATCCTTGAGTGAAAGGAGATCTTTGA
U_HW-SSH1_14b01.b1.seq+ AGTCCTCGACGAAGTGGAAGGAGTCGTCTGCGCCATCCTTGAGTGAGAGGAGAGCCTTGA
U_HW-SSH1_5g05.b1.seq-  AGTCCTTGAAGAAGGAGAAGGAGTGGTCTGTCCATCCAAATAGT-AGAGGAGAGCCGTGA
U_HW-SSH1_15c06.b1.seq- AGTCCTC
U_HW-SSH1_14c02.b1.seq+ ATTCCTCAACAAAGTGGAAGGAGTCGTCTGCGCCATCCTTGAGTGAGAGGAGAGCCTTGA
U_HW-SSH1_14c01.b1.seq+ AGTCCTCGACGAAGTGGAAGGAGTCGTCTGCCCCATCCTTGAGTGAGAGGAGAGCCTTGA
U_HW-SSH1_9d11.b1.seq+  AGTCCTCGACGAAGTGGAAGGAGTCGTCTGCGCCATCCTTGAGTGAAAGGAGAGCCTTGA
U_HW-SSH1_9c10.b1.seq+  ACTCCTAAACGAAAAGGAAAGGAGTCGTCTGCGCCCTCCTTGAGTGAGAGGAGAGCCTTGA
                        ____________________________________________________________
```

```
consensus                 AGTCCTCGACGAAGTGGAAGGAGTCGTCTGCGCCATCCTTGAGTGAGAGGAGAGCCTTGA

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_6e09.b1.seq-    TTCCACCGCAGCGGCTGTGGCCAATCACCACGATGACCTCAACCTTGAGGGCACAGACGG
U_HW-SSH1_5g12.b1.seq+    TTCC-CCGCATCG-CTGTGGCCAATCACCACGATGACCTCG-CCTTGAAAACACAGACTG
U_HW-SSH1_14b01.b1.seq+   TTCCACCGCAGCGGCTGTGGCCAATCACCACGATGACCTCAACCTTGAGAGCACAGACGG
U_HW-SSH1_5g05.b1.seq-    TTCCACCGCAGCGGCAG-GGCCAATCACCACGATGACCTCAACC
U_HW-SSH1_14c02.b1.seq+   TTCCACCGCAGCGGCTGTGGCCAATCACCACGATGACCTCAACCTTGAGAGCACAGACGG
U_HW-SSH1_14c01.b1.seq+   TTCCACCGCAGCGGCTGTGGCCAATCACCACGATGACCTCAACCTTGAGAGCACAGACGG
U_HW-SSH1_9d11.b1.seq+    TTCCACCGCAGCGGCTGTGGCCAATCACCACGATGACCTCAACCTTGAGAGCACAGACGG
U_HW-SSH1_9c10.b1.seq+    TTCCACCGCAGCGGCTGTGGCCAATCACCACGATGATCTCAACCTTGAAAGCATAGACGG

consensus                 TTCCACCGCAGCGGCTGTGGCCAATCACCACGATGACCTCAACCTTGAGAGCACAGACGG

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_6e09.b1.seq-    CGT-ATTCGATGGCCGATCCAACACCGGCGTTCCTCGGCCGCGACCACGCTA
U_HW-SSH1_5g12.b1.seq+    CGT-TTTCGATGGCC
U_HW-SSH1_14b01.b1.seq+   CGT-ATTCGATGGCCGATCCAACACCAGCGTACCTCGGCCGCGACCACGCTA
U_HW-SSH1_14c02.b1.seq+   CGT-ATTCGATGGCCGATCCAACACCAGCGTACCTCGGCCGCGACCACGCTA
U_HW-SSH1_14c01.b1.seq+   CGT-ATTCGATGGCCGATCCAACACCAGCGTACCTCGGCCGCGACCACGCTA
U_HW-SSH1_9d11.b1.seq+    CGT-TTTCGATGGCCGATCCAACACCAGCGTACCT-GCCCGGGCGGCCGCTCGAAATCAC
U_HW-SSH1_9c10.b1.seq+    CGTCTTTTGATGGCCGATCCAACACCCGCATACCT-GCCCGGGCGG

consensus                 CGT-ATTCGATGGCCGATCCAACACCAGCGTACCTCGGCCGCGACCACGCTAGAAATCAC

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_9d11.b1.seq+    AAGAGAATTCGCGGCCCCCTGCAGGTCTACCATATAGGAGAGCCCCAACGCGTTGGACCA

consensus                 AAGAGAATTCGCGGCCCCCTGCAGGTCTACCATATAGGAGAGCCCCAACGCGTTGGACCA

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_9d11.b1.seq+    TACCTTGAGTATTCTAAATGTAACCTAAATACCGCGGCGAAATCGTGTCATTTTCTTTCC

consensus                 TACCTTGAGTATTCTAAATGTAACCTAAATACCGCGGCGAAATCGTGTCATTTTCTTTCC

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_9d11.b1.seq+    AGAGTGTAATGTTTCCCCCTCAAA

consensus                 AGAGTGTAATGTTTCCCCCTCAAA

****************** Contig 27 *******************
                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7a02.b1.seq+    TAGCGTGGTCGCGGCCGAGGTACATGGACAAGAAGCTCCAAATCAAGCTGAATGCGAACC
U_HW-SSH1_8g09.b1.seq+       CGTGGTCCCGGCCGAGGTGCACGGACAAGAAGCTCCAA-TCAACCTGAATGCGAATC

consensus                 TAGCGTGGTCCCGGCCGAGGTACACGGACAAGAAGCTCCAAATCAACCTGAATGCGAACC

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7a02.b1.seq+    GTGTTGTCATTGGCACGCTTCGTGGATTTGATCAGTTCATGAATTTGGTGGTGGACAACA
U_HW-SSH1_8g09.b1.seq+    GTGTTGTCATTGGCACGCTTT-TGGATTTGATCAGTTCATGAATTTGGTGGTGGACAACA

consensus                 GTGTTGTCATTGGCACGCTTCGTGGATTTGATCAGTTCATGAATTTGGTGGTGGACAACA

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7a02.b1.seq+    CTGTGGAGGTCAATGGAGATGAAAAGACCGACATAGGGATGGTGGTTCTGAAAGGAAATA
U_HW-SSH1_8g09.b1.seq+    CTGTGCAGGTCAATGGACATGACCC-ACCGACATCGGGATGGTGGTTCTGAAAGGAAATA

consensus                 CTGTGCAGGTCAATGGACATGAAAAGACCGACATAGGGATGGTGGTTCTGAAAGGAAATA

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7a02.b1.seq+    GTGTTGTGATGATTGAAGCCCTTGAACC
U_HW-SSH1_8g09.b1.seq+    TTGTTGTGATGATTGAAGCCCTTGAACCCTTGCTTCAACTCGAACATCTTTTGCTTTGCC

consensus                 GTGTTGTGATGATTGAAGCCCTTGAACCCTTGCTTCAACTCGAACATCTTTTGCTTTGCC

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_8g09.b1.seq+    TGCTTCTGGTTTATTACCTGCCCGGGCAGCGGTTTCTCTCACATGACCACTCACGGTGGA

consensus                 TGCTTCTGGTTTATTACCTGCCCGGGCAGCGGTTTCTCTCACATGACCACTCACGGTGGA

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_8g09.b1.seq+    AGGGACAACACCGGCACCCCCGGCCCCCCCAACTGGGAGAACATCACCGCCGCCGCGACC

consensus                 AGGGACAACACCGGCACCCCCGGCCCCCCCAACTGGGAGAACATCACCGCCGCCGCGACC

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_8g09.b1.seq+    AGCCAAGTCGTGCTTGACTGGGCCGCCGCGGGGTATTGGAGCAGAAAGGACAGTTACCAC

consensus                 AGCCAAGTCGTGCTTGACTGGGCCGCCGCGGGGTATTGGAGCAGAAAGGACAGTTACCAC

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_8g09.b1.seq+    CACCTAGGACGCATTCCTCTCCTCTTCCAACGTGG

consensus                 CACCTAGGACGCATTCCTCTCCTCTTCCAACGTGG

****************** Contig 28 *******************
                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7d09.b1.seq+    TTCGATTACCGTGGGCCCCGCCGACGGGCACTTGTATGCATTTTCGACGGGGAAATCCCC
U_HW-SSH1_7e09.b1.seq+    TTCGATTACCGGGGGCCCGGCCGACGGGCACTTGTATGAATTTTAGACGGGGAACTCCCA

consensus                 TTCGATTACCGGGGGCCCCGCCGACGGGCACTTGTATGAATTTTAGACGGGGAAATCCCA

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7d09.b1.seq+    ACGAGTTTTTGATTTTTGGATTTTTTTCGCCATAATTTTTTT
U_HW-SSH1_7e09.b1.seq+    ATGAGTTTTTGTTTTTTCGATTTTTTGCGCCATAATTTTTTTTTGATAAACCCCGCGCTG

consensus                 ACGAGTTTTTGATTTTTCGATTTTTTGCGCCATAATTTTTTTTTGATAAACCCCGCGCTG

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7e09.b1.seq+    AAAATCTTTTATCCCTAATTAGTTTCTCCCTAGAAAGAGTGACTGGTTTTTCTTCTCGTG

consensus                 AAAATCTTTTATCCCTAATTAGTTTCTCCCTAGAAAGAGTGACTGGTTTTTCTTCTCGTG

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7e09.b1.seq+    GTTTTTTTGTTAGGGGCAGCCCACCCCTGACAGCGTCCTGTGTGGACAATTTTTTATATT

consensus                 GTTTTTTTGTTAGGGGCAGCCCACCCCTGACAGCGTCCTGTGTGGACAATTTTTTATATT

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7e09.b1.seq+    GCTTTGGGGGGGGAGGTTGTACAGATCCTCGGGGAAGTGCCCCCGGTGGGGAACATATCA

consensus                 GCTTTGGGGGGGGAGGTTGTACAGATCCTCGGGGAAGTGCCCCCGGTGGGGAACATATCA

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7e09.b1.seq+    ACGTGTGTTTAAAACCCCGTGCGCCCCGCGTGCACCATTAATAAATCTACATTGAATTCA

consensus                 ACGTGTGTTTAAAACCCCGTGCGCCCCGCGTGCACCATTAATAAATCTACATTGAATTCA

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7e09.b1.seq+    GAGCC

consensus                 GAGCC


****************** Contig 29 *******************
                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7g05.b1.seq+    TTCGATTACCGTGGGCCCCCCCGGCGGGCACCTGTATGCGACAACGCCGGGGAGCTACCC
U_HW-SSH1_7f05.b1.seq+          TACCGTGGGCCCCGCCGACGTTTACCTGTATACGAAAACGCCGGGGCGAACCCC
U_HW-SSH1_7h05.b1.seq+    TTCGATTACCGTGGGCCCCCCCGGAGGGCACCTGTATGCAAAATCGCCGGGGAGAACCCC
U_HW-SSH1_7g06.b1.seq+    TTCGATTACCGTGGGCCCCCCCGACGGGCACTTGTATGCAACATCGCCGGGGAGCTACCC
U_HW-SSH1_7f06.b1.seq+          TACCGTGGGCCCCGCCGAAGTTCACCTGGCTGCAACAACGCCGGGGCGCTACCC
U_HW-SSH1_7g08.b1.seq+    TTCGATTACCGTGGGCCCCCCCGGCGGGCACTTGTATGCATTTTCGCCGGGGAGC-CCCC
U_HW-SSH1_7f07.b1.seq+          TACCGTGGGCCCGGCCGACGGGCACTTGTATGCAACTTCGACGGGGAGATACCC
U_HW-SSH1_7g07.b1.seq+          TACCGTGGGCCGGGCCGGCGGGCACTTGTATGCATCTTCGCCGGGGAGCTACCC

consensus                 TTCGATTACCGTGGGCCCCCCCGACGGGCACCTGTATGCAACATCGCCGGGGAGCTACCC

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7g05.b1.seq+    ACCAGTTTTTGATTTTTGTAGTTTTTTCTGGCTAATTTTTTTTTGAAAAACCCGTCCCCC
U_HW-SSH1_7f05.b1.seq+    ACCAGTTTTTGAGTTTTGTAGTTTTTTCTGGCTAATTTTTTTTTGAAAAACCCGTCCCCC
U_HW-SSH1_7h05.b1.seq+    ACCATTTTTTGATTTTTCGAGTTTTTTCTGGCTAATTTTTTTTGTGAAAAACACGTCCCCC
U_HW-SSH1_7g06.b1.seq+    ACCAGTTTTTGAGTTTTCGAGTTTTTTCTGGCTAATTTTTTTGTGAAAAACCCGTCCCCC
U_HW-SSH1_7f06.b1.seq+    ACCGGTTTTTGAGTTGACGAGTTTTTGTTGGCTAATTTTAACGTGAAAAACCCGTCCCCC
U_HW-SSH1_7g08.b1.seq+    ACGAGTTTTTGATTTGACGATTTTTTGTTGGCTAATTTTTTTTTGAATAACCCGGCCCCC
U_HW-SSH1_7f07.b1.seq+    ATGACTTTTTGATTTGACGATTTTTTGTTGGCTAATTTTATTGTGAAAAACCCTGCCCCC
U_HW-SSH1_7g07.b1.seq+    ATGACTTTTTGATTTGACGATTTTTTTCGGGCTAATTTTTTTTTGAAAAACCCGGCCCCC

consensus                 ACCAGTTTTTGATTTGACGAGTTTTTTCTGGCTAATTTTTTTGTGAAAAACCCGTCCCCC

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7g05.b1.seq+    TCCGTCTTTTT-TTCCTCCTCAGCGTGACCAAGAGCAAGCCTGACACGGGTTAGGTGATG
U_HW-SSH1_7f05.b1.seq+    TCCATCTTTTT-TTCCTCCTCAGCGGGACCAAGAGCAAGCCTGTTACGGGTTAGGTGATG
U_HW-SSH1_7e04.b1.seq+                                       CAAGCCTGTTATCGGTTAGGTGATG
U_HW-SSH1_7h05.b1.seq+    TCCGTCTTTTT-TTCCTCGACAGCGCCTAAAA-AGGAAGCCTGAC-CGGGTTAGGTGTTG
U_HW-SSH1_7g06.b1.seq+    TCCATCTTTTT-ATCCTGCTCAGCGTGAA-AAGAGCAAGCCTGAGACGGGTTAGGTGATG
U_HW-SSH1_7f06.b1.seq+    TCCACGTTTTTCATCCCGCTCAGCGTGACCAAAAGCAAGCCGGAGACCGGTTAGGTGATG
U_HW-SSH1_7g08.b1.seq+    GCCAAATTTTT-ATTTGACTTAGCGGGTACAT-AGCAAGCCTGTTACGGGTTAGGTGATG
U_HW-SSH1_7f07.b1.seq+    TCCATCTTTTT-TTCCTGGACTGCGTTTAAAA-AGCAAGCCTGTTACGGGTTAGTTGATG
U_HW-SSH1_7g07.b1.seq+    GCCATCTTTTT-ATCCTCCTTAGCGGGAACAA-AGCAAGCCTGAGACGGGTTAGGTGACG

consensus                 TCCATCTTTTT-ATCCTCCTCAGCGTGAACAA-AGCAAGCCTGATACGGGTTAGGTGATG

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7g05.b1.seq+    GGTGTCTTTTAGAGGGGGCAGCCCCCCGATCCCAACCTCGGCGCCAAGGAATATTCGA-A
U_HW-SSH1_7f05.b1.seq+    GGTGTTTTTTATGTTGGGCATCCGCCAGATCCCAACCTCGGCGCCGGGGAATATTGGA-A
U_HW-SSH1_7e04.b1.seq+    GGTGTTTTCCGTGTTGGGCATCCCCCCGCTCCCAACCTCCTCGCCGGAAAATATTCTATA
U_HW-SSH1_7h05.b1.seq+    GGTGTTTTTTATAGGGGGCAGCCGCCCGATCCCAACCTCGGCGCTAAGGAATATTGGA-A
U_HW-SSH1_7g06.b1.seq+    GGTGTTTTTTATAGGGGGCAGCCCCCAGATCCCAACCTCGGCGCCAAGGAATCCTGGA-A
U_HW-SSH1_7f06.b1.seq+    GGTGTTTTCTAGAGGGGGCATCCGCCAGATCCCAACCTCGGCGCCAAGGAATCTTGGA-A
U_HW-SSH1_7g08.b1.seq+    GGGGTTTTTTGTATGGGGCACCCCACCCATGCCACCCTCCGCGCCAAGCAAGCCTTTCAA
U_HW-SSH1_7f07.b1.seq+    GGTGTTTTTTGTAGGGGGCATCCCCCCTATCCCACCCTCCGCGCCGGACAATATTCTATA
U_HW-SSH1_7g07.b1.seq+    GGGGTTTTTTGTGGGGGGCATCCCCCCCATCCCACCCTCCGCGCCAAGCAA

consensus                 GGTGTTTTTTATAGGGGGCATCCCCCCGATCCCAACCTCGGCGCCAAGGAATATTGGA-A

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7g05.b1.seq+    TTGCTTTGCGGGGGGGGGGGTACCAGCCCCTCCGGGAGAAATCCCCGGCGGCCAACACCT
U_HW-SSH1_7f05.b1.seq+    TTACTTTGGGGGGGGGGGAGGTACCAGCCCGGCCGGGAGAAATGCCCGGGGGGCAACACCT
U_HW-SSH1_7e04.b1.seq+    ATACTTTGGGGGGGGGGGGGGAACCAGCCCGGGGGGGAAAAATGCCCGGGGGGCAACACCT
U_HW-SSH1_7h05.b1.seq+    TTACTTTGCGGGGGGGGGGGGTACCAGCCCGGGCGGGAGAACTCCTCGGCGGGGAACACGT
U_HW-SSH1_7g06.b1.seq+    TCGCTTTCCAGGGGGAGAGGTACCAGCCCGGCCGGGAAATATCCCCGGCGCCCAACACGT
U_HW-SSH1_7f06.b1.seq+    TTGCTTGGGGGGGGGAGAGGTACCAGCCCGGGCGGGAAATATCCCCGGGGCGCAACATAT
U_HW-SSH1_7g08.b1.seq+    TTACTTTCGAGGGGGAGGGGTACCAGCCCCTCGGGGATATGCCCCCGGCGCCCAACATAT
U_HW-SSH1_7f07.b1.seq+    TTACTTTGGGGGGGGAGGGGTACCAGCCCGGGGGGGAGATGCACCCGGGGGGGAACACGT

consensus                 TTACTTTGGGGGGGGAGGGGTACCAGCCCGGCCGGGAGAAATCCCCGGCGGGCAACACCT

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7g05.b1.seq+    TAACGAGTGTTTAAAAACCCGTGTGCATCCCGGCCACCACTTGAG
U_HW-SSH1_7f05.b1.seq+    AATCGAGTGGTTATAAACCCCTGTGCACCCCGGCC
U_HW-SSH1_7e04.b1.seq+    AAACGAGGGGATTTAACCCCCTGTGCACC
U_HW-SSH1_7h05.b1.seq+    TAACGAGTGTTTAAAAACCCGTGTGCAGCCCGGCCCCCACTTGAG
U_HW-SSH1_7g06.b1.seq+    TAACGAGTGTTTATATCCCCGTGTGCAGGCCGGCCCCCACATGAG
U_HW-SSH1_7f06.b1.seq+    TATCGAGTGTTTATAAACCTGTGTGCACGCCGGCCGCCAC
U_HW-SSH1_7g08.b1.seq+    TAACGTGTGTTTATATCCCCGTGTGCCCGCCGGCCCCCACTTGAAAAATCTCTATTGACT
U_HW-SSH1_7f07.b1.seq+    TAACGAGTGTTTAAAGCCCCGTGT

consensus                 TAACGAGTGTTTATAAACCCGTGTGCACCCCGGCCCCCACTTGAGAAATCTCTATTGACT

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7g08.b1.seq+    TCGCAGCCGCATGCAGGTCTATCTTATGGGACACCTCCCTGGGTGGAGGTATGCATGGCC

consensus                 TCGCAGCCGCATGCAGGTCTATCTTATGGGACACCTCCCTGGGTGGAGGTATGCATGGCC

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7g08.b1.seq+    AAATTTTTCTCCTGTGTCAACTATGTAGACCGATCAAATTCCAGTCTAATTGTATCCTGA

consensus                 AAATTTTTCTCCTGTGTCAACTATGTAGACCGATCAAATTCCAGTCTAATTGTATCCTGA

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7g08.b1.seq+    GTGATATTGTTCACATCACGTGCTGCACACTAAATGCGCTCACTCAAGTTAATTGTGCTG

consensus                 GTGATATTGTTCACATCACGTGCTGCACACTAAATGCGCTCACTCAAGTTAATTGTGCTG

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7g08.b1.seq+    CCCTGCCTGTGCGTCTTTGCGTGACCGGACATCTCTCATGGCAGATTGCGTTAACGAATC

consensus                 CCCTGCCTGTGCGTCTTTGCGTGACCGGACATCTCTCATGGCAGATTGCGTTAACGAATC

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7g08.b1.seq+    CGCTCACTCCTCGGGAGCGCGCGTTTGCATTTTGCTTTGCTCATCCGCTCCCCTTCCAAG

consensus                 CGCTCACTCCTCGGGAGCGCGCGTTTGCATTTTGCTTTGCTCATCCGCTCCCCTTCCAAG

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7g08.b1.seq+    TGACAGGCTCACCTTCGTACTGATGCGCTCCTCCGATTCCTCATCACATCACTCGATGCC

consensus                 TGACAGGCTCACCTTCGTACTGATGCGCTCCTCCGATTCCTCATCACATCACTCGATGCC

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7g08.b1.seq+    GTAGTACGGATCATCCGCAGCAACAGGCATACAACTCAGCAAGAACAGTAGACGAAGCCA

consensus                 GTAGTACGGATCATCCGCAGCAACAGGCATACAACTCAGCAAGAACAGTAGACGAAGCCA

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7g08.b1.seq+    GCTAAAGGTGTGTAATCGTCGATGCCCTGTTCATGACATTCTTCAATAGCGTCCAGCCAC

consensus                 GCTAAAGGTGTGTAATCGTCGATGCCCTGTTCATGACATTCTTCAATAGCGTCCAGCCAC

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7g08.b1.seq+    CCAGAAGACGTACGTAATTG

consensus                 CCAGAAGACGTACGTAATTG

****************** Contig 30 *******************
                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7h01.b1.seq+    TTCGATTAGCGTGGTCGCGGCCGAGGTACCCCTTTGTGTCATTTGAGGACCCATTTCACC
U_HW-SSH1_7h02.b1.seq+          TAGCGTGGTCGCGGCCGAGGTACCCCATTGTGTCGATTGAGGACCCATTTGACC
U_HW-SSH1_7g03.b1.seq+          TAGCGTGGTCGCGGCCGAGGTACCCCATTGTGTCGATTGAGGACCCATTTGACC
U_HW-SSH1_7g02.b1.seq+          TAGCGTGGTCGCGGCCGAGGTACCCCTTTGTGTCGATTGAGGACCCATTTGACC
U_HW-SSH1_7f02.b1.seq+          TAGCGTGGTCGCGGCCGAGGTACCCCTTTGTGTCGATTGGGGACCCATTTCCCC
U_HW-SSH1_7h03.b1.seq+          TAGCGTGGTCGCGGCCGAGGTACCCCATTGTGTCAATTGAGGACCCATTTGACC

consensus                 TTCGATTAGCGTGGTCGCGGCCGAGGTACCCCATTGTGTCGATTGAGGACCCATTTGACC

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7h01.b1.seq+    ATGATGTTTGGGTGCATTATGCAAAAATGACTGAATATTGTTGAGTGGAAGTTCGCATTG
U_HW-SSH1_7h02.b1.seq+    AGGATGATTGGGTGCACTATGCTAAAATGACTGAATAATGTGGAGTGGAAGTTCAGATTG
U_HW-SSH1_7g01.b1.seq+              GGTGCACTATGCTAACATGACTGAATAATGTGGAGTGGAATTTCAGATTG
U_HW-SSH1_7g03.b1.seq+    AGGATGACTGGGTGCACTTTGCTAAAATGACTGAAGAATGTGGAGTGGAAGTTCAGATTG
U_HW-SSH1_7g02.b1.seq+    AGGATGACTGGGTGCACTATGCTAAAATGACTGAAGAATGTGGAGTGGAAGTTCAGATTG
U_HW-SSH1_7f02.b1.seq+    ATGATGTTTGGTTGTATTTTGCTAAAATGACTGAATATTGTTGATTGGAAGTTCATATTG
U_HW-SSH1_7h03.b1.seq+    AGGATGATTGGTTGCACTTTGCTAAAATGACTGAATATTGTGGAGTGGAATTTCACATTG

consensus                 AGGATGATTGGGTGCACTATGCTAAAATGACTGAATAATGTGGAGTGGAAGTTCAGATTG

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7h01.b1.seq+    TTGGTGATTACCTTCTACTCTCCAACCCCACCAAAGTGGGAAAGGCAATCCACTAAAAGT
U_HW-SSH1_7h02.b1.seq+    TTGGTGATGACCTTCTACCCCCCAACCCCACCAAAGTTGGTAAGGCAATCCAGGAGAAGT
U_HW-SSH1_7g01.b1.seq+    TTGGTGATAACCTTCTATTCTCCAACCCAACCAGAGTTGCAAAGGCAATCCAGGAAAATT
U_HW-SSH1_7g03.b1.seq+    TTGGTGATGACCTTCTAGTCACCAACCCAACCAGAGTTGCAAAGGCTATCCAGGAAAATT
U_HW-SSH1_7g02.b1.seq+    TTGGTGATGACCTTCTACTCACCAACCCAACCAAAGTTGCAAAGGCAATCCAGGAAAAGT
U_HW-SSH1_7f02.b1.seq+    TTGGTGATTACCTTCAACCCTCCACCCCCACCAAAGTTGGAAAGGCTATTTTGGAAAATT
U_HW-SSH1_7h03.b1.seq+    TTGGTGATTACCTTCTACTCACCAACCCCACCAAAGTTGCTAAGGCAATCCAGGACACGT

consensus                 TTGGTGATGACCTTCTACTCACCAACCCCACCAAAGTTGCAAAGGCAATCCAGGAAAAGT

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7h01.b1.seq+    CTTGTTTTGCTCTTCTGCAGACGGCCA-CTAAATTGGATCCGTAATTGAAAGTATCGAGG
U_HW-SSH1_7h02.b1.seq+    CATGTTT-GCTCTTCTGCTGACGGTTAACCAAATTGGATCCGTCACTGAGAGTATCGAGG
U_HW-SSH1_7g01.b1.seq+    CTTGCCATGCTCTTCTGCTGAAGGTTAACCAAATTGGATCCGTCACTGAGAGTATCGAGG
U_HW-SSH1_7g03.b1.seq+    CTTGCCATGCTCTTCTGCTGAAGGTTAACCAAATTGGATCCGTCACTGAAAGTATCGAGG
U_HW-SSH1_7g02.b1.seq+    CATGCATTGCTCTTCTGCTGAAGGTTAACCAAATTGGATCCGTCACTGAAAGTATCGAGG
U_HW-SSH1_7f02.b1.seq+    CTTGCCATGCTCTTCTGCTGACAACCA-CCAAATTGAATCCGTATTACTTAATTTCGAGG
U_HW-SSH1_7h03.b1.seq+    CATGT-TTGCTCTTCTGCTGAAGGTTAACCAAATTGGATCCGTCACTGAAAGTATCGAGG

consensus                 CTTGCCTTGCTCTTCTGCTGAAGGTTAACCAAATTGGATCCGTCACTGAAAGTATCGAGG

                                   .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7h01.b1.seq+    CCGTGAACATGTCGGAACTTGCTGGCTGGGGTGTCAAGACCACCCAGGGGAGTGGGGAGA
U_HW-SSH1_7h02.b1.seq+    CCGTGAACATGCCAAAACTTGCTGGCTGGGGTGTCATGACCAGCCACGGGAGTGGTGAGA
U_HW-SSH1_7g01.b1.seq+    CCGTGAACATGTCAAAACCTGCTGGCTGGGGTGTCATGACCACCCAGGGGAGTGGGGAGA
U_HW-SSH1_7g03.b1.seq+    CCGTGAACATGTCAAAACCTGCTGGCTGGGGTGTCATGACCAGCCACGGGAGTGGTGAGA
U_HW-SSH1_7g02.b1.seq+    CCGTGAACATGTCAAAACATGCTGGCTGGGGTGTCATGACCAGCCACAGGAGTGGTGAGA
U_HW-SSH1_7f02.b1.seq+    GCGGGAACATGCCAGAACTTGCTGGCTGGGGTGTCAAGACCACCCAGGGGAGTGGTGAGA
U_HW-SSH1_7h03.b1.seq+    CCGTGAAGATGTCAAAACTTGCTGGCTGGGGTGTCATGACCAGCCAGGGGAGTGGTGAAA
```

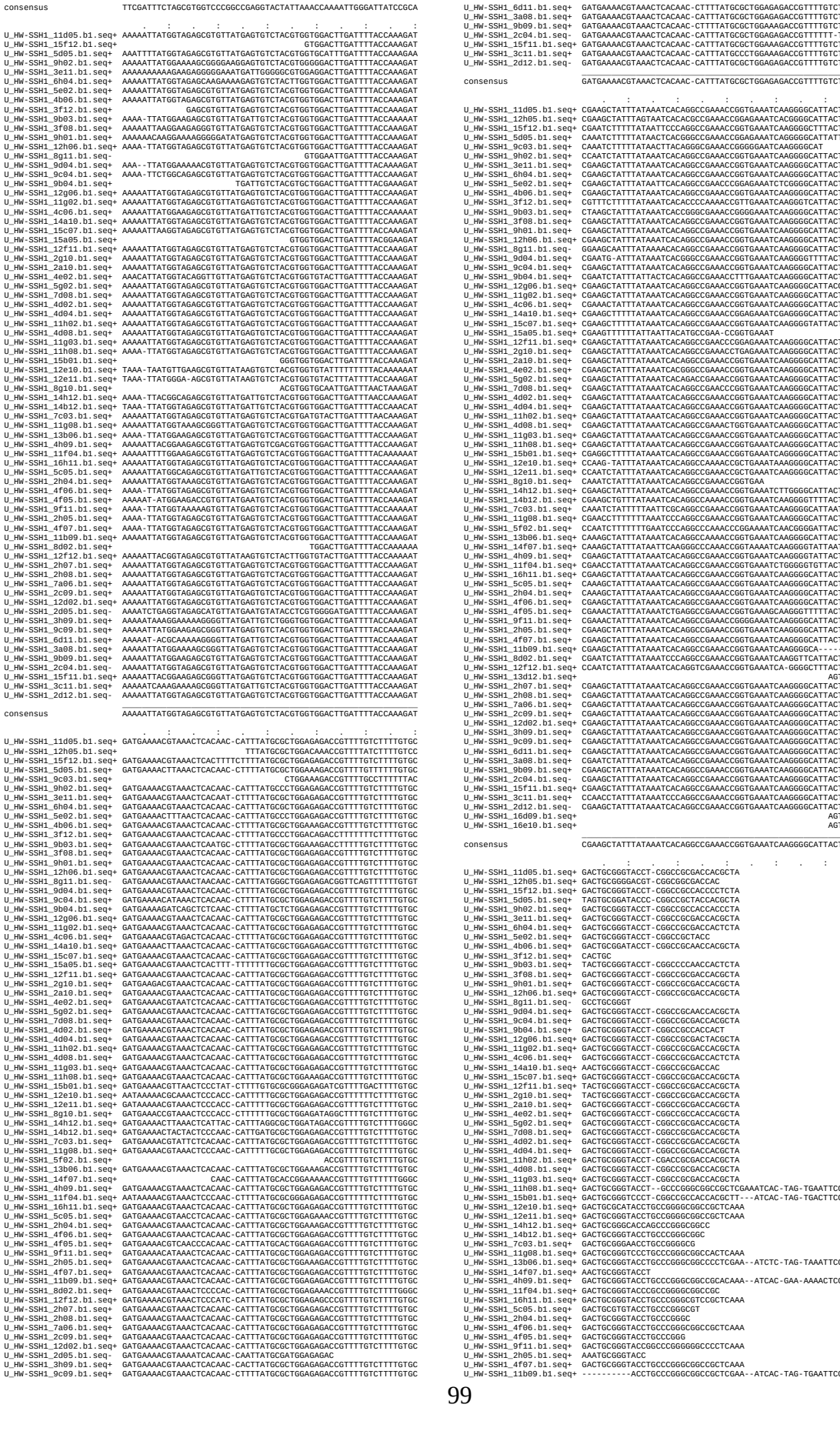
```
consensus                CCGTGAACATGTCAAAACTTGCTGGCTGGGGTGTCATGACCAGCCAGGGGAGTGGTGAGA

U_HW-SSH1_7h01.b1.seq+  CCAAGGACACATTCATTGCTGATTTGGCTGTTGGCCTGTCCACGGGTCAAATCAAGACCG
U_HW-SSH1_7h02.b1.seq+  CCGAGGACACATTCATTGCTGATTTGGCTGTTGGTCTGTCCACGGGTCAAATCAAGACCG
U_HW-SSH1_7g01.b1.seq+  CCGAGGACACATTCATTGCTGATTTGGCTGTTGGCCTGTCCACGGGTCAGATCAAGACCG
U_HW-SSH1_7g03.b1.seq+  CCGAGGACACATTCATTGCTGATTTGGCTGTTGGTCTGTCCACGGGTCAAATCAAGACCG
U_HW-SSH1_7g02.b1.seq+  CCGAGGACACATTCATTGCTGATTTGGCTGTTGGTCTGTCCACGGGTCAAATCAAGACCG
U_HW-SSH1_7f02.b1.seq+  CCAAGGACCCGTTCATTGCTGATTTGGCTGGTGGCCTGTCCACGGGTCAAATCAAGACCG
U_HW-SSH1_7h03.b1.seq+  CCGAGGACACATTCATTGCTGATTTGGCTGTTGGTCTGTCCACGGGTCAAATCAAGACCG

consensus                CCGAGGACACATTCATTGCTGATTTGGCTGTTGGTCTGTCCACGGGTCAAATCAAGACCG

U_HW-SSH1_7h01.b1.seq+  GGGCTCCCTGCCGGTCAGAGCGTCTTGCCAAGTACCTGCCC
U_HW-SSH1_7h02.b1.seq+  GGGCTCCCTGCCGGTCAGAGCGTCTTGCCAAGTACCTGCCC-GGGGGGACGTACCTGCTC
U_HW-SSH1_7g01.b1.seq+  GGGCTCCCTGCCGGTCAGAGCGTCTTGCCACGTACCTGCCC-GGGGG
U_HW-SSH1_7g03.b1.seq+  GGGCTCCCTGCCGGTCATAGCGTCTTGCCAAGTACCTGCCC-GGGGG
U_HW-SSH1_7g02.b1.seq+  GGGCTCCCTGCCGGTCAGAGCGTCTTGCCAAGTACCTGCCC
U_HW-SSH1_7f02.b1.seq+  GGGCTCCCTGCCGGTCATAGCGTCTTGCCAAGTACCTGCCC-GGGGGGACGTTCCTGCTC
U_HW-SSH1_7h03.b1.seq+  GGGCTCCCTGCCGGTCAGAGCGTCTTGCCAAGTACCTGCCCCGGGCGAACGTACCTGCTC

consensus                GGGCTCCCTGCCGGTCAGAGCGTCTTGCCAAGTACCTGCCC-GGGGGGACGTACCTGCTC

U_HW-SSH1_7h02.b1.seq+  GG
U_HW-SSH1_7f02.b1.seq+  GGACGTT
U_HW-SSH1_7h03.b1.seq+  GGACGTTCTTCGCGGCCGACTGTAAGGCTGGATAAGTGAGAGCTCCGAGGTGGTTAGAGG

consensus                GGACGTTCTTCGCGGCCGACTGTAAGGCTGGATAAGTGAGAGCTCCGAGGTGGTTAGAGG

U_HW-SSH1_7h03.b1.seq+  GATATCTTGAGTATTTTACTTGGTCCGCTAATAATGCCGGCTTAACGTGGGCTTAGCTGT

consensus                GATATCTTGAGTATTTTACTTGGTCCGCTAATAATGCCGGCTTAACGTGGGCTTAGCTGT

U_HW-SSH1_7h03.b1.seq+  CTCGGGAGTGCCATTGTGTCCGCTCACACTCCCGGGACATGCGACTCGCGAGGCGCTTGC

consensus                CTCGGGAGTGCCATTGTGTCCGCTCACACTCCCGGGACATGCGACTCGCGAGGCGCTTGC

U_HW-SSH1_7h03.b1.seq+  GAACGCTTGCGTGCCTAGTCACTTGGATTAACTAAAATGTGTGGCGGCGAGTACGTGCCC

consensus                GAACGCTTGCGTGCCTAGTCACTTGGATTAACTAAAATGTGTGGCGGCGAGTACGTGCCC

U_HW-SSH1_7h03.b1.seq+  GTTTCGGATAGGCACACTCTGCCGTCTCCTACATTAATGAACTGAACTACGACATGAGAT

consensus                GTTTCGGATAGGCACACTCTGCCGTCTCCTACATTAATGAACTGAACTACGACATGAGAT

U_HW-SSH1_7h03.b1.seq+  AGGCAGATAGGGTATTGGAC

consensus                AGGCAGATAGGGTATTGGAC

****************** Contig 31 ******************

U_HW-SSH1_8d02.b1.seq+  TAGCGTGGTCGCGGCCGAGGTACAGGCAGCAGCGTAGCAGCATGTTTTTGCTTATTCACA
U_HW-SSH1_9h04.b1.seq+  TAGCGTGGTCGCGGCCGAGGAACAGGCAGCAGCGTAGCAGCATGTTTTTGCTTATTCACA

consensus                TAGCGTGGTCGCGGCCGAGGAACAGGCAGCAGCGTAGCAGCATGTTTTTGCTTATTCACA

U_HW-SSH1_8d02.b1.seq+  TGATATACATCGATCGACCTCTGCTGAGAATAAGAGCGTTTTTTACACTAATAGTAGTTC
U_HW-SSH1_9h04.b1.seq+  TGATATACATCGATCGACCTCTGCTGAGAATAAGAGCGTTTTTTACACTAATAGTAGTTC
U_HW-SSH1_12b09.b1.seq+             GATCGACCTCTGCTGAAAATAAGAGGGTTTTTTACACTAAGAGGAGGGG

consensus                TGATATACATCGATCGACCTCTGCTGAGAATAAGAGCGTTTTTTACACTAATAGTAGTTC

U_HW-SSH1_8d02.b1.seq+  GTAGTAGCTGCTTGAGTTAGTTACTTGCTGGTTTGGTAGGGCGCCTCGCAAAACTCGCCG
U_HW-SSH1_9h04.b1.seq+  GTAGTAGCTGTTTGAGTTAGTTACTTGCTGGTTTGGTAGGGCGCCTCGCAAAACTCGCCG
U_HW-SSH1_12b09.b1.seq+ GTAGTGCCTGTTTGAGTTACTTACTTGCTGGTTTGGTAGGGCGCCTCGCAAAACTCGCCG

consensus                GTAGTAGCTGTTTGAGTTAGTTACTTGCTGGTTTGGTAGGGCGCCTCGCAAAACTCGCCG

U_HW-SSH1_8d02.b1.seq+  CCGAGATCGTCGCACGCCTCGTCCGGGAACACCGTTTTTGGCTCGTCGTAGGATAGGTAC
U_HW-SSH1_9h04.b1.seq+  CCGAGATCGTCGCACGCCTCGTCCGGGAACACCGTTTTTGGCTCGTCGTAGGATAGGTAC
U_HW-SSH1_12b09.b1.seq+ CCTATATCGCCGCACGCCTCGTCCGGGAACACCGTTTTTGGCTCGTCGTAGGATAGGTAC

consensus                CCGAGATCGTCGCACGCCTCGTCCGGGAACACCGTTTTTGGCTCGTCGTAGGATAGGTAC

U_HW-SSH1_8d02.b1.seq+  CTGCCCGGGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAGGTCGACCATA
U_HW-SSH1_9h04.b1.seq+  CTGCCCGGGCGGC
U_HW-SSH1_12b09.b1.seq+ CTGCCCGGGCGG

consensus                CTGCCCGGGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAGGTCGACCATA

U_HW-SSH1_8d02.b1.seq+  TGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGTCACCTAAATA

consensus                TGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGTCACCTAAATA

U_HW-SSH1_8d02.b1.seq+  GCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTC

consensus                GCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTC

U_HW-SSH1_8d02.b1.seq+  CACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCT

consensus                CACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCT

U_HW-SSH1_8d02.b1.seq+  AACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCC

consensus                AACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCC

U_HW-SSH1_8d02.b1.seq+  AGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTT

consensus                AGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTT

U_HW-SSH1_8d02.b1.seq+  CCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGCGAGCGTATCAGCT

consensus                CCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGCGAGCGTATCAGCT

U_HW-SSH1_8d02.b1.seq+  CACTCAGAGGCGGTATACGGTTATCCACAGAATCAGGGGATACGCAGAAGACATGTGAGC

consensus                CACTCAGAGGCGGTATACGGTTATCCACAGAATCAGGGGATACGCAGAAGACATGTGAGC

U_HW-SSH1_8d02.b1.seq+  AAACGTCAGCAATGCCAGACGTAGACG

consensus                AAACGTCAGCAATGCCAGACGTAGACG

****************** Contig 32 ******************

U_HW-SSH1_8d07.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACGGTGGGGTTCTACTTGCCAAGCGGCTCACCC
U_HW-SSH1_8e07.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACGGTCGGGTTCTG-TTGCAGAGCGGCTCCCGC

consensus                TTCGATTAGCGTGGTCGCGGCCGAGGTACGGTCGGGTTCTACTTGCAAAGCGGCTCACCC

U_HW-SSH1_8d07.b1.seq+  TCGACGCCCAATTTGTAGGAAGAGGACAGCTGACGCTCCTCCACGCCGCTGAAATTTGCG
U_HW-SSH1_8e07.b1.seq+  ACGACTTTTAATTTGGAAGATGAGGACAGCTAACGCTCCTCCACACCGCTGAAATTTGCG

consensus                ACGACGCCCAATTTGGAAGAAGAGGACAGCTAACGCTCCTCCACACCGCTGAAATTTGCG

U_HW-SSH1_8d07.b1.seq+  ACCTTGCGAATGGACCCGCCGATGGGGCCTTGCGGGTTGGATTTGCCGCTGCTGTCGCGC
U_HW-SSH1_8e07.b1.seq+  ACCTTCCTTATGGATCCGCAGATGGGGCCTCGCCCGTTGGATTTGCCGCTGCTGTCGAGT

consensus                ACCTTCCGAATGGACCCGCAGATGGGGCCTCGCCCGTTGGATTTGCCGCTGCTGTCGAGC

U_HW-SSH1_8d07.b1.seq+  ATGATGCCCCTCATGGAGGTGAGCAGGCTGCCGTAGGTGGTGCGCGGCTCAAACCTGCCC
U_HW-SSH1_8e07.b1.seq+  GTGATTCCCCTCAGGGAGGTGACCAGGCTGCCGAAAGTGGTGCGCGGCTC

consensus                ATGATGCCCCTCAGGGAGGTGACCAGGCTGCCGAAAGTGGTGCGCGGCTCAAACCTGCCC

U_HW-SSH1_8d07.b1.seq+  GGGCGGCCGCTCGAAATCTCTACTTATTTCCCGGCCGGTTGGCCCCTACGATTGGGAAGA

consensus                GGGCGGCCGCTCGAAATCTCTACTTATTTCCCGGCCGGTTGGCCCCTACGATTGGGAAGA

U_HW-SSH1_8d07.b1.seq+  GAA

consensus                GAA

****************** Contig 33 ******************

U_HW-SSH1_8f06.b1.seq+  TAGCGTGGTCGCGGCCGAGGTACCCAAAAATGAGCCTACAATTCACCCTAAACATACTAC
U_HW-SSH1_9h09.b1.seq+  TAGCGTGGTCGCGGCCGAGGGACCCAAAAATGAGCCTACAATTCACCCTAAACATACTA-

consensus                TAGCGTGGTCGCGGCCGAGGGACCCAAAAATGAGCCTACAATTCACCCTAAACATACTAC

U_HW-SSH1_8f06.b1.seq+  TTGTGCTAGTAAATCAGGGCGTAGGTTCCGTGCTCTCCAGCAGCAGGCATTTCAGTAGGT
U_HW-SSH1_9h09.b1.seq+  TAGAGCTAGTAAATCAGGGCGTAGGTTCCGTGCTCTCCAGCAGCAGGCATTTCAGTAGGT

consensus                TAGAGCTAGTAAATCAGGGCGTAGGTTCCGTGCTCTCCAGCAGCAGGCATTTCAGTAGGT

U_HW-SSH1_8f06.b1.seq+  TGGTTCAAATCACTTGGCAGGAATGCTACCACTGCCAGCAGGCCTTTTCAGCATTGCACC
U_HW-SSH1_9h09.b1.seq+  TGGTTCAAATCACTTGGCAGGAATGCTACCACTGCCAGCAGGCCTTTTCAGCATTGCACC

consensus                TGGTTCAAATCACTTGGCAGGAATGCTACCACTGCCAGCAGGCCTTTTCAGCATTGCACC

U_HW-SSH1_8f06.b1.seq+  TTGCAGGAGATACGACGCCTTGTTCCGGACCTTCGAAGCGTAAAACCTCCAGTCCGTGCA
U_HW-SSH1_9h09.b1.seq+  TTGCAGGAGATACGACGCCTTGTTCCGGACCTTCGAAGCGTAGAACCTCCAGTCCGTGCA

consensus                TTGCAGGAGATACGACGCCTTGTTCCGGACCTTCGAAGCGTAAAACCTCCAGTCCGTGCA

U_HW-SSH1_8f06.b1.seq+  TCCTATATGGGTCGAGCAGTTGCGTAGAAAAATTGCGCCATGCGTCAATTATCGCGGTCTT
U_HW-SSH1_9h09.b1.seq+  TCCTATATGGGTCGAGCAGTTGCGTAAAAAATTGCGCCATGCGTCGATTATCGCGGTCTT

consensus                TCCTATATGGGTCGAGCAGTTGCGTAAAAAATTGCGCCATGCGTCAATTATCGCGGTCTT

U_HW-SSH1_8f06.b1.seq+  GTTTCTGAACGCGTCGCTAGAAAAGAGCAGGTTGTCCATCAAAACTATGTGCACGTATAG
U_HW-SSH1_9h09.b1.seq+  GTTTCTGAACGCGTCGCTAAAGAAGAGCAGGTTGTCCATCAAAACTATGTGCACGTATAG

consensus                GTTTCTGAACGCGTCGCTAAAAAAGAGCAGGTTGTCCATCAAAACTATGTGCACGTATAG

U_HW-SSH1_8f06.b1.seq+  CACAAAGAAATTGCATTCTTTCTCCTTCACATTTATCGATGTGACCGACTTCAGGATCCT
U_HW-SSH1_9h09.b1.seq+  CACAAAGAAATTGCATTCTTTCTCCTTCACATTTATCGATGTGACCGACTTCAGGATCCT

consensus                CACAAAGAAATTGCATTCTTTCTCCTTCACATTTATCGATGTGACCGACTTCAGGATCCT

U_HW-SSH1_8f06.b1.seq+  TTCAACATTCGCCACTTTAAGGCAGAAGCTATTTTTGAGCAACTGAAGGGCCAGCTGGCT
U_HW-SSH1_9h09.b1.seq+  TTCAACATTCGCCACTTTAAGGCAGAAGCTATTTTTGAGCAACTGAAGGGCCAGCTGGCT

consensus                TTCAACATTCGCCACTTTAAGGCAGAAGCTATTTTTGAGCAACTGAAGGGCCAGCTGGCT

U_HW-SSH1_8f06.b1.seq+  CCTTAGGAATTTACCTGCCCGGGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCT
U_HW-SSH1_9h09.b1.seq+  CCTTAGGAATTTACCTGCCCGGGCGGCCGCTCGAAATCACTAGAGAATTCGCGGCCGCCT

consensus                CCTTAGGAATTTACCTGCCCGGGCGGCCGCTCGAAATCACTAGAGAATTCGCGGCCGCCT

U_HW-SSH1_8f06.b1.seq+  GCAGGTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATA
U_HW-SSH1_9h09.b1.seq+  GCGGGTCGACCATATGGGAGATCTCCCAACGGGTTGGATGCATAGCTTGA

consensus                GCAGGTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATA

U_HW-SSH1_8f06.b1.seq+  GTGTCACCTAAATAGCTTGCGTATCATGGATCATAGCTGTTTCCTGTGTGAAATTGTTAT

consensus                GTGTCACCTAAATAGCTTGCGTATCATGGATCATAGCTGTTTCCTGTGTGAAATTGTTAT

U_HW-SSH1_8f06.b1.seq+  CCGCTCACATTCCACACACATACGAGCCGGAGCATAAGTGTAAAGCCTGGGCTGCTAATG

consensus                CCGCTCACATTCCACACACATACGAGCCGGAGCATAAGTGTAAAGCCTGGGCTGCTAATG

U_HW-SSH1_8f06.b1.seq+  ATGAGCTACTCAATATGCGTGCGCTCACTGGCGCTTCAGTCGAAACTGTCTGGCAGCTGC

consensus                ATGAGCTACTCAATATGCGTGCGCTCACTGGCGCTTCAGTCGAAACTGTCTGGCAGCTGC

U_HW-SSH1_8f06.b1.seq+  ATAATGGATCCGCACGCGCGT

consensus                ATAATGGATCCGCACGCGCGT

****************** Contig 34 ******************

U_HW-SSH1_9f03.b1.seq+  TAGCGTGGTCGCGGCCGAGGGCCGCAAGACCGGAAGGAGCGGAGCCGCCGAGCCGGGAAG
U_HW-SSH1_9h03.b1.seq+                          ACCGGAAGGAGCGGAGCCGCCGAGCCGGGAAG

consensus                TAGCGTGGTCGCGGCCGAGGGCCGCAAGACCGGAAGGAGCGGAGCCGCCGAGCCGGGAAG

U_HW-SSH1_9f03.b1.seq+  AGCTCCACCCCATCCCATCGCCCGCCTCCGCTTCCGAAGGGTCAGAAATGGCGGACCGAG
U_HW-SSH1_9h03.b1.seq+  AGGCCCTCCCCATCCCATCGCCAACCTCCGCTTCCGAAGGGTCAGAGATGGCGGACCGAG

consensus                AGCCCCACCCCATCCCATCGCCAACCTCCGCTTCCGAAGGGTCAGAAATGGCGGACCGAG

U_HW-SSH1_9f03.b1.seq+  CTAACCCCCCGTCTGTCATGCAAAAGTTTGGTGGACAGTTCCACCTTGCCTCCAGCTTCT
U_HW-SSH1_9h03.b1.seq+  CT

consensus                CTAACCCCCCGTCTGTCATGCAAAAGTTTGGTGGACAGTTCCACCTTGCCTCCAGCTTCT

U_HW-SSH1_9f03.b1.seq+  CTGAGGGTGTTCGTGCTCGCAACATCTGCCCTTCTGTGCCATCCTATGAGAGGCCCTTCC

consensus                CTGAGGGTGTTCGTGCTCGCAACATCTGCCCTTCTGTGCCATCCTATGAGAGGCCCTTCC

U_HW-SSH1_9f03.b1.seq+  CCACAACCAGCTACATGACTCAAAACCTTGGGATCCCTGCCCCAATCATGTCATCTTCTC

consensus                CCACAACCAGCTACATGACTCAAAACCTTGGGATCCCTGCCCCAATCATGTCATCTTCTC

U_HW-SSH1_9f03.b1.seq+  CAATGTTTGCCAATGCACCCCCTGAAAAGAAAGGTGTCAAGAACTTTGCGATTGATTTCC

consensus                CAATGTTTGCCAATGCACCCCCTGAAAAGAAAGGTGTCAAGAACTTTGCGATTGATTTCC

U_HW-SSH1_9f03.b1.seq+  TCATGGGAGGAGTGTCAGCTGCATTTTCCAAGACTGCTGCAGCTCCCATTGCCCGTGTTA

consensus                TCATGGGAGGAGTGTCAGCTGCATTTTCCAAGACTGCTGCAGCTCCCATTGCCCGTGTTA

U_HW-SSH1_9f03.b1.seq+  ACCTGCTTATCCAGAACCAGAATGAGATGATCAAGGCTGGCAGGCTCTCTGAGCCATACA

consensus                ACCTGCTTATCCAGAACCAGAATGAGATGATCAAGGCTGGCAGGCTCTCTGAGCCATACA
```

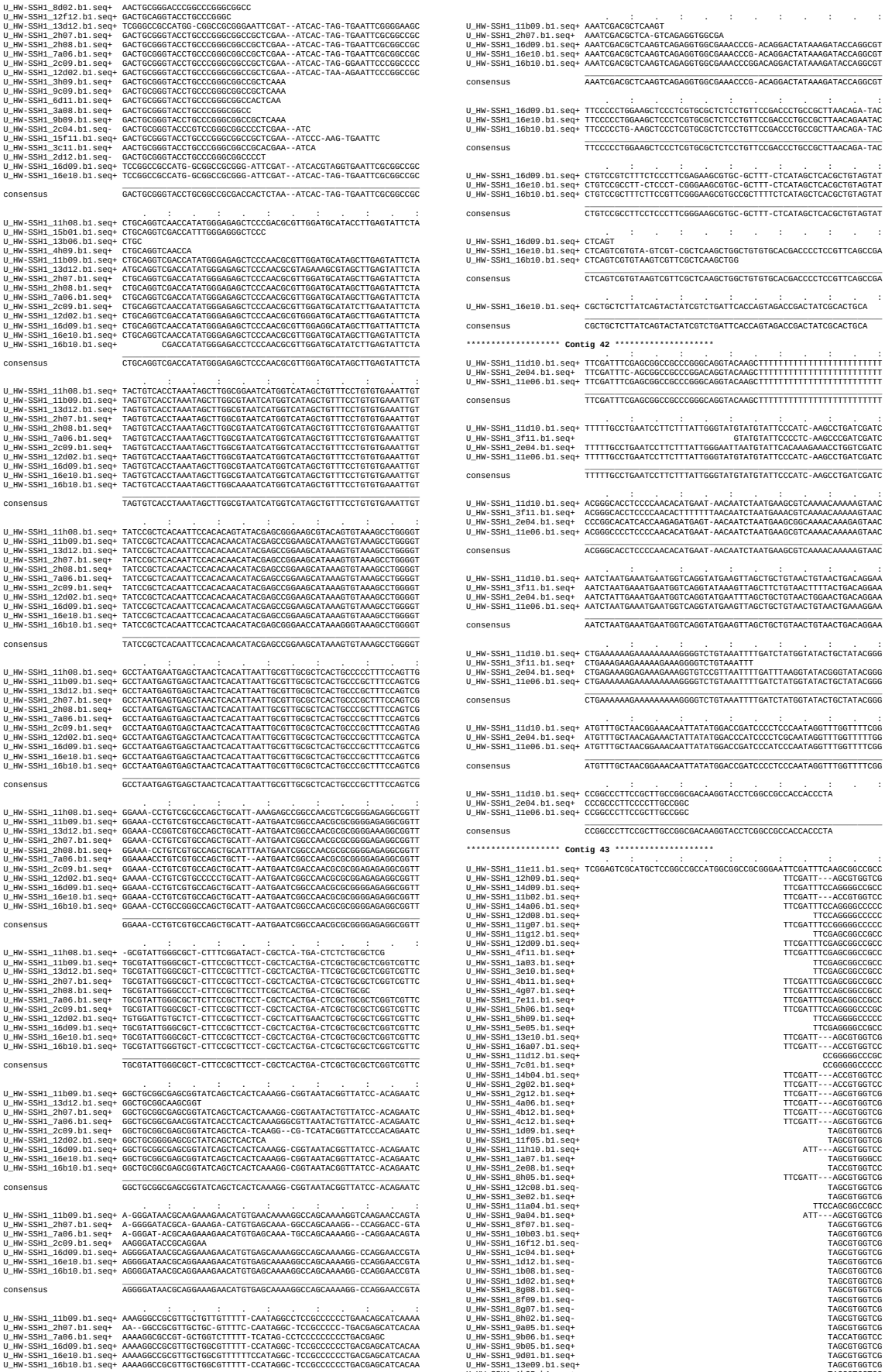


```
U_HW-SSH1_10e10.b1.seq+ ----------CT-GCCCGGGCGGCCCATCAAAATCA
U_HW-SSH1_3h07.b1.seq+  ----------CT-GC
U_HW-SSH1_9b12.b1.seq+  ----------CT-GCCCGGG
U_HW-SSH1_15g10.b1.seq+ ----------CT-GCCCGGGCCGCCCGCT
U_HW-SSH1_10e09.b1.seq+ ----------CT-GCCCGGGCCGCCCGCTCAAA
U_HW-SSH1_13g06.b1.seq+ ----------CT-GCCCGGGCGGCCGTTCAAAAA
U_HW-SSH1_3g07.b1.seq+  ----------CT-GCCCGGGCGGCC
U_HW-SSH1_13f06.b1.seq+ ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_13g08.b1.seq+ ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_10h11.b1.seq+ ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_13e06.b1.seq+ ----------CT-GCCCGGGCGGCCGCTAAAA
U_HW-SSH1_13h06.b1.seq+ ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_3e08.b1.seq+  ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_13e08.b1.seq+ ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_9f05.b1.seq+  ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_4d05.b1.seq+  ----------CT-GCCCGGGCGGTCGCTCGAAATCACAAGGGAATTC
U_HW-SSH1_11h01.b1.seq+ ----------CT-GCCCGGGCGGCGGCTCAAAATCA
U_HW-SSH1_11f02.b1.seq+ ----------CT-GCCCGGGCGGCCC
U_HW-SSH1_5h11.b1.seq+  ----------CT-GCCCGGGCG
U_HW-SSH1_3g11.b1.seq+  ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_11d02.b1.seq+ ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_13h09.b1.seq+ ----------CT-GCCCGGGCGGCCGTTCAAAATCACTATTGATTTCGGGGCCCCCTG
U_HW-SSH1_11f08.b1.seq- ----------CT-GCCCGGGCGGCCGCTCGAAATCGAA
U_HW-SSH1_3d12.b1.seq-  ----------CTC-CCCGGGCGGCCGCTCGAAATCGAA
U_HW-SSH1_8h09.b1.seq-  ----------CT-GCCCGGGCGGCCGCTCGAAATCGAA
U_HW-SSH1_5f04.b1.seq-  ----------CT-GCCCGGGCGGCCGCTCGAAATCGAA
U_HW-SSH1_14a11.b1.seq+ ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_4a04.b1.seq+  ----------CT-GCCCGGGCGGTCGC
U_HW-SSH1_13f02.b1.seq+ ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_13g09.b1.seq+ ----------CT-GCCCGGGCGGTCG
U_HW-SSH1_11f01.b1.seq+ ----------CT-GCCCGGGCGGCCAATCAAAATGACTAGTGAAT
U_HW-SSH1_11g10.b1.seq+ ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_13f08.b1.seq+ ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_5f05.b1.seq+  ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_5g04.b1.seq+  ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_8e12.b1.seq+  ----------CT-GCCCGGGCGGCCGCTCAAA
U_HW-SSH1_13g07.b1.seq+ ----------CT-GCCCGGGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAG
U_HW-SSH1_1f06.b1.seq+  AGTTAGAAACCTGCCCGGGCGGCCGCTCGAAATCACTATTGAATTCGCGGCCGCCTGCAG
U_HW-SSH1_2h09.b1.seq+  ----------CT-GCCCGGGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAG
U_HW-SSH1_3f09.b1.seq+  ----------CT-GCCCGGGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAG
U_HW-SSH1_16a08.b1.seq+ ----------CT-GCCCGGGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAG
U_HW-SSH1_10a10.b1.seq+ ----------CT-GCCCGGGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAG
U_HW-SSH1_10a09.b1.seq+ ----------CT-GCCCGGGCGGCCGCTCGAA

consensus               ----------CT-GCCCGGGCGGCCGCTCAAAATCAAAAGTGAATTCGCGGCCGCCTGCAG

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_11d04.b1.seq+ GCCCACCATATGGGAAACCTCCC
U_HW-SSH1_11e08.b1.seq+ GTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGT
U_HW-SSH1_13g07.b1.seq+ GTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGT
U_HW-SSH1_1f06.b1.seq+  GTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGT
U_HW-SSH1_2h09.b1.seq+  GTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGT
U_HW-SSH1_3f09.b1.seq+  GTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGT
U_HW-SSH1_16a08.b1.seq+ GTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGT
U_HW-SSH1_10a10.b1.seq+ GTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGT
                        ____________________________________________________________
consensus               GTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGT

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_11e08.b1.seq+ CACCTAAATAGCTTGGCGTAATCATGGTCATAGC-TGTTTCCTGTGTGAAATTGTTATCC
U_HW-SSH1_13g07.b1.seq+ CACCTAAATAGCTTGGCGTAATCATGGTCATAGC-TGTTTCCTGTGTGAAATTGTTATCC
U_HW-SSH1_1f06.b1.seq+  CACCTAAATAGCTTGGCGTAATCATGGTCATAGC-TGTTTCCTGTGAGAAATTGTTATCC
U_HW-SSH1_2h09.b1.seq+  CACCTAAATAGCTTGGCGTAATCATCGTCATAGCCTGTTTCCTGTGTGAAATTGTTATCC
U_HW-SSH1_3f09.b1.seq+  CACCTAAATAGCTTGGCGTAATCATGGTCATAGC-TGTTTCCTGTGTGAAATTGTTATCC
U_HW-SSH1_16a08.b1.seq+ CACCTAAATAGCTTGGCGTAATCATGGTCATAGC-TGTTTCCTGTGTGAAATTGTTATCC
U_HW-SSH1_10a10.b1.seq+ CACCTAAATAGCTTGGCGTAATCATGGTCATAGC-TGTTTCCTGTGTGAAATTGTTATCC
                        ____________________________________________________________
consensus               CACCTAAATAGCTTGGCGTAATCATGGTCATAGC-TGTTTCCTGTGTGAAATTGTTATCC

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_11e08.b1.seq+ GCTCACAATTCC-ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGG-TGCC
U_HW-SSH1_13g07.b1.seq+ GCTCACAATTCC-ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGGTGCC
U_HW-SSH1_1f06.b1.seq+  GCT
U_HW-SSH1_2h09.b1.seq+  GCTCACAATTCCCACACAACATACGAGCCGGAA
U_HW-SSH1_3f09.b1.seq+  GCTCACAATTCC-ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGG-TGCC
U_HW-SSH1_16a08.b1.seq+ GCTCACAATTCC-ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGG-TGCC
U_HW-SSH1_10a10.b1.seq+ GCTCACAATTCC-ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGG-TGCC
                        ____________________________________________________________
consensus               GCTCACAATTCC-ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGG-TGCC

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_11e08.b1.seq+ TAATGAGTGAGCTAA-CTCACATTAATTGCGTTGCGCTCACTGCCCGCTTT-CCAGTCGG
U_HW-SSH1_13g07.b1.seq+ TAATGAGTGAGCTAA-CTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTTCCAGTCGG
U_HW-SSH1_3f09.b1.seq+  TAATGAGTGAGCTAAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTT-CCAGTCGG
U_HW-SSH1_16a08.b1.seq+ TAATGAGTGAGCTAA-CTCACATTAATTGCGTTGCGCTCACTGCCCGCTTT-CCAGTCGG
U_HW-SSH1_10a10.b1.seq+ TAATGAGTGAGCTAA-CTCACATTATTTGCGTTGCGCTCACTGCCCGCTTTTCCAGTCGG
                        ____________________________________________________________
consensus               TAATGAGTGAGCTAA-CTCACATTAATTGCGTTGCGCTCACTGCCCGCTTT-CCAGTCGG

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_11e08.b1.seq+ GAAA--CCTGTCGTGCCAGC-TGCATTAAT-GAATC-GGCCAACGCGCGGGG-AGAGGCG
U_HW-SSH1_13g07.b1.seq+ GAAA--CCTGTCGTGCCAGC-TGAATTAAT-GAATC-GGCCAACGCGCGGGGGAGAGGCG
U_HW-SSH1_3f09.b1.seq+  GAAAACCTGTCGTGCCAGCCTGAATTAAT-GAATCCGGCCAACGCGCGGGGGAGAGGGG
U_HW-SSH1_16a08.b1.seq+ GAAA--CCTGTCGTGCCAGC-TGCATTAAT-GAATC-GGCCAACGCGCGGGG-AGAGGCG
U_HW-SSH1_10a10.b1.seq+ GAAA--CCTGTCGTGCCACC-TGCATTTATTGAATC-GGCCACCGCGCGGGGGAGAGGCG
                        ____________________________________________________________
consensus               GAAA--CCTGTCGTGCCAGC-TGCATTAAT-GAATC-GGCCAACGCGCGGGGGAGAGGCG

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_11e08.b1.seq+ GTTTGCGTATT-GGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTT
U_HW-SSH1_13g07.b1.seq+ GTTTGCGTATT-GGGTGCTCTTCACCTTCATCGCATACTGACTCGCTGCG
U_HW-SSH1_3f09.b1.seq+  GGTT
U_HW-SSH1_16a08.b1.seq+ GTTTGCGTATT-GGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTT
U_HW-SSH1_10a10.b1.seq+ GTTTGCGTATTTGGGCGCCCTTCCGCTTCC
                        ____________________________________________________________
consensus               GTTTGCGTATT-GGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTT

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_11e08.b1.seq+ CGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACTGTTATCCACAGATCAG
U_HW-SSH1_16a08.b1.seq+ CGGCTGCG-CGAGCG-TATCAGCTCACTCAAAGGCGGTAATACTGTTATC-ACAGATCAG
                        ____________________________________________________________
consensus               CGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACTGTTATCCACAGATCAG

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_11e08.b1.seq+ GGGATACGCAGAAAGAACATGTGAGCAACGCCAGCAAGCCAGACCGTAAAGCGCGTGCTG
U_HW-SSH1_16a08.b1.seq+ G--ATACGCAGAAAGA-CATGTGAGCAAG
                        ____________________________________________________________
consensus               GGGATACGCAGAAAGAACATGTGAGCAACGCCAGCAAGCCAGACCGTAAAGCGCGTGCTG

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_11e08.b1.seq+ TGTTTTCATACGC
                        ____________________________________________________________
consensus               TGTTTTCATACGC

****************** Contig 37 ******************
                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_10h09.b1.seq- TAGCGTGGTCGCGGCCGAGGTACTTGATTCCCCATTCGATTTACACACACTCACCCCAAAG
U_HW-SSH1_13e04.b1.seq+ TAGCGTGGTCGCGGCCGAGGAACTTGATTCCCCATTCTATTTACACACACACCCCAAAC
                        ____________________________________________________________
consensus               TAGCGTGGTCGCGGCCGAGGAACTTGATTCCCCATTCGATTTACACACACACCCCAAAC

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_10h09.b1.seq- AAGTCACGGACACACATACATTGCTGGTGCTTTTTTGACCTCCAGCCGATCCCATGCAAT
U_HW-SSH1_13e04.b1.seq+ AAGACACGGACACAGATACTTTGCTGCTGCTTCTTCCACCTCCAGCCGATCCCATGCAAT
                        ____________________________________________________________
consensus               AAGACACGGACACACATACATTGCTGCTGCTTCTTCCACCTCCAGCCGATCCCATGCAAT

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_10h09.b1.seq- CCATGCGTCC----TGATGCAATGCAACAACCCCTCTCCCACCACGCGCGCAAGCCAAAA
U_HW-SSH1_13e04.b1.seq+ CCGTGCGTCCGATCTGATGCAATGCAACAACCCCTCTCCCCCCACGCGCGCAACCCAAAA
                        ____________________________________________________________
consensus               CCATGCGTCCGATCTGATGCAATGCAACAACCCCTCTCCCACCACGCGCGCAACCCAAAA

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_10h09.b1.seq- ATCGTTTTATAGGCCGAGCGCGCCGAGCGGCGTCTTGCCCTGTCCGGCCTCGAAGTAGAA
U_HW-SSH1_13e04.b1.seq+ ATCTTCTTATAGGCCGAGCGCGCCGAGTGGCGTCTTGCCCTGCCCGGCCTCTAAGTAAAA
                        ____________________________________________________________
consensus               ATCGTCTTATAGGCCGAGCGCGCCGAGCGGCGTCTTGCCCTGCCCGGCCTCGAAGTAAAA

                                                   .    :    .    :    .    :    .

U_HW-SSH1_10h09.b1.seq- GATGAGCATGGCAAGCATGGCGAGGCGCGAGTGCTTGATCTCGGCCACCTTGAGCCGCTC
U_HW-SSH1_13e04.b1.seq+ AATGAGCATGGCAAGCATGGCGAGGCGCGAGTGCTTGATCTCGGCCACCTTGAGCCGCTC
                        ____________________________________________________________
consensus               AATGAGCATGGCAAGCATGGCGAGGCGCGAGTGCTTGATCTCGGCCACCTTGAGCCGCTC

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_10h09.b1.seq- GAGCTTCTCGGTGTCGGGGATGTAGACGCCGTCCTTGGTCTTGCCCCCGAGGCCGAGCGG
U_HW-SSH1_13e04.b1.seq+ GAGCTTCTCGGTGTCGGGGATGTAGACGCCGTCCTTGGTCTCACCACCGAGGCCGAGCGG
                        ____________________________________________________________
consensus               GAGCTTCTCGGTGTCGGGGATGTAGACGCCGTCCTTGGTCTCACCACCGAGGCCGAGCGG

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_10h09.b1.seq- GTCGAAGAACTTGCCGCCCCCCCCCCCCCCGGGCGGCCGCTCGAAATCGAA
U_HW-SSH1_13e04.b1.seq+ GTCAAAGAACTTGCCGCCC
                        ____________________________________________
consensus               GTCAAAGAACTTGCCGCCCCCCCCCCCCCGGGCGGCCGCTCGAAATCGAA

****************** Contig 38 ******************
                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_11b01.b1.seq- GGGGAAGCGGGGGGGGGGAGACATCCTCTCGTAAGCAGCATGGCGGCCGCCGATTTACTC
                        ____________________________________________________________
consensus               GGGGAAGCGGGGGGGGGGAGACATCCTCTCGTAAGCAGCATGGCGGCCGCCGATTTACTC

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_11b01.b1.seq- AATCTTTACCTCCTCCCCCTCGGGGTACTCCAGAATTGCCTCCCTCCCCCCGGGCGTTGT
                        ____________________________________________________________
consensus               AATCTTTACCTCCTCCCCCTCGGGGTACTCCAGAATTGCCTCCCTCCCCCCGGGCGTTGT

                           .    :    .    :    .    :    .    :    .    :    .    :

U_HW-SSH1_11b01.b1.seq- CAACTTTCACCCACCCCCAGGCCGCGCCGGGTTCATTAATGACTATGAGCGGCCCCCCGG
U_HW-SSH1_14g03.b1.seq+                                                 TTCGATTTCCAGGGGCCCCCCGG
U_HW-SSH1_11d07.b1.seq+                                                 TTCGATTTCCAGGGGCCCCCCGG
U_HW-SSH1_2g09.b1.seq+                                                  TTCGATTTCCAGGGGCCCCCCGG
U_HW-SSH1_10a02.b1.seq+                                                    TTCGAGGGGCCGCCCGG
U_HW-SSH1_5b12.b1.seq+                                                  TTCGATTACCAGGGGCCCGCCGG
U_HW-SSH1_12e02.b1.seq+                                                 TTCGATTTCCAGCGGCCGCCCGG
U_HW-SSH1_12f06.b1.seq+                                                 TTCGATTTCGAGCGGCCGCCCGG
U_HW-SSH1_9a07.b1.seq+                                                     TTCGAGCGGCCGCCCGG
U_HW-SSH1_5a02.b1.seq+                                                  TTCGATTACCAGGGGCCGCCCGG
U_HW-SSH1_5a06.b1.seq+                                                  TTCGATTACCAGGGTCCCCCCCG
U_HW-SSH1_4c02.b1.seq+                                                  TTCGATTTCCAGCGGCCGCCCGG
U_HW-SSH1_10c11.b1.seq+                                                    TTCGAGCGGCCGCCCGG
U_HW-SSH1_15h07.b1.seq+                                                    TTCGAGCGGCCGCCCGG
U_HW-SSH1_14e04.b1.seq+                                                    TTCCAGCGGCCGCCCGG
U_HW-SSH1_3a04.b1.seq+                                                     TTCGAGGGGCCGCCCGG
U_HW-SSH1_15h09.b1.seq+                                                       GAGCGGCCGCCCGG
U_HW-SSH1_4h06.b1.seq+                                                  ATTTCGAGCGGCCGCCCGG
U_HW-SSH1_4h05.b1.seq+                                                     TTCGAGCGGCCGCCCGG
U_HW-SSH1_4a08.b1.seq+                                                     TTCGAGCGGCCGCCCGG
U_HW-SSH1_2d08.b1.seq+                                                     TTCGAGCGGCCGCCCGG
U_HW-SSH1_5b06.b1.seq+                                                     TTCGAGCGGCCGCCCGG
U_HW-SSH1_14h01.b1.seq+                                                    TTCGAGCGGCCGCCCGG
U_HW-SSH1_12g07.b1.seq+                                                 ATTTCGAGCGGCCGCCCGG
U_HW-SSH1_9h11.b1.seq+                                                     TTCGAGCGGCCGCCCGG
U_HW-SSH1_7b08.b1.seq+                                                     TTCGAGCGGCCGCCCGG
U_HW-SSH1_2c08.b1.seq+                                                  TTCGATTTCGAGCGGCCGCCCGG
U_HW-SSH1_7b12.b1.seq+                                                  TTCGATTTCCAGCGGCCCCCCGG
U_HW-SSH1_11d11.b1.seq-                                                    GATTTTGAGCGGCCGCCCGG
U_HW-SSH1_5e12.b1.seq+                                                  TTCGATTTCGAGCGGCCGCCCGG
U_HW-SSH1_4f10.b1.seq+                                                  TTCGATTTCGAGCGGCCGCCCGG
U_HW-SSH1_5b02.b1.seq+                                                  TTCGATTTCGAGCGGCCGCCCGG
U_HW-SSH1_10g12.b1.seq+                                                 TTCGATTA-GCGTGGTCG-CGGC
U_HW-SSH1_11c06.b1.seq+                                                 TTCGATTACCGGGGTCCCCCCCG
U_HW-SSH1_11e07.b1.seq-                                                       CGGCCGCCCGG
U_HW-SSH1_13c04.b1.seq+                                                    TAGCGTGGTCGCGG
U_HW-SSH1_4g09.b1.seq+                                                  TTCGATT---AGCGTGGTCGCGG
U_HW-SSH1_11d06.b1.seq+                                                 TTCGATT---AGCGTGGTCGCGG
U_HW-SSH1_2c12.b1.seq+                                                     TACCGTGGTCCCGG
U_HW-SSH1_4e01.b1.seq+                                                  TTCGATT---AGCGGGGTCCCGG
U_HW-SSH1_8c06.b1.seq+                                                  TTCGATT---AGCGTGGTCGCGG
U_HW-SSH1_4g08.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_2g04.b1.seq+                                                  TTCGATT---AGCGTGGTCGCGG
U_HW-SSH1_8f04.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_7b03.b1.seq+                                                     TAGCGTGGTCCCCG
U_HW-SSH1_2d06.b1.seq+                                                  TTCGATT---ACCGTGGTCCCGG
U_HW-SSH1_8d04.b1.seq+                                                  TTCGATT---AGCGTGGTCGCGG
U_HW-SSH1_8c04.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_12e04.b1.seq+                                                    TAGCGTGGTCGCGG
U_HW-SSH1_2c06.b1.seq+                                                     TACCGTGGTCCCGG
U_HW-SSH1_2a04.b1.seq+                                                  TTCGATT---ACCGTGGTCGCGG
U_HW-SSH1_2a06.b1.seq+                                                     TACCGTGGTCCCGG
U_HW-SSH1_2b04.b1.seq+                                                  TTCGATT---ACCGTGGTCCCGG
U_HW-SSH1_7b04.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_11c09.b1.seq+                                                 TTCGAGCGGCCGCCCGG
U_HW-SSH1_16h12.b1.seq+                                                 TTCGATT---AGCGTGGTCGCGG
U_HW-SSH1_12e03.b1.seq+                                                    TAGCGTGGTCCCGG
U_HW-SSH1_2g05.b1.seq+                                                  TTCGATT---AGCGTGGTCGCGG
U_HW-SSH1_2c11.b1.seq+                                                     TACCGTGGTCCCGG
U_HW-SSH1_2g06.b1.seq+                                                     TAGCGTGGTCCCGC
U_HW-SSH1_7b07.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_8h06.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_7c07.b1.seq+                                                     TAGCGTGGTCCCGG
U_HW-SSH1_13a07.b1.seq-                                                    TAGCGTGGTCGCGG
U_HW-SSH1_12g10.b1.seq+                                                    TAGCGTGGTCGCGG
U_HW-SSH1_7c04.b1.seq+                                                  TTCGATT---ACCGTGGTCGCGG
U_HW-SSH1_11g06.b1.seq+                                                 ATTAGCGTGGTCCCGG
U_HW-SSH1_4c03.b1.seq+                                                     TAGCGTGGTCCCGC
U_HW-SSH1_7d11.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_7a08.b1.seq+                                                     TAGCGTGGTCCCGG
U_HW-SSH1_13e02.b1.seq-                                                    TAGCGTGGTCGCGG
U_HW-SSH1_13g01.b1.seq-                                                       GTGGTCGCGG
U_HW-SSH1_16d07.b1.seq-                                                       GTGGTCGCGG
U_HW-SSH1_13f03.b1.seq-                                                    TAGCGTGGTCGCGG
U_HW-SSH1_4d12.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_5b04.b1.seq+                                                     TACCGTGGTCGCGG
U_HW-SSH1_5e03.b1.seq+                                                        CGTGGTCGCGG
U_HW-SSH1_2g08.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_5c11.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_7c11.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_4f12.b1.seq+                                                  TTCGATT---AGCGTGGTCGCGG
U_HW-SSH1_5f11.b1.seq+                                                  TTCGATT---AGCGTGGTCGCGG
U_HW-SSH1_7d01.b1.seq+                                                     TAGCGTGGTCCCGG
U_HW-SSH1_5g06.b1.seq+                                                  TTCGATT---ACCGTGGTCGCGG
U_HW-SSH1_4a07.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_7a10.b1.seq+                                                  TTCGATT---AGCGTGGTCGCGG
U_HW-SSH1_8h11.b1.seq+                                                  TTCGATT---AGCGTGGCCCCGG
U_HW-SSH1_2e06.b1.seq+                                                  TTCGATA---AGCGTGGTCGCGG
U_HW-SSH1_11f10.b1.seq+                                                 TTCGATT---AGCGTGGTCGCGG
U_HW-SSH1_5e01.b1.seq+                                                  TTCGATT---ACCGTGGTCCCGG
U_HW-SSH1_5d01.b1.seq+                                                  TTCGATT---ACCGGGGCCCCGG
U_HW-SSH1_3e06.b1.seq+                                                  TTCGATT---AGCGTGGTCGGCG
U_HW-SSH1_12e05.b1.seq+                                                    TAGCGTGGTCGCGG
U_HW-SSH1_12g05.b1.seq+                                                 TTCGATT---AGCGTGGTCGCGG
U_HW-SSH1_7b01.b1.seq+                                                  ATTAGCGTGGTCGCGG
U_HW-SSH1_10g11.b1.seq+                                                    TAGCGTGGTCGCGG
U_HW-SSH1_1e04.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_13a05.b1.seq+                                                    TAGCGTGGTCGCGG
U_HW-SSH1_13b05.b1.seq+                                                    TAGCGTGGTCGCGG
U_HW-SSH1_3e03.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_13h05.b1.seq+                                                    TAGCGTGGTCGCGG
U_HW-SSH1_13h01.b1.seq+                                                    TAGCGTGGTCGCGG
U_HW-SSH1_13d05.b1.seq+                                                    TAGCGTGGTCGCGG
U_HW-SSH1_13g02.b1.seq+                                                    TAGCGTGGTCGCGG
U_HW-SSH1_4f08.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_9g07.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_14f04.b1.seq+                                                    TACCGTGGTCCCGG
U_HW-SSH1_15g04.b1.seq+                                                       CGTGGTCCCGG
U_HW-SSH1_1d08.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_14b07.b1.seq+                                                    TAGCGTGGTCGCGG
U_HW-SSH1_13c05.b1.seq+                                                    TAGCGTGGTCCCGG
U_HW-SSH1_1e05.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_3f07.b1.seq+                                                     TAGCGTGGTCGCGG
U_HW-SSH1_10a04.b1.seq+                                                    TAGCGTGGTCGCGG
U_HW-SSH1_8e06.b1.seq+                                                     TAGCGTGGTCGCGG
                                                   ____________________________________
consensus                                          CAACTTTCACCCACCCCCAGGCCGCGCCGGGTTCATTTTCGATTTCTAGCGTGGTCCCGG
```



```
U_HW-SSH1_8h11.b1.seq+  GGGGGGCCAATGAGGG-AGCAAACTCA
U_HW-SSH1_2e06.b1.seq+  GGTGC-CTAATGAGTG-AGCTAACTCACATTAA-TTGCGTTG-CGC-TCACTGCCCGTCT
U_HW-SSH1_11f10.b1.seq+ GGTGC-CTAATGAGTG-AGCTAACTCACATTAA-TTGCGTTG-CGC-TCACTGCCCGC-T
U_HW-SSH1_12g05.b1.seq+ GGTGC-CTAATGAGTG-AGCTAACTCACATTAA-TTGCGTTG-CGC-TCACAGCCCGC-T
U_HW-SSH1_7b01.b1.seq+  GGGGGCCAAATGAGTG-A
U_HW-SSH1_10g11.b1.seq+ GGTGC-CTAATGAGTG-AGCTAACTCACATTAAATTGCGTTG-CGC-TCACTGCCCGC-T
U_HW-SSH1_14f04.b1.seq+ GGTGC-CTAATGAGTG-AGCTAACTCACATTAG-TTGCGTGG-CGC-TCACTGCCCGCTT
U_HW-SSH1_14b07.b1.seq+ GGTGC-CTAATGAGTG-AGCTAACTCACATTAA-TTGCGTTG-CGC-TCACTGCCCGC-T
U_HW-SSH1_3f07.b1.seq+  GGGTGCCAAATGAGTGGAGCTAACCCACATAAA-TTGGGTTGGCGCCTCACTGCCCGCTT
U_HW-SSH1_8e06.b1.seq+  GGTGC-CTAATGAGTG-AGCTAACTCACATTAA-TTGCGTTG-CGC-TCACTGCCCGC-T
                        ____________________________________________________________
consensus               GGTGC-CTAATGAGTG-AGCTAACTCACATTAA-TTGCGTTG-CGC-TCACTGCCCGC-T

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_11d06.b1.seq+ TTCCAGTCGG-AAA-CCTGTCGTGCCAGCT-GCATTAATGAATCCGGCCAACGCGCGGGGG
U_HW-SSH1_2e06.b1.seq+  TTC-AGTCGGGAAA-CCTGTCGTGCCAGCT-GCATTAA-GAATCGGCCAACCGCGCGGGGG
U_HW-SSH1_11f10.b1.seq+ TTCGAGTCGGGAAA-CCTGTCGTGCCAGCT-GCAT-AATGAATCGGTCAA-CGCGCGGGG
U_HW-SSH1_12g05.b1.seq+ TTCCAGTCGGGAAA-CCTGTCGAGCCATCT-GCATTAATGAATCCGCCAA-CGCGCGGGG
U_HW-SSH1_10g11.b1.seq+ TTCCAGTCGGGAAA-CCTGTCGTGCCAGCT-GCATTAATGAATCGGCCAA-CGCGCGGGG
U_HW-SSH1_14f04.b1.seq+ TTACAGTCGGGAAAACTTGTCGTGCCATCT-GCATTATGAAATCGGCCAA-CGCGAAGGG
U_HW-SSH1_14b07.b1.seq+ TTCCAGTCGGGAAA-CCTGTCGTGCCAGCT-GCATTAATGAATCGGCCAA-CGCGCGGGG
U_HW-SSH1_3f07.b1.seq+  TCCCAGTCGG-AAACCCTGTCGCGCCCGCTTGCATTAATGAATCGGCCCCACGCGCGGGG
U_HW-SSH1_8e06.b1.seq+  TTCCAGTCGAGAAA-CCTGTCGTGCCAGCT-GCATTAATGAATCGGCCAA-CGCGCGGGG
                        ____________________________________________________________
consensus               TTCCAGTCGGGAAA-CCTGTCGTGCCAGCT-GCATTAATGAATCGGCCAA-CGCGCGGGG

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_11d06.b1.seq+ -AGAGGCGGTTTTGCGTATGGGGCCGCTCTTCCGCTTCCTTCGCTCACTGACTCGCTGCG
U_HW-SSH1_2e06.b1.seq+  -AGAGGCGGTTT--CCTATTGGGCGCCTCTTCCGCTTCCT-CGCTCACTGACTCCCTGCG
U_HW-SSH1_11f10.b1.seq+ GAGAGGCGGGTT-GCGTATTGGGCG-CTCTTCCGCTTTCTTCGCACACTGACTCGCTGCG
U_HW-SSH1_12g05.b1.seq+ GAGAGGAGGGTTTGCGTATTGG-CG-CTCTTTCGCCTTCCTCGCTCACTGACTC
U_HW-SSH1_10g11.b1.seq+ -AGAGGCGGTTT-GCGTATTGGGCG-CTCTTCCGCTTCCT-CGCTCACTGACTCGCTGCG
U_HW-SSH1_14f04.b1.seq+ GAAGAGCGGCTTTGCGTATTGGGCG-CTCTTCCGCTTC
U_HW-SSH1_14b07.b1.seq+ -AGAGGCGGTTT-GCGTATTGGGCG-CTCTT-CGCTTC--TCGCTCACTGACTCGCTGCG
U_HW-SSH1_3f07.b1.seq+  -AGAGG
U_HW-SSH1_8e06.b1.seq+  -AGAGGCGGTTT-GCGTATTGG-CG-CTCTTCCGCTACCT-CGCTCACTGACTCGCTGCG
                        ____________________________________________________________
consensus               -AGAGGCGGTTT-GCGTATTGGGCG-CTCTTCCGCTTCCTTCGCTCACTGACTCGCTGCG

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_11d06.b1.seq+ CTCGGGTGGGTCGGCTG-CGGCGAGCG
U_HW-SSH1_2e06.b1.seq+  CTCGG
U_HW-SSH1_11f10.b1.seq+ CTCGG-TCGTTCGGCTGACAGAGAGCGGTATCAGCTCACTC
U_HW-SSH1_10g11.b1.seq+ CTCGG-TCGTTCGGCTG-CGGCGAGCG-TATCAGCTCACTCAAAGGGCGGTATACGGTTA
U_HW-SSH1_14b07.b1.seq+ CTCGG-TCGTTCGGCTG-CGGCGAGCG-TATCAGCTCACTCGAAGG-CGGTATACGGTTA
U_HW-SSH1_8e06.b1.seq+  CTCGG-TCGTTCGGCTG--CGCGAGCTATATCAGCTCACTCAATGG-CG
                        ____________________________________________________________
consensus               CTCGG-TCGTTCGGCTG-CGGCGAGCG-TATCAGCTCACTCAAAGG-CGGTATACGGTTA

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_10g11.b1.seq+ TCTACAGATCAGGGATAACGCA
U_HW-SSH1_14b07.b1.seq+ TC-AC-GATCAGGGATA-CGCAAGAAAGAACATGTGAGCAAAGGCCAGCAAGGCCAGAAC
                        ____________________________________________________________
consensus               TCTACAGATCAGGGATAACGCAAGAAAGAACATGTGAGCAAAGGCCAGCAAGGCCAGAAC

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_14b07.b1.seq+ CG
                        ____________________________________________________________
consensus               CG

****************** Contig 39 ******************
                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_11b12.b1.seq+ TTCGATTAGCGTGGTCGCGGCCGAGGTACCCTGACGCGTATGTCCGCATCATCGGATTCA
U_HW-SSH1_2h11.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTGCCCTGACGCCTATGTCCGCATCATCGGATTCA
U_HW-SSH1_11h12.b1.seq+ TTCGATTAGCGTGGTCGCGGCCGAGGTACCCTGACGCGTATGTCCGCATCATCGGATTCG
U_HW-SSH1_8g04.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACCCTGACGCGTATGTCCGCATCATCGGATTCG
U_HW-SSH1_2e05.b1.seq+         TAGCGTGGTCGCGGCCGAGGTACCCTGACGCCTATGTCCGCATCATCGGATTCG
U_HW-SSH1_11b11.b1.seq+        TAGCGTGGTCGCGGCCGAGGTACCCTGACGCGTATGTCCGCATCATCGGATTCC
U_HW-SSH1_9e08.b1.seq+         TAGCGTGGTCGCGGCCGAGGAACACTGAGGCGTATGTCCGCATCATCAGATTCA
U_HW-SSH1_13e05.b1.seq+        TAGCGTGGTCGCGGCCGAGGGACCCTGACGCCTATGTCCGCATCATCGGATTCA
U_HW-SSH1_16a06.b1.seq+        CGTGGTCCCGGCCGAGGTACCCTGACGCGTATGTCCGCATCAGCACATCCG
U_HW-SSH1_11a10.b1.seq+        TAGCGTGGTCGCGGCCGAGGTAC-----------GTCCGCATCATCGGATTCA
U_HW-SSH1_16c09.b1.seq+        TAGCGTGGTCGCGGCCGAGGTAC-----------GTCCGCATCATCGGATTCA
U_HW-SSH1_4d10.b1.seq+         TAGCGTGGTCGCGGCCGAGGTAC-----------TTCCGCATCATCGGATTCA
U_HW-SSH1_11b10.b1.seq+        TAGCGTGGTCGCGGCCGAGGTAC-----------GTCCGCATCATCGGATTCA
U_HW-SSH1_16b06.b1.seq+           CGTGGTCCCGGCCGAGGTACCCGGCCGCGTATGTCCGCCTCATCTCATCCC
                        ____________________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACCCTGACGCGTATGTCCGCATCATCGGATTCA

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_11b12.b1.seq+ ACAACATGCGTCAGGTGCAGTGCGTCAGCTTCATCGCCTTCAACCCACCGGGCTGCAAGG
U_HW-SSH1_2h11.b1.seq+  ACAACATGCGTCAGGTGCAGTGCGTCACCTTCATCGCCTTCAAGCCACCGGGCTGCGAGG
U_HW-SSH1_11h12.b1.seq+ ACAACATGCGTCAGGTGCAGTGCGTCAGCTTCATCGCCTTCAAGCCACCGGGCTGCGAGG
U_HW-SSH1_8g04.b1.seq+  ACAACATGCGTCAGGTGCAGTGCGTCAGCTTCATCGCCTTCAAGCCACCGGGCTGCGAGG
U_HW-SSH1_2e05.b1.seq+  ACAACATGCGTCAGGTGCAGTGCGTCAGCTTCATCGCCTTCAAGCCACCGGGCTGCGAGG
U_HW-SSH1_11b11.b1.seq+ ACAACATGCGTCAGGTGCAGTGCGTCAGCTTCATCGCCTTCAAGCCACCGGGCTGCAAGG
U_HW-SSH1_9e08.b1.seq+  ACAACAGGGGCCAGGGGCAGTGCGTCATTTTCATCGCCTTCAAGCCACCAGGCTGCGAGG
U_HW-SSH1_13e05.b1.seq+ ACAACACGCGTCAGGGGCAGTGCGTCAGCTTCATCGCCTTCAAGCCACCGGGCTGCGAGG
U_HW-SSH1_3a09.b1.seq+                                                  CCGGGCTGCGAGG
U_HW-SSH1_16a06.b1.seq+ ACAACATGCGTCAGGGGCGGTGCATCATCTTCATCCCCTCCAAGCCACCGGGCTGCGAGG
U_HW-SSH1_11a10.b1.seq+ ACAACATGCGCCAGGTGCAGTGCGTCAGCTTCATTGCCTTCAAGCCACCGGGCTGCGAGG
U_HW-SSH1_16c09.b1.seq+ ACAACATGCGCCAGGTGTAGTGCGTCAGCTTCATTGCCTTCAAGCCACCGGGCTGCGAGG
U_HW-SSH1_4d10.b1.seq+  ACAACATGCGTCAGGTGCAGTGCGTCAGCTTCATCGCCTTCCTTCCAGCCCCGGGCTGCAAGG
U_HW-SSH1_11b10.b1.seq+ ACAACATGCGCCAGGTGCAGTGCGTCAGCTTCATTGCCTTCAAGCCACCGGGCTGCGAGG
U_HW-SSH1_16b06.b1.seq+ ACAACATGCGTCAAGGGCGGTGCATCAGCTTCATCGCCTCCAAGCCACCGGGCTGCCAGG
                        ____________________________________________________________
consensus               ACAACATGCGTCAGGTGCAGTGCGTCAGCTTCATCGCCTTCAAGCCACCGGGCTGCGAGG

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_11b12.b1.seq+ AGCCCGGCAAGGCCTAAACACCTC-ACTCACAAAAGGACATATATAAGGTGCCGTTGCTG
U_HW-SSH1_2h11.b1.seq+  AGTCCGGCAAGGCCTAAA
U_HW-SSH1_11h12.b1.seq+ AGTCCGGCAAGGCCTAAA
U_HW-SSH1_8g04.b1.seq+  AGTCCGGCAAGGCCTAAACAGCTC-ACTCACGACAGGCCATATATAAAGTGCCATTGCAG
U_HW-SSH1_2e05.b1.seq+  AGTCCGGCAAGGCCTAAA
U_HW-SSH1_11b11.b1.seq+ AGTCCGGCAAGTCCTAACCAGCTC-CCTCATAACAGGCCATATATAAATTCGCTTTGCAG
U_HW-SSH1_9e08.b1.seq+  AGTCCGGCAAGGCCTAAACAGCTC-ACTCACAACAGGCCATATATAAAGTGCCATTGCAG
U_HW-SSH1_13e05.b1.seq+ AGTCCGGCAAGGCCTAAACAGCTC-ACTCACGACAGGCCATATATAAGTGCCATTGCAG
U_HW-SSH1_3a09.b1.seq+  AGTCCGGCATGGCCTCACCACTTCGCCTCACGAAAGGCCTTATATGGAGTGCCCTTGCGG
U_HW-SSH1_16a06.b1.seq+ AGTCCGGCACGGCCTATCCAGCTC-CCTCACGACAGGCCATATATAAAGTGCCATTGCAT
U_HW-SSH1_11a10.b1.seq+ AGTCCGGCAAGGCCTAAACAGCTC-ACTCACCACGGGCCACATAAATAAAGTGCCATTGCAG
U_HW-SSH1_16c09.b1.seq+ AGTCCGGCAAGGCCTAAA
U_HW-SSH1_4d10.b1.seq+  AGTCCGGCAAGGCCTAAACACCTC-ACTCAAACAGGCCATAAATAAAGTGCCATTGCAG
U_HW-SSH1_11b10.b1.seq+ AGTCCGGCAAGGCCTAAACAGCTC-ACTCACCACGGGCCACATATAAAGTACCATTGCAG
U_HW-SSH1_16b06.b1.seq+ AGTCCGGCAAGGCCTATCCAGCTC-ACTCACGACAGGCCATATATAAGTGCCATTGCAG
U_HW-SSH1_16c06.b1.seq+                                                 AGTGCCATTGCTG
                        ____________________________________________________________
consensus               AGTCCGGCAAGGCCTAAACAGCTC-ACTCACGACAGGCCATATATAAAGTGCCATTGCAG

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_11b12.b1.seq+ TTTTGTCAACTCTGAGATGGCTTTG
U_HW-SSH1_8g04.b1.seq+  TTTTGTCAACTCTGACATTGCTTTGGGTTTTCCTTCTCCATTTATCTTTCTTATTTGTTC
U_HW-SSH1_11h11.b1.seq+ TTTTGTCAA
U_HW-SSH1_9e08.b1.seq+  TTTTGTCAACTCTGACATTGCTTTGGGTTTTCCTTCTCCATTTATCTTTCTTATTTGTTC
U_HW-SSH1_13e05.b1.seq+ TTTTGTCAACTCTGACATTGCTTTGGGTTTTCCTTCTCCATTTATCTTTCTTATTTGTTC
U_HW-SSH1_3a09.b1.seq+  TTTTGTCAACTCTGACGTTGCTTCGGGTTTTCCTTCTCCATTTTGCTTCTTTATTTGTCC
U_HW-SSH1_16a06.b1.seq+ TTTTGTCAACTCTGACATTGATTTGGGTTTTCCTTCTCCATTTATCTTTCTTATTTGTTC
U_HW-SSH1_11a10.b1.seq+ TTTTGTCAACTCTGACATTGCTTTGGGTTTTCCTTCTCCATTTATCTTTCTTATTTGTTC
U_HW-SSH1_16d10.b1.seq+                    TTTGGGTTTTCCTTCTCCATTTATCTTTCTTATTTGTTC
U_HW-SSH1_4d10.b1.seq+  TTTTGTCAACTCTGACTTTGCTTTGGGTTTTCCTTCTCCATTTATCTTTCTTATTTGTTC
U_HW-SSH1_11b10.b1.seq+ TTTTGTCAACTCTGACATTGCTTTGGGTTTTCCTTCTCCATTTATCTTTCTTATTTGTTC
U_HW-SSH1_16b06.b1.seq+ ATTTGTCAACTCTGACATTGCTTTGGGTTTTCCTTCTCCATTTATCATTCTTATTGGTTC
U_HW-SSH1_16c06.b1.seq+ ATTTGTCAACTCTGACTTTGCTTTGGGTTTTCCTTCTCCAATTCTCTTTCTTCTTGGTTC
                        ____________________________________________________________
consensus               TTTTGTCAACTCTGACATTGCTTTGGGTTTTCCTTCTCCATTTATCTTTCTTATTTGTTC

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_8g04.b1.seq+  CTAAAAATATGTGTATGTCCATGTTCATGTACCTGCCCGGG-CGGCCGCTCAAA
U_HW-SSH1_9e08.b1.seq+  CTAAAAATATGTGTATGTCCATGTTCATGTACCTGCCCGGG-CGGCCG
U_HW-SSH1_13e05.b1.seq+ CTAAAAATATGTGTATGTCCATGTTCATGTACCTGCCCGG
U_HW-SSH1_3a09.b1.seq+  CTAAGAATATGTGTCTGTCC
U_HW-SSH1_16a06.b1.seq+ CTAAAAATATGGGAAGGCCCATGTACATGTACCTGCCCGGGGCGGGCCGTCGGCTGCCTT
U_HW-SSH1_11a10.b1.seq+ CTAAAAATATGTGTATGTCCATGTTCATGTACCTGCCCGGG-CGGCCGCTCAAA
U_HW-SSH1_16d10.b1.seq+ CAAAAAATATGTGTATGTCCATGTTCATGTACCTGCCCGGGC
U_HW-SSH1_4d10.b1.seq+  CTAAGAATATGTGTATGTCCCCTTCATGTACCTGCCCGGG-CGG
U_HW-SSH1_11b10.b1.seq+ CTAAAAATATGTGTATGTCCATGTTCATGTACCTGCCCGGG-CGGCCGCTCAAA
U_HW-SSH1_16b06.b1.seq+ CTAAAAATATGTGAATGTCCATGTTCATGTACCTGCC
U_HW-SSH1_16c06.b1.seq+ CTAAAAATATGTGAATGTCCATGTTCAAGTAC
                        ____________________________________________________________
consensus               CTAAAAATATGTGTATGTCCATGTTCATGTACCTGCCCGGG-CGGCCGCTCAAATGCCTT

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_16a06.b1.seq+ TAGAATTACCAGGACCTCCCCGGCCCTACTATCGTCGAAAATTCTTGACACTTTCCAGCG
                        ____________________________________________________________
consensus               TAGAATTACCAGGACCTCCCCGGCCCTACTATCGTCGAAAATTCTTGACACTTTCCAGCG

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_16a06.b1.seq+ GCCGCGAACCTTCACTTCCGTATTGAATAGGACCCCGCGCGAGTTTGGACAGAGGCGGCA
                        ____________________________________________________________
consensus               GCCGCGAACCTTCACTTCCGTATTGAATAGGACCCCGCGCGAGTTTGGACAGAGGCGGCA

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_16a06.b1.seq+ AATCATGTCGTCTTGTAGGGGGCCATGGCTGTTCCCGACGGGACAATTAAATACATTGGG
                        ____________________________________________________________
consensus               AATCATGTCGTCTTGTAGGGGGCCATGGCTGTTCCCGACGGGACAATTAAATACATTGGG

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_16a06.b1.seq+ GAGCATTGGGCGAACACCGTCGGGATGCATAAAGTGAATGCATTTGCATTCAAAACAGTG
                        ____________________________________________________________
consensus               GAGCATTGGGCGAACACCGTCGGGATGCATAAAGTGAATGCATTTGCATTCAAAACAGTG

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_16a06.b1.seq+ TCCTAACTAAAATTTATTGGTTTGAACACACTGTTGTGTAATGCGAGAGCAAACTCCCCT
                        ____________________________________________________________
consensus               TCCTAACTAAAATTTATTGGTTTGAACACACTGTTGTGTAATGCGAGAGCAAACTCCCCT

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_16a06.b1.seq+ TAAAGGGTGAGGAAATGATTGCGTGCTTTATTCAGCGAAAAGCTGCTTGGGCTGCAAGAG
                        ____________________________________________________________
consensus               TAAAGGGTGAGGAAATGATTGCGTGCTTTATTCAGCGAAAAGCTGCTTGGGCTGCAAGAG

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_16a06.b1.seq+ ATCTTCAGCTGCAGCCTGCTGGTCGTAGGCGATCTGAATAAATGCAGCTCTCTGGCGCTA
                        ____________________________________________________________
consensus               ATCTTCAGCTGCAGCCTGCTGGTCGTAGGCGATCTGAATAAATGCAGCTCTCTGGCGCTA

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_16a06.b1.seq+ CTACCACAACTCACAAAGACGCACATCGTCTGCAGACACACAGTGAGAGACAGTCCACAA
                        ____________________________________________________________
consensus               CTACCACAACTCACAAAGACGCACATCGTCTGCAGACACACAGTGAGAGACAGTCCACAA

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_16a06.b1.seq+ AAGGTGGGAAGACGTTCTCGCCCGTTGTTCAGTGATCACTAAAGAGCGTCGTGCTGCCCA
                        ____________________________________________________________
consensus               AAGGTGGGAAGACGTTCTCGCCCGTTGTTCAGTGATCACTAAAGAGCGTCGTGCTGCCCA

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_16a06.b1.seq+ GATTGACAGAGACTCCCTGTA
                        ____________________________________________________________
consensus               GATTGACAGAGACTCCCTGTA

****************** Contig 40 ******************
                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_11c12.b1.seq- ATTCAAACAGCCGCCCGGGCAGGTACCGTAAGGTGCCCCTTTACCTCCTCCTATGCAGCA
U_HW-SSH1_7c06.b1.seq+                                GTGCCCCTTTACCTCCTCCTATGAAGCA
                        ____________________________________________________________
consensus               ATTCAAACAGCCGCCCGGGCAGGTACCGTAAGGTGCCCCTTTACCTCCTCCTATGAAGCA

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_11c12.b1.seq- AGAGATGGTGGGTGTGTATGGAGAATGTTCTAACCGTAGAAGGAACCAGTATTAATTGCA
U_HW-SSH1_7c06.b1.seq+  AGAGATGGTGGGTGTGTATGGAGAATGTTCTAACCTTAAAAGGAACCATTCTTCCTCGCT
                        ____________________________________________________________
consensus               AGAGATGGTGGGTGTGTATGGAGAATGTTCTAACCGTAAAAGGAACCAGTATTAATCGCA

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_11c12.b1.seq- TCCTGGTTAGCATCACCCAGAGCTGCCGGGGTCATGTAGGTGTCAACAAGGAGCACAAGC
U_HW-SSH1_7c06.b1.seq+  TCCTGTTTAGCATCACCCAGAGCTGCCTGGCTCATGTATGTGTCA
                        ____________________________________________________________
consensus               TCCTGGTTAGCATCACCCAGAGCTGCCGGGCTCATGTAGGTGTCAACAAGGAGCACAAGC

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_11c12.b1.seq- ACGACATTGTCCTTCTCCTATACGAGCATGCCCCGCCCCTCGGCCGCGACCACGCTAATC
                        ____________________________________________________________
consensus               ACGACATTGTCCTTCTCCTATACGAGCATGCCCCGCCCCTCGGCCGCGACCACGCTAATC

                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_11c12.b1.seq- GAA
                        ____________________________________________________________
consensus               GAA

****************** Contig 41 ******************
                              .   :   .   :   .   :   .   :   .   :   .   :   .   :

U_HW-SSH1_11d05.b1.seq+ TTCGATTTCGAGCGGCCGCCCGGGCA-GGTACTATTAAACCAAATTGGGATTATCCGCA
U_HW-SSH1_5d05.b1.seq+  TTCGATTTCCAGGGGCCCCCCGGACG-TGTACTATTACACCTAT-TTGGGATTATCCGCA
U_HW-SSH1_3h02.b1.seq+                                    CCAAATAGGGATTATCCGCA
U_HW-SSH1_3e11.b1.seq+                                AAACCAAATTGGGGATTATCCGCA
U_HW-SSH1_6h04.b1.seq+                                   ACCAAATTGGGATTATCCGCA
U_HW-SSH1_5e02.b1.seq+  TTCGATTTCCAGGGGCCGCCCGGACG-TGTACTATTA-AGTAAATTTGGGATTATCCGCA
U_HW-SSH1_4b06.b1.seq+         TTCGAGCGGCCGCCCGGGAG-GGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_9b03.b1.seq+               AGGGGCCCCCCGGGAG-GGCACTAATAAACAAAAATTGGGATTATCCGCA
U_HW-SSH1_3f08.b1.seq+  TTCGATTTCGAGCGGCCGCCCGGTCA-GGGATTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_1h01.b1.seq+         TTCGAGCGGCCGCCCCGGGA-GGAACAAAAAAAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_12h06.b1.seq+        TTCGAGCGGCCGCCCCGGGCA-GGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_9d04.b1.seq+         TTCGAGCGGCCGCCCCGGGCA-GGCACTGTTAAACCAAAATTGGAATTATCCGCC
U_HW-SSH1_9c04.b1.seq+            AGCGGCCGCCCCGACA-GGCACGATTAAACCAAATTTGGGATTATCCGCA
U_HW-SSH1_12g06.b1.seq+        TTCGAGCGGCCGCCCGGGCA-GGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_11g02.b1.seq+ TTCGATTTCCAGGGGCCGCCCGGGCG-GGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_4c06.b1.seq+  TTCGATTTCCAGCGGCCCCCCGGACG-TGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_14a10.b1.seq+        TTCCAGGGGCCGCCCGGGCG-GGTACTATTAAACCAAAATTGGAATTATCCGCA
U_HW-SSH1_15c07.b1.seq+           CGAGGGGCCCCCGGGGG-GGGACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_12f11.b1.seq+ TTCGATTTCCAGGGGCCCCCCGGGCG-TGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_2g10.b1.seq+         TTCCAGGGGCCGCCGGACG-TGTACTATTACACC-AGTTTGGGATTATCCGCA
U_HW-SSH1_2a10.b1.seq+         TTCCAGGGGCCGCCCGGACG-GGTACTATTAAACCAAATTTGGGATTATCCGCA
U_HW-SSH1_4e02.b1.seq+                                          TTTGGGATTATCCCCA
U_HW-SSH1_5g02.b1.seq+  TTCGATTTCGAGCGGCCGCCCGGGCA-GGTACTATTAAACCAAAATTGGAATTATCCGCA
U_HW-SSH1_7d08.b1.seq+  TTCGATTTCGAGCGGCCGCCGGGCG-GGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_4d02.b1.seq+         TTCGAGCGGCCGCCCCGGGCA-GGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_4d04.b1.seq+         TTCGAGCGGCCGCCCCGGGCA-GGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_11h02.b1.seq+ TTCGATTTCGAGCGGCCGCCCGGGCA-GGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_4d08.b1.seq+  TTCGATTTCGAGCGGCCGCCCGGGCA-GGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_11g03.b1.seq+ TTCGATTTCGAGCGGCCGCCCGGGCA-GGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_11h08.b1.seq+ TTCGATT---AGCGTGGTCCCGGCCGAGGTACTATTAAACCGAAATTGGGATTATCCGCA
U_HW-SSH1_12e10.b1.seq+ TTCGATTACC-GTGG--TCCCGGCCGAGGTGCACTTTAACCAATATTGGGATTATCCCCC
U_HW-SSH1_12e11.b1.seq+ TTCGATTACCGTGGTCCCCCCCG--A-GGTGCACTTAACCAATATTGGGATTATCCCCC
U_HW-SSH1_14h12.b1.seq+        TACCGCGGTCG--CGGCCGAGGTACTATTTAACCGAAAATGGGATTATCCGCA
U_HW-SSH1_14b12.b1.seq+ TTCGATTACC-GTGG--TCCCGGCCGAGGTACACTTAAACCGATGTTGGGATTATCCGCA
U_HW-SSH1_7c03.b1.seq+  TTCGATT---AGCGTGGTCCCGGCCGAGGTACTATTAAACCTAA-TTGGAATTATCCCCA
U_HW-SSH1_11g08.b1.seq+                  CCCGGCCGAGGTGCTCTTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_13b06.b1.seq+           TAGCGTGGTCGCGGCGGAGGAACAATTAAACCGAAATTGGAATTATCCGCA
U_HW-SSH1_4h09.b1.seq+  TTCGATT---AGCGTGGTCGCGGCCGAGGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_1d12.b1.seq+          ATTACCGTGGTCGCGGCCGAGGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_16h11.b1.seq+ TTCGATT---AGCGTGGTCGCGGCCGAGGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_5c05.b1.seq+          TACCGTGGTCGCGGCCGAGGTACTATTAAACCTTA-TTGGGATTATCCCCC
U_HW-SSH1_2h04.b1.seq+  TTCGATT---AGCGTGGTCCCGGCCGAGGTACTATTAAACCAAA-TTGGGATTATCCGCA
U_HW-SSH1_4f06.b1.seq+  TTCGATT---AGCGTGGTCGCGGCCGAGGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_4f05.b1.seq+          TAGCGTGGTCGCGGCCGAGGTACAATTAAACCAATATTGGAATTATCCGCA
U_HW-SSH1_9f11.b1.seq+          TAGCGTGGTCGCGGCCGAGGC-CTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_2h05.b1.seq+          TAGCGTGGTCGCGGCCGAGGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_4f07.b1.seq+  TTCGATT---AGCGTGGTCGCGGCCGAGGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_11b09.b1.seq+         TAGCGTGGTCGCGGCCGAGGGACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_12f12.b1.seq+         TAGCGTGGTCGCGGCCGAGGTACTATTAAACCAAAATGGGGATTATCCGCA
U_HW-SSH1_2h07.b1.seq+          TAGCGTGGTCGCGGCCGAGGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_2h08.b1.seq+          TAGCGTGGTCGCGGCCGAGGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_7a06.b1.seq+          TAGCGTGGTCGCGGCCGAGGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_2c09.b1.seq+          TAGCGTGGTCGCGGCCGAGGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_12d02.b1.seq+         TAGCGTGGTCGCGGCCGAGGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_2d05.b1.seq-                    GAGGTAATTAAACCAAAAA-GGGATTATCCACA
U_HW-SSH1_3h09.b1.seq+          TAGCGTGGTCGCGGCGGAGGAAAAATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_9c09.b1.seq+          TAGCGTGGTCGCGG-CGAGG-ACAATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_6d11.b1.seq+                              AAACCAAAATTGGGAT-ATCCGCA
U_HW-SSH1_3a08.b1.seq+          TAGCGTGGTCGCGGCCGAGGAACAATGAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_9b09.b1.seq+          TAGCGTGGTCGCGGCCGAGGAAAAAAAAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_2c04.b1.seq+             GTGGTCGCGGCCGAGGTACTATTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_15f11.b1.seq+         TAGCGTGGTCGCGGCCGAGGCATTTTAAACCAAAATTGGGATTATCCGCA
U_HW-SSH1_3c11.b1.seq+          TAGCGTGGTCGCGGCCGAGGAGCGATTAAACCAAAATTGGGATTATCCCCA
U_HW-SSH1_2d12.b1.seq-          TAGCGTGGTCGCGGCCGAGGTACTATTAAACCAAAATTGGGATTATCCGCA
                        ____________________________________________________________
```





U_HW-SSH1_8d02.b1.seq+ AACTGCGGGACCCGGCCCGGGCGGCC
U_HW-SSH1_12f12.b1.seq+ GACTGCAGGTACCTGCCCGGGC
U_HW-SSH1_13d12.b1.seq+ TCGGGCCGCCATGG-CGGCCGCGGGAATTCGAT--ATCAC-TAG-TGAATTCGGGGAAGC
U_HW-SSH1_2h07.b1.seq+ GACTGCGGGTACCTGCCCGGGCGGCCGCTCGAA--ATCAC-TAG-TGAATTCGCGGCCGC
U_HW-SSH1_2h08.b1.seq+ GACTGCGGGTACCTGCCCGGGCGGCCGCTCGAA--ATCAC-TAG-TGAATTCGCGGCCGC
U_HW-SSH1_7a06.b1.seq+ GACTGCGGGTACCTGCCCGGGCGGCCGCTCGAA--ATCAC-TAG-TGAATTCGCGGCCGC
U_HW-SSH1_2c09.b1.seq+ GACTGCGGGTACCTGCCCGGGCGGCCGCTCGAA--ATCAC-TAG-GGAATTCCCGGCCCC
U_HW-SSH1_12d02.b1.seq+ GACTGCGGGTACCTGCCCGGGCGGCCGCTCGAA--ATCAC-TAA-AGAATTCCCGGCCGC
U_HW-SSH1_3h09.b1.seq+ GACTGCGGGTACCTGCCCGGGCGGCCGCTCAAA
U_HW-SSH1_9c09.b1.seq+ GACTGCGGGTACCTGCCCGGGCGGCCGCTCAAA
U_HW-SSH1_6d11.b1.seq+ GACTGCGGGTACCTGCCCGGGCGGCCACTCAA
U_HW-SSH1_3a08.b1.seq+ GACTGCGGGTACCTGCCCGGGCGGCC
U_HW-SSH1_9b09.b1.seq+ GACTGCGGGTACCTGCCCGGGCGGCCGCTCAAA
U_HW-SSH1_2c04.b1.seq- GACTGCGGGTACCCGTCCGGGCGGCCCCTCGAA--ATC
U_HW-SSH1_15f11.b1.seq+ GACTGCGGGTACCTGCCCGGGCGGCCGCTCGAA--ATCCC-AAG-TGAATTC
U_HW-SSH1_3c11.b1.seq+ AACTGCGGGTACCTGCCCGGGCGGCCGCACGAA--ATCA
U_HW-SSH1_2d12.b1.seq- GACTGCGGGTACCTGCCCGGGCGGCCCCT
U_HW-SSH1_16d09.b1.seq+ TCCGGCCGCCATG-GCGGCCGCGGG-ATTCGAT--ATCACGTAGGTGAATTCGCGGCCGC
U_HW-SSH1_16e10.b1.seq+ TCCGGCCGCCATG-GCGGCCGCGGG-ATTCGAT--ATCAC-TAG-TGAATTCGCGGCCGC

consensus GACTGCGGGTACCTGCGGCCGCGACCACTCTAA--ATCAC-TAG-TGAATTCGCGGCCGC

U_HW-SSH1_11h08.b1.seq+ CTGCAGGTCAACCATATGGGAGAGCTCCCGACGCGTTGGATGCATACCTTGAGTATTCTA
U_HW-SSH1_15b01.b1.seq+ CTGCAGGTCGACCATTTGGGAGGGCTCCC
U_HW-SSH1_13b06.b1.seq+ CTGC
U_HW-SSH1_4h09.b1.seq+ CTGCAGGTCAACCA
U_HW-SSH1_11b09.b1.seq+ CTGCAGGTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTA
U_HW-SSH1_13d12.b1.seq+ ATGCAGGTCGACCATATGGGAGAGCTCCCAACGCGTAGAAAGCGTAGCTTGAGTATTCTA
U_HW-SSH1_2h07.b1.seq+ CTGCAGGTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTA
U_HW-SSH1_2h08.b1.seq+ CTGCAGGTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTA
U_HW-SSH1_7a06.b1.seq+ CTGCAGGTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTA
U_HW-SSH1_2c09.b1.seq+ CTGCAGGTCAACCATATGGGAGAGCTCCCAACGCGTTGGATGCATATCTTGAATATTCTA
U_HW-SSH1_12d02.b1.seq+ CTGCAGGTCGACCATATGGGAGAGCTCCCAACGCGTGGGATGCATAGCTTGAGTATTCTA
U_HW-SSH1_16d09.b1.seq+ CTGCAGGTCAACCATATGGGAGAGCTCCCAACGCGTTGGAGGCATAGCTTGATTATTCTA
U_HW-SSH1_16e10.b1.seq+ CTGCAGGTCAACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTA
U_HW-SSH1_16b10.b1.seq+ CGACCATATGGGAGACCTCCCAACGCGTTGGATGCATATCTTGAGTATTCTA

consensus CTGCAGGTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTA

U_HW-SSH1_11h08.b1.seq+ TACTGTCACCTAAATAGCTTGGCGGAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT
U_HW-SSH1_11b09.b1.seq+ TAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT
U_HW-SSH1_13d12.b1.seq+ TAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT
U_HW-SSH1_2h07.b1.seq+ TAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT
U_HW-SSH1_2h08.b1.seq+ TAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT
U_HW-SSH1_7a06.b1.seq+ TAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT
U_HW-SSH1_2c09.b1.seq+ TAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATACCTGTTTCCTGTGTGAAATTGT
U_HW-SSH1_12d02.b1.seq+ TAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT
U_HW-SSH1_16d09.b1.seq+ TAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT
U_HW-SSH1_16e10.b1.seq+ TAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT
U_HW-SSH1_16b10.b1.seq+ TACTGTCACCTAAAAATAGCTTGGCGAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT

consensus TAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT

U_HW-SSH1_11h08.b1.seq+ TATCCGCTCACAATTCCACACAGTATACGAGCGGGAAGCGTACAGTGTAAAGCCTGGGGT
U_HW-SSH1_11b09.b1.seq+ TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT
U_HW-SSH1_13d12.b1.seq+ TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT
U_HW-SSH1_2h07.b1.seq+ TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT
U_HW-SSH1_2h08.b1.seq+ TATCCGCTCACAACTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT
U_HW-SSH1_7a06.b1.seq+ TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT
U_HW-SSH1_2c09.b1.seq+ TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT
U_HW-SSH1_12d02.b1.seq+ TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT
U_HW-SSH1_16d09.b1.seq+ TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT
U_HW-SSH1_16e10.b1.seq+ TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT
U_HW-SSH1_16b10.b1.seq+ TATCCGCTCACAATTCCACTCAACATACGAGCGGGAACCATAAAGGGTAAAGCCTGGGGT

consensus TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT

U_HW-SSH1_11h08.b1.seq+ GCCTAATGAATGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCCCTTTCCAGTTG
U_HW-SSH1_11b09.b1.seq+ GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCG
U_HW-SSH1_13d12.b1.seq+ GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCG
U_HW-SSH1_2h07.b1.seq+ GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCG
U_HW-SSH1_2h08.b1.seq+ GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCG
U_HW-SSH1_7a06.b1.seq+ GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCG
U_HW-SSH1_2c09.b1.seq+ GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTAG
U_HW-SSH1_12d02.b1.seq+ GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCA
U_HW-SSH1_16d09.b1.seq+ GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCG
U_HW-SSH1_16e10.b1.seq+ GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCG
U_HW-SSH1_16b10.b1.seq+ GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCG

consensus GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCG

U_HW-SSH1_11h08.b1.seq+ GGAAA-CCTGTCGCGCCAGCTGCATT-AAAGAGCCGGCCAACGTCGCGGGAGAGGCGGTT
U_HW-SSH1_11b09.b1.seq+ GGAAA-CCTGTCGTGCCAGCTGCATT-AATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
U_HW-SSH1_13d12.b1.seq+ GGAAA-CCGGTCGTGCCAGCTGCATT-AATGAATCGGCCAACGCGCGGGGAAAGGCGGTT
U_HW-SSH1_2h07.b1.seq+ GGAAA-CCTGTCGTGCCAGCTGCATT-AATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
U_HW-SSH1_2h08.b1.seq+ GGAAA-CCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
U_HW-SSH1_7a06.b1.seq+ GGAAAACCTGTCGTGCCAGCTGCTT--AATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
U_HW-SSH1_2c09.b1.seq+ GGAAA-CCTGTCGTGCCAGCTGCATT-AATGAATCGACCAACGCGCGGAGAGGCGGTT
U_HW-SSH1_12d02.b1.seq+ GAAAA-CCTGTCGTGCCCCCTGCATT-AATGAATCGGCCAACGCGCGGAGAGGCGGTT
U_HW-SSH1_16d09.b1.seq+ GGAAA-CCTGTCGTGCCAGCTGCATT-AATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
U_HW-SSH1_16e10.b1.seq+ GGAAA-CCTGTCGTGCCAGCTGCATT-AATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
U_HW-SSH1_16b10.b1.seq+ GGAAA-CCTGCCGGGCCAGCTGCATT-AATGAATCGGCCAACGCGCGGGGAGAGGCGGTT

consensus GGAAA-CCTGTCGTGCCAGCTGCATT-AATGAATCGGCCAACGCGCGGGGAGAGGCGGTT

U_HW-SSH1_11h08.b1.seq+ -GCGTATTGGGCGCT-CTTTCGGATACT-CGCTCA-TGA-CTCTCTGCGCTCG
U_HW-SSH1_11b09.b1.seq+ TGCGTATTGGGCGCT-CTTCCGCTTCCT-CGCTCACTGA-CTCGCTGCGCTCGGTCGTTC
U_HW-SSH1_13d12.b1.seq+ TGCGTATTGGGCGCT-CTTCCGCTTTCT-CGCTCACTGA-TTCGCTGCGCTCGGTCGTTC
U_HW-SSH1_2h07.b1.seq+ TGCGTATTGGGCGCT-CTTCCGCTTCCT-CGCTCACTGA-CTCGCTGCGCTCGGTCGTTC
U_HW-SSH1_2h08.b1.seq+ TGCGTATTGGGCCCT-CTTCCGCTTCCTTCGCTCACTGA-CTCGCTGCGC
U_HW-SSH1_7a06.b1.seq+ TGCGTATTGGGCGCTTCTTCCGCTTCCT-CGCTCACTGA-CTCGCTGCGCTCGGTCGTTC
U_HW-SSH1_2c09.b1.seq+ TGCGTATTGGGCGCT-CTTCCGCTTCCT-CGCTCACTGA-ATCGCTGCGCTCGGTCGTTC
U_HW-SSH1_12d02.b1.seq+ TGTGGATTGTGCTCT-CTTCCGCTTCCT-CGCTCATTGAACTCGCTGCGCTCGGTCGTTC
U_HW-SSH1_16d09.b1.seq+ TGCGTATTGGGCGCT-CTTCCGCTTCCT-CGCTCACTGA-CTCGCTGCGCTCGGTCGTTC
U_HW-SSH1_16e10.b1.seq+ TGCGTATTGGGCGCT-CTTCCGCTTCCT-CGCTCACTGA-CTCGCTGCGCTCGGTCGTTC
U_HW-SSH1_16b10.b1.seq+ TGCGTATTGGGTGCT-CTTCCGCTTCCT-CGCTCACTGA-CTCGCTGCGCTCGGTCGTTC

consensus TGCGTATTGGGCGCT-CTTCCGCTTCCT-CGCTCACTGA-CTCGCTGCGCTCGGTCGTTC

U_HW-SSH1_11b09.b1.seq+ GGCTGCGGCGAGCGGTATCAGCTCACTCAAAGG-CGGTAATACGGTTATCC-ACAGAATC
U_HW-SSH1_13d12.b1.seq+ GGCTGCGGCAAGCGGT
U_HW-SSH1_2h07.b1.seq+ GGCTGCGGCGAGCGGTATCAGCTCACTCAAAGG-CGGTAATACTGTTATCC-ACAGAATC
U_HW-SSH1_7a06.b1.seq+ GGCTGCGGCGAACGGTATCACCTCACTCAAAGGGCGTTAATACTGTTATCC-ACAGAATC
U_HW-SSH1_2c09.b1.seq+ GGCTGCGGCGAGCGGTATCAGCTCA-TCAAGG--CG-TCATACGGTTATCCCACAGAATC
U_HW-SSH1_12d02.b1.seq+ GGCTGCGGGCGCTATCAGCTCACTCA----------CG-TCATACGGTTATCC-ACAGAATC
U_HW-SSH1_16d09.b1.seq+ GGCTGCGGCGAGCGGTATCAGCTCACTCAAAGG-CGGTAATACGGTTATCC-ACAGAATC
U_HW-SSH1_16e10.b1.seq+ GGCTGCGGCGAGCGGTATCAGCTCACTCAAAGG-CGGTAATACGGTTATCC-ACAGAATC
U_HW-SSH1_16b10.b1.seq+ GGCTGCGGCGAGCGGTATCAGCTCACTCAAAGG-CGGTAATACGGTTATCC-ACAGAATC

consensus GGCTGCGGCGAGCGGTATCAGCTCACTCAAAGG-CGGTAATACGGTTATCC-ACAGAATC

U_HW-SSH1_11b09.b1.seq+ A-GGGATAACGCAAGAAAGAACATGTGAACAAAAGGCCAGCAAAAGGTCAAGAACCAGTA
U_HW-SSH1_2h07.b1.seq+ A-GGGGATACGCA-GAAAGA-CATGTGAGCAAA-GGCCAGCAAAGG--CCAGGACC-GTA
U_HW-SSH1_7a06.b1.seq+ A-GGGAT-ACGCAAGAAAGAACATGTGAGCAAA-TGCCAGCAAAAGG--CAGGAACAGTA
U_HW-SSH1_2c09.b1.seq+ AAGGGATACCGCAGGAA
U_HW-SSH1_16d09.b1.seq+ AGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGG-CCAGGAACCGTA
U_HW-SSH1_16e10.b1.seq+ AGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGG-CCAGGAACCGTA
U_HW-SSH1_16b10.b1.seq+ AGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGG-CCAGGAACCGTA

consensus AGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGG-CCAGGAACCGTA

U_HW-SSH1_11b09.b1.seq+ AAAGGGCCGCGTTGCTGTTGTTTTT-CAATAGGCCTCCGCCCCCCCTGAACAGCATCAAAA
U_HW-SSH1_2h07.b1.seq+ AA--GGCCGCGTTGCTGC-GTTTTC-CAATAGGC-TCCGCCCCC-TGACGAGCATCACAA
U_HW-SSH1_7a06.b1.seq+ AAAAGGCGCCGT-GCTGGTCTTTTT-TCATAG-CCTCCCCCCCCCCTGACGAGC
U_HW-SSH1_16d09.b1.seq+ AAAAGGCCGCGTTGCTGGCGTTTTT-CCATAGGC-TCCGCCCCCCCTGACGAGCATCACAA
U_HW-SSH1_16e10.b1.seq+ AAAAGGCCGCGTTGCTGGCGTTTTTTCCATAGGC-TCCGCCCCCCCTGACGAGCATCACAA
U_HW-SSH1_16b10.b1.seq+ AAAAGGCCGCGTTGCTGGCGTTTTT-CCATAGGC-TCCGCCCCCCCTGACGAGCATCACAA

consensus AAAAGGCCGCGTTGCTGGCGTTTTT-CCATAGGC-TCCGCCCCCCCTGACGAGCATCACAA

U_HW-SSH1_11b09.b1.seq+ AAATCGACGCTCAAGT
U_HW-SSH1_2h07.b1.seq+ AAATCGACGCTCA-GTCAGAGGTGGCGA
U_HW-SSH1_16d09.b1.seq+ AAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG-ACAGGACTATAAAGATACCAGGCGT
U_HW-SSH1_16e10.b1.seq+ AAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG-ACAGGACTATAAAGATACCAGGCGT
U_HW-SSH1_16b10.b1.seq+ AAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGGACAGGACTATAAAGATACCAGGCGT

consensus AAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG-ACAGGACTATAAAGATACCAGGCGT

U_HW-SSH1_16d09.b1.seq+ TTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAACAGA-TAC
U_HW-SSH1_16e10.b1.seq+ TTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAACAGAATAC
U_HW-SSH1_16b10.b1.seq+ TTCCCCCTG-AAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAACAGA-TAC

consensus TTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAACAGA-TAC

U_HW-SSH1_16d09.b1.seq+ CTGTCCGTCTTTCTCCCCTCGAGAAGCGTGC-GCTTT-CTCATAGCTCACGCTGTAGTAT
U_HW-SSH1_16e10.b1.seq+ CTGTCCGCCTT-CTCCCT-CGGGAAGCGTGC-GCTTT-CTCATAGCTCACGCTGTAGTAT
U_HW-SSH1_16b10.b1.seq+ CTGTCCGCTTTCTTCCGTTCGGGAAGCGTGCCGCTTTTCTCATAGCTCACGCTGTAGTAT

consensus CTGTCCGCCTTCCTCCCTTCGGGAAGCGTGC-GCTTT-CTCATAGCTCACGCTGTAGTAT

U_HW-SSH1_16d09.b1.seq+ CTCAGT
U_HW-SSH1_16e10.b1.seq+ CTCAGTCGTGTA-GTCGT-CGCTCAAGCTGGCTGTGTGCACGACCCCTCCGTTCAGCCGA
U_HW-SSH1_16b10.b1.seq+ CTCAGTCGTGTAAGTCGTTCGCTCAAGCTGG

consensus CTCAGTCGTGTAAGTCGTTCGCTCAAGCTGGCTGTGTGCACGACCCCTCCGTTCAGCCGA

U_HW-SSH1_16e10.b1.seq+ CGCTGCTCTTATCAGTACTATCGTCTGATTCACCAGTAGACCGACTATCGCACTGCA

consensus CGCTGCTCTTATCAGTACTATCGTCTGATTCACCAGTAGACCGACTATCGCACTGCA

****************** **Contig 42** ******************

U_HW-SSH1_11d10.b1.seq+ TTCGATTTCGAGCGGCCGCCCGGGCAGGTACAAGCTTTTTTTTTTTTTTTTTTTTTTTTT
U_HW-SSH1_2e04.b1.seq+ TTCGATTTC-AGCGGCCGCCCGGACAGGTACAAGCTTTTTTTTTTTTTTTTTTTTTTTTT
U_HW-SSH1_11e06.b1.seq+ TTCGATTTCGAGCGGCCGCCCGGGCAGGTACAAGCTTTTTTTTTTTTTTTTTTTTTTTTT

consensus TTCGATTTCGAGCGGCCGCCCGGGCAGGTACAAGCTTTTTTTTTTTTTTTTTTTTTTTTT

U_HW-SSH1_11d10.b1.seq+ TTTTTGCCTGAATCCTTCTTTATTGGGTATGTATGTATTCCCATC-AAGCCTGATCGATC
U_HW-SSH1_3f11.b1.seq+ GTATGTATTCCCCTC-AAGCCCGATCGATC
U_HW-SSH1_2e04.b1.seq+ TTTTTGCCTGAATCCTTCTTTATTGGGAATTAATGTATTCACAAAGAAACCTGGTCGATC
U_HW-SSH1_11e06.b1.seq+ TTTTTGCCTGAATCCTTCTTTATTGGGTATGTATGTATTCCCATC-AAGCCTGATCGATC

consensus TTTTTGCCTGAATCCTTCTTTATTGGGTATGTATGTATTCCCATC-AAGCCTGATCGATC

U_HW-SSH1_11d10.b1.seq+ ACGGGCACCTCCCCAACACATGAAT-AACAATCTAATGAAGCGTCAAAACAAAAAGTAAC
U_HW-SSH1_3f11.b1.seq+ ACGGGCACCTCCCCAACACTTTTTTAACAATCTAATGAAACGTCAAAACAAAAAGTAAC
U_HW-SSH1_2e04.b1.seq+ CCCGGCACATCACCAAGAGATGAGT-AACAATCTAATGAAGCGGCAAAACAAAAAGTAAC
U_HW-SSH1_11e06.b1.seq+ ACGGGCCCCTCCCCAACACATGAAT-AACAATCTAATGAAGCGTCAAAACAAAAAGTAAC

consensus ACGGGCACCTCCCCAACACATGAAT-AACAATCTAATGAAGCGTCAAAACAAAAAGTAAC

U_HW-SSH1_11d10.b1.seq+ AATCTAATGAAATGAATGGTCAGGTATGAAGTTAGCTGCTGTAACTGTAACTGACAGGAA
U_HW-SSH1_3f11.b1.seq+ AATCTAATGAAATGAATGGTCAGGTATAAAGTTAGCTTCTGTAACTTTACTGACAGGAA
U_HW-SSH1_2e04.b1.seq+ AATCTATTGAAATGAATGGTCAGGTATGAAATTAGCTGCTGTAACTGGAACTGACAGGAA
U_HW-SSH1_11e06.b1.seq+ AATCTAATGAAATGAATGGTCAGGTATGAAGTTAGCTGCTGTAACTGTAACTGAAAGGAA

consensus AATCTAATGAAATGAATGGTCAGGTATGAAGTTAGCTGCTGTAACTGTAACTGACAGGAA

U_HW-SSH1_11d10.b1.seq+ CTGAAAAAAGGAAAAAAAAGGGGTCTGTAAATTTGATCTATGGTATACTGCTATACGGG
U_HW-SSH1_3f11.b1.seq+ CTGAAAGAAGAAAAAGAAAGGGGTCTGTAAATTT
U_HW-SSH1_2e04.b1.seq+ CTGAGAAAGGAGAAAAGAAAGGTGTCCGTTAATTTTGATTTAAGGTATACGGGTATACGGG
U_HW-SSH1_11e06.b1.seq+ CTGAAAAAAGAAAAAAAAAGGGGTCTGTAAATTTTGATCTATGGTATACTGCTATACGGG

consensus CTGAAAAAAGAAAAAAAAAGGGGTCTGTAAATTTTGATCTATGGTATACTGCTATACGGG

U_HW-SSH1_11d10.b1.seq+ ATGTTTGCTAACGGAAACAATTATATGGACCGATCCCCTCCCAATAGGTTTGGTTTTCGG
U_HW-SSH1_2e04.b1.seq+ ATGTTTGCTAACAGAAACTATTATATGGACCCATCCCCTCGCAATAGGTTTGGTTTTTGG
U_HW-SSH1_11e06.b1.seq+ ATGTTTGCTAACGGAAACAATTATATGGACCGATCCCATCCCAATAGGTTTGGTTTTCGG

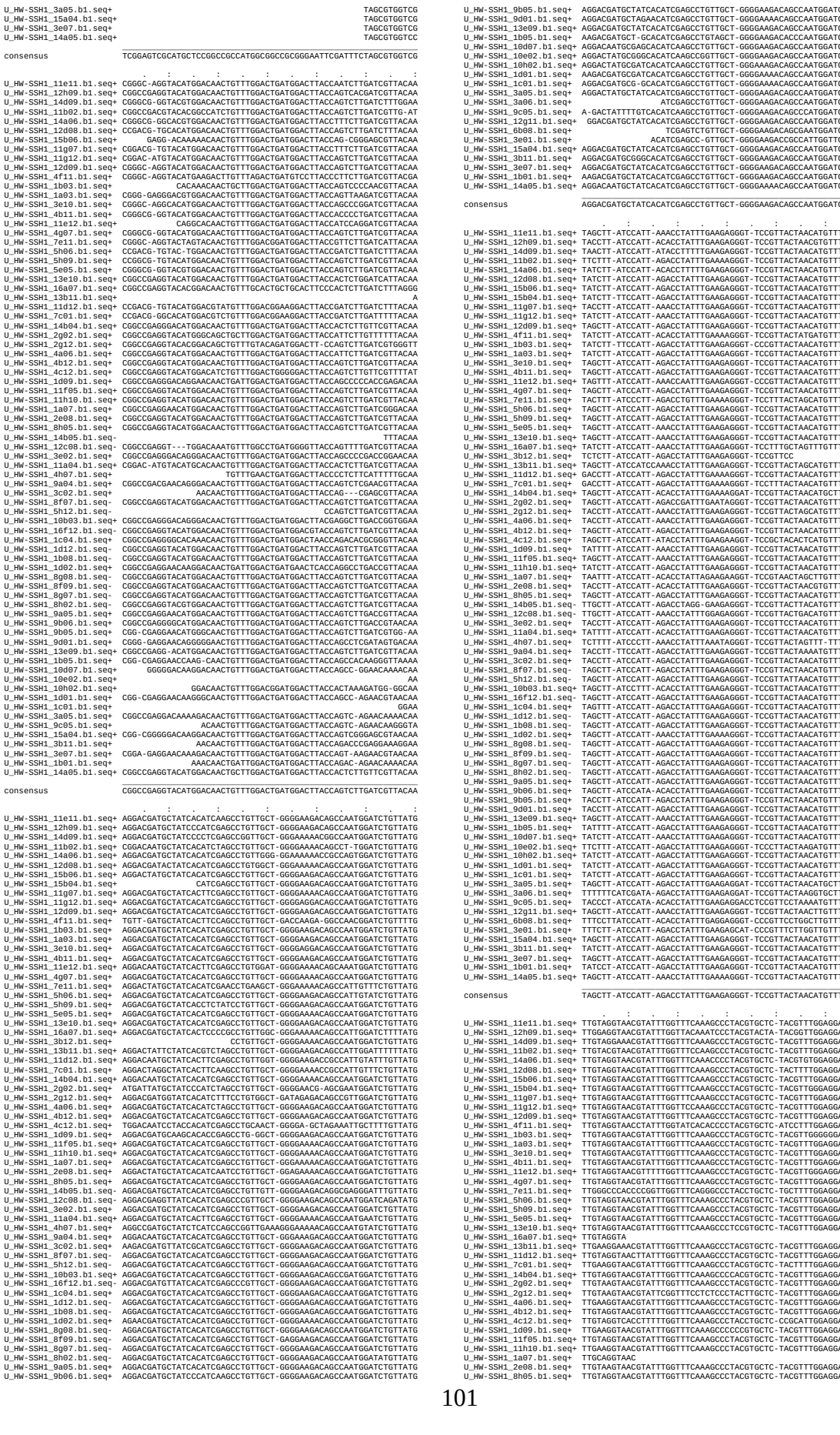
consensus ATGTTTGCTAACGGAAACAATTATATGGACCGATCCCCTCCCAATAGGTTTGGTTTTCGG

U_HW-SSH1_11d10.b1.seq+ CCGGCCCTTCCGCTTGCCGGCGACAAGGTACCTCGGCCGCCACCACCCTA
U_HW-SSH1_2e04.b1.seq+ CCCGCCCTTCCCCTTGCCGGC
U_HW-SSH1_11e06.b1.seq+ CCGGCCCTTCCGCTTGCCGGC

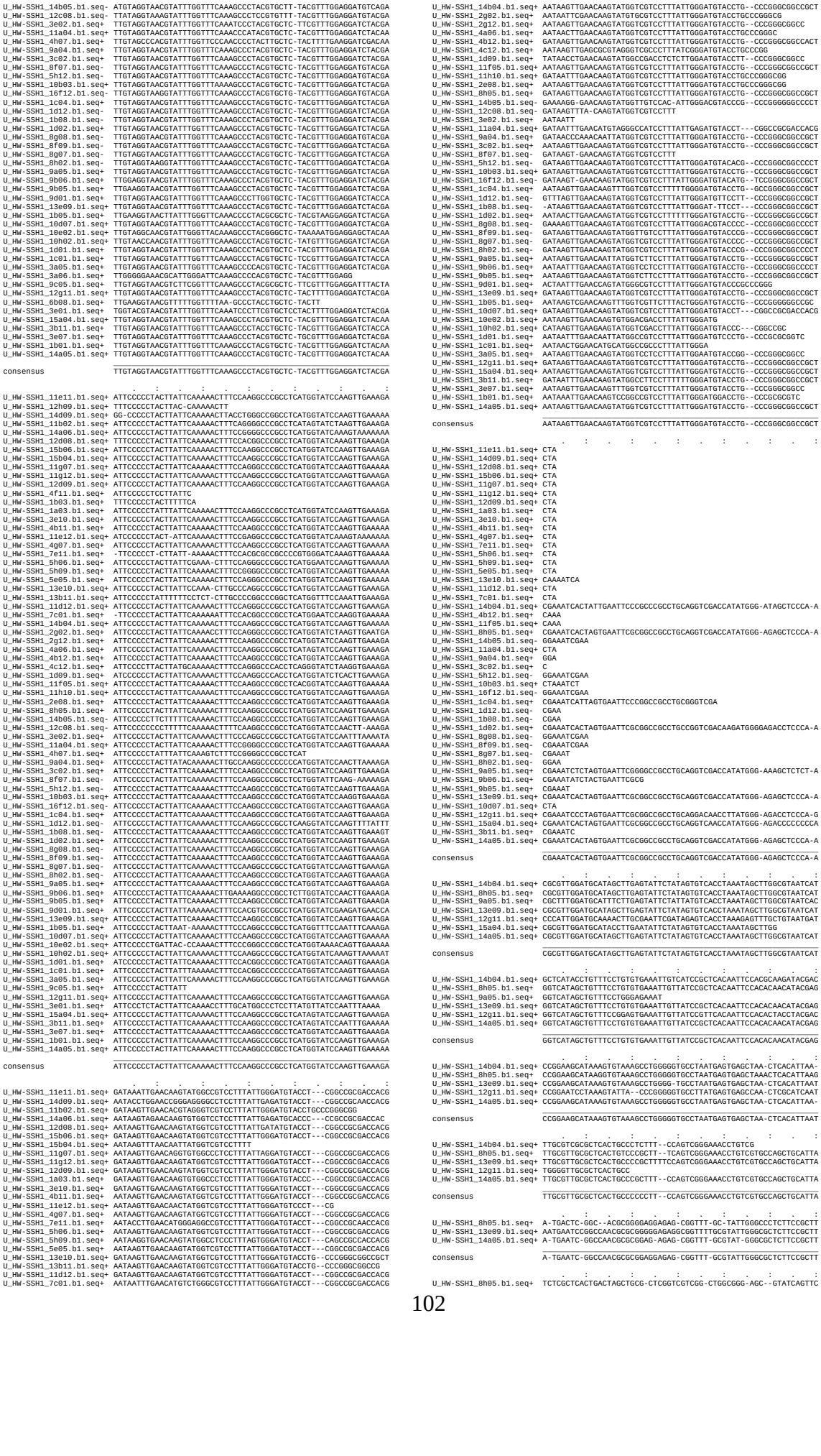
consensus CCGGCCCTTCCGCTTGCCGGCGACAAGGTACCTCGGCCGCCACCACCCTA

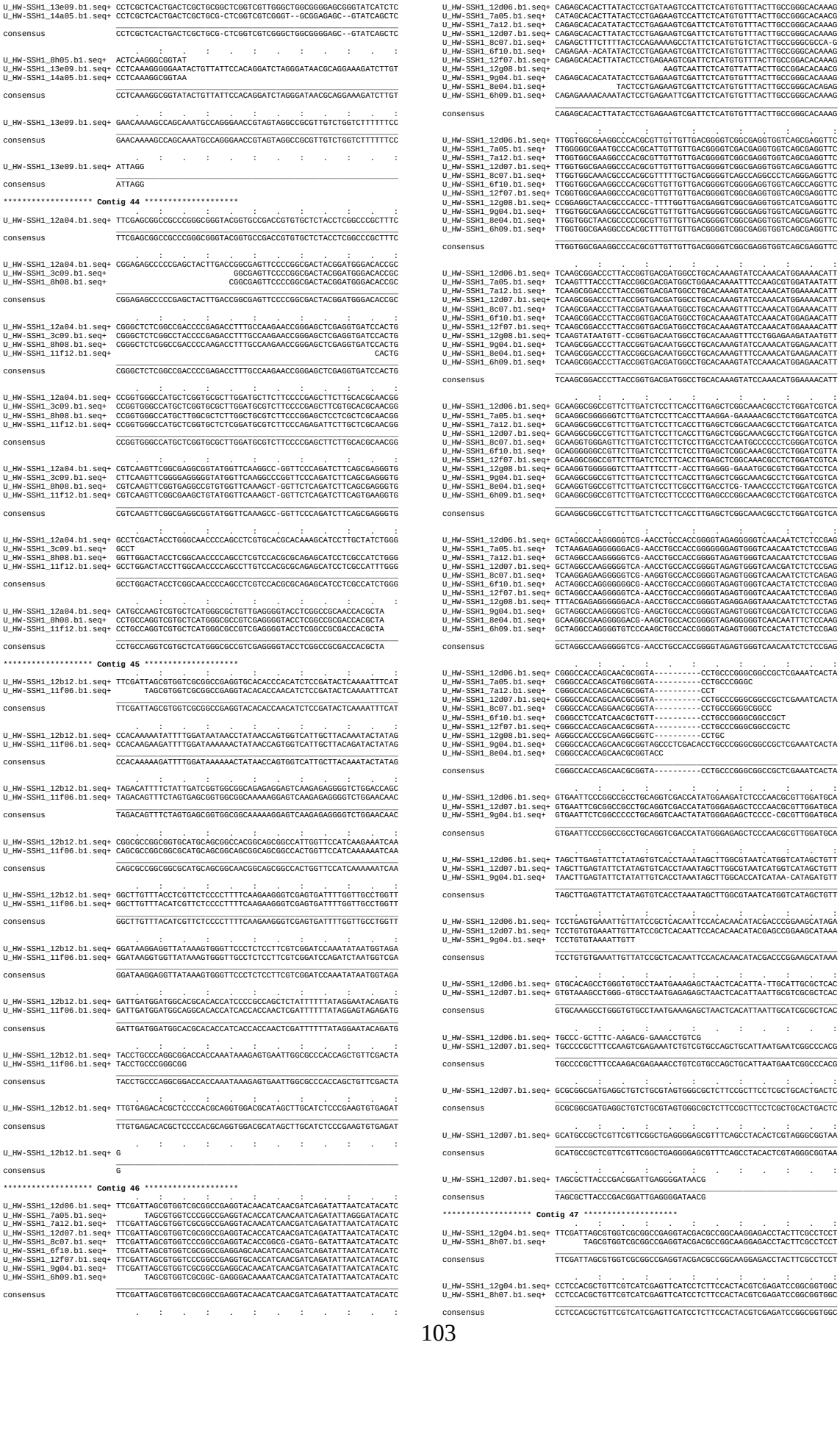
****************** **Contig 43** ******************

U_HW-SSH1_11e11.b1.seq+ TCGGAGTCGCATGCTCCGGCCGCCATGGCGGCCGCGGGAATTCGATTTCAAGCGGCCGCC
U_HW-SSH1_12h09.b1.seq+ TTCGATT---AGCGTGGTCG
U_HW-SSH1_14d09.b1.seq+ TTCGATTTCCAGGGGCCGCC
U_HW-SSH1_11b02.b1.seq+ TTCGATT---ACCGTGGTCC
U_HW-SSH1_14a06.b1.seq+ TTCGATTTCCAGGGGCCCCC
U_HW-SSH1_12d08.b1.seq+ TTCCAGGGGCCCCC
U_HW-SSH1_11g07.b1.seq+ TTCGATTTCCGGGGGCCCCC
U_HW-SSH1_11g12.b1.seq+ TTCGAGCGGCCGCC
U_HW-SSH1_12d09.b1.seq+ TTCGATTTCGAGCGGCCGCC
U_HW-SSH1_4f11.b1.seq+ TTCGATTTCGAGCGGCCGCC
U_HW-SSH1_1a03.b1.seq+ TTCGAGCGGCCGCC
U_HW-SSH1_3e10.b1.seq+ TTCGAGCGGCCGCC
U_HW-SSH1_4b11.b1.seq+ TTCGATTTCGAGCGGCCGCC
U_HW-SSH1_4g07.b1.seq+ TTCGATTTCCAGCGGCCGCC
U_HW-SSH1_7e11.b1.seq+ TTCGATTTCGAGCGGCCGCC
U_HW-SSH1_5h06.b1.seq+ TTCGATTTCCAGGGGCCCGC
U_HW-SSH1_5h09.b1.seq+ TTCCAGGGGCCCCC
U_HW-SSH1_5e05.b1.seq+ TTCGAGGGCCGCC
U_HW-SSH1_13e10.b1.seq+ TTCGATT---AGCGTGGTCG
U_HW-SSH1_16a07.b1.seq+ TTCGATT---ACCGTGGTCC
U_HW-SSH1_11d12.b1.seq+ CCGGGGGCCCGC
U_HW-SSH1_7c01.b1.seq+ CCGGGGGCCCGC
U_HW-SSH1_14b04.b1.seq+ TTCGATT---ACCGTGGTCC
U_HW-SSH1_2g02.b1.seq+ TTCGATT---ACCGTGGTCC
U_HW-SSH1_2g12.b1.seq+ TTCGATT---AGCGTGGTCG
U_HW-SSH1_4a06.b1.seq+ TTCGATT---AGCGTGGTCG
U_HW-SSH1_4b12.b1.seq+ TTCGATT---AGCGTGGTCG
U_HW-SSH1_4c12.b1.seq+ TTCGATT---AGCGTGGTCG
U_HW-SSH1_1d09.b1.seq+ TAGCGTGGTCG
U_HW-SSH1_11f05.b1.seq+ TAGCGTGGTCG
U_HW-SSH1_11h10.b1.seq+ ATT---AGCGTGGTCC
U_HW-SSH1_1a07.b1.seq+ TAGCGTGGGCC
U_HW-SSH1_2e08.b1.seq+ TACCGTGGTCC
U_HW-SSH1_8h05.b1.seq+ TTCGATT---AGCGTGGTCG
U_HW-SSH1_12c08.b1.seq- TAGCGTGGTCG
U_HW-SSH1_3e02.b1.seq+ TAGCGTGGTCG
U_HW-SSH1_11a04.b1.seq+ TTCCAGCGGCCGCC
U_HW-SSH1_9a04.b1.seq+ ATT---AGCGTGGTCG
U_HW-SSH1_8f07.b1.seq- TAGCGTGGTCG
U_HW-SSH1_10b03.b1.seq+ TAGCGTGGTCG
U_HW-SSH1_16f12.b1.seq- TAGCGTGGTCG
U_HW-SSH1_1c04.b1.seq+ TAGCGTGGTCG
U_HW-SSH1_1d12.b1.seq- TAGCGTGGTCG
U_HW-SSH1_1b08.b1.seq- TAGCGTGGTCG
U_HW-SSH1_1d02.b1.seq+ TAGCGTGGTCG
U_HW-SSH1_8g08.b1.seq- TAGCGTGGTCG
U_HW-SSH1_8f09.b1.seq- TAGCGTGGTCG
U_HW-SSH1_8g07.b1.seq- TAGCGTGGTCG
U_HW-SSH1_8h02.b1.seq- TAGCGTGGTCG
U_HW-SSH1_9a05.b1.seq+ TAGCGTGGTCG
U_HW-SSH1_9b06.b1.seq+ TACCATGGTCC
U_HW-SSH1_9b05.b1.seq+ TAGCGTGGTCG
U_HW-SSH1_9d01.b1.seq+ TAGCGTGGTCG
U_HW-SSH1_13e09.b1.seq+ TAGCGTGGTCG
U_HW-SSH1_1b05.b1.seq+ TAGCGTGGTCG
U_HW-SSH1_1d01.b1.seq+ TAGCGTGGTCG



U_HW-SSH1_3a05.b1.seq+ TAGCGTGGTCG
U_HW-SSH1_15a04.b1.seq+ TAGCGTGGTCG
U_HW-SSH1_3e07.b1.seq+ TAGCGTGGTCG
U_HW-SSH1_14a05.b1.seq+ TAGCGTGGTCC
consensus TCGGAGTCGCATGCTCCGGCCGCCATGGCGGCCGCGGGAATTCGATTTCTAGCGTGGTCG
U_HW-SSH1_11e11.b1.seq+ CGGGC-AGGTACATGGACAACTGTTTGGACTGATGGACTTACCAATCTTGATCGTTACAA
U_HW-SSH1_12h09.b1.seq+ CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCACGATCGTTACAA
U_HW-SSH1_14d09.b1.seq+ CGGGCG-GGTACGTGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCTTTGGAA
U_HW-SSH1_11b02.b1.seq+ CGGCCGAGGTACACGGCCATCTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTG-AT
U_HW-SSH1_14a06.b1.seq+ CGGGCG-GGCACGTGGACAACTGTTTGGACTGATGGACTTACCTTTCTTGATCGTTACAA
U_HW-SSH1_12d08.b1.seq+ CCGACG-TGCACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCTTTACAA
U_HW-SSH1_15b06.b1.seq+ GAGG-ACAAAAACAACTGTTTGGACTGATGGACTTACCAG-CGGGAGCGTTACAA
U_HW-SSH1_11g07.b1.seq+ CGGACG-TGTACATGGACAACTGTTTGGACTGATGGACTTACCTTTCTTGATCGTTACAA
U_HW-SSH1_11g12.b1.seq+ CGGAC-ATGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_12d09.b1.seq+ CGGGC-AGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_4f11.b1.seq+ CGGGC-AGGTACATAAAGACTTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACGA
U_HW-SSH1_1b03.b1.seq+ CACAAACAACTGTTTGGACTGATGGACTTACCAGTCCCCAACGTTACAA
U_HW-SSH1_1a03.b1.seq+ CGGG-GAGGGACGTGGACAACTGTTTGGACTGATGGACTTACCAGTTAAGATCGTTACAA
U_HW-SSH1_3e10.b1.seq+ CGGGC-AGGCACATGGACAACTGTTTGGACTGATGGACTTACCAGCCCGGATCGTTACAA
U_HW-SSH1_4b11.b1.seq+ CGGGCG-GGTACATGGACAACTGTTTGGACTGATGGACTTACCACCCCTGATCGTTACAA
U_HW-SSH1_11e12.b1.seq+ CAGGCACAACTGTTTGGACTGATGGACTTACCATCCAGGATCGTTACAA
U_HW-SSH1_4g07.b1.seq+ CGGGCG-GGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_7e11.b1.seq+ CGGGC-AGGTACTAGTACAACTGTTTGGACGGATGGACTTACCGTTCTTGATCATTACAA
U_HW-SSH1_5h06.b1.seq+ CCGGCG-TGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATTTTTACAA
U_HW-SSH1_5h09.b1.seq+ CCGGCG-TGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_5e05.b1.seq+ CGGGCG-GGTACGTGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_13e10.b1.seq+ CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACTTACCACTCTGGATCATTACAA
U_HW-SSH1_16a07.b1.seq+ CGGCCGAGGTACACGGACAACTGTTTGCACTGCTGCATTCCCACTCTGATCTTTAGGG
U_HW-SSH1_13b11.b1.seq+ A
U_HW-SSH1_11d12.b1.seq+ CCGACG-TGTACATGGACGTATGTTTGGACGGAAGGACTTACCGATCTTGATCTTTACA
U_HW-SSH1_7c01.b1.seq+ CCGACG-GGCACATGGACGTACTGTTTGGACGGAAGGACTTACCGATCTTGATTTTTACA
U_HW-SSH1_14b04.b1.seq+ CGGCCGAGGGACATGGACAACTGTTTGGACTGATGGACTTACCACTCTTGTTCGTTACAA
U_HW-SSH1_2g02.b1.seq+ CGGCCGAGGTACATGGGCAGCTGCTTGGACTGATGGACTTACCATTCTGTTTTTTACAA
U_HW-SSH1_2g12.b1.seq+ CGGCCGAGGTACACGGACAGCTGTTTGTACAGATGGACTT-CCAGTCTTGATCGTGGGTT
U_HW-SSH1_4a06.b1.seq+ CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACTTACCATTCTGATCGTTACAA
U_HW-SSH1_4b12.b1.seq+ CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_4c12.b1.seq+ CGGCCGAGGTACATGGACATCTGTTTGGACTGGGGACTTACCAGTCTTGTTCGTTTTAT
U_HW-SSH1_1d09.b1.seq+ CGGCCGAGGGACAGGAACAACTGATTGGACTGATGGACTTACCAGTCCCGACGAGAGCTA
U_HW-SSH1_11f05.b1.seq+ CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_11h10.b1.seq+ CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_1a07.b1.seq+ CGGCCGAGGAACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGGGACAA
U_HW-SSH1_2e08.b1.seq+ CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_8h05.b1.seq+ CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_14b05.b1.seq- TTTACAA
U_HW-SSH1_12c08.b1.seq- CGGCCGAGGT---TGGACAAATGTTTGGCCTGATGGGGTTACCAGTTTTGATCGTTACAA
U_HW-SSH1_3e02.b1.seq+ CGGCCGAGGGACAGGGACAACTGTTTGGACTGATGGACTTACCAGCCCGACCGAGAGCTA
U_HW-SSH1_11a04.b1.seq+ CGGAC-ATGTACATGCACAACTGTTTGGACTGATGGACTTACCACTCTTGATCGTTACAA
U_HW-SSH1_4h07.b1.seq+ TGTTTGAACTGATGGACTTACCCCTCTTCATTTTTGCAA
U_HW-SSH1_9a04.b1.seq+ CGGCCGACGAACAGGGACAACTGTTTGGACTGATGGACTTACCAGTCTCGAACGTTACAA
U_HW-SSH1_3c02.b1.seq+ AACAACTGTTTGGACTGATGGACTTACCAG---CGAGCGTTACAA
U_HW-SSH1_8f07.b1.seq- CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_5h12.b1.seq- CCAGTCTTGATCGTTACAA
U_HW-SSH1_10b03.b1.seq+ CGGCCGAGGGACAGGGACAACTGTTTGGACTGATGGACTTACCAGGCTGACCGGTGGAA
U_HW-SSH1_16f12.b1.seq- CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACGTACCAGTCTTGATCGTTACAA
U_HW-SSH1_1c04.b1.seq+ CGGCCGAGGGGCACAAACAACTGTTTGGACTGATGGACTAACCAGACACGCGGGTTACAA
U_HW-SSH1_1d12.b1.seq- CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_1b08.b1.seq- CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_1d02.b1.seq+ CGGCCGAGGAACAAGGACAACTGATTGGACTGATGAACTCACCAGGCCTGACCGTTACAA
U_HW-SSH1_8g08.b1.seq- CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_8f09.b1.seq- CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_8g07.b1.seq- CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_8h02.b1.seq- CGGCCGAGGTACGTGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_9a05.b1.seq+ CGGCCGAGGAACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGACCGTTACAA
U_HW-SSH1_9b06.b1.seq+ CGGCCGAGGGGCATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGACCGTAACAA
U_HW-SSH1_9b05.b1.seq+ CGG-CGAGGAACATGGGCAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTGG-AA
U_HW-SSH1_9d01.b1.seq+ CGGG-GAGGAACAGGGGGAACTGTTTGGACTGATGGACTTACCAGCCTCGATAGTGACAA
U_HW-SSH1_13e09.b1.seq+ CGGCCGAGG-ACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_1b05.b1.seq+ CGG-CGAGGAACCAAG-CAACTGTTTGGACTGATGGACTTACCAGCACAAGGGTTAAAA
U_HW-SSH1_10d07.b1.seq+ GGGGGACAAGGACAACTGTTTGGACTGATGGACTTACCAGCC-GGAACAAAACAA
U_HW-SSH1_10e02.b1.seq+ AA
U_HW-SSH1_10h02.b1.seq+ GGACAACTGTTTGGACGGATGGACTTACCACTAAAGATGG-GGCAA
U_HW-SSH1_1d01.b1.seq+ CGG-CGAGGAACAAGGGCAACTGTTTGGACTGATGGACTTACCAGCC-AGAACGTAACAA
U_HW-SSH1_1c01.b1.seq+ GGAA
U_HW-SSH1_3a05.b1.seq+ CGGCCGAGGACAAAAGACAACTGTTTGGACTGATGGACTTACCAGTC-AGAACAAAACAA
U_HW-SSH1_9c05.b1.seq+ ACAACTGTTTGGACTGATGGACTTACCAGTC-AGAACGAGGATA
U_HW-SSH1_15a04.b1.seq+ CGG-CGGGGGACAAGGACAACTGTTTGGACTGATGGACTTACCAGTCGGGAGCGTAACAA
U_HW-SSH1_3b11.b1.seq+ AACAACTGTTTGGACTGATGGACTTACCAGACCCGAGGAAAGGAA
U_HW-SSH1_3e07.b1.seq+ CGGA-GAGGAACAAAGACAACTGTTTGGACTGATGGACTTACCAGT-AAGAACGTAACAA
U_HW-SSH1_1b01.b1.seq+ AAACAACTGATTGGACTGATGGACTTACCAGAC-AGAACAAAACAA
U_HW-SSH1_14a05.b1.seq+ CGGCCGAGGTACATGGACAACTGCTTGGACTGATGGACTTACCACTCTTGTTCGTTACAA
consensus CGGCCGAGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCTTGATCGTTACAA
U_HW-SSH1_11e11.b1.seq+ AGGACGATGCTATCACATCAAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_12h09.b1.seq+ AGGACGATGCTATCCCATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_14d09.b1.seq+ AGGACGATGCTATCCCCTCGAGCCGGTTGCT-GGGAAAAACGGCCAATGGATCTGTTATG
U_HW-SSH1_11b02.b1.seq+ CGGACAATGCTATCACATCTAGCCTGTTGCT-GGGGAAAACAGCCT-TGGATCTGTTATG
U_HW-SSH1_14a06.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGGG-GGAAAAAACGGCCAATGGATCTGTTATG
U_HW-SSH1_12d08.b1.seq+ AGGACGATACTATCACATCGAGCCTGTGGCT-GGGGAAAAACAGCCAATGGATCTGTTATG
U_HW-SSH1_15b06.b1.seq+ AGGACTATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_15b04.b1.seq+ CATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_11g07.b1.seq+ AGGACGATGCTATCACTTCGAGCCTGTTGCT-GGGGAAAACAGCCAATGGATCTGTTATG
U_HW-SSH1_11g12.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGGACAGCCAATGGATCTGTTATG
U_HW-SSH1_12d09.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_4f11.b1.seq+ TGTT-GATGCTATCACTTCCAGCCTGTTGCT-GACCAAGA-GGCCAACGGATCTGTTTTG
U_HW-SSH1_1b03.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_1a03.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_3e10.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAGGACAGCCAATGGATCTGTTATG
U_HW-SSH1_4b11.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_11e12.b1.seq+ AGGACAATGCTATCACTTCGAGCCTGTGGAT-GGGGAAAACAGCAAATGGATCTGTTATG
U_HW-SSH1_4g07.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAAACAGCCAATGGATCTGTTATG
U_HW-SSH1_7e11.b1.seq+ AGGACTATGCTATCACATCGAACCTGAAGCT-GGGAAAAACAGCCATTGTTTCTGTTATG
U_HW-SSH1_5h06.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_5h09.b1.seq+ AGGACGATGCTATCACCTCTATCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_5e05.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAAACAGCCAATGGATCTGTTATG
U_HW-SSH1_13e10.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_16a07.b1.seq+ AGGACGATGCTATCACTCCCCGCCTGTTGGC-GGGAAAAACAGCCATTGGATCTTTTATG
U_HW-SSH1_3b12.b1.seq+ CCTGTTGCT-GGGGAAAACAGCCAATGGATCTGTTATG
U_HW-SSH1_13b11.b1.seq+ AGGACTATTCTATCAGTCTAGCCTGTTGCT-GGGGAAGACAGCCATTGGATTTTTATG
U_HW-SSH1_11d12.b1.seq+ AGGACAATGCTATCACATCTAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_7c01.b1.seq+ AGGACTAGGCTATCACTTCAAGCCTGTTGCT-GGGCAAGACAGCCAATGTTTCTGTTATG
U_HW-SSH1_14b04.b1.seq+ AGGACAATGCTATCACATCGAGCCTGTTGCT-GGGGAAAACAGCCAATGGATCTGTTATG
U_HW-SSH1_2g02.b1.seq+ ATGATTATGCTATCCCATCTAGCCTGTTGCT-GGGGAACG-AGCGAATGGATCTGTTATG
U_HW-SSH1_2g12.b1.seq+ AGGACGATGGTATCACATCTTTCCTGTGGCT-GATAGAGACAGCCGTTGGATCTGTTATG
U_HW-SSH1_4a06.b1.seq+ AGGACGATGCTATCACATCTAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_4b12.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_4c12.b1.seq+ TGGACAATCCTACCACATCGAGCCTGCAACT-GGGGA-GCTAGAAATTGCTTTTGTTATG
U_HW-SSH1_1d09.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_11f05.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAAACAGCCAATGGATCTGTTATG
U_HW-SSH1_11h10.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_1a07.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGAAAAACAGCCAATGGATCTGTTATG
U_HW-SSH1_2e08.b1.seq+ AGGACTATGCTATCACATCAATCCTGTTGCT-GGAGAAAACAGCCAATGGATCTGTTATG
U_HW-SSH1_8h05.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_14b05.b1.seq- AGGACGATGCTATCACATCGAGCCTGTTGTT-GGGGAAGACAGCGAGGGATTTGTTATG
U_HW-SSH1_12c08.b1.seq- AGGACGAGGTTTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCAGATTG
U_HW-SSH1_3e02.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_11a04.b1.seq+ AGGACGATGCTATCACTTCGAGCCTGTTGCT-GGGGAAGACAGCCAATGAATCTGTTATG
U_HW-SSH1_4h07.b1.seq+ AGGCCGATGCTATCTCATCCAGCCGGTTGAAAGGGAAAAACAGCCAATGTATCTGTTATG
U_HW-SSH1_9a04.b1.seq+ AGGACAATGCTATCACATCGAGCCTGTTGCT-GGGAAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_3c02.b1.seq+ AAGACGATGTTATCGCATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_8f07.b1.seq- AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_5h12.b1.seq- AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_10b03.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCGATGGATCTGTTATG
U_HW-SSH1_16f12.b1.seq- AGGACGATGTTATCACATCGAGCCCGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_1c04.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_1d12.b1.seq- AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_1b08.b1.seq- AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_1d02.b1.seq+ AGAACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAAACAGCCAATGGATCTGTTATG
U_HW-SSH1_8g08.b1.seq- AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_8f09.b1.seq- AGGACGATGCTATCACATCGAGCCTGTTGCT-GAGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_8g07.b1.seq- AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_8h02.b1.seq- AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGATATGTTATG
U_HW-SSH1_9a05.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_9b06.b1.seq+ AGGACGATGCTATCCCATCAAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_9b05.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_9d01.b1.seq+ AGGACGATGCTAGAACATCGAGCCTGTTGCT-GGGGAAAACAGCCAATGGATCTGTTTTG
U_HW-SSH1_13e09.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_1b05.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_10d07.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_10e02.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_10h02.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_1d01.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_1c01.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_3a05.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_3a06.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_9c05.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_12g11.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_6b08.b1.seq+ TCGAGTCTGTTGCT-GGGGAAGACAGCGAATGGATCTGTTATG
U_HW-SSH1_3e01.b1.seq+ ACATCGAGCC-GTTGCT-GGGGAAGACCGCCATTGGTTCTGTTCTG
U_HW-SSH1_15a04.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_3b11.b1.seq+ AGGACGATGCGGGCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_3e07.b1.seq+ AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_1b01.b1.seq+ AAGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_14a05.b1.seq+ AGGACAATGCTATCACATCGAGCCTGTTGCT-GGGGAAAACAGCCAATGGATCTGTTATG
consensus AGGACGATGCTATCACATCGAGCCTGTTGCT-GGGGAAGACAGCCAATGGATCTGTTATG
U_HW-SSH1_11e11.b1.seq+ TAGCTT-ATCCATT-AAACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_12h09.b1.seq+ TACCTT-ATCCATT-ACACCTATTTGAAGAGGGT-TCCGTTACTAACGTGTTTACTTCCA
U_HW-SSH1_14d09.b1.seq+ TAGCTT-ATCCATT-AAACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_11b02.b1.seq+ TTCTTT-ATCCATT-AGACCTATTTGAAAAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_14a06.b1.seq+ TATCTT-ATCCATT-ACACCTTTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCT
U_HW-SSH1_12d08.b1.seq+ TATCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_15b06.b1.seq+ TATCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_15b04.b1.seq+ TATCTT-TTCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_11g07.b1.seq+ TACCTT-ATCCATT-AAACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_11g12.b1.seq+ TATCTT-ATCCATT-AAACCTATTTGAAGAGGGT-TCCGTTACTATGATGTTTCCTTCCC
U_HW-SSH1_12d09.b1.seq+ TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_4f11.b1.seq+ TATCTT-ATCCATT-ACACCTATTTGAAAAGGGT-TCCGTTACTATGATGTTTCCTTCCC
U_HW-SSH1_1b03.b1.seq+ TATCTT-TTCCATT-AGACCTATTTGAAGAGGGT-CCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_1a03.b1.seq+ TATCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_3e10.b1.seq+ TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_4b11.b1.seq+ TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_11e12.b1.seq+ TAGTTT-ATCCATT-AAACAATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_4g07.b1.seq+ TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_7e11.b1.seq+ TACTTT-ATCCCTT-AGACCTGTTTGAAAAGGGT-TCCTTTACTAGCATGTTTACTTCCC
U_HW-SSH1_5h06.b1.seq+ TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_5h09.b1.seq+ TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCT
U_HW-SSH1_5e05.b1.seq+ TAGCTT-ATCCATT-AAACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_13e10.b1.seq+ TAGCTT-ATCCATT-AAACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_16a07.b1.seq+ TATCTT-ATCCATT-AAACCTATTTGAAGAGGGT-TCCTTTGCTAGTTTGTTTACTTCCA
U_HW-SSH1_3b12.b1.seq+ TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTCC
U_HW-SSH1_13b11.b1.seq+ TAGCTT-ATCCATCCAAACCTATTTGAAGAGGGT-TCCGTTACTAGCATGTTTCCTTCCA
U_HW-SSH1_11d12.b1.seq+ GACCTT-ATCCATT-AGACCTATTTGAAAAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_7c01.b1.seq+ GACCTT-ATCCATT-AGACCTATTTGAAAAGGGT-TCCTTTACTAACATGTTTACTTCCA
U_HW-SSH1_14b04.b1.seq+ TAGCTT-ATCCATT-ACACCTATTTGAAAAGGAT-TCCGTTACTAACATGCTTACTTCCA
U_HW-SSH1_2g02.b1.seq+ TAGCTT-ATCCATT-AGACCGATTTGAATAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_2g12.b1.seq+ TACCTT-ATCCATT-AAACCTATTTGAAGAGGGT-TCCGTTACTAGCATGTTTACTTCCA
U_HW-SSH1_4a06.b1.seq+ TACCTT-ATCCATT-AAACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_4b12.b1.seq+ TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_4c12.b1.seq+ TAGCTT-ATCCATT-ATACCTATTTGAAGAAGGT-TCCGCTACACTCATGTTTACTTCCG
U_HW-SSH1_1d09.b1.seq+ TATTTT-ATCCATT-AAACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_11f05.b1.seq+ TAGCTT-ATCCATT-AAACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_11h10.b1.seq+ TATCTT-ATCCATT-AAACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_1a07.b1.seq+ TAATTT-ATCCATT-AGACCTATTAGAAGAAGGT-TCCGTAACTAGCTTGTTTACTTCCA
U_HW-SSH1_2e08.b1.seq+ TAGCTT-ATCCATT-ACACCTATTTGAAGAGGGT-TCCGTTACTAACGTGTTTACTTCCT
U_HW-SSH1_8h05.b1.seq+ TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_14b05.b1.seq- TTGCTT-ATCCATT-AGACCTAGG-GAAGAGGGT-TCCGTTACTTACATGTTTACTTCCA
U_HW-SSH1_12c08.b1.seq- TTGCTT-ATCCATT-AAACCTATTTGGAAGAGGGT-TCCGTTACTGACATGTTTACTTCCG
U_HW-SSH1_3e02.b1.seq+ TACCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTCCTAACATGTTTACTTCCA
U_HW-SSH1_11a04.b1.seq+ TATTTT-ATCCATT-ACACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_4h07.b1.seq+ TCTTTT-ATCCCTT-AAACCTATTTAAATAGGGT-TCCGTTACTAGTTT-TTTCCTTCCA
U_HW-SSH1_9a04.b1.seq+ TACCTT-TTCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAAAATGTTTACTTCCT
U_HW-SSH1_3c02.b1.seq+ TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_8f07.b1.seq- TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_5h12.b1.seq- TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTATTAACATGTTTACTTCCA
U_HW-SSH1_10b03.b1.seq+ TAGCTT-ATCCTTT-ACACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_16f12.b1.seq- TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_1c04.b1.seq+ TAGTTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_1d12.b1.seq- TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_1b08.b1.seq- TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_1d02.b1.seq+ TAGCTT-ATCCATT-AAACCTATTTGAAAAGGGT-TCCGTTACTAACATGTTTACTTCCT
U_HW-SSH1_8g08.b1.seq- TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_8f09.b1.seq- TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_8g07.b1.seq- TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_8h02.b1.seq- TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_9a05.b1.seq+ TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_9b06.b1.seq+ TAGCTT-ATCCATA-ACACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCT
U_HW-SSH1_9b05.b1.seq+ TAGCTT-ATCCATT-AGACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTACTTCCA
U_HW-SSH1_9d01.b1.seq+ TACCTT-ATCCATT-ACACCTATTTGAAGAGGGT-TCCGTTACTAACATGTTTCCTTC





```
                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_12g04.b1.seq+ AGGACATCAAGAACCCGGGCTCCGTCAACCAGGACCCCATCTTCAAGAGCTACAGCCTCC
U_HW-SSH1_8h07.b1.seq+  AGGACATCAAGAACCCGGGCTCCGTCAACCAGGACCCCATCTTCAAGAGCTACAGCCTCC
U_HW-SSH1_12c09.b1.seq-                                                      AGCCTCC

consensus               AGGACATCAAGAACCCGGGCTCCGTCAACCAGGACCCCATCTTCAAGAGCTACAGCCTCC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_12g04.b1.seq+ CGCCCCACGAGTGCGGCTACCCCGGCAGCGTCTTCAACCCCCTCAACTTCGCCCCCACCC
U_HW-SSH1_8h07.b1.seq+  CGCCCCACGAGTGCGGCTACCCCGGCAGCGTCTTCAACCCCCTCAACTTCGCCCCCACCC
U_HW-SSH1_12c09.b1.seq- CGCCCCCCGAGTGCGGCTATCCCGGCAGCGTTTTCAACCCCCTCAACTTCGCCCCCACCC

consensus               CGCCCCACGAGTGCGGCTACCCCGGCAGCGTCTTCAACCCCCTCAACTTCGCCCCCACCC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_12g04.b1.seq+ TCGAGAACAAGGAGAAGGAGCTCGCCAACGGTAGACTGGCGATGCTGGCGTTCCTGGGGT
U_HW-SSH1_8h07.b1.seq+  TCGAGAACAAGGAGAAGGAGCTCGCCAACGGTAGACTGGCGATGCTGGCGTTCCTGGGGT
U_HW-SSH1_12c09.b1.seq- TCGAGAACAAGGAGAAGGAGCTCGCCAACGGGAGACTGGCGATGCTGGCCTTCCTGGGGT

consensus               TCGAGAACAAGGAGAAGGAGCTCGCCAACGGTAGACTGGCGATGCTGGCGTTCCTGGGGT

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_12g04.b1.seq+ TCCTGGTGCAGCACAACGTGACCGGCAAGGGCCCGTTCGAGAACCTGCAGCAGCACCTGG
U_HW-SSH1_8h07.b1.seq+  TCCTGGTGCAGCACAACGTGACCGGCAAGGGCCCGTTCGAGAACCTGCAGCAGCACCTGG
U_HW-SSH1_12c09.b1.seq- TCCTGGTGCAGCACAACGTGACCGGCAAGGGCCCGTTCGAGAACCTGCAGCAGCACCTGG

consensus               TCCTGGTGCAGCACAACGTGACCGGCAAGGGCCCGTTCGAGAACCTGCAGCAGCACCTGG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_12g04.b1.seq+ CCGACCCATGGCACACCACCATCATCCAGACCATCTCCGGCCAGTAAATCCGTCGATTTC
U_HW-SSH1_8h07.b1.seq+  CCGACCCATGGCACACCACCATCATCCAGACCATCTCCGGCCAGTAAATCCGTCGATTTC
U_HW-SSH1_12c09.b1.seq- CCGACCCATGGCACAACACCATCATCCAGACCATCTCCGGCCAATAAATCCGTTGATTTC

consensus               CCGACCCATGGCACACCACCATCATCCAGACCATCTCCGGCCAGTAAATCCGTCGATTTC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_12g04.b1.seq+ ACCGACCGGGGAGGTTTCAGGTGGTCTGAATTGTTATTTTGGGGT
U_HW-SSH1_8h07.b1.seq+  ACCGACCGGGGAGGTTTCAGGTGGTCTGAATTGTTATTTTGGGGTACCTGCCCGGGCGGC
U_HW-SSH1_12c09.b1.seq- ACCGACCGGGGAGGGTTCAGGTGGTTTGAATTGTTATTTTGGGGT

consensus               ACCGACCGGGGAGGTTTCAGGTGGTCTGAATTGTTATTTTGGGGTACCTGCCCGGGCGGC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_8h07.b1.seq+  CGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAGGTCGACCATATGGGAGAGCTCCC

consensus               CGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAGGTCGACCATATGGGAGAGCTCCC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_8h07.b1.seq+  AACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGTCACCTAAATAGCTTGGCGTAATC

consensus               AACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGTCACCTAAATAGCTTGGCGTAATC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_8h07.b1.seq+  ATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACATTTCCACACAACATACG

consensus               ATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACATTTCCACACAACATACG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_8h07.b1.seq+  AGCCGGGAAGCATAAAGTGTAAAGCCTGGGGGTGCCTAATGAGTGAGCTAACTCACATTA

consensus               AGCCGGGAAGCATAAAGTGTAAAGCCTGGGGGTGCCTAATGAGTGAGCTAACTCACATTA

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_8h07.b1.seq+  ATTGCGTTGCGCTCACTGCCCGCTTTCAGTCGGGAAAGCTTGTCGTGCCAGCTGCATTAA

consensus               ATTGCGTTGCGCTCACTGCCCGCTTTCAGTCGGGAAAGCTTGTCGTGCCAGCTGCATTAA

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_8h07.b1.seq+  TGAATCAGCAACGCCCGGGGGAAGAGGCGGTTTGCGTA

consensus               TGAATCAGCAACGCCCGGGGGAAGAGGCGGTTTGCGTA

****************** Contig 48 *******************
                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_13f10.b1.seq+ TTCGATTAGCGTGGTCGCGGCCGAGGTACAGGGGGAAACTCGACTGTGGAACCATACATA

consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACAGGGGGAAACTCGACTGTGGAACCATACATA

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_13f10.b1.seq+ GCAGCTCATAACAGGATACTGGCTCATGCATCAACTACCATACTTGACGGAGAAAAATAT
U_HW-SSH1_3g01.b1.seq+              ATGATACTGGCTCTTGCATCAACTACCAGACTTTACGGAGAAAAATAT
U_HW-SSH1_14g04.b1.seq+             ATGATACTGGCTCATGCATCAACTACCTTACTTTAAAGAAAAAAATAT

consensus               GCAGCTCATAACATGATACTGGCTCATGCATCAACTACCATACTTTACGGAGAAAAATAT

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_13f10.b1.seq+ CCAGCTGCCCAAAAGGGAGGTGTTGGCATAAATGTTTACTCTTCTTGGATTTATCCTATG
U_HW-SSH1_3g01.b1.seq+  CGAGCTGCCCAAAAGGGAGGTGTTGGCATAAATGTTTACTCTTCTTGGAGTTATCCTATG
U_HW-SSH1_14g04.b1.seq+ CGAACTGCCCTTTAGGGAGGTGTTGGCATAAATGTTTACTCTTCTTGGAGTTATCCTATG

consensus               CGAGCTGCCCAAAAGGGAGGTGTTGGCATAAATGTTTACTCTTCTTGGAGTTATCCTATG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_13f10.b1.seq+ ACGAACTCTGATGTGGATGTGGAAGCAACTCAAAGATACTTATACTTCGTGTTCGGAAGG
U_HW-SSH1_3g01.b1.seq+  ACGAACTCTGATGTGGATGTGGAAGCAGCTAAAAGATACTTAAACTTCGTGTTCGGATGG
U_HW-SSH1_14g04.b1.seq+ AGGAATTCTGATGTGGATGGGGAACCAGCTAAAAGATACTTGTACTTCGTGTTCTGATGG

consensus               ACGAACTCTGATGTGGATGTGGAAGCAGCTAAAAGATACTTATACTTCGTGTTCGGATGG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_13f10.b1.seq+ ATACTACAGCCCTTGGGGTCAGGAAATTACCCAGATGTGACGAGGAAAAATGTTGGGTCT
U_HW-SSH1_3g01.b1.seq+  ATACTAGAGCCCTTGGTGTCTGGAAATTACCC
U_HW-SSH1_14g04.b1.seq+ ATACTATAGCCCTTGGGGTCTGGAAATTACCCGGAGGGAAAGAGGAGGGGCCCCGGGTCT

consensus               ATACTACAGCCCTTGGGGTCTGGAAATTACCCAGAGGGAAAGAGGAAAAACCCCGGGTCT

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_13f10.b1.seq+ CGACTTCCATCGTTCACAAAGTCCCAGTCTCAAGTTGTCAAGGGAGCTGTTGATTTCATA
U_HW-SSH1_14g04.b1.seq+ CGACTTCTGTCAAAAA-ACCCCCCCCTCTCAAGTTGTCACGGGAGCTGTTGATTTCATA

consensus               CGACTTCCATCAAAAACAAACCCCCACTCTCAAGTTGTCAAGGGAGCTGTTGATTTCATA

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_13f10.b1.seq+ GGAATAAACCACTACTATTCCATGTATGTTAATGACCGTCCTTTAGACAAAGGCACTCGT
U_HW-SSH1_14g04.b1.seq+ GGAACAACCCACTACTATTCCATGTATTTAAATGACCCTCCTTTAGACAAAGGCACTCGT

consensus               GGAACAAACCACTACTATTCCATGTATGTAAATGACCCTCCTTTAGACAAAGGCACTCGT

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_13f10.b1.seq+ GACTATTCGGCAGACATGTCTCTTTACCAAAGAGCTTCTAAAACAATCCCAGGAAGTAGC
U_HW-SSH1_14g04.b1.seq+ GACTATTCGGCAGACGTGTCTCTTTACCGAAGAGCTTCTAAAGCCCTCCCAGGAGGCAGG

consensus               GACTATTCGGCAGACATGTCTCTTTACCAAAGAGCTTCTAAAACAATCCCAGGAAGCAGC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_13f10.b1.seq+ AAGAATGTCCCAGCATCTTCTCAAAGTGACCCGGAAGGATTCCAATATGTGCTGCAGTAC
U_HW-SSH1_14g04.b1.seq+ AAGAATGTCCCTCCCTCTTCTCAAAGTGACCCGGAAGGATTCCAATATGTGCTGCAGTAC

consensus               AAGAATGTCCCACCATCTTCTCAAAGTGACCCGGAAGGATTCCAATATGTGCTGCAGTAC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_13f10.b1.seq+ CTGCCCGGG
U_HW-SSH1_14g04.b1.seq+ CTGCCCGGGCGGCCGATTGAAATCGCTACCCAATTCGCGGCGAATTGCGTGTGCACCTTG

consensus               CTGCCCGGGCGGCCGATTGAAATCGCTACCCAATTCGCGGCGAATTGCGTGTGCACCTTG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14g04.b1.seq+ TGTTACAGCCGCAACGCTGTGGATGCATATGTTGACATGAATCTAGCACGCAGAGAGGAA

consensus               TGTTACAGCCGCAACGCTGTGGATGCATATGTTGACATGAATCTAGCACGCAGAGAGGAA

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14g04.b1.seq+ GAGGATCAATGCGTGGTGGAGCGCTGATCGTGTCTTCACATAATTGACGGCATACAGCTC

consensus               GAGGATCAATGCGTGGTGGAGCGCTGATCGTGTCTTCACATAATTGACGGCATACAGCTC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14g04.b1.seq+ GCACTACTTCGGAGCGAGAGGCATCAAGTGTAGAAGCGGGGGGGTGACTAGTGTCAGCCC

consensus               GCACTACTTCGGAGCGAGAGGCATCAAGTGTAGAAGCGGGGGGGTGACTAGTGTCAGCCC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14g04.b1.seq+ CTAGATCATTTTAATAGCGGTGGAATCGCACGGGTCGACTTCCAAGACGAGAAAAA

consensus               CTAGATCATTTTAATAGCGGTGGAATCGCACGGGTCGACTTCCAAGACGAGAAAAA

****************** Contig 49 *******************
                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14f06.b1.seq- GATCTTTTCATACGGTCGACCCTCAGGCGGGAACGAATTCACTTGTGATT--AGCGGAGT
U_HW-SSH1_1d10.b1.seq+                                                  TTCGAGCGGCCG
U_HW-SSH1_13c02.b1.seq+                                                 TTCGAGCGGCCG
U_HW-SSH1_5d08.b1.seq-                                                     TAGCGTGGT
U_HW-SSH1_14e06.b1.seq-                                                         TGGT
U_HW-SSH1_1d06.b1.seq+                                                     TAGCGTGGT
U_HW-SSH1_7c12.b1.seq+                                                     TAGCGTGGT
U_HW-SSH1_1a02.b1.seq+                                                  TTCGAGCGGCCG
U_HW-SSH1_11b06.b1.seq-                                                    TAGCGTGGT
U_HW-SSH1_11b07.b1.seq-                                                    TAGCGTGGT
U_HW-SSH1_4e10.b1.seq+                                                     TAGCGTGGT

consensus               GATCTTTTCATACGGTCGACCCTCAGGCGGGAACGAATTCACTTGTGATTCTAGCGTGGT

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14f06.b1.seq- TGGGTCCGAGGTACTTCAGGATCACCAACGGGCTTGAATTTGAGGACAAGGTCCACCCCG
U_HW-SSH1_1d10.b1.seq+  CCCGGGGGGGGGA-TACAGGATCACCAACGGACTGGAATTTGATGACAAGCCCCACCCAG
U_HW-SSH1_13c02.b1.seq+ CCCGGGC-AGGTACTACAGGATCACCAACGGACTGGAATTTGATGACAAGCTCCACCCAG
U_HW-SSH1_5d08.b1.seq-  CGCGGCCGAGGTACTACAGGATCACCAACGGGCTGGAATTTGACGACAAGCTCCACCCCG
U_HW-SSH1_14e06.b1.seq- CGCGGCCGAGGTACCCCAGGATCACCAACGGCCTGGAATTTGATGACAAGGTTCACCCCC
U_HW-SSH1_1d06.b1.seq+  CGCGGCCGAGGGACGACGGGATCACCAACGGACTGGAATTTGATGACAACCCCCACCCAG
U_HW-SSH1_7c12.b1.seq+  CGCGGCCGAGGTACTACAGGATCACCAACGGGCTGGAATTTGACGACAAGCTCCACCCCG
U_HW-SSH1_1a02.b1.seq+  CCCGGG-GAGGAAGTACAGGATCACCAACGGACTGGAATTTGATGACAAGCCCCACCCAG
U_HW-SSH1_11b06.b1.seq- CGCGGCCGAGGTATTACAGGATCACCAACGGACTGGAATTTGATGACAAGCTCCACCCAG
U_HW-SSH1_11b07.b1.seq- CGCGGCCGAGGTACTACAGGATCACCAACGGACTGGAATTTGATGACAAGCTCCACCCAG
U_HW-SSH1_4e10.b1.seq+  CGCGGCCGAGGTACTACCGGATCACCAACGGACTGGAATTTGATGACGAGCTCCACCCAG

consensus               CGCGGCCGAGGTACTACAGGATCACCAACGGACTGGAATTTGATGACAAGCTCCACCCAG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14f06.b1.seq- GGGGGGCAGTGGACCCGGTTGGCCTTACCACAGACCCCCCCCAGGCGGCGCTGGTCAATT
U_HW-SSH1_1d10.b1.seq+  GTGGCCCATTCGACCCGCTCGGCCTCGCCACCGACCCGGACCAGGCGGCGCTGCTCAAGG
U_HW-SSH1_13c02.b1.seq+ GTGGCCCATTCGACCCGCTCGGCCTCGCCACCGACCCGGACCAGGCGGCGCTGCTCAAGG
U_HW-SSH1_5d08.b1.seq-  GTGGGCCATTCGACCCGCTCGGCCTTACCACCGACCCCGACCAGGCGGCGCTGGTCAAGT
U_HW-SSH1_14e06.b1.seq- GTGGGCCATTGGACCCGTTTGGGCTTACCACAGACCCCCACCCAGGGGCGCTGGTTTTTT
U_HW-SSH1_1d06.b1.seq+  GGGGCCCATTCGACCCGCTCGGCCTCCCCACCGACCCGGACCAGGCGGCGCTGCTCAAGG
U_HW-SSH1_7c12.b1.seq+  GTGGCCCATTCGACCCGCTCGGCCTCGCCACCGACCCCGACCAGGCGGCGCTGCTCAAGG
U_HW-SSH1_1a02.b1.seq+  GTGGCCCATTCGACCCGCTCGGCCTCGCCACCGACCCGGACCAGGCGGCGCTGCTCAAGG
U_HW-SSH1_11b06.b1.seq- GTGGCCCATTCGACCCGCTCGGCCTCGCCACCGACCCGGACCAGGCGGCGCTGCTCAAGG
U_HW-SSH1_11b07.b1.seq- GTGGCCCATTCGACCCGCTCGGCCTCGCCACCGACCCGGGCCAGGGGGCGCTGCTCAAGG
U_HW-SSH1_4e10.b1.seq+  GTGGCCCATTCGACCCGCTCGGCCTCGCCACCGACCCGGACCAGGCGGCGCTGCTCAAGG

consensus               GTGGCCCATTCGACCCGCTCGGCCTCGCCACCGACCCGGACCAGGCGGCGCTGCTCAAGG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14f06.b1.seq- TGAAGGAGATCAAGAAGGGGGGGCGGGCCAAGTTTTCCATTG-GGGGTTCTTTATGCAGG
U_HW-SSH1_1d10.b1.seq+  TGAAGGAAATCAAGAACGGGCGGCTGGCCATGTTCTCCATGCTGGGGTTCTTCATCCAGG
U_HW-SSH1_13c02.b1.seq+ TGAAGGAGATCAAGAACGGGCGGCTGGCCATGTTCTCCATGCTGGGGTTCTTCATCCAGG
U_HW-SSH1_16e09.b1.seq+     GGAAATCAAAAACGGGCGGCTGCCCATGTACTCCATGCTGGGGTTCTTCATCCAGG
U_HW-SSH1_5d08.b1.seq-  TGAAGGAGATCAAGAACGGGCGGCCGGCCAAGTTCCTCATGG-GGGATTCTTCATTCATC
U_HW-SSH1_14e06.b1.seq- TTAAAGAGATCAAGAACGGGGGGCCGGCCACGTTTTCCATGG-GGGATTCTTAATTTCCT
U_HW-SSH1_1d06.b1.seq+  TGAAGGAGATCAAGAACGGGCGGCTGGCCATGTTCTCCATGCTGGGGTTCTTCATCCAGG
U_HW-SSH1_7c12.b1.seq+  TGAAGGAGATCAAGAACGGGCGGCTGGCCATGTTCTCCATGCTGGGCTTCTTCATCCAGG
U_HW-SSH1_1a02.b1.seq+  TGAAGGAAATCAAGAACGGGCGGCTGGCCATGTTCTCCATGCTGGGGTTCTTCATCCAGG
U_HW-SSH1_11b06.b1.seq- TGAAGGAGATCAAGAACGGGCGGCTGGCCATGTTCTCCATGCTGGGGTTCTTCATACAGG
U_HW-SSH1_11b07.b1.seq- TGAAGGAGATCAAGAACGGGCGGCTGGCCATGTTTTCCATGCTGGGGTTCTTCATTCAGG
U_HW-SSH1_4e10.b1.seq+  TGAAGGAGATCAAGAACGGGCGGCTGGCCATGTTCTCCATGCTGGGGTTCTTCATCCAGG

consensus               TGAAGGAGATCAAGAACGGGCGGCTGGCCATGTTCTCCATGCTGGGGTTCTTCATCCAGG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14f06.b1.seq- CGCACGTCACCGGAGAGGGAACTTTTGAGAACCTGTGAGCGCACGTCAGCGCCCCCTTCG
U_HW-SSH1_1d10.b1.seq+  CCTACGTCACCGGCGAGGGCCCCTTCGAGAACCTGTGCGCGCACCTCACCGACCCCTTCG
U_HW-SSH1_13c02.b1.seq+ CCTACGTCACCGGCGAGGGCCCCTTCGAGAACCTGTGCGCGCACCTCAGCGACCCCTTCG
U_HW-SSH1_16e09.b1.seq+ GCTACGTCACCGCCCAGGGCCCCTT-GCCAGGCTGAGCGCGCACCTCAGCGACCCCTTCG
U_HW-SSH1_5d08.b1.seq-  CGCACGTCACCGGCGAGGGCCCCTTCGAGAACCTGTGCGCGCACCTCAGCGACCCCTTCG
U_HW-SSH1_14e06.b1.seq- CCCACGTCACCGGCGAGGGACCCTTTGAGAACCTGTGCGCGCACATCAGCGACCCCTTCG
U_HW-SSH1_1d06.b1.seq+  CCTACGTCACCGGCGAGGGCCCCTTCGAGAACCTGTGCGCGCACCTCAGCGACCCCTTCG
U_HW-SSH1_7c12.b1.seq+  CCTACGTCACCGGCGAGGGCCCCTTCGAGAACCTGTGCGCGCACCTCAGCGACCCCTTCG
U_HW-SSH1_1a02.b1.seq+  CCTACGTCACCGGCGAGGGCCCCTTCAAGAACCTGTGCGCGCACCTCAGCGACCCCTTCG
U_HW-SSH1_11b06.b1.seq- CCTACGTCACCGGCGAGGGCCCCTTCGAGAACCTGTGCGCGCACCTCAGCGACCCCTTCG
U_HW-SSH1_11b07.b1.seq- CCTACGTCACCGGCGAGGGCCCCTTCGAGAACCTGTGCGCGCACCTCAGCGACCCCTTCG
U_HW-SSH1_4e10.b1.seq+  CCTACGTCACCGGCGAGGGCCCCTTCGAGAACCTGTGCCCGCACCTCAGCGACCCCTTCG

consensus               CCTACGTCACCGGCGAGGGCCCCTTCGAGAACCTGTGCGCGCACCTCAGCGACCCCTTCG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_14f06.b1.seq- GCAAAAAAATGCTCAC
U_HW-SSH1_1d10.b1.seq+  GCAACAACCTGCTCACCGTCATCTCCGGCGCCGCCGAGAGGGTGCCCAGCCTGTGAGCTG
U_HW-SSH1_13c02.b1.seq+ GCAACAACCTGCTCACCGTCATCTCCGGCGCCGCCGAGAGGGTGCCCAGCCTGTGAGCTG
U_HW-SSH1_16e09.b1.seq+ GGTACAACCTGCTCTCCGCCATCTCCGGCACCGCCGAGAGGGTGCTGAGCCTGGGAGCTG
U_HW-SSH1_5d08.b1.seq-  GCAACAAAATGCTCACCGTCATATCCGGAACCGCCGAGAGGGTGCCCAGCAAGTGAGGTG
U_HW-SSH1_14e06.b1.seq- ACAAAAAAATCCTCTCAGTCATATCCGGCTCCGCCGAGAGGGTGCCC
U_HW-SSH1_1d06.b1.seq+  GCAACAACCTGCTCACCGTCATCTCCGGCGCCGCCGAGAGGGTGCCCAGCCTGTGAGCTG
U_HW-SSH1_7c12.b1.seq+  GCAACAACCTGCTCACCGTCATCTCCGGCGCCGCCGAGAGGGTGCCCAGCCTGTGAGCTG
U_HW-SSH1_1a02.b1.seq+  GCAACAACCTGCTCACCGTCATCTCCGGCGCCGCCGAGAGGGTGCCCAGCCTGTGAGCTG
U_HW-SSH1_11b06.b1.seq- GCAACAACCTGCTCACCGTCATTTCCGGCGCCGTCGAGAGGGTGCCCAGCCTGCGAGCTG
U_HW-SSH1_11b07.b1.seq- GCAACAACCTGCTCACCGTCATTTCCGGCGCCGTTGAGAGGGTGCCCAGCCTGTGAGCTG
U_HW-SSH1_4e10.b1.seq+  GCAACAACCTGCTCACCGTCATCTCCGGCGCCGCCGAGAGGGTGCCCAGCCTGTGAGCTG

consensus               GCAACAACCTGCTCACCGTCATCTCCGGCGCCGCCGAGAGGGTGCCCAGCCTGTGAGCTG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_1d10.b1.seq+  GCCGTTAATTGCCCGTCCGCCGCCGTCGGCTGTTGATGATCAGCTGCATGCGCGCGATGC
U_HW-SSH1_13c02.b1.seq+ GCCGTTAATTGCCCGTCCGCCGCCGTCGGCTGTTGATGATCAGCTGCATGCGCGCGATGC
U_HW-SSH1_16e09.b1.seq+ GAGGT-AATTGCCCATCCGCCGCCGTCGGCTGT-GATGATCACCTGCATGCCCGCGATGC
U_HW-SSH1_5d08.b1.seq-  GCCGTTTATTGTCCGTCCCCCGCCGTCGGCAAA-GATGATCAGCTGCGTGCGCGCGATGC
U_HW-SSH1_1d06.b1.seq+  GCCGTTAATTGCCCGTCCGCCGCCGTCGGTTGTTGATGAACAGCTGCATGCGCGCGATGC
U_HW-SSH1_7c12.b1.seq+  GCCGTTTATTGCCCGTCCGCCGCCGTCGGTTGCTGATGATCAGCTGCGTGCGCGCGATGC
U_HW-SSH1_1a02.b1.seq+  GCCGTTAATTGCCCGTCCCCCGCCGTCGGCTGTTGATGATCAGCTGCATGCGCGCGATGC
U_HW-SSH1_11b06.b1.seq- GCCGTTAATTGCCCGTCCGCCGCCGTCGGCTGTTGATGATCAACTGCATGCGCGCGATGC
U_HW-SSH1_11b07.b1.seq- GCCGTTAATTGCCCGTCCGCCGCCGTCGGCTGTTGATGATCAACTGCATGCGCGCGATGC
U_HW-SSH1_4e10.b1.seq+  GCCGTTCATTGCCCGTCCGCCGCCGTCGGCTGTTGATGATCAGCTGCATGCGCGCAATGC

consensus               GCCGTTAATTGCCCGTCCGCCGCCGTCGGCTGTTGATGATCAGCTGCATGCGCGCGATGC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_1d10.b1.seq+  AGCATCATGTGCTGTGTGAATTTTACCGGGGAAAAGTATGAGAGTACCTCGGCCGCGACC
U_HW-SSH1_13c02.b1.seq+ AGCATCATGTGCTGTGTGAATTTTACCGGGGAAAAGTATGAGAGTACCTCGGCCGCGACC
U_HW-SSH1_16e09.b1.seq+ AGAATGGTGTGCTGTGTGCATTTTACCGGGGAAAAGTGAGAGAGTACCT
U_HW-SSH1_5d08.b1.seq-  ATCAGCATGTGTTGGGTGAATTTTTCCGGG-AAAAGTGTGAGAGTACC-CGTCCGGGGGG
U_HW-SSH1_1d06.b1.seq+  AGCATTATGTGCTGTGTGAATTTTACCGGGGAAAAATATAAGAGTCCCT-GCCCGGGCGG
U_HW-SSH1_7c12.b1.seq+  AGCAGCATGTGCTGTGTGAATTTTACCGGG-AAAAGTTTGAGAGTACCT-GCCCGGG
U_HW-SSH1_1a02.b1.seq+  AGCATCATGTGCTGTGTGAATTTTACCGGGGAAAAGTATGAGAGTACCTCGGCCGCGACC
U_HW-SSH1_11b06.b1.seq- AGCATCATGTGCTGTGTGAATTTTACCGGGGAAAAGTATGAGAGTACCT-GTCCGGGGGG
U_HW-SSH1_11b07.b1.seq- AGCATCATGTGCTGTGTGAATTTTACCGGGGAAAAGTATGAGAGTACA-CGTCCGGGGGG
U_HW-SSH1_4e10.b1.seq+  AACATCATGTGCTGTGTGAATTTTACCGGGGAAAAGTATGAGAGTACCT-GCCCGGGCGG

consensus               AGCATCATGTGCTGTGTGAATTTTACCGGGGAAAAGTATGAGAGTACCTCGCCCGGGAGG

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_1d10.b1.seq+  ACGCTA
U_HW-SSH1_13c02.b1.seq+ ACGCTA
U_HW-SSH1_5d08.b1.seq-  CCCCT
U_HW-SSH1_1d06.b1.seq+  CC
U_HW-SSH1_1a02.b1.seq+  ACGCTA
U_HW-SSH1_11b06.b1.seq- CCCCTGGAA
U_HW-SSH1_11b07.b1.seq- CCCCT
U_HW-SSH1_4e10.b1.seq+  CCTCGGAAACTCTGTTGAAATTTCACGGATGCCTGAGTCCCTGCCCGGTACCAGACCGGC

consensus               CCCCTAAAACTCTGTTGAAATTTCACGGATGCCTGAGTCCCTGCCCGGTACCAGACCGGC

                            .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_4e10.b1.seq+  CACGCCTTGTATGC

consensus               CACGCCTTGTATGC
```

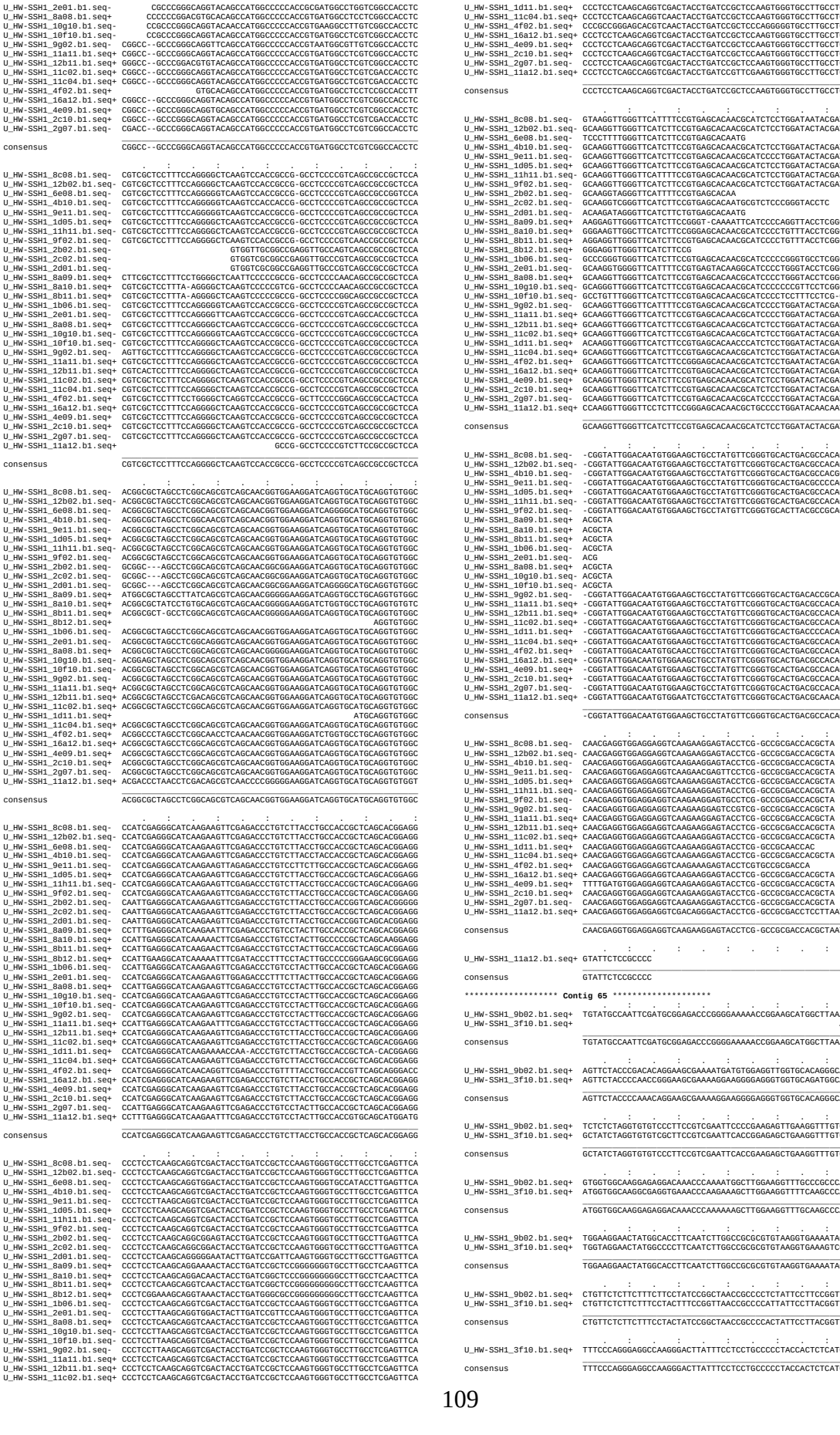
```
****************** Contig 50 *******************
                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16e05.b1.seq+ TTCGATTACCAGGGGCCCCCCGGACGTACACGTGTAAGTAAATGATTAAGAGATCTGTTT
U_HW-SSH1_16b05.b1.seq+                                             TGATTAAGAGAACTGTTT
U_HW-SSH1_16c05.b1.seq+       TACCATGGTCCCCCCCGACGTACACGTGTAAGTATGTGATAAAGAGCTCTGTTT
U_HW-SSH1_16b03.b1.seq+                                         TATGTGACAAAGAGATCTGTTT
U_HW-SSH1_16d04.b1.seq+           TCGTCCCCCCCGACGTACACGTGTAAGTAAGTTATAAAGAGAACTGTTT
U_HW-SSH1_16f04.b1.seq+                                                 AAGAGAACTGTTT
U_HW-SSH1_16g04.b1.seq+        CCAGCGGCCCCCCGGACGTGTACGTGTAAGTAAATGATTAAAAGATCTGTAT
U_HW-SSH1_16e04.b1.seq+            GTCCCCCCCGGGGTACACGTGTAAGTAAGTGATTAAGAGAACTGTTT
                        ____________________________________________________________
consensus               TTCGATTACCAGCGTCCCCCCCGACGTACACGTGTAAGTAAGTGATTAAGAGAACTGTTT

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16e05.b1.seq+ TTGCCTTTAAATTTTTGGGTTCCTATTGTAATGCATGACCACTTAGCGGGGGGATGCAGC
U_HW-SSH1_16b05.b1.seq+ TTGCCTTTCAATTATTGGGTTCCTATTGTAATGCATGACCATTTGGCGGGGGGATGCACC
U_HW-SSH1_16c05.b1.seq+ TTGCCTTTT--TTTGTGGGCTCCTATTGTC-TGCATGACCACCTGGCGGGGGGATGCAGC
U_HW-SSH1_16b03.b1.seq+ TTGCCATTT--TTTGTGGGCTCCTATTGTG-TGCGAGACCATTTGGCGGGGGGATGCACC
U_HW-SSH1_16d04.b1.seq+ TTGCCTTAAATTTTTTGTGCCCCTATTGTAATGCATGACCATTTGGGGGGAGGATGCAGC
U_HW-SSH1_16d05.b1.seq+                       CCTATTGTAATGCAAGACCATTTGGGGGGGGGATGCACC
U_HW-SSH1_16f04.b1.seq+ TTGCCTTAAAATTTTTGGGTCCCTATTGTAATGCATGACCACTTGGGGGGGGGATTCACC
U_HW-SSH1_16g04.b1.seq+ TTGCCTTAAAATTTTTGGGTTCCTATTGTAATGCATGACCATTTAGGGGGAGGATGCACC
U_HW-SSH1_16e04.b1.seq+ TTGCCTTTT-TTTTTTGTGTTCCTTTTGTAATGCATGACCATTTAGGGGGGGGATGCAGC
                        ____________________________________________________________
consensus               TTGCCTTTAAATTTTTGGGTTCCTATTGTAATGCATGACCATTTGGGGGGGGGATGCACC

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16e05.b1.seq+ GCAAATACAACTTTGTCTCATTATTGCCGCGAAAATGGCATACTTCTTCACTTTCTCCGT
U_HW-SSH1_16b05.b1.seq+ GCAAATACTACTTTGTCTCATTATTGCCGCGAAAATGGCCTACTTCTTCACATTCTCCGT
U_HW-SSH1_16c05.b1.seq+ GCAAATACAACTTTCTCTCATTATTGCCCCGAAAATGCCATACTTCTTCACTTTCTCCGT
U_HW-SSH1_16b03.b1.seq+ GCAAATTCAACTTTGTCTCATTAGCGCCCCGAAGATGCCATACTTCTTCACATTTTGCGT
U_HW-SSH1_16d04.b1.seq+ GCAAATACAACTTTCTCTCATTATTGCCGCGAAAATGCCATACTTCTTCACTTTCTCCGT
U_HW-SSH1_16d05.b1.seq+ GCAAATACTACTTTCTCTCATTTTTGCCCCCAAAATGCCCTACTTCTTCACTTTCTCCGG
U_HW-SSH1_16f04.b1.seq+ GCAAATACTACTGTGTCTCATTATTGCCGCGACAATGGCCTATTTCTTCACTTTTTCCGG
U_HW-SSH1_16g04.b1.seq+ GCAAATACTACTTTGGCTCATTATTGCCGCGAAAATGGCATACTTCTTCACTTTCTCCGT
U_HW-SSH1_16e04.b1.seq+ GCAAAAACAACTTTCTCTCATTAGCGCCGCGAAAATGGCATACTTCTTCACTTTCTCCGG
                        ____________________________________________________________
consensus               GCAAATACAACTTTGTCTCATTATTGCCGCGAAAATGGCATACTTCTTCACTTTCTCCGT

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16e05.b1.seq+ GTGGTGCATGCATTTATTGATAAACAAAAAAAACATGGTATGTTTTTCAGTATATTATAT
U_HW-SSH1_16b05.b1.seq+ GCAATGCATGCATTTATTGATAGACAAAAAAATCCTGGTATGTATTTCCGTGTATTATCT
U_HW-SSH1_16c05.b1.seq+ GTGTTGCTCCTATTTATTGAT-GACAAAACTCCCTTGGTATTTTTTTCAGTGTATTATAT
U_HW-SSH1_16b03.b1.seq+ GTGTT
U_HW-SSH1_16d04.b1.seq+ GTGTTGTTTGCATTTATTGATAGACAAAAATCTCTTGGTATGTTTTTCAGTATATTATAT
U_HW-SSH1_16d05.b1.seq+ GTTTTGCATGTATTTATTTATAAACAAAAATCTCTTGGTATTTATTTCCGTGTATTAGCT
U_HW-SSH1_16f04.b1.seq+ GTGTTGTTTGCAGTTTGTGATAAAAAAAAAAATCGTGGAATGTTTTTCCGTGTATTAGCT
U_HW-SSH1_16g04.b1.seq+ GTGGTGTTTGCATTTATTGAAAGACAAAAATCTCATGGTATGCTTTTCAGTGTATTATCT
U_HW-SSH1_16e04.b1.seq+ GTGATGTTTGCATTTATTGATAGACAAAAATATCTTGGTATGTTTTTCCGTGTATTATAT
                        ____________________________________________________________
consensus               GTGTTGCTTGCATTTATTGATAGACAAAAATATCTTGGTATGTTTTTCAGTGTATTATAT

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16e05.b1.seq+ AAAACTTTGCGTATGGGGGGGAGAGATAATATCCACTCCGGGACCCCGGGGGCGACCACA
U_HW-SSH1_16b05.b1.seq+ AAAAAATTGCGC-TGGGGGGGGGAGATCATATCCACTCGGGTACCTCGGCGGCGACCAC
U_HW-SSH1_16c05.b1.seq+ AACATTTTGCATGTGGGGGGGGGAGATTATCTCCTGTCCAGGACCTCGGGGGCGACCAC
U_HW-SSH1_16d04.b1.seq+ AAAACTTTGCATATGGGGGGGAGAGATCATCTCCTCTCCAGGACCTCGGGGGCGACCAC
U_HW-SSH1_16d05.b1.seq+ AAAGTTTTGCGTGTGGGGGGGGGAGATCATATCCTCTCCGGGCCCCCGGGGGCGACCA
U_HW-SSH1_16f04.b1.seq+ AAAACTTTGTTTGTGGGGGGGGGAGATCATCTCCGCTCCGGGACCTCGGGGGCGACC
U_HW-SSH1_16g04.b1.seq+ AAAACATTGCGTATGTGGGGGGGAGATTATATCCTCTCGAGGACCTCGGGGGCGACCACA
U_HW-SSH1_16e04.b1.seq+ AACGCTTTGCGTGTGGGGGGGGGAGATCATCTCCTCTCCGGGACCCCGGGGGCGACCACA
                        ____________________________________________________________
consensus               AAAACTTTGCGTGTGGGGGGGGGAGATCATATCCTCTCCGGGACCTCGGGGGCGACCACA

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16e05.b1.seq+ CTA
U_HW-SSH1_16g04.b1.seq+ CTA
U_HW-SSH1_16e04.b1.seq+ CTA
                        ____________________________________________________________
consensus               CTA

****************** Contig 51 *******************
                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f03.b1.seq+ TTCGATTACCGGGGTCCCCCCCGGCGTACACGGGCAAATATGTTACAAAGAGATCTGTTT
U_HW-SSH1_16e02.b1.seq+                                       TATGTAACAAAGAGATCTGTTT
                        ____________________________________________________________
consensus               TTCGATTACCGGGGTCCCCCCCGGCGTACACGGGCAAATATGTAACAAAGAGATCTGTTT

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f03.b1.seq+ GCGCCTTTTTTTGTGTTCCTCTTTTGTCTGATTGACCATATGGGGGGGGGATGCAGCGTA
U_HW-SSH1_16e02.b1.seq+ GTGCCATTTTTTGTGTTCCTCTTTTGTGTGCAAGACCATTTGGCGGGGGGATGCAGCGTA
                        ____________________________________________________________
consensus               GCGCCATTTTTTGTGTTCCTCTTTTGTCTGAAAGACCATATGGCGGGGGGATGCAGCGTA

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f03.b1.seq+ AAGCATCTGTCTCTCGATAGCGCCCCGAAGATGCCATGAATTTCCAGTTTCTGCGGGTGT
U_HW-SSH1_16e02.b1.seq+ AAGCATCTGTCTCTCATTGGCGCCCCGAAAATGCCAT
                        ____________________________________________________________
consensus               AAGCATCTGTCTCTCAATAGCGCCCCGAAAATGCCATGAATTTCCAGTTTCTGCGGGTGT

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f03.b1.seq+ TTTTACTTTTTATTTGATTACAAAAATCACTTGCTTCGTTTTTGAGTATATTATATAACA
                        ____________________________________________________________
consensus               TTTTACTTTTTATTTGATTACAAAAATCACTTGCTTCGTTTTTGAGTATATTATATAACA

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f03.b1.seq+ TTTTGCATGTGGGGGGGAAAGACTATCTTCACTTGAGCCGGCCGGGGGCAAAAATACTAA
                        ____________________________________________________________
consensus               TTTTGCATGTGGGGGGGAAAGACTATCTTCACTTGAGCCGGCCGGGGGCAAAAATACTAA

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f03.b1.seq+ TTTGAATTA
                        ____________________________________________________________
consensus               TTTGAATTA

****************** Contig 52 *******************
                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f08.b1.seq- GGCACGACGCATGACATATGATATCCATGTAGAAAGAGGAAGAAGGAGCGTCCCAAAGTC
                        ____________________________________________________________
consensus               GGCACGACGCATGACATATGATATCCATGTAGAAAGAGGAAGAAGGAGCGTCCCAAAGTC

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f08.b1.seq- TAGCGGCTCTCCCCATGAGTTGCGCGATGCAGTAACTCTAGTTGCAGGTCAGGTTTTGCC
U_HW-SSH1_13a01.b1.seq+                                                         TAGC
U_HW-SSH1_2f04.b1.seq+                                                          TAGC
U_HW-SSH1_16a09.b1.seq+                                                         TAGC
U_HW-SSH1_9e03.b1.seq+                                                          TAGC
                        ____________________________________________________________
consensus               TAGCGGCTCTCCCCATGAGTTGCGCGATGCAGTAACTCTAGTTGCAGGTCAGGTTTTAGC

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f08.b1.seq- GTCCGGCACGGCGCAGCTACTAGATGAAGAAAGATTTGCCTGGAGCCCACCTCCTTCACC
U_HW-SSH1_13a01.b1.seq+ GTG-GTCGCGGCCGAGGAACGAGATGAA-AAAGTTCTGCCTGGAGCCCACCTCCTTCACC
U_HW-SSH1_2f04.b1.seq+  GTG-GTCGCGGCCGAGGTACGAGATGAAGAA-GTTCTGCCTGGAGCCCACCTCCTTCACC
U_HW-SSH1_11e10.b1.seq+                                  TGCCTGGAGCCCACCTCCTTCACC
U_HW-SSH1_16a09.b1.seq+ GTG-GTCGCGGCCGAGGTACAAGATGAAGAA-TTTCTGCCTGGAGCCCACCTCCTTCACC
U_HW-SSH1_9e03.b1.seq+  GTG-GTCGCGGCCGAGGAACGAGATGAAGAA-GTTCTGCCTGGAGCCCACCTCCTTCACC
                        ____________________________________________________________
consensus               GTG-GTCGCGGCCGAGGTACGAGATGAAGAAAGTTCTGCCTGGAGCCCACCTCCTTCACC

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f08.b1.seq- GTCAAGGCCGAGGGCATCCAGAAGAATCGAGCCGCCGGCCTTCCAGAAGACCAAGCTCAT
U_HW-SSH1_13a01.b1.seq+ GGCAAGGGCGAGGGCATCCAGAAGAA-CGAGCCGCCGGCCTTCCAAAAAACCAAGCTCAT
U_HW-SSH1_2f04.b1.seq+  GTCAAGGCCGAGGGCATCCAGAAGAA-CGAGCCGCCGGCCTTCCAGAAAACCAAGCTCAT
U_HW-SSH1_11e10.b1.seq+ GTCAAGGCCGAGGGCATCCAAAAAAA-CGAGCCGCCGGCCTTCCAAAAAACCAAGCTCAT
U_HW-SSH1_16a09.b1.seq+ GTCAAGGCCGAGGGCATCCAGAAAAA-CGAGCCGCCGGCCTTCCAGAAAACCAAGCTCAT
U_HW-SSH1_9e03.b1.seq+  GGCAAGGCCGAGGGCATCCAGAAGAA-CGAGCCGCCGGCCTTCCAAAAAACCAAGCTCAT
                        ____________________________________________________________
consensus               GTCAAGGCCGAGGGCATCCAGAAGAA-CGAGCCGCCGGCCTTCCAGAAAACCAAGCTCAT

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f08.b1.seq- GACCCGTCTCACCTACACCCTCGACGAGATGGAAGGCCCGCTCGAGGTCGGCGCCGACGG
U_HW-SSH1_13a01.b1.seq+ GACCCGTCTCACCTACACCCTTGACGAGATGGAAGGCCCGCTCGAGGTCGGCGCCGACGG
U_HW-SSH1_2f04.b1.seq+  GACCCGTCTCACCTACACCCTTGACGAGATGGAAGGCCCGCTCGAGGTCGGCGCCGACGG
U_HW-SSH1_11e10.b1.seq+ GACCCGTCTCACCTACACCCTTGACGAGATGGAAGGCCCGCTCGAGGTCGGCGCCGACGG
U_HW-SSH1_16a09.b1.seq+ GACCCGTCTCACCTACACCCTTGACGAGATGGAAGGCCCGCTCGAGGTCGGCGCCGACGG
U_HW-SSH1_9e03.b1.seq+  GACCCGTCTCACCTACACCCTTGACGAGATGGAAGGCCCGCTCGAGGTCGGCGCCGACGG
U_HW-SSH1_16a11.b1.seq+                  CCCTTGACGAAAAGGAAGGCCCCCTCGAGGTCGGCGCCGACGG
                        ____________________________________________________________
consensus               GACCCGTCTCACCTACACCCTTGACGAGATGGAAGGCCCGCTCGAGGTCGGCGCCGACGG

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f08.b1.seq- CACCCTCAAGTTCGAGGAGAAGGACGGCATCGACTACGCGGCCGTCACCGTGCAGCTCCC
U_HW-SSH1_13a01.b1.seq+ CACCCTCAAGTTCGAGGAGAAGGACGGCATCGACTACGCGGCCGTCACCGTGCAGCTCCC
U_HW-SSH1_9e06.b1.seq+    CCCTCAAGTTCGAGGAGAAGGACGGCATCGACTACCCGGCCGTCACCGTGCAGCTCCC
U_HW-SSH1_3a10.b1.seq+   ACCCTCAAGTTCGAGGAGAAGGACGGCATCGACTACCCGGCCGTCACCGTGCATCTCCC
U_HW-SSH1_2f04.b1.seq+  CACCCTCAAGTTCGAGGAGAAGGACGGCATCGACTACGCGGCCGTCACCGTGCAGCTCCC
U_HW-SSH1_11e10.b1.seq+ CACCCTCAAGTTCGAGGAGAAGGACGGCATCGACTACGCGGCCGTCACCGTGCAGCTCCC
U_HW-SSH1_16a09.b1.seq+ CACCCTCAAGTTCGAGGAGAAGGACGGCATCGACTACGCGGCCGTCACCGTGCAGCTCCC
U_HW-SSH1_9e03.b1.seq+  CACCCTCAAGTTCGAGGAGAAGGACGGCATCGACTACGCGGCCGTCACCGTGCAGCTCCC
U_HW-SSH1_16a11.b1.seq+ CCCCCTCATTTTAGAGGATAAGGACGGCATCCTGTTTGCGGCGGTCCCCGTGCCTCTCCC
                        ____________________________________________________________
consensus               CACCCTCAAGTTCGAGGAGAAGGACGGCATCGACTACGCGGCCGTCACCGTGCAGCTCCC

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f08.b1.seq- CGGAGGCGAGCGCGTGCCCTTCCTATTCACCGTCAAGCAGCTCGTCGCCACCGGCAAGCC
U_HW-SSH1_13a01.b1.seq+ CGGAGGCGAGCGAGTGCCCTTCCTCTTCACCGCCAAGCAGCTCTTCGCTACCGGCAAGCC
U_HW-SSH1_9e06.b1.seq+  CGGAGGCGAGCGCGTGCCCTTCCTCTTCACCGTCAAGCAGCTCGTCGCCACCGGCAAGCC
U_HW-SSH1_3a10.b1.seq+  CGGAGGCGAGCGCGTGCCCTTCCTCTTCACCGTCAAGCAGCTCGTCGCCACCGGCAAGCC
U_HW-SSH1_2f04.b1.seq+  CGGAGGCGAGCGAGTGCCCTTCCTCTTCACCGCCAAGCAGCTCGTCGCTACCGGCAAGCC
U_HW-SSH1_11e10.b1.seq+ CGGAGGCGAGCGCGTGCCCTTCCTCTTCACCGTCAAGCAGCTCGTCGCCACCGGCAAGCC
U_HW-SSH1_16a09.b1.seq+ CGGAGGCGAGCGAGTGCCCTTCCTCTTCACCGCCAAGCAGCTCGTCGCTACCGGCAAGCC
U_HW-SSH1_9e03.b1.seq+  CGGAGGCGAGCGAGTGCCCTTCCTCTTCACCGCCAAGCAGCTCGTCGCTACCGGCAAGCC
U_HW-SSH1_16a11.b1.seq+ CGGAGGCGAACGAGTGGCCTTCCTCTTCACCCCCGCCCT-CTCGTCCCTACCCTCAAGCC
                        ____________________________________________________________
consensus               CGGAGGCGAGCGAGTGCCCTTCCTCTTCACCGCCAAGCAGCTCGTCGCCACCGGCAAGCC

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f08.b1.seq- CGAGAGCTTCAGCGGGCCCTTCCTCGTGCCCAGCTACAGGGGTTTGTTTTTCCTTGGCCC
U_HW-SSH1_13a01.b1.seq+ CGAGATCTTTAGCGGGCCCTTCCTCGTGCCCAGCTACTGGTGTTCCTCTTTCCTCGACCC
U_HW-SSH1_9e06.b1.seq+  CGAGAGCTTCAGCGGGCCCTTCCTCGTGCCCAGCTACAGGGGTTCGTCTTTCCTCGACCC
U_HW-SSH1_3a10.b1.seq+  CGAGAGCTTCAGCGGGCCCTTCCTCGTGCCCAGCTACAGGGGTTCGTCTTTCCTCGACCC
U_HW-SSH1_11d03.b1.seq-                                     TACAGGGGTTCGTCCCCCCGCGACCC
U_HW-SSH1_2f04.b1.seq+  CGAGAGCTTCAGCGGGCCCTTCCTCGTGCCCAGCTACAGGGGTTCGTCTTTCCTCGACCC
U_HW-SSH1_11e10.b1.seq+ CGAGAGCTTCAGCGGGCCCTTCCTCGTGCCCAGCTACAGGGGTTCGTCTTTCCTCGACCC
U_HW-SSH1_16a09.b1.seq+ CGAGAGCTTCAGCGGGCCCTTCCTCGTGCCCAGCTACAGGGGTTCGTCTTTCCTCGACCC
U_HW-SSH1_9e03.b1.seq+  CGAGAGCTTCAGCGGGCCCTTCCTCGTGCCCAGCTACAGGGGTTCGTCTTTCCTCGACCC
U_HW-SSH1_16a11.b1.seq+ CGAAAGCTTTT-CGGGCCCTTCCTCGTGCCCAGATACTGGGGTTCTTCTTTCCTCGACCG
                        ____________________________________________________________
consensus               CGAGAGCTTCAGCGGGCCCTTCCTCGTGCCCAGCTACAGGGGTTCGTCTTTCCTCGACCC

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f08.b1.seq- AAAGGGCCGTGGTGGCTCTACTGGCTACGACAACGCCGTGGCGCTACCCGCCGGAGGCAG
U_HW-SSH1_13a01.b1.seq+ AAATGGTCTTGGTGTCTCTTCTGGATACAACAA
U_HW-SSH1_9e06.b1.seq+  AAAGGGCCGTGGTGGCTCTACTGGCTACGACAACGCCGTGGCGCTACCCGCCGGAGGCAA
U_HW-SSH1_3a10.b1.seq+  AAAGGGCCGTGGTGGCTCTACTGGCTACAACAACGCCGTGGCGCTACCCGCCGGAGGCAG
U_HW-SSH1_11d03.b1.seq- AAAGGGCCGGGGAGGGTCTCCTGGCTGCGGCAACCCCGCGGGGCTTCCCGCAGGAGGCAG
U_HW-SSH1_2f04.b1.seq+  AAAGGGCCGTGGTGGCTCTACTGGCTACGACAACGCCGTGGCGCTACCCGCCGGAGGCAG
U_HW-SSH1_11e10.b1.seq+ AAAGGGCCGTGGTGGCTCTACTGGCTACAACAACGCCGTGGCGCTACCCGCCGGAGGCAA
U_HW-SSH1_16a09.b1.seq+ AAAGGGCCGTGGTGGCTCTACTGGCTACAACAACGCCGTGGCGCTACCCGCCGGAGGCAG
U_HW-SSH1_9e03.b1.seq+  AAAGGGCCGTGGTGGCTCTACTGGCTACAACAACGCCGTGGCGCTACCCGCCGGAGGCAG
U_HW-SSH1_16a11.b1.seq+ AAAGGGACGCGGGGGCTCTACTGGCTCCC-CTGGGCCGTGGCACTACCCGGGGGAATCAG
U_HW-SSH1_7e05.b1.seq+                                                    CCGGAGGCAG
                        ____________________________________________________________
consensus               AAAGGGCCGTGGTGGCTCTACTGGCTACAACAACGCCGTGGCGCTACCCGCCGGAGGCAG

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f08.b1.seq- AGGAGACGAGGAGGAGTTGGCCAAGGAGAACGTGAAGAACGCGTCCTCCTCCACGGGCAA
U_HW-SSH1_9e06.b1.seq+  AGGAAACGAGGAGGAGTTGGCCAAGGAGAACGTGAAGAACGCATCCTCCTCCACGGGCAA
U_HW-SSH1_3a10.b1.seq+  AGGAGACGAGGAGGAGTTGGCCAAGGAGAACGTGAAGAACGCGTCCTCCTCCACGGGCAA
U_HW-SSH1_11d03.b1.seq- AGGAGACGCAGAGGAGTTGGCCAAGGAGAAAGCGAAGAACGCGTCCTCATACACGGGCAA
U_HW-SSH1_2f04.b1.seq+  AGGAGACGAGGAGGAGTTGGCTAAGGAGAACGTGAAGAACGCGTCCTCGTCCACGGGCAA
U_HW-SSH1_11e10.b1.seq+ AGGAGACAAGGAGGAGTTGGCCAAGGAGAACGTGAAGAACGCGTCCTCCTCCACGGGCAA
U_HW-SSH1_16a09.b1.seq+ AGGAGACGAGGAGGAGTTGGCTAAGGAGAACGTGAAGAACGCGTCCTCGTCCACGGGCAA
U_HW-SSH1_9e03.b1.seq+  AGGAGACGAGGAGGAGTTGGCTAAGGAGAACGTGAAGAACGCGTCCTCGTCCACGGGCAA
U_HW-SSH1_16a11.b1.seq+ ACGATACGAGGAGGAGTTGGGTATGTACATGGTGAGGAACGCGTCCTCATCCACGGGCAA
U_HW-SSH1_7e05.b1.seq+  AGGATACGAGGAGGAGTTGGCTAAGGTTAACGTGAAAAACACGGCCTCCTCCAAATTCAA
                        ____________________________________________________________
consensus               AGGAGACGAGGAGGAGTTGGCCAAGGAGAACGTGAAGAACGCGTCCTCCTCCACGGGCAA

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f08.b1.seq- CATCACGCTCAGCGTCACCAA-GAGCAAGCCGGAGACCGGCGAGGTGATCGGCGTCTTCG
U_HW-SSH1_9e06.b1.seq+  CATCCCGCTCAGCGTCACCAA-GAGCAAGCCGGAGACCGGCGAGGTGATCGGCGTCTTCG
U_HW-SSH1_3a10.b1.seq+  CATCACGCTCAGCGTCACCAA-GAGCAAGCCGGAGACCGGCGAGGTGATCGGCGTCTTCG
U_HW-SSH1_11d03.b1.seq- CATCACCCTCAGCATAAACAA-GAGCAAGCCGGAGACCGTCGATGTTATGGGCGTCTTTG
U_HW-SSH1_2f04.b1.seq+  CATCACGCTCAGCGTGACCAA-GAGCAAGCCGGAGACCGGCGAGGTGATCGGTGTCTTCG
U_HW-SSH1_11e10.b1.seq+ CATCACGCTCAGCGTCACCAA-GAGCAAGCCGGAGACCGGCGAGGTGATCGGCGTCTTCG
U_HW-SSH1_16a09.b1.seq+ CATCACGCTCAGCGTGACCAAAGAGCAAGCCGGAGACCGGCGAGGTGATCGGTGTCTTCG
U_HW-SSH1_9e03.b1.seq+  CATCACGCTCAGCGTGACCAA-GAGCAAGCCGGAGACCGGCGAGGTGATCGGTGTCTTCG
U_HW-SSH1_16a11.b1.seq+ CATCACGCTCAGCGTGACCAA-AAGCAAGCCGGAGACCGGCGAGGTGATCGGTGTCTTCG
U_HW-SSH1_7e05.b1.seq+  CATTTCGCTCAGCGTGACCAA-AAGCAAGCCGGAAACCGGCGAGGTGATCGGTGTCTTCA
                        ____________________________________________________________
consensus               CATCACGCTCAGCGTCACCAA-GAGCAAGCCGGAGACCGGCGAGGTGATCGGCGTCTTCG

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f08.b1.seq- AGAGCGTGCAGCCGTCAGACACCGACCTCGGCGCCAAGGCGCCCAAGGATGTCAAGATCC
U_HW-SSH1_9e06.b1.seq+  AGAGCGTGCAGCCGTCAAACACCGACCTCGGCGCCAAGGCGCCCAAGGATGTCAAGATCC
U_HW-SSH1_3a10.b1.seq+  AGAGCGTGCAGCCGTCAGACACCGACCTCGGCGCCAAGGCGCCCAAGGATGTCAAGATCC
U_HW-SSH1_11d03.b1.seq- AGAGCGCGCAGCCGTCAGACACCGACCTTGGCGCCAAGGCGCCCAAGGATGTCAAGATAC
U_HW-SSH1_2f04.b1.seq+  AGAGCGTGCAGCCGTCAGACACCGACCTCGGCGCCAAGGCGCCCAAGGATGTCAAGATCC
U_HW-SSH1_11e10.b1.seq+ AGAGCGTGCAGCCGTCAGACACCGACCTCGGCGCCAAGGCGCCCAAGGATGTCAAGATCC
U_HW-SSH1_16a09.b1.seq+ AGAGCGTGCAGCCGTCAGACACCGACCTCGGCGCCAAGGCGCCCAAGGATGTCAAGATCC
U_HW-SSH1_9e03.b1.seq+  AGAGCGTGCAGCCGTCAAACACCGACCTCGGCGCCAAGGCGCCCAAGGATGTCAAGATCC
U_HW-SSH1_16a11.b1.seq+ AGAGCGTGCAGCCGTCAGACACCGACCTCGGCGCCAAGGCGCTCAAGGATGTCAAGATCT
U_HW-SSH1_7e05.b1.seq+  AAAT-GTCCAGCCCCCACCCCCCGACCTCCTCGCCAGGGCGCCTAAAGATGTCAAGATCC
                        ____________________________________________________________
consensus               AGAGCGTGCAGCCGTCAGACACCGACCTCGGCGCCAAGGCGCCCAAGGATGTCAAGATCC

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16f08.b1.seq- AGGG-TGTGGGGTACCTCGGCCG-CGACCACGCTA
U_HW-SSH1_9e06.b1.seq+  AGGG-TGTGTGGTACCTGCCCGGGCGGCC
U_HW-SSH1_3a10.b1.seq+  AGGG-TGTGTGGTACCTGCCCGGGCGGCC
U_HW-SSH1_11d03.b1.seq- AGGG-TGT
U_HW-SSH1_2f04.b1.seq+  AGGG-TGTGTGGTACCT
U_HW-SSH1_11e10.b1.seq+ AGGG-TGTGTGGTACCT
U_HW-SSH1_16a09.b1.seq+ AGGGGTGTGTGGTACCTG
U_HW-SSH1_9e03.b1.seq+  AGGG-TGTGTGGTACCTGCCCGGGCGG
U_HW-SSH1_16a11.b1.seq+ GGGG-TGTGTGGTACCTGCCC
U_HW-SSH1_7e05.b1.seq+  GGGG--GGGAGGAGCGGCCCCGGCCGACCTCTATACTCGCTGGAAAACACCCGAACGAGT
                        ____________________________________________________________
consensus               AGGG-TGTGTGGTACCTGCCCGGGCGACCACGATACTCGCTGGAAAACACCCGAACGAGT

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7e05.b1.seq+  GGGGATCAACCTGAGCGCAGACCCCGCCCGCTTTAATAAATATTTTTGTTTCTCACCCTT
                        ____________________________________________________________
consensus               GGGGATCAACCTGAGCGCAGACCCCGCCCGCTTTAATAAATATTTTTGTTTCTCACCCTT

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7e05.b1.seq+  CCGCCAAAAACTTAATGCAACCATCCCGGCCGATAACCCGCACACACTTATATTTTCCGC
                        ____________________________________________________________
consensus               CCGCCAAAAACTTAATGCAACCATCCCGGCCGATAACCCGCACACACTTATATTTTCCGC

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7e05.b1.seq+  CCCCAACTCAATGAAAAACTGAAGCCTAAGAAACGGTGGGAAAACTTATGACACTAATAA
                        ____________________________________________________________
consensus               CCCCAACTCAATGAAAAACTGAAGCCTAAGAAACGGTGGGAAAACTTATGACACTAATAA

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_7e05.b1.seq+  TCCCCATAAATTTCTC
                        ____________________________________________________________
consensus               TCCCCATAAATTTCTC

****************** Contig 53 *******************
                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_16h08.b1.seq+ TTCGATTTCCAGCGGCCGCCCGGGCATGTACTTATAATATTATGTGCATGTGCATATACA
U_HW-SSH1_2b01.b1.seq+        TTCGAGCGGCCGCCCGGGCAGGTACTTATAATATTATGTGCATGTGCATATACA
U_HW-SSH1_2c07.b1.seq+        TTCGAGCGGCCGCCCGGGCAGGTACTTATAATATTATGTGCATGTGCATATACA
U_HW-SSH1_15c08.b1.seq+       TTCGAGGGGCCGCCCCGGCAGGAACTTATAATATTATGTGCATGTGCATATACA
U_HW-SSH1_16g08.b1.seq+                               GTACTTATAATATTATGTGCATGTGCTTATACG
U_HW-SSH1_9d05.b1.seq+        TTCGAGGGGCCGCCCGGCCAGGCATTGATAATATTATGTGCATGTGCATATACA
U_HW-SSH1_1e09.b1.seq+         TCGAGCGGCCGCCCGGGCAGGAACTTATAATATTATGTGCATGTGCATATACA
U_HW-SSH1_2a07.b1.seq+         TCGAGCGGCCGCCCGGGCAGGTACTTATAATATTATGTGCATGTGCATATACA
U_HW-SSH1_2b07.b1.seq+         TCGAGCGGCCGCCCGGGCAGGTACTTATAATATTATGTGCATGTGCATATACA
                        ____________________________________________________________
consensus               TTCGATTTCGAGCGGCCGCCCGGGCAGGTACTTATAATATTATGTGCATGTGCATATACA
```

```
U_HW-SSH1_16h08.b1.seq+ TAGCCATCGGTAGCATTCACATACGAGCATGCTTTCTCAAGTCATGTCGGGAACATGGAC
U_HW-SSH1_2b01.b1.seq+  TAGCCATCGGTAGCATTCACATACGAGCATGCTTTCTCAAGTCATGTCGGGAACATGGAC
U_HW-SSH1_2c07.b1.seq+  TAGCCATCGGTAGCATTCACATACGAGCATGCTTTCTCGAGTCATGTCGGGAACATGGAC
U_HW-SSH1_15c08.b1.seq+ TAGCCACCGGTAGCATTCACATACTAGCATGCTTTCTCGAGTCATGTCGGGAACATGGAC
U_HW-SSH1_16g08.b1.seq+ -ACTTATCGGTAGCATTCACATACGACCATGCTTTCTCAAGTCATGTCGGGAACATGGAC
U_HW-SSH1_9d05.b1.seq+  TAGCCCCCGGTAGCATTCACATACGAGCATGCTTTCTCGAGTCATGTCGGGAACATGGAC
U_HW-SSH1_1e09.b1.seq+  TAGCCCCCGGGAGCATTCACATACGATCATGCTTTCTCGAGTCATGTCGGGAACATGGAC
U_HW-SSH1_2a07.b1.seq+  TAGCCATCGGTAGCATTCACATACGAGCATGCTTTCTCGAGTCATGTCGGGAACATGGAC
U_HW-SSH1_2b07.b1.seq+  TAGCCATCGGTAGCATTCACATACGAGCATGCTTTCTCGAGTCATGTCGGGAACATGGAC
                        ____________________________________________________________
consensus               TAGCCATCGGTAGCATTCACATACGAGCATGCTTTCTCGAGTCATGTCGGGAACATGGAC

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_16h08.b1.seq+ ATACACATATTCTTATCTTACGAACAAACAAAAAAGATAAATGGAAAAGGAAAACCCAAA
U_HW-SSH1_2b01.b1.seq+  ATACACATATTCTTATCTTAGGAACAAACAAGAAAGGTAAATGGAAAAGGAAAACCCAAG
U_HW-SSH1_2c07.b1.seq+  ATACACATATTCTTATCTTAGGAACAAACAAGAAAGATAAATGGAAAAGGAAAACCCAAA
U_HW-SSH1_15c08.b1.seq+ ATACACATATTCTTATCTTAGGAACAAACAAGAAAGATAAATGGAAAAGGAAAACCCAAA
U_HW-SSH1_2e03.b1.seq+                                          ATAAGTGGAAAAGGAAACACCACA
U_HW-SSH1_16g08.b1.seq+ TTGCACATATTCTTATCTTACGAACAAACAACAAAGATAAATGGAAAAGGAAAACCCAAA
U_HW-SSH1_9d05.b1.seq+  ATACACATATTCTTATCTTAGGAACAAACAAGAAAGGTAAATGGAAAAGGAAAACCCAAG
U_HW-SSH1_1e09.b1.seq+  ATACACATATTCTTATCTTAGGAACAAACAAGAAAGATAAATGGAAAAGGAAAACCCAAA
U_HW-SSH1_2a07.b1.seq+  ATACACATATTCTTATCTTAGGAACAAACAAGAAAGATAAATGGAAAAGGAAAACCCAAA
U_HW-SSH1_2b07.b1.seq+  ATACACATATTCTTATCTTAGGAACAAACAAGAAAGATAAATGGAAAAGGAAAACCCAAA
U_HW-SSH1_11a09.b1.seq-                  TTTTAGGAACAAACAAGAAAGATAAATGGAAAAGGAAAACCCAAA
U_HW-SSH1_14b02.b1.seq-                                                 AAATGGAGAAAGAAATCCCAAA
                        ____________________________________________________________
consensus               ATACACATATTCTTATCTTAGGAACAAACAAGAAAGATAAATGGAAAAGGAAAACCCAAA

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_16h08.b1.seq+ GCAATGTCAAAGTTGACAAAACCGCAATGGCACTTTATATGTGGCCCGTGGTGAGTGAGC
U_HW-SSH1_2b01.b1.seq+  GCAATGTCAGAGTTGACAAAACCGCAATGGCACTTTATATGTGGCCCGTGGTGAGTGAGC
U_HW-SSH1_2c07.b1.seq+  GCAATGTCAGAGTTGACAAAACCGCAATGGCACTTTATATGTGGCCCGTGGTGAGTGAGC
U_HW-SSH1_15c08.b1.seq+ GCAATGTCAGAGTTGACAAAACCGCAATGGCACTTTATATGTGGCCCGTGGTGAGTGAGC
U_HW-SSH1_2e03.b1.seq+  CCAATGTCACACTTGACAAACCCGCAATGGCACTTTTTATGTGGCCCGTGGTGAGTGAGC
U_HW-SSH1_16g08.b1.seq+ GCAATGATTAAGTTGACCAACCCGCAATGTCACTTTTTATGTGGCCCGTGGTGAGTGATT
U_HW-SSH1_9d05.b1.seq+  GCAATGTCATAGTTGACAAAACCGCAATGGCACTTTATATGTGGCCCGTGGTGAGTGAGC
U_HW-SSH1_1e09.b1.seq+  GCAATGTCAGAGTTGACAAAACCGCAATGGCACTTTATATGTGGCCCGTGGTGAGTGAGC
U_HW-SSH1_2a07.b1.seq+  GCAATGTCAGAGTTGACAAAACCGCAATGGCACTTTATATGTGGCCCGTGGTGAGTGAGC
U_HW-SSH1_2b07.b1.seq+  GCAATGTCAGAGTTGACAAAACCGCAATGGCACTTTATATGTGGCCCGTGGTGAGTGAGC
U_HW-SSH1_11a09.b1.seq- GCAATGTCAGAGTTGACAAAACCGCAATGGCACTTTATATGTGGCCTGTGGTGAGTGAGC
U_HW-SSH1_14b02.b1.seq- GCAATGTCAGAGTTGACAAATCCGCAATGGCGCTTTATATGTGGCCCTTGGTGAGTGAGC
                        ____________________________________________________________
consensus               GCAATGTCAGAGTTGACAAAACCGCAATGGCACTTTATATGTGGCCCGTGGTGAGTGAGC

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_16h08.b1.seq+ TGTTTAGGCCTTGCCGGACTCCTCGCAGCCCGGTGGCTTGAAGGCAATAAAGCTGACACA
U_HW-SSH1_2b01.b1.seq+  TGTTTAGGCCTTGCCGGACTCCTCGCAGCCCGGTGGCTTGAAGGCAATGAAGCTGACGCA
U_HW-SSH1_2c07.b1.seq+  TGTTTAGGCCTTGCCGGACTCCTCGCAGCCCGGTGGCTTGAAGGCGATGAAGCTGACGCA
U_HW-SSH1_15c08.b1.seq+ TGTTTAGGCCTTGCCGGACTCCTCGCAGCCCGGTGGCTTGAAGGCGATGAAGCTGACGCA
U_HW-SSH1_2e03.b1.seq+  TGTTTAGGCCTTGCCGGACTCCTCCCATCCCTTTGGTTTGAAGGCAATGAACCTGACGCA
U_HW-SSH1_16g08.b1.seq+ TGTTTAGGCCTTGCCGGACTCCTCCCATCCCGGTGGCTTGAAGGCAATAAAGCTAACACA
U_HW-SSH1_9d05.b1.seq+  TGTTTAGGCCTTGCCGGACTCCTCGCATCCCGGTGGTTTGAAGGCGATGAACCTGACGCA
U_HW-SSH1_1e09.b1.seq+  TGTTTAGGCCTTGCCGGACTCCTCGCAGCCCGGTGGCTTGAAGGCGATGAAGCTGACGCA
U_HW-SSH1_2a07.b1.seq+  TGTTTAGGCCTTGCCGGACTCCTCGCAGCCCGGTGGCTTGAAGGCGATGAAGCTGACGCA
U_HW-SSH1_2b07.b1.seq+  TGTTTAGGCCTTGCCGGACTCCTCGCAGCCCGGTGGCTTGAAGGCGATGAAGCTGACGCA
U_HW-SSH1_11a09.b1.seq- TGTTTAGGCCTTGCCGGACTCCTCGCAGCCCGGTGGCTTGAAGGCGATGAAGCTGACGCA
U_HW-SSH1_12a06.b1.seq-   TTTAGGCCTTGCCGGACTCCTTGCAGCCCGGTGGCTTGAAGGCAAAGAAGCCGATGCA
U_HW-SSH1_14b02.b1.seq- TTTTAGGCCTTGCCGGACTCCTAGCAACCTCGTGGCTTGAAGACGATGAAGCTGACCCA
                        ____________________________________________________________
consensus               TGTTTAGGCCTTGCCGGACTCCTCGCAGCCCGGTGGCTTGAAGGCGATGAAGCTGACGCA

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_16h08.b1.seq+ CTGCACCTGGCGCATGTTGTCAAATCCGATGATGCGGACATACGCGTCAGGGTACCTCGG
U_HW-SSH1_2b01.b1.seq+  CTGCACCTGGCGCATGTTGTCGAATCCGATGATGCGGACATACGCGTCAGGGTACCTCGG
U_HW-SSH1_2c07.b1.seq+  CTGCACCTGGCGCATGTTGTCGAATCCGATGATGCGGACATACGCGTCAGGGTACCTCGG
U_HW-SSH1_15c08.b1.seq+ CTGCACCTGGCGCATGTTGTCGAATCCGATGATGCGGACATACGCGTCAGGGTACCTCGG
U_HW-SSH1_2e03.b1.seq+  CTGCACCTGGCGCATGTTGTCGAATGGGATGATGCGGACATACGCGTCTTGGTACCTCGG
U_HW-SSH1_16g08.b1.seq+ CTGGACCTGGTTCATGTTGTCAAATCCGATGAGGTTTACATACTCGCCAGGGCACCTCGG
U_HW-SSH1_9d05.b1.seq+  CTGCACCTGGGGAATGTTGTCGAATCCGATGATGCGGACATACGCGTCAGGGTCCCTCGG
U_HW-SSH1_1e09.b1.seq+  CTGCACCTGGCGCATGTTGTCGAATCCGATGATGCGGACATACGCGTCAGGGTACCTCGG
U_HW-SSH1_2a07.b1.seq+  CTGCACCTGGCGCATGTTGTCGAATCCGATGATGCGGACATACGCGTCAGGGTACCTCGG
U_HW-SSH1_2b07.b1.seq+  CTGCACCTGGCGCATGTTGTCGAATCCGATGATGCGGACATACGCGTCAGGGTACCTCGG
U_HW-SSH1_11a09.b1.seq- CTGCACCTGGCGCATGTTGTTGAATCCGATGATGCGGACATACGCGTCAGGGTACCTCGG
U_HW-SSH1_12a06.b1.seq- AAACACCTGGCGCATGTTGTTGAATCCGATGATGCGG----------GGGTACCTCGG
U_HW-SSH1_14b02.b1.seq- CCGCCCCTGTCGCATGTTGTTGAATCCGAT
                        ____________________________________________________________
consensus               CTGCACCTGGCGCATGTTGTCGAATCCGATGATGCGGACATACGCGTCAGGGTACCTCGG

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_16h08.b1.seq+ CCGCGACCACGCTA
U_HW-SSH1_2b01.b1.seq+  CCGCGACCACGCTA
U_HW-SSH1_2c07.b1.seq+  CCGCGACCACGCTA
U_HW-SSH1_15c08.b1.seq+ CCGCGACCACGCTA
U_HW-SSH1_2e03.b1.seq+  CCGCGACCACGCTA
U_HW-SSH1_16g08.b1.seq+ CCGCCACCACGCTA
U_HW-SSH1_9d05.b1.seq+  CCGCGACCAC
U_HW-SSH1_1e09.b1.seq+  CCGCGACCACGCTA
U_HW-SSH1_2a07.b1.seq+  CCGCGACCACGCTA
U_HW-SSH1_2b07.b1.seq+  CCGCGACCACGCTA
U_HW-SSH1_11a09.b1.seq- CCGCGACCACGCTA
U_HW-SSH1_12a06.b1.seq- CCGCGACCACGCTA
                        ____________________________________________________________
consensus               CCGCGACCACGCTA

****************** Contig 54 ******************
                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2b03.b1.seq+  TTCATTTCGAGCGGCCGCCCGGGCAGGTACATTCATACTATTTCAACAGGGGCACGACGG
U_HW-SSH1_2a01.b1.seq+       TTCGAGGGGCCGCCCGGGCGGGTACATTCATACGAGTTCAACAGGGGCACGACGG
U_HW-SSH1_2c03.b1.seq+       TTCGAGCGGCCGCCCGGGCAGGTACATTCATACGAGTTCAACAGGGGCACGACGG
                        ____________________________________________________________
consensus               TTCATTTCGAGCGGCCGCCCGGGCAGGTACATTCATACGAGTTCAACAGGGGCACGACGG

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2b03.b1.seq+  CCTCAAAAGTCCATTCACTTCGTCACGGGGTGGGGTGATACTTTTGGCTGGTTATTTACG
U_HW-SSH1_2a01.b1.seq+  CCTCAAAAGTCCATTCACTTCGTCACGGGGTGGGGTGATACTTTTGGCTGGTTATTTACG
U_HW-SSH1_2c03.b1.seq+  CCTCAAAAGTCCATTCACTTCGTCACGGGGTGGGGTGATACTTTTGGCTGGTTATTTAGG
                        ____________________________________________________________
consensus               CCTCAAAAGTCCATTCACTTCGTCACGGGGTGGGGTGATACTTTTGGCTGGTTATTTACG

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2b03.b1.seq+  GGATAACGGTTCTGGCTCGGCGCATCCATGGTCACCAACTGGCCGTCAAGCTCTACCCCA
U_HW-SSH1_2a01.b1.seq+  TGATAACGGTTCTGGCTCGGCGCATCCATGGTCACCAGCTGGCCGTCAAGCTCTAGCCCA
U_HW-SSH1_2c03.b1.seq+  TGATAACGGTTCTGGCTCGGCGCATCCATGGTCACCAGCTGGCCGTCAAGCTCTAGCCCA
                        ____________________________________________________________
consensus               TGATAACGGTTCTGGCTCGGCGCATCCATGGTCACCAGCTGGCCGTCAAGCTCTAGCCCA

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2b03.b1.seq+  TGGCGTACCTCGGCCGCGACCACGCTA
U_HW-SSH1_2a01.b1.seq+  TGGCGTACCTCGGCCGCAACCACGCTA
U_HW-SSH1_2c03.b1.seq+  TGGCGTACCTCGGCCGCGACCACGCTA
                        ____________________________________________________________
consensus               TGGCGTACCTCGGCCGCGACCACGCTA

****************** Contig 55 ******************
                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2e12.b1.seq+  TTCGATTAGCGTGGTCCCGCCCGAGGTACACTAGTAGGTAAGTTAGAAGGGGAACGCGAA
U_HW-SSH1_16g02.b1.seq+          GGTCCCGCCCGAGGTGCACTAGTAAGTAAGTTATAAGGGGAACTCTTT
U_HW-SSH1_1b09.b1.seq+     CGATTAGCGTGGTCGCGGCCGAGGAACAGAAGGAGGTAAGTTAGAAGGGGAACGCGAA
U_HW-SSH1_2f10.b1.seq+        TAGCGTGGTCGCGGCCGAGGTACACTAGTAGGTAATTTAGAAGGGGAACGCCAA
U_HW-SSH1_5b01.b1.seq+        TAGCGTGGTCGCGGCCGAGGTACAGTAGTAGGTAAGTTAGAAGGGGAACGCGAA
                        ____________________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACACTAGTAGGTAAGTTAGAAGGGGAACGCGAA

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2e12.b1.seq+  ATGACTTTAGGTTTTGTTGATTTATTGCGCGATGATTTTATTGAAAAGATCGTGCTCGC
U_HW-SSH1_16f02.b1.seq+  TGCCTTTAGGTTTTGTTGATTTATTGCGCGATGATTTTATTGAAAAGGAGCATGCTCCC
U_HW-SSH1_16g02.b1.seq+ TTGCCTTTTGGTTTTTTGATTTATTGCGCGATGATTTTATTGAAAAGGAGGATGCTCCC
U_HW-SSH1_1b09.b1.seq+  ATGCCCA-AGGTGGGGTTGATTTATTGCGCGATGATTTTATTGAAAAAGATCGTGCTCGC
U_HW-SSH1_2f10.b1.seq+  ATGACTTTAGGTTTTGTTGATTTATTGCGCGATGATTTTATTGAAAAGATCGTGCTCGC
U_HW-SSH1_13c03.b1.seq-      CTTTAGGTTTTGTTGATTTATTTTCCGGTGATTTTTTTGAAAAAGATTGCACTCTC
U_HW-SSH1_5b01.b1.seq+  ATGACTTTAGGTTTTGTTGATTTATTGCGCGATGATTTTATTGAAAAGATCGTGCTCGC
                        ____________________________________________________________
consensus               ATGACTTTAGGTTTTGTTGATTTATTGCGCGATGATTTTATTGAAAAGATCGTGCTCGC

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2e12.b1.seq+  GGTATCTTTT-TCACTCAGGACTGGGTATCCATGCCAGGTGTTATACCGGAAGCTTCGGG
U_HW-SSH1_16f02.b1.seq+ GGTATCTTTTGTCTC
```

```
U_HW-SSH1_16g02.b1.seq+ GGTATCTTTTT
U_HW-SSH1_1b09.b1.seq+  GGTATCTTTT-TCACTCAGGACTGGGTATCCATGCCAGGTGTAATACCGGTAGCTTCAGG
U_HW-SSH1_2f10.b1.seq+  GGTATCTTTT-TCACTCAGGACTGGGTATCCATGCCAGGTGTTATACCGGTAGCTTCAGG
U_HW-SSH1_13c03.b1.seq- GGTATCTTTT-TCATTCACGAGTGGGTATCCGTGTCAGGTGTTATATCGGTAGTTTCAGG
U_HW-SSH1_5b01.b1.seq+  GGTATCTTTT-TCACTCAGGACTGGGTATCCATGCCAGGTGTTATACCGGTAGCTTCAGG
                        ____________________________________________________________
consensus               GGTATCTTTT-TCACTCAGGACTGGGTATCCATGCCAGGTGTTATACCGGTAGCTTCAGG

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2e12.b1.seq+  TGGTATTCATGTTTGGCATATGCCCGCTCTGACAGAAATCTTTGGGGACAATTCTGTATT
U_HW-SSH1_1b09.b1.seq+  TGGTATTCATGTTTGGCATATGCCAGCTCTGACCGAAATCTTCGGGGACGATTCTGTATT
U_HW-SSH1_2f10.b1.seq+  TGGTATTCATGTTTGGCATATGCCAGCTCTGACCGAAATCTTTGGGGACAATTCTGTATT
U_HW-SSH1_13c03.b1.seq- TGGTATTCATGTTTGGTATATGCCA
U_HW-SSH1_5b01.b1.seq+  TGGTATTCATGTTTGGCATATGCCAGCTCTGACCGAAATCTTTGGGGACGATTCTGTATT
                        ____________________________________________________________
consensus               TGGTATTCATGTTTGGCATATGCCAGCTCTGACCGAAATCTTTGGGGACAATTCTGTATT

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2e12.b1.seq+  ACTATTTGGTGGAGGGATATGATCTCCCCCATACATACCCTG-GCTTTGGCTAACACCC
U_HW-SSH1_1b09.b1.seq+  ACAATTTGGTGGAATGGATATGATCTCCCCCATACATACGCAATGCTTTATTTAATACAC
U_HW-SSH1_2f10.b1.seq+  ACAATTTGGTGGAGTGGATATGATCTCCCCCAAACATACGCAATGCTTTAGCTAAT
U_HW-SSH1_5b01.b1.seq+  ACAATTTGGTGGAGTGGATATGATCTCCCCCAGACATACGCAATGCTTTAGCTAAT
                        ____________________________________________________________
consensus               ACAATTTGGTGGAGTGGATATGATCTCCCCCATACATACGCAATGCTTTAGCTAATACAC

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2e12.b1.seq+  GGACATGCATACCATGATTTTTCTGTCTATCAATCACTGCTTGCATTGCAGGGTGAATGT
U_HW-SSH1_1b09.b1.seq+  TGAAATGCATACCATGATTTTTCTGTCTATCTTCCCCTGCTTGCATTGCATGTTGAATGC
                        ____________________________________________________________
consensus               GGAAATGCATACCATGATTTTTCTGTCTATCAACCACTGCTTGCATTGCAGGGTGAATGC

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2e12.b1.seq+  GAAGA
U_HW-SSH1_1b09.b1.seq+  GACCAATTAGTCCATTGTCTCGTAATAATGATCCAAATTATTATTTGCGGTGAATCCCCC
                        ____________________________________________________________
consensus               GAACAATTAGTCCATTGTCTCGTAATAATGATCCAAATTATTATTTGCGGTGAATCCCCC

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_1b09.b1.seq+  CTTTTTTTTTTTTTGCATTAAATACACCCCCCTTTTTTACTTTAAAATATTTCTCTCTT
                        ____________________________________________________________
consensus               CTTTTTTTTTTTTTGCATTAAATACACCCCCCTTTTTTACTTTAAAATATTTCTCTCTT

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_1b09.b1.seq+  AA
                        ____________________________________________________________
consensus               AA

****************** Contig 56 ******************
                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2h10.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACACAGCAACTAAAGTTCAACATCTCCTCTGAT
U_HW-SSH1_2d11.b1.seq+        TAGCGTGGTCGCGGCCGAGGTACAGAGCAGCTAGAGTTCAACATCTCCTCTGAT
                        ____________________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACACAGCAACTAAAGTTCAACATCTCCTCTGAT

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2h10.b1.seq+  CTAATGCATCTACTGGTAGGATTTACAAACACCCACACACTTCT-ATCGGTCTCATTCGC
U_HW-SSH1_2d11.b1.seq+  CTAGTGCATCTACTGGTAGGATTTACAAACACACACACACTTCACATCGGTCTCATTCGC
                        ____________________________________________________________
consensus               CTAATGCATCTACTGGTAGGATTTACAAACACACACACACTTCACATCGGTCTCATTCGC

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2h10.b1.seq+  CTCAGGTCGTTGCACGTCGCCGGTTGCCTACTACCAAATTTTCTTTGATCTACCACTCGG
U_HW-SSH1_2d11.b1.seq+  CTCAGGTCGTTGCACGTCGCCGGTTGCCTACTACCAAGTTTCCTTGAGCTACCACTCGG
                        ____________________________________________________________
consensus               CTCAGGTCGTTGCACGTCGCCGGTTGCCTACTACCAAATTTTCCTTGAGCTACCACTCGG

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2h10.b1.seq+  ATGTCGGATCCATCTAGCACATCCTTTGCTACGAAAACTCGCACCATCTCATGTGGAGTG
U_HW-SSH1_2d11.b1.seq+  ATGTCGGATCCATCTAGCACATCCTTTGCTACGAAAACTCGCACCATCTCACGTGGAGTG
                        ____________________________________________________________
consensus               ATGTCGGATCCATCTAGCACATCCTTTGCTACGAAAACTCGCACCATCTCACGTGGAGTG

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2h10.b1.seq+  GAGGTTTACAACGGAAGTAGTACTAGTAGTACCTGCCCGGG
U_HW-SSH1_2d11.b1.seq+  GATGTTTACAACGGAAGTAGTAGTAGTACCTGCCCGGGCGGCCGCTCGAAATCACTA
                        ____________________________________________________________
consensus               GAGGTTTACAACGGAAGTAGTACTAGTAGTACCTGCCCGGGCGGCCGCTCGAAATCACTA

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2d11.b1.seq+  GTGAATTCGCGGCCGCCTGCAGGTCCACCATATGGGAAAGCTCCCAACGCGTTGGATGCA
                        ____________________________________________________________
consensus               GTGAATTCGCGGCCGCCTGCAGGTCCACCATATGGGAAAGCTCCCAACGCGTTGGATGCA

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2d11.b1.seq+  TAGCTTGAGTATTCTATAGTGTCACCTAAATAGCTTGCCGAAATCATGGTCATAGCTGTT
                        ____________________________________________________________
consensus               TAGCTTGAGTATTCTATAGTGTCACCTAAATAGCTTGCCGAAATCATGGTCATAGCTGTT

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2d11.b1.seq+  TCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAAGCAAAA
                        ____________________________________________________________
consensus               TCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAAGCAAAA

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2d11.b1.seq+  GGGTAATGCCTGGGGTGCCTAATGAGTGACTAACTCACATTATTGCGTTGCGCTTCACTG
                        ____________________________________________________________
consensus               GGGTAATGCCTGGGGTGCCTAATGAGTGACTAACTCACATTATTGCGTTGCGCTTCACTG

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_2d11.b1.seq+  CCCGCTTTTCATCGAAAAATCTGTCGGGCCACCTGCATAATGAACCGCCCAACCC
                        ____________________________________________________________
consensus               CCCGCTTTTCATCGAAAAATCTGTCGGGCCACCTGCATAATGAACCGCCCAACCC

****************** Contig 57 ******************
                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_4b02.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACTTCAAGATGTGGAACATTTATTGCTCTGGGC
U_HW-SSH1_4b03.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACTTCAAGATGTGGAACATTTATTGCTCTGGGC
U_HW-SSH1_4b08.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACTTCAAGATGTGGAACATTTATTGCTCTGGGC
                        ____________________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACTTCAAGATGTGGAACATTTATTGCTCTGGGC

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_4b02.b1.seq+  GTCATCCGGAGCCGTTCAAGGTAAAAAAAGACGACAGTGAGTTCCCATATGACAGATGAG
U_HW-SSH1_4b03.b1.seq+  GTCATCCGGAGCCGTTCAAGGTAAAAGAAGACGACAGTGAGTTCCCATATGACAGATGAG
U_HW-SSH1_4b08.b1.seq+  GTCATCCGGAGCCGTTCAAGGTAAAAGAAACAACAGTGATTTCCCATATGACAGATGAG
                        ____________________________________________________________
consensus               GTCATCCGGAGCCGTTCAAGGTAAAAGAAGACGACAGTGAGTTCCCATATGACAGATGAG

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_4b02.b1.seq+  GAGCATGAAATCCCGGCTGTGTAAATAAAAAGCAAAGTTGTAGCGTAGTACCTGCCCGGG
U_HW-SSH1_4b03.b1.seq+  GAGCATGAAATCCCGGCTGTGTAAATAAAAAGCAAAGTTGTAGCGTAGTACCTGCCCGGG
U_HW-SSH1_4b08.b1.seq+  GAGCATGAAATCCCGGCTGTGTAGATAAAAAGCAGAGTTGTAGCGTAGTACCTGCCCGGG
                        ____________________________________________________________
consensus               GAGCATGAAATCCCGGCTGTGTAAATAAAAAGCAAAGTTGTAGCGTAGTACCTGCCCGGG

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_4b02.b1.seq+  CGGCCGCTCGAATCACTAGTGAATTCTGGGCCGCCTGCAAGCCAAGAAGGGGGGAGAGGC
U_HW-SSH1_4b03.b1.seq+  CGGCCGCTCGAATCAC
U_HW-SSH1_4b08.b1.seq+  CGGCCGCTCGA
                        ____________________________________________________________
consensus               CGGCCGCTCGAATCACTAGTGAATTCTGGGCCGCCTGCAAGCCAAGAAGGGGGGAGAGGC

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_4b02.b1.seq+  CCCGGCGGCGCTGATGTGCATATCCCCTTTGA-ATATTCAAACAGCTATTTGGGGGTGGC
U_HW-SSH1_4b01.b1.seq+    CGGCGGCGCTGATATGCATACCCCTTTGACATATTCAAACAGCTATTTGGGGGTGGC
                        ____________________________________________________________
consensus               CCCGGCGGCGCTGATATGCATACCCCTTTGACATATTCAAACAGCTATTTGGGGGTGGC

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_4b02.b1.seq+  GGTGGCGGCTTTGGAGGGGGTAGCTCAAAATGACACCCACAAAAGCGTGCTGAAAATGTG
U_HW-SSH1_4b01.b1.seq+  GGTGGCGGCTTTGGAGGGGGTAGCTCGAGAGGACACAAACAAAAGCGTGGTGAAGATGTG
                        ____________________________________________________________
consensus               GGTGGCGGCTTTGGAGGGGGTAGCTCAAAAGGACACAAACAAAAGCGTGCTGAAAATGTG

                           .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :  .  .  :
U_HW-SSH1_4b02.b1.seq+  GTGCATACCATGAAGGTTTCTATAGAAGACTTGTGCCTCGGGCGCGACCA
U_HW-SSH1_4b01.b1.seq+  GTGCATACCATGAAGGTTTCGTTAAAAGACTTGTACCTCGGCCGCGACCACGCTA
                        ____________________________________________________________
```

```
consensus              GTGCATACCATGAAGGTTTCGATAAAAGACTTGTACCTCGGCCGCGACCACGCTA

****************** Contig 58 ********************
                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_5d04.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACTACATCAGCTAAGCTTGCGGCCATTCATTGG
                        ________________________________________________________________________
consensus              TTCGATTAGCGTGGTCGCGGCCGAGGTACTACATCAGCTAAGCTTGCGGCCATTCATTGG

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_5d04.b1.seq+  ACGAATGCTCGTGGTCCACAAATAAGCTCCATGCTCTTAATAATTATCTGCATGCTGGAT
                        ________________________________________________________________________
consensus              ACGAATGCTCGTGGTCCACAAATAAGCTCCATGCTCTTAATAATTATCTGCATGCTGGAT

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_5d04.b1.seq+  ACATCAATAATAACCTTCGGTGTTGTTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
U_HW-SSH1_1a06.b1.seq+                                                          TAGCGTGGTC
U_HW-SSH1_8g06.b1.seq+                                                          TAGCGTGGTC
U_HW-SSH1_4g11.b1.seq+                                                          TAGCGTGGTC
U_HW-SSH1_8h12.b1.seq+                                                          TAGCGTGGTC
U_HW-SSH1_5h07.b1.seq+                                                            CGTGGTC
                        ________________________________________________________________________
consensus              ACATCAATAATAACCTTCGGTGTTGTTCTCAAAAAAAAAAAAAAAAAAAAAAAAGCGTGGTC

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_5d04.b1.seq+  AAGCTTGTAAA--CCCTGTTATTGTGAAAATTCTTAATTCAAGATTTATAGGGAGGGACT
U_HW-SSH1_1a06.b1.seq+  GCGGCCGAGGA--CCCTGTTATTGTGAGAATTCTTAATTCAAGAGTTATAGGGAGGGACT
U_HW-SSH1_5a12.b1.seq+                CCTGTTATTGTGAGAATTCTTAATTCCATAGTTATAGGGAGGGATT
U_HW-SSH1_11g11.b1.seq+                 CTGTTATTGTGAGAATTCTTAATTCAAGAGTTATAGGGAGGGACT
U_HW-SSH1_8g06.b1.seq+  CCGGCCGAGGT--C--TGTTATTGTGAGAATTCTTAATTCAAGAGTTATAGGGAGGGACT
U_HW-SSH1_4g11.b1.seq+  GCGGCCGAGGT--C--TGTTATTGTGAGAATTCTTAATTCAAGAGTTATAGGGAGGGACT
U_HW-SSH1_8h12.b1.seq+  GCGGCCGAGGT--CCCTGTTATTGTGAGAATTCTTAATTCAAGAGTTATAGGGAGGGACT
U_HW-SSH1_5h07.b1.seq+  CCGGCCGAGGTGACCCTGTTATTGTGATAATTCTTAATTCCAGAGTTATAGGGAGGGACT
U_HW-SSH1_11b05.b1.seq+                 GTTATTGTGATAATTCTTAATTCAAGATTTATAGGGAGGGACT
                        ________________________________________________________________________
consensus              GCGGCCGAGGT--CCCTGTTATTGTGAGAATTCTTAATTCAAGAGTTATAGGGAGGGACT

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_5d04.b1.seq+  TATGTCACCACAAACAAAAACTAAAGCAGGTGTTGGATTTAAAGCTGGTGTTAAAAATTA
U_HW-SSH1_1a06.b1.seq+  TATGTCACCACAAACAGAAACTAAAGCAGGTGTTGGATTTAAAGCTGGTGTTAAAGATTA
U_HW-SSH1_1c09.b1.seq+                        ACTAAAGCAGGTGTTGGATTTAAAGCTGGTGTTAAAGATTA
U_HW-SSH1_5a12.b1.seq+  TATGTCTCCACCAACAGAAACTAATGCTGGTGTTGGATTTAAAGCTGGTGTTTTT-TTA
U_HW-SSH1_11g11.b1.seq+ TATGTCACCACAAACAGAAACTAAAGCAGGTGTTGGATTTAAAGCTGGTGTTAAAGATTA
U_HW-SSH1_8g06.b1.seq+  TATGTCACCACAAACAGAAACTAAAGCAGGTGTTGGATTTAAACCTGGTGTTAAATATTA
U_HW-SSH1_4g11.b1.seq+  TATGTCACCACAAACAGAAACTAAAGCAGGTGTTGGATTTAAAGCTGGGGTTAAACATTA
U_HW-SSH1_8h12.b1.seq+  TATGTCACCACAAACAGAAACTAAAGCAGGTGTTGGATTTAAAGCTGGTGTTAAAAATTA
U_HW-SSH1_5h07.b1.seq+  TATGTCACCACAAACAGAAACTAAAGCAGGTGTTGGATTTAAAGCTGGTGTTAAAGATTA
U_HW-SSH1_11b05.b1.seq+ TATGTCACCACAAACAGAAACTAAACCAGGTGTTGAATTTAAAGCTGGTGTTAAAAATTA
                        ________________________________________________________________________
consensus              TATGTCACCACAAACAGAAACTAAAGCAGGTGTTGGATTTAAAGCTGGTGTTAAAGATTA

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_5d04.b1.seq+  TAAATTGACTTACTACACCCCAAAGTATGAAACTAAGGATACTGATATCTTGGCAGCATT
U_HW-SSH1_1a06.b1.seq+  TAAATTGACTTACTACACCCCAGAGTATGAAACTAAGGATACTGATATCTTGGCAGCATT
U_HW-SSH1_1c09.b1.seq+  TAAATTTACTTACCACACCCCAGAGTATGAAACTAAGGATACTGATATCTTGGCAGCATT
U_HW-SSH1_5a12.b1.seq+  TAAATTGACTTACTACACCCCAGAGTATGAAACTAAGGATACTGATATCTTGTCAGCTTT
U_HW-SSH1_11g11.b1.seq+ TAAATTGACTTACTACACCCCAAAGTATGAAACTAAGGATACTGATATCTTGGCAGCATT
U_HW-SSH1_8g06.b1.seq+  TAAATTGACTTACTACACCCCAGAGTATGAAACTAAGGATACTGATATCTTGGCAGCATT
U_HW-SSH1_4g11.b1.seq+  TAAATTGACTTACTACACCCCAAAGTATGAAACTAAGGATCCTGCTATCTTGGCACTATT
U_HW-SSH1_8h12.b1.seq+  TAAATTGACTTACTACACCCCAGAGTATGAAACTAAGGATACTGATATCTTGGCAGCACT
U_HW-SSH1_5h07.b1.seq+  TAAATTGACTTACTACACCCCAGAGTATGAAACTAAGGATACTGATATCTTGGCAGTATT
U_HW-SSH1_11b05.b1.seq+ TAAATTGACTTACTACACCCCTCAGTATGAAACTAAGGATACTGATATCTTGGCAGCATT
                        ________________________________________________________________________
consensus              TAAATTGACTTACTACACCCCAGAGTATGAAACTAAGGATACTGATATCTTGGCAGCATT

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_5d04.b1.seq+  CCGAGTAAGTCCTCAGCCTGGGGTCCGCCCAAAGAAGCAGGGGCTGCAGTAGCTGCCGA
U_HW-SSH1_1a06.b1.seq+  CCGAGTAAGTCCTCAGCCTGGGGTCCGCCCAAAGAAGCAGGGGCTGCAGTAGCTGCCGA
U_HW-SSH1_1c09.b1.seq+  CAGAGTAAGTCCTCACCCTGGGGTCCTCCCGA
U_HW-SSH1_5a12.b1.seq+  CCGAGTAACTCCTCGACCTGGGGTCCGCCCAAAAAATCCGGGGCTGCAGTAGCTGCCGA
U_HW-SSH1_11g11.b1.seq+ CCGAGTAAGTCCTCAGCCTGGGGTTCCGCCCAAAGAAGCAGGGGCTGCAGTAGCTGCCGA
U_HW-SSH1_8g06.b1.seq+  CCAAGTAAGTCCTCAGCCTGGGGTTCCGCCCTAAGAAGCAGGGGCTGCAGTAGCTGCCGA
U_HW-SSH1_4g11.b1.seq+  CCGAGTAAGTCCCCAGCCTGGGGTTCCCCCCGAAAAAGCAGGGGCTG
U_HW-SSH1_8h12.b1.seq+  CCGAGTAAGTCCTCAGCCTGGGGTTCCGCCCAAAGAAGCAGGGGCTGCAGTAGCTGCCGA
U_HW-SSH1_5h07.b1.seq+  CCGAGTAAGTCCTCAGCCTGGGGTTCCGCCCGAAAAAGCAGGGGCTGCAGTAGCTGCCGA
U_HW-SSH1_11b05.b1.seq+ CCGAGTAAGTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGTTGCAGTAGCTGCAGA
                        ________________________________________________________________________
consensus              CCGAGTAAGTCCTCAGCCTGGGGTCCGCCCAAAGAAGCAGGGGCTGCAGTAGCTGCCGA

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_5d04.b1.seq+  ATCTTCTACTGGTACCTGCCCGGGCGGC
U_HW-SSH1_1a06.b1.seq+  ATCTTCTACTGGTACCTGCCCGGGCGGCCGCTC
U_HW-SSH1_5a12.b1.seq+  ATCTTCTACTGGTACCT
U_HW-SSH1_11g11.b1.seq+ ATCTTCTACTGGTACCT
U_HW-SSH1_8g06.b1.seq+  ATCTTCTACTGGTACCTGCCCGGGCGGCCGCTC
U_HW-SSH1_8h12.b1.seq+  ATCTTCTACTGGTACCTGCCCGGGCGGCCGCTCGAAATCACTAATGAATTCGCGGCCGCC
U_HW-SSH1_5h07.b1.seq+  ATCTTCTACTGGTACCTGCCCGGGCGGCC
U_HW-SSH1_11b05.b1.seq+ ATCTTCTACTGGTCCCTGCCCGGGCGGCCCCTCGAGC-CACCCGTTCTTTATCGGCCGCC
                        ________________________________________________________________________
consensus              ATCTTCTACTGGTACCTGCCCGGGCGGCCGCTCGAAATCACCAATGAATTAGCGGCCGCC

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_8h12.b1.seq+  TGCAAGTCTAACATCGGGGAAGCCCCTACGCTATGAATCCATGGCTT
U_HW-SSH1_11b05.b1.seq+ TGTGGGCTGCCCCCCCCGGACAGCTCCCATCGGGTAGGATGAGGAGCTCGAATATTCCAT
                        ________________________________________________________________________
consensus              TGCAAGCCGAACACCCCGGAAAGCTCCCAACGCGAAGAATGAAGAGCTCGAATATTCCAT

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_11b05.b1.seq+ CTGGGCAAAAATATACCTCAGACTCCACCGGGTTGGAGATGTTTCATGTGCTAACTCGCT
                        ________________________________________________________________________
consensus              CTGGGCAAAAATATACCTCAGACTCCACCGGGTTGGAGATGTTTCATGTGCTAACTCGCT

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_11b05.b1.seq+ ACCCCCCTACACTTCCAGACATCCTCCGACGCGTGAACGTATACTGTATAGGATAGCTCG
                        ________________________________________________________________________
consensus              ACCCCCCTACACTTCCAGACATCCTCCGACGCGTGAACGTATACTGTATAGGATAGCTCG

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_11b05.b1.seq+ CCTCACGATAGATCCATAACTTGATT
                        ________________________________________________________________________
consensus              CCTCACGATAGATCCATAACTTGATT

****************** Contig 59 ********************
                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7d05.b1.seq+  TTCGATTACCGTGGCCCCCGCCGAGGGCACTGGTATGTACTAGACCGGGAGATCCCC
U_HW-SSH1_7f09.b1.seq+  TTCGATTACCGTGGGCCCCCGCCGAGGTGCACTTGTATGTATTTCGACGGGAAATCCCC
U_HW-SSH1_7g09.b1.seq+  TTCGATTACCGTGGGCCCCCCCGAGGGGTACTTGTATGTAATTTAGACGGGGAC-TCCCC
U_HW-SSH1_7d07.b1.seq+        TACCGTGGGCCCCCGCCGACGGGCACTTGTAAGTAAGTTAGACGGGGAGCGCCCA
U_HW-SSH1_7a07.b1.seq+        TACCGTGGGCCCCCCCGACGTACACTTGTATGCAACTTAGAAGGGGAAACCCCC
U_HW-SSH1_7h09.b1.seq+        TACCGTGGGCCCCCCGAGGGGCACTTGTATGTAACTTAGACGGGGAACTACCC
U_HW-SSH1_7e07.b1.seq+                      GCCGGCGGGCACTTGTATGTAACTTCGACGGGGAGATCCCC
                        ________________________________________________________________________
consensus              TTCGATTACCGTGGGCCCCGCCGAGGGGCACTTGTATGTAACTTAGACGGGGAAATCCCC

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7d05.b1.seq+  ATGAGTTTTTGTTTTGTTGATTTTTTGTTGGATAATTTTATTGAGAAAAACCCGGCCCCC
U_HW-SSH1_7f09.b1.seq+  ATGACTTTTTGTTTTTTTGATTTTTTGCGCCATAATTTTATTTTAAAAAATCCTGCCCCC
U_HW-SSH1_7g09.b1.seq+  ATGACTTTTTGTTTTGTCGATTTTTTGCGCGATAATTTTTTTTTGAAAAACCCCGCCCCC
U_HW-SSH1_7d07.b1.seq+  ATGACTTTTTGTTTTGTTGATTTTTTGTTGGATAATTTTATTGAAAAAAATCCTGCTCCC
U_HW-SSH1_7a07.b1.seq+  ATGACTTTTTGGATTTGTTGATTATT-GCGTGATAATTTTATTGAAAAAATCGTGCCCCC
U_HW-SSH1_7h09.b1.seq+  ATGACTTTTTGTTTTGTTGATTTTTTGCTGGATAATTTTATTGTAAAAAATCCTGCCCCC
U_HW-SSH1_7e07.b1.seq+  ATGACTTTTTGTTTTGTTGATTTTTTGCTGGATAATTTTATTGAAAAAAATCCTGCCCCC
                        ________________________________________________________________________
consensus              ATGACTTTTTGTTTTGTTGATTTTTTGCTGGATAATTTTATTGAAAAAAATCCTGCCCCC

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7d05.b1.seq+  GGTATCTTTTTCCC-CTGGACTGGGT-TTTATGCCAGGTGTGGTGCGGCGAGTTCAGGG
U_HW-SSH1_7f09.b1.seq+  GCTATCTTTTTCTC-CTGGACTGGGTATCCATAGCAAGTGTGTTACGGGTTAGTTCATGG
U_HW-SSH1_7g09.b1.seq+  GCTGTCTTTTTCCTTCTGGACTGGGTATCCATAGCAAGTGTTTACGGGTTGCTTCACGG
U_HW-SSH1_7d07.b1.seq+  GCTATCTTTTTCACTCTGGACTGGGTATCCATGCCAAGTGTTTTACCGGTTAGTTGAGGG
U_HW-SSH1_7a07.b1.seq+  GCCATCTTTTTCTC-CAGGACTGGGTATCCATGCCAAGTGTGA-ACCGGTTGCTTGATGG
U_HW-SSH1_7h09.b1.seq+  GCCATCTTTTTCACCCTGGACTGGGTATCCATAGCAAGTGTGA-ACCGGTTAGTTGATGG
U_HW-SSH1_7e07.b1.seq+  GCTTTCTTTTTCTC-CTGGACTGGTTTTCCCTGCCAAGTGTGA-CCCGGTTGCTTGAGGG
                        ________________________________________________________________________
consensus              GCTATCTTTTTCTC-CTGGACTGGGTATCCATGCCAAGTGTGATACCGGTTAGTTGAGGG

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7d05.b1.seq+  GGGATTTTTGTGGGGGGCATCCCCCCTATCACAACCTCCGTGGGGGACAATTTTGTATTA
U_HW-SSH1_7f09.b1.seq+  GGGTTTTTTGTAGGGCGCACCCCACCCCTGACACCCTCCGGGGCAGACAATTCTTTATAT
U_HW-SSH1_7g09.b1.seq+  GGGTTTTTTGTATGGAGCACCCCCCCCTGACCCCCTCCGTTGGGGACAATTTTTTATTT
U_HW-SSH1_7d07.b1.seq+  GGGTTTTCTGTTTGGGGCATCCCACCTATGACAACCTTCGTTGGGGAGAATTCTGTATTA
U_HW-SSH1_7a07.b1.seq+  GGGTTTTCTGTTTGGTGCATCCCACCTATGACAACCTTCGTTGGGGACAATTCTGTATTA
U_HW-SSH1_7h09.b1.seq+  GGGTTTTTTGTAGGGCGCACCCCACCCATGACCCCCTCCGCGGCAAGGAATTTTGTATAT
U_HW-SSH1_7e07.b1.seq+  GGGATTTTTGTTTGGCGCATCCCACCTCTGACAACCTCCGTTGGGGACAATTTTGTATAA
U_HW-SSH1_7c09.b1.seq+                                                          TGTATAT
                        ________________________________________________________________________
consensus              GGGTTTTTTGTATGGCGCATCCCACCTATGACAACCTCCGTTGGGGACAATTTTGTATAA

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7d05.b1.seq+  CACTTTGGGGGGGGAGGTTTACCAGCCCCCTCGGGGAAATGCACCCGGGGCACCCACTAAT
U_HW-SSH1_7f09.b1.seq+  TACTTTGGAGGGGGAGGAGTTTACCACCCCCCTCGGGGAAATGCCCCCGGCGCCCCACCTATT
U_HW-SSH1_7g09.b1.seq+  TACTTTGGAGGGGGAGGGGAACCACCCCCTCGGGGAAATGCCCCCGGCGCCCCACCTAAT
U_HW-SSH1_7d07.b1.seq+  CAATTTGGTGGGGGAGGGGTACGAGATCCTCGGGGAAATGCACCCGGTGCAGAACCTATT
U_HW-SSH1_7a07.b1.seq+  TAATTTGGGGGGGAGGGGTACCAGCCCCTCGGGGAAATGCACCCGGCGCAGAACCTATT
U_HW-SSH1_7h09.b1.seq+  TACTTTGGAGGGGGAGGGGTACCAGCCCCTCGGGGAAATGCCCCCGGCGCAAAACCTATT
U_HW-SSH1_7e07.b1.seq+  TACTTTGGGGGGGGAGGGGTTACGAGCCCCTCGGGGAAATGCACCCGGCGCCGAACATATT
U_HW-SSH1_7c09.b1.seq+  TACTTTGGGGGGGGAGGGGAACCAGACCCTCGGGGAAAAGCCCCCGGCGCCCAACCTCTT
                        ________________________________________________________________________
consensus              TACTTTGGGGGGGGAGGGGTACCAGCCCCTCGGGGAAATGCACCCGGCGCAGAACCTATT

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7d05.b1.seq+  CGCGAGGGTTTAGAACCCTGTGTACCTGCCCGGG
U_HW-SSH1_7f09.b1.seq+  AAAGTGTGTTTAAAACCCCGTGTACCTGCCCGGCCC
U_HW-SSH1_7g09.b1.seq+  AAAGAGTGTTTAAAACCCTGTGTACCTGCCGGGCCC
U_HW-SSH1_7d07.b1.seq+  CACGTGTGTTTATAACCCTGTGTCCCTGCCCGGCCC
U_HW-SSH1_7a07.b1.seq+  CAAGTGTGTTTAAAACCCTGTGTACCTGCCCGGG
U_HW-SSH1_7h09.b1.seq+  AACGTGTGTTTAAAACCCTGTGTACCTGCCCGGCCCCATTTGATAAATCTCTAGTGACTT
U_HW-SSH1_7e07.b1.seq+  AACGAGTGTTTAAAACCCTGTGTACCTGCCCGGGCCGC
U_HW-SSH1_7c09.b1.seq+  AACGTGTGTTTAAAACCCCGTGT
                        ________________________________________________________________________
consensus              AACGTGTGTTTAAAACCCTGTGTACCTGCCCGGCCCCATTTGATAAATCTCTAGTGACTT

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7h09.b1.seq+  CGCAGCCTATGTTGAAAATATGATGATGGACACCTCCCTGCGTGGAGTTATGCATGGGCC
                        ________________________________________________________________________
consensus              CGCAGCCTATGTTGAAAATATGATGATGGACACCTCCCTGCGTGGAGTTATGCATGGGCC

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7h09.b1.seq+  AAAATTGCTACCTGAGACAAAATGTAGCGCCTCATATTTCCAGTCAGAGGTGTATACGGA
                        ________________________________________________________________________
consensus              AAAATTGCTACCTGAGACAAAATGTAGCGCCTCATATTTCCAGTCAGAGGTGTATACGGA

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7h09.b1.seq+  GTGATCTGTGCACAGCATGTGCTGCCCACTGAATGC
                        ________________________________________________________________________
consensus              GTGATCTGTGCACAGCATGTGCTGCCCACTGAATGC

****************** Contig 60 ********************
                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7f10.b1.seq+  TACCGGGGGCCCCCCCGACGGGTACTAGTATGAATGTTTGGGGGATCCCCCCACGTTTTG
                        ________________________________________________________________________
consensus              TACCGGGGGCCCCCCCGACGGGTACTAGTATGAATGTTTGGGGGATCCCCCCACGTTTTG

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7f10.b1.seq+  GTAGATTTTGTTATTTTTTGTCCCGTTTTGAACTTGATTTAACCCGCGATGATTAAAACT
                        ________________________________________________________________________
consensus              GTAGATTTTGTTATTTTTTGTCCCGTTTTGAACTTGATTTAACCCGCGATGATTAAAACT

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7f10.b1.seq+  TTAACTCACAAACAGTTATGCGCTGGAGAGACTGTTTTGTCTTTTGTGCCGAAGCTTTTT
U_HW-SSH1_7e10.b1.seq+             ACAGTTATGCGCTAGAAAGACTGTTTTGTCTTTTGTGCCGAGGTTTTTT
                        ________________________________________________________________________
consensus              TTAACTCACAAACAGTTATGCGCTAGAAAGACTGTTTTGTCTTTTGTGCCGAAGCTTTTT

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7f10.b1.seq+  AGAAAGCACAAGCCCACCCCGGAGAAATCCCGGGGCATTAAATTATTGCTACTGCTGGGG
U_HW-SSH1_7e10.b1.seq+  TGAAAGCAGAAGCCCACCCCGGAGAAACCCCGGGGCATTAAATAATTGCTATTGCTTTGA
                        ________________________________________________________________________
consensus              AGAAAGCACAAGCCCACCCCGGAGAAACCCCGGGGCATTAAATAATTGCTACTGCTGGGA

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7f10.b1.seq+  CGGCGGAGGGGACCACCCTCCTCGGGAATGACTTCCCGGCCCCCCGCATGTCAACGAGA
U_HW-SSH1_7e10.b1.seq+  AGTCGGAGGGGAACACGCTCCTCGGGAATGAGTCCCCGGCCCCCCGCATATCAACGAGAG
                        ________________________________________________________________________
consensus              AGGCGGAGGGGAACACCCTCCTCGGGAATGACTCCCCGGCCCCCGCATATCAACGAGAG

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7e10.b1.seq+  GGGAAAGCCCCGTGCGCGTGCCATGCCCCC
                        ________________________________________________________________________
consensus              GGGAAAGCCCCGTGCGCGTGCCATGCCCCC

****************** Contig 61 ********************
                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7h12.b1.seq+  TGCGAGTCGCTGCTCCGGCCGCCATGGCGGCCGCGGGATTCGATATCGAGCGGCCGCCCG
                        ________________________________________________________________________
consensus              TGCGAGTCGCTGCTCCGGCCGCCATGGCGGCCGCGGGATTCGATATCGAGCGGCCGCCCG

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7h12.b1.seq+  GGCAGGTACCTGGGCCCCTTCTCCGCGCAGACGCC--GTCC--TACCTGAACGGCGAGTT
U_HW-SSH1_6c09.b1.seq+                        TTCGAGCGGCCGCCCGGGCAGGAACGGGAACGGCGAGTT
U_HW-SSH1_10a03.b1.seq+                       TTCGAGCGGCCGCCCGGGAGGGAACATGACCGGCGAGTT
U_HW-SSH1_9e10.b1.seq+                        TTCGAGCGGCCGCCCGGGCAGGTACCTGACCGGCGAGTT
U_HW-SSH1_14c04.b1.seq+                             GGCCGCCCGGGCGGGTACCTGACCGGCTGTTT
U_HW-SSH1_10c03.b1.seq+                             GGCCGCCCGGGGGGGAACCGAACCGGCAAGTT
                        ________________________________________________________________________
consensus              GGCAGGTACCTGGGCCCCTTCTTCGAGCGGCCGCCCGGGCGGGAACCTGACCGGCGAGTT

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7h12.b1.seq+  CCCCGGCGACTACGGCTGGGACACCGCCGAGCTTTCTGCCGACCCGGAGGCGTTCGCTAG
U_HW-SSH1_6c09.b1.seq+  CCCCGGCGACTACGGCTGGGACACCGGGGGGCTTTCTGCCGACCCGGAGGCGTTCGCGAG
U_HW-SSH1_10a03.b1.seq+ CCCCGGCGACTACGGGTGGGACACCGGGGGATTGTCTGCTGACCCCGAGACGTTCGCCAA
U_HW-SSH1_9e10.b1.seq+  CCCCGGCGACTACGGGTGGGACACCGCGGATTGTCTGCTGACCCCGAGACGTTCGCCAA
U_HW-SSH1_14c04.b1.seq+ CCCCGGCAACTACTGGTGGGACTCCGCCTGATTGTCTGCTGACCCCGAAACTTTCCCCAA
U_HW-SSH1_10c01.b1.seq+                                                 GACGTTCGCCAA
U_HW-SSH1_10c03.b1.seq+ CCCCGGCGACTACGGGTGGGAGACCGGCGGATTGTCTGCTGACCCCGAGACGTTCGCCAA
                        ________________________________________________________________________
consensus              CCCCGGCGACTACGGGTGGGACACCGCCGGATTGTCTGCTGACCCCGAGACGTTCGCCAA

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7h12.b1.seq+  GAACAGGGCGCTGGAGGTGATCCACGGGCGGTGGGCGATGCTCGGCGCTCTTGGCTGCGT
U_HW-SSH1_6c09.b1.seq+  GAACAGGGCGCTGGAGGTGATCCACGGGCGGTGGGCGATGCTTGGCGCTCTTGGGTGCGT
U_HW-SSH1_10a03.b1.seq+ GAACAGGGAGCTGGAGGTGATCCACTCGCGGTGGGCGATGCTCGGCGCCCTCGGGTGCGT
U_HW-SSH1_9e10.b1.seq+  GAACAGGGAGCTGGAGGTGATCCACTCGCGGTGGGCGATGCTCGGCGCCCTCGGGTGCGT
U_HW-SSH1_14c04.b1.seq+ GAACAGGGAGCTGGAGGTGATCCATTCGCGGTGGGCGATGCTCGGCGCCCTCGGGTGCGT
U_HW-SSH1_10c01.b1.seq+ GAACAGGGAGCTGGAGGTGATCCACG-GCGGGGGGCGATGCTCGGCGCCCTCGGGTGCGT
U_HW-SSH1_10c03.b1.seq+ GAACAGGGAGCTGGAGGTGATCCACTCGCGGTGGGCGATGCTCGGCGCCCTCGGGTGCGT
                        ________________________________________________________________________
consensus              GAACAGGGAGCTGGAGGTGATCCACTCGCGGTGGGCGATGCTCGGCGCCCTCGGGTGCGT

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7h12.b1.seq+  CTTCCCCGAGGTGCTCCAGAAGTGGGTGGGCGTCGAGTTCAAGGAGCCCGTCTGGTTCAA
U_HW-SSH1_6c09.b1.seq+  CTTCCCCGAGGTGCTCCAGAAGGGGGTGGGCGTCGAGTTCAAGGAGCCCGTCTGGTTCAA
U_HW-SSH1_10a03.b1.seq+ GTTCCCGGAGATCCTGTCCAAGAACG---GCATCAAGTTCGGCGAGGCCGTGTGGTTCAA
U_HW-SSH1_9e10.b1.seq+  GTTCCCGGAGATCCTGTCCAAGAACG---GCATCAAGTTCGGCGAGGCCGTGTGGTTCAA
U_HW-SSH1_14c04.b1.seq+ GTTCCCGGAGATCCTGTCCAAGAACG---GCATCAAGTTCGGCGAGGCCGTGTGGTTCAA
U_HW-SSH1_10c01.b1.seq+ GTTCCCGGAGATCCTGTCCAAGAACG---GCATCAAGTTCGGCGAGGCCGTGTGGTTCAA
U_HW-SSH1_10c03.b1.seq+ GTTCCCGGAGATCCTGTCCAAGAACG---GCATCAAGTTCGGCGAGGCCGTGTGGTTCAA
U_HW-SSH1_1a08.b1.seq+                       CGCAACG---GTGTGAAGTTCGGCGAGGCTGTTTGGTTCAA
                        ________________________________________________________________________
consensus              GTTCCCGGAGATCCTGTCCAAGAACG---GCATCAAGTTCGGCGAGGCCGTGTGGTTCAA

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7h12.b1.seq+  GGCCGGCTCGCAAATCTTCTCCGAGGGCGGCCTCGATTACCTTGGAAACCCCAACCTCGT
U_HW-SSH1_6c09.b1.seq+  GGCCGGCTCGCAGATCTTCTCCGAGGGTGGCCTCGATTACCTTGGGAACCCCAACCTCGT
U_HW-SSH1_10a03.b1.seq+ GGCCGGCGCCATATCTTCTCCGAGGGCGGCCTCGACTCCTGGGCAACCCCAACCTCGT
U_HW-SSH1_9e10.b1.seq+  GGCCGGCGCCCAGATCTTCTCCGAGGGCGGCCTCGACTACCTGGGCAACCCCAACCTGGT
U_HW-SSH1_14c04.b1.seq+ GGCCGGCGCCCAGATCTTCTCCGAGGGCGGCCTCGACTACCTGGGCAACCCCAACCTGGT
U_HW-SSH1_10c01.b1.seq+ GGCCGGCGCCCAGATCTTCTCCGAGGGCGGCCTCGACTACCTGGGCAACCCCAACCTGGT
U_HW-SSH1_10c03.b1.seq+ GGCCGGCGCCCAGATCTTCTCCGAGGGCGGCCTCGACTACCTGGGCAACCCCAACCTGGT
U_HW-SSH1_1a08.b1.seq+  GGCCGGATCCCAGATCTTCAGGGAGGGTGGCCTCGACTACCTGGGCAACCCCAAGCCTCGT
                        ________________________________________________________________________
consensus              GGCCGGCGCCCAGATCTTCTCCGAGGGCGGCCTCGACTACCTGGGCAACCCCAACCTGGT

                                 .   :   .   .   :   .   .   :   .   .   :   .   .   :   .   .   :
U_HW-SSH1_7h12.b1.seq+  CCACGCGCAAAGCATCCT
U_HW-SSH1_6c09.b1.seq+  CCACGCGCAGAGCATCCTTGCC
U_HW-SSH1_10a03.b1.seq+ GCACGCGCAAAGCATCCTCGCCATCTGGGCGGTGCAGGTGGTGCTCTTGGTTTTCTTCGA
```

```
U_HW-SSH1_9e10.b1.seq+  GCACGCGCAGAGCATCCTCGCCATCTGGGCGGTGCAGGTGGTGCTCATGGGCTTCATCGA
U_HW-SSH1_14c04.b1.seq+ GCCCGCGCAAAGCATCCTCGCCATCTGGGCGGTGCAGGTGGTGCTCATGGGCTTCATCGA
U_HW-SSH1_10c01.b1.seq+ GCACGCGCAGAGCATCCTCGCCATCTGGGCGGTGCAGGTGGTGCTCATGGGCTTCATCGA
U_HW-SSH1_10c03.b1.seq+ GCACGCGCAGAGCATCCTCGCCATCTGGGCGGTGCAGGTGGTGCTCATGGGCTTCATCGA
U_HW-SSH1_1a08.b1.seq+  GCACGCGCAAAGCATCCTTGCCATCTGGGCATGTCAGGTCGTTCTTATGGGCGCCGTTGA

consensus               GCACGCGCAAAGCATCCTCGCCATCTGGGCGGTGCAGGTGGTGCTCATGGGCTTCATCGA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_10a03.b1.seq+ GGTCTACCGCGTTGGTGGCCGGCCCCTCGGCGAGGGCCTCG
U_HW-SSH1_9e10.b1.seq+  GGGCTACCGTGTTGGTGGTGGGCCCCTCGGCGAGGGCCTCGACATCATCTACCCGGGCGG
U_HW-SSH1_14c04.b1.seq+ GGGCTACCGTGTTGGTGGCGGGCCCCTCGGCGAGGGCCTCGACATCATCTACCCGGGCGG
U_HW-SSH1_10c01.b1.seq+ GGGCTACCGTGTTGGTGGCGGGCCCCTCGGCGAGGGCCTCGACATCATCTACCCGGGCGG
U_HW-SSH1_10c03.b1.seq+ GGGCTACCGTGTTGGTGGCGGGCCCCTCGGCGAGGGCCTCGACATCATCTACCCGGGCGG
U_HW-SSH1_1a08.b1.seq+  GGGTTACCGCATTGCGGGCGGACCACTCGGTGAGATCGTAGACCCGCTCTACCCAGGCGG
                        ____________________________________________________________
consensus               GGGCTACCGTGTTGGTGGCGGGCCCCTCGGCGAGGGCCTCGACATCATCTACCCGGGCGG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_9e10.b1.seq+  CGCCTTCGACCCACTTGGCCTCGCCAACGACCCCGACACCGCCGCCGAGCTCAAGGTGAA
U_HW-SSH1_14c04.b1.seq+ CGCCTTCGACCCACTTGGTCTCCCCAACGACCCCGACACCGCCGCCGAGCTCGAGGTGAA
U_HW-SSH1_10c01.b1.seq+ CGCCTTCGACCCGCTCGGCCTCGCCGACGACCCCGACACCGCATCTGAGCTCAAGGTCAA
U_HW-SSH1_2e07.b1.seq+                                                          A
U_HW-SSH1_10c03.b1.seq+ CGCCTTCAACCCACTTGGTCTCGCCAACGACCCCGACACCGCCGCCGAGCTCGAGGTGAA
U_HW-SSH1_1a08.b1.seq+  CAGCTTCGATCCGCTCGGTCTTGCCAATGACCCCGAGGCATTTGCGGAGCTC-AGGTCAA
                        ____________________________________________________________
consensus               CGCCTTCGACCCACTTGGTCTCGCCAACGACCCCGACACCGCCGCCGAGCTCAAGGTGAA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_9e10.b1.seq+  GGAGCTCAAGAACGGCCGCCTCGCCATGTTCTCCATGTTCGGCTTCTTCGTGCAGGCCAT
U_HW-SSH1_14c04.b1.seq+ GGAGCTCAAGAACGGCCGCCTCACCATGTTCTCCATGTTCGGCTTCTTCATGCAGGCCAT
U_HW-SSH1_10c01.b1.seq+ GGAGCTCAAGAACGGCCGCCTCGCCATGTTCTCCATGTTCGGCTTCTTCGTGCAGGCCAT
U_HW-SSH1_2e07.b1.seq+  GGAGATCAAGAACGGCCGCCTCGCCATGTTCTCCATGTTCGGCTTCTTCGTCCAGGCCAT
U_HW-SSH1_10c03.b1.seq+ GGAGCTCAAGAACGGCCGCCTCGCCATGTTCTCCATGTTCGGCTTCTTCGTGCAGGCCAT
U_HW-SSH1_1a08.b1.seq+  GGAAATCAAGAACGGTTGTCTCGCCATGTTCTCCATGTTTGGTTTCTTTGTGCAAGCCAT
                        ____________________________________________________________
consensus               GGAGCTCAAGAACGGCCGCCTCGCCATGTTCTCCATGTTCGGCTTCTTCGTGCAGGCCAT

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_9e10.b1.seq+  CGTCACCGGGAAGGGGCCAGTTGAGAACCTCTTCGACCACGTCGCCGACCCGGTCAACAA
U_HW-SSH1_14c04.b1.seq+ CGCCACCGGTAAGGGGCCAGTTGAGAACCTCTTCTACCACGTCGCAGACCGGTGAGCAA
U_HW-SSH1_10c01.b1.seq+ CGTCACCGGAAAGGGGCCCGTAGAGAACCTCTTCGACCACGTCGCCGACCCGGTCAACAA
U_HW-SSH1_2e07.b1.seq+  CGTCACCGGCAAGGGCCCCCTCGAGAACCT
U_HW-SSH1_10c03.b1.seq+ CGTCACCGGGAAGGGGCCAGTTGAGAACCTCTTCGACCACGTCGCCGACCCGGTCAACAA
U_HW-SSH1_1a08.b1.seq+  TGTCACCGGCAAGGGTCCACTTGAGAACCTCGCTGACCCCCTC
                        ____________________________________________________________
consensus               CGTCACCGGCAAGGGGCCAGTTGAGAACCTCTTCGACCACGTCGCCGACCCGGTCAACAA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_9e10.b1.seq+  CAACGCCTGGGCCTTCGCCACCAACTTCGCCCCCGGAAGCTAAATGTGTTTAGCC----G
U_HW-SSH1_14c04.b1.seq+ CATCGCCTGGGCCTTCGCCACTAACTGCGCCCCGCGAAGTGAACTGTGTTCAGTC----G
U_HW-SSH1_10c01.b1.seq+ CAACGCGTGGGCCTTCGCCACCAACTTCGCCCCCGGAAGCTAAATGTGTTAAGCCATCTG
U_HW-SSH1_10c03.b1.seq+ CAACGCCTGGGCCTTCGCCACCAACTTCGCCCCCGGAAGCTAAATGTGTTTAGCC----G
                        ____________________________________________________________
consensus               CAACGCCTGGGCCTTCGCCACCAACTTCGCCCCCGGAAGCTAAATGTGTTTAGCC----G

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_9e10.b1.seq+  TCCGTCCATCGGACGAGATATGCATGTGTACCTCGGCC-GCGACCACGCTA
U_HW-SSH1_14c04.b1.seq+ TCCGTCCATCCGA-GAGATATGCATGTGTACCTCGGCC-GCGACCACTCTAATCACTATT
U_HW-SSH1_10c01.b1.seq+ TCCGTCCATCGGACGAGATATGCATGTGTACCTCGGCC-GCGACCACGCTA
U_HW-SSH1_10c03.b1.seq+ TCCCCCCATCGAACGAGATATGCATGTGTACCTCGGCCCGCGACCACGCTA
                        ____________________________________________________________
consensus               TCCGTCCATCGGACGAGATATGCATGTGTACCTCGGCC-GCGACCACGCTAATCACTATT

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_14c04.b1.seq+ GATACTG
                        _______
consensus               GATACTG

****************** Contig 62 ******************
                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8a04.b1.seq+  TTCGATTAGCGTGGTCCCGGCCGAGGTACACTGGACCGTATGTTAGCAGGCCAACCCTCC
                        ____________________________________________________________
consensus               TTCGATTAGCGTGGTCCCGGCCGAGGTACACTGGACCGTATGTTAGCAGGCCAACCCTCC

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8a04.b1.seq+  ATGCCTTTCGGCCCCCCCATCCCATTGCCCGCCCCCCCCCTTGGTAAAGATGGTGCTGGC
U_HW-SSH1_8a06.b1.seq+                                                  GTGCTAGC
U_HW-SSH1_8a05.b1.seq+                                                  GTGCTCGC
                        ____________________________________________________________
consensus               ATGCCTTTCGGCCCCCCCATCCCATTGCCCGCCCCCCCCCTTGGTAAAGATGGTGCTAGC

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8a04.b1.seq+  GGTTGGCTTTCCACTCAGCTTTATTGATCCATTCCGGGGGAAAAACCCTCCTTCCTCGT
U_HW-SSH1_8a06.b1.seq+  GGTTGGTTTTCCACTCCGCTTTATTGATCAATTCCAGTGGAAATACCCCCCTTTCCTCGT
U_HW-SSH1_8a05.b1.seq+  GGTTGGCTTTCCACTCAGGAGTAGGGATCCATTCCAGGGGAAATACCCTCCTTTCCTCGT
                        ____________________________________________________________
consensus               GGTTGGCTTTCCACTCAGCTTTATTGATCCATTCCAGGGGAAATACCCTCCTTTCCTCGT

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8a04.b1.seq+  GGGTTTAATATTAGGTTGCTGCCAGCTTTGACATAAATTTTTGTGGAGGATACTCTATTA
U_HW-SSH1_8a06.b1.seq+  GGGTTTCTTGTTAGTTTGCTTCCAGCTTTGACATAAATTTTTGTGGAGAATACTCTATTA
U_HW-SSH1_8a05.b1.seq+  GTTTTTCTTGTGAGTTTCATGCCAGCTTTGACACAAATTTTTGTGGAGAATACTGTATTA
                        ____________________________________________________________
consensus               GGGTTTCTTGTTAGTTTGCTGCCAGCTTTGACATAAATTTTTGTGGAGAATACTCTATTA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8a04.b1.seq+  CAATTTGGGGGAGGGGGTTTAAAACAACATCCGGGAAATGCGCCCCGCGGGCACGCCATT
U_HW-SSH1_8a06.b1.seq+  CAATTTGGGGGAGGAGGATTTGAACAAAATCCGGGAAATGCGCGCCGCG
U_HW-SSH1_8a05.b1.seq+  CAATTTGGGGGAGGGGGGTTTGAACAACATCGGGGGATGCGCCCGGCGCCCACGCCATC
                        ____________________________________________________________
consensus               CAATTTGGGGGAGGGGGGATTTGAACAACATCCGGGAAATGCGCCCCGCGCCCACGCCATC

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8a04.b1.seq+  AACTTGAAGGAAAACCCCTGTGCCCCTGGGGGCGACGGTTCAAAAAATCTCTC-GATTTG
U_HW-SSH1_8a05.b1.seq+  AACTTGTAGGAAAACCCCTGTGCACCTGTGGGGCGACGGTTCAAAAAATCTCGCAGACCCT
                        ____________________________________________________________
consensus               AACTTGAAGGAAAACCCCTGTGCACCTGGGGGCGACGGTTCAAAAAATCTCGCAGACCCG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8a04.b1.seq+  CCCCCCCTGGGGGGGGTACCCCATGGGATAGCCCCCACGGCTGGGGCTACCTATGGATTG
U_HW-SSH1_8a05.b1.seq+  CCCCCCCTGGGAGGACTACCCCATGCGATACCCCCCACGGCTGGG-CTGCATATGGTGTG
                        ____________________________________________________________
consensus               CCCCCCCTGGGAGGACTACCCCATGCGATACCCCCCACGGCTGGGGCTACATATGGAGTG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8a04.b1.seq+  AATTCGCTACTGTCCCCAAATTAGAATGGGGTGATCTTGGGCGCAAGGGTCTCACAGGAG
U_HW-SSH1_8a05.b1.seq+  AATTCGCTACCGTCCCCAAACTAGGATGAGATGATCTCGGGCGCAAGGGTCTCTGAGGAA
                        ____________________________________________________________
consensus               AATTCGCTACCGTCCCCAAACTAGAATGAGATGATCTCGGGCGCAAGGGTCTCACAGGAA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8a04.b1.seq+  TAAAAGTGTT
U_HW-SSH1_8a05.b1.seq+  TAAAAGTGTTGTTGATCACTGCTTCCACAACACGTGAAAGGAATTAACGTTTTGTGTCCA
                        ____________________________________________________________
consensus               TAAAAGTGTTGTTGATCACTGCTTCCACAACACGTGAAAGGAATTAACGTTTTGTGTCCA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8a05.b1.seq+  TGCCCGAGAGGCCACATTGAGACAGCAATCCCTTGTTTGGCAGTTGGGGTTTTTGAGTTG
                        ____________________________________________________________
consensus               TGCCCGAGAGGCCACATTGAGACAGCAATCCCTTGTTTGGCAGTTGGGGTTTTTGAGTTG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8a05.b1.seq+  GTTTTCGCGGGGAAATTGGGGGGGAGGCTCATTTTCCACTAACCCGATGTATCGCCCAGG
                        ____________________________________________________________
consensus               GTTTTCGCGGGGAAATTGGGGGGGAGGCTCATTTTCCACTAACCCGATGTATCGCCCAGG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8a05.b1.seq+  AAGTGGTTCTTGCAAAACGTCCGTTAAGGGGACCTGATTAATATTACCGCGATGTTCTCG
                        ____________________________________________________________
consensus               AAGTGGTTCTTGCAAAACGTCCGTTAAGGGGACCTGATTAATATTACCGCGATGTTCTCG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8a05.b1.seq+  TATACTGGTCGGGATACGTGACATATCTCGAAAGAGGTGGGATGCTTGCCCAGATTAGGG
                        ____________________________________________________________
consensus               TATACTGGTCGGGATACGTGACATATCTCGAAAGAGGTGGGATGCTTGCCCAGATTAGGG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8a05.b1.seq+  AAATAAACGGAAAAAAGCCCTGTAGCTTCACTT
                        _________________________________
consensus               AAATAAACGGAAAAAAGCCCTGTAGCTTCACTT

****************** Contig 63 ******************
                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8b07.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACACCGGCGTGTCCTCCTCCAGGCCATCGATCA
U_HW-SSH1_8b08.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACACCGGCGCGTCCGCCGCCAGGGCGTCGATCC
                        ____________________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACACCGGCGCGTCCGCCGCCAGGCCATCGATCA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8b07.b1.seq+  ATTATTTTCCTTTTTTGCGCTTATTGTGTTCTGATTCGATTGTGTAAAATACCGCCCGTC
U_HW-SSH1_8b08.b1.seq+  ATGTTGTGGCGTTTGGTTGCTTAAAGTGTTCTGATTCAACTGTGAAAAATACCGCCCGCC
                        ____________________________________________________________
consensus               ATGATGTGCCGTTTGGGCGCTTAAAGTGTTCTGATTCAACTGTGAAAAATACCGCCCGCC

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8b07.b1.seq+  GTTGGCAAACCAATATGGAGGGGGGTCACGTTTCAGGAGCCCTTCCCTCCTGAAGTCGAG
U_HW-SSH1_8b08.b1.seq+  GTTGGCAAGC-AATCTGGAGGGGGGTCACGATCCAGGACCCCTTCCCTCCTGAACTCAAG
                        ____________________________________________________________
consensus               GTTGGCAAACCAATATGGAGGGGGGTCACGATCCAGGACCCCTTCCCTCCTGAACTCAAG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8b07.b1.seq+  TGTTTATCCCTTTTGGATTCCCGAGGCAACGGACCTTTCCTTGAGAATAAGGGGGCA-AA
U_HW-SSH1_8b08.b1.seq+  TTGTTATCCCTTACGGATTCCCGAGGCAACATACCTTTTCTGGAGGGAAAGGGAGAACAA
                        ____________________________________________________________
consensus               TGGTTATCCCTTACGGATTCCCGAGGCAACAGACCTTTCCTGGAGAAAAAGGGAGAACAA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8b07.b1.seq+  TTTGGGAGGGGAGGAGAGGGACACAAACTTGGGGATGCCCCCGGCGGGCCCCCCCTCCAT
U_HW-SSH1_8b08.b1.seq+  TTTCGGAGGGGGGGGAGGGACAAAACCTTAGGGATGCCCCCGGGGGGCCCCCCCTCCAT
                        ____________________________________________________________
consensus               TTTCGGAGGGGAGGAGAGGGACAAAAACTTAGGGATGCCCCCGGCGGGCCCCCCCTCCAT

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8b07.b1.seq+  GCGAGGGAAACTCCCGGTGTGCCTGACGGCGCCAA
U_HW-SSH1_8b08.b1.seq+  GCAAAGGAACCTCCCCGGGTGCCTGAGGGCGCCAACTTGAAAAACCTCGGAGCGTTGGCG
                        ____________________________________________________________
consensus               GCAAAGGAAACTCCCCGGGTGCCTGACGGCGCCAACTTGAAAAACCTCGGAGCGTTGGCG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8b08.b1.seq+  AACGGATAGGCCGGCAGCGGAGTGGCGCCCCTGGAAGGGCGCGACGGATGTGACCAACAA
                        ____________________________________________________________
consensus               AACGGATAGGCCGGCAGCGGAGTGGCGCCCCTGGAAGGGCGCGACGGATGTGACCAACAA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8b08.b1.seq+  GGCCTTCAGGGTGGGGGCCATGGCGGTACCAGCGCGGGCGCCCGATTCAAATCTGAAGTA
                        ____________________________________________________________
consensus               GGCCTTCAGGGTGGGGGCCATGGCGGTACCAGCGCGGGCGCCCGATTCAAATCTGAAGTA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8b08.b1.seq+  AATTGTCGACCGCCTGTCGTTCCACAATAAGTGAAAAGCTTTCACTTTGTTGCATGTGTG
                        ____________________________________________________________
consensus               AATTGTCGACCGCCTGTCGTTCCACAATAAGTGAAAAGCTTTCACTTTGTTGCATGTGTG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8b08.b1.seq+  GGAGAGGCTATATTATAGAGGTCACATCACTTGCTTGGGCGAAGTGGGGTAACAAACTCT
                        ____________________________________________________________
consensus               GGAGAGGCTATATTATAGAGGTCACATCACTTGCTTGGGCGAAGTGGGGTAACAAACTCT

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8b08.b1.seq+  GGTTCACGCGGGGAAATTGCGGGGGGGCGCTTTTTTCCCCCATAATCCCGGCTGCGGGAA
                        ____________________________________________________________
consensus               GGTTCACGCGGGGAAATTGCGGGGGGGCGCTTTTTTCCCCCATAATCCCGGCTGCGGGAA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8b08.b1.seq+  AGAGGAACTCGTTTAGCCTCAAAGAGCCCATTAAAGGGTTTTCTATAATTTTTCTTCGTT
                        ____________________________________________________________
consensus               AGAGGAACTCGTTTAGCCTCAAAGAGCCCATTAAAGGGTTTTCTATAATTTTTCTTCGTT

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8b08.b1.seq+  TCCGCTTCTTCTTCTTATTGGGGTACGGGCTTATCTTGCGAGGACGTAGGAGGCCCCCCC
                        ____________________________________________________________
consensus               TCCGCTTCTTCTTCTTATTGGGGTACGGGCTTATCTTGCGAGGACGTAGGAGGCCCCCCC

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8b08.b1.seq+  GAAAAGGGTGAGAAACGTGTCATAACCCTGGTTATTCCA
                        _______________________________________
consensus               GAAAAGGGTGAGAAACGTGTCATAACCCTGGTTATTCCA

****************** Contig 64 ******************
                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8c08.b1.seq-  AGGCGGAGGAGCGCCCCAATATGCAAAGCTGCCTCTCCCGCGCGGTGGGCGGATTCATTA
                        ____________________________________________________________
consensus               AGGCGGAGGAGCGCCCCAATATGCAAAGCTGCCTCTCCCGCGCGGTGGGCGGATTCATTA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8c08.b1.seq-  ATGCACTGGCACGACAGGTTTCCGACTGGAAGGAGG-CAGTGAGCGCAACGCAAATAATG
U_HW-SSH1_12b02.b1.seq-                       GACTGCAAAGCGGGCAGTGAGCGCAACGCATCTAATG
                        ____________________________________________________________
consensus               ATGCACTGGCACGACAGGTTTCCGACTGCAAAGAGGGCAGTGAGCGCAACGCAAATAATG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8c08.b1.seq-  TGAGATAGCTCACTCAT--AGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATG
U_HW-SSH1_12b02.b1.seq- TGAGATAGCTCAATCAGTAAGACAGCCCAGACTTTACACTTTATGCTTCCAGCTCGTATG
U_HW-SSH1_11h11.b1.seq-                                     GCTTCCGGCTCGTTAG
                        ____________________________________________________________
consensus               TGAGATAGCTCAATCAGTAAGACACCCCAGACTTTACACTTTATGCTTCCGGCTCGTATG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8c08.b1.seq-  TTGTGTGGAAT-GT-GAGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGA-TA
U_HW-SSH1_12b02.b1.seq- TTGTGTCGAATTGT-GAACGGATAACA-TCTCACACAGGAAACAGCTATGACCATGAGTA
U_HW-SSH1_11h11.b1.seq- TTGTG-GGAATTGTTGAGCGG-TAACAATTTCACACAGGAAACAGCTATGACCATGATTT
                        ____________________________________________________________
consensus               TTGTGTGGAATTGT-GAGCGGATAACAATTTCACACAGGAAACAGCTATGACCATGAGTA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8c08.b1.seq-  CGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTATGCATCCAACGCGTTGGGAG
U_HW-SSH1_12b02.b1.seq- CGCCAAGCTATTTATGTGACACTATAGAATACTCAAGCTATGCATCCAACGCGTTGGGAG
U_HW-SSH1_11h11.b1.seq- CGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTATGCATCCAACGCGTTGGGAG
U_HW-SSH1_9f02.b1.seq-                                              ACGCGTGGGGAG
                        ____________________________________________________________
consensus               CGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTATGCATCCAACGCGTTGGGAG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8c08.b1.seq-  CTCTCCCATATGGTCGACCTGCAGGCGGCCGCGAATTCACTAGTGATTT------CGAG
U_HW-SSH1_12b02.b1.seq- CTCTCCCATATGGTCGACCTGCAGGCGGCCGCGAATTCACTAGTGATTT------CGAG
U_HW-SSH1_9e11.b1.seq-                    AGGCGGCCGGGAATTCATTATTGATTT------TGAG
U_HW-SSH1_1d05.b1.seq+                                                TT------CGAG
U_HW-SSH1_11h11.b1.seq- CTCTCCCATATGGTTGACCTGCAGGCGGCCGGGAATTCAATAGTGATTT------CGAG
U_HW-SSH1_9f02.b1.seq-  CTCTTCCATATGGGCGACCTGCAGGCGGCCGGGAATTCACTAGTGATATAATTGGCCGCC
U_HW-SSH1_8b11.b1.seq+                                                      CG
U_HW-SSH1_1b06.b1.seq-                                                    TTGAG
U_HW-SSH1_11a11.b1.seq+                                        TTCGATTT------CGAG
U_HW-SSH1_12b11.b1.seq+                                        TTCGATTT------CCAG
U_HW-SSH1_11c02.b1.seq+                                                 TTCGAG
U_HW-SSH1_11c04.b1.seq+                                        TTCGATTT------CGAG
U_HW-SSH1_16a12.b1.seq+                                        TTCGATTT------CGAG
U_HW-SSH1_4e09.b1.seq+                                         TTCGATTT------CGAG
U_HW-SSH1_2c10.b1.seq+                                         TTCGATTT------CGAG
U_HW-SSH1_2g07.b1.seq-                                            ATTT------CGAG
                        ____________________________________________________________
consensus               CTCTCCCATATGGTCGACCTGCAGGCGGCCGGGAATTCACTTTCGATTT------CGAG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH1_8c08.b1.seq-  CGGCC--GCCCGGGCAGGTACAGCCATGGCCCCCCACCGTGATGGCCTTGTTGGCCACCTC
U_HW-SSH1_12b02.b1.seq- CGGCC--GCCCGGGCAGGTACAGCCATGGCCCCCACCGTGATGGCCTCGTCGGCCACCTC
U_HW-SSH1_6e08.b1.seq-                    AGCCATGGCCCCCACCGTGATGGCCTCGTCGGCCACCTC
U_HW-SSH1_4b10.b1.seq-                          CCCCACCGAGATAGCCTCGTCGGCCCCCTC
U_HW-SSH1_9e11.b1.seq-  CGGCC--GCCCGGGCAGGTACAAACATGGCCCCCACCGTGATGACCAAGTCGGCCACCTC
U_HW-SSH1_1d05.b1.seq+  CGGCC--GCCCGGGCAGG-ACAGCCATGGCCCCCACCGTGATGGCCTCGTCGGCCCCCAC
U_HW-SSH1_11h11.b1.seq- CGGCC--GCCCGGGCAGGTACAGCCATGGCCCCCACCGTGATGGCCTCGTTGGCCACCTC
U_HW-SSH1_9f02.b1.seq-  CGGGCAGGTCCGGGCAGGTACAGCCATGGCCCCCCCCGTGATGGCCTCGTCGGCCACCTC
U_HW-SSH1_8a09.b1.seq+                    CACGGCCATGGCCCCCCACCAGGAGGGCCTCCCAGGCCTTTTC
U_HW-SSH1_8a10.b1.seq+     CC--CCCCCGACGTGCACGGCCATGGCCCCCACCGAGAGGGCCTCCCAGGCCACCTC
U_HW-SSH1_8b11.b1.seq+  TGGTCCCGGCCGAG-GTGCACCGGCATGGCCCCCACCGTGATGGCCTCGTCCGGCCACCTC
U_HW-SSH1_1b06.b1.seq-  CGGCC--GCCCGGGCAGGTACAGCCATGGCCCCCACCGTGATGGCCTCGTCGGCCACCTC
```



```
                                  .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_3f10.b1.seq+  AATTTTTCGCCCTCC
                        ________________________________________________________________
consensus               AATTTTTCGCCCTCC

******************* Contig 66 ********************
                                  .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_9g09.b1.seq+  TTCGATTTCGAGCGGCCGCCCGGGCGGGGACGTCGAGTTCCAGCGCAACGCGGAGCTGGA
U_HW-SSH1_4e08.b1.seq+                                  TCGAGTTCCAGCGCAACGCGGAGCTGGA
                        ________________________________________________________________
consensus               TTCGATTTCGAGCGGCCGCCCGGGCGGGGACGTCGAGTTCCAGCGCAACGCGGAGCTGGA

                                  .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_9g09.b1.seq+  CCCGGAGAGGAGGCTCTACCCCGGTGGCTCCTACTTCGACCCGCTGGGTCTCGCGGCGGA
U_HW-SSH1_4e08.b1.seq+  CCCGGAGAGGAGGCTCTACCCCGGTGGCTCCTACTTCGACCCGCTGGGGCTCGCGGCGGA
                        ________________________________________________________________
consensus               CCCGGAGAGGAGGCTCTACCCCGGTGGCTCCTACTTCGACCCGCTGGGGCTCGCGGCGGA

                                  .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_9g09.b1.seq+  CCCGGAGAAGAAGGAGACTCTGCAGCTGGCGGAGATCAAGCACGCCCGCCTCGCCATGGT
U_HW-SSH1_4e08.b1.seq+  CCTGGAAAAGAAGGAGACTCTGCAGCTGGCGGAGATCAAGCACGCCCGCCTCGCCATGGC
                        ________________________________________________________________
consensus               CCCGGAAAAGAAGGAGACTCTGCAGCTGGCGGAGATCAAGCACGCCCGCCTCGCCATGGC

                                  .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_9g09.b1.seq+  CGCCTTCCTCGGCTTCGCCGTGCAGGCCGCCGCCACCGGCAAGGGGCCGCTCAACAACTG
U_HW-SSH1_4e08.b1.seq+  CGCCTTCCTCGGCTTCGCCGTGCAGGCCGCCGCCACCGGCAAGGGGCCTCTCAACAACTG
                        ________________________________________________________________
consensus               CGCCTTCCTCGGCTTCGCCGTGCAGGCCGCCGCCACCGGCAAGGGGCCGCTCAACAACTG

                                  .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_9g09.b1.seq+  GGCCACCCACCTCAGCGACCCGCTGCACACCACCATCTTCGACACCTTGGGCTCCTCTTA
U_HW-SSH1_4e08.b1.seq+  GGCCACCCACCTCAGCGACCCGCTGCACACCACCATCTTCGACACCTTGGGTTCCTCTTA
                        ________________________________________________________________
consensus               GGCCACCCACCTCAGCGACCCGCTGCACACCACCATCTTCGACACCTTGGGCTCCTCTTA

                                  .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_9g09.b1.seq+  AGTGGTCGGTGGTCGAGCAATTTCTGTCAGCTCGGCTGCAAAATGGACGAACGCGCGTCC
U_HW-SSH1_4e08.b1.seq+  AGTGGTCGGTGGTCAAGCAATTTCTGTCAGCTCACCAACAAAATGGACAAACGCGCGTCC
                        ________________________________________________________________
consensus               AGTGGTCGGTGGTCAAGCAATTTCTGTCAGCTCACCAACAAAATGGACAAACGCGCGTCC

                                  .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_9g09.b1.seq+  GTGTAACGAACGTGCTTTGGTTTTGTATGACGAGTGATGGATGAGAGGGTATCGCA
U_HW-SSH1_4e08.b1.seq+  GTGTAACGAACGTGCTTTGGTTTTGTATGACGAGTGATGGATGAGAGGGTATCGCACAGA
                        ________________________________________________________________
consensus               GTGTAACGAACGTGCTTTGGTTTTGTATGACGAGTGATGGATGAGAGGGTATCGCACAGA

                                  .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_4e08.b1.seq+  TCCTTTGTTGATTAATGCAGGTCTGATCACAAAGGAGAGCTGCTGGGACTTGGTGATTTG
                        ________________________________________________________________
consensus               TCCTTTGTTGATTAATGCAGGTCTGATCACAAAGGAGAGCTGCTGGGACTTGGTGATTTG

                                  .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH1_4e08.b1.seq+  TAAAAAATGAACCATTGGTAACTTATTGCATCCACTTTGTACCTGCCCGGGCT
                        ________________________________________________________________
consensus               TAAAAAATGAACCATTGGTAACTTATTGCATCCACTTTGTACCTGCCCGGGCT
```

APPENDIX F

Detailed display of contig assemblies resulted from cluster analysis of SSH2 (R-D) sequence data by Cap3.

```
DETAILED DISPLAY OF CONTIGS
****************** Contig 1 ********************
                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10f06.b1.seq+ GTTTATTAAGCGAGTGCATGCTCCGGCCGCCATGGCGGCCGCGGGAATTCGATTTCAGGG
                        ________________________________________________________________
consensus               GTTTATTAAGCGAGTGCATGCTCCGGCCGCCATGGCGGCCGCGGGAATTCGATTTCAGGG

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10f06.b1.seq+ GCCGCCCGGGGGGGCACAAGTAGGTTATATATCAGCTGGGGATCTTCTACGGGCAGAAAT
U_HW-SSH2_12e12.b1.seq+                                 ATATATCAACTGGGGATCTTCTACGGGCTGAAGT
                        ________________________________________________________________
consensus               GCCGCCCGGGGGGGCACAAGTAGGTTATATATCAACTGGGGATCTTCTACGGGCAGAAAT

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10f06.b1.seq+ ATCTACTGGCACAGAGATAGGCAAAAAAGCAAAAGAATATATGGACAATGGCATGCTTGT
U_HW-SSH2_12e12.b1.seq+ ATCTTCTGGCACAGATATAGGCAAGAAAGCAAAAGAATATATGGACAATGGCATGCTTGT
                        ________________________________________________________________
consensus               ATCTACTGGCACAGAGATAGGCAAAAAAGCAAAAGAATATATGGACAATGGCATGCTTGT

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10f06.b1.seq+ CCCGGATCAAGTTGTGACAGATATGGTTGTATCACTACTATCACAGCCTGACGTGCGAGA
U_HW-SSH2_12e12.b1.seq+ CCCGGATCAAGTTGTGACAGATATGGTTGTATCACGACTATCACAGCCTGACGTGCGAGA
                        ________________________________________________________________
consensus               CCCGGATCAAGTTGTGACAGATATGGTTGTATCACGACTATCACAGCCTGACGTGCGAGA

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10f06.b1.seq+ AAGAGGGTGGCTTCTTGATGGTTACCCAGGGAGTTATGCTCAAGCACAAAGTCTTGGAAG
U_HW-SSH2_12e12.b1.seq+ AAGAGGGTGGCTTCTTGATGGTTACCCAAGGAGTTATGCTCAAGCACAAAGTCTTGGAAG
                        ________________________________________________________________
consensus               AAGAGGGTGGCTTCTTGATGGTTACCCAAGGAGTTATGCTCAAGCACAAAGTCTTGGAAG

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10f06.b1.seq+ TATGAAAAAAAAACCAGATATATTCATTTTACGGGAAGTTCCTGATGACAATCTAATCAA
U_HW-SSH2_12e12.b1.seq+ TATGAAAATAAAACCAGATATATTCATTTTACTGGAAGTTCCTGATGACAATCTAATCGA
                        ________________________________________________________________
consensus               TATGAAAAAAAAACCAGATATATTCATTTTACGGGAAGTTCCTGATGACAATCTAATCAA

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10f06.b1.seq+ TAGATGTGTTGGAAGAAGACTGGATCCTGTGACGGGCAAAATTTACCATGTAAAGAACTT
U_HW-SSH2_12e12.b1.seq+ TAGATGTGTTGAAAAAAGACTGGATCCTGTGACGGGCAAAATTTACCATGTAAAGAACTT
                        ________________________________________________________________
consensus               TAGATGTGTTGAAAAAAGACTGGATCCTGTGACGGGCAAAATTTACCATGTAAAGAACTT

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10f06.b1.seq+ CCCCCCAGAGAATGAGGAGATATCTGCCAGGCTTACTACACGCTCTGATGATACATTTGA
U_HW-SSH2_12e12.b1.seq+ CCCCCCAAAGAATGAGGAGATATCTGCCAGGCTTACTACACGCTCTGATGATACATTTGA
                        ________________________________________________________________
consensus               CCCCCCAAAGAATGAGGAGATATCTGCCAGGCTTACTACACGCTCTGATGATACATTTGA

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10f06.b1.seq+ AAAGGTTAAATCACGCCTTGAGACTTACAAACAAAATTCTGAAGCTGTTATTCCGACATA
U_HW-SSH2_12e12.b1.seq+ AAAGGTTAAATCACGCCTTGAGACTTACAAACAAAATTCTGAAGCTGTTATTCCGACATA
                        ________________________________________________________________
consensus               AAAGGTTAAATCACGCCTTGAGACTTACAAACAAAATTCTGAAGCTGTTATTCCGACATA

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10f06.b1.seq+ CTCAGATTTGCTTAACCAGATTGATGGAAATCGCCCAGTGGAAGTCATTTTTCATGAAAT
U_HW-SSH2_12e12.b1.seq+ CTCAGATTTGCTTAACCAGATTGATGGAAATCGCCCAGTGAAAGTCATTTTTCATGAAAT
                        ________________________________________________________________
consensus               CTCAGATTTGCTTAACCAGATTGATGGAAATCGCCCAGTGAAAGTCATTTTTCATGAAAT

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10f06.b1.seq+ AGAGTCCATGTTACAAAAGATTTGTACCTCGG
U_HW-SSH2_12e12.b1.seq+ AGAGTCCATGTTACAAAAGATTTGTACCTCGGGCCGCAAACCACGCTA
                        ________________________________________________________________
consensus               AGAGTCCATGTTACAAAAGATTTGTACCTCGGGCCGCAAACCACGCTA

****************** Contig 2 ********************
                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10g12.b1.seq+ TAGCGTGGTCGCGGCCGAGGAAGGGGGGGGATCCAGTCCGAAACTGCACTGCCGGTTTCC
U_HW-SSH2_10h01.b1.seq+                                   GATCCAGTCCGAAACTGCACTGCCGGTGACA
                        ________________________________________________________________
consensus               TAGCGTGGTCGCGGCCGAGGAAGGGGGGGGATCCAGTCCGAAACTGCACTGCCGGTGACA

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10g12.b1.seq+ GCACCCCAATCACCGGAGGAGAGACCCGCAAGAACGAATGGCCCGAATAGAATTGCTTGA
U_HW-SSH2_10h01.b1.seq+ GAAGCAAAAGCACAGGAGGAGAGACCCGCAAGAACGAATGGCCCGAATAGAATTGCTTGA
                        ________________________________________________________________
consensus               GAACCAAAAGCACAGGAGGAGAGACCCGCAAGAACGAATGGCCCGAATAGAATTGCTTGA

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10g12.b1.seq+ AGAGATGCATACTCCGGCCGGTCATCCTTGATTGCTTCGGTCCTTAGGGCAACTGGGAAT
U_HW-SSH2_10h01.b1.seq+ AGAGATGCATACTCCTGCCGGTCATCCTTGATTGCTTCGGACCTTAGGGCAACTGGGAAT
                        ________________________________________________________________
consensus               AGAGATGCATACTCCGGCCGGTCATCCTTGATTGCTTCGGACCTTAGGGCAACTGGGAAT

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10g12.b1.seq+ TGCAGTGATAGGTGATCGTTTGACCTCCACTGTTTGGTGACTGAAAGTAAAGAGCCTGGA
U_HW-SSH2_10h01.b1.seq+ TGCAGTGATAGGTGATCGTTTGAGCTCCACTGTTTGGTGACTGAAAGTAAAGAGCCTGGA
                        ________________________________________________________________
consensus               TGCAGTGATAGGTGATCGTTTGACCTCCACTGTTTGGTGACTGAAAGTAAAGAGCCTGGA

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10g12.b1.seq+ GTTACTGATCCCAAATCTTTGTCATTTAAAGTTGCTTTTGTGCCACTGGCAGATGTCCAT
U_HW-SSH2_10h01.b1.seq+ GTTACTGATCCCAAATCTTTGTCATTTAAAGTTGCTTTTGT
                        ________________________________________________________________
consensus               GTTACTGATCCCAAATCTTTGTCATTTAAAGTTGCTTTTGTGCCACTGGCAGATGTCCAT

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10g12.b1.seq+ GTTGGTATTCTCACATTCAATGTAACAGACTGACCATTTGTCTTCCCGGAAACAGAGAGT
                        ________________________________________________________________
consensus               GTTGGTATTCTCACATTCAATGTAACAGACTGACCATTTGTCTTCCCGGAAACAGAGAGT

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10g12.b1.seq+ GAAACTCGAAAGTTCATATCCGAGGAGCTGAGGGGCTCCAGTTGTTGGGTAACAGTAACC
                        ________________________________________________________________
consensus               GAAACTCGAAAGTTCATATCCGAGGAGCTGAGGGGCTCCAGTTGTTGGGTAACAGTAACC

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_10g12.b1.seq+ CCAGCTGTTTTCCAGTTGAAAGTGCTTGGTATGTACCTGCCCGGGCGGCCTATTGAA
                        ________________________________________________________________
consensus               CCAGCTGTTTTCCAGTTGAAAGTGCTTGGTATGTACCTGCCCGGGCGGCCTATTGAA

****************** Contig 3 ********************
                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11b01.b1.seq+ TTCCAGGGGCCCGCCGGACGTGTAGATGTTCCTCCGGTTAGGTTAAGTTACCATCACGGT
U_HW-SSH2_6f07.b1.seq+  TTCCGGGGGCCCCCCGGGCGTGTATATGTTCCTCCGGTTAGGTTAACTTACCATCTCGGT
                        ________________________________________________________________
consensus               TTCCAGGGGCCCCCCGGACGTGTAGATGTTCCTCCGGTTAGGTTAACTTACCATCACGGT

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11b01.b1.seq+ AACCATTATAATTCATTTGTTGATCCTCCTCGGCTGACAGTTGGGGCAGGCCTTGAATTT
U_HW-SSH2_6f07.b1.seq+  AACCATTATAATTCAGTTGTTGATCCCCGTCGGCTGACCGTTGGGGCAGGCCTTGAATTT
                        ________________________________________________________________
consensus               AACCATTATAATTCAGTTGTTGATCCCCCTCGGCTGACAGTTGGGGCAGGCCTTGAATTT

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11b01.b1.seq+ ACCTCCCTTAGAGGGACCAACATTGTTGACAGACACCAAGTGAAGGCTGCTTTAAAACCT
U_HW-SSH2_6f07.b1.seq+  ATCTCCCTTAGAGGGACCAACTGTGTTGACAGAGACCAAGTGAAGGCTGCAATAAAAGCT
                        ________________________________________________________________
consensus               ACCTCCCTTAGAGGGACCAACAGTGTTGACAGACACCAAGTGAAGGCTGCAATAAAACCT

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11b01.b1.seq+ CAGCAAGATCAGCAAATTGAGAACGCTCTTTTGGCTGAAGGGCGACTCTACTCTGATCTG
U_HW-SSH2_6f07.b1.seq+  CACCAAGATCAACAAATTGAGAACGCTCTTTTGGCTGAAGGGCGACTCTACTCTGATCTG
                        ________________________________________________________________
consensus               CACCAAGATCAACAAATTGAGAACGCTCTTTTGGCTGAAGGGCGACTCTACTCTGATCTG

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11b01.b1.seq+ GAGTTAGGTGAGAAGGAAATAAAGCGGATGGTGATGGAGGCCTCTCGGGCAAAGTATCTG
U_HW-SSH2_6f07.b1.seq+  GAGTTAACTGAAAAGGAAATAGAGCGGATGGTGATGGAGGCCTCTCGGGCAAATTATCTG
                        ________________________________________________________________
consensus               GAGTTAACTGAAAAGGAAATAAAGCGGATGGTGATGGAGGCCTCTCGGGCAAAGTATCTG

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11b01.b1.seq+ AACCAGCAGCAAGTTAACTTAAAAGAGTCATCAGGGTCAGGGGCACAACCATCTTCCTCC
U_HW-SSH2_6f07.b1.seq+  ACCCAGCAGCAAGTTAACTTCAAAGAGTCATCAAGGTCAGGGGCAGAGCCATCTTCCTCC
                        ________________________________________________________________
consensus               AACCAGCAGCAAGTTAACTTAAAAGAGTCATCAAGGTCAGGGGCACAACCATCTTCCTCC

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11b01.b1.seq+ GCCGCAATTATTGGATCATCTGGTTCGGCAGCGGATAGATGCGGTGATAATTGTATCATA
U_HW-SSH2_6f07.b1.seq+  GCCGCAATTAATGAATCATCTGGTTCGGCAGCGGATAAAGGCAGTGAGAATTGTTTCGTA
                        ________________________________________________________________
consensus               GCCGCAATTAATGAATCATCTGGTTCGGCAGCGGATAAAGGCAGTGAGAATTGTATCATA

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11b01.b1.seq+ CCTCGGCCGCAATCACGCTA
U_HW-SSH2_6f07.b1.seq+  CCTCGGCCGCGACCACGCTA
                        ________________________________________________________________
consensus               CCTCGGCCGCAACCACGCTA

****************** Contig 4 ********************
                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11f03.b1.seq- TAATAAGCAAACCCCGTGCAGGTGCCCCCCCTACCAATCGATTTTGGACATGATATCATA
                        ________________________________________________________________
consensus               TAATAAGCAAACCCCGTGCAGGTGCCCCCCCTACCAATCGATTTTGGACATGATATCATA

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11f03.b1.seq- TGTCGGAAGCCAGATATTCGGCCAGGCCTTTAGCACTAGGAAGGAGAGAGGGTGAGCCCG
                        ________________________________________________________________
consensus               TGTCGGAAGCCAGATATTCGGCCAGGCCTTTAGCACTAGGAAGGAGAGAGGGTGAGCCCG

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11f03.b1.seq- TCACTCACCACAGGCTTGCAACACGATCGTTCGATGCGTACATGAGGCGGATGTGTCAGG
                        ________________________________________________________________
consensus               TCACTCACCACAGGCTTGCAACACGATCGTTCGATGCGTACATGAGGCGGATGTGTCAGG

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11f03.b1.seq- GGATAAGGAACTCGCAGAGGAAATAGGAATGCCCACCCGGCACCGGAAGTGCAAGGTCCG
                        ________________________________________________________________
consensus               GGATAAGGAACTCGCAGAGGAAATAGGAATGCCCACCCGGCACCGGAAGTGCAAGGTCCG

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11f03.b1.seq- TGACAGGGATGCTCCGATTATTTAACCTCCCCTATTGATGTGCCCACTGTTGTCTAAAA
                        ________________________________________________________________
consensus               TGACAGGGATGCTCCGATTATTTAACCTCCCCTATTGATGTGCCCACTGTTGTCTAAAA

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11f03.b1.seq- GGTCGGGTTGTATTATGGGGCAATTATTGGCTCAGTTCCCGGGCAGGTTCGTTCACGGAC
U_HW-SSH2_5c11.b1.seq+                                      CCCGGGCAGGTACGTTCACGGAC
                        ________________________________________________________________
consensus               GGTCGGGTTGTATTATGGGGCAATTATTGGCTCAGTTCCCGGGCAGGTACGTTCACGGAC

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11f03.b1.seq- AAACATGTCTCCGGCGAAGGCGTTCGGGCATCTGATGTTGCCAAAAGTCGCACGGGGGAG
U_HW-SSH2_5c11.b1.seq+  AAACATGTCTCCGGTGAAGGTGTTCGGGCATCCGATGTTGACAAACGTCGCACGGGTGAT
                        ________________________________________________________________
consensus               AAACATGTCTCCGGCGAAGGCGTTCGGGCATCCGATGTTGACAAAAGTCGCACGGGGGAG

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11f03.b1.seq- GCTGTTCCTAGAAGAGATCGGGCCCGTGTACCCCGGCCCCGACCACGGTA
U_HW-SSH2_5c11.b1.seq+  GCTCTTCCTGGAGGAGGTCGGCGCCGAGTACCTCGGCCGCGACCACG
                        ________________________________________________________________
consensus               GCTCTTCCTAGAAGAGATCGGCCCCGAGTACCCCGGCCCCGACCACGGTA

****************** Contig 5 ********************
                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11g02.b1.seq+ TTCGATTTCGAGCGGCCGCCCGGGCAGGTACTGGAGCTAGCCCAATTAGCTCAATCAAGC
U_HW-SSH2_11h04.b1.seq+                                                 ATTATCTCAATCAACC
U_HW-SSH2_11h01.b1.seq+                                                 ATTAGCTCAATCAAGC
                        ________________________________________________________________
consensus               TTCGATTTCGAGCGGCCGCCCGGGCAGGTACTGGAGCTAGCCCAATTAGCTCAATCAAGC

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11g02.b1.seq+ ATGCTGGGGGTCCTTGGGAACTTGGTCTTACGGAAACACACCAGACACTCATACAAAATG
U_HW-SSH2_11h04.b1.seq+ ATGTTGGGGGTCCTTGGAAATTTGTTCTTACGGAAACACACAA-ACACTCATACGAAATG
U_HW-SSH2_11h01.b1.seq+ ATGCTGGGGGTCCTTGGGAACTTGGTCTTACGGAAACACACCAAACACTCATACAAAATG
                        ________________________________________________________________
consensus               ATGCTGGGGGTCCTTGGGAACTTGGTCTTACGGAAACACACCAAACACTCATACAAAATG

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11g02.b1.seq+ GATTGAGAACCTCGGCCGCGACCACGCTA
U_HW-SSH2_11h04.b1.seq+ GATTGAGAAC-TCGGCCGCAACCAC
U_HW-SSH2_11h01.b1.seq+ GATTGAGAACCTCGGCCGCGACCAC
                        ________________________________________________________________
consensus               GATTGAGAACCTCGGCCGCGACCACGCTA

****************** Contig 6 ********************
                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11h07.b1.seq+ TTCGATTAGCGTGGTCGCGGCCGAGGTACCT-TTATCTTATCTTTTAATTAGCTTTCCTC
U_HW-SSH2_5e02.b1.seq+         TAGCGTGGTCGCGGCCGAGGTACCT-TTTTCTTATCTTTTATTCAT-TTTCCTC
U_HW-SSH2_5c01.b1.seq+         TAGCGTGGTCGCGGCCGAGG-ACCT-TTATCTTATCTTTTAATTAGCTTTCCTC
U_HW-SSH2_11h08.b1.seq+        TAGCGTGGTCGCGGCCGAGGTACCT-TTATCTTATCTTTTAATTAGCTTTCCTC
U_HW-SSH2_1g12.b1.seq+                                  ATCTTATCTTTTAATTAGCTTTCCTC
U_HW-SSH2_1f11.b1.seq+         TAGCGTGGTCGCGGCGGAGGAACCAATTATCTTATTTTTTAATTAGCTTTCCTC
                        ________________________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACCT-TTATCTTATCTTTTAATTAGCTTTCCTC

                                 .   :   .   :   .   :   .   :   .   :   .   :   .   :   .
U_HW-SSH2_11h07.b1.seq+ TCCGACTT-CAGAGCCCCCTTTCAACATCGTCTTCCTCCAATGAGCGACACTTGAACATC
U_HW-SSH2_5e02.b1.seq+  TCCAACTT-CAGAGCCCCCTTGCAACATCATCTTCCTCCAATGATCGATGCTTGACCATC
U_HW-SSH2_5c01.b1.seq+  TCCGACTT-CAGAGCCCCCTTTCAACATCGTCTTCCTCCAATGAGCGACACTTGAACATC
U_HW-SSH2_11h08.b1.seq+ TCCGACTT-CAGAGCCCCCTTTCAACATCGTCTTCCTCCAATGAGCGACACTTGAACATC
U_HW-SSH2_1g12.b1.seq+  TCCTACCCACAAAACCCCCTTTCAACATCGTCTTCCTCCAATGAGCGACACTTGAACATC
U_HW-SSH2_1f11.b1.seq+  TCCGACAA-AAAAGCCCCCTTTCAACATCGTCTTCCTCCAATGAGCGACACTTGAACATC
                        ________________________________________________________________
```

```
consensus               TCCGACTT-CAGAGCCCCCTTTCAACATCGTCTTCCTCCAATGAGCGACACTTGAACATC

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11h07.b1.seq+ GCCTTCCTCCCCACTGTTGCTAGCACCCCAATCTCCTCTATTGACTCTCCTCGATTGTCAT
U_HW-SSH2_5e02.b1.seq+  CCCTTCCTCCCCACTGTTGCTAGCACCCCAATCTCCTCTATTGACTCTCCTCGATTG-CTT
U_HW-SSH2_5c01.b1.seq+  GCCTTCCTCCCCACTGTTGCTAGCACCCCAATCTCCTCTATTGACTCTCCTCGATTGTCAT
U_HW-SSH2_11h08.b1.seq+ GCCTTCCTCCCCACTGTTGCTAGCACCCCAATCTCCTCTATTGACTCTCCTCGATTGTCAT
U_HW-SSH2_1g12.b1.seq+  GCCTTCCTCCCCACTGTTGCTAGCACCCCAATCTCCTCTATTGACTCTCCTCGATTGTCAT
U_HW-SSH2_1f11.b1.seq+  CCCTTCCTCCCCACTGTTGCTACCACCCCAATCTCCTCTATTGACTCTCCTCGATTGTCAT
                        ____________________________________________________________
consensus               GCCTTCCTCCCCACTGTTGCTAGCACCCCAATCTCCTCTATTGACTCTCCTCGATTGTCAT

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11h07.b1.seq+ CCCAATCTCCTCTATTGACTCTCCTTGATTGTCATCCTAAATCTCCTTTGTTGACTCTCC
U_HW-SSH2_5e02.b1.seq+  CCCAATCTCCTCTATTGACTCTCTTGATTGGCACCCCAAATCTCCTTTGTTGACTCGCC
U_HW-SSH2_5c01.b1.seq+  CCCAATCTCCTCTATTGACTCTCCTTGATTGTCATCCTAAATCTCCTTTGTTGACTCTCC
U_HW-SSH2_11h08.b1.seq+ CCCAATCTCCTCTATTGACTCTCCTTGATTGTCATCCTAAATCTCCTTTGTTGACTCTCC
U_HW-SSH2_1g12.b1.seq+  CCCAATCTCCTCTATTGACTCTCCTTGATTGTCATCCTAAATCTCCTTTGTTGACTCTCC
U_HW-SSH2_1f11.b1.seq+  CCCAATCTCCTCTATTGACTCTCCTTGATTGGCATCCTAAATCTCCTTTGTTGACTCTCC
                        ____________________________________________________________
consensus               CCCAATCTCCTCTATTGACTCTCCTTGATTGTCATCCTAAATCTCCTTTGTTGACTCTCC

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11h07.b1.seq+ TCGATTGTCATCAGCTCCATCGATCAATGGATCAAGAATATC-TCTCTAGATGGCATCCA
U_HW-SSH2_5e02.b1.seq+  TCGATTGTCGTAAGATGGATCAATGAATGAATCAAAAATATC-TCTTGATATGGCATCCA
U_HW-SSH2_5c01.b1.seq+  TCGATTGTCATCAGCTCCATCAATCAATGGATCAAGAATATC-TCTCTAGATGGCATCCA
U_HW-SSH2_11h08.b1.seq+ TCGATTGTCATCAGCTCCATCGATCAATGGATCAAAAATATC-TCTCTAGATGGCATCCA
U_HW-SSH2_1g12.b1.seq+  TCGATTGTCATCAGCTCCATCGATCAATGGATCAAAAATATCCTCTCTAGATGGCATCCA
U_HW-SSH2_1f11.b1.seq+  TCGATTGTCATCAGCTCCATCGATCAATGGATCAAAAATATC-TCTCTAGATGGCATCCA
                        ____________________________________________________________
consensus               TCGATTGTCATCAGCTCCATCGATCAATGGATCAAAAATATC-TCTCTAGATGGCATCCA

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11h07.b1.seq+ AAAAACCTCTCTTTCCATCGTGCAAACGTGGTAAACTCACCCATCCCTATAATATCTCCC
U_HW-SSH2_5e02.b1.seq+  AAAAACCTCTCATTCCATCGTGCAATGTTGGAAAACTCACCCATCCCTATAAAATCTCCC
U_HW-SSH2_5c01.b1.seq+  AAAAACCTCTCTTTCCATCGTGCAAACGTGGTAAACTCAGCCATCCCTATAATATCTCCC
U_HW-SSH2_11h08.b1.seq+ AAAAACCTCTCTTTCCATCGTGCAAACGTGGTAAACTCAGCCATCCCTATAATATCTCCC
U_HW-SSH2_1g12.b1.seq+  AAAATC
U_HW-SSH2_1f11.b1.seq+  AAAATCCTCTCTTTCCAT
                        ____________________________________________________________
consensus               AAAAACCTCTCTTTCCATCGTGCAAACGTGGTAAACTCACCCATCCCTATAATATCTCCC

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11h07.b1.seq+ CCATGTAATGCTTCCACGGCCTCAGATATTAGGGTACCTGCCCGGGCGGCCGCTCTATCT
U_HW-SSH2_5e02.b1.seq+  CCATGTGATGCTACCTCGGCCATAAATATAAGGATACCTGCCCGGGCGG
U_HW-SSH2_5c01.b1.seq+  CCATGTAATGCTTCCACGGCCTCAAATATTAGGGTACCTGCCCGGGCGGCCGCTC
U_HW-SSH2_11h08.b1.seq+ CCATGTAATGCTTCCACGGCCTCAGATATTAGGGTACCTGCCCGGGCGGCCGCTC
                        ____________________________________________________________
consensus               CCATGTAATGCTTCCACGGCCTCAAATATTAGGGTACCTGCCCGGGCGGCCGCTCTATCT

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11h07.b1.seq+ CAATAGTTAAATTCACGGCCAACGGGCAGGTCCAACATATGGAACAACTCCCCACAACGC
                        ____________________________________________________________
consensus               CAATAGTTAAATTCACGGCCAACGGGCAGGTCCAACATATGGAACAACTCCCCACAACGC

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11h07.b1.seq+ AAAAAAG
                        _______
consensus               AAAAAAG

****************** Contig 7 ******************

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11h12.b1.seq+ TTCGATTAGCGTGGTCGCGGCCGAGGTACCCTACCGT-CTGCCTGGAGACGGGTCCCTAG
U_HW-SSH2_11h10.b1.seq+           CGTGGTCGCGGCCGAGGTACCCTACCAAGCTCGCTGGAGACGGATCCATAG
U_HW-SSH2_5b12.b1.seq+            CGTGGTCGCGGCCGAGGTACCCTACCGAGCTCGCTGGAGACGGATCCATAG
                                  __________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACCCTACCGAGCTCGCTGGAGACGGATCCATAG

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11h12.b1.seq+ GAGCACTGCCCCCAGCCCAAGTAATTTTAGCCACGGAACGTCCTGCTAATTTGCTGGAC
U_HW-SSH2_11h10.b1.seq+ GAGCACAGCCAGCAGCTCAAGTAGTTTTACCCGCGCAACCATCCTGCTAATTTGCTGGAC
U_HW-SSH2_5b12.b1.seq+  GAGCACAGCCAGCAGCTCAAGTAATTTTACCCGCGCAACCATCCTGCTAATTTGCTGGAC
                        ____________________________________________________________
consensus               GAGCACAGCCAGCAGCTCAAGTAATTTTACCCGCGCAACCATCCTGCTAATTTGCTGGAC

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11h12.b1.seq+ TTGAAGAATACCAACTAGTCGACGGACACAGGACGTTCCTGCAGGCTATGTCCTCCGAGC
U_HW-SSH2_11h10.b1.seq+ CTGAAGAATACCGACGAGTCGACGGACACAGGACGTTCCTGCAGGCTATGTCCTCCGAGC
U_HW-SSH2_5b12.b1.seq+  CTGAAGAATACCGACGAGTCGACGGACACAGGACGTTCCTGCAGGCTATGTCCTCCGAGC
                        ____________________________________________________________
consensus               CTGAAGAATACCGACGAGTCGACGGACACAGGACGTTCCTGCAGGCTATGTCCTCCGAGC

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11h12.b1.seq+ CTCGTGAAATCATGAGGACAAAGCTTCCGTGCCTACTTCACCTCGGCAGGACCAATGAT
U_HW-SSH2_11h10.b1.seq+ CTCGTGAAATCATGAGGACAGAAGCTTCCGTGCCTACTTCAACTCTGCAGGACCAATGAA
U_HW-SSH2_5b12.b1.seq+  CTCGTGAAATCATGAGGACAGAAGCTTCCGTGCCTACTTCAACTCTGCAGGACCAATGAA
                        ____________________________________________________________
consensus               CTCGTGAAATCATGAGGACAGAAGCTTCCGTGCCTACTTCAACTCTGCAGGACCAATGAA

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11h12.b1.seq+ GCTTGTTGTTTACACTTTGGGTGATGCAATTGATACTGATCTTGCACCCTGCTTGCTGCT
U_HW-SSH2_11h10.b1.seq+ GCTTGAAGTTTACAAGTTGGGGGATGCCAGTGATACTGATCTTGCACGCTGCTTGCTGCT
U_HW-SSH2_5b12.b1.seq+  GCTTGAAGTTTACAAGTTGGGGGATGCCAGTGATACTGATCTTGCACGCTGCTTGCTGCT
                        ____________________________________________________________
consensus               GCTTGAAGTTTACAAGTTGGGGGATGCCAGTGATACTGATCTTGCACGCTGCTTGCTGCT

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11h12.b1.seq+ GACTACTTGATGTTATAAAATTTAAGTCAAATTAAGCGTCATGTGACTTGATGCATTAGT
U_HW-SSH2_11h10.b1.seq+ GTCTACTTGATGTTTTTAAATTTAAGTCAAATTAAGCGTCATGTGTCGTTAAACTTTAGT
U_HW-SSH2_5b12.b1.seq+  GTCTACTTGATGTTTTTAAATTTAAGTCAAATTAAGCGTCGTGTGTCGTTAAACTTTATT
                        ____________________________________________________________
consensus               GTCTACTTGATGTTTTTAAATTTAAGTCAAATTAAGCGTCATGTGTCGTTAAACTTTAGT

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11h12.b1.seq+ TATGTGCAGTCTTGCCATTTTGGTTCTCGCGAATGTGTGCTAAACTACTGTTGGATCTTG
U_HW-SSH2_11h10.b1.seq+ TATGTCCAGTCTTGCGATTTTGGTTCGTGTGCCTGTGTGCTAAACTACTGTTGGATCTTG
U_HW-SSH2_5b12.b1.seq+  TATGTCCAGTCTTGCTATTTTGGTTCGTGTGCCTGTGTGCTAAACTACTGTTGGATCTTG
                        ____________________________________________________________
consensus               TATGTCCAGTCTTGCCATTTTGGTTCGTGTGCCTGTGTGCTAAACTACTGTTGGATCTTG

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5b12.b1.seq+  GATGCTATGTTTTGAGTCAAGATATGATTATGTACCTGCCCGGGCGGCCACTCGAAATCA
                        ____________________________________________________________
consensus               GATGCTATGTTTTGAGTCAAGATATGATTATGTACCTGCCCGGGCGGCCACTCGAAATCA

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5b12.b1.seq+  CTAGTGAATTCGCGGCCGCCTGCAGGTCGACTATATGGCATATCTCCCAACGCTCTGGAT
                        ____________________________________________________________
consensus               CTAGTGAATTCGCGGCCGCCTGCAGGTCGACTATATGGCATATCTCCCAACGCTCTGGAT

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5b12.b1.seq+  GCATAGCTTGAGTATTCTATAGTGCGACCTAGATAGAGTGGGCGTAATCACGGTCGTACT
                        ____________________________________________________________
consensus               GCATAGCTTGAGTATTCTATAGTGCGACCTAGATAGAGTGGGCGTAATCACGGTCGTACT

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5b12.b1.seq+  TGTTTCCTGCGTGAATTGTCATCCGCTCATACTTCGTGCCATATACTGATCCGAAAGTGT
                        ____________________________________________________________
consensus               TGTTTCCTGCGTGAATTGTCATCCGCTCATACTTCGTGCCATATACTGATCCGAAAGTGT

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5b12.b1.seq+  AAAGTGTAGAACCTGGGGTGCCTATGAGCGAACTAAATCCAGTAACTTGCGTCGCGCCTC
                        ____________________________________________________________
consensus               AAAGTGTAGAACCTGGGGTGCCTATGAGCGAACTAAATCCAGTAACTTGCGTCGCGCCTC

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5b12.b1.seq+  ACTGCCCGCTTACCAACGGGAAAACTGTCGTGCCAGCTGAATTTATGGATTCGGCCACTA
                        ____________________________________________________________
consensus               ACTGCCCGCTTACCAACGGGAAAACTGTCGTGCCAGCTGAATTTATGGATTCGGCCACTA

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5b12.b1.seq+  GCCGGCGAAATACG
                        ______________
consensus               GCCGGCGAAATACG

****************** Contig 8 ******************

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a04.b1.seq+ TTCGATTAGCGTGGTCGCGGCCGAGGGACTTCTTTGCCTCTCTTGTGATCGTAGTAAGAT

U_HW-SSH2_12a05.b1.seq+ TTCGATTAGCGGGGTCGCGGCCGAGGGACATCGTTGACTCCCTTGTCATCGTAGTAAGAT
                        ____________________________________________________________
consensus               TTCGATTAGCGGGGTCGCGGCCGAGGGACATCGTTGACTCCCTTGTCATCGTAGTAAGAT

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a04.b1.seq+ AAATTATGGCTAGGATCCAGTTCCTGGACTATGAATTGTTATTGGGTGT-TCCCCCCTTG
U_HW-SSH2_12a05.b1.seq+ AAGTTGTGGTTAGGAGCCAGTTCGTGGACAATGAATTGGTAGTAGGAGCATACTCCTTGG
                        ____________________________________________________________
consensus               AAATTATGGCTAGGAGCCAGTTCCTGGACAATGAATTGGTAGTAGGAGCATACCCCCTGG

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a04.b1.seq+ GTCATCTCAAAAGCAGGGACGGGGGCATTTCACCTGACCATCAACACG
U_HW-SSH2_12a05.b1.seq+ GTTGTCTCCATAGCAGGGACGGGGGCATTTCACCTGACCATCAACACGCAGGTGGTATAA
                        ____________________________________________________________
consensus               GTCATCTCAAAAGCAGGGACGGGGGCATTTCACCTGACCATCAACACGCAGGTGGTATAA

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a05.b1.seq+ TAGATACCCCCCCCAGACATTGATAAACGGGATGGGACGGGTTGGGGAATGGGGGTGGTG
                        ____________________________________________________________
consensus               TAGATACCCCCCCCAGACATTGATAAACGGGATGGGACGGGTTGGGGAATGGGGGTGGTG

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a05.b1.seq+ TAAAAAAGCTGAAAGTAATAAGAAAAGGCGTTGCTGGAAATGTACCTGGGCAGAAACCAC
                        ____________________________________________________________
consensus               TAAAAAAGCTGAAAGTAATAAGAAAAGGCGTTGCTGGAAATGTACCTGGGCAGAAACCAC

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a05.b1.seq+ CCTAATGGCTGGAGAATTCTGGGCCCCCACCCGGTCTACCGCTGGGGGAGGTCCCCACTT
                        ____________________________________________________________
consensus               CCTAATGGCTGGAGAATTCTGGGCCCCCACCCGGTCTACCGCTGGGGGAGGTCCCCACTT

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a05.b1.seq+ CTTTGATGACATAATAA
                        _________________
consensus               CTTTGATGACATAATAA

****************** Contig 9 ******************

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a07.b1.seq+ TTCGATTTCGAGCGGCCGCCCGGGCAGGTACTCTCCTCACTTCAATGACCGTGCCTATGT
U_HW-SSH2_12b06.b1.seq+ TTCGATTTCAAGGGGCCCCCCGGCCGGGAACTCTCCTCACTTCAATGACCGTGCCAATGT
U_HW-SSH2_12b07.b1.seq+ TTCGATTTCGAGCGGCCGCCCGGGCAGGTACTCTCCTCACTTCAATGAGCGTGCCTATGT
                        ____________________________________________________________
consensus               TTCGATTTCGAGCGGCCGCCCGGGCAGGTACTCTCCTCACTTCAATGACCGTGCCTATGT

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a07.b1.seq+ CAAGACCTCTTCCGATACACTTGAGCTCTAACGCGAATATAATTTTGGCATTCTCCCGCA
U_HW-SSH2_12b06.b1.seq+ AAAGACTTCTTAA-ATACACTTGAGCTCTAATGCGTATATAATTTTGGCATTCCCCCTCG
U_HW-SSH2_12b07.b1.seq+ CAAGACCTCTTCCAATAGACTTGAGCTCTAACGCGTATAGAATTTTGGCATTCTCCCGCA
                        ____________________________________________________________
consensus               CAAGACCTCTTCCAATACACTTGAGCTCTAACGCGTATATAATTTTGGCATTCTCCCGCA

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a07.b1.seq+ TAGCAATATCGATCTGATAGTCTGTGATCCCGAAAAGATGTTATAATGGAAGTATGAAGT
U_HW-SSH2_12b06.b1.seq+ TATCATTATCGATCTGGGA-TCTGTGATCCCCACAAGATGTTTAATGGAAGTATGAAAT
U_HW-SSH2_12b07.b1.seq+ TAGCAATATCGATCTGATAGTCTGTGATCCCAAAAAGATGTTTCCATGGAAGTATGAAGT
                        ____________________________________________________________
consensus               TAGCAATATCGATCTGATAGTCTGTGATCCCAAAAAGATGTTTAATGGAAGTATGAAGT

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a07.b1.seq+ CTGATGCATCACCAAAGACAAGATTTGACACTTTATTTAACTTTTGGAATGCATCGAGTC
U_HW-SSH2_12b06.b1.seq+ CTGATGCCTCTCCAAAAACAAGATTTGACACAAAAATTAACTTTTGGAATGCTTCGAGTC
U_HW-SSH2_12b07.b1.seq+ CTGATGCATCTCCAAAGACAAGATTTGACACAAAAATTAACTTTTGGAATGCATCGAGTC
                        ____________________________________________________________
consensus               CTGATGCATCTCCAAAGACAAGATTTGACACAAAAATTAACTTTTGGAATGCATCGAGTC

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a07.b1.seq+ TCTCTCTGTATAAGCGTCAACCAATCGCAATGTGCATATTTGCACCATCCACATCATCAA
U_HW-SSH2_12b06.b1.seq+ TCTCTCTGTATAAACGTCTACCAATCGCCATGTGCATATTTGCACCATCCACATCATCAA
U_HW-SSH2_12b07.b1.seq+ TCTCTCTGTATAAGCGTCTACCAATCGCCATGTGCATATTTGCAGCATCCACATCATCAA
                        ____________________________________________________________
consensus               TCTCTCTGTATAAGCGTCTACCAATCGCCATGTGCATATTTGCACCATCCACATCATCAA

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a07.b1.seq+ GTCAAAGAGCTTTTTTAAACTTTTTAATAGCTTCAACCTCAGTACCTCGGCCGCGACCAC
U_HW-SSH2_12b06.b1.seq+ GTCCAATAGCTTTTTTAATCTTTTTAATAGCTTCGACCTCAGTACCTCGGCCGCGACCAC
U_HW-SSH2_12b07.b1.seq+ GTCCAAGAGCTTTTTTAAACTTTTTAATAGCTTCAACCTCAGTACCTCGGCCGCGACCAC
                        ____________________________________________________________
consensus               GTCCAAGAGCTTTTTTAAACTTTTTAATAGCTTCAACCTCAGTACCTCGGCCGCGACCAC

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a07.b1.seq+ GCTA
U_HW-SSH2_12b06.b1.seq+ GCTA
U_HW-SSH2_12b07.b1.seq+ GCTA
                        ____
consensus               GCTA

****************** Contig 10 ******************

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c05.b1.seq+ TCGAGCGGCCGCCCCGGACGGAACTCATTGGGTCCCTTGGAAGAAGAATAGGAAAACTTG
                        ____________________________________________________________
consensus               TCGAGCGGCCGCCCCGGACGGAACTCATTGGGTCCCTTGGAAGAAGAATAGGAAAACTTG

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c05.b1.seq+ TTGCTAGGAGCCAATTCAGGGACCATGAATTGGAATTTGGTGTCAAACCCCTTGGTCATC
U_HW-SSH2_5b11.b1.seq+                                                  CTTGGTCATC
U_HW-SSH2_12b04.b1.seq+                                                 CTTGGTCATC
                        ____________________________________________________________
consensus               TTGCTAGGAGCCAATTCAGGGACCATGAATTGGAATTTGGTGTCAAACCCCTTGGTCATC

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c05.b1.seq+ TCCTTAGCAGGGACGGGGGCATTCCCCCTAGCCGTCAAGAAGTAGGTGCTCAAATTGATC
U_HW-SSH2_5b11.b1.seq+  TCCATAGCAGGGACGGTGGCGTTACCCCTAGCCATCGAGAAGTAGGTGCTCAAATTGATC
U_HW-SSH2_12b04.b1.seq+ TCCTTAACTGGGACGGGGGCATCCCCCCTAGCCATCAAGAAGTAGGTGCTCAAATTGATC
                        ____________________________________________________________
consensus               TCCTTAGCAGGGACGGGGGCATTCCCCCTAGCCATCAAGAAGTAGGTGCTCAAATTGATC

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c05.b1.seq+ TCCCCACCGGTCCATGAGTAACGGGCTGGGACGGCACCGAGAATGGGGGGGGGTGTCAAGA
U_HW-SSH2_5b11.b1.seq+  TCCCCACCGGTCCATGAGTAACGGTCTGGGACGGCACCGAGCATGGCGGTGGTGTCAAGA
U_HW-SSH2_12b04.b1.seq+ TCCCCCCCGGCCCATGATTAACCGGCTGGGACGGCACCGAGATTGGGGGGGGTGTCAAGA
                        ____________________________________________________________
consensus               TCCCCACCGGTCCATGAGTAACGGGCTGGGACGGCACCGAGAATGGGGGGGGTGTCAAGA

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c05.b1.seq+ ACCTGAACAAACTAGGAGAAGGTGTTGCTGGAAATGTCCCTCGGCCGCAACCAC
U_HW-SSH2_5b11.b1.seq+  ACCTGATCATAGTAAGAGAAGGTGTTGCTG
U_HW-SSH2_12b04.b1.seq+ ACCTGATCAAACTAAGAGAAGGCGTTGCTGAAATTGTCCCGCGGCAGCAACCACTCTAGT
                        ____________________________________________________________
consensus               ACCTGATCAAACTAAGAGAAGGTGTTGCTGAAAATGTCCCGCGGCAGCAACCACTCTAGT

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12b04.b1.seq+ GGCTTT
                        ______
consensus               GGCTTT

****************** Contig 11 ******************

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1a02.b1.seq+  TTCGATTTCGAGCGGCCGCCGGGGAAGAAAGGCTGAAAATTTGCAAAGCCCTGATTATGC
U_HW-SSH2_1h08.b1.seq+                                                  GCAAAGCCCTGATTATGC
                        ____________________________________________________________
consensus               TTCGATTTCGAGCGGCCGCCGGGGAAGAAAGGCTGAAAATTTGCAAAGCCCTGATTATGC

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1a02.b1.seq+  TGAAAA-CCGGAGTATGAAGCTTGTTGGCGGGACTTCCTTGAACGTTTGACAAATTATGA
U_HW-SSH2_1h08.b1.seq+  TGAAAAACCGGATAATGAAGCTGGATGGCAGGACTTCCTTGAACGTTTGACAAATTATGA
                        ____________________________________________________________
consensus               TGAAAAACCGGAGAATGAAGCTGGATGGCAGGACTTCCTTGAACGTTTGACAAATTATGA

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1a02.b1.seq+  AAAGGTCTACGAGCCAGTGCAGGAAGGCTCATATATCAAAATGATTGATATGGTAAAAGG
U_HW-SSH2_1h08.b1.seq+  AAAGGTCTACAAGCCAGTGCAGGAAGGCTCATATATCAAAATGATTGATATGGTAAAAGG
                        ____________________________________________________________
consensus               AAAGGTCTACAAGCCAGTGCAGGAAGGCTCATATATCAAAATGATTGATATGGTAAAAGG

                                .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1a02.b1.seq+  GGAGGGTGGCCAGTTACAGGTGAACAATATCAGTGGCTATCTCCCTGGGCGTATTGTCTT
```

```
U_HW-SSH2_1h08.b1.seq+  GGAGGGTGGCCAGTTACAGGTGAACAATATCAGTGGCTTTCTCCCGGGGCGTATTGTCTT
                        ____________________________________________________________
consensus               GGAGGGTGGCCAGTTACAGGTGAACAATATCAGTGGCTATCTCCCGGGGCGTATTGTCTT

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1a02.b1.seq+  TTTCTTGGTGAATTCTCATCTTGCGCCTCGGCCTATTTTGCTTACCAGGCAGGGGGAGAG
U_HW-SSH2_1h08.b1.seq+  TTTCTTGGTGAATTCTCTTCTTGCGCCTCGGCCTATTTTGCTTACCTGGCATGGGGAGAC
                        ____________________________________________________________
consensus               TTTCTTGGTGAATTCTCATCTTGCGCCTCGGCCTATTTTGCTTACCAGGCAGGGGGAGAC

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1a02.b1.seq+  TTTACACAATGTTAGAGGAAAAGTTGGTGGTGACACGGTGCTAAGTGAAGACGGAGACCT
U_HW-SSH2_1h08.b1.seq+  TTTCCCCAATGTTAAACGAAGATTTGGTGGTGAC
                        ____________________________________________________________
consensus               TTTACACAATGTTAAACGAAAAGTTGGTGGTGACACGGTGCTAAGTGAAGACGGAGACCT

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1a02.b1.seq+  TTACTCAAAGAAACTAGCCCACTTTATTGAAAACCG
                        ____________________________________
consensus               TTACTCAAAGAAACTAGCCCACTTTATTGAAAACCG

****************** Contig 12 ******************
                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1h07.b1.seq+  TTCGAGCGGCCGCCCGGGGAGGAACTAAGCCCTCCGTATTTCATGGGCCGCCGGGGGAAA
U_HW-SSH2_1a01.b1.seq+                                          TTCATGGGCCGCCGGGGGAAA
                        ____________________________________________________________
consensus               TTCGAGCGGCCGCCCGGGGAGGAACTAAGCCCTCCGTATTTCATGGGCCGCCGGGGGAAA

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1h07.b1.seq+  ACCGAAAACCACGCGACGTGCGGGGCTCTTCCGGCCACTGGACCCTACCTCCGGCTGAAC
U_HW-SSH2_1a01.b1.seq+  GCGAAAAACCACACTATTTGCGGGGCTCTTCCGGCCACTGGACCCTACCTCCGGCTGAAC
                        ____________________________________________________________
consensus               ACCAAAAACCACACGACGTGCGGGGCTCTTCCGGCCACTGGACCCTACCTCCGGCTGAAC

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1h07.b1.seq+  CGTTTCCAGTGCCCTGCAGGCCGTTAAGCAGAAAAGATAACTCTTCCCGAGGCCCCCGCC
U_HW-SSH2_1a01.b1.seq+  CGTTTCCGGGGTCG-GCAGGCCGTTAAGCAGAAAATATAACTCTTCCCGAGGCCCCCGCC
U_HW-SSH2_9c08.b1.seq-                  GCAGGCCGTTAAGCAGAAAAGATAACTCTTTCCGAGGCCCCAGCC
                        ____________________________________________________________
consensus               CGTTTCCAGGGCCCTGCAGGCCGTTAAGCAGAAAAGATAACTCTTCCCGAGGCCCCCGCC

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1h07.b1.seq+  GGCGTCTCCGGACTTCCTAACGTCGCCGTCAACCGCCACATCCCGGCTAGGGAAATCTTA
U_HW-SSH2_1a01.b1.seq+  GGCGTCTCCGGACTTCCTAACGTCGCCGTCCACCGCCACATCCCGGCTCGGGAAATCTTC
U_HW-SSH2_9c08.b1.seq-  GGCGTCTCCGGACTTCCTAACGTAGCCGTCAACCGCCACATCCCGGCTCAGGAAATCTTA
                        ____________________________________________________________
consensus               GGCGTCTCCGGACTTCCTAACGTCGCCGTCAACCGCCACATCCCGGCTCGGGAAATCTTA

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1h07.b1.seq+  ACCCGATTCCCTTTCGGGGGATGCGCGTGATCGCGCTATCTGCCGGGGTTACCCC
U_HW-SSH2_1a01.b1.seq+  ACCCGATTCCCTTTCGGGGGATGCGCTTGATTGCGCTATCTGCCGGGGTTTCCCC
U_HW-SSH2_9c08.b1.seq-  ACCCGATTCCCTTTTGGGGGATGCGCGTGATTGCGCTATCTGCAGGGGTTACCCCATCCC
                        ____________________________________________________________
consensus               ACCCGATTCCCTTTCGGGGGATGCGCGTGATTGCGCTATCTGCCGGGGTTACCCCATCCC

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9c08.b1.seq-  ATAAGATCCCCTTTCCCGTGTGCAAGTGCCGTTCACATGTTAATCTACGCCGTGCCCCTC
                        ____________________________________________________________
consensus               ATAAGATCCCCTTTCCCGTGTGCAAGTGCCGTTCACATGTTAATCTACGCCGTGCCCCTC

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9c08.b1.seq-  GGCCGCGACCACGCTA
                        ________________
consensus               GGCCGCGACCACGCTA

****************** Contig 13 ******************
                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_2c07.b1.seq+  TTCGAGCGGCCGCCCGGGCAGGAACCCAAGAAGCTTCAACAGGTGCTGGTGCCGGAACTC
                        ____________________________________________________________
consensus               TTCGAGCGGCCGCCCGGGCAGGAACCCAAGAAGCTTCAACAGGTGCTGGTGCCGGAACTC

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_2c07.b1.seq+  CCCAAGGAAGATCACCTCGGCCTGCAACCCCATCCCCAGGCATTGGAGTTAGTTGGGGCA
U_HW-SSH2_1d01.b1.seq+                                          AGGCTTTGGAGTT-GTTGGGGCA
                        ____________________________________________________________
consensus               CCCAAGGAAGATCACCTCGGCCTGCAACCCCATCCCCAGGCATTGGAGTTAGTTGGGGCA

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_2c07.b1.seq+  ATGGACTAGGACGAACAGCGGAAAGTAGTGGCTACTCTCAGGTGTATCGAATATTGGAAA
U_HW-SSH2_1d01.b1.seq+  ATGGACTAGGACTACCTGCGGAAAGTAGTGGCTACTCTCAGGTGTATCGAATATTGGAAG
                        ____________________________________________________________
consensus               ATGGACTAGGACGAACAGCGGAAAGTAGTGGCTACTCTCAGGTGTATCGAATATTGGAAA

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_2c07.b1.seq+  ATCATTATCAAACAATATCCAAAAAACTGCAATGTTGTGACAGCAAACTCTATCAAATGT
U_HW-SSH2_1d01.b1.seq+  ATCATTATCAAACAATATCCAAAAAACTGCAATGATGCGACACCAAACTCTATCAAATGT
                        ____________________________________________________________
consensus               ATCATTATCAAACAATATCCAAAAAACTGCAATGATGCGACACCAAACTCTATCAAATGT

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_2c07.b1.seq+  TTGAGGTTCTTACAAAATTTGATCCAAAAATAACATCCCTTCAGCCGTCACAAAAAAACA
U_HW-SSH2_1d01.b1.seq+  TTGAGGTTCTTACAAAATTTGATGCAAAAATAACATCCCTTCAGCCGTCACAAAAAAACC
                        ____________________________________________________________
consensus               TTGAGGTTCTTACAAAATTTGATCCAAAAATAACATCCCTTCAGCCGTCACAAAAAAACA

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_2c07.b1.seq+  AATCGCTGCTCAAAGTTTTGTGCACGGTTTGAGCAGCGTTGTTGTTTGGTTTGGTGGGTG
U_HW-SSH2_1d01.b1.seq+  ATTCGCTGCTCAAAGTTTTGTGCCCGGTTTCAGCAGCGTTGTTGTTTGGTTTGGTGGGTG
                        ____________________________________________________________
consensus               AATCGCTGCTCAAAGTTTTGTGCACGGTTTCAGCAGCGTTGTTGTTTGGTTTGGTGGGTG

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_2c07.b1.seq+  CTCCTGTGATGTTATTTTTGGA
U_HW-SSH2_1d01.b1.seq+  CTCCTGTGATGTTTTTTTTGGAATAAATTTTTGCACCCACCACAAATATTTGATATGGCT
                        ____________________________________________________________
consensus               CTCCTGTGATGTTATTTTTGGAATAAATTTTTGCACCCACCACAAATATTTGATATGGCT

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1d01.b1.seq+  GGGCGTCGAAAAATTTTAGATTTTGCTGCACCAGGAAATCTCACTTCT
                        _______________________________________________
consensus               GGGCGTCGAAAAATTTTAGATTTTGCTGCACCAGGAAATCTCACTTCT

****************** Contig 14 ******************
                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_2g06.b1.seq+  TAGCGTGGTCGCGGCAGAGGGAAAACAAACAGCTCAATAGAGCAGTTGACTTCTGCCAAA
                        ____________________________________________________________
consensus               TAGCGTGGTCGCGGCAGAGGGAAAACAAACAGCTCAATAGAGCAGTTGACTTCTGCCAAA

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_2g06.b1.seq+  AACGAGGGGTCTATCACCGTGTTGGGAAGCCTGAAAATCTTCTTCTTGATGAGAACCGCA
U_HW-SSH2_2h06.b1.seq+                                          AAAATCTTCTTCTTGATGA-AACCGCA
                        ____________________________________________________________
consensus               AACGAGGGGTCTATCACCGTGTTGGGAAGCCTGAAAATCTTCTTCTTGATGAGAACCGCA

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_2g06.b1.seq+  ATTTAAGGATCTCTCTCTGTGGGTTTGAGTGCACTTGCAAAATGCAAGAGACAAGATGGG
U_HW-SSH2_2h06.b1.seq+  ATTTAAGGATCTCTTTCTTTGG-TTTGAGTGCACTTGCATAATGCAAGAGACAAGATGGG
                        ____________________________________________________________
consensus               ATTTAAGGATCTCTCTCTGTGGGTTTGAGTGCACTTGCAAAATGCAAGAGACAAGATGGG

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_2g06.b1.seq+  CTGTTTCACACAACTTGTGGTACCTGCCCGGGCGG
U_HW-SSH2_2h06.b1.seq+  CTGCTTCACTCAATTTGTTTTACCTGCCC
                        ____________________________________________
consensus               CTGCTTCACACAACTTGTGGTACCTGCCCGGGCGG

****************** Contig 15 ******************
                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a08.b1.seq+  TAGCGTGGTCGCGGCGGAGGAACAGGGAAGGAATTGAGACGCGACAAAATGAAGCTTAGA
U_HW-SSH2_3e06.b1.seq+  TAGCGTGGTCGCGGCCGAGGTACATGAAAGGAATTGAGACGCGACAAAATGAAGCTTACC
U_HW-SSH2_9d05.b1.seq+  TAGCGTGGTCGCGGCCGAGGAACACGAAAGGAATTGAGACGCGACAAAATGAAGCTTACC
                        ____________________________________________________________
consensus               TAGCGTGGTCGCGGCCGAGGAACACGAAAGGAATTGAGACGCGACAAAATGAAGCTTACC

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a08.b1.seq+  C-CATAAGGGCCCCGACCTCGGCATGACACCTTCATCAAGTGCAACGACTCCAGGCATCT
U_HW-SSH2_3e06.b1.seq+  CTCATACGGTCACCGACCTCGTCATGACACCTTCATCAAGTGCAACGACTCCAGGCAGCT
U_HW-SSH2_9d05.b1.seq+  CAAAAACGGGCACCGACCTCGTCATGACACCTTCATCAAGTGCAACGACTCCAGGCAGCT
U_HW-SSH2_3a07.b1.seq+                                                  TCAAGTGCAACAACTCCAGGCACCT
                        ____________________________________________________________
consensus               CACATACGGGCACCGACCTCGTCATGACACCTTCATCAAGTGCAACGACTCCAGGCAGCT

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a08.b1.seq+  CCTTTCCTTCCAACAGCTCCAAGCTAGCGC-ACCACCAGTTGAGATGTGGCTCATAACAT
U_HW-SSH2_3e06.b1.seq+  CCTTTCCTTCCAACAGCTCCAAGCTAGCGCCACCACCAGTTGAGATGTGGCTCATAACAT
U_HW-SSH2_9d05.b1.seq+  CCTTTCCTTCCAACAGCTCCAAGCTAGCGCCACCACCAGTTGAGATGTGGCTCATAACAT
U_HW-SSH2_3a07.b1.seq+  CCTTTCCTTCCTT-AGCTCCAAACTAGCGC-ACCATG-GTTGAGATGTGGCTCATAACAT
                        ____________________________________________________________
consensus               CCTTTCCTTCCAACAGCTCCAAGCTAGCGCCACCACCAGTTGAGATGTGGCTCATAACAT

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a08.b1.seq+  CGGCCACTCCCACCTTCTCAACAGCCGCAACGGAGTCTCCACCTCCAATGATAGTTGTCA
U_HW-SSH2_3e06.b1.seq+  CAGCCACTCCCACCTTCTCAACAGCCGCAACGGAGTCTCCACCTCCAATGATAGTTGTCA
U_HW-SSH2_9d05.b1.seq+  CAGCCACTCCCACCTTCTCAACAGCCGCAACGGAGTCTCCACCTCCAATGATAGTTGTCA
U_HW-SSH2_3a07.b1.seq+  CGGC-ACTCCCACCTTCTCAACAGCCGCAACGGAGTCTCCACCTGGTAAGTGAGTTGTCA
                        ____________________________________________________________
consensus               CAGCCACTCCCACCTTCTCAACAGCCGCAACGGAGTCTCCACCTCCAATGATAGTTGTCA

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a08.b1.seq+  CACCCTTTTTGCTAAGCTCGGCCAACTTCTTTGCAATAGACTCAGTTCCTACTGCAAACT
U_HW-SSH2_3e06.b1.seq+  CACCCTTTTTGCTAAGCTCGGCCAACTTCTTTGCAATAGACTCAGTTCCTACTGCAAACT
U_HW-SSH2_9d05.b1.seq+  CACCCTTTTTGCTAAGCTCGGCCAACTTCTTTGCAATAGACTCAGTTCCTACTGCAAACT
U_HW-SSH2_3a07.b1.seq+  CACCCTTTTTGCTAACCTCGGCCAACTTCTTTGCAATAGAATCGGTTCCGACTGAAAACT
                        ____________________________________________________________
consensus               CACCCTTTTTGCTAAGCTCGGCCAACTTCTTTGCAATAGACTCAGTTCCTACTGCAAACT

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a08.b1.seq+  TGTCAAATTCAAAGACACCCATTGGTCCGTCCCAAATGATTGTCTGTGTTGTGTCCAGGG
U_HW-SSH2_3e06.b1.seq+  TGTCAAATTCAAAGACACCCATTGGTCCGTCCCAAATGATTGTCTGTGTTGTGTCCAGGG
U_HW-SSH2_9d05.b1.seq+  TGTCAAATTCAAAGACCCCCATTGGTCCGTCCCAAATGATTGTCTGTGTTGTGTCCAGGG
U_HW-SSH2_3a07.b1.seq+  TGTCAAATTCAAAGACACCCCTTGGTCCGTCCCAAATGATTGGCTGTGTTGACTCCAGGG
                        ____________________________________________________________
consensus               TGTCAAATTCAAAGACACCCATTGGTCCGTCCCAAATGATTGTCTGTGTTGTGTCCAGGG

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a08.b1.seq+  CATCATTAAATGTTTTGACTGAATCGGGGCCAATGTCCAGCCCCCTCCAACCATCAGGAA
U_HW-SSH2_3e06.b1.seq+  CATCATTAAATGTTTTGACTGAATCTGGGCCAATGTCCAGCCCCATCCAACCATCAGGAA
U_HW-SSH2_9d05.b1.seq+  CATCATTAAATGTTTTGACTGAATCTGGGCCAATGTCCAGCCCCATCCAACCATCAGGAA
U_HW-SSH2_3a07.b1.seq+  ATTAATTAATTGTTTGGCCTGAGTCGGGGCCAATGTCCAGCCCCCTCCCACCGTCATGAA
                        ____________________________________________________________
consensus               CATCATTAAATGTTTTGACTGAATCGGGGCCAATGTCCAGCCCCATCCAACCATCAGGAA

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a08.b1.seq+  TTGCATATGCAGGGACGGTCTGACTGTTACCATCC
U_HW-SSH2_3e06.b1.seq+  TTGCAGATGCAGGGACGGTCTGACTGTTAGCATCAGGAGC
U_HW-SSH2_9d05.b1.seq+  TTGCAGATGCGGGGACGGTCTGACTGTTAGCATCAGGAGC
U_HW-SSH2_3a07.b1.seq+  TTGAAAATGCGGGGACGGTCTGATTGTTACCATCCGGAGCCAACTAATCATGAAGGTTAC
                        ____________________________________________________________
consensus               TTGCAGATGCAGGGACGGTCTGACTGTTACCATCAGGAGCCAACTAATCATGAAGGTTAC

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a07.b1.seq+  CGTCACCTGGCAACAAAAGGGAGACCCTTTTTCTTTTGCCTCTGCCGGAGGATGTTGCAA
                        ____________________________________________________________
consensus               CGTCACCTGGCAACAAAAGGGAGACCCTTTTTCTTTTGCCTCTGCCGGAGGATGTTGCAA

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a07.b1.seq+  ACTTTAATACTGCTGCCCCGCCAGGAAAAACTAACTAATAATTTTTGTTCCCTGGTAAAG
                        ____________________________________________________________
consensus               ACTTTAATACTGCTGCCCCGCCAGGAAAAACTAACTAATAATTTTTGTTCCCTGGTAAAG

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a07.b1.seq+  GTGAATATCCCACCACCACATAAACAGGGAAATTCTTCTTCTTCAAAGGGGAACAACCC
                        ____________________________________________________________
consensus               GTGAATATCCCACCACCACATAAACAGGGAAATTCTTCTTCTTCAAAGGGGAACAACCC

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a07.b1.seq+  CGCCAAGCTGGATCGCCCCTTGGAACTCCTCTCCATTGCCCCCAAACGTGGATCCTTCTG
                        ____________________________________________________________
consensus               CGCCAAGCTGGATCGCCCCTTGGAACTCCTCTCCATTGCCCCCAAACGTGGATCCTTCTG

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a07.b1.seq+  GGTTTAAACCTCTTCCTTCCGGTTAGCTAATTTCCTTTTA
                        _______________________________________
consensus               GGTTTAAACCTCTTCCTTCCGGTTAGCTAATTTCCTTTTA

****************** Contig 16 ******************
                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3f04.b1.seq+  TAGCGTGGTCGCGGC-GAGGAAAAAAAAGCTGAAGGAGTTGGCAGGCAGCGACGTTCAGA
U_HW-SSH2_9b04.b1.seq+  TAGCGTGGTCGCGGCCGAGGGCAACAAAGCTGAAGGAGC-GGCAGGCAGCGACGTTCAAA
U_HW-SSH2_3g01.b1.seq+  TAGCGTGGTCGCGGC-GAGGAGAAAAAAGCTGAAGGAGTTGGCAGGCAGCGACGTTCAAA
U_HW-SSH2_3f02.b1.seq+                                  AAGGAGTTGGCAGGAACCGACTTTCATA
                        ____________________________________________________________
consensus               TAGCGTGGTCGCGGC-GAGGAAAAAAAAGCTGAAGGAGTTGGCAGGCAGCGACGTTCAAA

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3f04.b1.seq+  AAGGAGTCGACAATGGATTCAACAATGGAAAGCAGGACTAGAGAGAGGTTGGCTTCAGAG
U_HW-SSH2_9b04.b1.seq+  AAGGAATCAACAATGGATTCAACAAGGGAAAGCAGGACTAGAGAGAGGTTGGCTTCAGAG
U_HW-SSH2_3g01.b1.seq+  AAGGAGACGACAATGGATTCAACAGTGGAAAGCAGGACTAGAGAGAGGTTGGCTTCAGAG
U_HW-SSH2_3f02.b1.seq+  AAGGAGTCAACAATGGATTCAACAATGGAAAGCAAGACTAGAGAGAGGTTGACTTCAGAG
                        ____________________________________________________________
consensus               AAGGAGTCAACAATGGATTCAACAATGGAAAGCAGGACTAGAGAGAGGTTGGCTTCAGAG

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3f04.b1.seq+  GAC
U_HW-SSH2_9b04.b1.seq+  GAC
U_HW-SSH2_3g01.b1.seq+  GAC
U_HW-SSH2_3f02.b1.seq+  GACTCTTGGTCATACAAATCCTATCACTAATTCAAGTGGTCTCCGGAGTATATCCCCATG
                        ____________________________________________________________
consensus               GACTCTTGGTCATACAAATCCTATCACTAATTCAAGTGGTCTCCGGAGTATATCCCCATG

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3f02.b1.seq+  AAGGAGTACCTGCCCGAGCGGCCGCTCAAA
                        _____________________________
consensus               AAGGAGTACCTGCCCGAGCGGCCGCTCAAA

****************** Contig 17 ******************
                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3f08.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGA-CCTCTTCACCAACACCAACGTCCGCAAGATCG
U_HW-SSH2_3e07.b1.seq+        TAGCGTGGTCGCGGCCGAGGAACCCCTTCACCAACACCAACGTCCGCAAGATCG
U_HW-SSH2_3f07.b1.seq+        TAGCGTGGTCGCGGCCGAGGGACCGCTCCACCAACACCAACGTCCGCAAGATCG
U_HW-SSH2_3g07.b1.seq+                        CTTCACCAACACCAACGTCCGCAAGAGCG
U_HW-SSH2_3g02.b1.seq+        TAGCGTGGTCGCGGCCGAGGAACCCCTGCACCAACACCAACGTCCGCAAGATCG
U_HW-SSH2_3e08.b1.seq+        TAGCGTGGTCGCGGCCGAGGAACATCGGCACCAACACCAACGTCCGCAAGATCG
                              ____________________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGAACCCCTTCACCAACACCAACGTCCGCAAGATCG

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3f08.b1.seq+  GGCCAAAGGAGTTCACTTCTGTGTTTTACAGTCTTCAGAATTGGAGGGGCATATTTGAGA
U_HW-SSH2_3e07.b1.seq+  GGCCCAAAAAAAACACTTCTGTGTTTTACAGTCTTCAAAATTGGAGGGGCATATTTGAGA
U_HW-SSH2_3f07.b1.seq+  GGCCAAAGGAGATCACTTCTGTGTTTTACAGTCTTCAGAATTGGAGGGGCATTTTTGAGA
U_HW-SSH2_3g07.b1.seq+  GGCCAAAGGAGTTCACTTCTGTGTTTTACAGTCTTCAGAATTGGAGGGGGATTTTTGAGA
U_HW-SSH2_3g02.b1.seq+  GGCCAAAGGAGTTCACTTCTGTGTTTTACAGTCTTCAGAATTGGAGGGGCATATTTGAGA
U_HW-SSH2_3e08.b1.seq+  GGCCAAAGGAGTTCACTTCTGTGTTTTACAGTCTTCAAAATTGGAGGGGCATATTTGAGA
                        ____________________________________________________________
consensus               GGCCAAAGGAGTTCACTTCTGTGTTTTACAGTCTTCAGAATTGGAGGGGCATATTTGAGA

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3f08.b1.seq+  GGTTTGACCGTGACCAAAGTGGTAGAATTGATGCACCAGAACTGCGTGATGCTCTTCTAG
U_HW-SSH2_3e07.b1.seq+  GGTTTGACCGTGACCAAAGTGTTAGAATTGATGCACCAAAACTGCGAGATGCTCTTCTAG
U_HW-SSH2_3f07.b1.seq+  GGTTTGACCGTGACCAAAGTGGTAGAATTGATGCACCAGAACTGCGTGATGCTCTTCTAG
U_HW-SSH2_3g07.b1.seq+  GGTTTGACCGTGACCAAAGTGGTATAATTGATGCACCGGAACTGCGTGATGCTCTTCCTG
U_HW-SSH2_3g02.b1.seq+  GGTTTGACCGTGACCAAAGTGGTAGAATTGATGCACCAGAACTGCGTGATGCTCTTCTAG
U_HW-SSH2_3e08.b1.seq+  GGTTTGACCGTGACCAAAGTGGTAGAATTGATGCACCAAAACTGCGTGATGCTCTTCTAG
                        ____________________________________________________________
consensus               GGTTTGACCGTGACCAAAGTGGTAGAATTGATGCACCAGAACTGCGTGATGCTCTTCTAG

                                .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3f08.b1.seq+  ATCTTGGATATTCCGTTTCTCCTACTGTGCTAGACTTGCTTGTGTCTAAATTTGACAAGA
U_HW-SSH2_3e07.b1.seq+  ATCTTGGATATTCCGTTTCTCCTACTGTGCTAGACTTGCTTGTCTAAATTTGACAAGA
U_HW-SSH2_3f07.b1.seq+  ATCTTGGATATTCCGTTCCTCCTACTGTGCTAGACTTGCTTGTGTCTAAATTTGACAAGA
U_HW-SSH2_3g07.b1.seq+  ATTTTGGATTTCCCGTTTCCCGACTGTTTTTGACTTGCTTGTGTC
U_HW-SSH2_3g02.b1.seq+  ATCTTGAATATTCCGTTTCTCCTACTGTGCTAGACTTGCTTGTGTCTAAATTTGACAAGA
U_HW-SSH2_3e08.b1.seq+  ATCTTGGATATTCCGTTTCTCCTACTGTGCTAGACTTGCTTGTGTCTAAATTTGACAAGA
                        ____________________________________________________________
consensus               ATCTTGGATATTCCGTTTCTCCTACTGTGCTAGACTTGCTTGTGTCTAAATTTGACAAGA
```

```
                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3f08.b1.seq+  CTGGGGGCAAGAACAAAGCGGTTGAATATGACAACTTCATTGAATGCTGCCTTACAGTGA
U_HW-SSH2_3e07.b1.seq+  CTGGGGGCAAGAACAAAGCGGTTGAATATGACAACTTCATTGAATGCTGCCTTACAGTGA
U_HW-SSH2_3f07.b1.seq+  CTGGGGGCAAGAACAAAGCGGTTGAATATGACATCTTCATTGAATGCTGCCTTACAGGGA
U_HW-SSH2_3g02.b1.seq+  CTGGGGGCAAGAACAAAGGGGTTGAATATGACAACTTCATTGAATGCTGCCTTACAGTGA
U_HW-SSH2_3e08.b1.seq+  CTGGGGGCAAGAACAAAGCGGTTGAATATGACAACTTCATTGAATGCTGCCTTACAGTGA
                        ____________________________________________________________
consensus               CTGGGGGCAAGAACAAAGCGGTTGAATATGACAACTTCATTGAATGCTGCCTTACAGTGA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_3f08.b1.seq+  AGGGCCTGACCGAAAAGTTCAAGGAGAAGGACACGGTGTACCTGCCCGGGCGGCCGCTC
U_HW-SSH2_3e07.b1.seq+  AGGGCCTGACCAAAAAGTTCAAGGAAAAGGACACGGTGTACCGCCCGGG
U_HW-SSH2_3f07.b1.seq+  AGGGCCTGACCAAAAATTTCAAGGAAAAGGACACGGTGTCCCTGCCCGGGCGGCC
U_HW-SSH2_3g02.b1.seq+  AGGGCCTGACCCAAAAGTTCAAAGAAAAGGACACGTTGTACCTGCCCGGGC
U_HW-SSH2_3e08.b1.seq+  AGGGCCTGACCGAAAAGTTCAAGGAGAAGGACACGGTGTACCTGCCCGGGCGGCCGCTCG
                        ____________________________________________________________
consensus               AGGGCCTGACCAAAAAGTTCAAGGAAAAGGACACGGTGTACCTGCCCGGGCGGCCGCTCG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_3e08.b1.seq+  AAATCACTAGTGAATTCGCGGCCGCCCCGCGGGGCAACCATATGGGAGACCTCCCAACGCG
                        ____________________________________________________________
consensus               AAATCACTAGTGAATTCGCGGCCGCCCGCGGGGCAACCATATGGGAGACCTCCCAACGCG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_3e08.b1.seq+  TTGGATGCATAGTTTGAGTATTCTATAATGCCACCTAAAAAGCTTGGGGTAATCATGGTC
                        ____________________________________________________________
consensus               TTGGATGCATAGTTTGAGTATTCTATAATGCCACCTAAAAAGCTTGGGGTAATCATGGTC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_3e08.b1.seq+  ATAACTGTGTCCTGAGTGAAATTGTTATCCCCTCACAATTCCCAACAACATACGCCCCCC
                        ____________________________________________________________
consensus               ATAACTGTGTCCTGAGTGAAATTGTTATCCCCTCACAATTCCCAACAACATACGCCCCC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_3e08.b1.seq+  CGAAACATAAAATGATAACCTTGC
                        ________________________
consensus               CGAAACATAAAATGATAACCTTGC


****************** Contig 18 ******************
                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a09.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACAGGAATACTGACCCGTTGTCT-TCGACTACG
U_HW-SSH2_5a10.b1.seq+            GTGGTCGCGGCCGAGGTACAGGAATATTGACCTGTTGTCCATCGACTACG
                        ____________________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACAGGAATACTGACCCGTTGTCCATCGACTACG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a09.b1.seq+  CCTTTCGGCCTGATCTTAGGCCCTGACTCACCCTCCGTGGACCATGCTTGCGGAGGAACC
U_HW-SSH2_5a10.b1.seq+  CCTTTCGGCCTGATCTTAGGCCCTGACTCACCCTCCGTGGACGAACCTTGCGGAGGAAAC
                        ____________________________________________________________
consensus               CCTTTCGGCCTGATCTTAGGCCCTGACTCACCCTCCGTGGACCAACCTTGCGGAGGAAAC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a09.b1.seq+  CGGGGGTTTTCGGGGCATTGAATT-TCAA-AATGTTTACATTACACATCCCGACATTCGC
U_HW-SSH2_5a10.b1.seq+  CTTGGGTTTTCGGGGCATTGGATTCTCACCAATGTTTTCGTTACTCAAGCCGACATTCTC
                        ____________________________________________________________
consensus               CGGGGGTTTTCGGGGCATTGAATTCTCAACAATGTTTACATTACACAACCCGACATTCGC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a09.b1.seq+  GGTTCCGCTTCGACCACCCCCGCTTTCGCTGT-GCTTCCCTCCAAAAAGGAAAGCTCCCC
U_HW-SSH2_5a10.b1.seq+  GCTTCCGCTTCGTCAACCCCCGCTTTCACGGTTGCTTCCCTCTAAGGCGGAACGCTCCCC
                        ____________________________________________________________
consensus               GCTTCCGCTTCGACAACCCCCGCTTTCACGGTTGCTTCCCTCCAAAAAGGAAAGCTCCCC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a09.b1.seq+  TACCGATGCATTTTGACTTCCCACAACTACGACAAATAACTTACCCCCGTTGATCTTCAG
U_HW-SSH2_5a10.b1.seq+  TACCGATGCATTTTGACATCCCACATCTTCGGCAGATCGCTTAGCCCCGTTCATCTTCAA
                        ____________________________________________________________
consensus               TACCGATGCATTTTGACATCCCACAACTACGACAAATAACTTACCCCCGTTCATCTTCAA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a09.b1.seq+  CGCAAGGGCCCACAATCATTGAGCTATTCCGCCTTCTTTAAAGGGTGGCTGTTTCTAAGA
U_HW-SSH2_5a10.b1.seq+  CGCAAGGGCGCTCGATCAGTGAGCTATTACGCACTCTTTAAAGGGTGGCTGTTTCTAGGC
                        ____________________________________________________________
consensus               CGCAAGGGCCCACAATCAGTGAGCTATTACGCACTCTTTAAAGGGTGGCTGTTTCTAAGA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a09.b1.seq+  AAACCTCCTGGCTGCCATAGCACCCCCCAGTCCTTTAT-ATTGACCGGTCATTTAGGGGC
U_HW-SSH2_5a10.b1.seq+  AAACCTCCTGGCTGTCTTTCGCACCCCCACCTCCTTTATCACTGAGCGGTCATTTAGGGGC
                        ____________________________________________________________
consensus               AAACCTCCTGGCTGCCATAGCACCCCCCAACTCCTTTATCACTGACCGGTCATTTAGGGGC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a09.b1.seq+  CT
U_HW-SSH2_5a10.b1.seq+  CTTAGCTGGCGATCCGGGCTGTTTCCCTCTCAAAGATGAAGCTTATCCCCCCATCGTCTC
                        ____________________________________________________________
consensus               CTTAGCTGGCGATCCGGGCTGTTTCCCTCTCAAAGATGAAGCTTATCCCCCCATCGTCTC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a10.b1.seq+  ACTGGCCGACCTTGACCCCTGTTTATTTTTGGGTCATATCTAATATTCAGAGTTTGCCTC
                        ____________________________________________________________
consensus               ACTGGCCGACCTTGACCCCTGTTTATTTTTGGGTCATATCTAATATTCAGAGTTTGCCTC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a10.b1.seq+  GATTTGGCACCTGCCCGGGGCG
                        _____________________
consensus               GATTTGGCACCTGCCCGGGGCG


****************** Contig 19 ******************
                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a11.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACTTCGTGGGTATAAACAAAACTTTAAAGGGCT
U_HW-SSH2_11h05.b1.seq+       TAGCGTGGTCGCGGCCGAGGTACTTCGTGGGTATAAACAAAACTTTAAAGGGCT
                        ____________________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACTTCGTGGGTATAAACAAAACTTTAAAGGGCT

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a11.b1.seq+  ATACAGACGCTATATCTTGAAATTTGGTCAACCTGTGCCCTAGAAAGAAACCAGCAAAAT
U_HW-SSH2_11h05.b1.seq+ ATACAGACCCTATATCTTGAAATTTGGTCAACCTGTGCCCTAGAAAGAAACCAGCAAAAT
                        ____________________________________________________________
consensus               ATACAGACCCTATATCTTGAAATTTGGTCAACCTGTGCCCTAGAAAGAAACCAGCAAAAT

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a11.b1.seq+  TCACAAGTAGAATGCTCCTCAATCAGGATAATCTTCACTCGGTCTTTTGCAGCCATCCAA
U_HW-SSH2_11h05.b1.seq+ TCACAAGTAGAATGCTCCTCAATCAGGATAATCTTCACTCGGTCTTTTGCAGCCATCCAA
                        ____________________________________________________________
consensus               TCACAAGTAGAATGCTCCTCAATCAGGATAATCTTCACTCGGTCTTTTGCAGCCATCCAA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a11.b1.seq+  GCTTCCACGCATACATCACGAAAAAGGCGACTGTATCTGCTGACCAGACAACCGCAAACG
U_HW-SSH2_11h05.b1.seq+ GCTTCCACGCATACATCACGAAAAAGGCGACTGTATCTGCTGACCAGACAACCGCAAACG
                        ____________________________________________________________
consensus               GCTTCCACGCATACATCACGAAAAAGGCGACTGTATCTGCTGACCAGACAACCGCAAACG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a11.b1.seq+  ATTTCACAAAAAACGGGATGATCACGTTGATCAAAGGGACCAGGATGAACAAATAATTGA
U_HW-SSH2_11h05.b1.seq+ ATTTCACGAAGAACGGGATGATCCCGTTGATCAAAGGGACCAGGATGAACAAATAATTGA
                        ____________________________________________________________
consensus               ATTTCACAAAAAACGGGATGATCACGTTGATCAAAGGGACCAGGATGAACAAATAATTGA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a11.b1.seq+  GAGCCTCTTTCTCCTTGTTTGAGCAGTCACGGGCCCGTAAAGAAGGTATAGTGAACATCC
U_HW-SSH2_11h05.b1.seq+ GAGCCTCTTTCTCCTTGTTTGACCAGTCACGGGCCCGTAAAGAAGGTATAGTGAACATCC
                        ____________________________________________________________
consensus               GAGCCTCTTTCTCCTTGTTTGACCAGTCACGGGCCCGTAAAGAAGGTATAGTGAACATCC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a11.b1.seq+  AGATGGACCACATCCCCATGAGCCTCCAAATGTCCGGTTCGCTGGAGGGAAAGACGAGGT
U_HW-SSH2_11h05.b1.seq+ AGATGGACCACATCCCCATGAGCCTCCAAATGTCCGGTTCGCTGGAGGGAAAAACAAGGT
                        ____________________________________________________________
consensus               AGATGGACCACATCCCCATGAGCCTCCAAATGTCCGGTTCGCTGGAGGGAAAAACAAGGT

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5a11.b1.seq+  TGAAGGAAAGGGCGCCGCCGGCAAGCATGGAGGCGTACCTGCCCGGGCGGCCGCTCGAAT
U_HW-SSH2_11h05.b1.seq+ TGAAGGAAAGGGCGCCGCCGGCAAGCATGGAGGCGTACCTGCCCGGGCG
                        ____________________________________________________________
consensus               TGAAGGAAAGGGCGCCGCCGGCAAGCATGGAGGCGTACCTGCCCGGGCGGCCGCTCGAAT


****************** Contig 20 ******************
                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5c08.b1.seq+  TTCCAGGGGCCCCCCGGACTTGTACCAAATGGACTGGATTGAAGGCCAGCTTGACAATGA
U_HW-SSH2_5c09.b1.seq+  TTCCATGGGCCCCCCGGACGTGTACCAAATGGACTGGATTGAAGGCCGGCTTAACAAGGA
                        ____________________________________________________________
consensus               TTCCAGGGGCCCCCCGGACGTGTACCAAATGGACTGGATTGAAGGCCAGCTTAACAAGGA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5c08.b1.seq+  ATCCTTATTTCCTCAGAAACTTGAAGATTGACAGCCTCAAGGAGGAGGCTCATCTTAACT
U_HW-SSH2_5c09.b1.seq+  ATCCTTATTTCCTAAAAAAATTGAAGATTGACAGACTCAAGGAGGAGGCTCACCTTAACT
                        ____________________________________________________________
consensus               ATCCTTATTTCCTAAAAAAATTGAAGATTGACAGACTCAAGGAGGAGGCTCACCTTAACT

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5c08.b1.seq+  CCTGCTTCAAGCACTTCATTCTGTTTACGAACGAATTTGGGCTGATTGACAAGGAAGAAC
U_HW-SSH2_5c09.b1.seq+  CCTGCTTCACGCACTTCATTCTGTTTACCAGCGAATTTGGGCTGATTGTCAAGGAAGAAC
                        ____________________________________________________________
consensus               CCTGCTTCAAGCACTTCATTCTGTTTACCAACGAATTTGGGCTGATTGACAAGGAAGAAC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5c08.b1.seq+  TGGCTCCCCTCCAGGAGCTCATCAAATCAATCATCGTTCCCTACTGAAAAGGAAACACTG
U_HW-SSH2_5c09.b1.seq+  TGGCTCCCCTACAAGAGCTCG-CTAATGCATCATCGTTCCCTACTGATAAGGAAACACGG
                        ____________________________________________________________
consensus               TGGCTCCCCTACAAGAGCTCATCAAATCAATCATCGTTCCCTACTGAAAAGGAAACACGG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5c08.b1.seq+  AGGCTGAACCGAACAAAACATGGTTGCTACCGAGTCCTCTACAGGAATGGTCGAGCGATT
U_HW-SSH2_5c09.b1.seq+  AAGATGAACCCAACTACCCGTGGCTGCTACCGAATCCCCCTCAGGAATGGTCGAGCGATT
                        ____________________________________________________________
consensus               AAGATGAACCCAACAAAACATGGCTGCTACCGAATCCCCCACAGGAATGGTCGAGCGATT

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5c08.b1.seq+  GGGCTATCTGCGCCAATAATTTACTGGCTAAATCTTCTTGTTCCATTTCTTTGACATAAA
U_HW-SSH2_5c09.b1.seq+  GGGCTATCTGCCCCAATAATTTACTGGCTCTATCTTCTTGTTCCATTTCTTTGACATAAA
                        ____________________________________________________________
consensus               GGGCTATCTGCCCCAATAATTTACTGGCTAAATCTTCTTGTTCCATTTCTTTGACATAAA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5c08.b1.seq+  AAAACAAAGACATGTCCCTCGGCCGCGACCACGCTA
U_HW-SSH2_5c09.b1.seq+  AA
                        ___________________________________
consensus               AAAACAAAGACATGTCCCTCGGCCGCGACCACGCTA


****************** Contig 21 ******************
                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5c10.b1.seq+  TCCGAATCCCCTGCCTCCGGCCGCCTGGCGGGCCGCGGGATTTCAATTACCGTGGTCGCG
U_HW-SSH2_5c05.b1.seq+                                                  ATTAGCGTGGTCGCG
                        ____________________________________________________________
consensus               TCCGAATCCCCTGCCTCCGGCCGCCTGGCGGGCCGCGGGATTTCAATTACCGTGGTCGCG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5c10.b1.seq+  GCCGACGTTCA-AAGAACCTGTTGCTTCAGGTAGGGCAGCGTCTGGTATGTCTAGTGATG
U_HW-SSH2_5c05.b1.seq+  GCCGAGGTACACATGAACCTGGTGCTTCAGGTAGGGCATCGTCTGGAATGTCGAGTGATA
                        ____________________________________________________________
consensus               GCCGACGTACACAAGAACCTGGTGCTTCAGGTAGGGCAGCGTCTGGAATGTCGAGTGATA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5c10.b1.seq+  AAAG-AACCACCGGCAGACAGATGCTCGGGTGCTTATGCCACCACCTCGCTCATTACCAC
U_HW-SSH2_5c05.b1.seq+  AAAACAACCAGCGGCAGAGTAATGCTCGGGGGCTTATGCCACCCCCTCTCTCATTACCAC
                        ____________________________________________________________
consensus               AAAACAACCACCGGCAGACAAATGCTCGGGGGCTTATGCCACCACCTCGCTCATTACCAC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5c10.b1.seq+  CTAATATAGCTAGATCTGCGGATAAACGTGCGGTGTCCAGCTCTAGCAATGCTTCGACCA
U_HW-SSH2_5c05.b1.seq+  CTAATAGATCTGGATCTGCGGATAAACGTTCGGTGTCCAGCTGTAACAATGCTTCTACCA
                        ____________________________________________________________
consensus               CTAATAGAGCTAGATCTGCGGATAAACGTGCGGTGTCCAGCTCTAACAATGCTTCGACCA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5c10.b1.seq+  CCACAAGCGG-ATCTCATTCAAAACAAG-AAAGCATCCA-TCTTTCTGGAGATCACA-CC
U_HW-SSH2_5c05.b1.seq+  ACACAAGCGGTAACTCATTCAAAAATAGGAAAGCATTCAATCTTTCGGGAGATCACAACA
                        ____________________________________________________________
consensus               ACACAAGCGGTAACTCATTCAAAAAAGGAAAGCATCCAATCTTTCGGGAGATCACAACA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5c10.b1.seq+  CCACTCTGAGTTCGCTTTCTGATGCTCATAACCCACGCCCAAAA
U_HW-SSH2_5c05.b1.seq+  TCACTCTGAGTTCT-TTTCTGATGCTCATAAGCCACGCCGAAAAAGGAGACCGAAGAAAA
                        ____________________________________________________________
consensus               CCACTCTGAGTTCGCTTTCTGATGCTCATAACCCACGCCCAAAAAGGAGACCGAAGAAAA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5c05.b1.seq+  CTAATCAGTTGTGAATGAATATTCCAATCCTCCAAAAGAGCAAAAGCCAAAATCCGTTCC
                        ____________________________________________________________
consensus               CTAATCAGTTGTGAATGAATATTCCAATCCTCCAAAAGAGCAAAAGCCAAAATCCGTTCC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5c05.b1.seq+  TACCAAAGCGCGTCTTCTTTTTGATTCGATCGTTCTCCTATGGAGGAATATTCCTAAAGA
                        ____________________________________________________________
consensus               TACCAAAGCGCGTCTTCTTTTTGATTCGATCGTTCTCCTATGGAGGAATATTCCTAAAGA


****************** Contig 22 ******************
                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5e03.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACAACATCATCTGGTCTATTACCTCAAATGGTT
U_HW-SSH2_10g10.b1.seq+                                        CTGGTCTATTAGCTCAAATGGTT
U_HW-SSH2_12a10.b1.seq+                                        CTGGACTATTATCTCAAATGGTT
                        ____________________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACAACATCATCTGGTCTATTACCTCAAATGGTT

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5e03.b1.seq+  TCTATGAGTGCTGATGTTGCACGCGAGTATCTTGAAAAGTGGCAGATCTTCTTTTGGAG
U_HW-SSH2_10g10.b1.seq+ TCTATGAGGGCTGATGTTGCACGCTAGTATCTTGAGAAAGTGGCAGATCTTCTTTTGGAG
U_HW-SSH2_12a10.b1.seq+ TCTATGAGTGCTGATGTTGCACGCGAGTATCTTGAGAAACTGCTCCATCTTCTTTTGGAG
U_HW-SSH2_5g05.b1.seq-             ATGTTGCACGCGGGTATCTTG-GAAAGGGGCAGATCTTTTTTTGGAG
U_HW-SSH2_10f11.b1.seq+                                CTTGAGAAAATGGCAGATCTTCTTTTGGAG
                        ____________________________________________________________
consensus               TCTATGAGTGCTGATGTTGCACGCGAGTATCTTGAGAAAGTGGCAGATCTTCTTTTGGAG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5e03.b1.seq+  TTTGCACAAGCAGACACTGTTGTAAAATCTCTCATGTCTAGCCAAAGCCTTCTCGCACGG
U_HW-SSH2_10g10.b1.seq+ TTTGCACAAGCAGACACTGTTGTAAAATCTCTCATGTCTAGCCAAAGCCTTCTCGCACGG
U_HW-SSH2_12a10.b1.seq+ TTTGCACAAGTCCAC-CTGTTGTAAAATCTCTCATGTCTATCCAAAGCCTTCTCGCACGG
U_HW-SSH2_5g05.b1.seq-  TATGCACAAGCAGACACTGT-GTAAAATCTATCATGTCTAGCCAAAGCCTTCTTGCACGG
U_HW-SSH2_10f11.b1.seq+ TTGGCACAAGCAAACCCTGTTGTAAAGTCTCTCCTGCCTGGCCAAACCCTTCCCGCCCT
                        ____________________________________________________________
consensus               TTTGCACAAGCAGACACTGTTGTAAAATCTCTCATGTCTAGCCAAAGCCTTCTCGCACGG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5e03.b1.seq+  CTTTTCCAGATGTTCAACAAGATAGAATCTCCTATTCTTCTGAAGATTCTTAGGTGCATC
U_HW-SSH2_10g10.b1.seq+ CTTTTCCAGATGTTCAACAAGATAGAATCTCCTATTCTTCTGAAGATTCTTAGGTGCATC
U_HW-SSH2_12a10.b1.seq+ CTTTTCCAGATGTTCAAAAAGAAACAATCTCCTATTCTTCTGAACATTCTTAGGTGCATC
U_HW-SSH2_5g05.b1.seq-  CTTT-CCAGATGTTCAACAAGATAGAATCTCCTATTTTTTTGAAGATTTTTAGGTGCATC
U_HW-SSH2_10f11.b1.seq+ CTTTCCTGTATGTTCAAAACAAAATATTCTCCTATTCGTCGGAAGATTCTTAGGTGCATC
                        ____________________________________________________________
consensus               CTTTTCCAGATGTTCAACAAGATAGAATCTCCTATTCTTCTGAAGATTCTTAGGTGCATC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_5e03.b1.seq+  AATCATTTGTCTGGGGATCCTAATTGTCTAGAGACACTTCAA
U_HW-SSH2_10g10.b1.seq+ AATCATTTGTCTGGTGATCCTAATTGTCTAGAGACACTTCAACGCACAGATGCTATCAAG
U_HW-SSH2_12a10.b1.seq+ AATCATTTGTCTGGGGATCCTAATTGTCTACACACACTTCAACCCCCCCATGCTATCGAG
U_HW-SSH2_5g05.b1.seq-  AATCATTTGTCTGGTGATCCTAATTGTCTAGAGACACTTCAACGCACAGATGCTATCAAG
U_HW-SSH2_10f11.b1.seq+ ACTCATTTGTCTGGTGCTCCTACTTGTCTAGAGACAGTTCCACGCACGGATGCTATCAAT
                        ____________________________________________________________
consensus               AATCATTTGTCTGGTGATCCTAATTGTCTAGAGACACTTCAACGCACAGATGCTATCAAG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_10g10.b1.seq+ CATTTGATACCAATTCTCGAACTTCGTGATGGACCTCTAGTTTTTTCAAATACATAGCGAG
U_HW-SSH2_12a10.b1.seq+ CATTTGATACCCCTTCCCGAACTTCGGGATGGCCCTCTATTTTTTCAAATACGTATCGAG
U_HW-SSH2_5g05.b1.seq-  CATTTGATACCAATTCTCGAACTTCGTGATGGACCTCTAGTTTTTCAAATACATAGCGAG
U_HW-SSH2_10f11.b1.seq+ GATTTTATTCCTATTCTCAAACTCCCTGAAGGACCCTTAGTATTTGTAAAACAAAGAAAG
                        ____________________________________________________________
consensus               CATTTGATACCAATTCTCGAACTTCGTGATGGACCTCTAGTTTTTCAAATACATAGCGAG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .
U_HW-SSH2_10g10.b1.seq+ G-TCCTCAATGCGCTGTTCAACCTTTGTAAGATCAATAAAAGAAGACAGGAACAGGCAGC
U_HW-SSH2_12a10.b1.seq+ G-TCCTCAATGCGCTGTTCAACCTTTGTAAGATCAATAAAAGAAAACAGGAACAGGCAAC
U_HW-SSH2_5g05.b1.seq-  G-TCCTCAATGCGCTGTTCAACCTTTGTAAGATCAATAAAAGAAGACAGGAACAAGCAGC
U_HW-SSH2_10f11.b1.seq+ GGTCCTCCATGCCCTGTTCTTCCTTTGTAAGATCACTAGAAAAAAA-AGGA-CAGGCAGC
```

```
consensus                G-TCCTCAATGCGCTGTTCAACCTTTGTAAGATCAATAAAAGAAGACAGGAACAGGCAGC

U_HW-SSH2_10g10.b1.seq+ TGAAAATGGG-ATCATTCCTCACTTGATGAATTTTTGTCATGTCAGACTCGCCGCTAAGGC
U_HW-SSH2_12a10.b1.seq+ TGAAAATGGGGATCATTCCTCACTTGATGAATTTTTGTCATGACAGACTCGCCGCTAAGGC
U_HW-SSH2_5g05.b1.seq-  TGAAAATGGG-ATCATTCCTCACTTGATGAATTTTTGTCATGTCAGACTCGCCGCTAAGGC
U_HW-SSH2_10f11.b1.seq+ TGAAAATGGA-ATCATTCCTCACTTG-TAATGCTTGTCATGTCAGACTCCCCGCTAAGGG
consensus                TGAAAATGGG-ATCATTCCTCACTTGATGAATTTTGTCATGTCAGACTCGCCGCTAAGGC

U_HW-SSH2_10g10.b1.seq+ AGTATGCTTTGCCTCTTCTTTGTGATATGGCTCATGCTTCTCGCAACTCTAGAGAGCAGT
U_HW-SSH2_12a10.b1.seq+ AGAATGCTTTGCCTCTTCTTTGTGATATGGCTCATGCTTCTCGCAACTCTAGAGAGCAGT
U_HW-SSH2_5g05.b1.seq-  AGTATGCTTTGCCTTTTCTTTGTGATATGGCTCATGCTTCTCGCAACTCTAGAGAGCAGT
U_HW-SSH2_10f11.b1.seq+ CTTGTGCTTTGCCTCTTCTTTGTGATTTGGCTTATGCTTCT-GCAACA--AAAAAGCAAA
consensus                AGTATGCTTTGCCTCTTCTTTGTGATATGGCTCATGCTTCTCGCAACTCTAGAGAGCAGT

U_HW-SSH2_10g10.b1.seq+ TGAGAGCTCATGGAGGCCTGGATGTGTACCTGCCCGGGCGGCCGCTC
U_HW-SSH2_12a10.b1.seq+ TGAGAGCTCATGGAGGCCTGTATGTGTACCTGCCCGGGCG
U_HW-SSH2_5g05.b1.seq-  TGAGAGCTCATGGAGGCCTGGATGTGTACCTGCCCGGGCG
U_HW-SSH2_10f11.b1.seq+ TGAAACCTCATGGAAGCCAAAATGAGTACA-GCCGGGGCGGTTTCTAAAATCCTAGTGTA
consensus                TGAGAGCTCATGGAGGCCTGGATGTGTACCTGCCCGGGCGGCCGCTAAAATCCTAGTGTA

U_HW-SSH2_10f11.b1.seq+ ATCGCCCCTCGGCCAGAGGAATATGTCTTGACGGCCTCCTCTTTTGACGCCGTCTAAGT
consensus                ATCGCCCCTCGGCCAGAGGAATATGTCTTGACGGCCTCCTCTTTTGACGCCGTCTAAGT

U_HW-SSH2_10f11.b1.seq+ GTTTCGGATATATAGTAAGACGCCTCGGCTCGATCGATGCAAATGCGTTACCGTGTGTCA
consensus                GTTTCGGATATATAGTAAGACGCCTCGGCTCGATCGATGCAAATGCGTTACCGTGTGTCA

U_HW-SSH2_10f11.b1.seq+ TCCCCTCAATCACCACTGCTATATTGGA
consensus                TCCCCTCAATCACCACTGCTATATTGGA

****************** Contig 23 ******************

U_HW-SSH2_5e07.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACGGCTTTATAAGCACAACAGCACTGTGATAGT
U_HW-SSH2_3h10.b1.seq+           CGTGGTCGCGGCCGAGGAACGGCTTTATAAGCACAACTGCACTGTGAAAGG
U_HW-SSH2_11a11.b1.seq+          CGTGGTCGCGGCCGAGGTACAGCTTTATAACCACTTCAGCACTGTGATAGT
consensus                TTCGATTAGCGTGGTCGCGGCCGAGGTACGGCTTTATAAGCACAACAGCACTGTGATAGT

U_HW-SSH2_5e07.b1.seq+  GAAGGATCTGAACTTGAAGTCAAAGCACAAGAAAGGCACTGAGGATGAACCGGGTGAAAT
U_HW-SSH2_3h10.b1.seq+  GAATGACCCGAACTTGAAGTCAAAGAACAAGAAAGGCACTGAGGATGAACCGGGTGAAAT
U_HW-SSH2_11a11.b1.seq+ GAAGGATCTGAACTTGAAGTCAAAGCACAACAAAGGCACTGAGGATGAACCGGGTGAAAT
consensus                GAAGGATCTGAACTTGAAGTCAAAGCACAAGAAAGGCACTGAGGATGAACCGGGTGAAAT

U_HW-SSH2_5e07.b1.seq+  TGTCATGATTGAAGGCCCCATTCATAGCTCGAACATGATGCTCTACTCAAAGGAAAAGAA
U_HW-SSH2_3h10.b1.seq+  TGTAATGATTGAAGGCCCTTTTCTTAGATCGAACATGATGCTCTACTCAAAGGAAAAAAA
U_HW-SSH2_11a11.b1.seq+ TGTCATGATTGAAGGCCCCATTCATAGCTCGAACATGATGCTCTACTCAAAGGAGAAAAA
consensus                TGTCATGATTGAAGGCCCCATTCATAGCTCGAACATGATGCTCTACTCAAAGGAAAAAAA

U_HW-SSH2_5e07.b1.seq+  CGTGACGAGTAGGGTTGGGCACAAAATCCTCGAGGATGGCACCAAGGTCCGCTACCTGAA
U_HW-SSH2_3h10.b1.seq+  CGTGACAAGTAGGGTTGGACAAAATATCCTCGAGGAAGGCACCAAGGTCCGCTACCTGAA
U_HW-SSH2_11a11.b1.seq+ CGTGACTAGTAGGGTTGGGCACAAAATCCTCGAGGATGGCACCAAGGTCCGCTACCTGAA
consensus                CGTGACAAGTAGGGTTGGGCACAAAATCCTCGAGGATGGCACCAAGGTCCGCTACCTGAA

U_HW-SSH2_5e07.b1.seq+  AAAGACCGGTGAATTAATCGACAGCGTTGACAACTGGGTGAAGGTGTTCAAGGAAGGAGA
U_HW-SSH2_3h10.b1.seq+  AAAAACCGGTGAAGTAATCGACAGCGTTGACAACTGGGTGAAGGTGTTCAAGGAAGGAAA
U_HW-SSH2_11a11.b1.seq+ AAAGACCGGTGAAGTAATCGACAGCGTTGACAACTGGGTGAAGGTGTTCAAGGAAGGAGA
consensus                AAAGACCGGTGAAGTAATCGACAGCGTTGACAACTGGGTGAAGGTGTTCAAGGAAGGAGA

U_HW-SSH2_5e07.b1.seq+  TTCTGACTCATCATCGTAGTATGGAAATGCTGCGCATGCTCTCAACCTTAGCTGCGC-TT
U_HW-SSH2_3h10.b1.seq+  TTCTGAATCATCATCGTAAAATGGAAATGCTGCGCATGCTCTCAACCTTAGCTGCCCCTT
U_HW-SSH2_11a11.b1.seq+ TTCTGAGTCATCATCGTAGTATGGAAATGCTGCGCATGCTCTCAACCTTAGCTGCGC-TT
consensus                TTCTGAATCATCATCGTAGTATGGAAATGCTGCGCATGCTCTCAACCTTAGCTGCGC-TT

U_HW-SSH2_5e07.b1.seq+  ATTGCTGCCCAAACGCTTACTCGGCTGGTGCCACTGCTTGTACCTGCCCGGGCGCG
U_HW-SSH2_3h10.b1.seq+  ATTGCTGCCCAAACTCTTACTCGGCTGGTGCCACTGCTTGTACCTGCCCGG
U_HW-SSH2_11a11.b1.seq+ ATTGCTGCCCAAACGCTTACTCGGCTGGTGCCACTGCTTGTACCTGCCCGGGCGGCCGCT
consensus                ATTGCTGCCCAAACGCTTACTCGGCTGGTGCCACTGCTTGTACCTGCCCGGGCGGCCGCT

U_HW-SSH2_11a11.b1.seq+ AAAAATCATTAGGGAATTCACGGCTTCCTGCAGGACGAACGTATGCAACAGCTCGAGAGG
consensus                AAAAATCATTAGGGAATTCACGGCTTCCTGCAGGACGAACGTATGCAACAGCTCGAGAGG

U_HW-SSH2_11a11.b1.seq+ GTTTAATTCGCTCTTGGCTATTCCGTAGGAGACTTGTTGAATGTGCAAATCCCCGTTGAT
consensus                GTTTAATTCGCTCTTGGCTATTCCGTAGGAGACTTGTTGAATGTGCAAATCCCCGTTGAT

U_HW-SSH2_11a11.b1.seq+ CCCGGGTCCAGATTAAAAGAGTATATCCTGACAATCGACTCGACGAACTTATCTCGCAGT
consensus                CCCGGGTCCAGATTAAAAGAGTATATCCTGACAATCGACTCGACGAACTTATCTCGCAGT

U_HW-SSH2_11a11.b1.seq+ ACAGCTGAAACCCGGTGGCGCTTTACAGGAGAGAAACCGAAATGCGTAGGGTGAATATTC
consensus                ACAGCTGAAACCCGGTGGCGCTTTACAGGAGAGAAACCGAAATGCGTAGGGTGAATATTC

U_HW-SSH2_11a11.b1.seq+ ATGCCCCACTTGGCATGTGGTAAACAAGTCGCGTATATCTTTTTCAC
consensus                ATGCCCCACTTGGCATGTGGTAAACAAGTCGCGTATATCTTTTTCAC

****************** Contig 24 ******************

U_HW-SSH2_5f04.b1.seq+  TTCGATTTCGAGCGGCCGCCCGGGCAGGTACCTGCATCTTGGACACCACCTTCTAGATTG
U_HW-SSH2_5g03.b1.seq+  TTCGATTTCGAGGGGCCGCCCGGGCAGGTACCTGCATCTTGGACACCACCTTCTAGATTG
consensus                TTCGATTTCGAGCGGCCGCCCGGGCAGGTACCTGCATCTTGGACACCACCTTCTAGATTG

U_HW-SSH2_5f04.b1.seq+  GGCCACTCAATGTCTGTGTATGATGGTAGGAAAATTCTGATGTTCGGCGGTCTTGCTAAG
U_HW-SSH2_5g03.b1.seq+  GGCCACTCAATGTCTGTGTATGATGGTAGGAAAATTCTGATGTTCGGCGGTCTTGCTAAA
consensus                GGCCACTCAATGTCTGTGTATGATGGTAGGAAAATTCTGATGTTCGGCGGTCTTGCTAAA

U_HW-SSH2_5f04.b1.seq+  AGTGGTCCTCTCCGACTACGATCTAATGATGTGTTCACAATGGACCTAAGCGAAAAAGAG
U_HW-SSH2_5g03.b1.seq+  AGTGGTCCTCTCCGACTACGATCTATTGATGTGTTCACAATGCACCTAAGCGAAGAAGAG
consensus                AGTGGTCCTCTCCGACTACGATCTAATGATGTGTTCACAATGCACCTAAGCGAAAAAGAG

U_HW-SSH2_5f04.b1.seq+  CCCTGTTGGCGGTGCCTAACCGGGAGTGGAATGCCTGGGGCGGGAAATCCGGCTGGAGCT
U_HW-SSH2_5g03.b1.seq+  CCCTGTTGGCGGTGCCTAACCGGGAGTGGAATGCCTGGGGCGGGAAATCCGGCTGGAGCT
consensus                CCCTGTTGGCGGTGCCTAACCGGGAGTGGAATGCCTGGGGCGGGAAATCCGGCTGGAGCT

U_HW-SSH2_5f04.b1.seq+  GGTCCCCCTCCTCGTCTTGATCATGTTGCTGTGAGTTTGCCAGGGGAAAAAGTGTTGATA
U_HW-SSH2_5g03.b1.seq+  GGTCCACCTCCTCTTCTTGATCATGTTGCTGTGATTTTGCCAGGGGAAAAAGTGTTGATT
consensus                GGTCCACCTCCTCGTCTTGATCATGTTGCTGTGAGTTTGCCAGGGGAAAAAGTGTTGATA

U_HW-SSH2_5f04.b1.seq+  TTTGGTGGATCCGTGGCGGGCCTCCACTCGGAGTTACAGCTGTATCTCTTGTATCCGACT
U_HW-SSH2_5g03.b1.seq+  TTTGGTG
consensus                TTTGGTGGATCCGTGGCGGGCCTCCACTCGGAGTTACAGCTGTATCTCTTGTATCCGACT

U_HW-SSH2_5f04.b1.seq+  GAAGAAAAACCTACGTGGACGATAGTTAATGTTCCCGGGCT
consensus                GAAGAAAAACCTACGTGGACGATAGTTAATGTTCCCGGGCT

****************** Contig 25 ******************

U_HW-SSH2_5h12.b1.seq+  TTCGATTTCGAGCGGCCGCCCGGGCAGGTCAGAATTATCCCCAGCTTCATGATCCAAGGA
consensus                TTCGATTTCGAGCGGCCGCCCGGGCAGGTCAGAATTATCCCCAGCTTCATGATCCAAGGA

U_HW-SSH2_5h12.b1.seq+  GGTGACTTCACTCTTGGCGATGGAAGGGGCGGTGAATCAATCTACGGCACAAAGTTCGCC
U_HW-SSH2_11a07.b1.seq+                                                 GGGTTCGCC
consensus                GGTGACTTCACTCTTGGCGATGGAAGGGGCGGTGAATCAATCTACGGCACAAAGTTCGCC

U_HW-SSH2_5h12.b1.seq+  GATGAGAACTTCAAGCTCAAGCACACTGGACCAGGCTACCTTTCCATGGCCAATGCTGGG
U_HW-SSH2_11a07.b1.seq+ GATAATAACTTCAAGCTCAAGCGCGCTGGACCGGGCTACCTTTCCATGGCCAATGGGGGG
consensus                GATAAGAACTTCAAGCTCAAGCACACTGGACCAGGCTACCTTTCCATGGCCAATGCGGGG

U_HW-SSH2_5h12.b1.seq+  AGAGATACCAATGGATCCCAGTTCTTCATCACCACTGTAACCACGAGCTGGTTGGATGGC
U_HW-SSH2_11a07.b1.seq+ AGAGATACCAATGGATCCCATTTCTTCATCACCACTGTAACCACGAGCTGGTTGGATGGC
consensus                AGAGATACCAATGGATCCCAGTTCTTCATCACCACTGTAACCACGAGCTGGTTGGATGGC

U_HW-SSH2_5h12.b1.seq+  AAGCACGTCGTGTTCGGCAAGGTGTTGTCTGGAATGGACGTGGTCTACAAGGTCGAGGCC
U_HW-SSH2_11a07.b1.seq+ AAGCACCTCGTGTTCCGCACGGGGTTGTCTGGAATGAACTTGGTCTACAGGGGCCAGGCG
consensus                AAGCACCTCGTGTTCCGCAAGGGGTTGTCTGGAATGAACGTGGTCTACAAGGGCCAGGCC

U_HW-SSH2_5h12.b1.seq+  GAGGGCAAGCAGAACGGGACACCAAAGAGCAAAGTTGTCATTGCTGACAGCGGGGAAGTG
U_HW-SSH2_11a07.b1.seq+ GAAGGCTAACAAAAAGGCACACCAAAGATCGC-GTTGTCATTGCTGACAGCCGGGAAATG
consensus                GAAGGCAAACAAAAAGGCACACCAAAGAGCAAAGTTGTCATTGCTGACAGCCGGGAAATG

U_HW-SSH2_5h12.b1.seq+  CCGCTGTGATGACCTGAAACGGTCTCTGGTGGAA
U_HW-SSH2_11a07.b1.seq+ CCGCTGTGATGACTTCAAACGGTCTCTGGAGGAACCTACAGAGATCTGGGTCCGATCAAA
consensus                CCGCTGTGATGACCTCAAACGGTCTCTGGAGGAACCTACAGAGATCTGGGTCCGATCAAA

U_HW-SSH2_11a07.b1.seq+ AAAAATCATATGTCGGAACTGTTTTCATGCACACGCCCGCGACCACGCTAATCATTATTG
consensus                AAAAATCATATGTCGGAACTGTTTTCATGCACACGCCCGCGACCACGCTAATCATTATTG

U_HW-SSH2_11a07.b1.seq+ ATTTCCCGGCAGCCTGCAGTTCCACGTATGATATATCTCCCATCTCGTTGGAAGTAAATT
consensus                ATTTCCCGGCAGCCTGCAGTTCCACGTATGATATATCTCCCATCTCGTTGGAAGTAAATT

U_HW-SSH2_11a07.b1.seq+ TGAGTATCTTTACA
consensus                TGAGTATCTTTACA

****************** Contig 26 ******************

U_HW-SSH2_6b08.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACCCTCAGGATTTCTACCGGTTAGATTCTCTTG
consensus                TTCGATTAGCGTGGTCGCGGCCGAGGTACCCTCAGGATTTCTACCGGTTAGATTCTCTTG

U_HW-SSH2_6b08.b1.seq+  TGCACCAGCTCAAAGGCAGCGGATCCAGCATTGGAGCAGTGAGGATGAAGAACGAGTGCT
U_HW-SSH2_2b07.b1.seq+                                  GGAGCAGTGAGGATGAAGAACGAGTGCT
consensus                TGCACCAGCTCAAAGGCAGCGGATCCAGCATTGGAGCAGTGAGGATGAAGAACGAGTGCT

U_HW-SSH2_6b08.b1.seq+  CGGTGTTTAAGGCACACTGCAATG-ACAGGAATCTGGAAGGATGCCGCAGGTCACTGCAA
U_HW-SSH2_2b07.b1.seq+  CGGTGTTAAAGGCACACTGAAATTTACAGGAATCTGGAAGGATCCCCCAGGTCACTGCAA
consensus                CGGTGTTAAAGGCACACTGAAATGTACAGGAATCTGGAAGGATCCCCCAGGTCACTGCAA

U_HW-SSH2_6b08.b1.seq+  AAAATGAAGAGGGAGCATGCCACTCTGAAGCAGAAGCTGGAGTCATATTTTCAGTTACTG
U_HW-SSH2_2b07.b1.seq+  AAGAAAAACAGGGAGCATGCCACTCTGAAGCAGAACCTGGATTCATATTTTCATTTACTG
consensus                AAAAAAAACAGGGAGCATGCCACTCTGAAGCAGAACCTGGAGTCATATTTTCAGTTACTG

U_HW-SSH2_6b08.b1.seq+  CGGCAAGTCGGGCCTCGCGAGCATGCCGTGAACTCAAGGAAGTAAAAAAATAGCATATGG
U_HW-SSH2_2b07.b1.seq+  CAACAAGTCGGGCCTCACAAACATGCCATGAAATCAAGGAATCAACAAAATAGCCTATGA
consensus                CAACAAGTCGGGCCTCACAAACATGCCATGAAATCAAGGAAGCAAAAAAATAGCATATGA

U_HW-SSH2_6b08.b1.seq+  AATGCAGTTCCAAGGGAACTAAGGGACCAGCTACCTCTCTCCCTTGGGAGCTTTTATCAT
U_HW-SSH2_2b07.b1.seq+  AATGCAGTTCCAAGGGAACTAAGGGACCAGCTACCTCTCCCCCTTGGGAGCTTTTATCAT
consensus                AATGCAGTTCCAAGGGAACTAAGGGACCAGCTACCTCTCCCCCTTGGGAGCTTTTATCAT

U_HW-SSH2_6b08.b1.seq+  CCATAATTTTTGCTTGCTTTTAACCTGGGCCCTTTTGTCGTTCATGGGTGGCCTAGTTCT
U_HW-SSH2_2b07.b1.seq+  CCATTTTTTTTGCTTGCTTTTACCTGGGCCCTTTTGTCGACCATGGGTGGCCTATTTCT
consensus                CCATAATTTTTGCTTGCTTTTAACCTGGGCCCTTTTGTCGACCATGGGTGGCCTAGTTCT

U_HW-SSH2_6b08.b1.seq+  TTGTTGTGTGAAGCTTGCTCATGCATACACAGCCCCTGCCTTGCTGGGGAATGCCATGAT
U_HW-SSH2_2b07.b1.seq+  TTGTGGGGTGAAGCTTGCTCTTGCAT-CACAGCCCCTGCCTTGCTGGG
consensus                TTGTGGGGTGAAGCTTGCTCATGCATACACAGCCCCTGCCTTGCTGGGGAATGCCATGAT

U_HW-SSH2_6b08.b1.seq+  GTAATCTAACTCCTTTCTTTTACGAATACGCAAAGCTTGCTTTCGCGAAACACGTGTTGT
consensus                GTAATCTAACTCCTTTCTTTTACGAATACGCAAAGCTTGCTTTCGCGAAACACGTGTTGT

U_HW-SSH2_6b08.b1.seq+  ACCTGCCCGGGCGGCCGCTCAAATAAAAACTGAATTCACGGTCGCTGAAGACAA
consensus                ACCTGCCCGGGCGGCCGCTCAAATAAAAACTGAATTCACGGTCGCTGAAGACAA

****************** Contig 27 ******************

U_HW-SSH2_6c06.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACTACTTCGCTATCGGTCACCCAGGAGTATTTA
U_HW-SSH2_6c07.b1.seq+        TAGCGTGGTCGCGGCCGAGGTACTACTTCGCTATCGGTCACCCAGGAGTATTTA
U_HW-SSH2_5h06.b1.seq+              AGGTACTACTTCGCTATCGGTCACCCAGGAGTATTTA
U_HW-SSH2_12g07.b1.seq+       TAGCGTGGTCGCGGCCGAGGTACTACTTCGCTATCGGTCACCCAGGAGTATTTA
U_HW-SSH2_3a05.b1.seq-        TAGCGTGGTGGCGGCCGAGGTACTACTTCGCTATTGGTCACCCAGGAGTATTTA
consensus                TTCGATTAGCGTGGTCGCGGCCGAGGTACTACTTCGCTATCGGTCACCCAGGAGTATTTA

U_HW-SSH2_6c06.b1.seq+  GCCTTGCAAGGTGGTCCTTGCTGATTCACACGGGATTCCACGTGCCCCATGCTACTCGGG
U_HW-SSH2_10c03.b1.seq+                           CGGGATTCAACATGCCCCATGCCACTCGGG
U_HW-SSH2_6c07.b1.seq+  GCCTTGCAAGGTGGTCCTTGCTGATTCACACGGGATTCCACGTGCCCCATGCTACTCGGG
U_HW-SSH2_5h06.b1.seq+  GCCTTGCAAGGTGGTCCTTGCTGATTCACACGGGATTCCACGTGCCCCATGCTACTCGGG
U_HW-SSH2_12g07.b1.seq+ GCCTTGCAAGGTGGTCCTTGCTGATTCACACGGGATTCCACGTGCCCCATGCTACTCGGG
U_HW-SSH2_3a05.b1.seq-  GCCTTGCAAGGTGGTCCTTGCTGATTCACACGGGATTCCACGTGCCCCATGCCACTCGGG
consensus                GCCTTGCAAGGTGGTCCTTGCTGATTCACACGGGATTCCACGTGCCCCATGCTACTCGGG

U_HW-SSH2_6c06.b1.seq+  TCAGAGCGTAAGCTAGTGATGCTTTCGGCTACTGGACTTTAGCCATCTAGGGTGCGGCAC
```

```
U_HW-SSH2_10c03.b1.seq+ TCATAGCGTAAGCTAGTGATGCTTTCGGCTGCTGGACTTTATCCATCTAGGGTGCGGCAC
U_HW-SSH2_6c07.b1.seq+  TCAAAGCGTAAGCTAGTGATGCTTTCGGCTACTGGACTTTAGCCATCTAGGGTGCGGCAC
U_HW-SSH2_5h06.b1.seq+  TCAAAGCGTAAGCTAGTGATGCTTTCGGCTACTGGACTTTAGCCATCTAGGGTGCGGCAC
U_HW-SSH2_12g07.b1.seq+ TCAAAGCGTAAGCTAGTGATGCTTTCGGCTACTGGACTTTACCCATCTAGGGTGCGGCAC
U_HW-SSH2_3a05.b1.seq-  TCAGAGAGTAAGCTAGTGATGCTTTCGGCTACTGGACTTTAGCCATCTAGGGTGCGGCAC

consensus               TCAAAGCGTAAGCTAGTGATGCTTTCGGCTACTGGACTTTAGCCATCTAGGGTGCGGCAC

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c06.b1.seq+  TCAACCGCTTCGCCTAGCAGCACAACGCTTGTATTGCTCTCCCACAACCCCGTTTTCACG
U_HW-SSH2_10c03.b1.seq+ TCAACCGCTTCGCCAAGCACCACAACGCTTGTTTTGCTCTCCCCCAACCCTTTTTTTTCT
U_HW-SSH2_6c07.b1.seq+  TCAACCGCTTCGCCTAGCAGCACAACGCTTGTATTGCTCTCCCACAACCCCGTTTTCACG
U_HW-SSH2_5h06.b1.seq+  TCAACCGCTTCGCCTATCAGCACAACGCTTGTATTGCTCTCCCACAACCCCGTTTTCACG
U_HW-SSH2_12g07.b1.seq+ TCACCCGCTTCGCCTAGCAGCACAACGCTTGTATTGCTCTCCCACAACCCCGTTTTCACG
U_HW-SSH2_3a05.b1.seq-  TCAACCGCTTCGCCTAGCAGCACAACGCTTGTATTGCTCTCCCACAACCCCGTTTTCACG
                        ____________________________________________________________

consensus               TCAACCGCTTCGCCTAGCAGCACAACGCTTGTATTGCTCTCCCACAACCCCGTTTTCACG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c06.b1.seq+  GTTTAGGCTGCTCCCATTTCGCTCGCCGCTACTACGGGAATCGCTTTTGCTTTCTTTTCC
U_HW-SSH2_10c03.b1.seq+ GTTTAGGCTGCTCCCATTTCGCTCACCGCTACTACGGGAATCGCTTTTGCTTTCTTTTCC
U_HW-SSH2_6c07.b1.seq+  GTTTAGGCTGCTCCCATTTCGCTCGCCGCTACTACGGGAATCGCTTTTGCTTTCTTTTCC
U_HW-SSH2_5h06.b1.seq+  GTTTAGGCTGCTCCCATTTCGCTCGCCGCTACTACAGGAATCGCTTTTGCTTTCTTTTCC
U_HW-SSH2_12g07.b1.seq+ GTTTAGGCTGCTCCCATTTCGCTCGCCGCTACTACGGGAATCGCTTTTGCTTTCTTTTCC
U_HW-SSH2_3a05.b1.seq-  GTTTAGGCTGCTCCCATTTCGCTCGCCGCTACTACGGGAATCGCTTTTGCTTTCTTTTCC
                        ____________________________________________________________

consensus               GTTTAGGCTGCTCCCATTTCGCTCGCCGCTACTACGGGAATCGCTTTTGCTTTCTTTTCC

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c06.b1.seq+  TCTGGCTACTAAAATGTTTCAGTTCGCCAGGTTGTCTCTTGCCTGCTCATGGATTCAGCA
U_HW-SSH2_10c03.b1.seq+ TCTGGCTACTAAAATGTTTCCGTTCCCCAGGATGTCTCTTGCCTGCTAAGGTTTTCAAGA
U_HW-SSH2_6c07.b1.seq+  TCTGGCTACTAAGATGTTTCAGTTCGCCAGGTTGTCTCTTGCCTGCTCATGGATTCAGCA
U_HW-SSH2_5h06.b1.seq+  TCTGGCTACTAAAATGTTTCAGTTCGCCAGGTTGTCTCTTGCCTGCTCATGGATTCACCA
U_HW-SSH2_12g07.b1.seq+ TCTGGCTACTAAGATGTTTCAGTTCGCCAGGTTGTCTCTTGCCTGCTCATGGATTCAGCA
U_HW-SSH2_3a05.b1.seq-  TCTGGCTACTAAGATGTTTCAGTTCGCCAGGTTGTCTCTTGCCTGCTCATGGATTCAGCA
                        ____________________________________________________________

consensus               TCTGGCTACTAAGATGTTTCAGTTCGCCAGGTTGTCTCTTGCCTGCTCATGGATTCAGCA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c06.b1.seq+  GGCAGTTTAAAAGGTTGACCTATTTGGGAATCTCCGGATCTATGCTTATTTTCAACTCCC
U_HW-SSH2_10c03.b1.seq+ GGCAGTTTAAAAGGTTGACCTATTTGGGAATCTCCGGATCTATGCTTATTTTCAACTCCC
U_HW-SSH2_6c07.b1.seq+  GGCAGTTTAAAAGGTTGACCTATTTGGGAATCTCCGGATCTATGCTTATTTTCAACTCCC
U_HW-SSH2_5h06.b1.seq+  GGCACTTTAAAAGGTTGACCTATTTGGAAATCTCCGGATCTATGCTTATTTTCAACTCCC
U_HW-SSH2_12g07.b1.seq+ GGCAGTTTAAAAGGTTGACCTATTTGGGAATCTCCGGATCTATGCTTATTTTCAACTCCC
U_HW-SSH2_3a05.b1.seq-  GGCAGTTTAAAAGGTTGACCTATTTGGGAATCTCCGGATCTATGCTTATTTTCAACTCCC
                        ____________________________________________________________

consensus               GGCAGTTTAAAAGGTTGACCTATTTGGGAATCTCCGGATCTATGCTTATTTTCAACTCCC

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c06.b1.seq+  C-GAAGCATTTCGTCGCTTGCTACGCCCTTCCTCGTCTCTGGGTGCCAAGGTATCCACCG
U_HW-SSH2_10c03.b1.seq+ C-GAAGAATTTCTTCGCTTGCTACGCCCTTCCACGTCT
U_HW-SSH2_6c07.b1.seq+  C-GAAGCATTTCGTCGCTTGCTACGCCCTTCCTCGTCTCTGGGTGCCTAGGTATCCACCG
U_HW-SSH2_5h06.b1.seq+  C-GAAGCATTTCGTCGCTTGCTACGCCCTTCCTCGTCTCTGGGTGCCTAGGTATCCACCG
U_HW-SSH2_12g07.b1.seq+ CCGAATTATTTCGTCGCTTGCTACGCCCTTCCTCGTCTCTGGGTGCCTAGGTAACCACAA
U_HW-SSH2_3a05.b1.seq-  C-GAAGCATTTCGTCGCTTGTTACGCCCTTCCTCGTCTCTGGGTGCCTAGGTATCCACCG
                        ____________________________________________________________

consensus               C-GAAGCATTTCGTCGCTTGCTACGCCCTTCCTCGTCTCTGGGTGCCTAGGTATCCACCG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c06.b1.seq+  CAAGCTACCTGCCC
U_HW-SSH2_6c07.b1.seq+  CAAGCTACCTGCCCGGGCGGCCACTCGAAATCACTAGTGAATTCGCGGCCGCCCGGAGGT
U_HW-SSH2_5h06.b1.seq+  CAAGC
U_HW-SSH2_12g07.b1.seq+ CAAGCTACCTGCCC
U_HW-SSH2_3a05.b1.seq-  CCAGCCCCCTCCCCGGGCGGCCCCTCGAAATC
                        _______________________________

consensus               CAAGCTACCTGCCCGGGCGGCCACTCGAAATCACTAGTGAATTCGCGGCCGCCCGGAGGT

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c07.b1.seq+  CGACCGAAGGGGAGACTCCCAAGAAGTTGGATGCGATCCTGAAATACTAAATGCACCTAA
                        ____________________________________________________________

consensus               CGACCGAAGGGGAGACTCCCAAGAAGTTGGATGCGATCCTGAAATACTAAATGCACCTAA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c07.b1.seq+  GAGTAGTGCAGATCTGATCTACCTGTATCTG
                        _______________________________

consensus               GAGTAGTGCAGATCTGATCTACCTGTATCTG

****************** Contig 28 ******************
                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c11.b1.seq-  TAGTGTGGTCGCGTCCGAGGTGCAGGAATATTGACCATTGTCCATTCACTACGCCTATCG
                        ____________________________________________________________

consensus               TAGTGTGGTCGCGTCCGAGGTGCAGGAATATTGACCATTGTCCATTCACTACGCCTATCG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c11.b1.seq-  GCCTGATCATAGGTCCTGCATCACCCTCCGTTGACGAACCATGCGGAGGAAACCATGCGT
                        ____________________________________________________________

consensus               GCCTGATCATAGGTCCTGCATCACCCTCCGTTGACGAACCATGCGGAGGAAACCATGCGT

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c11.b1.seq-  CTTAGGGGCAGTGGATTCTCACCAATGTTTTCGTTACACAAGCCGACATTATTCACTAGT
                        ____________________________________________________________

consensus               CTTAGGGGCAGTGGATTCTCACCAATGTTTTCGTTACACAAGCCGACATTATTCACTAGT

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c11.b1.seq-  GATTTCGAGAGGCCGCCCGGGCAGGTACCGGGTTGCCGGCGGCCCACTTGGCGAGATCGT
U_HW-SSH2_12h05.b1.seq+                                                 GAGATCGT
                        ____________________________________________________________

consensus               GATTTCGAGAGGCCGCCCGGGCAGGTACCGGGTTGCCGGCGGCCCACTTGGCGAGATCGT

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c11.b1.seq-  CGACCCACTATATCCAGGAGGCAGCTTGACCCTCTCGGCCTAGCCGATGACCCCGAGGC
U_HW-SSH2_12h05.b1.seq+ CGACCCACTCTACCCCGGTGGCAGCTTCGACCCCCTTGGCCTAGCCGACGACCCGGAGGC
U_HW-SSH2_3h12.b1.seq-                                          GGCCTTGCCGACGACCCTGAGGC
                        ____________________________________________________________

consensus               CGACCCACTATACCCAGGAGGCAGCTTCGACCCCCTCGGCCTAGCCGACGACCCGAGGC

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c11.b1.seq-  ATTCGCCGAGCTCAAGGTGAAGGAGATCAAGAACGGTCGCCTCGCCATGTTCTCAATGTT
U_HW-SSH2_12h05.b1.seq+ GTTTGCTGAGCTCAAGGTGAAGGAAATCAAGAACGGCCGCCTTGCAATGTTCTCCATGTT
U_HW-SSH2_3h12.b1.seq-  ATTCGCCGAGCTTAAGGTTAAGGAGATCAAGAACGGTCGCCTCGCCATGTTCTCCATGTT
U_HW-SSH2_12g05.b1.seq+                 GTGAAGGAAATCAAGAACGGCCGCCTTGCAATGTTCTCCATGTT
U_HW-SSH2_12g04.b1.seq+                 GTGAAAGAAATCAAGAACGGCCGCCTTGAAATGTTCTG-ATGTT
                        ____________________________________________________________

consensus               ATTCGCCGAGCTCAAGGTGAAGGAAATCAAGAACGGCCGCCTTGCAATGTTCTCCATGTT

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c11.b1.seq-  CGGCTTCTTTGTCCAAGCTATCGTCACGGGCAAGGGACCACTTGAGAACCTCGCTGACCA
U_HW-SSH2_12h05.b1.seq+ TGGATACTTTGTGCAGGCCATCGTCACTGGTAAGGGTCCGCTGGAAAACCTCGCTGACCA
U_HW-SSH2_9f08.b1.seq-                          TCACTAGTAAGGGTCCGCTGGAGAACCTCGCTGACCA
U_HW-SSH2_3h12.b1.seq-  CGGGTTCTTTGTGCAAGCCATCGTCACCGGCAAGGGTCCACTCGAGAACCTCGCAGACCA
U_HW-SSH2_12g05.b1.seq+ TGGATACTTTGTGCAGGCCATCACTGGTAAGGGTCCGCTGGAAAACCTCGCTGACCA
U_HW-SSH2_12g04.b1.seq+ TGAATACTGTGTGCAGGCCATCCTCAACCTGGGGGGTCCGTTGGA-AACCTCGCTAACCC
                        ____________________________________________________________

consensus               TGGATACTTTGTGCAGGCCATCGTCACTGGTAAGGGTCCGCTGGAGAACCTCGCTGACCA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c11.b1.seq-  CATCGCTGACCCCGTCAACAACAACGCCTGGGCATTCGCCACCAACTTTGTCCCCGGCAA
U_HW-SSH2_12h05.b1.seq+ CCTCGCCGACCCTGTCAACAACAACGCGTGGGCCTTCGCCACCAACTTTGTGCCCGGCAA
U_HW-SSH2_9f08.b1.seq-  CCTGGCGGACCCTGTCAACAACAACGCGTGGGCCTTCGCCACCAACTTTGTGCCCGGCAA
U_HW-SSH2_3h12.b1.seq-  CCTTGCCGACCCCGTCAACAACAATGCCTGGGCATTTGCCACCAACTTCGTTCCTGGCAA
U_HW-SSH2_12g05.b1.seq+ CCTCCCCGACCCTGTCAACAACAACGCGTGGGCCTTCCCCACCAACTTTGTGCCCGGCAA
U_HW-SSH2_12g04.b1.seq+ CCTCGCCGACCCTGTCAACAACAACCCGTGGGCGTTCGCCACCAACTTTGTGCCCGGCAA
                        ____________________________________________________________

consensus               CCTCGCCGACCCTGTCAACAACAACGCGTGGGCCTTCGCCACCAACTTTGTGCCCGGCAA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6c11.b1.seq-  GTAA
U_HW-SSH2_12h05.b1.seq+ GTAAACACATGAAAATCGACTTCTCAGGAGTATATGTGTACCTG
U_HW-SSH2_9f08.b1.seq-  GTAAACACATGAAAATCGACTTCTCAGGAG
U_HW-SSH2_3h12.b1.seq-  GTAAG
U_HW-SSH2_12g05.b1.seq+ GTAAACACATGAAAATCGACTTCTCAGGAGTATATGTGTAC
U_HW-SSH2_12g04.b1.seq+ GTAAACCCATGAAAATCGACTTCTCAGGAGTATATGTGTACATATCTACGGAAGTTCTAT
                        ____________________________________________________________

consensus               GTAAACACATGAAAATCGACTTCTCAGGAGTATATGTGTACATATCTACGGAAGTTCTAT

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_12g04.b1.seq+ CAACCCAAGTGACATAACCTACCCAAAGGATTGATTCAAACATGCATATCTACAATTGAT
                        ____________________________________________________________

consensus               CAACCCAAGTGACATAACCTACCCAAAGGATTGATTCAAACATGCATATCTACAATTGAT

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_12g04.b1.seq+ GTCATGAACTCCATTGCTCGAGGGCAAAGATTCCTCTCTTTTCTGCTGCTGGTCTTCCTC
                        ____________________________________________________________

consensus               GTCATGAACTCCATTGCTCGAGGGCAAAGATTCCTCTCTTTTCTGCTGCTGGTCTTCCTC

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_12g04.b1.seq+ ATAATGAAACCGCTGCCTCAAATTTCTCGCCAGGCTGGTCTTGTCAAAAGGCTGGAAAAA
                        ____________________________________________________________

consensus               ATAATGAAACCGCTGCCTCAAATTTCTCGCCAGGCTGGTCTTGTCAAAAGGCTGGAAAAA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_12g04.b1.seq+ AGGAAAACATGCAGAGGGTGGGGGGCGAAACATGAACTATTTTTACTTTTGTGTTTGCAT
                        ____________________________________________________________

consensus               AGGAAAACATGCAGAGGGTGGGGGGCGAAACATGAACTATTTTTACTTTTGTGTTTGCAT

****************** Contig 29 ******************
                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6e07.b1.seq+  TTCGATTACCGTGGTCCCGGCCGAGGTACCTCCTCAACGGTTATGATGACCACCAAAAGG
U_HW-SSH2_6e09.b1.seq+          CGTGGTCGCGGCCGAGGTATCTCCTCAACGGTTATGATGACCAACAGAAGG
U_HW-SSH2_6b10.b1.seq+          CGTGGTCGCGGCGGAGGGAGCTCCTCAACGGTTATGATGACCAGCAGAAGG
                        ____________________________________________________________

consensus               TTCGATTACCGTGGTCGCGGCCGAGGTACCTCCTCAACGGTTATGATGACCAACAGAAGG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6e07.b1.seq+  CTCTCATACAGAAGGAAAGGGCAAGACGGATCATGGAACAGCACACGATGTTTTCATCGA
U_HW-SSH2_6e09.b1.seq+  CTCTCATACAGAAGGAAAGGGCAAGACGGATCATGGAACAGCACACGATGTTTTCATCGA
U_HW-SSH2_3h02.b1.seq+            AAGGAAAGGGCATTATGGATCATGGAACACCACACGATGTTTTCATCGA
U_HW-SSH2_6b10.b1.seq+  CTCTCAAACAGAAGGAAAGGGCAAGACGGATCATGGAACACCACACGATGTTTTCATCGA
                        ____________________________________________________________

consensus               CTCTCATACAGAAGGAAAGGGCAAGACGGATCATGGAACACCACACGATGTTTTCATCGA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6e07.b1.seq+  GGAAACTTTGTTTAGTGCTTGATTTGGATCACCCCTCTCCTCAATTCTGCTAAGTTTATAG
U_HW-SSH2_6e09.b1.seq+  GGAAACTTTGTTTAGTGCTTGATTTGGATCACACCTCTCCTCAATTCTGCTAAGTTTATAG
U_HW-SSH2_3h02.b1.seq+  GGAAACTTTGTTTAGTGCTTTATTTGGATCACCCTCTCCTCAATTCTGCTAAGTTTATAG
U_HW-SSH2_6b10.b1.seq+  GGAAACTTTGTTTAGTGCTTGATTTGGATCACACTCTCCTCAATTCTGCTAAGTTTATAG
                        ____________________________________________________________

consensus               GGAAACTTTGTTTAGTGCTTGATTTGGATCACACTCTCCTCAATTCTGCTAAGTTTATAG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6e07.b1.seq+  AAGTGGATCCTATTCATGAAGAGATTTTGCGGAAAAAAGAGGAACAAGACCGGGAAAGGT
U_HW-SSH2_6e09.b1.seq+  AAGTGGATCCTATTCATGAAGAGATTTTGCGGAAGAAAGAGGAACAAGACCGGGAAAGGT
U_HW-SSH2_3h02.b1.seq+  AAGTGGATCCTATTCATGAAGAGATTTTGCGGAAGAAAGAGGAACAAGACCGGGAAAGGT
U_HW-SSH2_6b10.b1.seq+  AAGTGGATCCTATTCATGAAAGATTTTGCGGAAGAAAGAGGAACAAGACCGGGAAAGGT
                        ____________________________________________________________

consensus               AAGTGGATCCTATTCATGAAGAGATTTTGCGGAAGAAAGAGGAACAAGACCGGGAAAGGT

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6e07.b1.seq+  CAAAGCGGCATCTGTTCCGATTCCATCATATGCAAATGTGGACTAAACTAAGACCAGGAA
U_HW-SSH2_6e09.b1.seq+  CAGAGCGGCATCTGTTCCGATTCCATCATATGCAAATGTGGACTAAACTAAGACCAGGAA
U_HW-SSH2_3h02.b1.seq+  CAGAGCGGCATCTGTTCCGATTCCTTCATATGCAAATGTGGACTAAACTAACACCCGGAA
U_HW-SSH2_6b10.b1.seq+  CAGAGCGGCTTCTGTTCCAATTCCATCATATGCAAATGTGGACTAAACAAAAACAAGGAA
                        ____________________________________________________________

consensus               CAGAGCGGCATCTGTTCCGATTCCATCATATGCAAATGTGGACTAAACTAAGACCAGGAA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6e07.b1.seq+  TATGGAATCTTCTCAAGAAGGCGAGCAAGCTTTATGAGTTACATCTGTACCTGCCCGGGC
U_HW-SSH2_6e09.b1.seq+  TATGGAATCTTCTCGAGAAGGCGAGCAAGCTTTATGAGTTACATCTGTACCTGCCCGGGC
U_HW-SSH2_3h02.b1.seq+  TATGGAATCTCCCCGAGAAGGCGAGCAAGCTTTATGAGTTTTTTCTGTCGCTGCCCGGGC
U_HW-SSH2_6b10.b1.seq+  TATGGAATCTTCTCGAGAAGGCGAGCAAGCTTTATGAGTTACTTCTGTACCTGCCCGGGC
                        ____________________________________________________________

consensus               TATGGAATCTTCTCGAGAAGGCGAGCAAGCTTTATGAGTTACATCTGTACCTGCCCGGGC

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6e07.b1.seq+  GGGAAGGAAAAATCTAAAGCGAATTCTCGCCCGCCAGCATATGCGGGTAATTAAAATGTC
U_HW-SSH2_6e09.b1.seq+  GG
U_HW-SSH2_3h02.b1.seq+  G
U_HW-SSH2_6b10.b1.seq+  G
                        ____________________________________________________________

consensus               GGGAAGGAAAAATCTAAAGCGAATTCTCGCCCGCCAGCATATGCGGGTAATTAAAATGTC

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6e07.b1.seq+  CCATCTTCCGCTACCCCTTGCGTGAGAATGCCTTGAAGCCCCAAAAAAGGGTGCAAAAAA
                        ____________________________________________________________

consensus               CCATCTTCCGCTACCCCTTGCGTGAGAATGCCTTGAAGCCCCAAAAAAGGGTGCAAAAAA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6e07.b1.seq+  AAAGTCTAACCTGGACCGGCTTGATTTATACCGAACTAGCGCTTCATGGGGATTCCATTC
                        ____________________________________________________________

consensus               AAAGTCTAACCTGGACCGGCTTGATTTATACCGAACTAGCGCTTCATGGGGATTCCATTC

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6e07.b1.seq+  CCGACCCGAG
                        __________

consensus               CCGACCCGAG

****************** Contig 30 ******************
                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6f08.b1.seq+  TTCGATTTCCAGGGGCCGCCCGGGCAGGTACCCGGAGGCATCAGGATGGCAACCCCCCCA
U_HW-SSH2_6g05.b1.seq+                                                AACCCCGCA
U_HW-SSH2_6g06.b1.seq+                                                AACCCCGCC
                        ____________________________________________________________

consensus               TTCGATTTCCAGGGGCCGCCCGGGCAGGTACCCGGAGGCATCAGGATGGCAACCCCCGCA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6f08.b1.seq+  CTTACATCAAGAGGATTTGTTGAGGAGGACTTCCCCAAGGTTGCTGACTTCTTCAATTCG
U_HW-SSH2_6g05.b1.seq+  CTTACATCAAAAGGATTTGTTGAGGAGGACTTCGCCAAGGTTGCTGACTTCTTCGATTCG
U_HW-SSH2_6g06.b1.seq+  CTTACTTCAAAAGGATTTGGTGAGGAGGACTTCGCCAAGGTTGCTGACTTCTTCGATTCG
                        ____________________________________________________________

consensus               CTTACATCAAAAGGATTTGTTGAGGAGGACTTCGCCAAGGTTGCTGACTTCTTCGATTCG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6f08.b1.seq+  GCAGTGAACTTGGCCTTGAAGGTTAAAGCTGCAGCAGCAGGTACCTCGGCCGCGACCAC
U_HW-SSH2_6g05.b1.seq+  GCAGTGAACTTGGCCTTGAAGGTTAAAGCTGCAGCAGCAGGTACCTCGGCCGCGACCAC
U_HW-SSH2_6g06.b1.seq+  GCTTTGAACTTGGCCTTGAAGGTTAAAGCTGCAGCACCAGGTACCTCGGCCGCGACCACT
                        ____________________________________________________________

consensus               GCAGTGAACTTGGCCTTGAAGGTTAAAGCTGCAGCAGCAGGTACCTCGGCCGCGACCACT

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6g06.b1.seq+  CTAATC
                        ______

consensus               CTAATC

****************** Contig 31 ******************
                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6f10.b1.seq+  TTCAATTAGCGTGGTCGCGGCCGAGGTACAACGTCGGCGTACTCTCCTTCGTCGACAAGG
U_HW-SSH2_1b02.b1.seq+        TAGCGTGGTCGCGGCCGAGGAACAACGTCAGCATACTCTCCTTCGTCGACAAGG
U_HW-SSH2_1g08.b1.seq+                                                CCTTCGTCGACAAGG
                        ____________________________________________________________

consensus               TTCAATTAGCGTGGTCGCGGCCGAGGAACAACGTCAGCATACTCTCCTTCGTCGACAAGG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6f10.b1.seq+  ACCACCTCAAGCCAGGATGCTCCATCCTCATGCACAACAAGGTTCTTTCGGTGGTTGGAA
U_HW-SSH2_1b02.b1.seq+  ACCACCCCGAGCCAGGATGCTCCATCCTCATGCACAACAAGGTTCTTTCTGTGGTTGGAA
U_HW-SSH2_1d12.b1.seq+              AGGATGCTCCTTTCTCGTGCACAACAAGGTTCTTTCTGTGGTTGGAA
U_HW-SSH2_1g08.b1.seq+  ACCATAAAAAGCAAGGATGCTCCTTCCTCATGCACAACAAGGTTCTTTCTGTGGTTGGAA
                        ____________________________________________________________

consensus               ACCACCACAAGCCAGGATGCTCCATCCTCATGCACAACAAGGTTCTTTCTGTGGTTGGAA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6f10.b1.seq+  TTAAGTTTTACTAAGTTGACCCTTTGGAATCTGTAGTAAAAGTTGACAATGCTCCACTAA
U_HW-SSH2_1b02.b1.seq+  TTCTGCAAGACGAAGTTGACCCTATGGTATCTGTGATGAAAGTTGAAAAAGCTCCACTAA
U_HW-SSH2_1d12.b1.seq+  TTCTGCAAGACGAAGTTGACCCTATGGTATCTGTGATGAAAGTTGAAAAAGCTCCACTAG
U_HW-SSH2_1g08.b1.seq+  TTCTGCAAGACGAAGTTGACCCTATGGTATCTGTGATGAAAGTTGAAAAAGCTCCACTAA
                        ____________________________________________________________

consensus               TTCTGCAAGACGAAGTTGACCCTATGGTATCTGTGATGAAAGTTGAAAAAGCTCCACTAA

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :

U_HW-SSH2_6f10.b1.seq+  AATCGTATGCAAACATTGGAGGGATAAAGGCTAAGATTCAGGAAATAAAGGAGGAGGTTG
U_HW-SSH2_1b02.b1.seq+  AATCATATGCAGACATTGGAGGGTTAGATGCTCAGATTCAAGAAATAAAGGAGGCGGTTG
U_HW-SSH2_1d12.b1.seq+  AATCATATGCAGACATTGGAGGGTTAGATGCTCACATTCAAGAAATAAAGGAGGCGGTTG
U_HW-SSH2_1g08.b1.seq+  AATCATATGCAGACATTGGAGGGTTAGATGCTCAGATTCAAGAAATAAGGAGGCGGTTG
                        ____________________________________________________________

consensus               AATCATATGCAGACATTGGAGGGTTAGATGCTCAGATTCAAGAAATAAAGGAGGCGGTTG

                           .  :  .  .  .  :  .  .  .  :  .  .  .  :  .  .  .  :
```

```
U_HW-SSH2_6f10.b1.seq+  AACTTCCGCTTACCCACCCTTACAAAAATGAGCACGTGGGAATAAGGCCACCCAAGGAAG
U_HW-SSH2_1b02.b1.seq+  AGCTTCCGCTGACCCACCCTGAGCTATATGAAGACATTGGAATAAGGCCACCCAAGGGGG
U_HW-SSH2_1d12.b1.seq+  AGCTTCCGCTGACCCACCCTGACCTATATGAAGACATTGGAATAAGGCCACCCAAGGGGG
U_HW-SSH2_1g08.b1.seq+  AGCTTCCGCTGACCCACCCTGAGCTATATGAAGACTTTGGAATAAGGCCACCCAGGGGG
                        ____________________________________________________________
consensus               AGCTTCCGCTGACCCACCCTGACCTATATGAAGACATTGGAATAAGGCCACCCAAGGGGG

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6f10.b1.seq+  TCATATTACTTGGCGAAGCTGGAAGAGGGAAATTTCTACTTGCCCGGGCTGTGGCTAGCC
U_HW-SSH2_1b02.b1.seq+  TCATATTATATGGAGAACCTGGAACAGGGAAAACTCTACTTGCCAAGGCTGTTGCTAACT
U_HW-SSH2_1d12.b1.seq+  TCTTATTATTTGGAGAACCTGGAACCGGGAAAACTCTACTTGCCAAGGCTGTTGCTCACT
U_HW-SSH2_1g08.b1.seq+  TCATATTATATGGAGAACCTGGAACAGGGAAAACTCTACTTGCCAAGGCTGTTGCTAACT
                        ____________________________________________________________
consensus               TCATATTATATGGAGAACCTGGAACAGGGAAAACTCTACTTGCCAAGGCTGTTGCTAACT

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6f10.b1.seq+  CCAAATCTGAAACTTCCTTACGTGTCGTTGGAAGTAAACTTATTCA
U_HW-SSH2_1b02.b1.seq+  CCACATCTGCAACTTTCTTACGTGTCGTTGGAAGTGAACTTATTCAAAAGTACCTGCCCG
U_HW-SSH2_1d12.b1.seq+  CCACATCTGCAACTTTCTTACGTGTCGT
U_HW-SSH2_1g08.b1.seq+  CCACATCTGCAATTTTCTTACGTGTCGT
                        ____________________________________________________________
consensus               CCACATCTGCAACTTTCTTACGTGTCGTTGGAAGTAAACTTATTCAAAAGTACCTGCCCG

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1b02.b1.seq+  GGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAGGTCGACCATATGGGAGA
                        ____________________________________________________________
consensus               GGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAGGTCGACCATATGGGAGA

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1b02.b1.seq+  GCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATATTGTCACCTAAATACCTTGCC
                        ____________________________________________________________
consensus               GCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATATTGTCACCTAAATACCTTGCC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1b02.b1.seq+  GTAATCATGGCAACCCTC
                        _________________
consensus               GTAATCATGGCAACCCTC

****************** Contig 32 ********************
                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6g01.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACCTAGTGAAGTGGGCTTCCTCGATAGTAGAGA
U_HW-SSH2_6g02.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACCTAGTGAAGTGGGCTTCCTCGATAGTAGAGA
                        ____________________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACCTAGTGAAGTGGGCTTCCTCGATAGTAGAGA

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6g01.b1.seq+  GAAGGGGAAGAACTGAAAAACAAGTTATTTTTGAAGATGCAGAACATTCCTCAACATGTT
U_HW-SSH2_6g02.b1.seq+  GAAGGGGAAGAACTGAAAAACAAGTTATTTTTGAAGATGCAGAACATTCCTCAACATGTT
                        ____________________________________________________________
consensus               GAAGGGGAAGAACTGAAAAACAAGTTATTTTTGAAGATGCAGAACATTCCTCAACATGTT

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6g01.b1.seq+  GCTTTGCATTTAGAGTGGTCAATCCAAATTATTTACCTCCTTTGAAGGAGCTGCAAAAGT
U_HW-SSH2_6g02.b1.seq+  GCTTTGCATTTAGAGTGGTCAATCCAAATTATTTACCTCCTTTGAAGGAGCTGCAAAAGT
                        ____________________________________________________________
consensus               GCTTTGCATTTAGAGTGGTCAATCCAAATTATTTACCTCCTTTGAAGGAGCTGCAAAAGT

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6g01.b1.seq+  TGATGAGAATCCAGTCACTGCGTTGCCATGCTCTTTATAACCACAGTGCTACCAGGCTAT
U_HW-SSH2_6g02.b1.seq+  TGATGAGAATCCAGTCACTGCGTTGCCATGCTCTTTATAACCACAGTGCTACCAGGCTAT
                        ____________________________________________________________
consensus               TGATGAGAATCCAGTCACTGCGTTGCCATGCTCTTTATAACCACAGTGCTACCAGGCTAT

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6g01.b1.seq+  CTGTAATTCCAATTCATGCATCACGGTCCCAGGCTCTAAGGTACCTGCCCGGGCGGCCGC
U_HW-SSH2_6g02.b1.seq+  CTGTAATTCCAATTCATGCATCACGGTCCCAGGCTCTAAGGTACCTGCCCGGGCGGCCGC
                        ____________________________________________________________
consensus               CTGTAATTCCAATTCATGCATCACGGTCCCAGGCTCTAAGGTACCTGCCCGGGCGGCCGC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6g01.b1.seq+  TCAAA
U_HW-SSH2_6g02.b1.seq+  TCAAA
                        _____
consensus               TCAAA

****************** Contig 33 ********************
                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6g03.b1.seq-  CTCCCAAGTGATTCGCGAGGTTGCTGGCCATGTACAACGCACGGTACTTAATCCACCCTC
                        ____________________________________________________________
consensus               CTCCCAAGTGATTCGCGAGGTTGCTGGCCATGTACAACGCACGGTACTTAATCCACCCTC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6g03.b1.seq-  GAAAACAAGCTTACATGAAGTGCCTTCAGTTTGGTTGAAAAAACGCCCGGGCAGGTACTG
                        ____________________________________________________________
consensus               GAAAACAAGCTTACATGAAGTGCCTTCAGTTTGGTTGAAAAAACGCCCGGGCAGGTACTG

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6g03.b1.seq-  CCCAAGAAACGATGCTCGCGTCTTGGCTCGCTTTGTCAGAAGATCTTCCGATGAGGATCA
U_HW-SSH2_1g04.b1.seq+                                                  GGATCA
                        ____________________________________________________________
consensus               CCCAAGAAACGATGCTCGCGTCTTGGCTCGCTTTGTCAGAAGATCTTCCGATGAGGATCA

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6g03.b1.seq-  GCTGGTTTTATCCGCAGCTCTGCCTCTGACTCCATGAGGGGTGTGTTCACGCTCTGCTT
U_HW-SSH2_1g04.b1.seq+  GCTCCTTTCATCCGGCAGCTCTGCCTCTGACTCCATGAGGGGGGTGTTCCCCCTCTGCTT
                        ____________________________________________________________
consensus               GCTCCTTTCATCCGGCAGCTCTGCCTCTGACTCCATGAGGGGGGTGTTCACCCTCTGCTT

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6g03.b1.seq-  GCTGCAGTCAGTAGTCGCTCGTCTAAAGCTTCCCGGGTGACCCTACAAAAGCGTTGCGTG
U_HW-SSH2_1g04.b1.seq+  GCTCTAGTCAGAAGTCCCTCGTCTAAAGCTGCCCGGGTGACCCCAAAAAAGCGTTGCGTG
                        ____________________________________________________________
consensus               GCTCCAGTCAGAAGTCCCTCGTCTAAAGCTGCCCGGGTGACCCCAAAAAAGCGTTGCGTG

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6g03.b1.seq-  GTAAAATAAGAAACGGAGCCTTGTAATAGCGTGGCTTTTAGCTTCAGCAGCGACGACAGT
U_HW-SSH2_1g04.b1.seq+  CTAAAATAAGATACGGAGCCTAGGAATACCGGGGCTTTTAGCCTCCGCAGCAACGACAGT
                        ____________________________________________________________
consensus               CTAAAATAAGAAACGGAGCCTAGGAATACCGGGGCTTTTAGCCTCAGCAGCAACGACAGT

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6g03.b1.seq-  CACTGCACTAGTGTACCTCGGCCGCGACCC
U_HW-SSH2_1g04.b1.seq+  CACTGCACTTGTGTCCCTCCGCCGCGACCCCTCTAATCACATTATAATTAAAAGCCGTCC
                        ____________________________________________________________
consensus               CACTGCACTAGTGTACCTCGGCCGCGACCCCTCTAATCACATTATAATTAAAAGCCGTCC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1g04.b1.seq+  TTCTCTCATCTATTTGTGAGAGCTCCCCTCACGTTGGATTATTTGCATCCTCTTGCTAAC
                        ____________________________________________________________
consensus               TTCTCTCATCTATTTGTGAGAGCTCCCCTCACGTTGGATTATTTGCATCCTCTTGCTAAC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1g04.b1.seq+  CCCCCCCC
                        ________
consensus               CCCCCCCC

****************** Contig 34 ********************
                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7a12.b1.seq+  TTCGATTTCCGGGGGCCCGCCCGAGGTGCACTTGATTGTGCTACTGCCTACCCTAATGGC
                        ____________________________________________________________
consensus               TTCGATTTCCGGGGGCCCGCCCGAGGTGCACTTGATTGTGCTACTGCCTACCCTAATGGC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7a12.b1.seq+  CACACTAGATCCCTTCTCATTGGAGGTGGAATGACCAACTACTCTGATGGCCCTGCCACT
                        ____________________________________________________________
consensus               CACACTAGATCCCTTCTCATTGGAGGTGGAATGACCAACTACTCTGATGGCCCTGCCACT

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7a12.b1.seq+  TTTAGGGACCTCATTCTGGCCTTAAGAAAGAGGGAATCCGGGTGGTGGGCATCCAGGATG
U_HW-SSH2_10a08.b1.seq+                                                 TCCAGGATG
                        ____________________________________________________________
consensus               TTTAGGGACCTCATTCTGGCCTTAAGAAAGAGGGAATCCGGGTGGTGGGCATCCAGGATG

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7a12.b1.seq+  CACCTCTATGTTCAACGAGGCGGTCCAAATCACGAAACTGGACTGGCGAAAATCCACACG
U_HW-SSH2_10a08.b1.seq+ CACCTCTATGTTCAAGGAGGCGGTCCAAATTACCAAACTGGACTGGCGAAAATGAACATT
                        ____________________________________________________________
consensus               CACCTCTATGTTCAACGAGGCGGTCCAAATCACCAAACTGGACTGGCGAAAATCAACACG

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7a12.b1.seq+  CGGGGGATACAAATCGGTGTTCCAATTGAGGTGTATGGACCGGAAGAGACAATGACGGGC
U_HW-SSH2_10a08.b1.seq+ CTTGGTGGATAAATCGCTGTTCCGATTGAGGTGTATGGACCGAACGAGACAATGGCTGGT
                        ____________________________________________________________
consensus               CGGGGGAGACAAATCGCTGTTCCAATTGAGGTGTATGGACCGAAAGAGACAATGACGGGC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7a12.b1.seq+  ATCTGCAAGCAAGAAATTGAATGCATTATGGCGGCCTCATAAATCAGGATACAGTTGAGA
U_HW-SSH2_10a08.b1.seq+ -TCTGCACTTTTGAAATTGAATGCATCTTGCCCCGGTCATTGGTGGGGATACAAATGATA
                        ____________________________________________________________
consensus               ATCTGCAAGCAAGAAATTGAATGCATCATGCCCCCCTCATAAATCAGGATACAAATGAGA

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7a12.b1.seq+  AGTATTTTAAGATCTACAAACAATAAACTGGCTGCCGCATAAATGAGAGCATATTGGCAC
U_HW-SSH2_10a08.b1.seq+ AGTCCTTTGAGATCTACAAAGCAAATACTGGCTGCCGCCTAAATGAAAGCATGGTGGCAC
                        ____________________________________________________________
consensus               AGTACTTTAAGATCTACAAACAAAAAACTGGCTGCCGCATAAATGAAAGCATAGTGGCAC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7a12.b1.seq+  TAGGTTCACATCGCATGGTTGATTAGTTTCTTCTGAAGTTATTTGGACAAAAACACATAT
U_HW-SSH2_10a08.b1.seq+ TAGGTTCTCATCACTTGGTTGATTAGTTTTTTCAAAAAAGAAAGAGACTAAGACCCCCGG
                        ____________________________________________________________
consensus               TAGGTTCACATCACATGGTTGATTAGTTTCTTCAAAAAAGAAAGAGACAAAAACACACAG

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7a12.b1.seq+  CTTGTTGTCGTACAGGACCCTGTACCTCGGCCGCTACCACGCTA
U_HW-SSH2_10a08.b1.seq+ CCTGTTGTCGTAAACGAACCTGTACCTCGGCCGCAACCACGCTAATCACTATTAGAATTC
                        ____________________________________________________________
consensus               CCTGTTGTCGTAAACGAACCTGTACCTCGGCCGCAACCACGCTAATCACTATTAGAATTC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10a08.b1.seq+ GCGCCCCCCCCGCAGGTCTACTTTAGGGGAAA
                        ________________________________
consensus               GCGCCCCCCCCGCAGGTCTACTTTAGGGGAAA

****************** Contig 35 ********************
                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7b02.b1.seq+  TACCGGGGTCCCGCCCGAGGGGCACCTGCGTTTTGGATTTGAAGGG
U_HW-SSH2_7b03.b1.seq+  TACCGTGGTCCCGCCCGAGGGGCACCTGCGTTTTGGATTTGAAGGGAAAATGGCCCCACC
                        ____________________________________________________________
consensus               TACCGGGGTCCCGCCCGAGGGGCACCTGCGTTTTGGATTTGAAGGGAAAATGGCCCCACC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7b03.b1.seq+  AGAGTCTGCAAGGGATGGAAAAGAGATGCGATTACCCGGAGGGATGGTACCGGTTTGTTA
                        ____________________________________________________________
consensus               AGAGTCTGCAAGGGATGGAAAAGAGATGCGATTACCCGGAGGGATGGTACCGGTTTGTTA

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7b03.b1.seq+  TGGTGGAAAATGTCTTGGAGACTTTCTTCTACGCCCCAACCTACGTGGTTTTCCCTGGTT
                        ____________________________________________________________
consensus               TGGTGGAAAATGTCTTGGAGACTTTCTTCTACGCCCCAACCTACGTGGTTTTCCCTGGTT

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7b03.b1.seq+  GATCTCCAAACCCATTGAATTCCCGGCGGATTTCCCTCTATTGCGGTCCCCCCACCGCCG
                        ____________________________________________________________
consensus               GATCTCCAAACCCATTGAATTCCCGGCGGATTTCCCTCTATTGCGGTCCCCCCACCGCCG

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7b03.b1.seq+  TTCTCGGAAAAGAACATGATGGTCAAATGCAACACGGACCTGCTCCGCCGTACACGGACA
                        ____________________________________________________________
consensus               TTCTCGGAAAAGAACATGATGGTCAAATGCAACACGGACCTGCTCCGCCGTACACGGACA

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7b03.b1.seq+  TCCCGAGATGGCAGATTACCCTTTTGAATTTCTATGGCACTTCAATTCACGCGGATGGGA
                        ____________________________________________________________
consensus               TCCCGAGATGGCAGATTACCCTTTTGAATTTCTATGGCACTTCAATTCACGCGGATGGGA

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7b03.b1.seq+  GAATGGATAGCTGGCTGGGCCCGCTGGCAGGCCGATTGACCGCTACTGTTTTATAATTTT
                        ____________________________________________________________
consensus               GAATGGATAGCTGGCTGGGCCCGCTGGCAGGCCGATTGACCGCTACTGTTTTATAATTTT

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7b03.b1.seq+  AAACAAGGAAAAAGATACCGCGCTCACCGCTGCAACCTCATAGAAAACAGAAGCGAGACG
                        ____________________________________________________________
consensus               AAACAAGGAAAAAGATACCGCGCTCACCGCTGCAACCTCATAGAAAACAGAAGCGAGACG

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7b03.b1.seq+  GACATGGGGCCATCCAACCCCTATGGGCGAAAACCAAAGGGAAGGTTTAAATTCTTTATC
                        ____________________________________________________________
consensus               GACATGGGGCCATCCAACCCCTATGGGCGAAAACCAAAGGGAAGGTTTAAATTCTTTATC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7b03.b1.seq+  CAACCCAGTTAAAGATCAAAAATTCTGCGTTTCGATGCCCCCCTTCCAAGTGAAGGGACC
                        ____________________________________________________________
consensus               CAACCCAGTTAAAGATCAAAAATTCTGCGTTTCGATGCCCCCCTTCCAAGTGAAGGGACC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7b03.b1.seq+  CAGGACCACGGTGATTCTCGTTAAATTATGCTGTCCAAAAAAAGTGCGTATAAAAGAGAG
                        ____________________________________________________________
consensus               CAGGACCACGGTGATTCTCGTTAAATTATGCTGTCCAAAAAAAGTGCGTATAAAAGAGAG

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7b03.b1.seq+  GGGTCCCCTGTCCTGGTAAAGAAACCCCAACCACCCCCACCACACTTAATGAGAGCGTAC
                        ____________________________________________________________
consensus               GGGTCCCCTGTCCTGGTAAAGAAACCCCAACCACCCCCACCACACTTAATGAGAGCGTAC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7b03.b1.seq+  TCGGGAGGTGAGTGGGACAAAGCGAAAATGTGGAGCTGTTGACATTTATGCCTCTCTTCT
                        ____________________________________________________________
consensus               TCGGGAGGTGAGTGGGACAAAGCGAAAATGTGGAGCTGTTGACATTTATGCCTCTCTTCT

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7b03.b1.seq+  TGTGTTGCCTGAGGGGTCCAATTTCGAGTAATGGGCCACACTAGACTATACGCCAGAAAC
                        ____________________________________________________________
consensus               TGTGTTGCCTGAGGGGTCCAATTTCGAGTAATGGGCCACACTAGACTATACGCCAGAAAC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7b03.b1.seq+  GCG
                        ___
consensus               GCG

****************** Contig 36 ********************
                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7d10.b1.seq+  TTCGATTTCGAGCGGCCGCCCGGGCAGGTATGGAGAATCGCCTCCGAAATAGCAGGACGC
U_HW-SSH2_10e02.b1.seq+                                                 AGCAGGACGC
U_HW-SSH2_10e05.b1.seq+                                                  GCAGGACGC
                        ____________________________________________________________
consensus               TTCGATTTCGAGCGGCCGCCCGGGCAGGTATGGAGAATCGCCTCCGAAATAGCAGGACGC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7d10.b1.seq+  TCGGAGAATGAAGTTGTCACAGTAAATGAAGATGATTTGTCACTCAAGAAACTTGAGGAG
U_HW-SSH2_10e02.b1.seq+ TCGGAGAAAGAAAGGGTCACAGTAAATGAGGATGATTTGTCACTCAAGAAACTTGAGGAG
U_HW-SSH2_10e05.b1.seq+ TCGGAGAAAGAAGTTGTCACAGTAAATGAAGATGATTTGTCACTCAAGAATCTTGAGGAG
                        ____________________________________________________________
consensus               TCGGAGAAAGAAGTTGTCACAGTAAATGAAGATGATTTGTCACTCAAGAAACTTGAGGAG

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7d10.b1.seq+  CACCAAAGTGAGCTGCAACGACTTAAAAGA
U_HW-SSH2_10e02.b1.seq+ CACCAAAGTGAGCTGCCACGACTTAAAAGA
U_HW-SSH2_10e05.b1.seq+ CACCAAATTGAGCTGCCACGACTTAAAAGACAAGAAGGGCGATCGCCTGTGCAAAGTTGAA
                        ____________________________________________________________
consensus               CACCAAAGTGAGCTGCCACGACTTAAAAGACAAGAAGGGCGATCGCCTGTGCAAAGTTGAA

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10e05.b1.seq+ GAGTATAAAGTTTTAATTTGCAATTTCCCAAAAATTATGGGGATGGATCCCTCAAACGTT
                        ____________________________________________________________
consensus               GAGTATAAAGTTTTAATTTGCAATTTCCCAAAAATTATGGGGATGGATCCCTCAAACGTT

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10e05.b1.seq+ CTTGCTAGGGTTCACCCCCCCCTTGCTAATTGGAGCAAATGAACAACAGAAAAAGAACCTC
                        ____________________________________________________________
consensus               CTTGCTAGGGTTCACCCCCCCCTTGCTAATTGGAGCAAATGAACAACAGAAAAAGAACCTC

                        .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10e05.b1.seq+ ATTGACCACATCTTTAACCCGCTCAATACTATGGGCCAGCAGCTTAAAAAAAAAAGAAC
```

```
consensus                ATTGACCACATCTTTAACCCGCTCAATACTATGGGCCAGCAGCTTAAAAAAAAAAAGAAC

U_HW-SSH2_10e05.b1.seq+ CACAGATTGGAAAAGCTCCACAGCCTTGGAAAAGCCTTGGCAAACTTATGGAATATACTA

consensus                CACAGATTGGAAAAGCTCCACAGCCTTGGAAAAGCCTTGGCAAACTTATGGAATATACTA

U_HW-SSH2_10e05.b1.seq+ AATACTGCGATGGAAGAACGCCAGCCTTACGGGCAAATTAATATATTTTCATTGTCTTCA

consensus                AATACTGCGATGGAAGAACGCCAGCCTTACGGGCAAATTAATATATTTTCATTGTCTTCA

U_HW-SSH2_10e05.b1.seq+ GCCAATGGTATGCTAGGTCCTGGAAGTCTAAGACTAGAGAAAATTCAGCAGATTGAATCT

consensus                GCCAATGGTATGCTAGGTCCTGGAAGTCTAAGACTAGAGAAAATTCAGCAGATTGAATCT

U_HW-SSH2_10e05.b1.seq+ GAAGTTCAGCGACTAGATCAGTTAAAAGCAAGCAAAATGAAAGAGCTATTCATCAAAAAG

consensus                GAAGTTCAGCGACTAGATCAGTTAAAAGCAAGCAAAATGAAAGAGCTATTCATCAAAAAG

U_HW-SSH2_10e05.b1.seq+ AAAGCTGAGATTGAGGAAATTTGCAAGATATCCCACATGGATGTGCCTTACCAGACAGAA

consensus                AAAGCTGAGATTGAGGAAATTTGCAAGATATCCCACATGGATGTGCCTTACCAGACAGAA

U_HW-SSH2_10e05.b1.seq+ ATGGACAACATAATGAACTGATAATGTCAGGAGATGTGCACCACGATAATCTACTTTACA

consensus                ATGGACAACATAATGAACTGATAATGTCAGGAGATGTGCACCACGATAATCTACTTTACA

U_HW-SSH2_10e05.b1.seq+ CCATGGATGGATTATATATACAAAACAAAGAGGAGGTCCCCAGCCGTAAAGAAATTACTG

consensus                CCATGGATGGATTATATATACAAAACAAAGAGGAGGTCCCCAGCCGTAAAGAAATTACTG

U_HW-SSH2_10e05.b1.seq+ GACAAAGTCCAAATAATTGAATAACTTCATGGTGAATGAGGAGCCGTTGGCTTAACAAAT

consensus                GACAAAGTCCAAATAATTGAATAACTTCATGGTGAATGAGGAGCCGTTGGCTTAACAAAT

U_HW-SSH2_10e05.b1.seq+ TTACCCAGGATGAGAGGGAGGTACTCTCGGCCGGCGACCATCCTCTATTCCACTTGTGAT

consensus                TTACCCAGGATGAGAGGGAGGTACTCTCGGCCGGCGACCATCCTCTATTCCACTTGTGAT

U_HW-SSH2_10e05.b1.seq+ ATTCCGCGGCCCGCCCTCGGCCGAGTCGACGAT

consensus                ATTCCGCGGCCCGCCCTCGGCCGAGTCGACGAT

****************** Contig 37 ******************

U_HW-SSH2_7d11.b1.seq+  TAGCGTGGTCGCGGCCGAGGTAGAAGGCGCAACCGCCGGCCGCCAAGGTACTGGTGGTAG
U_HW-SSH2_10a12.b1.seq+                          GCAGCCGCCCGCCGCCAAGGTACAGGTGGAAA
U_HW-SSH2_10a10.b1.seq+                          GCAGCCGCCGGCCGCCAAGGTACAGGTGGTAG

consensus                TAGCGTGGTCGCGGCCGAGGTAGAAGGCGCAGCCGCCGGCCGCCAAGGTACAGGTGGTAG

U_HW-SSH2_7d11.b1.seq+  GATGGCCACCAATCCGCTGTTACGGGAAAAACACCATGGGGACAAACTTATCTGCTCCCA
U_HW-SSH2_10a12.b1.seq+ GAAAGCCACCAATCCGCATTAACAGGAAGAACACCATGGCGACGAACTTATCTGCTCCCA
U_HW-SSH2_10a10.b1.seq+ GAGGGCCACCAATCCGCATTTACAGGAAGAACACCTTGGCGACGAACTTATCTGCTCCCA

consensus                GAAGGCCACCAATCCGCATTTACAGGAAGAACACCATGGCGACGAACTTATCTGCTCCCA

U_HW-SSH2_7d11.b1.seq+  AAAGCAAAGACAAGGCCGAGGCGAAGCAGGCCCCGGCCCCAGGCTGCCTTTATGTCAGGG
U_HW-SSH2_10a12.b1.seq+ GAAGCAAAGACGAGGCCGAGGCGAAGCAGGCACCGGCACCAGGCTGCCTTTATGTCAAGG
U_HW-SSH2_10a10.b1.seq+ AAAGCAAAGACGAGGCCGAGGCGAAACAGGCACCGGCACCAGGCTGCCTTTATGTCAAGG

consensus                AAAGCAAAGACGAGGCCGAGGCGAAGCAGGCACCGGCACCAGGCTGCCTTTATGTCAAGG

U_HW-SSH2_7d11.b1.seq+  TTAGCATGGATGGTGCTCCTTACCTCAGGAAGG
U_HW-SSH2_10a12.b1.seq+ TTAGCATGGATGGTGCTCCTTACCTCAGGAAGG
U_HW-SSH2_10a10.b1.seq+ TTAGCATGGATGGGGCTCCTTACCTCAGGAAGGTGGATCTCAAAATGTATAAAAACTATA

consensus                TTAGCATGGATGGTGCTCCTTACCTCAGGAAGGTGGATCTCAAAATGTATAAAAACTATA

U_HW-SSH2_10a10.b1.seq+ AGGACCTCCCGCTGGAGCTGGAGAAAAAATTCAGCGGCTTTACTGTTGGTCATGGTGAAT

consensus                AGGACCTCCCGCTGGAGCTGGAGAAAAAATTCAGCGGCTTTACTGTTGGTCATGGTGAAT

U_HW-SSH2_10a10.b1.seq+ CGACTGGAAAATCGGAAAGAGATGGATTATCTGATTGCCGGCTGATGGATCTTAAAAGCG

consensus                CGACTGGAAAATCGGAAAGAGATGGATTATCTGATTGCCGGCTGATGGATCTTAAAAGCG

U_HW-SSH2_10a10.b1.seq+ GCACTGAACTTGTGCTCACTTATGAGGATAAGGATGGTGATTGGATGCTTGTTGGTGATG

consensus                GCACTGAACTTGTGCTCACTTATGAGGATAAGGATGGTGATTGGATGCTTGTTGGTGATG

U_HW-SSH2_10a10.b1.seq+ TTCCTTGGCGAATGTTCACATACAGCTGTAGGAGGATGAGGATCATGAGGGGGTCAGATG

consensus                TTCCTTGGCGAATGTTCACATACAGCTGTAGGAGGATGAGGATCATGAGGGGGTCAGATG

U_HW-SSH2_10a10.b1.seq+ CAGTGGGCCTCCCTCCGAGGGCCGCCGAGAAAAATAATACCCAGAAGAACCCGAACGATG

consensus                CAGTGGGCCTCCCTCCGAGGGCCGCCGAGAAAAATAATACCCAGAAGAACCCGAACGATG

U_HW-SSH2_10a10.b1.seq+ AACCCCGATCTGTTTCCTTCCCCGCATCGCATCTTACAAGGGTGATGGACTTTATGTGGA

consensus                AACCCCGATCTGTTTCCTTCCCCGCATCGCATCTTACAAGGGTGATGGACTTTATGTGGA

U_HW-SSH2_10a10.b1.seq+ AAGAAGAAAAGGGATTTACTTATATATATATAACCTCCTGTTTTCTCTTTGTTTTTCCTTTG

consensus                AAGAAGAAAAGGGATTTACTTATATATATATAACCTCCTGTTTTCTCTTTGTTTTTCCTTTG

U_HW-SSH2_10a10.b1.seq+ TTCTTTCCTCAAAACAACAAGGTAGAATGTGTAAACTGAGGTGTGTGAATCCTCCCACAC

consensus                TTCTTTCCTCAAAACAACAAGGTAGAATGTGTAAACTGAGGTGTGTGAATCCTCCCACAC

U_HW-SSH2_10a10.b1.seq+ CGCACTAACTAGATCTTATTCGGGGGGGGTTGTATGCCGTTTCCCTTGGAAATTGGGCGG

consensus                CGCACTAACTAGATCTTATTCGGGGGGGGTTGTATGCCGTTTCCCTTGGAAATTGGGCGG

U_HW-SSH2_10a10.b1.seq+ GATCAGTCTCCCCCCCGCCCCGGGGCGTGGGACCTAAAACAGGATGGGAGTGTTTCTGCC

consensus                GATCAGTCTCCCCCCCGCCCCGGGGCGTGGGACCTAAAACAGGATGGGAGTGTTTCTGCC

U_HW-SSH2_10a10.b1.seq+ TGCCCTTCGGTGCTGCGCTACCCTTCCGACTG

consensus                TGCCCTTCGGTGCTGCGCTACCCTTCCGACTG

****************** Contig 38 ******************

U_HW-SSH2_8h09.b1.seq+  TAGCGTGGTCGCGGCCGAAAAAACACAAAAGCCCAAAATAGAAGCGAATGTCATCTACAC
U_HW-SSH2_7h04.b1.seq+                           AGCCCAAAACAGAAGCGAATGTCATCTACAC

consensus                TAGCGTGGTCGCGGCCGAAAAAACACAAAAGCCCAAAACAGAAGCGAATGTCATCTACAC

U_HW-SSH2_8h09.b1.seq+  AAAAAAGCCCGAAGTCCCAACACGAAAAAACTGAATGTGATTGATACATTTCTGTCACGC
U_HW-SSH2_7h04.b1.seq+  CACACGGTCTAGAGTTCCAACACCATAAAACTGAATGTGATTGATACATTTCTGTCACGC

consensus                AAAAAAGCCCAAAGTCCCAACACCAAAAAACTGAATGTGATTGATACATTTCTGTCACGC

U_HW-SSH2_8h09.b1.seq+  GGCCAAGGCACCATCTTTCTCTGGAAGAGCACACACACTATGACAATAGACTAAATCACC
U_HW-SSH2_7h04.b1.seq+  GGCCAAGGCACCATCACCAGCA--AAGAGCACACACACTATGACGATAGACTAAATCACC

consensus                GGCCAAGGCACCATCACCAGCAGGAAGAGCACACACACTATGACAATAGACTAAATCACC

U_HW-SSH2_8h09.b1.seq+  AGAGGCAGCAAGAAGTACAAAAATAACCTGATTTCGT-GGCTACGAATACCCTTTGATAA
U_HW-SSH2_7h04.b1.seq+  AGAGGCAGCAAGAAGTACAAAAATAACCTGATTTCATTGGCTACGAATACCCTATGATGA

consensus                AGAGGCAGCAAGAAGTACAAAAATAACCTGATTTCATTGGCTACGAATACCCTATGATAA

U_HW-SSH2_8h09.b1.seq+  TCACGTTTCTTTCATAACT-ACTGCTTGCTTCTC
U_HW-SSH2_7h04.b1.seq+  TCACGTTTCTTTCATAACAGACTGCTTGCTTCTCCGCTGGTGCACGTCCCAGTTAAATAT

consensus                TCACGTTTCTTTCATAACAGACTGCTTGCTTCTCCGCTGGTGCACGTCCCAGTTAAATAT

U_HW-SSH2_7h04.b1.seq+  CCGAGCAATTGTAACCTGAGTTATCGTTTGCTGGTCCCGTAAGAAATGAAGATCGCCAAC

consensus                CCGAGCAATTGTAACCTGAGTTATCGTTTGCTGGTCCCGTAAGAAATGAAGATCGCCAAC

U_HW-SSH2_7h04.b1.seq+  AAGGACTTCCAAACTGGCCCTCGCATTTTCCAAGTTACTTTTCAAGAGCTCATTGGCCTC

consensus                AAGGACTTCCAAACTGGCCCTCGCATTTTCCAAGTTACTTTTCAAGAGCTCATTGGCCTC

U_HW-SSH2_7h04.b1.seq+  GTCACAGGAGTATTCCAGCATCACATTTGCACCCAACCATAGGCACACTGAGTCAGAGTC

consensus                GTCACAGGAGTATTCCAGCATCACATTTGCACCCAACCATAGGCACACTGAGTCAGAGTC

U_HW-SSH2_7h04.b1.seq+  CTCAATTTTAGCACGCGAATAGATTCCCTCGGATAATTCAAAATCAGCTATGAGTGCCTC

consensus                CTCAATTTTAGCACGCGAATAGATTCCCTCGGATAATTCAAAATCAGCTATGAGTGCCTC

U_HW-SSH2_7h04.b1.seq+  ACCCAAAGCTTTTTTAGCTTTCAATGTCGCAACAATATCCAAGCACTTCTCTATATCAGG

consensus                ACCCAAAGCTTTTTTAGCTTTCAATGTCGCAACAATATCCAAGCACTTCTCTATATCAGG

U_HW-SSH2_7h04.b1.seq+  AATTTTCGCCTGAAGTTCTCTTTGTTGTGCTAAAAGTTTCATCTCCACCATTTGTACCTG

consensus                AATTTTCGCCTGAAGTTCTCTTTGTTGTGCTAAAAGTTTCATCTCCACCATTTGTACCTG

U_HW-SSH2_7h04.b1.seq+  CCCGGGCGGCCACTCAAAATCCATAGGGATTCCCGCCGCTTGCAGCCGACAATGTGCACA

consensus                CCCGGGCGGCCACTCAAAATCCATAGGGATTCCCGCCGCTTGCAGCCGACAATGTGCACA

U_HW-SSH2_7h04.b1.seq+  CTCTCACGTGTAGATGGCAAGTTTTAA

consensus                CTCTCACGTGTAGATGGCAAGTTTTAA

****************** Contig 39 ******************

U_HW-SSH2_9b05.b1.seq+  TAGCGTGGTCGCGGCAGAGAAAACAAAAAGGAAACAATCTTCTGCAACCCAACAAAGCTT

consensus                TAGCGTGGTCGCGGCAGAGAAAACAAAAAGGAAACAATCTTCTGCAACCCAACAAAGCTT

U_HW-SSH2_9b05.b1.seq+  GAAAAAGGGACTGTCTTTCTGCAGCTTCTGCTGATTTAACATCCCGC-CTAGATTGTGGG
U_HW-SSH2_9a04.b1.seq+                  TCTGCAGCTTCTGCTGATTTAACATACATAACTAGATTGTAGG
U_HW-SSH2_9a05.b1.seq+                  TCTGCAGCTTCTGCTGATTTAACATACATAACTAGATTGTAGG

consensus                GAAAAAGGGACTGTCTTTCTGCAGCTTCTGCTGATTTAACATACATAACTAGATTGTAGG

U_HW-SSH2_9b05.b1.seq+  ACTTTCCCTCTTCTTTGTGCATGCCCCAGAACCCAGGGTTGTAAATGCCAACGCCGCCGG
U_HW-SSH2_9a04.b1.seq+  ACTTTCCATCTTCTTTGTTCATGCCCCAAAACCCAGGGTTGTAAATGCCAACGCCACCGG
U_HW-SSH2_9a05.b1.seq+  ACTTTCCATCTTCTATGTTCATGCCCCAGAACCCAGGGTTGTAAATGCCAACGCCACCGG

consensus                ACTTTCCATCTTCTTTGTTCATGCCCCAGAACCCAGGGTTGTAAATGCCAACGCCACCGG

U_HW-SSH2_9b05.b1.seq+  CCTGGGCATTCCTCACCCATACCCGCCATCCTACGAGCGATGATTTTTCGACTGAAACAT
U_HW-SSH2_9a04.b1.seq+  C-TGGGCATTCATCACAAAGAACCTCCATCCTAAGAGCGATGATGTTTCGACTGAAACAT
U_HW-SSH2_9a05.b1.seq+  C-TGGGCATTCATCAAAGAGAACCTCCATCCTAAGAGCGATGATGTTTCGACTGAAACAT

consensus                C-TGGGCATTCATCACAAAGAACCTCCATCCTAAGAGCGATGATGTTTCGACTGAAACAT

U_HW-SSH2_9b05.b1.seq+  GATG
U_HW-SSH2_9a04.b1.seq+  GATGTACCTGCCCGGGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAGGTC
U_HW-SSH2_9a05.b1.seq+  GATG

consensus                GATGTACCTGCCCGGGCGGCCGCTCGAAATCACTAGTGAATTCGCGGCCGCCTGCAGGTC

U_HW-SSH2_9a04.b1.seq+  GACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGTCAC

consensus                GACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTATAGTGTCAC

U_HW-SSH2_9a04.b1.seq+  CTAAATAGCTTGGCGTAATCATGGACATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTC

consensus                CTAAATAGCTTGGCGTAATCATGGACATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTC

U_HW-SSH2_9a04.b1.seq+  ACAATTCCACCCCACATACGAGCCCGGAAGCATAAAGTGTAAAGGCCTGGGGGTGCCTAA

consensus                ACAATTCCACCCCACATACGAGCCCGGAAGCATAAAGTGTAAAGGCCTGGGGGTGCCTAA

U_HW-SSH2_9a04.b1.seq+  TGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAAA

consensus                TGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAAA

U_HW-SSH2_9a04.b1.seq+  CCTGGTCGTGCCATCTG

consensus                CCTGGTCGTGCCATCTG

****************** Contig 40 ******************

U_HW-SSH2_9c03.b1.seq+  TTCGAGCGGCCGCCCGGGCAGGTACCTGGGCCCCTTCTCTGCGCAGACGCCGTCCTACCT
U_HW-SSH2_9d08.b1.seq+                          GGGCCCCTTCTCTGCGCAGACGCCGTCCTACCT

consensus                TTCGAGCGGCCGCCCGGGCAGGTACCTGGGCCCCTTCTCTGCGCAGACGCCGTCCTACCT

U_HW-SSH2_9c03.b1.seq+  GAACGGCGAGTTCCCGGGCGACTACGGCTGGGACACCGCCGGGCTTTCCGCCGACCCGGA
U_HW-SSH2_9d08.b1.seq+  GAACGGGGAGTTCCCGGGCGACTACGGCTGGGACACCGCCGGGCTTTCCGCCGACCCGGA

consensus                GAACGGCGAGTTCCCGGGCGACTACGGCTGGGACACCGCCGGGCTTTCCGCCGACCCGGA

U_HW-SSH2_9c03.b1.seq+  GGCGTTCGCTAGGAACAGGGCGCTGGAGGTGATCCACGGGCGGTGGGCGATGCTCGGCGC
U_HW-SSH2_9d08.b1.seq+  GGCGTTCGCTAGGAACAGGGCGCTGGAGGTGATCCACGGGCGGTGGGCGATGCTCGGCGC

consensus                GGCGTTCGCTAGGAACAGGGCGCTGGAGGTGATCCACGGGCGGTGGGCGATGCTCGGCGC

U_HW-SSH2_9c03.b1.seq+  TCTTGGCTGCGTCTTCCCCGAGGTGCTCCAGAAGTGGGTGGGCGTGGAGTTCAAGGAGCC
U_HW-SSH2_9d08.b1.seq+  TCTTGGCTGCGTCTTCCCCGAGGTGCTCCAAAAGTGGGTGGGCGTGGAGTTCAAGGAGCC

consensus                TCTTGGCTGCGTCTTCCCCGAGGTGCTCCAAAAGTGGGTGGGCGTGGAGTTCAAGGAGCC

U_HW-SSH2_9c03.b1.seq+  CGTCTGGTTCAAGGCCGGCTCGCATATCTTCTCCGAGGGTGGCCTCGACTACCTTGGGAA
U_HW-SSH2_9d08.b1.seq+  CGTCTGGTTCAAGGCCGGCTCGCAAATCTTCTCCGAGGGTGGCCTCGACTACCTTGGGAA

consensus                CGTCTGGTTCAAGGCCGGCTCGCAAATCTTCTCCGAGGGTGGCCTCGACTACCTTGGGAA
```

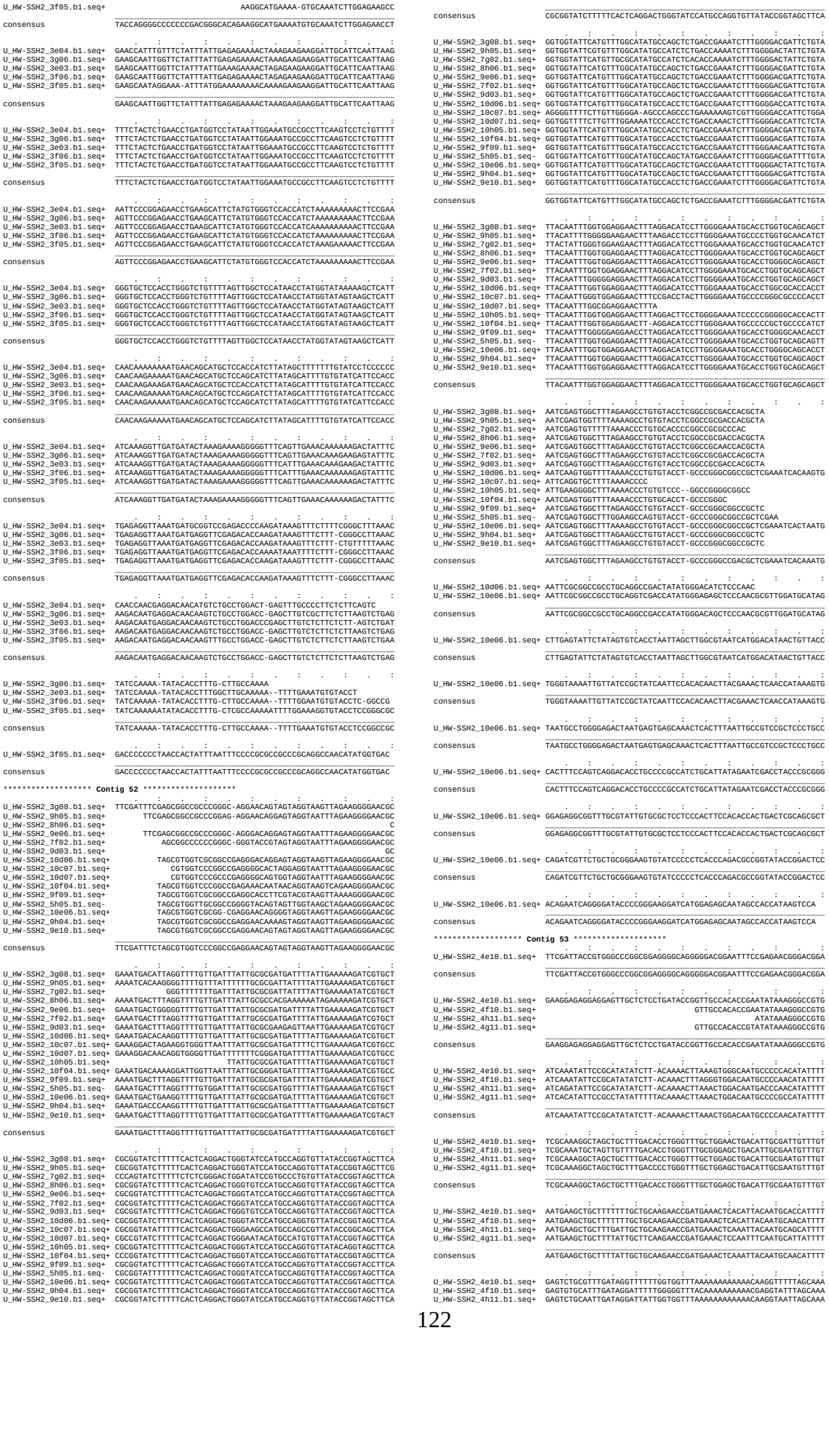
```
consensus               CGTCTGGTTCAAGGCCGGCTCGCAAATCTTCTCCGAGGGTGGCCTCGACTACCTTGGGAA

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9c03.b1.seq+  CCCCAACCTCGTCCACGCGCAGAGCATCCTTGCCGTGCTGGGCTTCCAGGTCCTTCTCAT
U_HW-SSH2_9d08.b1.seq+  CCCCAACCTCGTCCACGCACAAAGCATCCTTGCCGTGCTGGGCTTCCAGGTCCTTCTCAT

consensus               CCCCAACCTCGTCCACGCACAAAGCATCCTTGCCGTGCTGGGCTTCCAGGTCCTTCTCAT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9c03.b1.seq+  GGGCCTGGTAGAAGGGTTCCGCATCAATGGTCTCGACGGTGTCGGCGAGGGCAACGACCT
U_HW-SSH2_9d08.b1.seq+  GGGCCTGGTAGAAGGGTTCCGCATCAATGGTCTCGACGGTGTCGGCGAGGGCAA      
                        ___________________________________________________________
consensus               GGGCCTGGTAGAAGGGTTCCGCATCAATGGTCTCGACGGTGTCGGCGAGGGCAACGACCT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9c03.b1.seq+  CTACCCCGGCGGCCAGTACCTCGGCCGCGACCACGCTA
                        ______________________________________
consensus               CTACCCCGGCGGCCAGTACCTCGGCCGCGACCACGCTA

****************** Contig 41 ******************
                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9h10.b1.seq+  TAGCGTGGTCGCGGCTGAGGACAACTAGAGTCCCATCATTAACAAAACACAACAACCATT
                        ___________________________________________________________
consensus               TAGCGTGGTCGCGGCTGAGGACAACTAGAGTCCCATCATTAACAAAACACAACAACCATT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9h10.b1.seq+  CCCCAATGTCGGTTATCTTTAGCGGGGGCCGCTCCTGCGCGAGGCCATGTCCACGCCCGT
U_HW-SSH2_9h09.b1.seq+                          CGGGGGCCGCTCCTGCGCGAGGCCATGTCGACGCCCGT
                        ___________________________________________________________
consensus               CCCCAATGTCGGTTATCTTTAGCGGGGGCCGCTCCTGCGCGAGGCCATGTCCACGCCCGT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9h10.b1.seq+  GCTTATGGTCACAGGGGAGCTGGCGCTGGTGGAGGTTGAAGGCCGCTTCCAGCTGGGGTC
U_HW-SSH2_9h09.b1.seq+  GCTGATGGTCACAGTGGAGCAGGCGCTGGTGGAGGTTGACAGCCACTTTTAGTTTGTGTC

consensus               GCTGATGGTCACAGGGGAGCAGGCGCTGGTGGAGGTTGAAAGCCACTTCCAGCTGGGGTC

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9h10.b1.seq+  TTGCCTCCCGGTTGACCCCACCTCTCACAAATCCTTCTGGGTC
U_HW-SSH2_9h09.b1.seq+  CGGCCTCCCGGTTGACCACACCTCTTGCAAATCCTTCGGGGTCTTCGTCAAAAACAATCT
                        ___________________________________________________________
consensus               CGGCCTCCCGGTTGACCACACCTCTCACAAATCCTTCGGGGTCTTCGTCAAAAACAATCT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9h09.b1.seq+  TGTGAGGGCTTTCCTTTTGGTAAATGTCCGGATAGCCCATGTGGTGACATCTCCAACAGT
                        ___________________________________________________________
consensus               TGTGAGGGCTTTCCTTTTGGTAAATGTCCGGATAGCCCATGTGGTGACATCTCCAACAGT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9h09.b1.seq+  CAGGTTATAATTTGATAAATTATTTCTGTCTTCCCTATTTTTTTTTTTAGAAATC
                        ______________________________________________________
consensus               CAGGTTATAATTTGATAAATTATTTCTGTCTTCCCTATTTTTTTTTTTAGAAATC


****************** Contig 42 ******************
                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10d05.b1.seq+ TACAGGGGCCGCCCCGGGGGGCACAAGGAAACCAAAAAAGGATTATCCGCAAAAAAAAA
                        ___________________________________________________________
consensus               TACAGGGGCCGCCCCGGGGGGCACAAGGAAACCAAAAAAGGATTATCCGCAAAAAAAAA

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10d05.b1.seq+ CGGAGAAGCGGGAAATGAGTGTCGACGAGGTGAACTTGATTTTACCAAAGATGATGAAAA
U_HW-SSH2_5b10.b1.seq+                  ATGAGTGTCTACGTGGTGGACTTGATTTTACCAAAGATGATGAAAA
U_HW-SSH2_4b09.b1.seq-                  ATGAGTGTTTACGTGGTGGACTTGATTTTACCAAAGATGATGAAAA
                        ___________________________________________________________
consensus               CGGAGAAGCGGGAAATGAGTGTCTACGTGGTGGACTTGATTTTACCAAAGATGATGAAAA

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10d05.b1.seq+ CTTATCCTCACAGCCTTTTATGCGCTGGAGAAGACCGTTTTGTCTTTTGTGCCGAAGCTAT
U_HW-SSH2_5b10.b1.seq+  CGTAAACTCACAACCATTTATGCGCTGGAGAAGACCGTTTTGTCTTTTGTGCCGAAGCTAT
U_HW-SSH2_4b09.b1.seq-  CGTAAACTCACAACCATTTATGCGCTGGGGAGACCGTTTTGTTTTTTGTGCCGAAGCTAT
                        ___________________________________________________________
consensus               CGTAAACTCACAACCATTTATGCGCTGGAGAGACCGTTTTGTCTTTTGTGCCGAAGCTAT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10d05.b1.seq+ TTATTAATCACAGGCCGAACCCGGAGAAATCGGGGGGGATTCCTTGAATGCTACTGCGG-
U_HW-SSH2_5b10.b1.seq+  TTATAAATCACAGGCCGAAACCGGTGAAATCAAGGGGCATTACTTGAATGCGACTGCGG-
U_HW-SSH2_4b09.b1.seq-  TTATAAATCACAGGCCGAAACCGGTGAAATCAAGGGGCATTACTTGAATGCGACTGCGG-
U_HW-SSH2_12g10.b1.seq+                                          TTCGATTAGCGCGGTCGCGCC
U_HW-SSH2_12g11.b1.seq+                                       TTCGATTACCGTGGCCCCGCC
U_HW-SSH2_4a12.b1.seq+                                           ATTAGCGTGGTCGCGCC
U_HW-SSH2_10e01.b1.seq-                                             TAGCGTGGTCGCGGC
U_HW-SSH2_12h12.b1.seq+                                          TTCGATTAGCGTGGTCGCGGC
U_HW-SSH2_10d02.b1.seq+                                          ATTAGCGTGGTCGCGGC
U_HW-SSH2_10g06.b1.seq+                                             TAGCGTGGTCGCGGC
U_HW-SSH2_9h12.b1.seq+                                              TAGCGTGGTCGCGGC
U_HW-SSH2_5e10.b1.seq-                                              TAGCGTGGTCGCGGC
U_HW-SSH2_5f11.b1.seq+                                              TAGCGTGGTCGCGGC
U_HW-SSH2_6f06.b1.seq-                                              TAGCGTGGTCGCGGC
                        ___________________________________________________________
consensus               TTATAAATCACAGGCCGAAACCGGTGAAATCAAGGGGCATTCCATTAGCGTGGTCGCGGC

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10d05.b1.seq+ ----G
U_HW-SSH2_5b10.b1.seq+  ----GTAC
U_HW-SSH2_4b09.b1.seq-  ----GTACATGTGAAGAAATGATTAAGAGAGCTGTATTTGCAAGAGAATTAGGGGTTCCT
U_HW-SSH2_12g10.b1.seq+ CGACGTACCTGTGCACAAATGATTAAGAGAGCTGTATTTGCAAAATAATTAGGGGTTCCT
U_HW-SSH2_12g11.b1.seq+ CGAGGTACATGTGAACAAATGATTAAGAAAGGTGTTTTTGCAAAAAAATTAGGGGTTCCT
U_HW-SSH2_4a12.b1.seq+  CGAGGAGAGGGGGAAAAATGATTAAAAGAGCTGTATTTGCAAAAAAAAGGGGTTCCT
U_HW-SSH2_10e01.b1.seq-  CGAGGTACATGTGAAGAAATGATTAAGAGAGCTGTATTTGCAAGAGAATTAGGGGTTCCT
U_HW-SSH2_6c05.b1.seq+                                                GAGAATTAGGGGTTCCT
U_HW-SSH2_12h12.b1.seq+ CGAGGTACATGTGAAGAAATGATTAAGAGAGCTGTATTTGCAAAAGAATTAGGGGTTCCT
U_HW-SSH2_10d02.b1.seq+ CGAGG-ACAGGGGAAGAAATAATTAAGAGAGCTGTATTTGCAAAAAAAATAGGGGTTCCT
U_HW-SSH2_10g06.b1.seq+ CGAGGAACATGTGAAGAAATGATTAAGAGAGCTGTATTTGCAAGAGAATTAGGGGTTCCT
U_HW-SSH2_9h12.b1.seq+  CGAGGAACGTGTGAAGAAATGATTAAGAGAGCTGTATTTGCAAG
U_HW-SSH2_8e11.b1.seq+                  AAGAAATGACTAAGAGAGCTGTATTTGAAAGAGAACAAAAGGAACCT
U_HW-SSH2_5e10.b1.seq-  CGAGGTACATGTGAAGAAATGATTAAGAGAGCTGTATTTGCAAGAGAATTAGGGGTTCCT
U_HW-SSH2_5f11.b1.seq+  CGAGGTACATGTGATCAAATGATTAAAAGAGCTGTATTTGCAAGATACTTAGGGGTTCCT
U_HW-SSH2_12h02.b1.seq+       ACATGTGAAGAAATGATTAAGAGAGCTGTATTTGCAAGAGAATTAGGGGTTCCT
U_HW-SSH2_10d12.b1.seq-                           AGAGAGCCGTATTTGCAAGAGAAATAGGGGTTCGT
U_HW-SSH2_5a01.b1.seq+                                  CTGTATTTGCAAGACAATTAGGGGTTCCT
U_HW-SSH2_5f10.b1.seq+    AGGTACATGTGAAGAAATGATTAAGAGAGCTGTATTTGCAAGAGAATTAGGGGTTCCT
U_HW-SSH2_6f06.b1.seq-  CGAGGTACATGTGAAGAAATGATTAAGAGAGCTGTATTTGCAAGAGAATTAGGGGTTCCT
                        ___________________________________________________________
consensus               CGAGGTACATGTGAAGAAATGATTAAGAGAGCTGTATTTGCAAGAGAATTAGGGGTTCCT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_4b09.b1.seq-  ATTGTAATGCATGACTACTTAAGTGGGGATTCACCGCAAATACTACTTTGGCTCAT-TA
U_HW-SSH2_12g10.b1.seq+ ATTGTAATGCATGACTACTTAAGTGGGGATTCACCGCAAATACTAATTTGGCTCAT-TA
U_HW-SSH2_12g11.b1.seq+ ATTGTAATGCAGGACTACTTAAGTGGGGATTCACCGCAAATTCTAATTTGGGTCAT-TA
U_HW-SSH2_4a12.b1.seq+  ATTGTAATGCATGACTACTTAACTGGGGGATTCACCGCAAATACTACTTTGGCTCAT-TA
U_HW-SSH2_10e01.b1.seq-  ATTGTAATGCATGACTACTTAACTGGGGGATTCACCGCAAATACTACTTTGGCTCAT-TA
U_HW-SSH2_3d11.b1.seq+                  ACTTAACTGGGGGATTCACCGCAAATACTACTTGGCCTCAT-TA
U_HW-SSH2_6c05.b1.seq+  ATTGTAATGCATGACTACTTAACTGGGGCATTCACGGGAAATACTACTTTGGCTCTT-TA
U_HW-SSH2_12h12.b1.seq+ ATTGTAATGCATGACTACTTAACTGGGGATTCACCGCAAATACTACTTTGGCTCAT-TA
U_HW-SSH2_10d02.b1.seq+ ATTGTAATGCCTGACTACTTACCTGGGGGATTCACCGCCAATACTACTTTGGCTCAT-TA
U_HW-SSH2_10g06.b1.seq+ ATTGTAATGCATGACTACTTAACTGGGGATTCACCGCAAATACTACTTTGGCTCAT-TA
U_HW-SSH2_6g10.b1.seq+      ATGCAGGACTACTTAACTGGGGATTCCCCACAAATACTACTTTGGCTCAT-TA
U_HW-SSH2_8e11.b1.seq+  ATTGAAAAGCATGACTACTTAACTGGGGATTCACCGCAAATACTACTTTGGCTCTCTT
U_HW-SSH2_5e10.b1.seq-  ATTGTAATGCATGACTACTTAACTGGGGATTCACCGCAAATACTACTTTGGCTCAT-TA
U_HW-SSH2_5f11.b1.seq+  ATTGCAATGCATGACTACTTAACTGGGGATTCACCGCAGATACTACTTTGGCTCAT-TA
U_HW-SSH2_12h02.b1.seq+ ATTGTAATGCATGACTACTTAACTGGGGATTCACCGCAAATACTACTTTGGCTCAT-TA
U_HW-SSH2_10d12.b1.seq- ATTTTAATGCATGACCACGTAAATGGGGGGTTCACGGCAAAAAATACTTTGGATCAT-TA
U_HW-SSH2_5a01.b1.seq+  ATTGTAATGCATGACTACTTAACTGGGGATTCACCGCAAATACTACTTTGGCTCAT-TA
U_HW-SSH2_5f10.b1.seq+  ATTGTAATGCATGACTACTTAACTGGGGATTCACCGCAAATACTACTTTGGCTCAT-TA
U_HW-SSH2_6f06.b1.seq-  ATTGTAATGCATGACTACTTAACTGGGGATTCACCGCAAATACTACTTTGGCTCAT-TA

consensus               ATTGTAATGCATGACTACTTAACTGGGGATTCACCGCAAATACTACTTTGGCTCAT-TA

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_4b09.b1.seq-  TTGCCGCGACAATGGCCTACTTCTTCACATTCACCGTGCAATGCATGCAGTT-ATTGATA
U_HW-SSH2_12g10.b1.seq+ TTGCCCCGACAATGGCCTACTTCTTCACATTGGCGGTGCAATGCATGCCTTT-ATTGATA
U_HW-SSH2_12g11.b1.seq+ TTGCCCCCACAATGGCCTACTTCTTCACATTGGCCGTGCAATGCATGCCTTT-ATTGATA
U_HW-SSH2_4a12.b1.seq+  TTGCCGCGACAATGGCCTACTTCTTCACATTCACCGTGCTATGCATGCCTTTTATTGATA
U_HW-SSH2_10e01.b1.seq-  TTGCCGCGACAATGGCCTACTTCTTCACATTCACCGTGCAATGCATGCAGTT-ATTGATA
U_HW-SSH2_3d11.b1.seq+  TTGCCGCGACAAGGGCCTACTTCTTCACCTTCACCGTGC
U_HW-SSH2_6c05.b1.seq+  TTGCATCGACC-GGGCCTACTTCTTCACATTCGCCGTGCA
```

```
U_HW-SSH2_12h12.b1.seq+ TTGCCGCGACAATGGCCTACTTCTTCACATTCACCGTGCAATGCATGCAGTT-ATTGATA
U_HW-SSH2_10d02.b1.seq+ TTGCCGAAACAATGGCCTACTTCTTCACATTCACCGTGCAATGCATGCGGTT-ATTGATA
U_HW-SSH2_10g06.b1.seq+ TTGCCGCGACAATGGCCTACTTCTTCACATTCACCGTGCAATGCATGCAGTT-ATTGATA
U_HW-SSH2_6g10.b1.seq+  TTGCCGCGACAAGGGCCTATTTCTTCACTTTCACCGTGCAATGCATGCAGTT-ATTGATA
U_HW-SSH2_8e11.b1.seq+  TAGCCGCGACAATGGCCTACTTCTTCACATTCACCGTGCAATGCATGCAGTT-ATTGATA
U_HW-SSH2_5e10.b1.seq-  TTGCCGCGACAATGGCCTACTTCTTCACATTCACCGTGCAATGCATGCAGTT-ATTGATA
U_HW-SSH2_5f11.b1.seq+  TTGCCGCGACAATGGCCTACTTCTTCACATTCACCGTGCAATGCATGCAGTA-ATTGATA
U_HW-SSH2_12h02.b1.seq+ TTGCCGCGACAATGGCCTACTTCTTCACATTCACCGTGCAATGCATGCAGTT-ATTGATA
U_HW-SSH2_10d12.b1.seq- TT
U_HW-SSH2_5a01.b1.seq+  TTGCCTCGACAATGGCCTACTTCTTCACATTCACCGTGCAATGCATGCAATT-ATTGATA
U_HW-SSH2_5f10.b1.seq+  TTGCCGCGACAATGGCCTACTTCTTCACATTCACCGTGCAATGCATGCAGTT-ATTGATA
U_HW-SSH2_6f06.b1.seq-  TTGCCGCGACAATGGCCTACTTTTTCACATTCACCGTGCAATGCATGCAGTT-ATTGATA

consensus               TTGCCGCGACAATGGCCTACTTCTTCACATTCACCGTGCAATGCATGCAGTT-ATTGATA

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_4b09.b1.seq-  GACAGAAAAATCATGGTATGCATTTCCGTGTATTAGCTTTTGCATTGCGTATGTCTGGGG
U_HW-SSH2_12g10.b1.seq+ AAAAGAAAAATCATGGTATGCGTTTCCAGCGAATAAAATAAAGAATTGCTTAGGGGTGGGG
U_HW-SSH2_12g11.b1.seq+ AAAAGAAAAATCATGGTATGCGTTTCCAGGAATAAAATAAAGAATTGCTTATGGGGGGGG
U_HW-SSH2_4a12.b1.seq-  GACAAAAAAATCATGGTATGCATTTCCGTGTATTACCTAAAGCATTGCGTATTTCTGGGG
U_HW-SSH2_10e01.b1.seq-  GACAGAAAAATCATGGTATGCAATTCCGTGTATTT
U_HW-SSH2_12h12.b1.seq+ AACAAAAAAATCATGGTATGCATTTCCGTGTATTAGCTAAAGCATTGCGTATGTCTGGGG
U_HW-SSH2_10d02.b1.seq+ GACAAAAAAATCATGGTATGCATTTCCGTGTATTT-CTAAAGATTTGCGTATGTCTGGGG
U_HW-SSH2_10g06.b1.seq+ GACAGAAAAATCATGGTATGCATTTCCGTGTATTAGCTAAAGCATTGCGTATGTCTGGGG
U_HW-SSH2_6g10.b1.seq+  GAAAGAAAAATCATGGTATGCATTTCCATGAATTAACTAAAGCTTTGCGTATGTCTGGGG
U_HW-SSH2_8e11.b1.seq+  AAAAGAAAAATCATGGTATGCATTTCCGTGTATTAGCTAAAGTTTTGCGTATGTCTGGGG
U_HW-SSH2_5e10.b1.seq-  GACAGAAAAATCATGGTATGCATTTCCGTGTATTAGCTAAAGCATTGCGTATGTCTGGGG
U_HW-SSH2_5f11.b1.seq+  CACAGAAAAATCATGGTATGCATTTCCCGTGTATTAGCTAAAGCATTGCGTATGTCGGGGG
U_HW-SSH2_12h02.b1.seq+ GACAAAAAAATCATGGTATGCATTTCCGTGTATTAGCTAAAGCATTGCGTATGTCTGGGG
U_HW-SSH2_5a01.b1.seq+  GACAGAAAAATCATGGTATGCATTTCCATGTATTAACTAAATCATTGCGTATGTCTGGGG
U_HW-SSH2_5f10.b1.seq+  GACAAAAAAATCATGGTATGCATTTCCGTGTATTAGCTAAAGCATTGCGTATGTCTGGGG
U_HW-SSH2_6f06.b1.seq-  GACAGAAAAATCATGGTATGCATTTCCGTGTATTAGCTAAAGCATTGCGTATGTCTGGGG
                        ___________________________________________________________
consensus               GACAGAAAAATCATGGTATGCATTTCCGTGTATTAGCTAAAGCATTGCGTATGTCTGGGG

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_4b09.b1.seq-  GAGATCATATCCACTCCGGTGCCT-CCCCGGGCGGCCGCTCGAA
U_HW-SSH2_12g10.b1.seq+ GAGATCATTTCCACTCGGGAACCT-GCCCGGGCGGCCG
U_HW-SSH2_12g11.b1.seq+ GAGATCATATCCACTCGGGAACCC-GCCCGGGCGGC
U_HW-SSH2_4a12.b1.seq+  GAAATCATATCCACTCCTGTACCT-GCCCGGGCG
U_HW-SSH2_12h12.b1.seq+ GAGATCATATCCACTCCGGTACCG-GCCCGGGCGGCCGCT
U_HW-SSH2_10d02.b1.seq+ AAAATCATATCCAACCCGGTACCT-GCCCGGG
U_HW-SSH2_10g06.b1.seq+ GAGATCATATCCACTCCGGTACCT-GCCCGGGCGGCCGCTC
U_HW-SSH2_6g10.b1.seq+  GAGATCGAATCCACCCCGGT
U_HW-SSH2_8e11.b1.seq+  AAAAT
U_HW-SSH2_5e10.b1.seq-  GAGATCATATCCACTCCGGTACCT-GCCCGGGCGGCCGCTCGAAATCGAA
U_HW-SSH2_5f11.b1.seq+  GA
U_HW-SSH2_12h02.b1.seq+ GAGATCATATCCACTCCGGTACCTCGGCCGCGACCACGCT
U_HW-SSH2_5a01.b1.seq+  GAAATCATATCCACTCCGGTACCTCGGCCGCGACC
U_HW-SSH2_5f10.b1.seq+  GAGATCATATCCACTCCGGTACCTCGGCCGCGACCACGCT
U_HW-SSH2_6f06.b1.seq-  GAGATCATATCCACTCCGGTACCT-GCCCGGGCGGCCGCTCGAAATC
                        ___________________________________________________________
consensus               GAGATCATATCCACTCCGGTACCT-GCCCGGGCGGCCGCTCGAAATCGAA

****************** Contig 43 ******************
                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10h08.b1.seq+ TTCGAGCGGCCGCCCGGGCAGGCACCAAGAGGGTGCTGTTTGTCGAAACTTGATTAGGG
U_HW-SSH2_10h11.b1.seq+   CGAGGGGCCGCCCGGGAAAGAACCAAAAGGGTGCTGATTGTCAGGAACTTGATTACCG
                        ___________________________________________________________
consensus               TTCGAGCGGCCGCCCGGGAAAGAACCAAAAGGGTGCTGATTGTCAGGAACTTGATTACCG

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10h08.b1.seq+ AGGTCTGGATT-TGCTCCCTATTGAGAAGCGTATCACTGACCTTCTTAAGGTTGGAAAG
U_HW-SSH2_10h11.b1.seq+ AGGAACCTGGAAAATGCTCCCGAGGAGAAGCGTATCACTGAGCTTCTTAAGGTTGGAAAG
                        ___________________________________________________________
consensus               AGGAACCTGGAAAATGCTCCCGAGGAGAAGCGTATCACTGACCTTCTTAAGGTTGGAAAG

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10h08.b1.seq+ GACAAGCGTGCACTCAA-GGTCGCCAAGAGGAAGCTTGGTACCTCGGCCGCGACCACGCT
U_HW-SSH2_10h11.b1.seq+ GACAAGCGTGCCCTTTTGGTCGCCAAGAGGAAGCTTGGAACATCGGCCGCGACCACGCT
                        ___________________________________________________________
consensus               GACAAGCGTGCACTCAATGGTCGCCAAGAGGAAGCTTGGAACATCGGCCGCGACCACGCT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10h08.b1.seq+ A
U_HW-SSH2_10h11.b1.seq+ A
                        ___
consensus               A

****************** Contig 44 ******************
                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11b02.b1.seq+ TTCGATTACCGTGGTCGCGGCCGAGGTACACCTGCGCCTTTTATTTTACTA-AAAA-CAA
U_HW-SSH2_11d01.b1.seq+          CGTGGTCCCGGCCGAGGTACACCTGCGCCTTTTATTTTACTA-AAAAACAA
U_HW-SSH2_11c02.b1.seq+          CGTGGTCCGCGGCCGAGGTACACCTGCGCCTTTTATTTTACTACAAAAACAA
U_HW-SSH2_11c03.b1.seq+             GGTCCCGGCCGAGGTGCACGTGCGCCTTTTTTTTAGTG-ACAATCAC
U_HW-SSH2_11b03.b1.seq+          CGTGGTCGCGGCCGAGGTACACCTGCGCCTTTTGTTTTATTG-ACTGACAA
U_HW-SSH2_11e02.b1.seq+          CGTGGTCGCGGCCGAGGTACACCTGCGCCTTTATTTTACTA-AAAAACAA
U_HW-SSH2_11d02.b1.seq+          CGTGGTCGCGGCCGAGGTACACCTGCGCCTTTTATTTTACTG-AAAAACAA
U_HW-SSH2_11c01.b1.seq+          CGTGGTCGCGGCCGAGGTACAACTGCGCCTTTTATTTTACTACAAAAACAA
                        ___________________________________________________________
consensus               TTCGATTACCGTGGTCGCGGCCGAGGTACACCTGCGCCTTTTATTTTACTA-AAAAACAA

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11b02.b1.seq+ ATAATGATACACTACTCCAGGTCTATCTTTTCAG-CCGCATAGAAAGAGGAAGAGGGGTA
U_HW-SSH2_11d01.b1.seq+ ATAATGATACACTATTCCAGGTCTAGCTTTTCAG-CCGCATAGAAAGAGGAACAGGGGTA
U_HW-SSH2_11c02.b1.seq+ ATAATGATACACTAGTCCAGGTCTAGCTTTTCAG-CCGCATAGAAAGAGGAACAGGGGTA
U_HW-SSH2_11c03.b1.seq+ ATAATTTTATCTTACTGGAGGAGGATATTTTCCCACCGCATAAAAATCGAAGGAGGA-TA
U_HW-SSH2_11b03.b1.seq+ ATAATGATACACTATGGGAGGTCT-GATTTTCCAACCGCATTGGCAT-GGAAGGGGGGTA
U_HW-SSH2_11a02.b1.seq+                                                  AGGGGTA
U_HW-SSH2_11e02.b1.seq+ ATAATGATACACTAGTCCAGGTCTATCTTTTCAG-CCGCATAGAAAGAGGAACAGGGGTA
U_HW-SSH2_11d02.b1.seq+ ATAATGATACACTAGTCCAGGTCTAGCTTTTCAG-CCGCATAGAAAGAGGAACGGGGGTA
U_HW-SSH2_11c01.b1.seq+ ATAATGATACACTAGTCCAGGTCTAGCTTTTCAG-CCGCATAGAAAGAGGAACAGGGGTA
U_HW-SSH2_11e01.b1.seq+                                          GAACAGGGTTA
                        ___________________________________________________________
consensus               ATAATGATACACTAGTCCAGGTCTAGCTTTTCAG-CCGCATAGAAAGAGGAACAGGGGTA

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11b02.b1.seq+ ATAACATATCATGAGCTTGAAAAGTGTGCAATCGATTGTGCCATCATCAAAACAAACCTT
U_HW-SSH2_11d01.b1.seq+ ATAGCAAATCATGAGCTTGTAAAGTGTGCAATCGATTGTGCCATCATCAAACCAGACCTT
U_HW-SSH2_11c02.b1.seq+ ATAACAAATCATGAGCTTGTAAAGTGTGCAATCGATTGTGCCATCATCAAAGCAAACCTT
U_HW-SSH2_11c03.b1.seq+ ATAACTGATCATGAGCTTTAAATTAGAGCTTACAATTGTGCCATCATGGTACCGAACCTT
U_HW-SSH2_11b03.b1.seq+ ATAACAATTCATGAGTTTG-AAACTGTGCCATCGATGGCGCCATCATCGGGACGAACCTT
U_HW-SSH2_11a02.b1.seq+ ATAGCATTTCATGAGCTTGTAAAGTGTGCCACCGATTGCGCCATCATCAAACCAAACCTT
U_HW-SSH2_11e02.b1.seq+ ATAACAAATCATGAGCTTGTAAAGTGTGCAATCGATTGTGCCATCATCAAACCAAACCTT
U_HW-SSH2_11d02.b1.seq+ ATAACAAATCATGAGCTTGTAAAGTGTGCAATCGATTGTGCCATCATCAAACCAAACCTT
U_HW-SSH2_11c01.b1.seq+ ATAACAAATCATGAGCTTGTAAAGTGTGCAATCGATTGTGCCATCATCAAAGCAGACCTT
U_HW-SSH2_11e01.b1.seq+ ATAGCAATTCATGAGCTTGAAAAATGTGCAATCGATTGTGCCATCATCAAACGATAACTT
U_HW-SSH2_11a03.b1.seq+                                 CGATTGCGCCATCATCAAACCTAACCTT
                        ___________________________________________________________
consensus               ATAACAAATCATGAGCTTGTAAAGTGTGCAATCGATTGTGCCATCATCAAACCAAACCTT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11b02.b1.seq+ TTGAACAACCATATGCACAGTAATAGGGGGCGATTAATAGATCGGAACAACGCTGTCGGG
U_HW-SSH2_11d01.b1.seq+ TTGCACAACCATATGCACAGTAATAGGGGGCGATTAAAGATCGGAACACCGCTGTCGTG
U_HW-SSH2_11c02.b1.seq+ TTGCACAACCATATGCACAGTAATAGGGGGCGATTAAAGATCGGCACAACGCTGTCGTG
U_HW-SSH2_11c03.b1.seq+ TTGCACAACCTTATGCACAGTAATAGGGGGCTATTAAAGATCCGAACAT-GATGTCATG
U_HW-SSH2_11b03.b1.seq+ TTGCACAACCATATGCACAGTAATAGGGGGAGATTAA
U_HW-SSH2_11a02.b1.seq+ TTGAACAACCATATGCACAGTAATAGGGGGCGATGAAATGATCGGCACATCGCTGTCAGG
U_HW-SSH2_11e02.b1.seq+ TTGCACAACCATATGCACAGTAATAGGGGGCGATTAAAGATCGGCACAACGCTGTCGTG
U_HW-SSH2_11d02.b1.seq+ TTGCACAACCATATGCACAGTAATAGGGGGCGATTAAAGATCGGCACAACGCTGTCATG
U_HW-SSH2_11c01.b1.seq+ TTGCACAACCATATGCACAGTAATAGGGGGCGATTAAAAATCGGACCATCGATGTCGTG
U_HW-SSH2_11e01.b1.seq+ TTGACCAACCATATGCAAAAAAATCGGGGGCGATTACTTGATCTTCCTCCCGTTGTAATG
U_HW-SSH2_11a03.b1.seq+ TTGCACAACCGTATGCACAGAAATAGGGGGCGATTAAAAATCGGACCATCGATGTCAGG
                        ___________________________________________________________
consensus               TTGCACAACCATATGCACAGTAATAGGGGGCGATTAAAGATCGGCACAACGCTGTCATG

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11b02.b1.seq+ GACCCTGTTCTTCTGGTGCTGGGCAACGCATTCCGATATCCACATCAGGTTCCTTATCTC
U_HW-SSH2_11d01.b1.seq+ GACCCTGTTCTTCTGGTTCTGGGCAACGCATTCCGAGATCCACATCAAGTTCCTTATCTC
U_HW-SSH2_11c02.b1.seq+ GACCCTGTTCTTCTGGTTCTGGGCAACGCATTCCGAGATCCACATCAAGTTCCTTATCTC
U_HW-SSH2_11c03.b1.seq+ GACCCTGTTCTTCTGGTCCCGGGCTTTTT-TTCCCACATTCAAGGCCCC--CGTTATCTC
U_HW-SSH2_11a02.b1.seq+ GACCCTGTTCTTCTGGTGCTGGACAACTT-TTCCGATATCTACATCAAGTTCCTTATCTC
U_HW-SSH2_11e02.b1.seq+ GACCCTGTTCTTCTGGTTCTGGGCAACGCATTCCGAGATCCAAATCAAGTTCCTTATCTC
U_HW-SSH2_11d02.b1.seq+ GACCCTGTTCTTCTGGTTCTGGGCAACGCATTCCGAGATCCACATCAAGTTCCTTATCTC
U_HW-SSH2_11c01.b1.seq+ GACCCTGTTCTTCTGGTTCTGGGCAACGCATTCCGAGATCCACATCAAGTTCCTTATCTC
U_HW-SSH2_11e01.b1.seq+ GACCCTGTTCTTCTGGTTCGGGGCATCTT-TTCACAAATCCA-ATCAAGTTCCTTATCTC
U_HW-SSH2_11a03.b1.seq+ GAGCCTGTTCTTCGGGTGGGGGGGTTTTT-TTCCGACATCCACATCATGTTCCTTATCTC
                        ___________________________________________________________
```

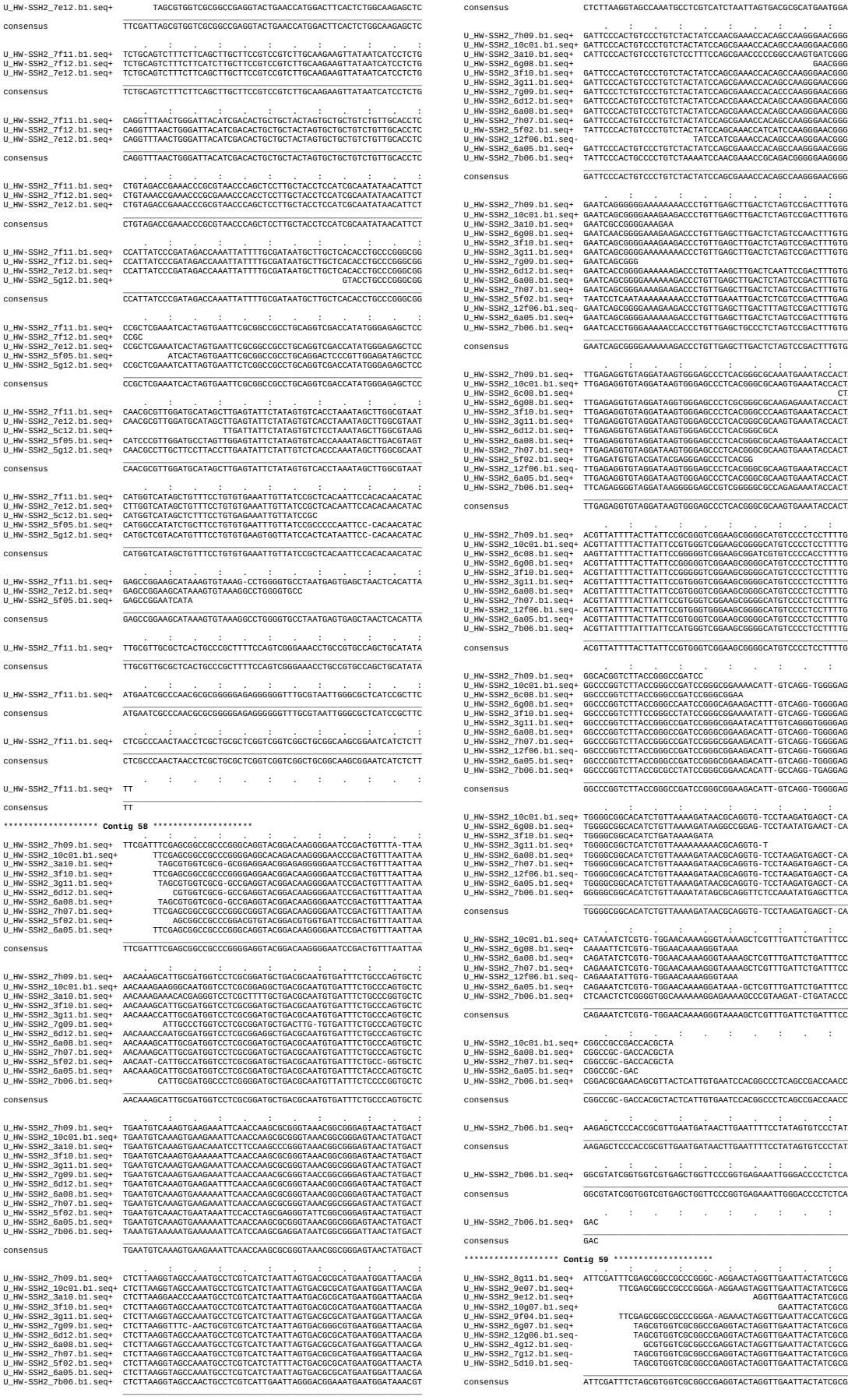
```
consensus               GACCCTGTTCTTCTGGTTCTGGGCAACGCATTCCGAGATCCACATCAAGTTCCTTATCTC

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11b02.b1.seq+ CTGCTCTCGTAGCCTCATGTATGCGAAAAAAAACAGCGTAGTGGAACTGCTGTTCAAATGA
U_HW-SSH2_11d01.b1.seq+ CTGCTCTCGCAGCCTCATGTATGCCAATAAAACAGCGTAGTGGAACTGCTGTTCAAATGA
U_HW-SSH2_11c02.b1.seq+ CTGCTCTCGTAGCCTCATGTATGCAAAAAAAACAGCGTAGTGGAACTGCTGTTCAAATGA
U_HW-SSH2_11c03.b1.seq+ CTGCTCTTG-AGCCTCATGTACGCAAACAAAACAGCCTACTTTTATTGCTGGTCAA-TGA
U_HW-SSH2_11a02.b1.seq+ CTGCTCCCGTAACCTCATGTATGCAAAGAAAACAGCGTAGTGGATCTGCTGTTCAAACGA
U_HW-SSH2_11e02.b1.seq+ CTGCTCTCGTACCCTCATGTATGCAAAGAAAACAGCGTAGTGGAACTGCTGTTCAAATGA
U_HW-SSH2_11d02.b1.seq+ CTGCTCTCGTAGCCTCATGTATGCAAAAAAAACAGCGTAGTGGAACTGCTGTTCAAATGA
U_HW-SSH2_11c01.b1.seq+ CTGCTCTCGTAGCCTCATGTATGCAAAAAAAACAGCGTAGTGGAACTGCTGTTCAAATGA
U_HW-SSH2_11e01.b1.seq+ CTGCTCTCTCAACCTCATGCATGCCAATAAAACATCTTAGAGCAACTGCTGTTCAATTGA
U_HW-SSH2_11a03.b1.seq+ CTGCTCTCGCAGCCTCATGTATGCAAATAAAGCGCTTACTGGATCTACTGTTCAAATGA
                        ____________________________________________________________

consensus               CTGCTCTCGTAGCCTCATGTATGCAAAAAAAACAGCGTAGTGGAACTGCTGTTCAAATGA

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11b02.b1.seq+ CTGGCTCAGCCTCTTTCCTTCCTCCTCATAAAAGGCCTTGTCCAACATCTGGCTTTCGCC
U_HW-SSH2_11d01.b1.seq+ CTGGCACACCCTCTTTACTTCCTCCTCATAAAAGGCCTTGTCCAACATCTGGCTTTCGCC
U_HW-SSH2_11c02.b1.seq+ CTGGCACAGCCTCTTTACTTCCTCCTCATAAAAGGCCTTGTCCAACATCTGGCTTTCGCC
U_HW-SSH2_11c03.b1.seq+ CTGGCACACCCTCTTTCCTTCCTCCTTATAACAGGCCTTGTCCAAGATCTGGCTTTAGCC
U_HW-SSH2_11a02.b1.seq+ CTGGCACTCCCTCTTTACTTCCTCCTCATAAAAAAC-TTG-CCAAGATCTGGGTTTCACC
U_HW-SSH2_11e02.b1.seq+ CTGGCACAGCCTCTTTACTTCCTCCTCATAAAGGGCCTTGTCCAACATCTGGCTTTCGCC
U_HW-SSH2_11d02.b1.seq+ CTGGCACAGCCTCTTTACTTCCTCCTCATAAAAGCCTTGTCCAACATCTGGCTTTCGCC
U_HW-SSH2_11c01.b1.seq+ CTGGCACAGCCTCTTTACTTCCTCCTCATAAAAGGCCTTGTCCAACATCTGGCTTTCGCC
U_HW-SSH2_11e01.b1.seq+ CTGGCACAGCCTCTTTACTTCCTCCTCATAAGAGCACTTGTCCCCACATCTGGCTTTCGCC
U_HW-SSH2_11a03.b1.seq+ CTGGCTCACCCTCTTTACTTCCTCCTTATGAAAGGCCTTGTCCAAGATCTGGCTTTAGCC

consensus               CTGGCACAGCCTCTTTACTTCCTCCTCATAAAAGCCTTGTCCAACATCTGGCTTTCGCC

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11b02.b1.seq+ ATATG-ATATCTTGGCAAAAAT
U_HW-SSH2_11d01.b1.seq+ ATATG-ATATCTTGGCAA
U_HW-SSH2_11c02.b1.seq+ ATATG-ATATCTTGGCAAAAATAGACTGGTATGGGGGGTACCT-GCCCGG
U_HW-SSH2_11c03.b1.seq+ ATATG-ATATCTTGGCAAAAATAGACTGGTA
U_HW-SSH2_11a02.b1.seq+ ATATG-ATATCTTGTCAAAAATA
U_HW-SSH2_11e02.b1.seq+ AAATGTATATCTTGACAAAAATAGACT
U_HW-SSH2_11d02.b1.seq+ ATATG-ATATCTTGGCAA
U_HW-SSH2_11c01.b1.seq+ ATATG-ATATCTTGGCAAAAATAGACTGGTATGGGGGGTACCT-GCCCGG
U_HW-SSH2_11e01.b1.seq+ AGATG-ATATCTTGGCAATA-TACACTGCTATGAGGGGTACCTAGCCCGGATGATGGCAG
U_HW-SSH2_11a03.b1.seq+ ATATG-ATATCTTGCCAAAAATACACTGGTACGGGAGGCACCT-GCCCGG
                        ____________________________________________________________

consensus               ATATG-ATATCTTGGCAAAAATAGACTGGTATGGGGGGTACCT-GCCCGGATGATGGCAG

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11e01.b1.seq+ TGCGTTATCTTCAATGAATGAACTGTTCTCGTTAGCATGGTTTGACCCAACGTACGACAT
                        ____________________________________________________________

consensus               TGCGTTATCTTCAATGAATGAACTGTTCTCGTTAGCATGGTTTGACCCAACGTACGACAT

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11e01.b1.seq+ CAAATGTGCAGCATTCGTGTCCAAAGATCCATATTGCATCACATGGGACCATGGCTGTAT
                        ____________________________________________________________

consensus               CAAATGTGCAGCATTCGTGTCCAAAGATCCATATTGCATCACATGGGACCATGGCTGTAT

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11e01.b1.seq+ GAGTCTGAGCTGCTGTTCTCCTCTGACCCGTTATACTGCAGCTGAGAGATCGCTTCTCAG
                        ____________________________________________________________

consensus               GAGTCTGAGCTGCTGTTCTCCTCTGACCCGTTATACTGCAGCTGAGAGATCGCTTCTCAG

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11e01.b1.seq+ TTGGGGACATCCCTGTCTCCACTCAGAGAGTGCTGTACCTCGTCCGCACCACCCTATCAC
                        ____________________________________________________________

consensus               TTGGGGACATCCCTGTCTCCACTCAGAGAGTGCTGTACCTCGTCCGCACCACCCTATCAC

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11e01.b1.seq+ TACTGAATCGCGGCCCGCCAGCAAGTCGACCAATGGGAAGTCCCCGCGCGTTGCATGCAT
                        ____________________________________________________________

consensus               TACTGAATCGCGGCCCGCCAGCAAGTCGACCAATGGGAAGTCCCCGCGCGTTGCATGCAT

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11e01.b1.seq+ GGCTGGCTATTTCGTATGGTCACTCACACTAGGTAGGCTCATCACAGTCCAGTCGTGTGC
                        ____________________________________________________________

consensus               GGCTGGCTATTTCGTATGGTCACTCACACTAGGTAGGCTCATCACAGTCCAGTCGTGTGC

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_11e01.b1.seq+ TGGAGG
                        ____________________________________________________________

consensus               TGGAGG

****************** Contig 45 ********************
                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c07.b1.seq+ TTCGATTAGCGTGGTCGCGGCCGAGGTACTACTTTGGCTCTGAGGAAGCCATGATCAGGC
U_HW-SSH2_12c08.b1.seq+       TAGCGTGGTCCCGGCCGAGGTACTACTTTGGCTCTGAGGAAGCCATGATCAGGC
U_HW-SSH2_5c03.b1.seq+        TAGCGTGGTCGCGGCCGAGGTACTACTTTGGCTCTGAGGAAGCCATGATCAGGC
U_HW-SSH2_5d03.b1.seq+        TAGCGTGGTCCCGGCCGAGGTACTACTTTGGCTCTGAGGAA-CCTTGATCAGGC
U_HW-SSH2_5e01.b1.seq+        TAGCGTGGTCGCGGCCGAGGTACTACTTTGGCTCTGAGGAAGCCATGATCAGGC
U_HW-SSH2_5d02.b1.seq+        TAGCGTGGTCGCGGCCGAGGTACTACTTTGGCTCTGAGGAAGCCATGATCAGGC
                              ______________________________________________________

consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACTACTTTGGCTCTGAGGAAGCCATGATCAGGC

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c07.b1.seq+ TTAATATGAGTGAGTTCATGGAGAGACATACTGTTTCAAAACTAATTGGGTCGCCACCCG
U_HW-SSH2_12c08.b1.seq+ TTAATATGAGTGAATTCATGGAGAGACATACTGTTTCAAA-CTAATTGGGTCGCCACCCG
U_HW-SSH2_5c03.b1.seq+  TTAATATGAGTGAGTTCATGGAGAGACATACTGTTTCAAAACTAATTGGGTCGCCACCCG
U_HW-SSH2_4c09.b1.seq+                                              AAACTAATTGGGTCGCCCCCCG
U_HW-SSH2_5d03.b1.seq+  TTAATATGAGTGAGTTCATGGAGAGACATACTGTTTCAAAACTAATTGGGTCGCCACCCG
U_HW-SSH2_5e01.b1.seq+  TTAATATGAGTGAGTTCATGGAGAGACATACTGTTTCAAAACTAATTGGGTCGCCACCCG
U_HW-SSH2_5d02.b1.seq+  TTAATATGAGTGAGTTCATGGAGAGACATACTGTTTCAAAACTAATTGGGTCGCCACCCG
                        ____________________________________________________________

consensus               TTAATATGAGTGAGTTCATGGAGAGACATACTGTTTCAAAACTAATTGGGTCGCCACCCG

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c07.b1.seq+ GATATGTTGGCTATACTGAGGGTGGTCAATTAACTGAAGCAGTTCGTCG-TCGCCCTTAC
U_HW-SSH2_12c08.b1.seq+ GATATGTTGGCTCTACTGAGGGTGGTCAATTAACTGATGCAGTTCGTCC-TCGCCCTTAC
U_HW-SSH2_5c03.b1.seq+  GATATGTTGGCTATACTGAGGGTGGTCAATTAACTGAAGCAGTTCGTCG-TCGCCCTTAC
U_HW-SSH2_4c09.b1.seq+  GATATGTTGGCTACACGGAGGGTGGTCAATTAACTGACGCTGTTCCCCCCTCGCCCTTAC
U_HW-SSH2_5d03.b1.seq+  GATATGTTGGCTATACTGAGGGTGGTCAATTAACTGAAGCAGTTCGTCG-TCGCCCTTAC
U_HW-SSH2_5e01.b1.seq+  GATATGTTGGCTATACTGAGGGTGGTCAATTAACTGAAGCAGTTCGTCG-TCGCCCTTAC
U_HW-SSH2_5d02.b1.seq+  GATATGTTGGCTATACTGAGGGTGGTCAATTAACTGAAGCAGTTCGTCG-TCGCCCTTAC
                        ____________________________________________________________

consensus               GATATGTTGGCTATACTGAGGGTGGTCAATTAACTGAAGCAGTTCGTCG-TCGCCCTTAC

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c07.b1.seq+ ACAGTATTTCTCTTTGATGAAATCGAAAAGGCACATCCAGACGTCTTCAGCATGATGCTT
U_HW-SSH2_12c08.b1.seq+ ACAGAAGTTCTCTTTGATGAAATCGAAAAGGCACATCCAAACTTCTTCGTGATGATGCTT
U_HW-SSH2_5c03.b1.seq+  ACAGTATTTCTCTTTGATGAGATCGAAAAGGCACATCCAGACGTCTTCAGCATGATGCTT
U_HW-SSH2_4c09.b1.seq+  CCAGAATTTCTCATTGATCAGATCGTAAAGGCACCTCCC-ACGTCTTCGGGTTGATGCTT
U_HW-SSH2_5d03.b1.seq+  ACAGTAATTCTCTTTGATGAGATCGAAAAGGCACATCCAGACGTCTTC-TCATGATGCTT
U_HW-SSH2_5e01.b1.seq+  ACAGTATTTCTCTTTGATGAGATCGAAAAGGCACATCCAGACGTCTTCAGCATGATGCTT
U_HW-SSH2_5d02.b1.seq+  ACAGTAGTTCTCTTTGATGAGATCGAAAAGGCACATCCAGACGTCTTCAGCATGATGCTT
                        ____________________________________________________________

consensus               ACAGTATTTCTCTTTGATGAGATCGAAAAGGCACATCCAGACGTCTTCAGCATGATGCTT

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c07.b1.seq+ CAAATACTGAAAAATGGAAGATTGACTGACAGCAAGGGGCGGACTGTTGATTTCAAGAAT
U_HW-SSH2_12c08.b1.seq+ CAAATACTGAAAAATGGAAAATTGACTGACTGCAAGGGGCGGACTGTTCATTTCAACAAT
U_HW-SSH2_5c03.b1.seq+  CAAATACTGGAAGATGGAAGATTGACTGACAGCAAGGGGCGGACTGTTGATTTCAAGAAT
U_HW-SSH2_4c09.b1.seq+  CATATACTGGAAGATGGAAGATTGACTGACAGCAAGGGGCGGACTGCTCATTTCAAAAAT
U_HW-SSH2_5d03.b1.seq+  CAATACTGGAAGATGGAAACATTGACTGACCTGAGGGGCGGACTGTTGATTTCAAGAAT
U_HW-SSH2_5e01.b1.seq+  CAAATACTGGAAGATGGAAGATTGACTGACAGCAAGGGGCGGACTGTTGATTTCAAGAAT
U_HW-SSH2_5d02.b1.seq+  CAAATACTGGAAGATGGAAGATTGACTGACAGCAAGGGGCGGACTGTTGATTTCAAGAAT
                        ____________________________________________________________

consensus               CAAATACTGGAAGATGGAAGATTGACTGACAGCAAGGGGCGGACTGTTGATTTCAAGAAT

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c07.b1.seq+ ACGCTGTTGATCATGACATCTAATGTTGGAAGCAGTGTCATTGAAAGGGAGGCCGCAAG
U_HW-SSH2_12c08.b1.seq+ ACCCTGTTGATCATGACATCTAATGTTGGAAGCAGTGTCATTGAAAACGGAGGCCCCCAG
U_HW-SSH2_5c03.b1.seq+  ACGCTGTTGATCATGACATCTAATGTTGGAAGCAGTGTCATTGAGAAGGGAGGCCGCAAG
U_HW-SSH2_4c09.b1.seq+  ATCCTGTCGATCATGACACCTAATGT
U_HW-SSH2_5d03.b1.seq+  ACGCTGTTGATCATGACATCTAATGTTGGAACCAGTGTCATTGAGAAGGGAGGCCGCAAG
U_HW-SSH2_5e01.b1.seq+  ACGCTGTTGATCATGACATCTAATGTCGGAAGCAGTGTCATTGAGAAGGGAGGCCGCAAG
U_HW-SSH2_5d02.b1.seq+  ACGCTGTTGATCATGACATCTAATGTTGGAAGCAGTGTCATTGAGAAGGGAGGCCGCAAG
                        ____________________________________________________________

consensus               ACGCTGTTGATCATGACATCTAATGTTGGAAGCAGTGTCATTGAGAAGGGAGGCCGCAAG

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c07.b1.seq+ ATCGGATTTGACCTTGACTATGATGAGAAGGACACCAGCTACAACAGGATTAAGAGCCTG
U_HW-SSH2_12c08.b1.seq+ ATCGAATTTGACCTTGACTATGATGAAAAGGACACCCTCTACAACAGGATTACTAGCCTG
U_HW-SSH2_5c03.b1.seq+  ATCGGATTTGACCTTGACTATGATGAGAAGGACACCAGCTACAACAGGATTAAGAGCCTG
U_HW-SSH2_5d03.b1.seq+  ATCCGATTTGACCTTGACTATGATGAGAAGGACACCCGCTACAAAAGAATTAAAAGCCTG
U_HW-SSH2_5e01.b1.seq+  ATCGGATTTGACCTTGACTATGAAGAAAGGACACC-TCTACAACAGGATTAAGAGCCTG
U_HW-SSH2_5d02.b1.seq+  ATCGGATTTGACCTTGACTATGATGAGAAGGACACCAGCTACAACAGGATTAAGAGCCTG
                        ____________________________________________________________

consensus               ATCGGATTTGACCTTGACTATGATGAGAAGGACACCAGCTACAACAGGATTAAGAGCCTG

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c07.b1.seq+ GTGACTGAGGAGCTAAAGCAGTACCTGCCCGGGCGGCCGCTCGAAATCACTAGTGAATTC
U_HW-SSH2_12c08.b1.seq+ GTGACTGAGGAGCTAAAGCAGTACCTGCCCGGGCGGCC
U_HW-SSH2_5c03.b1.seq+  GTGACTGAGGAGCTAAAGCAGTACCTGCCCGGGCGGCCGCTCGAAATCACTATTGAATTC
U_HW-SSH2_5d03.b1.seq+  GTGACTGAGGAGCT
U_HW-SSH2_5e01.b1.seq+  GTGATTGAGGAGCTAAAGCA
U_HW-SSH2_5d02.b1.seq+  GTGACTGAGGAGCTAAAGCAGTACCTGCCCGGGCGGCCGCTC
                        ____________________________________________________________

consensus               GTGACTGAGGAGCTAAAGCAGTACCTGCCCGGGCGGCCGCTCGAAATCACTAGTGAATTC

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c07.b1.seq+ GCGGCCGCCTGCAGGTCGACCATATGGGAGAGCTCCC-AACGCGTTG-GATGCATAGCTT
U_HW-SSH2_5c03.b1.seq+  GCGGCCGCCTGCAGGTCGACCATATGGGAGAGCTCCCCAACGCGTTGAGATGCATAGCTT
                        ____________________________________________________________

consensus               GCGGCCGCCTGCAGGTCGACCATATGGGAGAGCTCCCCAACGCGTTGAGATGCATAGCTT

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c07.b1.seq+ GAGTATTCTATAGTGTCACCTAA-TGGCTTTGGCGTAAATCATGG-TCATAGCTGTTTCC
U_HW-SSH2_5c03.b1.seq+  GA-TATTCTATAGTGTCACCTAAATAGCTTTGACGTAA-TCATGGGTCATAGCTGTTTCC
                        ____________________________________________________________

consensus               GAGTATTCTATAGTGTCACCTAAATAGCTTTGACGTAAATCATGGGTCATAGCTGTTTCC

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c07.b1.seq+ CTGTGTGAAATT--GTTAACCCGCTCCCAATTCCACACACA-TACGAGCCGGAAGCATAA
U_HW-SSH2_5c03.b1.seq+  A-GAGTGAAATTTTGTTATCCCGCTCCCAATTCTACACAAAATACGAGCCG
                        ____________________________________________________________

consensus               ATGAGTGAAATTTTGTTAACCCGCTCCCAATTCCACACAAAATACGAGCCGGAAGCATAA

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12c07.b1.seq+ AGTGTAAGCCTGGGGTGCCAAATGAGA
                        ____________________________

consensus               AGTGTAAGCCTGGGGTGCCAAATGAGA

****************** Contig 46 ********************
                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12d04.b1.seq+ TTCGATTAGCGTGGTCGCGGCCGACGTACCAGGGCTGGTGCAATTGGAGGCCCAGGAGGG
U_HW-SSH2_12d09.b1.seq+     ATTAGCGTGGTCGCGGCCCACGAACCAGGGCTGGTGCAATTGGAGGCCCAGGAGGG
U_HW-SSH2_12d08.b1.seq+ TTCGATTAGCGTGGTCGCGGCCGAGGTACCAGGGCTGGTGCAATTGGAGGCCCAGGAGGG
U_HW-SSH2_12e04.b1.seq+       TAGCGTGGTCGCGGCCGAGGTACCATGGTTGGTGCATTTGGAGGCCCAGGAGGG
U_HW-SSH2_12c11.b1.seq+     ATTAGCGTGGTCGCGGCCGAGGGACCGGGGGGGGTGCAATTGGAGGCCCATTAGGG
U_HW-SSH2_12d11.b1.seq+ TTCGATTAGCGTGGTCGCGGCCGAGGGACCTGGGCTGGTGCATTTGGAGGCCCAGGAGGG
U_HW-SSH2_12d10.b1.seq+ TTCGATTAGCGTGGTCGCGGCCGAGGAACCAGGGCTGGTGCAATTGGAGGCCCAGGAGGG
                        ____________________________________________________________

consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACCAGGGCTGGTGCAATTGGAGGCCCAGGAGGG

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12d04.b1.seq+ CTGGGTT-CAGCAAATTTGAGCAGCCTGCTCGGTGGTCTTGGTGGGAATGCAAGAACTGG
U_HW-SSH2_12d09.b1.seq+ CTGGGTT-CATCAAATTTGAGCACCCTGCTCGGTGGTCTTGGTGGGAATGCAAGAACTGG
U_HW-SSH2_12d08.b1.seq+ CTGGGTT-CAGCAAATTGAGCAGCCTGCTCGGTGGTCTTGGTGGGAATGCAAGAACTGG
U_HW-SSH2_12e04.b1.seq+ CTGACTTTCAGGTTATTTGAATTTCCTGCTCGGTGATCTTGGTGGAAATGCAAGAACTGG
U_HW-SSH2_12c11.b1.seq+ CTGGCTT-CATAAAATTTGAGCAGCCTGCTCGGTGTTCTTGGTGGTAATGCAAGAACTGG
U_HW-SSH2_12d11.b1.seq+ TTGGCTT-CATCAAATTTGACCAGCCTGCTCGGGGGTCTTGGTGGGAATGCAAGAACTGG
U_HW-SSH2_12d10.b1.seq+ CTGGTTT-CAACAAATTTGAGCAGCCTGCTCGGTGGTCTTGGTGGAAATGCAAGAACTGG
                        ____________________________________________________________

consensus               CTGGCTT-CAGCAAATTTGAGCAGCCTGCTCGGTGGTCTTGGTGGGAATGCAAGAACTGG

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12d04.b1.seq+ TGCTGCAGGTGGTCTAGGAGGGTTGGGTTCAGCAAATTTGGGGAGTATGCTTGGTGGT
U_HW-SSH2_12d09.b1.seq+ TGCTGCAGGTGGTCTAGGAGGGTTGGGTTCAACAAATTTGGGGAGTATGCTTGGTGGT
U_HW-SSH2_12d08.b1.seq+ TGCTGCAGGTGGTCTAGGAGGGTTGGGTTCAGCAAATTTGGGGAGTATGCTTGGTGGTCC
U_HW-SSH2_12e04.b1.seq+ TGCTGCTT-TGGTCTAGGAGGGTTGGGTTCAGCAAATTTGGGGAGTATGCTTGGTGGT
U_HW-SSH2_12c11.b1.seq+ TGCTGCAGGGGGTCTAGGAGGGTTGGGTTCAACAGATTTGGGGA
U_HW-SSH2_12d11.b1.seq+ TGCTGCGGGTGGTCTAGGGGGGTTGGGTTCCCCAGATTTGGGGAGTATGCTTGG
U_HW-SSH2_12d10.b1.seq+ TGCTGCAGGTGGTCTAGGAGGGTTGGGTTCAGCAAATTTGGGGAGTATGCTTGGTGGT
                        ____________________________________________________________

consensus               TGCTGCAGGTGGTCTAGGAGGGTTGGGTTCAGCAAATTTGGGGAGTATGCTTGGTGGTCC

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12d08.b1.seq+ ACCTGATGCTGCTCTTTTGAGTCAAATGCTGCAAAACCCTGCTATGATGCAAATGATGCA
                        ____________________________________________________________

consensus               ACCTGATGCTGCTCTTTTGAGTCAAATGCTGCAAAACCCTGCTATGATGCAAATGATGCA

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12d08.b1.seq+ AAACATTATGTCTGACCCACAGTCAATGAACCAGTTGCTTAGCATGAACCCAAATGCACG
                        ____________________________________________________________

consensus               AAACATTATGTCTGACCCACAGTCAATGAACCAGTTGCTTAGCATGAACCCAAATGCACG

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12d08.b1.seq+ TAGCCTGATGGAGTCAAACACTCAGTTGAGGGATATGTTCCAAAACCCAGAATTTCTTCG
                        ____________________________________________________________

consensus               TAGCCTGATGGAGTCAAACACTCAGTTGAGGGATATGTTCCAAAACCCAGAATTTCTTCG

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12d08.b1.seq+ CCAGATGGCATCCCCAAAGGCTTTGCAACAATTACTCTCATTCCAACAAACACTGTCATC
                        ____________________________________________________________

consensus               CCAGATGGCATCCCCAAAGGCTTTGCAACAATTACTCTCATTCCAACAAACACTGTCATC

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12d08.b1.seq+ ACAGCTTGGCCAAAATCAACCTACCCAGGCTGGTAACCTAGGAGGCAATGGCACAGGCAC
                        ____________________________________________________________

consensus               ACAGCTTGGCCAAAATCAACCTACCCAGGCTGGTAACCTAGGAGGCAATGGCACAGGCAC

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12d08.b1.seq+ GCGGGGAAATGTTGGCCTGCACACCTTGATGGGCATGCTTAGTGGGCTTGGTGCTGGAGG
                        ____________________________________________________________

consensus               GCGGGGAAATGTTGGCCTGCACACCTTGATGGGCATGCTTAGTGGGCTTGGTGCTGGAGG

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12d08.b1.seq+ TGGCTTAGGTGTACCTGCCCCGGGCGGCCGCTCAA
                        ____________________________________

consensus               TGGCTTAGGTGTACCTGCCCCGGGCGGCCGCTCAA

****************** Contig 47 ********************
                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12e02.b1.seq+ TTCGATTCGCGCGGCCGCCCCGGAGGGTCCTGACAACCATGAGTATATCAGAACCTATGT
                        ____________________________________________________________

consensus               TTCGATTCGCGCGGCCGCCCCGGAGGGTCCTGACAACCATGAGTATATCAGAACCTATGT

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12e02.b1.seq+ ATTTCTCTAACGAGAAAACCGGCCTCTCCTCCTTTCAAAAAAAACAGAACCGTGTCAGTT
                        ____________________________________________________________

consensus               ATTTCTCTAACGAGAAAACCGGCCTCTCCTCCTTTCAAAAAAAACAGAACCGTGTCAGTT

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12e02.b1.seq+ TGCGTTACCATGCTTTTATTGCCCTTAAGGAGGGTTCATCTGTGTATGAATAAAACTTCC
U_HW-SSH2_12e01.b1.seq+           TGCTTTTATTGCCCGTATGGAGGGTGCGTCTGTGAATGAATATCAGTTCC
                        ____________________________________________________________

consensus               TGCGTTACCATGCTTTTATTGCCCGTAAGGAGGGTGCATCTGTGAATGAATAAAACTTCC

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12e02.b1.seq+ TGTACCTCCCTGAGAGGTTGAGAAGGCTTCCTTTTCTCAGGTCGCAACCTGAAGGGTCTC
U_HW-SSH2_12e01.b1.seq+ TGTAACTCCCTGAGAGGTTGAAAAGGCCTCCTTTTCTCCGCTCGCAACCTGAACGGGCTC
                        ____________________________________________________________

consensus               TGTAACTCCCTGAGAGGTTGAAAAGGCCTCCTTTTCTCAGCTCGCAACCTGAACGGGCTC

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12e02.b1.seq+ CATTTCTCCTTCTGTGTAATCAGCCCAGAACTTCGGCTTTTCACCCGCGCTTGAATCATC
U_HW-SSH2_12e01.b1.seq+ GACTTCTTTAGCAGGGAAATCAGGAAAGACTTTGGGGTTTACGCCCGCGCTTGAAGCATC
                        ____________________________________________________________

consensus               CACTTCTCCAGCAGGGAAATCAGCAAAGAACTTCGGCTTTACACCCGCGCTTGAAGCATC

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12e02.b1.seq+ TTAGGCTTCTTTTGGGGCTAAAGTGCCTGCTGGAGCCTCTATCGAGGCCGTTGCATCAAC
U_HW-SSH2_12e01.b1.seq+ TTGAGCTTCTTTAGGGGCTGAGGCCCAT-CTTGAGCATCTATCGAGGCCGTTACATCAAC
                        ____________________________________________________________

consensus               TTGAGCTTCTTTAGGGGCTAAAGCCCATGCTGGAGCATCTATCGAGGCCGTTACATCAAC

                             .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12e02.b1.seq+ TTCCCACCTCAAAAAACTATAGTTTAATAAAGCTTCCCTTCACGGTCCTCACATTCCAAA
U_HW-SSH2_12e01.b1.seq+ TTCCCGCCTCAAAAAACTATAGTTTCATAATGCTTCACTTCACTGACCTCACATTCCACA
                        ____________________________________
```

```
consensus                TTCCCACCTCAAAAAACTATAGTTTAATAAAGCTTCACTTCACGGACCTCACATTCCAAA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12e02.b1.seq+ TGGTTGTTCTTCTCCTCCGTGTTCTTGCTCTCAATCTCATTTTCTACATCAGTTCCACCA
U_HW-SSH2_12e01.b1.seq+ TGGTTGTTCTTCTCCTGCGTGTTCTTGCTCTCA-TCTCAGCTTCATCATCAGTTCCCCCT

consensus                TGGTTGTTCTTCTCCTCCGTGTTCTTGCTCTCAATCTCAGCTTCAACATCAGTTCCACCA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12e02.b1.seq+ GATGTATCATTTCCTTCAGGAATTTGTCTCACTAGTTTCACACACTTGTAGGGAAGCAAC
U_HW-SSH2_12e01.b1.seq+ GATGTATTATTTCCTTCAA-AACTAGTCTCACTAGTTTCAGACACTTGTGGGGAAGCA
                        ____________________________________________________________
consensus                GATGTATCATTTCCTTCAAGAACTAGTCTCACTAGTTTCACACACTTGTAGGGAAGCAAC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12e02.b1.seq+ GTGGGTGACTCGACTGTACCTCGGACGCTACCACGCTTATCACTAGTTTAATTCGCGGCC
                        ____________________________________________________________
consensus                GTGGGTGACTCGACTGTACCTCGGACGCTACCACGCTTATCACTAGTTTAATTCGCGGCC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12e02.b1.seq+ GCCTGCAAGTCGAACATATGGCGAGAGCTCCCAACGCGATGGATGAGTAGATGGATTATT
                        ____________________________________________________________
consensus                GCCTGCAAGTCGAACATATGGCGAGAGCTCCCAACGCGATGGATGAGTAGATGGATTATT

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12e02.b1.seq+ GTATAGTGTCACCTATATACCTAAGCGAGACACATGATCATACCTGCTTCCTGAGCAAAT
                        ____________________________________________________________
consensus                GTATAGTGTCACCTATATACCTAAGCGAGACACATGATCATACCTGCTTCCTGAGCAAAT

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12e02.b1.seq+ TCCTACTCCGCGCACTTTCCCCACAAGATACTTGGCGTATGCATGCAGCGCACCGCCCTG
                        ____________________________________________________________
consensus                TCCTACTCCGCGCACTTTCCCCACAAGATACTTGGCGTATGCATGCAGCGCACCGCCCTG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12e02.b1.seq+ ATGGTGCCTTATTGAGAGACTCAACTTCCAATGAGGTGGGATCTCCGTCAAGGCCCCGCT
                        ____________________________________________________________
consensus                ATGGTGCCTTATTGAGAGACTCAACTTCCAATGAGGTGGGATCTCCGTCAAGGCCCCGCT

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12e02.b1.seq+ TTCCCAGAAGAAGAAAGCCCGGCTCT
                        _________________________
consensus                TTCCCAGAAGAAGAAAGCCCGGCTCT

****************** Contig 48 ******************
                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1f04.b1.seq-  AGGGCAGCGGGGTCAGAGAGCGAGGAAAGGGGAAGAGAGCCCAAAACGCAAACCGCCTCT
                        ____________________________________________________________
consensus                AGGGCAGCGGGGTCAGAGAGCGAGGAAAGGGGAAGAGAGCCCAAAACGCAAACCGCCTCT

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1f04.b1.seq-  CCCCGCGCGTTGGCCGATTCATTAAAACAGGGGGCACGACAGGTTTCCCGACTGGAAAGC
                        ____________________________________________________________
consensus                CCCCGCGCGTTGGCCGATTCATTAAAACAGGGGGCACGACAGGTTTCCCGACTGGAAAGC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1f04.b1.seq-  GGGCAGGGAGCGCAACGCAATTAAAGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTT
                        ____________________________________________________________
consensus                GGGCAGGGAGCGCAACGCAATTAAAGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTT

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1f04.b1.seq-  ACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACAC
U_HW-SSH2_1h06.b1.seq-                                                GTGAGGGGAAAACAAATTAACAC
                        ____________________________________________________________
consensus                ACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAAACAATTTAACAC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1f04.b1.seq-  AGGAAACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAA
U_HW-SSH2_1h06.b1.seq-  AGGAAACAGCTATGACCACGATTACGGCCAGGTATTTATGTGCCACCATAGAAAACTCAA
                        ____________________________________________________________
consensus                AGGAAACAGCTATGACCACGATTACGCCAAGCTATTTAGGTGACACCATAGAAAACTCAA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1f04.b1.seq-  GCTATGCATCCAACGCGTTGGGAGCTCTCCCATATGGTCGACCTGCAGGCGGTCGCGAAT
U_HW-SSH2_1h06.b1.seq-  GGTAAGCATCCAACGCGTTGGGAGCTCTCCCATATGGTCGACCCGCAGGCGGCCGTGAAT
                        ____________________________________________________________
consensus                GCTAAGCATCCAACGCGTTGGGAGCTCTCCCATATGGTCGACCCGCAGGCGGCCGCGAAT

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1f04.b1.seq-  TCACTAGTGATTTCGAGCGACC-GCCCGGGCAGGTACTCCTTCTTGACCTCCTCCACCTC
U_HW-SSH2_1h06.b1.seq-  TCACTAGTGATTTCGAGCAAAAAGCCCGGGCAGGTACTCCTTCTTGACCTCCTCCACCTC
U_HW-SSH2_12a11.b1.seq-                                          TACTCCTTCTTGACCTCCTCCACCTC
                        ____________________________________________________________
consensus                TCACTAGTGATTTCGAGCAAAAAGCCCGGGCAGGTACTCCTTCTTGACCTCCTCCACCTC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_1f04.b1.seq-  GTTGATCACCTGCGAGGAGTCGGTGCATCCGTTCGTTGGCAGCTTCCACATTGTCCA
U_HW-SSH2_1h06.b1.seq-  GTTGATCACCTCCGTGGCGTCGGTGCA
U_HW-SSH2_12a11.b1.seq- GTTGATCACCTGTGTGGCGTCAGTGCACCCGAACATAGGCAGCTTCCACATTGTCCAATA
U_HW-SSH2_3g05.b1.seq+                                                          TA
U_HW-SSH2_9h07.b1.seq-                                                TTCCACATTTTCCAATC
U_HW-SSH2_3h04.b1.seq+                                                          TA
U_HW-SSH2_5g09.b1.seq+                                                          TA
U_HW-SSH2_5d09.b1.seq-                                      AGGCAGATTCCACTTTGTTCAATA
                        ____________________________________________________________
consensus                GTTGATCACCTGCGTGGCGTCGGTGCACCCGAACATAGGCAGCTTCCACATTGTCCAATA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a11.b1.seq- CCG-----GCCATCGTAGTATCCAGGAGATGCGTTGTGCTCACGGAAGATGAACCCAACC
U_HW-SSH2_11h09.b1.seq+                                                       CCAACC
U_HW-SSH2_3g05.b1.seq+  GCGTGGTCGCGGCCGAGGGACCCAGGGGATGCGTTGTGCTCACGGAAAATGAACCCAACC
U_HW-SSH2_9h07.b1.seq-  CCG-----GCCATCGTAGTATCCAGGAGATGAGTTGTGCTCACGGAAGATGAACCCAATC
U_HW-SSH2_3h04.b1.seq+  GCGTGGTCGCGGCCGAGGAACCCAGGGGATGCGTTGTGCTCACGGAAGATGAACCCAACC
U_HW-SSH2_5g09.b1.seq+  GCGTGGTCGCGGCCGAGGTACCCACGGGATGCGTTGTCCTCACAGATGATGAACCCAAC
U_HW-SSH2_5d09.b1.seq-  CCG-----GCCATCGTAGT-TCCAGGAGATGCGTTGTGCTCACGGAAGATGAACCCAACC
U_HW-SSH2_10a05.b1.seq+                                     TTGTGCTCACGGAAAATGAACCCAACC
                        ____________________________________________________________
consensus                CCGTGGTCGCCACCGAAGTACCCAGGAGATGCGTTGTGCTCACGGAAGATGAACCCAACC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a11.b1.seq- TTGCTGAACTCGAGGCAAGGCACCCACTTGGAGCGGATCAGGTAGTCGACCTGCTTGAGG
U_HW-SSH2_11h09.b1.seq+ TTGCTGAACTCGAGGCTGGGCACCCTCTTGGAGCGGATCATGTCTTCGACCTGCTTCACG
U_HW-SSH2_3g05.b1.seq+  CGGCTGAACTCAAGGCAAGGCACCCATTTGGAGCGGATCAGGTAGTCGACCTGCTTGAGG
U_HW-SSH2_9h07.b1.seq-  CTTCCGAACTAAAGGCAAGCCACCCATTTGGAGCGGATCAGGTAGTCGACCTGCTTGAGG
U_HW-SSH2_1e04.b1.seq+                                  CCCACTTGGAGCGGATCAGGTAGTCGACCTGCTTGAGG
U_HW-SSH2_3h04.b1.seq+  CTGCTGAACTCGAGGCAAGGCACCCACTTGGAGCGGATCAGGTAGTCGACCTGCTTGAGG
U_HW-SSH2_5d09.b1.seq-  TTGCTGAACTCGAGGCAAGGCACCCACTTGGAGCGGATCAGGTAGTCGACCTGCTTGAGG
U_HW-SSH2_10a05.b1.seq+ TTGCTGAACTCGAGGCAAGGCACCCCCTTGAAGCGGATCAGGTAGTCGACCTGCTTGAGG
                        ____________________________________________________________
consensus                TTGCTGAACTCGAGGCAAGGCACCCACTTGGAGCGGATCAGGTAGTCGACCTGCTTGAGG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a11.b1.seq- AGGGCCTCCGTG-CTGAGCGGTGGCAGGTAAGACAGGGTCTCGAACTTCTTGATGCCCTC
U_HW-SSH2_11h09.b1.seq+ AGGGCCTCCGTG-GAGAGGGGTGGCAAGTAAAACACGGTCTCGAACTTCGTGATGCCCTC
U_HW-SSH2_3g05.b1.seq+  AGGGCCTCCGTG-CTGAGCGGTGGCAGGTAGGACAGGGTCTCGAACTTCTTGATGCCCTC
U_HW-SSH2_9h07.b1.seq-  AGGGCCTCCGTG-CTGAGCGGTGGCAGGTAGGACAGGGTCTCGAAATTCTTGATGCCCTC
U_HW-SSH2_1e04.b1.seq+  AGGGCCTCCTTTTCTGAGCGGTGGCAGGTAGGACAGGAACTCTAACTTCTTAATGCCCTC
U_HW-SSH2_3h04.b1.seq+  AGGGCCTCCGTG-CTGAGCGGTGGCAAGTAGGACAGGGTCTCGAACTTCTTGATGCCCTC
U_HW-SSH2_5d09.b1.seq-  AGGGCCTCCGTG-CTGAGCGGTGGCAGGTAAGACAGGGTCTCGAAATTCTTGATGCCCTC
U_HW-SSH2_10a05.b1.seq+ AGGGCCTCCGTG-TTAATCGGTGGAAGGAAAGACAGGGACTCAAACTTTTTGAGGCCCTC
                        ____________________________________________________________
consensus                AGGGCCTCCGTG-CTGAGCGGTGGCAGGTAAGACAGGGTCTCGAACTTCTTGATGCCCTC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a11.b1.seq- GATGGGCCACACCTGCATGCACCTGATCCTTCCACCGTTGCTGACGCTGCCGAGGCTAGC
U_HW-SSH2_11h09.b1.seq+ ATTCGGCCACACCTGGATGCACCTGATCCTTCCGCCATTGCTGACGCTGCCGAGGCT---
U_HW-SSH2_3g05.b1.seq+  GATGGGCCACACCTGCATGCACCTGATCCTTCCACCGTTGCTGACGCTGCCGAGGCTAGC
U_HW-SSH2_9h07.b1.seq-  GATGGGCCACACCTGCATGCACCAGATCCTTCCCCCGATGCTGACGCTACCGAGGCTAGC
U_HW-SSH2_1e04.b1.seq+  G
U_HW-SSH2_3h04.b1.seq+  AATGGGCCACACCTGCATGCACCTGATCCTTCCACCGTTGCTGACGCTGCCGAGGCTAGC
U_HW-SSH2_5d09.b1.seq-  GATGGGCCACACCTGCATGCACCTGATCCTTCCACCGTTGCTGACGCTGCCGAGGCTAGC
U_HW-SSH2_10a05.b1.seq+ GATGGGCCACACCTGCATGCACCTGATCCTTCCACCGTTGCTGACCCTGCCGAGGCTAGC
                        ____________________________________________________________
consensus                GATGGGCCACACCTGCATGCACCTGATCCTTCCACCGTTGCTGACGCTGCCGAGGCTAGC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a11.b1.seq- GCCGTTGGAGCGGCGGCTGACGGGGAGGCCGGCGGTGGA-CTTGAGCCCCTGGAAAGGAG
U_HW-SSH2_11h09.b1.seq+ GCCGCTGGACCGGCGGTTGACGGGCCGACCGGCCGTGGA-CTTGAGCCC
```

```
U_HW-SSH2_3g05.b1.seq+  GCCGTTGGACCGGCGGCTGACGGGGAGGCCGGCGG
U_HW-SSH2_9h07.b1.seq-  GCCGTTGGAGCGGCGGCTGACGGGGAGACAGGCGGTGGA-CATGAGCCCCTGGAAAGGAG
U_HW-SSH2_3h04.b1.seq+  GCCGTTGGAGCGGCGGCTGACGGGGAGGCCGGCGGTGGA-CTTGACCCCCTGGAAAGGAG
U_HW-SSH2_5d09.b1.seq-  GCCGTTGGAGCGGCGGCTGACGGGGAGGCCGGCGGTGGA-CTTGAGCCCCTGGAAAGGAG
U_HW-SSH2_10a05.b1.seq+ GCCATTGGAGCGGCGGTTGACGGGGAGGCCGGCGGAGAAACCTGCCCGGGCGGCCTCTTG

consensus                GCCGTTGGAGCGGCGGCTGACGGGGAGGCCGGCGGTGGA-CTTGAGCCCCTGGAAAGGAG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a11.b1.seq- CGACGGAGGTGGCCGACGAGGCCATCACGGTGGGGGCCATGGCTGTGCTATGTAGGTATA
U_HW-SSH2_9h07.b1.seq-  CGACGGAGGTGGCCGACGAGGCCTCACG
U_HW-SSH2_3h04.b1.seq+  CGACGGAGGTGGCCAACGAGGCCATCACGGGGGGGGCCATGGCTGTGCTATGTAGGTATA
U_HW-SSH2_5d09.b1.seq-  CGACGGAGGTGGCCGACGAGGCCATCACGGTGGGGGCCATGGCTGTGCTATGTAGGTATA
U_HW-SSH2_10a05.b1.seq+ TAAAGAAACTGGAGGGTGGG-----CGCGTGCCGGGACCTGG-TATACAAGATATGTATC
                        ____________________________________________________________
consensus                CGACGGAGGTGGCCGACGAGGCCATCACGGGGGGGGCCATGGCTGTGCTATGTAGGTATA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_12a11.b1.seq- TAGCTTGCTAGGAGGAGGCAC
U_HW-SSH2_3h04.b1.seq+  TAGCTTGCTAGGAG
U_HW-SSH2_5d09.b1.seq-  TAGCTTGCTAGGAGGAGGCAC
U_HW-SSH2_10a05.b1.seq+ ------GCTAAGAAGAATTATTTGGGTTCATTATCGGCCAATCCACCAGGGTATTAAAAA
                        ____________________________________________________________
consensus                TAGCTTGCTAGGAGGAGGCACTTGGGTTCATTATCGGCCAATCCACCAGGGTATTAAAAA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10a05.b1.seq+ CCTTATCCAGGGCTCCATACGAGTCCACCAGATAGCCGAGCTCCAGGGGAGGGGCCCCGT
                        ____________________________________________________________
consensus                CCTTATCCAGGGCTCCATACGAGTCCACCAGATAGCCGAGCTCCAGGGGAGGGGCCCCGT

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10a05.b1.seq+ TTTGCTGGGATGGAAATTCTGAGCCTTCCAACCCCCCAACTCCATTAAGGGGGCAAAACA
                        ____________________________________________________________
consensus                TTTGCTGGGATGGAAATTCTGAGCCTTCCAACCCCCCAACTCCATTAAGGGGGCAAAACA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10a05.b1.seq+ TTTTCTTTTTTCCTTCCGTACCCACCTTTCTAATTCGTATATCAGTCGTGTCAGTTTCGT
                        ____________________________________________________________
consensus                TTTTCTTTTTTCCTTCCGTACCCACCTTTCTAATTCGTATATCAGTCGTGTCAGTTTCGT

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10a05.b1.seq+ AACCGATATGGGTAAAGTTGCCGCGCTGGTGTATCCTACCTATGATTAATTTTCCTCTCC
                        ____________________________________________________________
consensus                AACCGATATGGGTAAAGTTGCCGCGCTGGTGTATCCTACCTATGATTAATTTTCCTCTCC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10a05.b1.seq+ TCGCGCTGCCGTAGCGGCCGGAACGACCGTGGTGGTTTCTAGCA
                        ____________________________________________________________
consensus                TCGCGCTGCCGTAGCGGCCGGAACGACCGTGGTGGTTTCTAGCA

****************** Contig 49 ******************
                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a06.b1.seq+  TAGCGTGGTCGCGGC-GAGG-ACCCCTAGATTGCTATATGCGTTTAAGCTGGCACCAAGG
U_HW-SSH2_7h05.b1.seq+  TAGCGTGGTCGCGGCCGAGGTACCCCTAGATTGCTATATGCGTTTAAGCTGGCACCAAGG
                        ____________________________________________________________
consensus                TAGCGTGGTCGCGGCCGAGGTACCCCTAGATTGCTATATGCGTTTAAGCTGGCACCAAGG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a06.b1.seq+  A-AAATACGAAGGCAAATGGAACATCAAGGTCAACGATACTCAAATCTGAAGAAACCCGG
U_HW-SSH2_7h05.b1.seq+  TTAAATACGAAGGCAAATGGAACATCAAGGTCAACGATACTCAAATCTGAAGAAACCCGG
                        ____________________________________________________________
consensus                ATAAATACGAAGGCAAATGGAACATCAAGGTCAACGATACTCAAATCTGAAGAAACCCGG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a06.b1.seq+  CTAAGAACCCTTCCTAGCGGAGTAAAATCAAAAAAGGACATTGGTGCACGGAATAATGAA
U_HW-SSH2_7h05.b1.seq+  CTAAGAACCCTTCCTAGCGGAGTAAAATCAAAAAAGGACATTGGTGCACGGAATAATGAA
                        ____________________________________________________________
consensus                CTAAGAACCCTTCCTAGCGGAGTAAAATCAAAAAAGGACATTGGTGCACGGAATAATGAA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a06.b1.seq+  TTGAGTAGCTGGGAAAATAAGGATCGTGATGTCTGGATCCCAAGAATAACGACTGCCAAA
U_HW-SSH2_7h05.b1.seq+  TTGAGTAGCTGGGAAAATAAGGATCGTGATGTCTGGATCCCAAGAATAACGACTGCCAAA
                        ____________________________________________________________
consensus                TTGAGTAGCTGGGAAAATAAGGATCGTGATGTCTGGATCCCAAGAATAACGACTGCCAAA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a06.b1.seq+  GATCTTGATAGCAAAAAAAACATTGTGCAAACTCCAATAATAATGTACCTGCCCGGGCGG
U_HW-SSH2_7h05.b1.seq+  GATCTTGATAGCAAGAAAAACATTGTGCAAACTCCGATAATAATGTACCTGCCCGGGCGG
                        ____________________________________________________________
consensus                GATCTTGATAGCAAAAAAAACATTGTGCAAACTCCAATAATAATGTACCTGCCCGGGCGG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a06.b1.seq+  CCGCACAAAATCAGAAAAAAAAATTCGCGCCCGCCTGTTGGTTTTCTGTGAGCCCTCCCTC
U_HW-SSH2_7h05.b1.seq+  CCGCTCAAA
                        _________
consensus                CCGCACAAAATCAGAAAAAAAATTCGCGCCCGCCTGTTGGTTTTCTGTGAGCCCTCCCTC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a06.b1.seq+  CCCTCATGTTTTGTGCTTACCGTGCCTGGCCCCTTGTTTGGCCCCCTCCCCCTGTCGTGA
                        ____________________________________________________________
consensus                CCCTCATGTTTTGTGCTTACCGTGCCTGGCCCCTTGTTTGGCCCCCTCCCCCTGTCGTGA

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3a06.b1.seq+  TTTTTTCCTCGCGGTCTCCCGGGGGGGATTCTATCCCCCTCCCACTATATTCTCCAA
                        ____________________________________________________________
consensus                TTTTTTCCTCGCGGTCTCCCGGGGGGGATTCTATCCCCCTCCCACTATATTCTCCAA

****************** Contig 50 ******************
                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3c05.b1.seq-  TGATTTGCTGCAGGCCGGGGAATCAGTAGCAGGTTCGTGTGGCCGCCCGGGCAGGTACGT
U_HW-SSH2_9d04.b1.seq+                                                TAGCGTGGTCGCGGCCG-AGGAACGT
U_HW-SSH2_9c04.b1.seq+                                                        AGGTACGT
                        ____________________________________________________________
consensus                TGATTTGCTGCAGGCCGGGGAATCAGTAGCAGGTTAGCGTGGCCGCCCCCGCAGGTACGT

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3c05.b1.seq-  TCAAGTTGACCCTGCAATTTACAGAAGATTACCCCAACAAGCCACCAACTGTTCGGTTTG
U_HW-SSH2_9d04.b1.seq+  TCAAGCTGACCCTGCAATTCACAGAAGATTACCCCAACAAGCCACCAACTGTTCGGTTTG
U_HW-SSH2_9c04.b1.seq+  TCAAGCTGACCCTGCAATTCACAGAAGATTACCCCAACAAGCCACCAACTGTTCGGTTTG
U_HW-SSH2_8h07.b1.seq+   CAAGCTGACCCTGCAATTCACAGAAGATCCCCCCACCAAAAAACGAACTGTTCGGTAAA
                        ____________________________________________________________
consensus                TCAAGCTGACCCTGCAATTCACAGAAGATTACCCCAACAAGCCACCAACTGTTCGGTTTG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3c05.b1.seq-  TCTCAAGGATGTTTCACCCAAACATTTATGCAGATGGAAGCATTTGCTTGGATATCCTAC
U_HW-SSH2_9d04.b1.seq+  TCTCAAGGATGTTTCACCCAAACATTTATGCAGATGGAAGCATCTGCTTGGACATCCTAC
U_HW-SSH2_9c04.b1.seq+  TCTCAAGGATGTTTCACCCAAACATTTATGCAGATGGAAGCATCTGCTTGGATATCCTAC
U_HW-SSH2_8h07.b1.seq+  AAGCGAGGATGTTTCACCCAAACATTTATGCAGATGGAAGCTTCTGCTTTTTCATCCTAC
                        ____________________________________________________________
consensus                TCTCAAGGATGTTTCACCCAAACATTTATGCAGATGGAAGCATCTGCTTGGACATCCTAC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3c05.b1.seq-  AGAACCAGTGGAGCCCTATATATGATGTTGCGGCGATATTGACCTCTATCCAGTCCCTGC
U_HW-SSH2_9d04.b1.seq+  AGAACCAGTGGAGCCCTATATATGATGTTGCAGCAATATTGACCTCTATCCAGTCCCTGC
U_HW-SSH2_9c04.b1.seq+  AGAACCAGTGGAGCCCTATATATGATGTTGCAGCAATATTGACCTCTATCCAGTCCCTGC
U_HW-SSH2_8h07.b1.seq+  AGAACCAGTGGAGCCCTATATATGATGTTGCAGCAATATTGACCTCTATCCACTCCCTGC
                        ____________________________________________________________
consensus                AGAACCAGTGGAGCCCTATATATGATGTTGCAGCAATATTGACCTCTATCCAGTCCCTGC

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3c05.b1.seq-  TGTGCCACCCGGTGCCGAATTCTCCTGCGAACTCTGAAGCAGCC
U_HW-SSH2_9d04.b1.seq+  TGTGCGACCCGAACCCGAATTCTCCTGCGAACTCTGAAGCAGCC
U_HW-SSH2_9c04.b1.seq+  TGTGCGACCCGAACCCGAATTCTCCTGCGAACTCTGAAGCAGCC
U_HW-SSH2_8h07.b1.seq+  TGTGCGACCCGAACCTTATTTTTCCTGCGT-CTCTGAAGCAGCCAGAATTACCTGTCCGG
                        ____________________________________________________________
consensus                TGTGCGACCCGAACCCGAATTCTCCTGCGAACTCTGAAGCAGCCAGAATTACCTGTCCGG

                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_8h07.b1.seq+  GCC
                        ___
consensus                GCC

****************** Contig 51 ******************
                                 .    :    .    :    .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3e04.b1.seq+  TACCAGGGGCCCCCCGACGGGCACATAAGGCAAGAAAATGTGCAAATCTTGGAGAACCT
U_HW-SSH2_3g06.b1.seq+                          ACATAAGGCATGAAAATGTGCAAATCTTGGAGAAGCT
U_HW-SSH2_3e03.b1.seq+                             GAAGGCAAGAAAATGTGCAAATCTTGGAGAACCT
U_HW-SSH2_3f06.b1.seq+                             GAAGGCATGAAAATGTGCAAATCTTGGAGAACCT
```

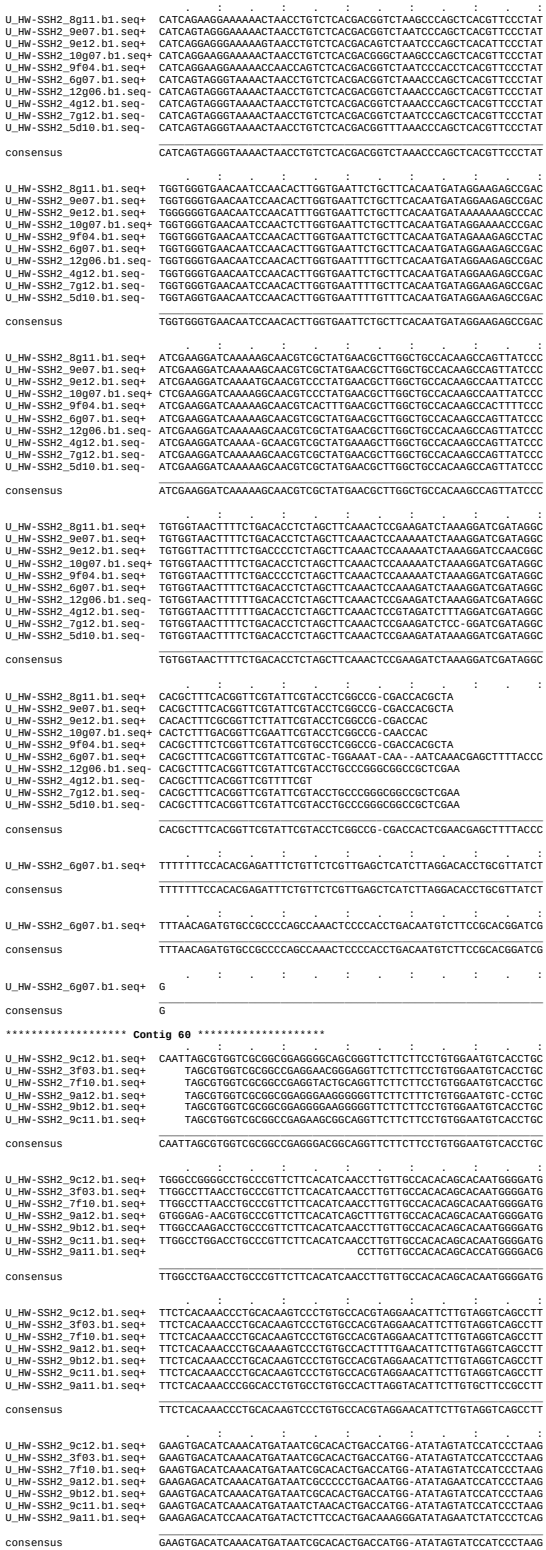


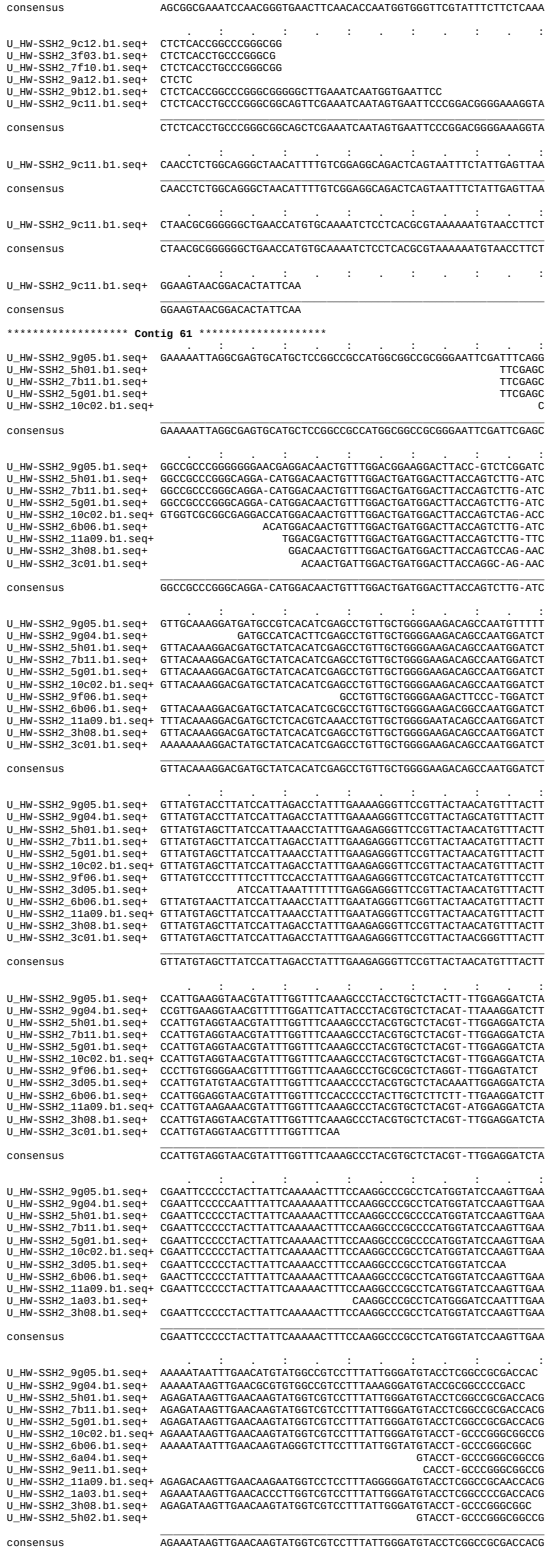
```
U_HW-SSH2_4g11.b1.seq+  GAGTCTGCATTTGATAGGATTTTTGGGGGTTTAGAAAAAAAAAACGAGGGATTTAGCAAA
                        ____________________________________________________________
consensus               GAGTCTGCATTTGATAGGATTTTTGGGGGTTTAAAAAAAAAAACAAGGTATTTAGCAAA

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_4e10.b1.seq+  CTGGAGCGACTTTCCTGCCCGGGGGGCAGCTCAA
U_HW-SSH2_4f10.b1.seq+  CTGAGGCGACTTACCTGCCCGGGCGGC
U_HW-SSH2_4h11.b1.seq+  CTGGAGCGACGTACCTGCCCGGGCGGCCGCTCAA
U_HW-SSH2_4g11.b1.seq+  CTGGAGCGACGTGCCTGCCCGGGCGGCAGGTCAAACTCAGAAGGGGGTTCGGGACCTGCC
                        ____________________________________________________________
consensus               CTGGAGCGACGTACCTGCCCGGGCGGCAGCTCAAACTCAGAAGGGGGTTCGGGACCTGCC

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_4g11.b1.seq+  CCCGGACGGCCTTTTGGAAATCCGTCCTTTCCTGGTTGTCTGTCTTTGAGTGATGTCGAA
                        ____________________________________________________________
consensus               CCCGGACGGCCTTTTGGAAATCCGTCCTTTCCTGGTTGTCTGTCTTTGAGTGATGTCGAA

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_4g11.b1.seq+  ACGCGTTCCCCCTTTGCTTAACAAAACCGACGGCTTGTCGGCATCCGGGGGGTCCCGGGC
                        ____________________________________________________________
consensus               ACGCGTTCCCCCTTTGCTTAACAAAACCGACGGCTTGTCGGCATCCGGGGGGTCCCGGGC

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_4g11.b1.seq+  CGCCGCTGCCTATTCCCCCTAG
                        ____________________________________________________________
consensus               CGCCGCTGCCTATTCCCCCTAG

****************** Contig 54 ******************
                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5b08.b1.seq+  TTCGATTACCGTGGTCCCGGCCGAGGTACATGAGCGTGTTTATGATGAGTTTGTTGACAA
U_HW-SSH2_5d08.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACATGACCCTGCTTATGATGATTTTGTTGACAT
U_HW-SSH2_5e08.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACATGAGCGTGTTTATGATGAGTTTGTTGACAA
U_HW-SSH2_6h08.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACATGAGCGTGTTTATGATGAGTTTGTTGAGAA
U_HW-SSH2_7a10.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGAACATGAGCGTGTTTATGATGAGTTTGTTGAGAA
U_HW-SSH2_6h09.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACATGAGCGTGTTTATGATGAGTTTGTTGAGAA
U_HW-SSH2_5h03.b1.seq+           CGTGGTCCCGGCGGAGGTGTATGAGCGTGTTTATGATAAGTTTGTTGACAA
U_HW-SSH2_5f03.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACATGAGCGTGTTTATGATGAGTTTGTTGAGAA
U_HW-SSH2_1h12.b1.seq+        TAGCGTGGTCGCGGCCGAGGAACAAGAGCGTGTTTATGATGAGTTTGTTGAGAA
U_HW-SSH2_5f07.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACATGAGCGTGTTTATGATGAGTTTGTTGAGAA
U_HW-SSH2_3h07.b1.seq+        TAGCGTGGTCGCGGCCGAGGAACAGGGGCGTGTTTATGATGAGTTGGATGAAAA
                        ____________________________________________________________
consensus               TTCGATTAGCGTGGTCGCGGCCGAGGTACATGAGCGTGTTTATGATGAGTTTGTTGAGAA

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5b08.b1.seq+  GTTTGAGGCTCGCTTTTGAAGCTTGTAGTTGGTGATCTATTCAAGAAGGGTGTTGA-CA
U_HW-SSH2_5d08.b1.seq+  -TCCAAGGGTCGCGCTTTGAATCGAGTACTTGGTGATCCTTTCGGGATGGGTGTT
U_HW-SSH2_5e08.b1.seq+  GTCCAAGGCTCGCGCTTTGAACCGTGTAGTTGGTGATCCATTCAGGAAGGGTGTTGAGCA
U_HW-SSH2_6h08.b1.seq+  GTCCAAGGCTCGCGCTTTGAAGCGTGTAGTTGGTGATCCATTCAGGAAGGGTGTTGAGCA
U_HW-SSH2_7a10.b1.seq+  GTCCAAGGCTCGCGCTTTGAAGCGTGTAGTTGGTGATCCATTCAGGAAGGGTGTTGAGCA
U_HW-SSH2_6h09.b1.seq+  GTCCAAGGCTCGCGCTTTGAAGCGTGTAGTTGGTGATCCATTCAGGAAGGGTGTTGAGCA
U_HW-SSH2_5h03.b1.seq+  GTCCAAGGCTCGTTCTTTGAAGCGTGTAGTTGGTGATCCATTCGCGAAGGGTGTTGAGCA
U_HW-SSH2_5f03.b1.seq+  GTCCAAGGCTCGCGCTTTGAAGCGTGTAGTTGGTGATCCATTCAGGAAGGGTGTTGAGCA
U_HW-SSH2_1h12.b1.seq+  GCCCCAAGAAGGCGCTTAGAAGTTTGTAGGTGGTGATCCATTCAGGAAGGGTGTTGAGCA
U_HW-SSH2_1a06.b1.seq+                                  TGGTGATCCATTCAGGAAGGGTGTTGAGCA
U_HW-SSH2_5f07.b1.seq+  GTCCAAGGCTCGCGCTTTGAAGCGTGTAGTTGGTGATCCATTCAGGAAGGGTGTTGAGCA
U_HW-SSH2_3h07.b1.seq+  GTCCAAGGCTCGCGCTTTGAAGCATGTAGTTGGTGATCCCTTGAGGAAGGGTGTTAAGCC
                        ____________________________________________________________
consensus               GTCCAAGGCTCGCGCTTTGAAGCGTGTAGTTGGTGATCCATTCAGGAAGGGTGTTGAGCA

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5b08.b1.seq+  CGGTCCTTTA-TTGATGATGTT-AATTCAAAAACATCTT-CGCTACGTC-AAGTCGGGTG
U_HW-SSH2_5e08.b1.seq+  GGGTCCTCAAATTGATGATGAGCAATTCAAGAAGATCTTGCGCTACATC-AAGTCGGGTG
U_HW-SSH2_6h08.b1.seq+  GGGTCCTCAAATTGATGATGAGCAATTCAAGAAGATCTTGCGCTACATC-AAGTCGGGTG
U_HW-SSH2_7a10.b1.seq+  GGGTCCTCAAATTGATGATGAGCAAT
U_HW-SSH2_6h09.b1.seq+  GGGTCCTCAAATTGATGATGAGCAATTCAAGAAGATCTTGCGCTACATC-AAGTCGGGTG
U_HW-SSH2_5h03.b1.seq+  GGGTCCTCAAATTGATGATGAGCAATTCATGAATATCTTGCGCTACATC-AAGTCGGGTG
U_HW-SSH2_5f03.b1.seq+  GGGTCCTCAGATTGATGATGAGCAATTCAAGAAGATCTTGCGCTACATC-AAGTCGGGTG
U_HW-SSH2_1h12.b1.seq+  GGGTCCTCAGATTGAT
U_HW-SSH2_1a06.b1.seq+  GGGTCCTCTTATTGATCATTATCAATTCTCGAACATCTTGCACTACATCCAATTCGGTTG
U_HW-SSH2_5f07.b1.seq+  GGGTCCTCAGATTGATGATGAGCAATTCAAAAGATCTTGCGCTACATC-AAGTCGGGTG
U_HW-SSH2_3h07.b1.seq+  GGGTCCTCATATTGATGATGATCAATTCAAGAACATCTTGCGCAACATC-CCGTCGGGTG
                        ____________________________________________________________
consensus               GGGTCCTCAAATTGATGATGAGCAATTCAAGAAGATCTTGCGCTACATC-AAGTCGGGTG

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5b08.b1.seq+  TGTACAGTGGACCCACCCTTGTGACTAGTGGTTACAATTTGGTCGACAAAGGTTACT-CA
U_HW-SSH2_5e08.b1.seq+  TGGACAGGGGAGCCACCCTTGTGACGAGTGGTGACAAGTTGGGCGACAAAGGTTACTACA
U_HW-SSH2_6h08.b1.seq+  TGGACAGTGGAGCCACCCTTGTGACGAGTGGTGACAAGTTGGGTGACAAAGGTTACTACA
U_HW-SSH2_6h09.b1.seq+  TGGACAGTGGAGCCACCCTTGTGACGAGTGGTGACAAGTTGGGTGACAAAGGTTACTACA
U_HW-SSH2_5h03.b1.seq+  TGGACAGTGGAGCCACCCTTGTGACGAGTGGTGACAAGTTGGGCGACAAAGGTTACTACA
U_HW-SSH2_5f03.b1.seq+  TGGACAGTGGAGCCACCCTTGTGACGAGTGGTGACAAGTTGGGTGACAAAGGTTACTACA
U_HW-SSH2_1a06.b1.seq+  TGGACAGTGTACCCACCCTTGTGACCCATGGTGACTAGTTGGGTGACAAAGGTTACTACA
U_HW-SSH2_5f07.b1.seq+  TGGACAGTGGAGCCACCCTTGTGACGAGTGGTGACAAGTTGGGTGACAAAGGTTACTACA
U_HW-SSH2_3h07.b1.seq+  TGGACAGTGGAGCCACCCTTGTGACGAGTGGGGACAAGTTGGGTGACAAAGGTTACTACA
                        ____________________________________________________________
consensus               TGGACAGTGGAGCCACCCTTGTGACGAGTGGTGACAAGTTGGGTGACAAAGGTTACTACA

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5b08.b1.seq+  TCCAGTCAACATTTTTCCCACATGTGCTGGATGCCATGATAATTGCCAAAAAGGAGATTT
U_HW-SSH2_5e08.b1.seq+  TCCAGCCAACAATTTTCTCAGATGTGCAGGATGGAATGAAAATTGCCCAAGAGGAGATAT
U_HW-SSH2_6h08.b1.seq+  TCCAGCCAACAATTTTCTCAAATGTGCAGGATGGCATGAAAATTGCCCAAAAGGAGATAT
U_HW-SSH2_6h09.b1.seq+  TCCAGCCAACAATTTTCTCAGATGTGCAGGATGGCATGAAAATTGCCCAAAAGGAGATAT
U_HW-SSH2_5h03.b1.seq+  TCCAGCCAACAATTTTCTCAGATCTGCAGGATGGCATGAAAATTGCCCAAGAGGAGATAT
U_HW-SSH2_5f03.b1.seq+  TCCAGCCAACAATTTTCTCAGATGTGCAGGATGGCATGAAAATTGCCCAAAAGGAGATAT
U_HW-SSH2_1a06.b1.seq+  TCCCTCCAACTTTTTTCCCTGATGTGCGGGATGGAATGAATATTGCCCAAGAGGGGATAT
U_HW-SSH2_5f07.b1.seq+  TCCAGCCAACAATTTTCTCAAATGTGCAGGATGGCATGAAAATTGCCCAAGAGGAGATAT
U_HW-SSH2_3h07.b1.seq+  TCCAGCCAACAATTTTCTCAGATGTGCAGGATGGCATGAAAATTGCCCAAAAGGAGATTT
                        ____________________________________________________________
consensus               TCCAGCCAACAATTTTCTCAGATGTGCAGGATGGCATGAAAATTGCCCAAAAGGAGATAT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5b08.b1.seq+  TCGGGCCTGTTCAATCAATCTT
U_HW-SSH2_5e08.b1.seq+  TTGGGCCTGTTCAGTCAATCTTCAA-TTCAATGACCTCCAAGAGGTGATCAAGAGGGCGA
U_HW-SSH2_6h08.b1.seq+  TTGGGCCTGTTCAGTCAATCTTCAAGTTCAATGACCTCAACGAGGTGATCAAGAGGGCGA
U_HW-SSH2_6h09.b1.seq+  TTGGGCCTGTTCAGTCAATCTTCAAGTTCAATGACCTCAACGAGGTGATCAAGAGGGCGA
U_HW-SSH2_5h03.b1.seq+  TTGGGCCTGTTCATTCAATCTTCAAGTTCAATGACCTCAACGAGGTGATAAAGAGGGCGA
U_HW-SSH2_5f03.b1.seq+  TTGGGCCTGTTCAGTCAATCTTCAAGTTCAATGACCTCAACGAGGTGATCAAGAGGGCGA
U_HW-SSH2_1a06.b1.seq+  TTGGTCCTGTTCACTCAATCTTCAAGTTCTATGACCTC
U_HW-SSH2_5f07.b1.seq+  TTGGGCCTGTTCACTCAATCTTCAAGTTCAATGACCTCAACGAGGTGATCAAGAGGGCGA
U_HW-SSH2_3h07.b1.seq+  TTGGGCCTGTTCAATCAATCTTCAAGTTCAATGACCTCAACTAGGTGATCAAGAGGGCCA
                        ____________________________________________________________
consensus               TTGGGCCTGTTCAGTCAATCTTCAAGTTCAATGACCTCAACGAGGTGATCAAGAGGGCGA

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5e08.b1.seq+  ACGCAAGCCATTACCTGCCCGGGCGGCCGCTCAAA
U_HW-SSH2_6h08.b1.seq+  ACGCAAGCCAGTACCTGCCCGGGCGGCCGCTCAAA
U_HW-SSH2_6h09.b1.seq+  ACGCAAGCCAGTACCTGCCCGGGCGGCCGCTCAAA
U_HW-SSH2_5h03.b1.seq+  ACGCAC-CCAGTACCTCCCCGGGC
U_HW-SSH2_5f03.b1.seq+  ACGCAAGCCAGTACCTGCCCGGGCGGC
U_HW-SSH2_5f07.b1.seq+  ACGCAAGCCAGTACCTGTCCGGG
U_HW-SSH2_3h07.b1.seq+  ACGCAAGCCAGTACCTGCCCGGGGGGCCGCTCGAAATCACTACAGAATTCGCGGCCGCCT
                        ____________________________________________________________
consensus               ACGCAAGCCAGTACCTGCCCGGGCGGCCGCTCAAAATCACTACAGAATTCGCGGCCGCCT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3h07.b1.seq+  GCAGCTTCCACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTTT
                        ____________________________________________________________
consensus               GCAGCTTCCACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGAGTATTCTTT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_3h07.b1.seq+  GGGTCACCTAAATAGCTTGT
                        ____________________________________________________________
consensus               GGGTCACCTAAATAGCTTGT

****************** Contig 55 ******************
                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5d01.b1.seq-  TAGCGTGGTCGCGGCCGAGGTGTTATTGTGAGAATTCTTAATTCAAGAGTTATAGGGAGG
U_HW-SSH2_11c12.b1.seq+                          TTGTGAGATTTCTTAATTCGAGAGTTATAGGGAGG
U_HW-SSH2_9g11.b1.seq+                         ATTGTGATAATTCTAAATTCAAGAGTTATAGGGAGG
U_HW-SSH2_12h03.b1.seq+                         TTGTGAGAATTCTTAATTCAAGAGTTATAGGGAGG
U_HW-SSH2_9f11.b1.seq+                                             AGGGAGG
                        ____________________________________________________________
consensus               TAGCGTGGTCGCGGCCGAGGTGTTATTGTGAGAATTCTTAATTCAAGAGTTATAGGGAGG

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5d01.b1.seq-  GACTTATGTCACCACAAACAGAAACTAAAGCAGGTGTTGGATTTAAAGCTGGTGTTAAAG
U_HW-SSH2_11c12.b1.seq+ GACTTATGTCCCCACAAACAAAAACTAAAGCAGGTGTTGTATTTAAAGCTGGTGTTAAAG
U_HW-SSH2_9g11.b1.seq+  GATTTATGTCACCACAAACAGAAACTAAAGCATGTGTTGAATTTAAAGCTGGTGTTAAAG
U_HW-SSH2_12h03.b1.seq+ GACTTATGTCACCACAAACAGAAACTAAAGCAGGTGTTGGATTTAAAGCTGGTGTTAAAG
U_HW-SSH2_9f11.b1.seq+  GATTTATGTCACCACAAACAGAAATTAAATCTTGTGTTAAATTTAAACCTGGTGTTGA-G
                        ____________________________________________________________
consensus               GACTTATGTCACCACAAACAGAAACTAAAGCAGGTGTTGGATTTAAAGCTGGTGTTAAAG

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5d01.b1.seq-  ATTATAAATTGACTTACTACACCCCAGAGTATGAAACTAAGGATACTGATATCTTGGCAG
U_HW-SSH2_11c12.b1.seq+ ATTATAAATTGACTTACTACACCCCAAAGTATGAAACTAAGGATACTGATATCTTGGCAG
U_HW-SSH2_9g11.b1.seq+  ATTATAAATTGACTAACTACCCCCCAGAGAATGAAACTAAGGATTCTGATATCTGGGCAG
U_HW-SSH2_12h03.b1.seq+ ATTATAAATTGACTTACTACACCCCAGAGTATGAAACTAAGGATACTGATATCTTGGCAG
U_HW-SSH2_9f11.b1.seq+  ATTATAAATTGTCAAACAACCCCCCATAGAATAAAACTAACGATTCTGATTTTTTGTTTG
                        ____________________________________________________________
consensus               ATTATAAATTGACTTACTACACCCCAGAGTATGAAACTAAGGATACTGATATCTTGGCAG

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5d01.b1.seq-  CATTCCGAGTAAGTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGTAGCTG
U_HW-SSH2_11c12.b1.seq+ CTTTCCGAGTAAGTCCTCAGCCTGGGGTTCC
U_HW-SSH2_9g11.b1.seq+  CATTCCGAGTAACTCCTCAGCCTGGGGTTCCCCCCGAAGAAGCAGGGGCTGCATTATCTG
U_HW-SSH2_12h03.b1.seq+ CATTCCGAGTAAGTCCTCAGCCTGGGGTTCCGCCCAAAGAAGCAGGGGCT
U_HW-SSH2_9f11.b1.seq+  CCTTCCGAGTGACTCCTCATCTGGGGGATCCTCCCGAAGAATCCCGGGCTTCAATATCTG
                        ____________________________________________________________
consensus               CATTCCGAGTAAGTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAATATCTG

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5d01.b1.seq-  CCGAATCTTCTACTGGTACATGCCCGGGCGGCCG
U_HW-SSH2_9g11.b1.seq+  CCGAATCTTCTACTGGAAACCTGCC
U_HW-SSH2_9f11.b1.seq+  CCAAATCTTCTACTGGTACCTGCCGGGGAGGCCGGATGTGATGACTCCTCAAATCATGAGT
                        ____________________________________________________________
consensus               CCGAATCTTCTACTGGTACCTGCCGGGGAGGCCGATGTGATGACTCCTCAAATCATGAGT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9f11.b1.seq+  GTATCAAGCCATGCATGGTGGGCACCCCTGACTAATATCCTCATGAAAAAAGATGCCCAC
                        ____________________________________________________________
consensus               GTATCAAGCCATGCATGGTGGGCACCCCTGACTAATATCCTCATGAAAAAAGATGCCCAC

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9f11.b1.seq+  ATTACGTATACTAAATGGGAGCCCTCCCATCGTGGGGGATGCTAGCCTTGAGTATTTTCT
                        ____________________________________________________________
consensus               ATTACGTATACTAAATGGGAGCCCTCCCATCGTGGGGGATGCTAGCCTTGAGTATTTTCT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9f11.b1.seq+  TGTGGCATATAAATACCTGGTCAAATTTCCGCACAAAATTGTTCCCTGAAAGGGAATTGT
                        ____________________________________________________________
consensus               TGTGGCATATAAATACCTGGTCAAATTTCCGCACAAAATTGTTCCCTGAAAGGGAATTGT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9f11.b1.seq+  GATCCGCTCGCGGTTCCAAATGAAAGAACTGCCGGACACTTAAAGGGGTAACGCTTGGGG
                        ____________________________________________________________
consensus               GATCCGCTCGCGGTTCCAAATGAAAGAACTGCCGGACACTTAAAGGGGTAACGCTTGGGG

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9f11.b1.seq+  TGCGTAATGAAGGAGGAAAATCTGTTTAGTGGGGTGCATACAAGGGCCCGCCATCGGGTG
                        ____________________________________________________________
consensus               TGCGTAATGAAGGAGGAAAATCTGTTTAGTGGGGTGCATACAAGGGCCCGCCATCGGGTG

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9f11.b1.seq+  GGGAAAAGGGGGGGTGCCATCTGTTTTATGGATCCGGTCACCGCCCGCTGAAAACGCTGT
                        ____________________________________________________________
consensus               GGGAAAAGGGGGGGTGCCATCTGTTTTATGGATCCGGTCACCGCCCGCTGAAAACGCTGT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_9f11.b1.seq+  TTTCGTTGGT
                        ____________________________________________________________
consensus               TTTCGTTGGT

****************** Contig 56 ******************
                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6h04.b1.seq-  CTGCGAAGTGGGTGGATTTTGATGGATAACTATTTCTCTCCGGAAAAAAATAACGCCCTT
                        ____________________________________________________________
consensus               CTGCGAAGTGGGTGGATTTTGATGGATAACTATTTCTCTCCGGAAAAAAATAACGCCCTT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6h04.b1.seq-  GCAGGGCCCAGCTTCTTTTTTGGCTCTATTGAATTATCAAGCTAAGCATAGCGCGGGTTG
                        ____________________________________________________________
consensus               GCAGGGCCCAGCTTCTTTTTTGGCTCTATTGAATTATCAAGCTAAGCATAGCGCGGGTTG

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6h04.b1.seq-  GGAGGGCTAACATATAGTTAGCTTGCAGGAGGCCGAGAATTCATTAGTGATTTAGAGAAG
U_HW-SSH2_11f02.b1.seq+                                                  TAGCGTGG
U_HW-SSH2_3f11.b1.seq+                                                   TAGCGTGG
U_HW-SSH2_12h11.b1.seq+                                                        G
U_HW-SSH2_8h11.b1.seq-                                                   TAGCGTGG
                        ____________________________________________________________
consensus               GGAGGGCTAACATATAGTTAGCTTGCAGGAGGCCGAGAATTCATTAGTGATTTAGCGTGG

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6h04.b1.seq-  CCGCCCGGGCAGGTACCCTGACGCGTATGTCCGCATCATTGGATTTGACAACATCGGTCA
U_HW-SSH2_3e11.b1.seq+                                                     GCGCCA
U_HW-SSH2_3a11.b1.seq+                    CCTGACGCGTATGTCCGCATCATCGGATTCGACAACAAGCGCCA
U_HW-SSH2_11f02.b1.seq+ TCGCGGCCG-AGGTACCCTGACGCGTATGTCCGCATCATCGGATTCAACAACATCGCCA
U_HW-SSH2_3f11.b1.seq+  TCGCGGCCG-AGGTACCCTGACGCGTATGTCCGCATCATCGGATTCAACAACCTCGCCA
U_HW-SSH2_12h11.b1.seq+ CCGCCCGGGCAGGTACCCTGACACCTATGTCCGCATCATCGGATTCCACAACATCGCTCG
U_HW-SSH2_8h11.b1.seq-  TCGCGGCCG-AGGTACCTTGACGCGTATGTCCGCATCATCGGATTCGACAACATCGCCA
                        ____________________________________________________________
consensus               TCGCGGCCG-AGGTACCCTGACGCGTATGTCCGCATCATCGGATTCGACAACATCGCCA

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6h04.b1.seq-  GGTGCAGTGCGTCAGCTTCATTGCCTTCAAGCCACCGGGCTGCGAGGAGTCCGGCAAGGC
U_HW-SSH2_3e11.b1.seq+  GGGGCAGCGCGTTAGCTTCATCCCCTTCAATCCACCGGGCTGCTAGGAGTCCGGCAAGGC
U_HW-SSH2_3a11.b1.seq+  GGGGCAGTGCGTCAGCTTCATCGCCTTCAAGCCACCGGGCTGCGAGGAGTCCGGCAAGGC
U_HW-SSH2_11f02.b1.seq+ GGTGCAGTGCGTCAGCTTCATCGCCTTCAAGCCACCGGGCTGCGAGGAGTCCGGCAAGGC
U_HW-SSH2_3f11.b1.seq+  GGGGCAGTGCGTCAGCTTCATCGCCTTCAAGCCACCGGGCTGCGAGGAGTCCGGCAAGGC
U_HW-SSH2_12h11.b1.seq+ GGTGCAGTGCGTCAGCTTCATCGCCTTCAAGCCACCGGGCTGCGAGGAGTCCGGCAAGGC
U_HW-SSH2_8h11.b1.seq-  GGTGCAGTGCGTCAGCTTCATCTCCTTCAAGCCACCGGGCTGGGAGGAGTCCGGCAAGGC
                        ____________________________________________________________
consensus               GGTGCAGTGCGTCAGCTTCATCGCCTTCAAGCCACCGGGCTGCGAGGAGTCCGGCAAGGC

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6h04.b1.seq-  CTAAACAGCTCACTCACCACGGGCCACATATAAAGTGCCATTGCGGTTTTGTCAACTCTG
U_HW-SSH2_3e11.b1.seq+  CTAAACAGCAAATTCACCACGGGCCAAATATAAAGTGCCATTGCAGTTTTGA-AACTCTC
U_HW-SSH2_3a11.b1.seq+  CTAAA
U_HW-SSH2_11f02.b1.seq+ CTAAA
U_HW-SSH2_3f11.b1.seq+  CTAAA
U_HW-SSH2_12h11.b1.seq+ CTAAACAGCTCACTCACGACAGGCCATATATAAAGTGCCATTGCAGTTTTGTCAACTCTG
U_HW-SSH2_8h11.b1.seq-  CTAAACAGCTCACTCACCACGGGCCACATATAAAGTGCCATTGCGGTTTTGTCAACTCTG
                        ____________________________________________________________
consensus               CTAAACAGCTCACTCACCACGGGCCACATATAAAGTGCCATTGCAGTTTTGTCAACTCTG

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6h04.b1.seq-  ACATTGCTTTGGGTTTTCCTTTTCCATTTATCTTTCTTGTTTGTTCCTAA-GATAAGAAT
U_HW-SSH2_3e11.b1.seq+  ACATTGCTTTGGGTTTTCCTTTCGCCATTGATCTTTCTTATTTGATCCTAA
U_HW-SSH2_12h11.b1.seq+ ACATTGCTTTGGGTTTTCCTTTCTCCATTTATCTTTCTTATTTGTTC
U_HW-SSH2_8h11.b1.seq-  ACATTGCTTTGGGTTTTCCTTTTCCATTTATCTTTCTTGTTTGTTCCAAAAGATAAGAAT
                        ____________________________________________________________
consensus               ACATTGCTTTGGGTTTTCCTTCTCCATTTATCTTTCTTATTTGTTCCTAAAGATAAGAAT

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6h04.b1.seq-  ATGTGTATGTCCATGTTCCCGACATGACTCGAGAAAGCATGCTCGTATGTGAATGCTACC
U_HW-SSH2_8h11.b1.seq-  ATGTGTATGTCCATGTTCCCGACATGACTCGAGAAAGCCTCCTCGTATGTGAATGCTTTC
                        ____________________________________________________________
consensus               ATGTGTATGTCCATGTTCCCGACATGACTCGAGAAAGCATCCTCGTATGTGAATGCTACC

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6h04.b1.seq-  GATGGCTATGTATATGCACATGCACATAATATTATAAGTACCTGCCCGGGCGGCCGCTCG
U_HW-SSH2_8h11.b1.seq-  GTTGGGTATGTATATGCACATGCACATCATATTCTTAGTTTCTTCCCGGGCGGCCGCTCG
                        ____________________________________________________________
consensus               GATGGCTATGTATATGCACATGCACATAATATTATAAGTACCTGCCCGGGCGGCCGCTCG

                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_6h04.b1.seq-  AA
U_HW-SSH2_8h11.b1.seq-  AA
                        ____________________________________________________________
consensus               AA

****************** Contig 57 ******************
                           .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7f11.b1.seq+  TTCGATTAGCGTGGTCGCGGCCGAGGTACTGAACCATGGACTTCACTCTGGCAAGAGCTC
U_HW-SSH2_7f12.b1.seq+        TAGCGTGGTCGCGGCCGAGGTACTGAACCATGGACTTCACTCTGGCAAGATCTC
```



Contig 58

Contig 59





```
U_HW-SSH2_7h02.b1.seq+  CGCGTTGGATGCATAGCTTGAGTATTCTATAGTGTCACCTAAATAGCTTGGCGTAATCAT
                        ____________________________________________________________
consensus               CGCGTTGGATGCATAGCTTGAGTATTCTATAGTGTCACCTAAATAGCTTGGCGTAATCAT

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10c02.b1.seq+ GGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAG
U_HW-SSH2_6a04.b1.seq+  GGTCATACCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAG
U_HW-SSH2_9e11.b1.seq+  GGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAG
U_HW-SSH2_5h02.b1.seq+  GGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAG
U_HW-SSH2_7h02.b1.seq+  GGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACAAG
                        ____________________________________________________________
consensus               GGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAG

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10c02.b1.seq+ CCGGAAGCATAAAGTGTAAAGCCT-GGGGTGCCTAAT-GAGTGAGCTAACTCACATTAAT
U_HW-SSH2_6a04.b1.seq+  CCGGAAACATAAAGTGTAAAGCCTCGGGGTGCCTAAA-GAGTGACCTACCTCACATTAAT
U_HW-SSH2_9e11.b1.seq+  CCGGAAGCATAAAGTGTAAAGGCG-GGCGTGCCTAAATGAGTGAGCTAAC-CAAATTAAT
U_HW-SSH2_5h02.b1.seq+  CCGGAAGCATAAAGTGTAAAGCCT-GGGGTGCCTAAT-GAGTGAGCTAACTCACATTAAT
U_HW-SSH2_7h02.b1.seq+  CCGGAAGCATAAAGTGTAAAGCCT-GGGGTGCCTAAT-GAGTGAGCTAACTCACATTAAT
                        ____________________________________________________________
consensus               CCGGAAGCATAAAGTGTAAAGCCT-GGGGTGCCTAAT-GAGTGAGCTAACTCACATTAAT

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10c02.b1.seq+ TGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATG
U_HW-SSH2_6a04.b1.seq+  TGCGTTGCGCACACTGCCCACTTTCCAGTAGG-AAACCTGTCGCGCCAT-TGAATTAATG
U_HW-SSH2_9e11.b1.seq+  TGCGTTGCGCTCACTGCCC-CTTTTCAGTCGGGAAAC
U_HW-SSH2_5h02.b1.seq+  TGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCTATAATG
U_HW-SSH2_7h02.b1.seq+  TGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATG
                        ____________________________________________________________
consensus               TGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATG

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10c02.b1.seq+ AATCGGCCAACGCGCGGGGGAGAGGCGGTTTGCGTATTTGGGCGCTCTTCCGCTTCCTCG
U_HW-SSH2_6a04.b1.seq+  AATCGGCCCACGCGCGGAG-AGAGGCGGTTTG
U_HW-SSH2_5h02.b1.seq+  AATCGGCCAACGCGCGGAG-AGAGGCGGTTTGCGAATT-GGGCGCTCTTCCGCTTCCTCG
U_HW-SSH2_7h02.b1.seq+  AATCGGCCAACGCGCGGGG-AGAGGCGGTTTGCGTATT-GGGCGCTCTTCCGCTTCCTCG
                        ____________________________________________________________
consensus               AATCGGCCAACGCGCGGAG-AGAGGCGGTTTGCGTATT-GGGCGCTCTTCCGCTTCCTCG

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_10c02.b1.seq+ CTCA-TGACTCGCTGCGCTCGGTCGTTCGG
U_HW-SSH2_5h02.b1.seq+  CTCACTGACTCGCTGCGCTCGGTCGTTCGGGCTGCAGCGAGCAGAATCAGCTCAATCAAG
U_HW-SSH2_7h02.b1.seq+  CTCACTGACTCGCTGCGCTCGGTCGTTCGG-CTGCGGCGAGCGGTATCAGCTCACTCAAA
                        ____________________________________________________________
consensus               CTCACTGACTCGCTGCGCTCGGTCGTTCGGGCTGCAGCGAGCAGAATCAGCTCAATCAAA

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_5h02.b1.seq+  GTCGTAATTACGGTTATCCACAGATTCAGGGGATAACGCAG
U_HW-SSH2_7h02.b1.seq+  GGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGAAAA
                        ____________________________________________________________
consensus               GGCGGAAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGAAAA

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7h02.b1.seq+  AGGCCAGCAAATGGCCAGGAACCATAAAAAGGCCGCGTTGCTGGCGTTTTTCCATTAGGC
                        ____________________________________________________________
consensus               AGGCCAGCAAATGGCCAGGAACCATAAAAAGGCCGCGTTGCTGGCGTTTTTCCATTAGGC

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7h02.b1.seq+  TCCCCCCCCCCCTAAAAAGTATCAAAAAAATCGACTCTCAAGTAAGAGGGGGCTAATCCC
                        ____________________________________________________________
consensus               TCCCCCCCCCCCTAAAAAGTATCAAAAAAATCGACTCTCAAGTAAGAGGGGGCTAATCCC

                               .    :    .    :    .    :    .    :    .    :    .    :
U_HW-SSH2_7h02.b1.seq+  TACAGGATATAAAGATACCCGGCGTCTCCCCCCTGGAACCCCCTTATG
                        ____________________________________________________________
consensus               TACAGGATATAAAGATACCCGGCGTCTCCCCCCTGGAACCCCCTTATG
```

APPENDIX G

Detailed display of Blast N analysis results of SSH1 (D-R) classified according to function or origin categories.

The singletons and contigs are presented in separate tables.

The contig assembly program Cap 3 detected that some sequences were within some other sequences. These cases are indicated under the clone numbers of these sequences, (as "In SSH...").

First coloumn shows the clone number, second coloumn shows the length of read sequence (after sequencing), third coloumn indicates E-Value and identity and the fourth coloumn displays Blast N Homology Result.

"Representative" is used to indicate that not all clones representing a particular contig are shown.

Metabolism and Energy

Singletons

SSH1-1 a05	420	Expect = 0.0 Identities = 388/399 (97%)	Triticum aestivum plastid glutamine synthetase isoform GS2c (GS2) mRNA, complete cds; nuclear gene for plastid product gi|71362639|gb|DQ124214.1|
SSH1-1 g02	68	Expect = 0.18 Identities = 21/21 (100%)	Anopheles gambiae putative secreted carbonic anhydrase mRNA, complete cds gi|99082887|gb|DQ518577.1|
SSH1-1 h03	170	Expect = 2.2 Identities = 20/20 (100%)	PREDICTED: Pan troglodytes plasma membrane calcium ATPase 4, transcript variant 7 (ATP2B4), mRNA gi|114571943|ref|XM_001156333.1|
SSH1-2 b05	149	Expect = e-173 Identities = 326/331 (98%)	Triticum aestivum plastid glutamine synthetase isoform GS2c GS2)mRNA, complete cds; nuclear gene for plastid product gi|71362454|gb|DQ124212.1|
SSH1-2 b09	183	Expect = 6e-004 Identities = 39/42 (92%)	Hordeum vulgare HVP1 mRNA for vacuolar proton-inorganic pyrophosphatase, complete cds gi|11527560|dbj|AB032839.1|
SSH1-2 d07	428	Expect = e-157 Identities = 316/327 (96%)	Hordeum vulgare mRNA for vacuolar membrane proton-translocating inorganic pyrophosphatase, complete cds gi|6012171|dbj|D13472.2|BLYINOPP
SSH1-2 f02	406	Expect = e-149 Identities = 334/354 (94%)	Triticum aestivum leucine zipper protein zip1 (zip1) Mrna complete cds gi|58339282|gb|AY738114.1|
		Expect = 1e-044 Identities = 171/197 (86%)	Hordeum vulgare aerobic Mg-protoporphyrin IX monomethyl ester cyclase(Xantha-l) gene, complete cds gi|58617795|gb|AY887063.1|
SSH1-2 f04	651	Expect = 0.0 Identities = 569/596 (95%)	Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II gi|21843|emb|X57408.1|TAPSB0
		Expect = 0.0 Identities = 526/588 (89%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC clone:B1080D07 gi|116011070|dbj|AK241705.1|
SSH1-2 f12	504	Expect = e-126 Identities = 241/244 (98%)	Triticum aestivum putative glycine decarboxylase subunit mRNA, complete cds gi|22204117|gb|AY123417.1|
		Expect = 2e-052 Identities = 186/212 (87%)	Zea mays glycine cleavage H-protein mRNA, partial cds gi|17017276|gb|AF439730.1|AF439730
SSH1-3 b06	59	Expect = 2.3 Identities = 19/19 (100%)	Streptomyces griseus fredericamycin biosynthetic gene cluster, complete sequence gi|85674271|gb|AF525490.2|
SSH1-3 c05	79	Expect = 0.88 Identities = 20/20 (100%)	Triticum aestivum cultivar Biggar myo-inositol 1-phosphate synthase(MIPS) mRNA, complete cds gi|4589065|gb|AF120148.1|AF120148
		Expect = 3.5 Identities = 19/19 (100%)	PREDICTED: Canis familiaris similar to Gap junction alpha-7 protein(Connexin 45) (Cx45) (LOC607294), mRNA gi|73975455|ref|XM_843919.1|
SSH1-4 a11	429	Expect = 0.098 Identities = 47/55 (85%)	Arabidopsis thaliana N-acetyltransferase (AT1G32070) mRNA, complete cds gi|18398251|ref|NM_102941.1|
SSH1-4 b07	511	Expect = e-112 Identities = 390/450 (86%)	Triticum aestivum cysteine protease (CP) mRNA, complete cds gi|56682916|gb|AY841792.1|
SSH1-4 c05	316	Expect = e-134 Identities = 277/286 (96%)	Wheat PsbP mRNA for 23 kDa oxygen evolving protein of photosystem II gi|21836|emb|X57407.1|TAPPSBP
SSH1-4 d09	232	Expect = 7e-026 Identities = 119/137 (86%)	Zea mays gene for Ferredoxin-NADP reductase binding protein gi|407028|emb|Z26824.1|ZMFNRBP
SSH1-4 e06	385	Expect = e-142 Identities = 274/279 (98%)	Triticum aestivum **vacuolar ATP synthase subunit E** (VATE) mRNA,complete cds gi|85375921|gb|DQ344624.1|
		Expect = e-114 Identities = 262/279 (93%)	Hordeum vulgare **vacuolar proton-translocating ATPase** subunit E(Ylp) mRNA, complete cds gi|4099149|gb|U84269.1|HVU84269
SSH1-5 a07	442	Expect = e-130 Identities = 251/255 (98%)	H.vulgare mRNA PsaN for photosystem I subunit N gi|19094|emb|X66428.1|HVPSANMR
SSH1-5 f03	495	Expect = 0.029 Identities = 30/32 (93%)	Oryza sativa mRNA for manganese-binding PsbY-like protein precursor(MgBP1 gene) gi|57282598|emb|AJ437536.2|OSA437536
SSH1-5 h05	461	Expect = 1e-019 Identities = 68/73 (93%)	Hordeum vulgare carbonic anhydrase mRNA, complete cds gi|558498|gb|L36959.1|BLYCA
SSH1-7 e06	344	Expect = 0.005 Identities = 50/57 (87%)	Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II gi|21843|emb|X57408.1|TAPSB0
SSH1-7 f01	363	Expect = 0.33 Identities = 34/38 (89%)	Cynodon dactylon pollen 2-phosphoglycerate dehydrogenase 2 precursor,mRNA, complete cds gi|37222050|gb|AY344113.2|

SSH1-7 g04	337	Expect = 1.2 Identities = 27/29 (93%)	Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II gi|21843|emb|X57408.1|TAPSB0
SSH1-7 h08	304	Expect = 1.1 Identities = 21/21 (100%)	Sorghum bicolor **flavonoid 3'-hydroxylase** (F3'H1) mRNA, complete cds gi|110180150|gb|DQ787855.1|
SSH1-8 a01	506	Expect = 3e-036 Identities = 147/169 (86%)	H.chilense x T.turgidum conv. durum (Tritordeum) mRNA for S-adenosylmethionine decarboxylase gi|1403043|emb|X83881.1|HCTTSAMDC
SSH1-8 c05	308	Expect = 5e-009 Identities = 111/135 (82%)	H.vulgare mRNA for photosysteme I antenna protein gi|666053|emb|X84308.1|HVLHCA2
SSH1-8 d10	499	Expect = 7.1 Identities = 20/20 (100%)	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 1(ABCB1) gene, complete cds gi|58802448|gb|AY910577.1|
SSH1-8 f03	276	Expect = 0.96 Identities = 21/21 (100%)	Caldicellulosiruptor lactoaceticus lac gene for beta-galactosidase gi|15144247|emb|AJ316560.1|CLA316560
SSH1-8 h10	94	Expect = 2e-033 Identities = 75/75 (100%)	Triticum aestivum glyceraldehyde-3-phosphate dehydrogenase-like mRNA, complete sequence gi|10946206|gb|AF273738.1|AF273738
SSH1-9 f09	711	Expect = 0.0 Identities = 540/579 (93%)	Triticum aestivum adenine phosphoribosyltransferase form 1 (APT1) mRNA, complete cds gi|726304|gb|U22442.1|TAU22442
SSH1-10 d06	658	Expect = 2e-034 Identities = 111/122 (90%)	Sorghum propinquum putative aconitate hydratase 1 gene, exons 16,17 and partial cds gi|94961050|gb|DQ463100.1|
SSH1-10 g09	419	Expect = 0.38 Identities = 31/34 (91%)	Triticum aestivum partial mRNA for putative fructose 1-,6-biphosphate aldolase (ald gene) gi|18496064|emb|AJ420778.1|TAE420778
SSH1-11 a05	872	Expect = 1e-027 Identities = 293/367 (79%),	Triticum aestivum S-adenosylmethionine decarboxylase precursor, mRNA, complete cds gi|4325044|gb|AF117660.1|AF117660
SSH1-11 c11	386	Expect = 0.006 Identities = 31/33 (93%)	Triticum aestivum chloroplast inositol phosphatase-like protein mRNA, complete cds; nuclear gene for chloroplast product gi|52548245|gb|AY736122.1|
		Expect = 0.006 Identities = 31/33 (93%)	Triticum aestivum chloroplast-localized Ptr ToxA-binding protein1 (TaThf1) mRNA, complete cds; nuclear gene for chloroplast product gi|38570260|gb|AY377991.1|
SSH1-11 d09	387	Expect = 5.4 Identities = 20/20 (100%)	Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds gi|5669918|gb|AF146689.1|AF146689
SSH1-11 g04	405	Expect = 0.001 Identities = 32/34 (94%)	Zea mays ferredoxin-dependent glutamate synthase mRNA, complete cds gi|168476|gb|M59190.1|MZEFEGLU
SSH1-11 h05	256	Expect = 0.22 Identities = 22/22 (100%)	Aspergillus fumigatus Af293 phosphatidyl synthase (Afu3g12330)partial mRNA gi|70999337|ref|XM_749295.1|
SSH1-12 a05	356	Expect = 1e-031 Identities = 221/270 (81%)	Triticum aestivum beta-1,3-glucanase precursor (Glb3) mRNA, complete cds gi|4741845|gb|AF112965.1|
SSH1-12 a10	505	Expect = 2e-074 Identities = 273/313 (87%),	Triticum aestivum petF gene for ferredoxin gi|403032|emb|X75089.1|TAPETFFE
SSH1-12 b04	291	Expect = 2e-069 Identities = 197/217 (90%)	Hordeum vulgare catalase (Cat2) mRNA, complete cds gi|684947|gb|U20778.1|HVU20778
SSH1-12 e01	345	Expect = 1.2 Identities = 30/33 (90%)	Homo sapiens vWF-CP(ADAMTS13) mRNA for von Willebrand factor-cleaving protease, complete cds gi|16117337|dbj|AB069698.2|
SSH1-13 a03	136	Expect = 6.8 Identities = 22/23 (95%)	PREDICTED: Bos taurus similar to N-acetylglutamate synthase,transcript variant 2 (LOC538004), mRNA gi|76644975|ref|XM_618194.2|
SSH1-13 b04	382	Expect = 2e-092 Identities = 256/283 (90%)	H.vulgare mRNA for xylose isomerase gi|1296808|emb|X95257.1|HVXYLISOP
SSH1-13 c07	427	Expect = 0.38 Identities = 22/22 (100%)	Arabidopsis thaliana ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase (AT5G24360) mRNA, complete cds gi|42568060|ref|NM_122344.3|
SSH1-13 g03	126	Expect = 6.2 Identities = 19/19 (100%)	Bacillus stearothermophilus xylan 1,4-beta-xylosidase (xylA) gene,complete cds gi|560029|gb|U15984.1|BSU15984
SSH1-14 c06	62	Expect = 9.8 Identities = 18/18 (100%)	Arabidopsis thaliana mRNA for anthranilate N-benzoyltransferase,complete cds, clone: RAFL04-15-L12 gi|110740544|dbj|AK226213.1|
SSH1-14 c07	377	Expect = 5.3 Identities = 23/24 (95%)	Mesorhizobifum loti pno gene for pyridoxine 4-oxidase, complete cds gi|56790043|dbj|AB197054.1|
SSH1-14 d05	221	Expect = 0.75 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-184C23 on chromosome 6 Contains the gene for a novel protein similar to FK506-binding protein(FKBP-12) (Peptidyl-prolyl cis-trans isomerase)(PPiase)(Rotamase), a pseudogene similar to part of serine palmitoyltransferase long chain base subunit 1(SPTLC1) and a novel pseudogene, complete sequence gi|12331145|emb|AL450346.4|
SSH1-14 d07	678	Expect = 2.5 Identities = 24/25 (96%)	Human DNA sequence from clone RP11-100G15 on chromosome 9 Contains the 5' end of the SPTLC1 gene for serine palmitoyltransferase long chain base subunit 1, a pseudogene similar to part of ATP synthase 6 (MTATP6), a cytochrome c oxidase III(MTCO3) pseudogene, pseudogenes for NADH dehydrogenases 3, 4 and 4L (MTND3, MTND4L, MTND4), a protein tyrosine phosphatase pseudogene, a novel gene (LOC158314), two novel genes, part of a novel gene and a CpG island, complete sequence gi|9187237|emb|AL354751.7|
SSH1-14 e03	332	Expect = 4.6 Identities = 20/20 (100%)	Human DNA sequence from clone RP5-1077I2 on chromosome 20 Contains the 3' end of the SPTLC2L gene for serine palmitoyltransferase long chain base subunit 2-like (aminotransferase 2), the 5' end of C20orf82 gene for a novel protein similar to Xenopus Isthmin protein, two novel genes and a putative CpG island, complete sequence gi|7263998|emb|AL050320.19|HSJ1077I2
SSH1-14 e08	783	21Expect = 2.9 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-428L19 on chromosome 9 Contains the 5' end of the PCSK5 gene for proprotein convertase subtilisin/kexin type 5 and two CpG islands, complete sequence gi|14596321|emb|AL359253.17|
SSH1-14 e12	350	Expect = 4.9 Identities = 20/20 (100%)	Helicobacter pylori isolate 43 urease protein UreA (ureA) gene,complete cds gi|14583062|gb|AF373579.1|
SSH1-14 g12	132	Expect = 2e-009 Identities = 48/51 (94%)	Hordeum vulgare carbonic anhydrase mRNA, complete cds gi|558498|gb|L36959.1|BLYCA
SSH1-15 a01	188	Expect = 9.8 Identities = 22/23 (95%)	PREDICTED: Strongylocentrotus purpuratus similar to peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor(LOC588352), mRNA gi|72029206|ref|XM_788041.1|
SSH1-15 a07	90	Expect = 4.1 Identities = 22/23 (95%)	Pseudomma truncatum voucher ZMBN68267 cytochrome c oxidase subunit 1 (COX1) gene, partial cds; mitochondrial gi|54398594|gb|AY624278.1|
SSH1-15 b08	360	Expect = 1.3 Identities = 21/21 (100%)	Homo sapiens adiponectin, C1Q and collagen domain containing(ADIPOQ), mRNA gi|44890057|ref|NM_004797.2|
SSH1-15 b09	419	Expect = 0.38 Identities = 28/30 (93%)	Myiagra rubecula voucher UWBM57515 NADH dehydrogenase subunit 2(NADH2) gene, partial cds; mitochondrial gi|99030008|gb|DQ468930.1|
SSH1-15 b12	261	Expect = 3.6 Identities = 23/24 (95%)	PREDICTED: Macaca mulatta similar to beta 3-glycosyltransferase-like(LOC713498), mRNA gi|109120406|ref|XR_012519.1|
SSH1-15 c06	326	Expect = 6e-095 Identities = 240/263 (91%)	Hordeum vulgare carbonic anhydrase mRNA, complete cds gi|558498|gb|L36959.1|BLYCA
SSH1-15 e12	272	Expect = 3.7 Identities = 23/24 (95%)	Trypanosoma brucei TREU927 clone RPCI93-6H23 diadenosine tetraphosphatase (Tb927.8.8040) partial mRNA gi|71850566|ref|XM_819960.1|

		Expect = 3.7 Identities = 23/24 (95%)	Human DNA sequence from clone RP11-153P4 on chromosome 9 Contains the 3' end of the VAV2 gene for vav 2 oncogene, the 5' end of the SARDH gene for sarcosine dehydrogenase (SAR, SDH,SARD, DMGDHL1) and a CpG island, complete sequence gi|17065766|emb|AL606970.12|
SSH1-15 f01	105	Expect = 4.9 Identities = 22/23 (95%)	Anolis distichus REG648 NADH dehydrogense subunit I (ND1) gene,partial cds; tRNA-Ile, tRNA-Glx, and tRNA-Met genes, complete sequence; NADH dehydrogenase subunit II (ND2) gene, complete cds; tRNA-Trp, tRNA-Ala, tRNA-Asx, tRNA-Cys, and tRNA-Tyr genes, complete sequence; and cytochrome oxidase subunit I (CO1) gene, partial cds; mitochondrial genes for mitochondrial products gi|33113529|gb|AY263004.1|
SSH1-15 g01	126	Expect = 0.10 Identities = 25/26 (96%)	H.sapiens DNA for enhancer elements gi|577565|emb|Z46773.1|HSMYCENH2
		Expect = 6.2 Identities = 29/31 (93%)	Diachasmimorpha sp. RMNH-Jo804 cytochrome oxidase subunit I (COI)gene, partial cds; mitochondrial gi|62465282|gb|AY935349.1|
SSH1-15 g05	123	Expect = 1.5 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-181K3 on chromosome 1 Contains the 3' end of the LAMC1 for laminin, gamma 1 (formerly LAMB2) the LAMC2 gene for laminin, gamma 2 and the 3' end of the NMNAT2 gene for nicotinamide nucleotide adenylyltransferase 2, complete sequence gi|16973821|emb|AL354953.16|
SSH1-16 a01	420	Expect = 1.5 Identities = 21/21 (100%)	Mus musculus olfactory receptor 1230, mRNA (cDNA clone MGC:123494 IMAGE:40040284), complete cds gi|80474696|gb|BC108938.1|
		Expect = 5.9 Identities = 26/28 (92%)	Sphingomonas sp. HL4 PAH ring-hydroxylating dioxygenase alpha subunit gene, partial cds gi|77543316|gb|DQ192650.1|
SSH1-16 a04	317	Expect = 4.4 Identities = 20/20 (100%)	Cystophora cristata NADH dehydrogenase subunit 5 (ND5) gene, complete cds; mitochondrial gene for mitochondrial product gi|37620689|gb|AY377375.1|
SSH1-16 a10	834	Expect = 0.0 Identities = 558/596 (93%),	Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II gi|21843|emb|X57408.1|TAPSB0
SSH1-16 c12	555	Expect = 0.002 Identities = 26/26 (100%)	EST from a gravity versus microgravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103472690|emb|CT979074.1|
		Expect = 0.008 Identities = 28/29 (96%)	Nicotiana tabacum serine/threonine kinase mRNA, partial cds gi|90654202|gb|DQ459385.1|
SSH1-16 d06	310	Expect = 4.3 Identities = 23/24 (95%)	Mus musculus Phgdh gene for 3-phosphoglycerate dehydrogenase,complete cds gi|41529269|dbj|AB128936.1|
SSH1-16 f06	142	Expect = 7.1 Identities = 19/19 (100%)	PREDICTED: Canis familiaris similar to TPR domain, ankyrin-repeat and coiled-coil-containing (LOC478760), mRNA gi|74004633|ref|XM_535925.2|
		Expect = 7.1 Identities = 25/27 (92%)	Bambusa oldhamii sucrose-phosphate synthase mRNA, complete cds gi|38305299|gb|AY445835.1|
SSH1-16 g12	540	Expect = 1e-069 Identities = 281/325 (86%),	Oryza sativa (japonica cultivar-group) Os02g0817900 (Os02g0817900) mRNA, complete cds gi|115449680|ref|NM_001055061.1|
		Expect = 4e-014 Identities = 98/116 (84%)	Arabidopsis thaliana heme binding / iron ion binding / monooxygenase/ oxygen binding (AT1G31800) mRNA, complete cds gi|30692603|ref|NM_102914.2|
SSH1-16 h03	260	Expect = 3.6 Identities = 20/20 (100%)	Leishmania major aromatic amino acid hydroxylase-like (AAAHL) gene, complete cds gi|33304619|gb|AY273788.1|

Metabolism and Energy

Contigs

CONTIG 3	(3 clones)		
SSH1-10 e05	593	Expect = 4e-039 Identities = 128/142 (90%)	Sorghum propinquum putative aconitate hydratase 1 gene, exons 16, 17 and partial cds gi|94961050|gb|DQ463100.1|
		Expect = e-113 Identities = 417/482 (86%)	Oryza sativa (japonica cultivar-group) Os03g0136900 (Os03g0136900) mRNA, complete cds gi|115450594|ref|NM_001055433.1|
SSH1-10 f09 In SSH1-10 e05	429	Expect = 2e-074 Identities = 241/273 (88%)	Oryza sativa (japonica cultivar-group) Os03g0136900 (Os03g0136900)mRNA, complete cds gi|115450594|ref|NM_001055433.1|
		Expect = 2e-039 Identities = 125/138 (90%)	Sorghum propinquum putative aconitate hydratase 1 gene, exons 16,17 and partial cds gi|94961050|gb|DQ463100.1|
SSH1-5 e06 In SSH1-10 e05	640	Expect = e-149 Identities = 514/590 (87%)	Oryza sativa (japonica cultivar-group) Os03g0136900 (Os03g0136900) mRNA, complete cds gi|115450594|ref|NM_001055433.1|
		Expect = 2e-041 Identities = 129/142 (90%)	Sorghum propinquum putative aconitate hydratase 1 gene, exons 16,17 and partial cds gi|94961050|gb|DQ463100.1|
CONTIG 4	(5 clones)		
SSH1-10 h10	363	Expect = e-118 Identities = 295/318 (92%)	Triticum aestivum vacuolar proton-inorganic pyrophosphatase mRNA,complete cds gi|31580800|gb|AY296911.1|
SSH1-11 h04	838	Expect = 0.0 Identities = 432/445 (97%)	Cloning vector pGEM-WIZ, complete sequence gi|114846943|gb|DQ917671.1|
SSH1-9 a08 In SSH1-11 h04	371	Expect = 7e-058 Identities = 232/273 (84%)	Hordeum vulgare mRNA for vacuolar membrane proton-translocating inorganic pyrophosphatase, complete cds gi|6012171|dbj|D13472.2|BLYINOPP
SSH1-2 a09 In SSH1-11 h04	559	Expect = e-115 Identities = 292/317 (92%)	Hordeum brevisubulatum vacuolar proton-inorganic pyrophosphatase(AVP1) mRNA, complete cds gi|30027156|gb|AY255181.1|
SSH1-4 d03 In SSH1-11 h04	359	Expect = e-159 Identities = 320/331 (96%)	Hordeum brevisubulatum vacuolar proton-inorganic pyrophosphatase (AVP1) mRNA, complete cds gi|30027156|gb|AY255181.1|
CONTIG 6	(4 clones)		
SSH1-11 c07	620	Expect = 2e-028 Identities = 152/180 (84%)	Arabidopsis thaliana mRNA for putative chloroplast FtsH protease,clone: RAFL08-16-K08 gi|110742013|dbj|AK226853.1|
		Expect = 2e-028 Identities = 152/180 (84%)	Arabidopsis thaliana FTSH1; ATP-dependent peptidase/ ATPase/ metallopeptidase (FTSH1) mRNA, complete cds gi|42562642|ref|NM_103909.3|
SSH1-2 c01 In SSH1-11 c07	691	Expect = 2e-028 Identities = 152/180 (84%)	Arabidopsis thaliana putative chloroplast FtsH protease (At1g50250) mRNA, complete cds gi|21689846|gb|AY123034.1|
		Expect = 6e-026 Identities = 148/176 (84%)	Arabidopsis thaliana VAR1 (VARIEGATED 1); ATP-dependent peptidase/ ATPase/ metallopeptidase (VAR1) mRNA, complete cds gi|30694023|ref|NM_123592.2|

SSH1-14 e01	803	Expect = 0.0 Identities = 552/556 (99%)	Triticum aestivum clone wl1n.pk0059.g7:fis, full insert mRNA sequence gi|32128699|gb|BT009148.1|
		Expect = 5e-045 Identities = 149/160 (93%)	Photobacterium damselae subsp. piscicida partial coi genes for putative cytochrome C oxidase proteins, clone pRDA19 gi|57635372|emb|AJ749800.1|
SSH1-14 g01 In SSH1-14 e01	707	Expect = 0.0 Identities = 527/548 (96%)	Triticum aestivum clone wl1n.pk0059.g7:fis, full insert mRNA sequence gi|32128699|gb|BT009148.1|
		Expect = 5e-017 Identities = 142/173 (82%)	Arabidopsis thaliana FTSH1; ATP-dependent peptidase/ ATPase/metallopeptidase (FTSH1) mRNA, complete cds gi|42562642|ref|NM_103909.3|
CONTIG 8	(2 clones)		
SSH1-11 h09	692	Expect = 0.0 Identities = 626/653 (95%)	Triticum aestivum zeaxanthin epoxidase (WZE) mRNA, partial cds gi|69054056|gb|AF384103.2|
SSH1-3 g08 In SSH1-11 h09	393	Expect = e-155 Identities = 315/325 (96%)	Triticum aestivum zeaxanthin epoxidase (WZE) mRNA, partial cds gi|69054056|gb|AF384103.2|
CONTIG 9	(4 clones)		
SSH1-14 a04	511	Expect = 0.0 Identities = 473/485 (97%)	Triticum aestivum RNA for phosphoribulokinase gi|21840|emb|X51608.1|TAPRKGEN
SSH1-2 f07 In SSH1-14 a04	513	Expect = 6e-053 Identities = 149/161 (92%)	Triticum aestivum RNA for phosphoribulokinase gi|21840|emb|X51608.1|TAPRKGEN
		Expect = 3e-030 Identities = 77/79 (97%)	T.aestivum PRK gene for ribulose-5-phosphate kinase gi|21838|emb|X57952.1|TAPRK
SSH1-3 h08 In SSH1-14 a04	432	Expect = 0.0 Identities = 400/410 (97%)	Triticum aestivum RNA for phosphoribulokinase gi|21840|emb|X51608.1|TAPRKGEN
SSH1-11 e04	797	Expect = 0.0 Identities = 693/712 (97%)	Triticum aestivum RNA for phosphoribulokinase gi|21840|emb|X51608.1|TAPRKGEN
CONTIG 11	(4 clones)		
SSH1-16 b12	370	Expect = 6e-080 Identities = 202/218 (92%)	Triticum aestivum Na+/H+ antiporter (NHX2) mRNA, complete cds gi|28575020|gb|AY040246.2|
SSH1-1 a09 In SSH1-16 b12	364	Expect = 7e-098 Identities = 208/216 (96%)	Triticum aestivum Na+/H+ antiporter (NHX2) mRNA, complete cds gi|28575020|gb|AY040246.2|
SSH1-13 c09	363	Expect = 4e-010 Identities = 115/141 (81%)	Triticum aestivum Na+/H+ antiporter (NHX2) mRNA, complete cds gi|28575020|gb|AY040246.2|
SSH1-13 b07	391	Expect = 5.5 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-19G1 on chromosome 9 Contains part of a variant of the PTPRD gene for protein tyrosine phosphatase, receptor type, D (HPTP, PTPD, HPTPD),complete sequence gi|14270148|emb|AL390723.21|
CONTIG 17	(2 clones)		
SSH1-3 g05	313	Expect = 1.1 Identities = 21/21 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 4 gi|58530790|dbj|AP008210.1|
SSH1-4 a02 In SSH1-3 g05	275	Expect = 2e-026 Identities = 85/92 (92%)	Zea mays clone Contig96 mRNA sequence gi|54651044|gb|BT016263.1|
		Expect = 3e-007 Identities = 53/60 (88%)	Musa acuminata nitrilase associated protein-like mRNA, partial cds gi|94982650|gb|DQ493958.1|
		Expect = 6e-005 Identities = 28/28 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483934|emb|CT989287.1|
CONTIG 23	(2 clones)		
SSH1-5 a07	442	Expect = e-130 Identities = 251/255 (98%)	H.vulgare mRNA PsaN for photosystem I subunit N gi|19094|emb|X66428.1|HVPSANMR
SSH1-14 h08	748	Expect = e-133 Identities = 252/255 (98%)	H.vulgare mRNA PsaN for photosystem I subunit N gi|19094|emb|X66428.1|HVPSANMR
CONTIG 24	(4 clones)		
SSH1-5 e11	359	Expect = e-163 Identities = 321/330 (97%)	Triticum aestivum S-adenosylmethionine decarboxylase precursor,mRNA, complete cds gi|4325044|gb|AF117660.1|AF117660
SSH1-4 a10	439	Expect = 0.0 Identities = 384/402 (95%)	Triticum aestivum S-adenosylmethionine decarboxylase precursor, mRNA, complete cds gi|4325044|gb|AF117660.1|AF117660
SSH1-4 g05	516	Expect = e-119 Identities = 281/300 (93%)	H.chilense x T.turgidum conv. durum (Tritordeum) mRNA for S-adenosylmethionine decarboxylase gi|1403043|emb|X83881.1|HCTTSAMDC
SSH1-8 a02 In SSH1-4 g05	510	Expect = e-145 Identities = 418/468 (89%)	H.chilense x T.turgidum conv. durum (Tritordeum) mRNA for S-adenosylmethionine decarboxylase gi|1403043|emb|X83881.1|HCTTSAMDC
CONTIG 26	(9 clones)		
SSH1-6 e09	536	Expect = e-121 Identities = 266/280 (95%)	Hordeum vulgare carbonic anhydrase mRNA, complete cds gi|558498|gb|L36959.1|BLYCA
SSH1-5 g12 In SSH1-6 e09	437	Expect = e-138 Identities = 332/356 (93%)	Hordeum vulgare carbonic anhydrase mRNA, complete cds gi|558498|gb|L36959.1|BLYCA
SSH1-14 b01 In SSH1-6 e09	467	Expect = 2e-095 Identities = 309/352 (87%)	Oryza sativa chloroplast carbonic anhydrase mRNA, complete cds gi|606816|gb|U08404.1|OSU08404
SSH1-5 g05 In SSH1-14 b01	467	Expect = 8e-086 Identities = 313/360 (86%)	Hordeum vulgare carbonic anhydrase mRNA, complete cds gi|558498|gb|L36959.1|BLYCA
SSH1-15 c06 In SSH1-14 b01	326	Expect = 6e-095 Identities = 240/263 (91%)	Hordeum vulgare carbonic anhydrase mRNA, complete cds gi|558498|gb|L36959.1|BLYCA
SSH1-14 c02 In SSH1-14 b01	467	Expect = e-179 Identities = 386/408 (94%)	Hordeum vulgare carbonic anhydrase mRNA, complete cds gi|558498|gb|L36959.1|BLYCA
SSH1-14 c01 In SSH1-14 b01	467	Expect = 0.0 Identities = 390/408 (95%)	Hordeum vulgare carbonic anhydrase mRNA, complete cds gi|558498|gb|L36959.1|BLYCA
SSH1-9 d11	615	Expect = e-172 Identities = 363/381 (95%)	Hordeum vulgare carbonic anhydrase mRNA, complete cds gi|558498|gb|L36959.1|BLYCA
SSH1-9 c10 In SSH1-9 d11	594	Expect = 3e-052 Identities = 275/328 (83%	Hordeum vulgare carbonic anhydrase mRNA, complete cds gi|558498|gb|L36959.1|BLYCA
CONTIG 30	(7 clones)		
SSH1-7 h01	466	Expect = 8e-015 Identities = 90/105 (85%)	Arabidopsis thaliana LOS2; phosphopyruvate hydratase (LOS2) mRNA, complete cds gi|30686823|ref|NM_129209.2|
SSH1-7 h02	547	Expect = 3e-067 Identities = 308/365 (84%)	Cynodon dactylon pollen 2-phosphoglycerate dehydrogenase 2 precursor, mRNA, complete cdsgi|37222050|gb|AY344113.2|

SSH1-7 g01 In SSH1-7 h02	450	Expect = 2e-052 Identities = 264/316 (83%)	Cynodon dactylon pollen 2-phosphoglycerate dehydrogenase 2 precursor,mRNA, complete cds gi|37222050|gb|AY344113.2|
SSH1-7 g03 In SSH1-7 h02	400	Expect = 1e-081 Identities = 313/365 (85%)	Cynodon dactylon pollen 2-phosphoglycerate dehydrogenase 2 precursor,mRNA, complete cds gi|37222050|gb|AY344113.2|
SSH1-7 g02 In SSH1-7 h02	417	Expect = 1e-081 Identities = 313/365 (85%)	Cynodon dactylon pollen 2-phosphoglycerate dehydrogenase 2 precursor, mRNA, complete cds gi|37222050|gb|AY344113.2|
SSH1-7 f02	425	Expect = 7e-009 Identities = 86/103 (83%)	Cynodon dactylon pollen 2-phosphoglycerate dehydrogenase 2 precursor, mRNA, complete cds gi|37222050|gb|AY344113.2|
SSH1-7 h03	733	Expect = 3e-055 Identities = 303/365 (83%)	Cynodon dactylon pollen 2-phosphoglycerate dehydrogenase 2 precursor, mRNA, complete cds gi|37222050|gb|AY344113.2|
CONTIG 34	(2 clones)		
SSH1-9 f03	819	Expect = e-160 Identities = 427/465 (91%)	T.turgidum mRNA for ADP/ATP carrier gi|944841|emb|X80023.1|TTADPATP
SSH1-9 h03 In SSH1-9 f03	116	Expect = 5.6 Identities = 22/23 (95%)	PREDICTED: Pan troglodytes chitinase domain containing 1, transcript variant 8 (CHID1), mRNA gi|114635502|ref|XM_001152026.1|

Signal Transduction

Singletons

SSH1-1 a11	342	Expect = 4.8 Identities = 20/20 (100%)	Mus musculus receptor interacting protein kinase 5 (Ripk5), Mrna gi|70794791|ref|NM_172516.3|
		Expect = 4.8 Identities = 20/20 (100%)	Mus musculus dusty protein kinase mRNA, complete cds gi|45181424|gb|AY429676.1|
SSH1-1 c07	183	Expect = 0.003 Identities = 25/25 (100%)	Nicotiana tabacum serine/threonine kinase mRNA, partial cds gi|90654202|gb|DQ459385.1|
SSH1-1 e02	55	Expect = 2.1 Identities = 25/27 (92%)	PREDICTED: Rattus norvegicus low density lipoprotein-related protein 1B (deleted in tumors) (predicted) (Lrp1b_predicted), mRNA gi|109469831|ref|XM_001055209.1|
SSH1-3 h06	548	Expect = 2e-096 Identities = 314/358 (87%)	Oryza sativa (japonica cultivar-group) Os01g0205700 (Os01g0205700)mRNA, partial cds gi|115435165|ref|NM_001048876.1|
		Expect = 6e-019 Identities = 163/200 (81%)	partial cDNA sequence from a Lambda ZAP II normalized full-length cDNA library of differentiating xylem from Eucalyptus gi|103473805|emb|CT980189.1|
		Expect = 6e-010 Identities = 49/53 (92%)	Arabidopsis thaliana shaggy related protein kinase, ASK-GAMMA(At3g05840) mRNA, complete cds gi|20259997|gb|AY093347.1|
SSH1-4 a01	627	Expect = 1e-088 Identities = 178/181 (98%)	Triticum aestivum chloroplast-localized Ptr ToxA-binding protein1 TaThf1) mRNA, complete cds; nuclear gene for chloroplast product gi|38570260|gb|AY377991.1|
		Expect = 8e-059 Identities = 122/123 (99%)	Triticum aestivum chloroplast inositol phosphatase-like protein mRNA, complete cds; nuclear gene for chloroplast product gi|52548245|gb|AY736122.1|
SSH1-5 b09	642	Expect = 1e-088 Identities = 178/181 (98%)	Triticum aestivum chloroplast-localized Ptr ToxA-binding protein1(TaThf1) mRNA, complete cds; nuclear gene for chloroplast product gi|38570260|gb|AY377991.1|
		Expect = 8e-059 Identities = 122/123 (99%)	Triticum aestivum chloroplast inositol phosphatase-like protein mRNA, complete cds; nuclear gene for chloroplast product gi|52548245|gb|AY736122.1|
SSH1-6 e11	61	Expect = 0.61 Identities = 20/20 (100%)	Aspergillus nidulans FGSC A4 hypothetical protein (AN1807.2), mRNA
		Expect = 9.5 Identities = 18/18 (100%)	PREDICTED: Rattus norvegicus homeodomain interacting protein kinase 2(predicted), transcript variant 2 (Hipk2_predicted), mRNA gi|109473301|ref|XM_001066649.1|
SSH1-6 f11	428	Expect = 6.0 Identities = 20/20 (100%)	Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630058K11 product:oxysterol binding protein-like 3, full insert sequence gi|26088823|dbj|AK042104.1|
SSH1-6 g07	215	Expect = 0.047 Identities = 26/27 (96%)	Human chromosome 14 DNA sequence BAC R-247L20 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence gi|13872735|emb|AL359397.3|
		Expect = 2.9 Identities = 26/28 (92%)	PREDICTED: Macaca mulatta similar to Kelch repeat and BTB domain-containing protein 11 (Kelch domain-containing protein 7B) (KBTBD11), mRNA gi|109085506|ref|XR_011828.1|
		Expect = 2.9 Identities = 23/24 (95%)	Medicago truncatula clone mth2-57b3, complete sequence gi|75750613|gb|AC146632.23|
SSH1-6 g08	422	Expect = 1.5 Identities = 21/21 (100%)	Lactate dehydrogenase-elevating virus Plagemann strain, complete genome gi|564002|gb|U15146.1|LDU15146
		Expect = 6.0 Identities = 23/24 (95%)	PREDICTED: Macaca mulatta similar to plasminogen activator, tissue type isoform 3 precursor (LOC704475), mRNA gi|109086246|ref|XM_001095260.1|
		Expect = 6.0 Identities = 20/20 (100%)	PREDICTED: Gallus gallus similar to integrin alpha 11 subunit precursor (LOC415560), mRNA gi|85677427|dbj|AB214651.1|
		Expect = 6.0 Identities = 20/20 (100%)	Aspergillus oryzae ku80 gene for Ku80 protein, complete cds gi|85677427|dbj|AB214651.1|
SSH1-7 f12	653	Expect = 3e-009 Identities = 159/200 (79%)	Glycine max putative receptor-like protein kinase 2 mRNA, complete cds gi|51847837|gb|AY687391.1|
SSH1-9 d07	190	Expect = 0.010 Identities = 24/24 (100%)	Zebrafish DNA sequence from clone CH211-188C22 in linkage group 7 Contains a novel gene similar PLCB (phospholipase C beta),a novel gene similar to PPP1R14B (protein phosphatase 1,regulatory inhibitor subunit 14B) and part of a novel gene similar to BRMS1 (breast cancer metastasis-suppressor 1),complete sequence gi|21912723|emb|AL772136.5|
SSH1-10 c02	90	Expect = 4.1 Identities = 19/19 (100%)	Arabidopsis thaliana catalytic/ protein phosphatase type 2C(AT1G79630) mRNA, complete cds gi|30699437|ref|NM_106612.3|
SSH1-10 c09	315	Expect = 4.4 Identities = 20/20 (100%)	PREDICTED: Rattus norvegicus similar to nitric oxide synthase interacting protein (LOC365171), mRNA gi|109516300|ref|XR_009345.1|
SSH1-10 h03	61	Expect = 2.4 Identities = 19/19 (100%)	Trypanosoma cruzi strain CL Brener serine/threonine protein kinase (Tc00.1047053508153.970) partial mRNA gi|71660867|ref|XM_817047.1|
SSH1-11 a01	193	Expect = 2.6 Identities = 20/20 (100%)	Caenorhabditis elegans acetyl choline receptor alpha subunit DES-2(des-2) mRNA, complete cds gi|72000729|ref|NM_073497.2|
SSH1-13 b02	586	Expect = 8.4 Identities = 23/24 (95%)	PREDICTED: Rattus norvegicus similar to Leucine-rich repeat-containing G-protein coupled receptor 5 precursor (G-protein coupled receptor 49) (Orphan G-protein coupled receptor FEX) (LOC687868), mRNA gi|109481886|ref|XM_001078728.1|
SSH1-13 c08	278	Expect = 3.8 Identities = 20/20 (100%)	Dictyostelium discoideum AX4 G-protein-coupled receptor (GPCR)family protein (grlN) mRNA, complete cds gi|66810360|ref|XM_633812.1|

SSH1-14 f08	178	Expect = 9.2 Identities = 22/23 (95%)	Human DNA sequence from clone RP11-461N23 on chromosome 13 Contains part of a novel gene (FLJ30001), a H2A histone family, pseudogene, the GPR18 gene for G protein-coupled receptor 18, the EBI2 gene for Epstein-Barr virus induced gene 2(lymphocyte-specific G protein-coupled receptor), two novel genes and a CpG island, complete sequence gi|13234836|emb|AL160155.19|
		Expect = 2.3 Identities = 23/24 (95%)	Mus musculus BAC clone RP23-69D2 from chromosome 9, complete sequence gi|76150689|gb|AC167250.2|
SSH1-14 g05	607	Expect = 8.7 Identities = 20/20 (100%)	PREDICTED: Gallus gallus protein-tyrosine-phosphatase alpha(LOC396060), mRNA gi|50747440|ref|XM_426359.1|
SSH1-14 h03	355	Expect = 1.3 Identities = 21/21 (100%)	Gallus gallus mitogen-activated protein kinase 6 (MAPK6), mRNA gi|71895652|ref|NM_001030549.1|
SSH1-15 a09	387	Expect = 0.35 Identities = 22/22 (100%)	Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930014J05 product:serine/arginine-rich protein specific kinase 2,full insert sequence gi|26091910|dbj|AK047059.1|
SSH1-15 e02	61	Expect = 9.5 Identities = 18/18 (100%)	Stenella coeruleoalba transferrin receptor (TFRC) mRNA, partial cds gi|107098804|gb|DQ533608.1|
SSH1-15 e03	134	Expect = 6.6 Identities = 19/19 (100%)	Silurus meridionalis growth hormone receptor II (GHR2) mRNA, complete cds gi|68160557|gb|AY973231.1|
SSH1-15 e04	60	Expect = 9.3 Identities = 18/18 (100%)	Homo sapiens zinc finger protein 764, mRNA (cDNA clone MGC:13138 IMAGE:4130947), complete cds gi|33988978|gb|BC008821.2|
		Expect = 9.3 Identities = 18/18 (100%)	Human guanine nucleotide-binding protein alpha-subunit gene(G-s-alpha), exon 1 gi|183397|gb|M21139.1|HUMGNAS1
SSH1-15 e06	56	Expect = 8.4 Identities = 18/18 (100%)	Bos taurus G-protein signalling modulator 1 (AGS3-like, C. elegans)(GPSM1), mRNA, complete cds gi|110331994|gb|BT026264.1|
SSH1-15 e07	90	Expect = 1.0 Identities = 20/20 (100%)	Mus musculus Rho GTPase-activating protein, mRNA (cDNA clone IMAGE:3481952), partial cds gi|23958261|gb|BC023261.1|
SSH1-15 f05	85	Expect = 3.8 Identities = 19/19 (100%)	Dictyostelium minutum SpkA gene, partial cds; and cAMP receptor 1 and DtmA genes, complete cds gi|45360218|gb|AY518271.1|
SSH1-15 f08	189	Expect = 0.63 Identities = 21/21 (100%)	Theileria annulata strain Ankara hypothetical protein (TA19520)partial mRNA gi|84999969|ref|NW_001091929.1|
		Expect = 2.5 Identities = 20/20 (100%)	Homo sapiens RPGR gene for retinitis pigmentosa GTPase regulator, exons 1-19 gi|18073942|emb|AJ318463.1|HSA318463
SSH1-15 g06	56	Expect = 2.1 Identities = 19/19 (100%)	Gallus gallus receptor tyrosine-protein kinase erbB-2 precursor(ERBB2) mRNA, complete cds gi|87128734|gb|DQ376139.1|
SSH1-15 g07	390	Expect = 0.0 Identities = 356/362 (98%)	Triticum aestivum GTP-binding protein mRNA, complete cds gi|37548543|gb|AY135021.1|
SSH1-15 h06	543	Expect = 2e-022 Identities = 153/181 (84%)	Triticum aestivum GTP-binding protein mRNA, complete cds gi|37548543|gb|AY135021.1|
SSH1-16 d02	662	Expect = 9.5 Identities = 20/20 (100%)	PREDICTED: Pan troglodytes Ras-related protein Rab-23, transcript variant 1 (RAB23), mRNA gi|114607988|ref|XM_001158655.1|
		Expect = 9.5 Identities = 23/24 (95%)	Triticum aestivum tat binding protein mRNA, partial cds gi|32400783|gb|AF475102.1|
		Expect = 9.5 Identities = 20/20 (100%)	Rattus norvegicus gene for aldolase C, complete cds gi|4519575|dbj|AB017483.1|
SSH1-16 h01	793	Expect = 2e-004 Identities = 49/56 (87%)	Oryza sativa (japonica cultivar-group) Os01g0896500 (Os01g0896500)mRNA, complete cds gi|115441602|ref|NM_001051616.1|
		Expect = 2.9 Identities = 21/21 (100%)	Homo sapiens interleukin 1 receptor, type II (IL1R2) gene, complete cds gi|21655314|gb|AY124010.1|

Signal Transduction

Contigs

CONTIG 7	(3 clones)		
SSH1-11 e05	475	Expect = 2e-080 Identities = 300/351 (85%)	Oryza sativa (japonica cultivar-group) Os01g0674800 (Os01g0674800)mRNA, partial cds gi|115439126|ref|NM_001050378.1|
		Expect = 0.002 Identities = 26/26 (100%)	Rattus norvegicus REST/NRSF-interacting lim domain protein (Rilp) mRNA, complete cds gi|33307741|gb|AF399843.1|
SSH1-11 e09 In SSH1-11 e05	476	Expect = 2e-064 Identities = 291/344 (84%)	Oryza sativa (japonica cultivar-group) Os01g0674800 (Os01g0674800)mRNA, partial cds gi|115439126|ref|NM_001050378.1|
		Expect = 4e-004 Identities = 39/43 (90%)	Arabidopsis thaliana ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase (AT5G45840) mRNA, complete cds gi|18422598|ref|NM_123952.1|
SSH1-11 f09 In SSH1-11 e05	475	Expect = 1e-044 Identities = 146/163 (89%)	Oryza sativa (japonica cultivar-group) cDNA clone:001-023-E07, full insert sequence gi|32969187|dbj|AK059169.1|
		Expect = 0.028 Identities = 24/24 (100%)	Sesbania drummondii clone SSH-40_01_C12_T3 mRNA sequence gi|99126125|gb|DQ465793.1|
CONTIG 12	(2 clones)		
SSH1-16 c04	306	Expect = 1.1 Identities = 21/21 (100%)	Homo sapiens estrogen-related receptor gamma (ESRRG) gene, complete cds gi|41324139|gb|AY528719.1|
SSH1-16 c03	298	Expect = 1.0 Identities = 21/21 (100%)	Gadus morhua steroidogenic acute regulatory protein (StAR) precursor RNA, complete cds gi|31323271|gb|AY291435.1|
CONTIG 18	(2 clones)		
SSH1-4 b09	642	Expect = 1e-088 Identities = 178/181 (98%)	Triticum aestivum chloroplast-localized Ptr ToxA-binding protein1(TaThf1) mRNA, complete cds; nuclear gene for chloroplast product gi|38570260|gb|AY377991.1|
		Expect = 8e-059 Identities = 122/123 (99%	Triticum aestivum chloroplast inositol phosphatase-like protein mRNA, complete cds; nuclear gene for chloroplast product gi|52548245|gb|AY736122.1|
SSH1-4 a09 In SSH1-4 b09	368	Expect = 2e-086 Identities = 177/181 (97%)	Triticum aestivum chloroplast-localized Ptr ToxA-binding protein1(TaThf1) mRNA, complete cds; nuclear gene for chloroplast product gi|38570260|gb|AY377991.1|
		Expect = 7e-058 Identities = 120/121 (99%)	Triticum aestivum chloroplast inositol phosphatase-like protein mRNA, complete cds; nuclear gene for chloroplast product gi|52548245|gb|AY736122.1|

Apoptosis

Singletons

SSH1-1 c03	125	Expect = 6.1 Identities = 22/23 (95%)	Mus musculus apoptosis, caspase activation inhibitor, mRNA (cDNA clone MGC:124011 IMAGE:40045263), complete cds gi|71680756|gb|BC100725.1|
SSH1-2 a11	793	Expect = 0.74 Identities = 22/22 (100%)	PREDICTED: Rattus norvegicus similar to cell division cycle and apoptosis regulator 1 (predicted), transcript variant 2 (RGD1560358_predicted), mRNA gi|109510124|ref|XM_001058883.1|

Defence Related

Singletons

SSH1-3 c03	287	Expect = 0.25 Identities = 22/22 (100%)	PREDICTED: Pan troglodytes similar to defensin alpha 1, transcript variant 2 (LOC742808), mRNA gi|114618713|ref|XM_001146692.1|
		Expect = 0.25 Identities = 22/22 (100%)	Homo sapiens chromosome 8 clone SCb-540n10 map p22-p21, complete sequence gi|50057838|gb|AF200455.5|
SSH1-7 b06	871	Expect = 1e-048 Identities = 188/214 (87%),	Haynaldia villosa clone kong28 mRNA gi|21902322|gb|AF498268.1|
		Expect = 2e-004 Identities = 52/60 (86%)	Oryza sativa (indica cultivar-group) brown planthopper-induced resistance protein 1 (Bi1) mRNA, complete cds gi|33771377|gb|AY346466.1|
		Expect = 2e-004 Identities = 52/60 (86%)	Oryza sativa (indica cultivar-group) putative brown planthopper susceptibility protein Hd002A mRNA, complete cds gi|33771375|gb|AY346465.1|
SSH1-13 b09	314	Expect = 4.3 Identities = 20/20 (100%)	B.vulgaris Chitinase Ch1 gene gi|488730|emb|X79301.1|BVCHCH1
SSH1-13 b12	172	Expect = 8.9 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-430K10 on chromosome 13 Contains a peptidylprolyl isomerase (cyclophilin) pseudogene and a CpG island, complete sequence gi|10862753|emb|AL353734.12|
SSH1-14 a07	597	Expect = 2.2 Identities = 24/25 (96%)	Brassica napus disease resistance-like protein (RGA9) gene, partial cds gi|11761657|gb|AF209484.1|
SSH1-16 f05	295	Expect = 4.1 Identities = 20/20 (100%)	Bacillus thuringiensis serovar entomocidus cry30Aa like gene for putative mosquitocidal toxin and hypothetical protein gene, complete cds gi|37999233|dbj|AB125059.1|

Defence Related

Contigs

CONTIG 21	(5 clones)		
SSH1-4 e11	479	Expect = 3e-017 Identities = 103/121 (85%)	Oryza sativa (indica cultivar-group) putative brown planthopper susceptibility protein Hd002A mRNA, complete cds gi|33771375|gb|AY346465.1|
		Expect = 2e-015 Identities = 104/122 (85%)	Oryza sativa (indica cultivar-group) brown planthopper-induced resistance protein 1 (Bi1) mRNA, complete cds gi|33771377|gb|AY346466.1|
		Expect = 0.028 Identities = 24/24 (100%)	Photobacterium damselae subsp. piscicida trpA gene for putative transposase and partial ORF1 DNA for hypothetical protein, clone pRDA13 gi|57635359|emb|AJ749794.1|
SSH1-11 e01 In SSH1-4 e11	330	Expect = 6e-024 Identities = 188/228 (82%)	Homo sapiens, clone IMAGE:5196881, mRNA gi|20809724|gb|BC029142.1|
SSH1-1 e08	487	Expect = 2e-040 Identities = 175/204 (85%)	Oryza sativa (indica cultivar-group) putative brown planthopper susceptibility protein Hd002A mRNA, complete cds gi|33771375|gb|AY346465.1|
SSH1-9 g10	428	Expect = e-132 Identities = 343/382 (89%)	Haynaldia villosa clone kong28 mRNA gi|21902322|gb|AF498268.1|
SSH1-4 g10 In SSH1-9 g10	266	Expect = 2e-032 Identities = 164/194 (84%)	Oryza sativa (indica cultivar-group) putative brown planthopper susceptibility protein Hd002A mRNA, complete cds gi|33771375|gb|AY346465.1|

Stress Related

Contigs

		Expect = 4e-014 Identities = 65/72 (90%)	Antrodia camphorata partial mnsod gene for manganese superoxide dismutase, exons 1-3, strain B85 gi|33186703|emb|AJ496411.1|ACA496411
CONTIG 10	(2 clones)		
SSH1-10 b02	621	Expect = 7e-023 Identities = 131/153 (86%)	Zea mays PCO073953 mRNA sequence gi|21280907|gb|AY106929.1|
SSH1-14 d01	631	Expect = 0.003 Identities = 157/174 (90%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood

		Identities = 35/38 (92%)	SSH libraries gi|103481661|emb|CT988393.1|
CONTIG 14	(3 clones)		
SSH1-16 g09	626	Expect = 0.0 Identities = 559/580 (96%)	Triticum aestivum mRNA for Thiol-specific antioxidant protein, partial cds gi|1783180|dbj|AB000405.1|
SSH1-16 f09	695	Expect = 0.0 Identities = 538/581 (92%)	Secale cereale thioredoxin peroxidase (TPx1) mRNA, complete cds gi|3328220|gb|AF076920.1|AF076920
SSH1-11 b03 In SSH1-16 f09	647	Expect = 9e-071 Identities = 283/330 (85%)	Triticum aestivum mRNA for Thiol-specific antioxidant protein, partial cds gi|1783180|dbj|AB000405.1|

Protein Degradation and Ubiquitinylation

Singletons

SSH1-3 g02	301	Expect = 1.1 Identities = 21/21 (100%)	PREDICTED: Strongylocentrotus purpuratus similar to ubiquitin specific protease 9 (LOC586751), mRNA gi|115893591|ref|XR_026466.1|
		Expect = 4.2 Identities = 20/20 (100%)	Corynebacterium glutamicum ATCC 13032 DNA, complete genome gi|42602314|dbj|BA000036.3|
SSH1-12 a01	293	Expect = 0.065 Identities = 23/23 (100%)	Human DNA sequence from clone RP11-137D19 on chromosome X Contains an ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast) (UBE2D2) pseudogene, complete sequence gi|18476877|emb|AL645638.10|
SSH1-15 d05	131	Expect = 1.6 Identities = 20/20 (100%)	PREDICTED: Macaca mulatta similar to ubiquitin-binding protein homolog, transcript variant 1 (LOC700601), mRNA gi|109127913|ref|XM_001094767.1|

Protein Degradation and Ubiquitinylation

Contigs

CONTIG 2	(3 clones)		
SSH1-10 d10	678	Expect = e-127 Identities = 278/286 (97%)	Uncultured soil fungus partial 18S rRNA gene, clone F47 (S2) gi|86604434|emb|AM229059.1|
		Expect = e-116 Identities = 260/268 (97%)	Cloning vector pGEM-WIZ, complete sequence gi|114846943|gb|DQ917671.1|
SSH1-12 e06 In SSH1-10 d10	370	Expect = 4e-093 Identities = 284/317 (89%)	Triticum aestivum mRNA for triticain gamma, complete cds gi|111073718|dbj|AB267409.1|
		Expect = 2e-055 Identities = 174/193 (90%)	Barley gene for thiol protease aleurain gi|19020|emb|X05167.1|HVLEU
		Expect = 6e-046 Identities = 136/149 (91%)	Lolium multiflorum mRNA for cysteine protease (see1 gene) gi|6851029|emb|AJ249847.1|LMU249847
SSH1-10 d09 In SSH1-10 d10	394	Expect = 2e-095 Identities = 252/273 (92%)	Triticum aestivum mRNA for triticain gamma, complete cds gi|111073718|dbj|AB267409.1|
		Expect = 5e-059 Identities = 170/187 (90%)	Barley gene for thiol protease aleurain gi|19020|emb|X05167.1|HVLEU
		Expect = 2e-055 Identities = 140/149 (93%)	Lolium multiflorum mRNA for cysteine protease (see1 gene) gi|6851029|emb|AJ249847.1|LMU249847

Transcription and Translation

Singletons

SSH1-1 f11	167	Expect = 8.6 Identities = 19/19 (100%)	Branchiostoma floridae **runt protein** (runt) mRNA, complete cds gi|34335169|gb|AY146617.1|
SSH1-7 d03	277	Expect = 0.062 Identities = 23/23 (100%)	Mus musculus chromosome 1, clone RP23-366C1, complete sequence gi|60115814|gb|AC091266.8|
		Expect = 3.8 Identities = 20/20 (100%)	PREDICTED: Strongylocentrotus purpuratus translation elongation factor 1B beta subunit, transcript variant 3 (eef1Bb),mRNA gi|115960244|ref|XM_001176862.1|
SSH1-8 a03	799	Expect = 0.19 Identities = 23/23 (100%)	Paralabrax clathratus isolate NaplesReef1-15 tRNA-Pro gene and control region, partial sequence; mitochondrial gi|75991473|gb|DQ192362.1|
SSH1-10 d08	366	Expect = 0.33 Identities = 25/26 (96%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|40949809|gb|AY461597.1|
		Expect = 5.1 Identities = 20/20 (100%)	PREDICTED: Canis familiaris similar to Forkhead box protein C2(Forkhead-related protein FKHL14) (Mesenchyme fork head protein 1) (MFH-1 protein) (Transcription factor FKH-14),transcript variant 1 (LOC489671), mRNA gi|73956864|ref|XM_546791.2|
SSH1-10 f07	49	Expect = 1.7 Identities = 19/19 (100%)	Chenopodium rubrum mRNA for transcription factor (E2F gene) gi|11558191|emb|AJ278884.1|CRU278884
SSH1-11 c03	265	Expect = 0.001 Identities = 26/26 (100%)	Agaricus bisporus partial mRNA for putative stress protein (sp gene) gi|26984412|emb|AJ534349.1|ABI534349
		Expect = 0.015 Identities = 24/24 (100%)	Platanus x acerifolia partial mRNA for putative transcription factor (tf gene), clone L9B gi|110681479|emb|AM293617.1|
		Expect = 0.059 Identities = 23/23 (100%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6653_6821_etc genomic sequence gi|109390341|gb|DQ518956.1|
SSH1-11 e02	383	Expect = 1.4 Identities = 21/21 (100%)	Dictyostelium discoideum AX4 putative homeobox transcription factor (warA) mRNA, complete cds gi|66803129|ref|XM_630316.1|

SSH1-14 f10	821	Expect = 0.76 Identities = 22/22 (100%)	Trifolium pratense RNA for putative eukaryotic translation initiation factor 6, complete cds, clone: C213

Transcription and Translation

Contigs

CONTIG 5	(2 clones)		
SSH1-11 b04 In SSH1-11 b04	508	Expect = 6e-059 Identities = 304/368 (82%)	Capsicum annuum elongation factor 2 mRNA, partial sequence gi|40287590|gb|AY480021.1|
SSH1-4 c09	440	Expect = 7e-049 Identities = 252/305 (82%)	Capsicum annuum elongation factor 2 mRNA, partial sequence gi|40287590|gb|AY480021.1|

Cellular Organization

Singletons

SSH1-2 b11	749	Expect = e-140 Identities = 303/319 (94%)	Oryza sativa triose phosphate/phosphate translocator mRNA, complete Cds gi|13518112|gb|AY028422.1|
SSH1-3 h01	305	Expect = 1.1 Identities = 21/21 (100%)	Homo sapiens BAC clone RP11-319A7 from 2, complete sequence gi|10048012|gb|AC007400.4|
		Expect = 4.2 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-428P16 on chromosome 10 Contains the 5' end of the KCNMA1 gene for potassium large conductance calcium-activated channel subfamily M alpha member 1, a novel zinc finger pseudogene (KIAA1629) and two CpG islands, complete sequence gi|22449771|emb|AL731556.11|
SSH1-16 e03	312	Expect = 4.3 Identities = 23/24 (95%)	Human DNA sequence from clone RP13-42E14 on chromosome Xq13.1-13.3 Contains the 3' end of the ABCB7 gene for ATP-binding cassette sub-family B (MDR/TAP) member 7, complete sequence gi|13897100|emb|AL359545.12|

Cellular Organization

Contigs

CONTIG 22	(2 clones)		
SSH1-5 a05	522	Expect = 2e-046 Identities = 170/194 (87%)	Zea mays hexose transporter (pGlcT) mRNA, partial cds; nuclear gene for chloroplast product gi|8347247|gb|AF215854.1|AF215854
SSH1-10 a08	435	Expect = 4e-041 Identities = 167/193 (86%)	Zea mays hexose transporter (pGlcT) mRNA, partial cds; nuclear gene for chloroplast product gi|8347247|gb|AF215854.1|AF215854

Other

Singletons

SSH1-1 e12	170	Expect = 0.56 Identities = 21/21 (100%)	PREDICTED: Danio rerio **similar to Zinc finger protein** 184 (Kruppel-like) (LOC569436), mRNA gi|68398836|ref|XM_692820.1|
SSH1-2 d10	482	Expect = 1.7 Identities = 21/21 (100%)	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds gi|2088550|gb|U91328.1|HSU91328
		Expect = 1.7 Identities = 24/25 (96%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 9 gi|58531196|dbj|AP008215.1|
SSH1-3 g12	125	Expect = 0.39 Identities = 21/21 (100%)	Drosophila melanogaster strain 2CPA 129 attacin A gene, 5' flanking region gi|16555210|gb|AY056902.1|
		Expect = 1.5 Identities = 23/24 (95%)	PREDICTED: Rattus norvegicus zinc finger protein 46 (predicted)(Zfp46_predicted), mRNA gi|109475673|ref|XM_233568.4|
SSH1-3 h10	197	Expect = 2.6 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-330O11 on chromosome 10 Contains the 3' end of the gene for a novel protein (LOC220929)(FLJ32761), a DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDH10) pseudogene and a CpG island,complete sequence gi|22204156|emb|AL359532.26|
		Expect = 2.6 Identities = 20/20 (100%)	Leishmania major HEXBP DNA binding protein (HEXBP) gene, complete cds gi|159341|gb|M94390.1|LEIHEXBP

SSH1-4 e07	258	Expect = 1e-046 Identities = 101/102 (99%)	Triticum aestivum cultivar Soissons thioredoxin H mRNA, complete cds gi|46200294|gb|AF286593.2|
SSH1-4 h01	45	Expect = 5.8 Identities = 18/18 (100%)	Psilotum nudum class III homeodomain-leucine zipper protein C3HDZ3(C3HDZ3) mRNA, partial cds gi|89514858|gb|DQ385523.1|
SSH1-4 h02	22	Expect = 3.7 Identities = 17/17 (100%)	Mouse DNA sequence from clone RP23-10M12 on chromosome 11 Contains a novel gene (MOR280-1) similar to the olfactory receptor family, a novel gene (D330012D11Rik), the Zfp62 gene for zinc finger protein 62, the Mgat1 gene for mannoside acetylglucosaminyltransferase 1, a novel gene (MOR256-24) similar to the olfactory receptor family, a novel gene (MOR256-25) similar to the olfactory receptor family, a novel gene (LOC216715) similar to the olfactory receptor MOR256 family, a novel gene (MOR256-27) similar to the olfactory receptor family, a novel gene (MOR256-2) similar to the olfactory receptor family and three CpG islands, complete sequence gi|20068543|emb|AL606829.13|
SSH1-5 b07	568	Expect = 0.008 Identities = 34/37 (91%)	Triticum aestivum partial mRNA for Putative **NBS-LRR** protein gi|40641570|emb|AJ606014.1|
SSH1-5 d10	561	Expect = 0.13 Identities = 23/23 (100%)	Simian foamy virus proviral partial pol gene for integrase, strain SFVora, isolate Popp_De gi|60302535|emb|BX537261.7|
SSH1-5 f10	362	Expect = 5.1 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-669M2 on chromosome 1 Contains the 3' end of a novel gene and apolipoprotein L 3 (APOL3)pseudogene, complete sequence gi|30523816|emb|AL929288.4|
SSH1-5 h02	156	Expect = 0.13 Identities = 22/22 (100%)	Human DNA sequence from clone RP4-608E8 on chromosome 6p22.1-22.3 Contains the 5' end of the DTNBP1 gene for dystobrevin binding protein 1 and a CpG island, complete sequence gi|6523647|emb|AL022343.6|HS608E8
SSH1-6 f08	195	Expect = 3e-012 Identities = 70/80 (87%)	Oryza sativa (japonica cultivar-group) Os02g0197600 (Os02g0197600) mRNA, complete cds gi|115444840|ref|NM_001052735.1|
		Expect = 0.66 Identities = 21/21 (100%)	PREDICTED: Pan troglodytes cleavage and polyadenylation specific factor 4, 30kDa, transcript variant 3 (CPSF4), mRNA gi|114675278|ref|XM_524103.2|
SSH1-6 f12	297	Expect = 0.26 Identities = 22/22 (100%)	Trypanosoma cruzi strain CL Brener hypothetical protein (Tc00.1047053511167.20) partial mRNA gi|71650153|ref|XM_808687.1|
		Expect = 4.1 Identities = 20/20 (100%)	Mouse DNA sequence from clone RP23-248G11 on chromosome 11 Contains a heterogeneous nuclear ribonucleoprotein pseudogene and a CpG island, complete sequence gi|20069468|emb|AL663065.9|
SSH1-7 b10	420	Expect = 3e-060 Identities = 181/201 (90%)	Triticum aestivum lipid transfer protein 3 (LTP3) mRNA, complete cds gi|30385243|gb|AY226580.1|
SSH1-7 c10	739	Expect = 8e-050 Identities = 161/180 (89%)	Triticum aestivum ltp9.4b gene for type 1 non specific lipid transfer protein precursor, exons 1-2 gi|84617192|emb|AJ852541.1|
		Expect = 5e-020 Identities = 82/90 (91%),	Elymus sibiricus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) mRNA, complete cds; chloroplast gi|54401455|gb|AY772669.1|
SSH1-8 e03	783	Expect = 5e-045 Identities = 194/224 (86%),	T.turgidum mRNA for ADP/ATP carrier gi|944841|emb|X80023.1|TTADPATP
SSH1-8 h01	464	Expect = 0.0 Identities = 378/382 (98%)	Triticum aestivum leucine-rich repeat protein mRNA, complete cds gi|52548247|gb|AY736123.1|
SSH1-8 h03	359	Expect = 1.3 Identities = 30/33 (90%)	Influenza A virus (A/swine/Korea/S109/2004(H9N2)) PA gene, complete cds gi|55925937|gb|AY790325.1|
SSH1-9 e12	66	Expect = 0.044 Identities = 22/22 (100%)	Sarcophyton glaucum large subunit ribosomal RNA gene, partialsequence; NADH dehydrogenase subunits 2 (ND2), 5 (ND5),nd 4 (ND4) genes, complete cds; tRNA-Met gene, complete sequence; cytochrome oxidase subunit III (COIII), ATPsynthetase subunit 6 (ATPase 6), ATP synthetase subunit 8 (ATPase 8)cytochrome oxidase subunit II (COII), and cytochrome oxidase subunit I (COI) genes, complete cds; small subunit ribosomal RNA gene, complete sequence; and NADH dehydrogenase subunit 1 (ND1) gene, partial cds,mitochondrial genes for mitochondrial products gi|4091912|gb|AF064823.1|AF064823
SSH1-9 f10	776	Expect = 0.18 Identities = 23/23 (100%)	TPA_exp: Homo sapiens neuregulin 1 isoform (NRG1) gene, alternatively spliced, complete cds gi|22004070|tpg|BK000383.1|
SSH1-10 b08	177	Expect = 2.3 Identities = 20/20 (100%)	Homo sapiens genomic sequence surrounding NotI site, clone NR1-CC5C gi|15870974|emb|AJ326580.1|HSA326580
		Expect = 9.2 Identities = 19/19 (100%)	Homo sapiens RNA binding motif protein 15B (RBM15B), mRNA gi|54607123|ref|NM_013286.3|
		Expect = 9.2 Identities = 19/19 (100%)	Myxococcus xanthus strain CECT 422 milk-clotting protease (cltA)and milk-clotting protease (cltB) genes, complete cds gi|108460647|gb|CP000113.1|
SSH1-10 b09	419	Expect = 7e-009 Identities = 35/35 (100%)	Uncultured Campylobacter sp. clone BES1 16S ribosomal RNA gene,partial sequence gi|75709287|gb|DQ184691.1|
		Expect = 7e-009 Identities = 35/35 (100%)	Homo sapiens clone ps1-6-T7 MHC class II antigen (HLA-DRB4) mRNA,HLA-DRB4*01030101 variant allele, complete cds gi|84796220|gb|DQ284433.1|
SSH1-10 c08	298	Expect = 0.26 Identities = 22/22 (100%)	Paramecium tetraurelia H immobilization antigen gene 5'terminus gi|10065|emb|X05696.1|PTHIAG5
SSH1-10 g01	345	Expect = 5e-006 Identities = 109/134 (81%)	Triticum aestivum translationally controlled tumor protein mRNA,complete cds gi|21070378|gb|AF508970.1|
SSH1-10 g02	349	Expect = 3e-010 Identities = 37/37 (100%)	Homo sapiens clone ps1-6-T7 MHC class II antigen (HLA-DRB4) mRNA,HLA-DRB4*01030101 variant allele, complete cds gi|84796220|gb|DQ284433.1|
SSH1-10 g08	227	Expect = 2e-017 Identities = 92/105 (87%)	PREDICTED: Gallus gallus similar to histone protein Hist2h3c1(LOC417953), mRNA gi|50728591|ref|XM_416193.1|
SSH1-11 a08	853	Expect = 0.79 Identities = 25/26 (96%)	PREDICTED: Pan troglodytes sorting nexin 19, transcript variant 6 (SNX19), mRNA gi|114641319|ref|XM_508865.2|
SSH1-11 h07	305	Expect = 1.1 Identities = 21/21 (100%)	Homo sapiens coagulation factor VIII, procoagulant component (hemophilia A) (F8) gene, complete cds gi|56385011|gb|AY769950.1|
SSH1-12 d01	341	Expect = 1.2 Identities = 21/21 (100%)	Lactococcus lactis cremoris mismatch repair protein homolog (hexB) gene, partial cds gi|2281331|gb|U82817.1|LLU82817
SSH1-12 f09	516	Expect = 0.47 Identities = 22/22 (100%)	PREDICTED: Mus musculus sorbin and SH3 domain containing 2,transcript variant 9 (Sorbs2), mRNA gi|94384930|ref|XM_989675.1|
SSH1-12 g02	354	Expect = 0.32 Identities = 22/22 (100%)	Homo sapiens mahogunin, ring finger 1, mRNA (cDNA clone MGC:51963 IMAGE:5755971), complete cds gi|29792177|gb|BC050389.1|
		Expect = 1.3 Identities = 27/29 (93%)	Murdannia sp. BH 75-650 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|37959631|gb|AY298838.1|
SSH1-12 h10	173	Expect = 8.9 Identities = 19/19 (100%)	Drosophila melanogaster SET domain binding factor CG6939-RB,transcript variant B (Sbf), mRNA gi|28573078|ref|NM_169430.2|
		Expect = 8.9 Identities = 19/19 (100%)	Erythroplusia pyropia mitochondrial cytb gene for cytochrome b,partial cds gi|47076358|dbj|AB125684.1|
SSH1-12 h12	79	Expect = 3.5 Identities = 19/19 (100%)	PREDICTED: Gallus gallus similar to PHD finger protein 7 isoform 1(LOC415934), mRNA gi|50754186|ref|XM_414278.1|
SSH1-13 a04	311	Expect = 0.28 Identities = 22/22 (100%)	Macaca mulatta Major Histocompatibility Complex BAC MMU025A04, complete sequence gi|46358453|gb|AC148667.1|
SSH1-13 b08	259	Expect = 0.90 Identities = 24/25 (96%)	Rhizopus oligosporus chs1 gene for chitin synthase, complete cds gi|218030|dbj|D10159.1|RCHCHS1

		Expect = 3.5 Identities = 20/20 (100%)	Gallus gallus zinc transporter 7 (ZnT7) mRNA, complete cds gi|56555152|gb|AY703477.1|
SSH1-13 b10	420	Expect = 0.096 Identities = 35/39 (89%)	Ictalurus punctatus isolate C6MMD03 chaperonin containing TCP1 subunit 2 beta mRNA, partial cds gi|85719954|gb|DQ353755.1|
		Expect = 1.5 Identities = 21/21 (100%)	PREDICTED: Rattus norvegicus similar to inositol hexaphosphate kinase 3 (LOC688862), mRNA gi|109509162|ref|XM_001068612.1|
		Expect = 1.5 Identities = 24/25 (96%)	Homo sapiens DNA for O6-methylguanine-DNA- methyltransferase promoter gi|34556|emb|X61657.1|HSMETDMET
		Expect = 5.9 Identities = 53/64 (82%)	Arabidopsis thaliana ATP binding / protein binding (AT5G20890)mRNA, complete cds gi|30688032|ref|NM_122097.2|
SSH1-13 d04	127	Expect = 6.2 Identities = 22/23 (95%)	PREDICTED: Rattus norvegicus similar to RPE-spondin (predicted)(RGD1559717_predicted), mRNA gi|109474542|ref|XM_216317.4|
SSH1-13 h02	355	Expect = 1.3 Identities = 21/21 (100%)	PREDICTED: Canis familiaris similar to basic leucine zipper nuclear factor 1 (LOC490354), mRNA gi|73961389|ref|XM_547475.2|
		Expect = 1.3 Identities = 21/21 (100%)	Bos taurus prosaposin, mRNA (cDNA clone MGC:128268 IMAGE:7986319),complete cds gi|88682885|gb|BC105409.1|
SSH1-14 b08	705	Expect = 2.6 Identities = 21/21 (100%)	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds gi|8650408|gb|AF217490.1|AF217491S3
SSH1-14 b09	372	Expect = 0.33 Identities = 25/26 (96%)	Cryptosporidium parvum putative telomeric DNA binding protein (TRF1) gene, complete cds gi|6691168|gb|AF220540.1|AF220540
SSH1-14 c11	323	Expect = 1.1 Identities = 24/25 (96%)	Aplysia californica reductase-related protein mRNA, complete cds gi|3043930|gb|AF042739.1|AF042739
		Expect = 1.1 Identities = 21/21 (100%)	Trichoderma reesei creA gene for DNA-binding protein, complete cds gi|940428|dbj|D63514.1|TRRCREA
		Expect = 4.5 Identities = 23/24 (95%)	Homo sapiens UDP-glucose ceramide glucosyltransferase-like 2, mRNA(cDNA clone IMAGE:40124682), complete cds gi|115529098|gb|BC125234.1|
SSH1-14 e07	280	Expect = 0.97 Identities = 21/21 (100%)	Litoria infrafrenata mRNA for frenatin 3 precursor (fre3 gene) gi|62318094|emb|AJ937524.1|
		Expect = 3.8 Identities = 20/20 (100%)	Human DNA sequence from clone RP3-364I1 on chromosome Xq23 Contains a novel gene, part of the AMMECR1 gene for Alport syndrome(mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1) (FLJ341111), the gene for a novel protein similar to guanine nucleotide binding protein (G protein) gamma 5 (GNG5) and a CpG island,complete sequence gi|4469068|emb|AL031319.5|HS364I1
SSH1-14 e11	601	Expect = 8.6 Identities = 20/20 (100%)	Homo sapiens CDC14 cell division cycle 14 homolog B (S. cerevisiae)(CDC14B) gene, complete cds gi|50234990|gb|AY675321.1|
SSH1-14 g02	146	Expect = 7.4 Identities = 22/23 (95%)	Human DNA sequence from clone RP5-1027G4 on chromosome 20 Contains part of the SLC24A3 gene for solute carrier family 24(sodium/potassium/calcium exchanger) member 3 and a novel gene, complete sequence gi|5791522|emb|AL049647.7|HSJ1027G4
SSH1-14 g06	115	Expect = 5.5 Identities = 19/19 (100%)	Homo sapiens casein kinase 1, epsilon (CSNK1E), transcript variant 2,mRNA gi|40549399|ref|NM_001894.4|
		Expect = 5.5 Identities = 19/19 (100%)	Bos taurus cyclin-dependent kinase 4, mRNA (cDNA clone MGC:133903 IMAGE:8041087), complete cds gi|81674381|gb|BC109858.1|
		Expect = 5.5 Identities = 19/19 (100%)	Mus musculus 3 beta-hydroxysteroid dehydrogenase isomerase VI(Hsd3b6) gene, promoter and exon 1 gi|15667241|gb|AY046511.1|
SSH1-14 g07	615	Expect = 8.8 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-191A15 on chromosome 6 Contains the 5' end of the CMAH gene for cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) (CSAH), an aryl hydrocarbon receptor (AHR) pseudogene and an ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast) (UBE2D3) (UBCH5C) pseudogene, complete sequence gi|14018311|emb|AL590084.9|
SSH1-14 g11	123	Expect = 0.38 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-8C21 on chromosome 9 Contains the 5'end of a novel gene (SHC3), a novel gene (HFSE-1), the CSK2 gene for CDC28 protein kinase regulatory subunit 2(CKSHS2), the 5' end of the gene for SECIS binding protein 2 (SBP2) and three CpG islands, complete sequence gi|13872562|emb|AL160054.14|
SSH1-15 b05	178	Expect = 9.2 Identities = 19/19 (100%)	PREDICTED: Canis familiaris similar to spermatid perinuclear RNA-binding protein, transcript variant 3 (LOC482974),mRNA gi|73979762|ref|XM_852125.1|
SSH1-15 d02	58	Expect = 8.8 Identities = 18/18 (100%)	Human DNA sequence from clone RP1-24M15 on chromosome 1q24-25 Contains part of the TNR gene fortenascin R (restrictin, janusin),complete sequence gi|1944546|emb|Z94055.1|HS24M15
SSH1-15 d04	93	Expect = 1.1 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-51D15 on chromosome Xq26.2-27.3 Contains part of the GPR112 gene for G protein-coupled receptor 112, complete sequence gi|11830771|emb|AL161778.19|
		Expect = 1.1 Identities = 20/20 (100%)	Cynops pyrrhogaster mRNA for alpha1 type II collagen, complete cds gi|5360531|dbj|AB022046.1|
		Expect = 4.2 Identities = 19/19 (100%)	PREDICTED: Macaca mulatta similar to DNA polymerase zeta catalytic subunit (Seizure-related protein 4) (LOC703920), mRNA gi|109131260|ref|XM_001096699.1|
SSH1-15 d05	131	Expect = 1.6 Identities = 20/20 (100%)	PREDICTED: Macaca mulatta similar to ubiquitin-binding protein homolog, transcript variant 1 (LOC700601), mRNA gi|109127913|ref|XM_001094767.1|
SSH1-15 d09	237	Expect = 0.81 Identities = 21/21 (100%)	PREDICTED: Mus musculus TatD DNase domain containing 3 (Tatdn3),mRNA gi|94364756|ref|XM_129661.9|
SSH1-15 e09	87	Expect = 3.9 Identities = 22/23 (95%)	Haemophilus influenzae ORF1 gene, partial cds; CDP diglyceride synthetase (cds), ORF3, and D15 (d15) genes, complete cds; and ORF4 (skp) gene, partial cds gi|2231182|gb|U60831.1|HIU60831
		Expect = 3.9 Identities = 19/19 (100%)	Human DNA sequence from clone RP4-608O15 on chromosome 1 Contains the 5' end of FHR5 gene for factor H-related protein 5, the HFL3 gene for H factor (complement)-like 3 protein and the 3' end of the FHR-4 gene for the complement factor H-related protein 4, complete sequence gi|16555445|emb|AL139418.9|
SSH1-15 e10	53	Expect = 1.9 Identities = 19/19 (100%)	Bacillus mojavensis isolate RO-C-2 quorum-sensing gene locus, partial sequence gi|18307868|gb|AF456134.1|
SSH1-15 f02	416	Expect = 0.024 Identities = 27/28 (96%)	Mus musculus chromosome 8, clone RP23-314K9, complete sequence gi|42475639|gb|AC113098.12|
		Expect = 5.9 Identities = 20/20 (100%)	PREDICTED: Gallus gallus similar to coproporphyrinogen oxidase;coproporphyrinogen oxidase (coproporphyria,harderoporphyria) (LOC418377), mRNA gi|50729639|ref|XM_416596.1|
SSH1-15 g02	25	Expect = 5.5 Identities = 17/17 (100%)	Oryza sativa (japonica cultivar-group) mRNA for squalene synthase,complete cds gi|2463564|dbj|AB007501.1|
SSH1-15 h03	124	Expect = 6.1 Identities = 19/19 (100%)	Mus musculus adaptor-related protein complex AP-3 beta 1 subunit(Ap3b1) gene, exons 23 and 24 gi|10802826|gb|AF255587.1|F255566S22
SSH1-16 a05	851	Expect = 0.20 Identities = 23/23 (100%)	Zea mays OCL1 gene for homeobox protein OCL1, exons 1-9 gi|67966272|emb|AJ748731.1|
		Expect = 3.1 Identities = 21/21 (100%)	PREDICTED: Apis mellifera similar to Gram-negative bacteria binding protein 1 CG6895-PA (LOC411899), mRNA gi|110759447|ref|XM_395368.3|

SSH1-16 b01	871	Expect = 0.81 Identities = 25/26 (96%)	Tetrahymena vorax telomerase RNA gene, complete sequence gi|790631|gb|U22354.1|TVU22354
		Expect = 3.2 Identities = 21/21 (100%)	Heterodera schachtii clone gCMB011 chorismate mutase gene, partial cds gi|75750697|gb|DQ176600.1|
		Expect = 3.2 Identities = 21/21 (100%)	Caenorhabditis elegans Nematode AStacin protease family member(nas-39) (nas-39) mRNA, complete cds gi|71989479|ref|NM_078271.3|
SSH1-16 b02	292	Expect = 1.0 Identities = 21/21 (100%)	Arabidopsis thaliana katanin 1 (KTN1) gene, complete cds gi|14133601|gb|AF359248.1|AF359248
		Expect = 1.0 Identities = 39/45 (86%)	Piptatherum miliaceum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds;chloroplast gi|51511894|gb|AY622898.1|
SSH1-16 c10	859	Expect = 0.051 Identities = 24/24 (100%)	Hevea brasiliensis isolate SSH41 mRNA sequence gi|83727986|gb|DQ306770.1|
		Expect = 0.051 Identities = 24/24 (100%)	Agaricus bisporus partial mRNA for putative inorganic phosphate transporter (ipt gene), clone pm8 gi|26984428|emb|AJ534357.1|ABI534357
SSH1-16 c11	330	Expect = 1.2 Identities = 24/25 (96%)	Rabbit T-cell receptor germline beta-chain gene C-region 2 (C-beta-2), complete cds gi|165717|gb|M26312.1|RABTCBCA3
SSH1-16 d01	849	Expect = 3.1 Identities = 21/21 (100%)	PREDICTED: Bos taurus similar to phosphatidylinositol-binding clathrin assembly protein isoform 1 (LOC513579), mRNA gi|76657042|ref|XM_591279.2|
SSH1-16 e07	374	Expect = 0.085 Identities = 26/27 (96%)	Human DNA sequence from clone RP4-785G19 on chromosome 20q11.1-11.23 Contains the XPOTP1 gene for exportin tRNA (nuclear export receptor for tRNAs) pseudogene 1, a UTRN (utrophin(homologous to dystrophin)) pseudogene, the ASIP gene for agouti (mouse)-signaling protein, the 3' end of AHCY gene for S-adenosylhomocysteine hydrolase and three CpG islands, complete sequence gi|6624641|emb|AL035458.35|HS785G19
SSH1-16 g07	301	Expect = 4.2 Identities = 20/20 (100%)	Apis mellifera telomerase reverse transcriptase (Tert), mRNA gi|100815791|ref|NM_001040681.1|
SSH1-16 h02	313	Expect = 4.3 Identities = 23/24 (95%)	Human DNA sequence from clone RP11-248N6 on chromosome 13 Contains two olfactory receptor pseudogenes and a nucleophosmin(nucleolar phosphoprotein B23, numatrin) NPM1 pseudogene,complete sequence gi|9944152|emb|AL353580.7|
SSH1-16 h10	381	Expect = 0.34 Identities = 25/26 (96%)	PREDICTED: Rattus norvegicus chromodomain helicase DNA binding protein 6 (predicted) (Chd6_predicted), mRNA gi|109471239|ref|XM_001068943.1|

Other

Contigs

CONTIG 13	(4 clones)		
SSH1-16 g05	305	Expect = 7e-005 Identities = 47/52 (90%)	Araucaria bidwillii ribulose biphosphate carboxylase (rbcL) gene, chloroplast gene encoding chloroplast protein, partial cds gi|3982522|gb|U96472.1|U96472
SSH1-16 g06 In SSH1-16 g05	304	Expect = 4.2 Identities = 20/20 (100%)	Pan troglodytes RBP4 gene for retinol binding protein4, complete cds gi|46401567|dbj|AB124586.1|
SSH1-16 h05	850	Expect = 3.1 Identities = 21/21 (100%)	Dictyostelium discoideum AX4 C-module-binding factor (cbfA) mRNA,complete cds gi|66815396|ref|XM_636623.1|
SSH1-16 h06 In SSH1-16 h05	317	Expect = 4.4 Identities = 20/20 (100%)	Dictyostelium discoideum AX4 replication factor C subunit (rfc5) mRNA, complete cds gi|66812243|ref|XM_635209.1|
CONTIG 16	(2 clones)		
SSH1-3 d09	397	Expect = 4e-013 Identities = 77/86 (89%)	Triticum turgidum A genome HMW glutenin A gene locus, sequence gi|40849982|gb|AY494981.1|
		Expect = 1e-010 Identities = 54/58 (93%)	Triticum aestivum pinb gene for puroindoline b protein, complete cds gi|109240245|dbj|AB262660.1|
		Expect = 6e-009 Identities = 76/87 (87%)	Aegilops tauschii transposons Caspar, XJ, Angela, and XJ, complete equence; LRR protein WM1.7 (WM1.7) and LRR protein WM1.12 (WM1.12) genes, complete cds; transposons Ophelia2,Angela3s, and XJ3, complete sequence; LRR protein WM1.3(WM1.3) gene, complete cds; Stowaway MITE, transposons XJ1, Jody, Angela, and XJ and Stowaway MITE, complete sequence; LRR protein WM1.2 (WM1.2) and LLR protein WM1.1(WM1.1) genes, complete cds; transposons XJ, XA, Angela,and Fred and WM1.11 gene, complete sequence; RPM1-like sequence and LRR protein WM1.10 (WM1.10) genes, complete cds; and transposon XJ, complete sequence gi|44888773|gb|AY534123.1|SEG_AY534122S2
SSH1-3 d10 In SSH1-3 d09	384	Expect = 9e-008 Identities = 68/77 (88%)	Triticum turgidum A genome HMW glutenin A gene locus, sequence gi|40849982|gb|AY494981.1|
		Expect = 2e-005 Identities = 57/65 (87%)	Triticum aestivum pinb gene for puroindoline b protein, complete cds gi|109240245|dbj|AB262660.1|
		Expect = 2e-005 Identities = 67/77 (87%)	Aegilops tauschii transposons Caspar, XJ, Angela, and XJ, complete equence; LRR protein WM1.7 (WM1.7) and LRR protein WM1.12 (WM1.12) genes, complete cds; transposons Ophelia2,Angela3s, and XJ3, complete sequence; LRR protein WM1.3(WM1.3) gene, complete cds; Stowaway MITE, transposons XJ1, Jody, Angela, and XJ and Stowaway MITE, complete sequence; LRR protein WM1.2 (WM1.2) and LLR protein WM1.1(WM1.1) genes, complete cds; transposons XJ, XA, Angela,and Fred and WM1.11 gene, complete sequence; RPM1-like sequence and LRR protein WM1.10 (WM1.10) genes, complete cds; and transposon XJ, complete sequence gi|44888773|gb|AY534123.1|SEG_AY534122S2
CONTIG 19	(6 clones)		
SSH1-4 c04	500	Expect = 0.0 Identities = 443/463 (95%)	Triticum aestivum **translationally controlled tumor protein** mRNA,complete cds gi|21070378|gb|AF508970.1|
SSH1-15 f09 In SSH1-4 c04	351	Expect = 3e-041 Identities = 155/177 (87%)	Triticum aestivum translationally controlled tumor protein mRNA,complete cds gi|21070378|gb|AF508970.1|
SSH1-12 a09 In SSH1-4 c04	421	Expect = 0.0 Identities = 362/373 (97%)	Triticum aestivum translationally controlled tumor protein mRNA, complete cds gi|21070378|gb|AF508970.1|
SSH1-15 h12	391	Expect = 0.0 Identities = 355/364 (97%)	Triticum aestivum translationally controlled tumor protein mRNA,complete cds gi|21070378|gb|AF508970.1|
SSH1-11 h03 In SSH1-15 h12	360	Expect = e-117 Identities = 245/257 (95%)	Triticum aestivum translationally controlled tumor protein mRNA,complete cds gi|21070378|gb|AF508970.1|
		Expect = 4e-010	partial cDNA sequence from a Lambda ZAP II normalized full-length cDNA library of

		Identities = 103/125 (82%)	differentiating xylem from Eucalyptus gunnii gi|103479622|emb|CT985810.1|
SSH1-2 g01	631	Expect = e-112 Identities = 243/257 (94%)	Triticum aestivum translationally controlled tumor protein mRNA,complete cds gi|21070378|gb|AF508970.1|
		Expect = 7e-093 Identities = 237/256 (92%)	Uncultured soil fungus partial 18S rRNA gene, clone F47 (S2) gi|86604434|emb|AM229059.1|
		Expect = 1e-091 Identities = 238/258 (92%)	Cloning vector psiLentGene Neomycin, complete sequence gi|45655412|gb|AY508733.1|
		Expect = 1e-091 Identities = 235/254 (92%)	Homo sapiens mRNA for polyglutamine binding protein variant 4(PQBP1 gene) gi|67508866|emb|AJ973596.1|
CONTIG 20	(3 clones)		
SSH1-4 d11	345	Expect = 1e-080 Identities = 245/275 (89%)	Triticum aestivum lipid transfer protein 3 (LTP3) mRNA, complete cds gi|30385243|gb|AY226580.1|
SSH1-7 b09	455	Expect = e-138 Identities = 309/328 (94%)	Triticum aestivum lipid transfer protein 3 (LTP3) mRNA, complete cds gi|30385243|gb|AY226580.1|
		Expect = 1.6 Identities = 21/21 (100%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103482172|emb|CT988582.1|
SSH1-7 b11 In SSH1-7 b09	341	Expect = e-147 Identities = 273/275 (99%)	Triticum aestivum lipid transfer protein 3 (LTP3) mRNA, complete cds gi|30385243|gb|AY226580.1|
CONTIG 27	(2 clones)		
SSH1-7 a02	296	Expect = 1e-052 Identities = 168/189 (88%)	Oryza sativa (japonica cultivar-group) Os07g0608700 (Os07g0608700)mRNA, complete cds gi|115473290|ref|NM_001066779.1|
		Expect = 3e-016 Identities = 122/147 (82%)	Arabidopsis thaliana putative small nuclear ribonucleoprotein polypeptide G (At3g11500; F24K9.17) mRNA, complete cds gi|17065483|gb|AY062818.1|
		Expect = 5e-012 Identities = 136/168 (80%)	partial cDNA sequence from a Lambda ZAP II normalized full-length cDNA library of differentiating xylem from Eucalyptus gunnii gi|103479591|emb|CT985779.1|
SSH1-8 g09	452	Expect = 3e-023 Identities = 155/183 (84%)	Oryza sativa (japonica cultivar-group) cDNA, clone: J100001P06, full insert sequence gi|116012389|dbj|AK243024.1|
CONTIG 35	(2 clones)		
SSH1-9 h08	313	Expect = 4e-022 Identities = 96/109 (88%)	Oryza sativa S-phase-specific ribosomal protein (RSPSP94) mRNA,complete cds gi|4079799|gb|AF052503.1|AF052503
		Expect = 2e-085 Identities = 163/163 (100%)	Triticum aestivum 40S ribosomal protein mRNA, partial cds gi|32400860|gb|AF479043.1|
SSH1-9 g05	308	Expect = 4e-071 Identities = 157/163 (96%)	Triticum aestivum 40S ribosomal protein mRNA, partial cds gi|32400860|gb|AF479043.1|
		Expect = 2e-017 Identities = 91/105 (86%)	Oryza sativa S-phase-specific ribosomal protein (RSPSP94) mRNA,complete cds gi|4079799|gb|AF052503.1|AF052503
CONTIG 52	(11 clones)		
REPRESENTATIVE			
SSH1-16 f08	758	Expect = 0.0 Identities = 551/578 (95%)	Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II gi|21843|emb|X57408.1|TAPSB0
SSH1-7 e05	500	Expect = 4e-023 Identities = 110/127 (86%)	Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II gi|21843|emb|X57408.1|TAPSB0
		Expect = 0.46 Identities = 40/46 (86%)	partial cDNA sequence from a Lambda ZAP II normalized full-length cDNA library of differentiating xylem from Eucalyptus gunnii gi|103480929|emb|CT987506.1|

Unknown

Singletons

SSH1-1 a01	172	Expect = 0.57 Identities = 21/21 (100%)	Mus musculus chromosome 8, clone RP23-389O4, complete sequence gi|46395428|gb|AC102050.13|
SSH1-1 a04	464	Expect = 0.42 Identities = 22/22 (100%)	Frankia alni str. ACN14A chromosome, complete sequence gi|111147037|emb|CT573213.2|
SSH1-1 a10	70	Expect = 0.012 Identities = 23/23 (100%)	Human DNA sequence from clone RP13-408A12 on chromosome 10, complete sequence gi|14547264|emb|AL392045.9|
SSH1-1 b10	39	Expect = 4.4 Identities = 18/18 (100%)	Zebrafish DNA sequence from clone DKEY-165L22 in linkage group9, complete sequence gi|115312874|emb|CR753862.32|
SSH1-1 c05	251	Expect = 3.4 Identities = 20/20 (100%)	Mus musculus chromosome 5, clone RP23-384P12, complete sequence gi|74356144|gb|AC161442.5|
SSH1-1 e01	171	Expect = 2.2 Identities = 20/20 (100%)	Mus musculus BAC clone RP23-126F14 from 14, complete sequence gi|23499677|gb|AC122858.2|
SSH1-1 e06	515	Expect = 0.12 Identities = 23/23 (100%)	Homo sapiens BAC clone RP11-150L12 from 2, complete sequence SSH1-1 e08 gi|18464273|gb|AC079344.5|
SSH1-1 e07	70	Expect = 0.74 Identities = 20/20 (100%)	Bradyrhizobium japonicum USDA 110 DNA, complete genome gi|47118316|dbj|BA000040.2|
SSH1-1 e11	308	Expect = 0.27 Identities = 22/22 (100%)	Loxodonta africana clone VMRC15-519D8, complete sequence gi|63094058|gb|AC153773.3|
		Expect = 1.1 Identities = 30/33 (90%)	Human DNA sequence from clone RP11-360J11 on chromosome 6, complete sequence gi|14272323|emb|AL451108.11|
SSH1-1 f07	454	Expect = 1.6 Identities = 27/29 (93%)	Pan troglodytes BAC clone CH251-728G7 from chromosome 7, complete sequence gi|113462216|gb|AC187606.2|
SSH1-1 f08	362	Expect = 3e-032 Identities = 146/170 (85%)	Oryza sativa (japonica cultivar-group) cDNA clone:001-101-D05, full insert sequence gi|115444902|ref|NM_001052766.1|
SSH1-1 f09	473	Expect = 1.7 Identities = 21/21 (100%)	Pig DNA sequence from clone CH242-217L7 on chromosome 17, complete sequence gi|83306421|emb|CR974477.12|
SSH1-1 f10	380	Expect = 0.34 Identities = 22/22 (100%)	Mouse DNA sequence from clone RP23-105O1 on chromosome 2, complete sequence gi|28412549|emb|AL954315.6|

SSH1-1 f12	206	Expect = 2.8 Identities = 20/20 (100%)	Salmo salar BAC S0188I22, partial sequence gi|76445911|gb|DQ156150.1|
SSH1-1 g01	178	Expect = 0.59 Identities = 21/21 (100%)	Mus musculus chromosome 7, clone RP23-218E6, complete sequence gi|69752496|gb|AC101690.7|
SSH1-1 g03	168	Expect = 0.55 Identities = 21/21 (100%)	Arabidopsis thaliana DNA chromosome 4, BAC clone T30C3 (ESSA project) gi|5123922|emb|AL079350.1|ATT30C3
SSH1-1 g04	187	Expect = 0.63 Identities = 24/25 (96%)	Canis Familiaris chromosome 5, clone XX-212F17, complete sequence gi|110835818|gb|AC186051.8|
SSH1-1 g06	245	Expect = 2e-004 Identities = 39/43 (90%)	Oryza sativa (japonica cultivar-group) Os01g0914200 (Os01g0914200)mRNA, partial cds gi|115441798|ref|NM_001051714.1|
SSH1-1 g07	241	Expect = 3e-031 Identities = 93/100 (93%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 7 gi|58531194|dbj|AP008213.1|
SSH1-1 g09	510	Expect = 0.47 Identities = 22/22 (100%)	Homo sapiens chromosome 5 clone RP11-182I21, complete sequence gi|16303417|gb|AC091903.2|
SSH1-1 g10	471	Expect = 1.7 Identities = 21/21 (100%)	Pan troglodytes BAC clone CH251-87A18 from Y, complete sequence gi|40539157|gb|AC147161.2|
SSH1-1 g11	161	Expect = 0.034 Identities = 23/23 (100%)	Opossum DNA sequence from clone XX-158F12, complete sequence gi|52694609|emb|CR387990.9|
SSH1-1 g12	214	Expect = 2.9 Identities = 26/28 (92%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6 gi|58531193|dbj|AP008212.1|
SSH1-1 h01	221	Expect = 0.19 Identities = 22/22 (100%)	Homo sapiens chromosome 3 clone RP11-169K17 map 3p, complete sequence gi|29788796|gb|AC022001.5|
SSH1-1 h05	298	Expect = 1.0 Identities = 21/21 (100%)	Plasmodium falciparum chromosome 6, complete sequence; segment 2/5 gi|46361038|emb|CR382399.1|
SSH1-1 h12	201	Expect = 0.68 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-733D4 on chromosome 10 Containspart of a novel gene, complete sequence gi|14596303|emb|AL356157.14|
SSH1-2 a02	191	Expect = 2.5 Identities = 20/20 (100%)	Homo sapiens chromosome 8, clone RP11-642D21, complete sequence gi|21629410|gb|AC103853.2|
SSH1-2 a12	460	Expect = 6.5 Identities = 20/20 (100%)	Mus musculus BAC clone RP24-399O5 from chromosome 9, complete sequence gi|77020569|gb|AC125370.4|
SSH1-2 d02	408	Expect = 0.37 Identities = 25/26 (96%)	Mus musculus BAC clone RP23-122O10 from 10, complete sequence gi|21844711|gb|AC098889.3|
SSH1-2 d03	327	Expect = 0.074 Identities = 26/27 (96%)	Homo sapiens BAC clone RP11-153O16 from 2, complete sequence gi|15145546|gb|AC019064.6|
SSH1-2 e11	461	Expect = 1.7 Identities = 21/21 (100%)	Oryza sativa (japonica cultivar-group) Os04g0667100 (Os04g0667100)mRNA, complete cds gi|115461167|ref|NM_001060719.1|
		Expect = 1.7 Identities = 24/25 (96%)	PREDICTED: Canis familiaris similar to calpain 10 isoform c, transcript variant 2 (LOC607311), mRNA gi|73994219|ref|XM_843215.1|
SSH1-2 f01	238	Expect = 0.21 Identities = 29/30 (96%)	Pseudomonas sp. YMAS3006 16S ribosomal RNA gene, partial sequence gi|93141197|gb|DQ315377.1|
		Expect = 0.82 Identities = 21/21 (100%)	Mus musculus BAC clone RP23-122C18 from 3, complete sequence gi|23683313|gb|AC099414.4|
SSH1-2 f03	223	Expect = 0.19 Identities = 28/30 (93%)	Mouse DNA sequence from clone RP23-239L12 on chromosome 12, complete sequence gi|84992945|emb|CT010497.9|
SSH1-2 h06	294	Expect = 1e-006 Identities = 40/43 (93%)	Zea mays subsp. parviglumis mitochondrion, complete genome gi|102567956|gb|DQ645539.1|
SSH1-2 h12	162	Expect = 8.3 Identities = 19/19 (100%)	C.jacchus DNA sequence from clone CH259-147B13, complete sequence gi|113207708|emb|CR925829.3|
SSH1-3 a01	171	Expect = 0.57 Identities = 21/21 (100%)	Mus musculus chromosome 6, clone RP23-186F2, complete sequence gi|40217714|gb|AC113021.10|
SSH1-3 a02	298	Expect = 6e-030 Identities = 123/140 (87%)	Oryza sativa (japonica cultivar-group) Os02g0259600 (Os02g0259600)mRNA, complete cds gi|115445398|ref|NM_001053014.1|
SSH1-3 b01	295	Expect = 0.066 Identities = 23/23 (100%)	Bos taurus BAC CH240-475A10 (Children's Hospital Oakland Research Institute Bovine BAC Library (male)) complete sequence gi|52000547|gb|AC150888.5|
SSH1-3 b07	146	Expect = 0.47 Identities = 21/21 (100%)	Mus musculus chromosome 8, clone RP23-29G4, complete sequence gi|33285122|gb|AC102527.6|
SSH1-3 b09	510	Expect = 0.47 Identities = 22/22 (100%)	Mus musculus BAC clone RP23-64O5 from 17, complete sequence gi|58332983|gb|AC154378.2|
SSH1-3 b10	43	Expect = 1.4 Identities = 19/19 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 8 gi|58531195|dbj|AP008214.1|
SSH1-3 c01	77	Expect = 0.21 Identities = 21/21 (100%)	Mus musculus chromosome 8, clone RP24-280K15, complete sequence gi|70909440|gb|AC138593.14|
SSH1-3 c06	88	Expect = 0.25 Identities = 24/25 (96%)	Mus musculus chromosome X, clones RP21-438P10, RP21-382F2, RP21-118B24, Map qA7.1, complete sequences gi|50428585|gb|AC091454.2|
SSH1-3 c07	45	Expect = 1.5 Identities = 19/19 (100%)	Mouse DNA sequence from clone RP23-292J9 on chromosome 11 Contains a reduced expression 3 (Rex3) pseudogene, complete sequence gi|25168718|emb|AL928702.7|
SSH1-3 c08	209	Expect = 0.18 Identities = 22/22 (100%)	Homo sapiens chromosome 3 clone RP11-1035L22, complete sequence gi|20340479|gb|AC093418.2|
SSH1-3 c12	51	Expect = 1.8 Identities = 19/19 (100%)	Arabidopsis thaliana BAC F4H6, chromosome IV, complete sequence gi|3309259|gb|AF074021.1|
SSH1-3 d04	137	Expect = 0.44 Identities = 21/21 (100%)	Mus musculus chromosome 1, clone RP24-150D10, complete sequence gi|51870870|gb|AC131976.6|
SSH1-3 d07	261	Expect = 0.058 Identities = 23/23 (100%)	Mus musculus BAC clone RP24-187P11 from chromosome 9, complete sequence gi|71725582|gb|AC161593.2|
SSH1-3 d08	351	Expect = 1.2 Identities = 21/21 (100%)	Oryza sativa (japonica cultivar-group) chromosome 11 clone P0036H01 gi|56550758|gb|AC148235.2|
SSH1-3 d11	313	Expect = 0.28 Identities = 22/22 (100%)	Takifugu rubripes frRHCE, frSMP1, frNPD014, and frP29 genes, complete sequence; frRUNX3 (frRUNX3) gene, complete cds; and frCLIC4, frSRRM1, frMTMR9L, frLCK, frHD, and frKCP3 genes,complete sequence gi|51944934|gb|AY739096.1|
		Expect = 1.1 Identities = 21/21 (100%)	Mus musculus BAC clone RP24-497G20 from chromosome 12, complete sequence gi|69752552|gb|AC159616.2|
SSH1-3 e04	64	Expect = 2.6 Identities = 19/19 (100%)	Mus musculus BAC clone RP24-338L20 from chromosome 16, complete sequence gi|39979573|gb|AC134837.3|
SSH1-3 e05	251	Expect = 0.22 Identities = 22/22 (100%)	Human DNA sequence from clone GS1-215N23 on chromosome 1q24.1-31.1 Contains the 3' end of the C1orf19 gene for chromosome 1 open reading frame 19, complete sequence gi|16304891|emb|AL158011.13|
		Expect = 0.22 Identities = 22/22 (100%)	Homo sapiens BAC clone RP11-303D3 from 1, complete sequence gi|8748872|gb|AC009481.4|AC009481
SSH1-3 e12	134	Expect = 6.6 Identities = 19/19 (100%)	Mus musculus BAC clone RP23-309L12 from chromosome 14, complete sequence gi|42716243|gb|AC146602.3|
SSH1-3 f01	131	Expect = 1.6 Identities = 20/20 (100%)	Mus musculus BAC clone RP23-269O24 from chromosome 10, complete sequence gi|73853590|gb|AC150314.5|
SSH1-3 f03	260	Expect = 0.015	Lycopersicon esculentum clone BAC 19, complete sequence

		Identities = 30/32 (93%)	gi|9858768|gb|AF273333.1|AF273333
SSH1-3 f04	165	Expect = 2.1 Identities = 20/20 (100%)	Pan troglodytes BAC clone CH251-352M13 from chromosome unknown gi|89994810|gb|AC182471.3|
SSH1-3 f05	306	Expect = 0.27 Identities = 22/22 (100%)	Mus musculus chromosome 5, clone RP23-58C20, complete sequence gi|71834811|gb|AC164004.3|
SSH1-3 f06	82	Expect = 3.6 Identities = 19/19 (100%)	Homo sapiens chromosome 3 clone RP11-754F19, complete sequence gi|18139446|gb|AC099559.2|
SSH1-3 g03	63	Expect = 2.5 Identities = 19/19 (100%)	Zebrafish DNA sequence from clone CH211-173O4 in linkage group 9,complete sequence gi|110224930|emb|BX936339.11|
SSH1-3 g05	313	Expect = 1.1 Identities = 21/21 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 4 gi|58530790|dbj|AP008210.1|
SSH1-3 g06	31	Expect = 0.71 Identities = 19/19 (100%)	Oryza sativa (japonica cultivar-group) cDNA, clone: J065121D09, full insert sequence gi|116014145|dbj|AK241194.1|
SSH1-3 g10	221	Expect = 0.012 Identities = 24/24 (100%)	Zebrafish DNA sequence from clone CH211-261H19 in linkage group 1,complete sequence gi|62750974|emb|BX901886.8|
SSH1-3 h03	126	Expect = 6.2 Identities = 19/19 (100%)	(TEK HIT) Xenopus tropicalis clone CH216-123D2, complete sequence gi|113199804|gb|AC147822.3|
SSH1-4 c01	191	Expect = 3e-006 Identities = 33/34 (97%)	Uncultured bacterium clone SB121 16S ribosomal RNA gene, partial sequence gi|28864937|gb|AY187463.1|
SSH1-4 d06	271	Expect = 0.24 Identities = 22/22 (100%)	Homo sapiens BAC clone RP11-454B3 from 2, complete sequence gi|18855149|gb|AC104697.2|
SSH1-4 e03	263	Expect = 0.91 Identities = 21/21 (100%)	Pan troglodytes BAC clone RP43-9D19 from 7, complete sequence gi|47903423|gb|AC145898.4|
SSH1-4 g03	70	Expect = 0.74 Identities = 20/20 (100%)	Caenorhabditis elegans F44B9.9 (F44B9.9) mRNA, complete cds gi|17553437|ref|NM_066350.1|
SSH1-4 h03	173	Expect = 2.3 Identities = 20/20 (100%)	Drosophila melanogaster chromosome 3R, complete sequence gi|55380579|gb|AE014297.2|
SSH1-4 h04	740	Expect = 0.011 Identities = 25/25 (100%)	Belgica antarctica clone Ba-U40 CG32816-like mRNA, partial cds gi|104531276|gb|DQ507301.1|
SSH1-4 h08	479	Expect = 5e-013 Identities = 118/142 (83%),	Oryza sativa (japonica cultivar-group) cDNA clone:J013110J02, full insert sequence gi|32982078|dbj|AK072055.1|
		Expect = 0.002 Identities = 26/26 (100%)	Triticum aestivum clone wlsu2.pk0001.h3:fis, full insert mRNA sequence gi|32129009|gb|BT009458.1|
SSH1-5 a03	471	Expect = 0.43 Identities = 25/26 (96%)	Zebrafish DNA sequence from clone CH211-271C18 in linkage group 7,complete sequence gi|48374137|emb|BX294178.13|
SSH1-5 a11	437	Expect = 0.10 Identities = 23/23 (100%)	Mus musculus BAC clone RP23-226I10 from 3, complete sequence gi|23499683|gb|AC111007.4|
SSH1-5 b11	638	Expect = 0.59 Identities = 22/22 (100%)	Zebrafish DNA sequence from clone CH211-132F21, complete sequence gi|50344681|emb|BX248113.22|
SSH1-5 c07	784	Expect = 0.012 Identities = 25/25 (100%)	Human DNA sequence from clone CTA-21C21 on chromosome 1p22.2-31.1 Contains STSs and GSSs, complete sequence gi|6523665|emb|AL049861.18|HSBK21C21
SSH1-5 c08	672	Expect = 0.16 Identities = 23/23 (100%)	Homo sapiens chromosome 11, clone RP11-290F24, complete sequence gi|21427860|gb|AC022762.8|
SSH1-5 c10	381	Expect = 0.087 Identities = 23/23 (100%)	Gallus gallus BAC clone CH261-103G12 from chromosome z, complete sequence gi|109689964|gb|AC187108.2|
SSH1-5 c12	85	Expect = 0.062 Identities = 22/22 (100%)	Human DNA sequence from clone RP11-301B7 on chromosome 6 Contains part of the gene for a novel protein highly similar to FLJ30899, complete sequence gi|11121072|emb|AL365508.19|
SSH1-5 d02	837	Expect = 2e-004 Identities = 64/76 (84%)	Triticum aestivum clone wl1n.pk0059.g7:fis, full insert mRNA sequence gi|32128699|gb|BT009148.1|
SSH1-5 d06	272	Expect = 3.7 Identities = 23/24 (95%)	Pan troglodytes BAC clone CH251-530L13 from chromosome 7, complete sequence gi|113700391|gb|AC187741.3|
SSH1-5 d12	391	Expect = 0.089 Identities = 41/47 (87%)	Oryza sativa (japonica cultivar-group) chromosome 3 clone OSJNBa0064E16, complete sequence gi|24211087|gb|AC105731.2|
SSH1-5 e07	126	Expect = 6.2 Identities = 19/19 (100%)	Chromohalobacter salexigens DSM 3043, complete genome gi|91795226|gb|CP000285.1|
SSH1-5 e08	411	Expect = 1.5 Identities = 21/21 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 4 gi|58530790|dbj|AP008210.1|
SSH1-5 f06	127	Expect = 0.10 Identities = 22/22 (100%)	Mus musculus 10 BAC RP24-444M16 (Roswell Park Cancer Institute(C57BL/6J Male) Mouse BAC Library) complete sequence gi|71274227|gb|AC153950.8|
SSH1-5 f08	178	Expect = 2.3 Identities = 20/20 (100%)	Mus musculus BAC clone RP24-177F21 from chromosome 12, complete sequence gi|74039309|gb|AC159631.2|
SSH1-5 f12	432	Expect = 1.5 Identities = 21/21 (100%)	Mus musculus chromosome 3, clone RP24-130I14, complete sequence gi|51854561|gb|AC113989.6|
SSH1-5 g01	51	Expect = 1.8 Identities = 19/19 (100%)	Rhodobacter sphaeroides 2.4.1 chromosome 2, complete genome gi|77389406|gb|CP000144.1|
SSH1-5 g07	629	Expect = 0.58 Identities = 25/26 (96%)	Mus musculus BAC clone RP23-169M10 from 8, complete sequence gi|21844686|gb|AC112258.4|
SSH1-5 g08	665	Expect = 2.4 Identities = 21/21 (100%)	Pan troglodytes BAC clone RP43-165H20 from 7, complete sequence gi|47131405|gb|AC147069.2|
SSH1-5 g10	735	Expect = 0.044 Identities = 24/24 (100%)	Hyphomonas neptunium ATCC 15444, complete genome gi|114737225|gb|CP000158.1|
SSH1-5 h01	794	Expect = 0.19 Identities = 23/23 (100%)	Caenorhabditis elegans cosmid F47F6, complete sequence gi|3844606|gb|U80838.1|
SSH1-6 e12	40	Expect = 1.2 Identities = 19/19 (100%)	Mus musculus BAC clone RP23-405E15 from chromosome 9, complete sequence gi|84095250|gb|AC174457.2|
SSH1-6 f02	181	Expect = 0.15 Identities = 22/22 (100%)	Mus musculus chromosome 10, clone RP23-271A21, complete sequence gi|32441357|gb|AC101709.11|
SSH1-6 f03	197	Expect = 0.17 Identities = 22/22 (100%)	Zebrafish DNA sequence from clone CH211-145G9 in linkage group 17, complete sequence gi|41060330|emb|BX548032.5|
SSH1-6 f05	272	Expect = 0.94 Identities = 24/25 (96%)	Drosophila melanogaster chromosome 3L, complete sequence gi|113194865|gb|AE014296.4|
SSH1-6 f06	130	Expect = 0.10 Identities = 22/22 (100%)	Mus musculus BAC clone RP24-409C23 from chromosome 18, complete sequence gi|24158593|gb|AC116597.3|
SSH1-6 g02	86	Expect = 3.9 Identities = 19/19 (100%)	Pan troglodytes BAC clone CH251-51M20 from chromosome unknown, complete sequence gi|63025486|gb|AC159133.2|
SSH1-6 g03	82	Expect = 3.6 Identities = 19/19 (100%)	Carboxydothermus hydrogenoformans Z-2901, complete genome gi|77994731|gb|CP000141.1|
SSH1-6 g09	220	Expect = 3.0 Identities = 20/20 (100%)	Pelodictyon luteolum DSM 273, complete genome gi|78165794|gb|CP000096.1|
		Expect = 3.0 Identities = 20/20 (100%)	PREDICTED: Bos taurus hypothetical LOC513620, transcript variant 3 (LOC513620), mRNA gi|76628617|ref|XM_591329.2|
SSH1-6 g11	268	Expect = 0.23 Identities = 22/22 (100%)	Mus musculus BAC clone RP24-155I11 from chromosome 1, complete sequence gi|23462963|gb|AC121892.3|

		Expect = 3.7 Identities = 20/20 (100%)	Equus caballus CRISP3 gene for cysteine-rich secretory protein 3 and TPX1 gene for testis specific protein 1 gi|26189923|emb|AJ459965.1|ECA459965
SSH1-6 h01	143	Expect = 7.2 Identities = 19/19 (100%)	Homo sapiens chromosome X clone RP11-185O17 map p11.4, complete sequence gi|50726746|gb|AC092268.4|
SSH1-6 h02	169	Expect = 0.56 Identities = 24/25 (96%)	Hordeum vulgare jekyll gene, exons 1-3 gi|107593775|emb|AM261729.1|
SSH1-6 h05	60	Expect = 2.4 Identities = 19/19 (100%)	Homo sapiens chromosome 17, clone RP11-655D3, complete sequence gi|26051022|gb|AC026591.15|
SSH1-6 h06	60	Expect = 2.4 Identities = 19/19 (100%)	Mouse DNA sequence from clone RP23-456K21 on chromosome 12, complete sequence gi|111185871|emb|CT025683.13|
SSH1-6 h07	246	Expect = 0.85 Identities = 21/21 (100%)	Mus musculus BAC clone RP23-73N8 from chromosome 1, complete sequence gi|47078043|gb|AC122204.3|
SSH1-6 h10	53	Expect = 1.9 Identities = 19/19 (100%)	Silicibacter sp. TM1040, complete genome gi|99036121|gb|CP000377.1|
SSH1-6 h11	110	Expect = 0.085 Identities = 22/22 (100%)	Oryza sativa (japonica cultivar-group) chromosome 11 BAC clone B1112E06, complete sequence gi|46559437|gb|AC146766.2|
SSH1-6 h12	218	Expect = 0.048 Identities = 26/27 (96%)	Mus musculus BAC clone RP23-290H17 from chromosome 7, complete sequence gi|45774267|gb|AC127306.3|
SSH1-7 a01	324	Expect = 0.29 Identities = 25/26 (96%)	Pan troglodytes BAC clone RP43-16G11 from 7, complete sequence gi|34419748|gb|AC146035.2|
SSH1-7 a03	376	Expect = 0.085 Identities = 26/27 (96%)	Homo sapiens chromosome 17, clone RP11-1148O4, complete sequence gi|19849376|gb|AC104996.4|
SSH1-7 a04	340	Expect = 0.077 Identities = 29/31 (93%)	Mus musculus BAC clone RP23-480P21 from chromosome 5, complete sequence gi|24111065|gb|AC121829.3|
SSH1-7 a11	341	Expect = 4.7 Identities = 20/20 (100%)	Drosophila melanogaster CG16904-RA (CG16904), mRNA gi|24645537|ref|NM_141700.1|
SSH1-7 c02	660	Expect = 2e-075 Identities = 214/239 (89%)	Oryza sativa (japonica cultivar-group) cDNA, clone: J090088O10, full insert sequence gi|116012316|dbj|AK242951.1|
SSH1-7 d04	140	Expect = 1.8 Identities = 20/20 (100%)	Populus trichocarpa clone Pop1-72K24, complete sequence gi|114158738|gb|AC182699.2|
SSH1-7 d06	435	Expect = 0.100 Identities = 23/23 (100%)	Homo sapiens 3 BAC RP11-280F2 (Roswell Park Cancer Institute Human BAC Library) complete sequence gi|16554309|gb|AC068776.17|
SSH1-7 e01	837	Expect = 0.78 Identities = 22/22 (100%)	Sulfolobus acidocaldarius DSM 639, complete genome gi|68566501|gb|CP000077.1|
SSH1-7 e03	561	Expect = 2.0 Identities = 21/21 (100%)	Homo sapiens cDNA FLJ40226 fis, clone TESTI2022086 gi|21757347|dbj|AK097545.1|
SSH1-7 e12	103	Expect = 0.31 Identities = 27/29 (93%)	Homo sapiens BAC clone RP11-703P11 from 7, complete sequence gi|14010935|gb|AC073137.7|
SSH1-7 f08	306	Expect = 1.1 Identities = 21/21 (100%)	Medicago truncatula clone mth2-145n10, complete sequence gi|41151876|gb|AC146721.7|
SSH1-7 f11	428	Expect = 6.0 Identities = 23/24 (95%)	Mus musculus BAC clone RP24-140P18 from chromosome 8, complete sequence gi|47825164|gb|AC122409.4|
SSH1-7 g10	377	Expect = 1.3 Identities = 21/21 (100%)	Mus musculus BAC clone RP24-320J12 from chromosome 7, complete sequence gi|38348225|gb|AC133653.4|
SSH1-7 g11	502	Expect = 1.8 Identities = 21/21 (100%)	Homo sapiens BAC clone RP11-318E19 from 4, complete sequence gi|22002306|gb|AC104796.4|
SSH1-7 g12	380	Expect = 1.3 Identities = 21/21 (100%)	Pan troglodytes BAC clone CH251-557M20 from Y, complete sequence gi|48958801|gb|AC148934.2|
SSH1-7 h04	57	Expect = 2.2 Identities = 19/19 (100%)	Mus musculus chromosome 10, clone RP24-417L12, complete sequence gi|50511609|gb|AC124614.11|
SSH1-7 h06	404	Expect = 1.4 Identities = 21/21 (100%)	Helicobacter acinonychis str. Sheeba complete genome, strain Sheeba gi|109713861|emb|AM260522.1|
SSH1-7 h11	621	Expect = e-155 Identities = 313/324 (96%)	Triticum aestivum (wali7) mRNA, 3' end, partial cds gi|451192|gb|L28008.1|WHTWALI
SSH1-8 a11	769	Expect = 2.8 Identities = 24/25 (96%)	Frankia alni str. ACN14A chromosome, complete sequence gi|111147037|emb|CT573213.2|
SSH1-8 a12	741	Expect = 2.7 Identities = 21/21 (100%)	Medicago truncatula clone mth2-18f6, complete sequence gi|48717587|gb|AC148242.14|
SSH1-8 b01	670	Expect = 6e-041 Identities = 173/201 (86%)	Oryza sativa (japonica cultivar-group) Os04g0591100 (Os04g0591100) mRNA, complete cds gi|115460221|ref|NM_001060246.1|
SSH1-8 b06	801	Expect = 0.74 Identities = 22/22 (100%)	Oncorhynchus mykiss clone B21 VHSV-induced mRNA, partial sequence gi|20270929|gb|AF483544.1|
SSH1-8 b09	766	Expect = 0.71 Identities = 22/22 (100%)	Mus musculus BAC clone RP23-460I18 from chromosome 14, complete sequence gi|77020644|gb|AC154528.2|
SSH1-8 b10	364	Expect = 5.1 Identities = 20/20 (100%)	Mus musculus BAC clone RP24-349B6 from chromosome 9, complete sequence gi|75991827|gb|AC157994.2|
SSH1-8 d05	441	Expect = 6.2 Identities = 20/20 (100%)	Streptomyces avermitilis MA-4680 genomic DNA, complete genome gi|57546753|dbj|BA000030.2|
SSH1-8 d09	455	Expect = 1.6 Identities = 21/21 (100%)	Homo sapiens chromosome 16 clone CTD-2517O22, complete sequence gi|18057084|gb|AC093514.2|
SSH1-8 e01	293	Expect = 0.017 Identities = 24/24 (100%)	Homo sapiens mRNA expressed only in placental villi, clone SMAP77 gi|3885370|dbj|AB019567.1|
SSH1-8 e02	154	Expect = 5e-004 Identities = 26/26 (100%)	Belgica antarctica clone Ba-U40 CG32816-like mRNA, partial cds gi|104531276|gb|DQ507301.1|
SSH1-8 e09	779	Expect = 2.9 Identities = 21/21 (100%)	Mus musculus chromosome 7, clone RP23-290H21, complete sequence gi|76443729|gb|AC163402.5|
SSH1-8 f02	378	Expect = 4e-004 Identities = 27/27 (100%)	Belgica antarctica clone Ba-U40 CG32816-like mRNA, partial cds gi|104531276|gb|DQ507301.1|
SSH1-8 g03	384	Expect = 2e-024 Identities = 115/133 (86%)	Oryza sativa (japonica cultivar-group) Os06g0213400 (Os06g0213400) mRNA, complete cds gi|115467057|ref|NM_001063663.1|
SSH1-9 a03	297	Expect = 0.066 Identities = 23/23 (100%)	M.spretus DNA sequence from clone XX-CH35_123K8 on chromosome 7, complete sequence gi|112702989|emb|CU074422.1|
SSH1-9 a09	75	Expect = 0.82 Identities = 20/20 (100%)	Desulfitobacterium hafniense Y51 genomic DNA, complete genome gi|89332194|dbj|AP008230.1|
SSH1-9 a10	588	Expect = e-105 Identities = 421/496 (84%)	Oryza sativa (japonica cultivar-group) Os06g0684000 (Os06g0684000) mRNA, complete cds gi|115469589|ref|NM_001064929.1|
SSH1-9 a11	33	Expect = 0.21 Identities = 20/20 (100%)	Canis familiaris MHC class I DLA-88 (dla88), mRNA gi|62339251|ref|NM_001014767.1|
SSH1-9 a12	138	Expect = 6.9 Identities = 19/19 (100%)	Streptomyces avermitilis MA-4680 genomic DNA, complete genome gi|57546753|dbj|BA000030.2|
SSH1-9 b08	385	Expect = 0.088 Identities = 23/23 (100%)	Homo sapiens chromosome 15, clone CTD-2280M1, complete sequence gi|22539146|gb|AC129907.3|

SSH1-9 b10	241	Expect = 0.83 Identities = 30/33 (90%)	Oryza sativa (japonica cultivar-group) mitochondrial DNA, complete genome gi|47118326|dbj|BA000029.3|
SSH1-9 b11	40	Expect = 4.7 Identities = 18/18 (100%)	Gallus gallus BAC clone CH261-113G6 from chromosome ul, complete sequence gi|110835863|gb|AC174985.4|
SSH1-9 c01	113	Expect = 5.4 Identities = 19/19 (100%)	Cryptococcus neoformans var. neoformans JEC21 chromosome 7, complete sequence gi|57227952|gb|AE017347.1|
SSH1-9 c12	80	Expect = 0.89 Identities = 20/20 (100%)	Mus musculus chromosome 5, clone RP23-471H10, complete sequence gi|50540834|gb|AC121500.6|
SSH1-9 d08	346	Expect = 1.2 Identities = 21/21 (100%)	Mus musculus BAC clone RP23-299A12 from chromosome X, complete sequence gi|31746707|gb|AC121595.3|
SSH1-9 e05	153	Expect = 0.032 Identities = 23/23 (100%)	Gallus gallus BAC clone TAM31-31H9 from chromosome z, complete sequence gi|116063648|gb|AC186874.3|
SSH1-9 f06	364	Expect = 0.021 Identities = 27/28 (96%)	Mus musculus chromosome 18, clone RP24-92N23, complete sequence gi|30581669|gb|AC121523.6|
		Expect = 0.33 Identities = 40/46 (86%)	Micraira subulifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gi|54303883|gb|AY632366.1|
SSH1-9 g03	60	Expect = 0.60 Identities = 20/20 (100%)	Mus musculus BAC clone RP23-419G4 from 8, complete sequence gi|51011346|gb|AC145211.3|
SSH1-9 g06	483	Expect = 0.44 Identities = 22/22 (100%)	Homo sapiens BAC clone RP11-455K24 from 7, complete sequence gi|15638857|gb|AC092441.4|
SSH1-9 g08	335	Expect = 0.30 Identities = 22/22 (100%)	Caenorhabditis elegans Fosmid H15M21, complete sequence gi|2253135|emb|Z92793.1|CEH15M21
SSH1-9 g11	806	Expect = 0.75 Identities = 28/30 (93%)	Mus musculus BAC clone RP24-385N13 from chromosome 1, complete sequence gi|46559522|gb|AC134332.2|
SSH1-9 g12	112	Expect = 0.34 Identities = 21/21 (100%)	Rhesus Macaque BAC CH250-53N5 (Children's Hospital Oakland Research Institute Rhesus macaque Adult Male BAC Library) complete sequence gi|77797856|gb|AC170424.1|
SSH1-9 h06	256	Expect = 0.014 Identities = 24/24 (100%)	Bacillus thuringiensis serovar konkukian str. 97-27, complete genome gi|49328240|gb|AE017355.1|
SSH1-9 h07	133	Expect = 0.11 Identities = 22/22 (100%)	Zebrafish DNA sequence from clone CH73-95A24 in linkage group 12,complete sequence gi|115530345|emb|CT033796.7|
SSH1-10 b01	58	Expect = 2.2 Identities = 22/23 (95%)	Mus musculus BAC clone RP24-199J23 from chromosome 19, complete sequence gi|42544099|gb|AC131756.3|
SSH1-10 b04	70	Expect = 2.9 Identities = 19/19 (100%)	Arabidopsis thaliana ATPDIL5-4; electron transporter (ATPDIL5-4)mRNA, complete cds gi|30687467|ref|NM_118842.3|
SSH1-10 b05	242	Expect = 9e-044 Identities = 117/125 (93%)	Triticum aestivum ribosomal protein S7 mRNA, complete cds gi|57471723|gb|AY846832.1|
SSH1-10 d02	178	Expect = 0.59 Identities = 21/21 (100%)	Homo sapiens BAC clone RP11-16I14 from 4, complete sequence gi|15668092|gb|AC092581.2|
SSH1-10 d04	70	Expect = 0.74 Identities = 20/20 (100%)	PREDICTED: Pan troglodytes similar to Family with sequence similarity 26, member C (LOC466194), mRNA gi|114632665|ref|XM_521596.2|
SSH1-10 d05	338	Expect = 1.2 Identities = 21/21 (100%)	PREDICTED: Mus musculus tetratricopeptide repeat domain 18,transcript variant 2 (Ttc18), mRNA gi|94397844|ref|XM_972945.1|
SSH1-10 e04	91	Expect = 0.26 Identities = 21/21 (100%)	Mus musculus chromosome 3, clone RP24-220A11, complete sequence gi|58082541|gb|AC115017.11|
SSH1-10 e06	147	Expect = 0.12 Identities = 22/22 (100%)	Caenorhabditis elegans cosmid F08F3, complete sequence gi|1458326|gb|U64847.1|
SSH1-10 e08	64	Expect = 2.6 Identities = 19/19 (100%)	Gibberella zeae PH-1 chromosome 1 hypothetical protein (FG01488.1)partial mRNA gi|46109211|ref|XM_381664.1|
SSH1-10 f01	122	Expect = 0.096 Identities = 22/22 (100%)	Aspergillus oryzae RIB40 genomic DNA, SC020 gi|83773123|dbj|AP007167.1|
SSH1-10 f02	300	Expect = 0.27 Identities = 22/22 (100%)	Zebrafish DNA sequence from clone DKEY-156H23 in linkage group 9,complete sequence gi|72060665|emb|BX005408.12|
SSH1-10 f03	696	Expect = 2.5 Identities = 21/21 (100%)	Rattus norvegicus 7 BAC CH230-33J22 (Children's Hospital Oakland Research Institute) complete sequence gi|49615130|gb|AC102999.7|
SSH1-10 f04	64	Expect = 0.66 Identities = 20/20 (100%)	Aedes aegypti ASAP ID: 35685 unknown mRNA sequence gi|42763662|gb|AY431520.1|
SSH1-10 g03	90	Expect = 1.0 Identities = 20/20 (100%)	Homo sapiens 3 BAC RP11-131O20 (Roswell Park Cancer Institute Human BAC Library) complete sequence gi|22532525|gb|AC092931.8|
SSH1-10 g04	85	Expect = 0.062 Identities = 22/22 (100%)	Mus musculus chromosome 1, clone RP23-202A19, complete sequence gi|46931440|gb|AC102127.11|
SSH1-10 g05	22	Expect = 0.93 Identities = 18/18 (100%)	Arabidopsis thaliana BAC T3F12 from chromosome IV near 24 cM, complete sequence gi|2443899|gb|AC002983.1|
SSH1-10 h01	127	Expect = 0.026 Identities = 23/23 (100%)	Mus musculus chromosome 16, clone RP23-345L20, complete sequence gi|32813514|gb|AC109213.6|
SSH1-10 h04	68	Expect = 0.18 Identities = 21/21 (100%)	PREDICTED: Strongylocentrotus purpuratus similar to KIAA0261(LOC588586), mRNA gi|115977076|ref|XM_001195836.1|
SSH1-10 h05	188	Expect = 2.5 Identities = 20/20 (100%)	Pseudomonas fluorescens PfO-1, complete genome gi|77380231|gb|CP000094.1|
SSH1-10 h06	25	Expect = 1.4 Identities = 18/18 (100%)	Silicibacter pomeroyi DSS-3, complete genome gi|56676665|gb|CP000031.1|
SSH1-10 h12	226	Expect = 0.003 Identities = 25/25 (100%)	Homo sapiens mRNA differentially expressed in malignant melanoma,clone NN f4 gi|27526548|emb|AJ293411.1|HSA293411
SSH1-11 a03	683	Expect = 8e-016 Identities = 77/87 (88%)	Lolium perenne light-induced protein 1-like (LIR1) mRNA, complete cds gi|77023865|gb|DQ206624.1|
		Expect = 0.003 Identities = 26/26 (100%)	Zea mays clone Zmcoi6.18 cold-inducible unknown mRNA gi|71067860|gb|DQ078775.1|
SSH1-11 g01	371	Expect = 0.005 Identities = 25/25 (100%)	Zebrafish DNA sequence from clone DKEY-221N16 in linkage group 18,complete sequence gi|82653559|emb|CR385047.19|
SSH1-11 h06	404	Expect = 1.4 Identities = 21/21 (100%)	Arabidopsis thaliana chromosome I BAC F14I3 genomic sequence,complete sequence gi|5391457|gb|AC007980.1|
SSH1-12 a02	175	Expect = 0.009 Identities = 27/28 (96%)	Streptomyces coelicolor A3(2) complete genome; segment 2/29 gi|24418991|emb|AL939105.1|SCO939105
SSH1-12 a03	523	Expect = 2e-018 Identities = 93/107 (86%)	Oryza sativa (japonica cultivar-group) chromosome 11 clone OSJNBa0058P12, complete sequence gi|46849659|gb|AC139170.2|
SSH1-12 b05	418	Expect = 1.5 Identities = 21/21 (100%)	Mus musculus Crn, crooked neck-like 1 (Drosophila), mRNA (cDNA clone MGC:35710 IMAGE:3495255), complete cds gi|22137399|gb|BC029187.1|
SSH1-12 b07	721	Expect = 0.67 Identities = 25/26 (96%)	EST from a gravity versus microgravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
		Expect = 0.67 Identities = 22/22 (100%)	Burkholderia mallei ATCC 23344 chromosome 1, complete sequence gi|52426793|gb|CP000010.1|

SSH1-12 c01	725	Expect = 2.6 Identities = 21/21 (100%)	Medicago truncatula clone mth2-11j1, complete sequence gi|56542330|gb|AC137995.31|
SSH1-12 c05	248	Expect = 0.86 Identities = 27/29 (93%)	Mus musculus chromosome 7, clone RP23-207N5, complete sequence gi|76362876|gb|AC158582.2|
SSH1-12 d03	384	Expect = 0.35 Identities = 25/26 (96%)	Hordeum vulgare contig 211252, complete sequence gi|31296707|gb|AF521177.1|
SSH1-12 e08	401	Expect = 9e-070 Identities = 239/273 (87%)	Oryza sativa (japonica cultivar-group) Os01g0221500 (Os01g0221500)mRNA, complete cds gi|115435347|ref|NM_001048967.1|
SSH1-12 f01	171	Expect = 2.2 Identities = 20/20 (100%)	Mus musculus BAC clone RP24-165J6 from chromosome 12, complete sequence gi|68268208|gb|AC161253.2|
SSH1-12 f02	339	Expect = 0.019 Identities = 24/24 (100%)	Zebrafish DNA sequence from clone CH211-170N20 in linkage group 6,complete sequence gi|76666366|emb|BX927362.10|
SSH1-12 f08	86	Expect = 3.9 Identities = 19/19 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 9 gi|58531196|dbj|AP008215.1|
SSH1-12 g01	349	Expect = 0.31 Identities = 22/22 (100%)	Mus musculus BAC clone RP23-140M6 from chromosome 6, complete sequence gi|46518692|gb|AC130220.3|
SSH1-12 g03	475	Expect = 0.43 Identities = 22/22 (100%)	Drosophila melanogaster chromosome 2L, complete sequence gi|113194944|gb|AE014134.5|
SSH1-12 g12	288	Expect = 0.064 Identities = 29/31 (93%)	Medicago truncatula chromosome 5 clone mth2-181g12, COMPLETE SEQUENCE gi|109627511|emb|CT963113.2|
SSH1-12 h01	588	Expect = 2.1 Identities = 21/21 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1 gi|58530787|dbj|AP008207.1|
SSH1-12 h02	341	Expect = 1.2 Identities = 24/25 (96%)	Thermoanaerobacter tengcongensis MB4, section 74 of 244 of the complete genome gi|20515794|gb|AE013047.1|
SSH1-12 h03	77	Expect = 3.4 Identities = 19/19 (100%)	Zebrafish DNA sequence from clone CH211-53P9 in linkage group 5,complete sequence gi|54888656|emb|BX629349.6|
SSH1-12 h07	673	Expect = 0.16 Identities = 23/23 (100%)	Zebrafish DNA sequence from clone DKEY-93N13 in linkage group 3,complete sequence gi|50470893|emb|BX682550.7|
SSH1-13 a02	63	Expect = 10.0 Identities = 18/18 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2 gi|58530788|dbj|AP008208.1|
SSH1-13 a06	71	Expect = 3.0 Identities = 19/19 (100%)	Corynebacterium diphtheriae gravis NCTC13129, complete genome; segment 6/8 gi|38200531|emb|BX248359.1|
SSH1-13 a08	187	Expect = 0.63 Identities = 24/25 (96%)	Mus musculus BAC clone RP24-318O6 from chromosome 9, complete sequence gi|59797224|gb|AC131777.2|
SSH1-13 a09	323	Expect = 0.29 Identities = 22/22 (100%)	S.cerevisiae chromosome XV reading frame ORF YOR301w gi|1420664|emb|Z75209.1|SCYOR301W
SSH1-13 a10	33	Expect = 3.3 Identities = 18/18 (100%)	Mus musculus chromosome 1, clone RP24-317E14, complete sequence gi|77734982|gb|AC166493.6|
SSH1-13 a11	51	Expect = 7.2 Identities = 18/18 (100%)	Bacillus halodurans C-125 DNA, complete genome gi|47118318|dbj|BA000004.3|
SSH1-13 b01	658	Expect = 2.4 Identities = 21/21 (100%)	Mus musculus BAC clone RP24-383B2 from chromosome 17, complete sequence gi|29336282|gb|AC122488.3|
SSH1-13 e01	370	Expect = 0.33 Identities = 22/22 (100%)	Mus musculus chromosome 1, clone RP23-272H13, complete sequence gi|45120352|gb|AC107837.11|
SSH1-13 e03	425	Expect = 0.097 Identities = 23/23 (100%)	Arabidopsis thaliana chromosome 1 BAC T24P22 genomic sequence,complete sequence gi|12321108|gb|AC084242.4|AC084242
SSH1-13 h03	132	Expect = 1.7 Identities = 20/20 (100%)	Mus musculus chromosome 5, clone RP23-354E8, complete sequence gi|46931416|gb|AC117663.13|
SSH1-14 a01	499	Expect = 0.45 Identities = 22/22 (100%)	Colobus guereza clone CH272-157M1, complete sequence gi|80751223|gb|AC153740.3|
SSH1-14 a03	403	Expect = 0.36 Identities = 28/30 (93%)	PREDICTED: Tribolium castaneum similar to CG9494-PA (LOC660004),mRNA gi|91090122|ref|XM_966268.1|
		Expect = 0.36 Identities = 22/22 (100%)	Human chromosome 14 DNA sequence BAC R-663F5 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence gi|14139938|emb|AL512414.2|CNS07EFC
SSH1-14 a08	645	Expect = 0.002 Identities = 26/26 (100%)	Tetraodon nigroviridis BAC sequence gi|50880313|emb|BX629360.1|CNS09SBS
SSH1-14 b03	375	Expect = 0.085 Identities = 23/23 (100%)	Mus musculus BAC clone RP23-90K8 from chromosome 19, complete sequence gi|37060010|gb|AC133099.3|
SSH1-14 b11	327	Expect = 0.019 Identities = 27/28 (96%)	Microtus arvalis haplotype CZve02 control region, partial sequence; mitochondrial gi|54288866|gb|AY708415.1|
SSH1-14 c05	571	Expect = 2.1 Identities = 24/25 (96%)	Oryza sativa (japonica cultivar-group) chromosome 5 clone OJ1045_C06, complete sequence gi|55167974|gb|AC104272.5|
		Expect = 8.2 Identities = 20/20 (100%)	TPA_exp: Mus musculus immunoglobulin heavy chain variable region locus, strain C57BL/6 gi|90704841|tpe|BN000872.1|
SSH1-14 d02	290	Expect = 1.0 Identities = 24/25 (96%)	Mus musculus chromosome 15, clone RP23-236P20, complete sequence gi|29501916|gb|AC099600.5|
SSH1-14 d03	801	Expect = 2.9 Identities = 21/21 (100%)	Homo sapiens chromosome 15, clone RP11-684B21, complete sequence gi|18693519|gb|AC040918.7|
SSH1-14 d08	846	Expect = 0.013 Identities = 46/53 (86%)	Oryza sativa (japonica cultivar-group) Os03g0136900 (Os03g0136900)mRNA, complete cds gi|115450594|ref|NM_001055433.1|
SSH1-14 d11	671	Expect = 0.040 Identities = 27/28 (96%)	Mouse DNA sequence from clone RP23-132H1 on chromosome X, complete sequence gi|21537501|emb|AL671982.4|
SSH1-14 e02	652	Expect = 0.15 Identities = 26/27 (96%)	Triticum aestivum clone wlp1c.pk007.f6:fis, full insert mRNA sequence gi|32129008|gb|BT009457.1|
SSH1-14 e05	848	Expect = 0.20 Identities = 23/23 (100%)	Human DNA sequence from clone RP3-429O6 on chromosome 6 Contains part of a novel gene and a CpG island, complete sequence gi|10443389|emb|AL158817.11|
SSH1-14 e10	317	Expect = 4.4 Identities = 20/20 (100%)	Mus musculus BAC clone RP23-395A17 from chromosome 7, complete sequence gi|38154138|gb|AC127296.4|
SSH1-14 f01	117	Expect = 5.6 Identities = 19/19 (100%)	Carassius auratus preprogalanin 1B mRNA, complete cds; alternatively spliced gi|29122966|gb|AF416925.1|
SSH1-14 f02	813	Expect = 0.048 Identities = 55/64 (85%)	Triticum aestivum clone wl1n.pk0059.g7:fis, full insert mRNA sequence gi|32128699|gb|BT009148.1|
SSH1-14 f05	811	Expect = 1e-039 Identities = 186/219 (84%)	Triticum aestivum clone wl1n.pk0059.g7:fis, full insert mRNA sequence gi|32128699|gb|BT009148.1|
SSH1-14 f11	345	Expect = 1.2 Identities = 21/21 (100%)	Homo sapiens 12 BAC RP11-474P2 (Roswell Park Cancer Institute Human BAC Library) complete sequence gi|16258903|gb|AC025031.30|
SSH1-14 g09	811	Expect = 0.19 Identities = 23/23 (100%)	Gallus gallus BAC clone CH261-85J8 from chromosome ul, complete sequence gi|88196911|gb|AC161470.3|
SSH1-14 g10	822	Expect = 0.76 Identities = 22/22 (100%)	Mus musculus BAC clone RP23-127P22 from chromosome 19, complete sequence gi|33004992|gb|AC132454.3|

SSH1-14 h02	702	Expect = 2.6 Identities = 21/21 (100%)	Human DNA sequence from clone RP5-1158H2 on chromosome Xp11.23-11.4 Contains part of gene FLJ22843, a KIAA0218 pseudogene, and a ribonucleotide reductase M2 polypeptide (RRM2)pseudogene, complete sequence gi|9581533|emb|AL133344.28|
SSH1-14 h05	498	Expect = 0.45 Identities = 22/22 (100%)	Homo sapiens PAC clone RP5-826E18 from 7p22-p21, complete sequence gi|11120929|gb|AC005282.4|AC005282
SSH1-14 h06	583	Expect = 0.034 Identities = 24/24 (100%)	Human DNA sequence from clone RP11-478P15 on chromosome 1, complete sequence gi|16508251|emb|AL589789.7|
SSH1-14 h10	304	Expect = 1.1 Identities = 21/21 (100%)	Mus musculus BAC clone RP24-232D3 from chromosome 12, complete sequence gi|78190185|gb|AC155300.2|
SSH1-14 h11	804	Expect = 0.75 Identities = 28/30 (93%)	Mouse DNA sequence from clone RP23-256J17 on chromosome X, complete sequence gi|56368511|emb|AL671118.30|
SSH1-15 a02	474	Expect = 0.11 Identities = 23/23 (100%)	Mus musculus BAC clone RP23-375H15 from 3, complete sequence gi|55734067|gb|AC131686.4|
SSH1-15 a08	309	Expect = 1.1 Identities = 21/21 (100%)	Listeria innocua Clip11262 complete genome, segment 11/12 gi|16415123|emb|AL596173.1|
SSH1-15 a10	308	Expect = 0.27 Identities = 22/22 (100%)	Mus musculus strain C57BL6/J chromosome 6 clone RP23-287D23, complete sequence gi|45736651|gb|AC084163.4|
		Expect = 1.1 Identities = 21/21 (100%)	Human DNA sequence from clone RP3-402L9 on chromosome 6q25-26.1 Contains the 3' end of the OPRM1 gene for opiate receptor,mu 1 (MOR-1) and the 3' end of the gene for phosphoinositide-binding protein PIP3-E (KIAA0403), complete sequence gi|6706887|emb|AL132774.20|HSDJ402L9
SSH1-15 a11	327	Expect = 0.29 Identities = 22/22 (100%)	Mus musculus BAC clone RP23-105B9 from chromosome 14, complete sequence gi|77020691|gb|AC164437.2|
		Expect = 0.29 Identities = 28/30 (93%)	Human DNA sequence from clone RP11-65E10 on chromosome 10 Contains part of the gene for alpha-catenin-like protein (MGC26194)(VR22), complete sequence gi|16973196|emb|AL607023.3|
SSH1-15 a12	437	Expect = 0.025 Identities = 24/24 (100%)	Pan troglodytes protamine 2 (PRM2) gene, complete cds gi|6979757|gb|AF215711.1|AF215711
		Expect = 6.2 Identities = 20/20 (100%)	Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 7(lysophosphatidic acid acyltransferase, eta), mRNA (cDNA clone IMAGE:5288401) gi|29476891|gb|BC048430.1|
SSH1-15 b02	347	Expect = 4.8 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-22B10 on chromosome X Contains the GSPT2 gene for G1 to S phase transition 2, a pseudogene similar to part of p30 (nuclear protein p30), a zinc finger protein pseudogene, the 5' end of a variant of the MAGED1 gene for melanoma antigen, family D, 1 and two CpG islands, complete sequence gi|25168760|emb|AL929101.4|
SSH1-15 b07	432	Expect = 1.5 Identities = 21/21 (100%)	Mus musculus chromosome 14, clone RP23-97N1, complete sequence gi|46849829|gb|AC091464.8|
SSH1-15 b11	145	Expect = 7.3 Identities = 19/19 (100%)	X. tropicalis BAC clone containing gene for egr, complete sequence gi|50253587|gb|AC146894.4|
SSH1-15 c02	499	Expect = 0.45 Identities = 22/22 (100%)	Zebrafish DNA sequence from clone DKEY-59H7 in linkage group 20,complete sequence gi|34850305|emb|BX511133.4|
		Expect = 7.1 Identities = 20/20 (100%)	Arabidopsis thaliana DNA, chromosome 1 centromere region, BAC clone:T24F19 gi|18148660|dbj|AB062087.1|
SSH1-15 c04	57	Expect = 8.6 Identities = 18/18 (100%)	Yarrowia lipolytica CLIB122, YALI0C21131g predicted mRNA gi|49647136|emb|CR382129.1|
SSH1-15 c05	137	Expect = 1.7 Identities = 26/28 (92%)	Drosophila melanogaster bithorax complex (BX-C), complete sequence gi|969077|gb|U31961.1|DMU31961
SSH1-15 c09	56	Expect = 8.4 Identities = 18/18 (100%)	Nitrosomonas europaea ATCC 19718, complete genome; segment 5/10 gi|30180445|emb|BX321860.1|
SSH1-15 c10	300	Expect = 4.1 Identities = 26/28 (92%)	Uncultured methanogenic archaeon RC-I complete genome gi|110619806|emb|AM114193.1|
SSH1-15 c11	345	Expect = 4.8 Identities = 20/20 (100%)	Leishmania major chromosome 35, complete sequence gi|70905590|gb|CP000081.1|
SSH1-15 d03	57	Expect = 8.6 Identities = 18/18 (100%)	Burkholderia cepacia complex phage BcepC6B, complete genome gi|47778996|gb|AY605181.1|
SSH1-15 d08	56	Expect = 0.54 Identities = 20/20 (100%)	Mus musculus BAC clone RP24-91A16 from chromosome 9, complete sequence gi|74039312|gb|AC161257.2|
SSH1-15 d10	58	Expect = 8.8 Identities = 18/18 (100%)	Nitrobacter winogradskyi Nb-255, complete genome gi|74419069|gb|CP000115.1|
SSH1-15 d11	270	Expect = 0.24 Identities = 22/22 (100%)	Xanthomonas oryzae pv. oryzae MAFF 311018 DNA, complete genome gi|84365597|dbj|AP008229.1|
SSH1-15 e08	89	Expect = 1.0 Identities = 26/28 (92%)	Mus musculus BAC clone RP23-4P1 from chromosome 5, complete sequence gi|78190353|gb|AC162528.5|
SSH1-15 e11	270	Expect = 3.7 Identities = 23/24 (95%)	Burkholderia pseudomallei strain K96243, chromosome 1, complete sequence gi|52208053|emb|BX571965.1|
SSH1-15 f07	55	Expect = 2.1 Identities = 19/19 (100%)	Oryza sativa chromosome 3 BAC OSJNBb0122C16 genomic sequence, complete sequence gi|41393267|gb|AC135228.5|
SSH1-15 g03	119	Expect = 5.8 Identities = 19/19 (100%)	Mus musculus chromosome 15, clone RP23-197P10, complete sequence gi|56744365|gb|AC129583.15|
SSH1-15 g08	133	Expect = 0.11 Identities = 22/22 (100%)	Mus musculus BAC clone RP23-428H16 from 16, complete sequence gi|51854654|gb|AC150034.2|
SSH1-15 g12	141	Expect = 7.1 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-272M24 on chromosome 13 Contains a novel pseudogene, complete sequence gi|13234845|emb|AL162373.16|
SSH1-15 h01	204	Expect = 2.7 Identities = 20/20 (100%)	Brassica rapa subsp. pekinensis clone KBrH031P22, complete sequence gi|110797287|gb|AC189607.1|
SSH1-15 h02	101	Expect = 4.7 Identities = 19/19 (100%)	Acinetobacter sp. ADP1 ben operon and cat operon, complete sequence gi|49529273|emb|CR543861.1|
SSH1-16 a03	739	Expect = 2.7 Identities = 21/21 (100%)	Human DNA sequence from clone RP3-401P4 on chromosome 6q11.2-12 Contains part of the gene for a novel EGF-like domain containing protein, complete sequence gi|6434774|emb|AL109922.9|HSDJ401P4
SSH1-16 b07	368	Expect = 0.33 Identities = 22/22 (100%)	Guillardia theta complete plastid genome gi|3602932|gb|AF041468.1|
SSH1-16 b09	880	Expect = 0.21 Identities = 23/23 (100%)	Mus musculus chromosome 19, clone RP24-555M16, complete sequence gi|55831516|gb|AC117797.9|
		Expect = 3.2 Identities = 21/21 (100%)	Human Chromosome 16 BAC clone CIT987SK-A-1000D7, complete sequence gi|2815547|gb|AC002990.1|HUAC002990
SSH1-16 c01	319	Expect = 1.1 Identities = 21/21 (100%)	PREDICTED: Pan troglodytes APG16 autophagy 16-like, transcript variant 1 (ATG16L1), mRNA gi|114583981|ref|XM_001149307.1|

		Expect = 4.4 Identities = 20/20 (100%)	Hyla versicolor voucher INHS399T clone 1 18S ribosomal RNA gene,partial sequence; internal transcribed spacer 1,complete sequence; and 5.8S ribosomal RNA gene, partial sequence gi|60267646|gb|AY831367.1|
SSH1-16 d03	310	Expect = 0.27 Identities = 25/26 (96%)	Human DNA sequence from clone CTA-211A9 on chromosome 22q12.1, complete sequence gi|3482999|emb|Z95889.1|HS211A9
SSH1-16 e01	306	Expect = 0.27 Identities = 22/22 (100%)	J-virus, complete genome gi|62546304|gb|AY900001.1|
SSH1-16 e08	882	Expect = 0.053 Identities = 24/24 (100%)	Oryza sativa (japonica cultivar-group) cDNA, clone: J065196L09, full insert sequence gi|116011070|dbj|AK241705.1|
SSH1-16 f01	327	Expect = 1.1 Identities = 21/21 (100%)	PREDICTED: Danio rerio similar to solute carrier family 26 member 6 c (LOC559448), mRNA gi|68362497|ref|XM_682786.1|
SSH1-16 f07	331	Expect = 4.6 Identities = 20/20 (100%)	Human DNA sequence from clone RP4-625H18 on chromosome 6p22.2-23 Contains the ID4 gene for dominant negative helix-loop-helix inhibitor of DNA binding 4 protein, a novel gene, the 5' end of two novel genes and four CpG islands, complete sequence gi|3676217|emb|AL022726.1|HS625H18
		Expect = 0.29 Identities = 22/22 (100%)	PREDICTED: Mus musculus RIKEN cDNA 4930463M05 gene (4930463M05Rik),mRNA gi|94394275|ref|XM_976043.1|
SSH1-16 f10	623	Expect = 2e-043 Identities = 204/233 (87%)	Triticum aestivum 14-3-3 protein mRNA, complete cds gi|40781604|gb|AY386126.1|
SSH1-16 g01	302	Expect = 1.1 Identities = 21/21 (100%)	Arabidopsis thaliana unknown protein (AT1G61970) mRNA, complete cds gi|30696642|ref|NM_104877.2|
		Expect = 4.2 Identities = 20/20 (100%)	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230114A16 product:hypothetical Acyl-CoA dehydrogenase (flavoprotein), N-terminal and middle domains structure containing protein, full insert sequence gi|26348766|dbj|AK080793.1|
SSH1-16 h04	479	Expect = 6.8 Identities = 20/20 (100%)	Mus musculus BAC clone RP23-204P24 from chromosome 16, complete sequence gi|84000499|gb|AC174448.2|
SSH1-16 h07	850	Expect = 0.20 Identities = 23/23 (100%)	Zebrafish DNA sequence from clone RP71-70D16 in linkage group 9,complete sequence gi|52075519|emb|BX323013.3|

Unknown

Contigs

CONTIG 15	(5 clones)		
SSH1-2 f05	183	Expect = 1e-017 Identities = 100/117 (85%)	Oryza sativa (japonica cultivar-group) Os02g0259600 (Os02g0259600)mRNA, complete cds gi|115445398|ref|NM_001053014.1|
SSH1-2 f06 In SSH1-2 f05	184	Expect = 2e-031 Identities = 120/136 (88%)	Zea mays PCO077438 mRNA sequence gi|21207382|gb|AY104304.1|
SSH1-16 h09	178	Expect = 1e-032 Identities = 107/118 (90%)	Oryza sativa (japonica cultivar-group) Os02g0259600 (Os02g0259600) mRNA, complete cds gi|115445398|ref|NM_001053014.1|
SSH1-2 h02 In SSH1-16 h09	178	Expect = 3e-027 Identities = 104/117 (88%)	Oryza sativa (japonica cultivar-group) Os02g0259600 (Os02g0259600)mRNA, complete cds gi|115445398|ref|NM_001053014.1|
		Expect = 0.038 Identities = 23/23 (100%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6908 genomic sequence gi|109390333|gb|DQ518948.1|
SSH1-14 a02	187	Expect = 3e-012 Identities = 76/88 (86%)	Oryza sativa (japonica cultivar-group) Os02g0259600 (Os02g0259600) mRNA, complete cds gi|115445398|ref|NM_001053014.1|
CONTIG 25	(2 clones)		
SSH1-5 f09	548	Expect = 0.50 Identities = 22/22 (100%)	Zebrafish DNA sequence from clone CH211-275D22 in linkage group 8, complete sequence gi|56368649|emb|CR450804.7|
SSH1-5 g09 In SSH1-5 f09	304	Expect = 0.068 Identities = 23/23 (100%)	Mouse DNA sequence from clone RP23-61E13 on chromosome X, complete sequence gi|55700730|emb|AL731774.11|
CONTIG 28	(2 clones)		
SSH1-7 d09	345	Expect = 1.2 Identities = 21/21 (100%)	Mus musculus BAC clone RP23-211E20 from chromosome 13, complete sequence gi|73695564|gb|AC159304.2|
SSH1-7 e09	365	Expect = 5.1 Identities = 20/20 (100%)	Homo sapiens 3 BAC RP11-564P9 (Roswell Park Cancer Institute Human BAC Library) complete sequence gi|20334518|gb|AC107302.4|
CONTIG 29	(9 clones)		
SSH1-7 g05	345	Expect = 1.2 Identities = 21/21 (100%)	Uncultured archaeon clone pEPR210 16S ribosomal RNA gene, partial sequence gi|21842351|gb|AF526972.1|
SSH1-7 f05 In SSH1-7 g05	339	Expect = 0.076 Identities = 23/23 (100%)	Medicago truncatula chromosome 7 BAC clone mth2-93e11, complete sequence gi|50198862|gb|AC147482.2|
SSH1-7 e04 In SSH1-7 f05	342	Expect = 1.2 Identities = 21/21 (100%)	Ralstonia eutropha H16 chromosome 1 gi|113524807|emb|AM260479.1|
SSH1-7 h05 In SSH1-7 g05	343		NO HIT
SSH1-7 g06 In SSH1-7 g05	344	Expect = 1.2 Identities = 21/21 (100%)	Mus musculus chromosome 14, clone RP23-114J12, complete sequence gi|37992003|gb|AC108416.5|
SSH1-7 f06 In SSH1-7 g06	340	Expect = 8e-005 Identities = 43/48 (89%)	Wheat PsbO mRNA for 33kDa oxygen evolving protein of photosystem II gi|21843|emb|X57408.1|TAPSB0
SSH1-7 g08	857	Expect = 0.80 Identities = 22/22 (100%)	Mus musculus BAC clone RP23-406I17 from chromosome 2, complete sequence gi|27413944|gb|AC124525.3|
SSH1-7 f07 In SSH1-7 g08	338	Expect = 0.076 Identities = 26/27 (96%)	Zebrafish DNA sequence from clone DKEYP-55D11 in linkage group 6,complete sequence gi|46878997|emb|BX664627.16|
SSH1-7 g07 In SSH1-7 g08	345	Expect = 4.8 Identities = 20/20 (100%)	Homo sapiens chromosome 8, clone CTD-2006H14, complete sequence gi|22450655|gb|AC120053.4|
CONTIG 31	(3 clones)		
SSH1-8 b02	747	Expect = 0.0 Identities = 425/429 (99%)	Cloning vector pGEM-WIZ, complete sequence gi|114846943|gb|DQ917671.1|
SSH1-9 h04	254	Expect = 1e-012	O.sativa light-induced mRNA

In SSH1-8 b02		Identities = 68/77 (88%)	gi|20262|emb|X68807.1|OSLIAA
SSH1-12 b09 In SSH1-9 h04	258	Expect = 2e-011 Identities = 75/87 (86%)	Lolium perenne light-induced protein 1-like (LIR1) mRNA, complete cds gi|77023865|gb|DQ206624.1|
CONTIG 32	(2 clones)		
SSH1-8 d07	303	Expect = 9e-023 Identities = 109/126 (86%)	Oryza sativa (japonica cultivar-group) cDNA, clone: J100078J12, full insert sequence gi|116012907|dbj|AK243542.1|
SSH1-8 e07 In SSH1-8 d07	283	Expect = 2e-005 Identities = 29/29 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
CONTIG 51	(2 clones)		
SSH1-16 f03	309	Expect = 0.069 Identities = 23/23 (100%)	Homo sapiens BAC clone RP11-492I5 from 2, complete sequence gi|13443263|gb|AC067947.6|
SSH1-16 e02 In SSH1-16 f03	306	Expect = 0.27 Identities = 22/22 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2 gi|58530788|dbj|AP008208.1|
CONTIG 65	(2 clones)		
SSH1-9 b02	409	Expect = 0.006 Identities = 25/25 (100%)	Mus musculus BAC clone RP23-81P21 from chromosome 18, complete sequence gi|31074941|gb|AC127353.3|
SSH1-3 f10	424	Expect = 1.5 Identities = 27/29 (93%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103484047|emb|CT989400.1|
		Expect = 1.5 Identities = 21/21 (100%)	Mus musculus BAC clone RP23-173L24 from chromosome 3, complete sequence gi|78190287|gb|AC165162.4|

Rubisco

Singletons

SSH1-1 b02	50	Expect = 0.002 Identities = 24/24 (100%)	Atrichum angustatum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|113910703|gb|DQ645986.1|
SSH1-1 b04	350	Expect = 1.2 Identities = 31/33 (93%),	Notholaena sulphurea ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, chloroplast gene encoding chloroplast protein, partial cds gi|886804|gb|U28254.1|NSU28254
SSH1-1 c02	230	Expect = 2e-010 Identities = 71/81 (87%)	Hordeum vulgare subsp. vulgare ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene,complete cds; chloroplast gene for chloroplast product gi|31087904|gb|AY137454.1|
SSH1-1 c10	307	Expect = 0.017 Identities = 58/68 (85%)	Puccinellia stricta ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493537|gb|AY691643.1|
SSH1-1 c11	492	Expect = 1e-026 Identities = 128/149 (85%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-1 d03	256	Expect = 6e-005 Identities = 70/84 (83%)	Zotovia thomsonii ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493539|gb|AY691644.1|
SSH1-1 d07	402	Expect = 3e-014 Identities = 65/72 (90%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-1 f05	63	Expect = 0.64 Identities = 20/20 (100%)	Cyanidium sp. MonteRotaro 20 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|45332758|gb|AY541301.1|
SSH1-1 g05	542	Expect = 6e-010 Identities = 113/137 (82%)	Wheat (T. aestivum) chloroplast ribulosebisphosphate carboxylase small subunit mRNA, clone pTS406, 3' end gi|170760|gb|K02324.1|WHTRBCC
SSH1-1 g08	374	Expect = e-158 Identities = 315/325 (96%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|12343|emb|X62117.1|CHTAHSRA
SSH1-1 h06	396	Expect = 4e-084 Identities = 225/244 (92%)	Wheat mRNA fragment for small subunit precursor of RuBPCase (EC 4.1.1.39 ribulosebisphosphate carboxylase) clones 234 and 406 gi|21867|emb|X00235.1|TARUB2
SSH1-1 h07	262	Expect = e-104 Identities = 212/218 (97%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-1 h09	368	Expect = e-175 Identities = 323/326 (99%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I
SSH1-1 h10	384	Expect = 1e-065 Identities = 187/206 (90%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-1 h11	472	Expect = 0.11 Identities = 29/31 (93%)	Pinus sabiniana voucher WTU-330593 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|74315455|gb|DQ156489.1|
SSH1-2 a03	284	Expect = 0.063 Identities = 23/23 (100%)	Hordeum vulgare ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds gi|1167947|gb|U43493.1|HVU43493
SSH1-2 a05	349	Expect = 3e-007 Identities = 65/76 (85%)	Puccinellia stricta ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493537|gb|AY691643.1|
SSH1-2 b08	467	Expect = 2e-006 Identities = 52/59 (88%)	Zoysia sp. JID-2004 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gi|54303901|gb|AY632375.1|
SSH1-2 b10	522	Expect = 5e-010 Identities = 52/57 (91%)	Wheat (T. aestivum) chloroplast ribulosebisphosphate carboxylase small subunit mRNA, clone pTS406, 3' end gi|170760|gb|K02324.1|WHTRBCC
SSH1-2 b12	508	Expect = 1e-007 Identities = 66/77 (85%)	Fargesia sp. Asmussen 105 plastid partial rbcL gene for ribulose bisphosphate carboxylase large subunit, specimen voucher Asmussen 105 (CP) gi|90968367|emb|AM110249.1|
SSH1-2 c05	409	Expect = 2e-006 Identities = 55/63 (87%)	Enkianthus campanulatus ribulose 1,5-bisphosphate carboxylase large subunit (rbcL) gene, partial cds; chloroplast gene for chloroplast product gi|37194740|gb|L12616.2|ENKCPRBCLA
SSH1-2 d04	306	Expect = 0.069 Identities = 23/23 (100%)	Agdestis clematidea chloroplast ribulose 1,5-bisphosphate carboxylase-like (rbcL) gene, partial sequence gi|8927055|gb|AF132092.1|AF132092
SSH1-2 e02	193	Expect = 7e-007 Identities = 49/55 (89%)	Wheat mRNA fragment for small subunit precursor of RuBPCase (EC 4.1.1.39 ribulosebisphosphate carboxylase) clones 234 and 406 gi|21867|emb|X00235.1|TARUB2
SSH1-2 f08	657	Expect = 7e-090 Identities = 199/206 (96%)	Elymus solanderi ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493535|gb|AY691642.1|
SSH1-2 f11	614	Expect = 1e-017 Identities = 72/78 (92%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-2 h01	790	Expect = 2.9 Identities = 45/53 (84%)	Amphibromus fluitans ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493513|gb|AY691631.1|
SSH1-3 a11	258	Expect = 0.014	Brachypodium pinnatum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL)

		Identities = 71/84 (84%)	gene, partial cds; plastid gi|54303873|gb|AY632361.1|
SSH1-3 a12	269	Expect = 7e-011 Identities = 60/66 (90%)	Wheat (T. aestivum) chloroplast ribulosebisphosphate carboxylase small subunit mRNA, clone pTS406, 3' end gi|170760|gb|K02324.1|WHTRBCC
SSH1-3 b02	185	Expect = 3e-009 Identities = 53/59 (89%)	Hordeum vulgare ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds gi|1167947|gb|U43493.1|HVU43493
SSH1-3 b08	258	Expect = 3.5 Identities = 20/20 (100%)	Corydalis incisa ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|115490367|gb|DQ912903.1|
SSH1-3 d02	308	Expect = 3e-004 Identities = 39/43 (90%)	Trisetum youngii ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493543|gb|AY691646.1|
SSH1-3 d03	178	Expect = 1e-005 Identities = 32/33 (96%)	Parrotia persica chloroplast partial rbcL gene for ribulose 1,5-bisphosphate carboxilase/oxigenase large subunit gi|115564968|emb|AM183411.1|
SSH1-3 e09	374	Expect = 2e-027 Identities = 156/186 (83%)	A.squarrosa chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|11324|emb|X62119.1|CHASHSRA
SSH1-3 g04	263	Expect = 2e-017 Identities = 74/81 (91%)	Festuca pratensis ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|41056394|gb|AY395536.1|
SSH1-4 a03	467	Expect = 2e-006 Identities = 46/51 (90%)	Fargesia sp. Asmussen 105 plastid partial rbcL gene for ribulose bisphosphate carboxylase large subunit, specimen voucher Asmussen 105 (CP) gi|90968367|emb|AM110249.1|
SSH1-4 b04	306	Expect = 0.004 Identities = 31/33 (93%)	Promenaea ovatiloba ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit-like (rbcL) gene, partial sequence; chloroplast gene for chloroplast product gi|37223054|gb|AY368369.1|
SSH1-4 d01	424	Expect = 0.002 Identities = 99/122 (81%)	Glyceria grandis ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gi|54303879|gb|AY632364.1|
SSH1-4 e05	434	Expect = 5e-019 Identities = 98/112 (87%)	Fargesia sp. Asmussen 105 plastid partial rbcL gene for ribulose bisphosphate carboxylase large subunit, specimen voucher Asmussen 105 (CP) gi|90968367|emb|AM110249.1|
SSH1-4 f04	638	Expect = 9e-074 Identities = 201/220 (91%)	Elymus solanderi ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493535|gb|AY691642.1|
SSH1-4 g06	238	Expect = 3e-093 Identities = 199/207 (96%)	Psathyrostachys fragilis subsp. villosus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, complete cds; chloroplast gene for chloroplast product gi|31087918|gb|AY137461.1|
SSH1-4 h11	694	Expect = e-116 Identities = 245/257 (95%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-4 h12	490	Expect = 1.8 Identities = 30/33 (90%)	Platycerium grande ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|82470467|gb|DQ164451.1|
SSH1-5 a04	431	Expect = 4e-010 Identities = 62/69 (89%)	Psathyrostachys lanuginosa isolate A voucher H8803 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, complete cds; chloroplast gi|51859654|gb|AY607051.1|
SSH1-5 b03	340	Expect = 4.7 Identities = 20/20 (100%)	Dendrobium equitans voucher TARI.F.D0101.0 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|98647393|gb|DQ449484.1|
SSH1-5 b05	396	Expect = 0.001 Identities = 26/26 (100%)	Onychium japonicum chloroplast large subunit ribulose-1,5-bisphosphate carboxylase/oxygenase (rbcL) gene, partial cds gi|21628864|gb|AF360359.1|
SSH1-5 b10	504	Expect = 1e-010 Identities = 84/98 (85%)	Psathyrostachys caduca voucher H6702 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, complete cds; chloroplast gi|51859672|gb|AY607060.1|
SSH1-5 c02	501	Expect = 5e-007 Identities = 56/64 (87%)	Puccinellia stricta ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493537|gb|AY691643.1|
SSH1-5 c03	346	Expect = 2e-011 Identities = 78/91 (85%)	Xyris bicephala ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gene for plastid product gi|27461543|gb|AY123243.1|
SSH1-5 c06	631	Expect = e-111 Identities = 220/223 (98%)	Elymus solanderi ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493535|gb|AY691642.1|
SSH1-5 d01	594	Expect = 3e-027 Identities = 108/122 (88%)	Elymus sibiricus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) mRNA, complete cds; chloroplast gi|54401455|gb|AY772669.1|
SSH1-5 e10	366	Expect = 1.3 Identities = 32/36 (88%)	T.portulacastrum chloroplast ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, complete cds gi|343473|gb|M62572.1|TIACPRBCL
SSH1-5 f07	272	Expect = 0.015 Identities = 27/28 (96%)	Psathyrostachys stoloniformis ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; rbcL-psaI intergenic spacer, complete sequence; and photosystem I subunit VIII (psaI) gene, partial cds; chloroplast gi|61378670|gb|AY836180.1|
SSH1-5 g11	329	Expect = 1e-018 Identities = 57/59 (96%)	Brachypodium pinnatum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gi|54303873|gb|AY632361.1|
SSH1-5 h04	519	Expect = 1e-041 Identities = 156/178 (87%)	Triticum aestivum RNA for phosphoribulokinase gi|21840|emb|X51608.1|TAPRKGEN
SSH1-7 b02	759	Expect = 7e-004 Identities = 39/43 (90%)	Fargesia sp. Asmussen 105 plastid partial rbcL gene for ribulose bisphosphate carboxylase large subunit, specimen voucher Asmussen 105 (CP) gi|90968367|emb|AM110249.1|
SSH1-7 b05	474	Expect = 0.007 Identities = 46/53 (86%)	Raddia brasiliensis chloroplast partial rbcL gene for ribulose bisphosphate carboxylase large chain gi|57283829|emb|AJ746275.1|
SSH1-7 c05	345	Expect = 0.020 Identities = 66/80 (82%)	Brachypodium pinnatum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gi|54303873|gb|AY632361.1|
SSH1-7 c08	347	Expect = 1.2 Identities = 21/21 (100%)	Leucobryum albidum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|113910713|gb|DQ645991.1|
SSH1-7 d02	715	Expect = e-158 Identities = 297/301 (98%)	Australopyrum calcis subsp. calcis ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493523|gb|AY691636.1|
SSH1-7 d10	670	Expect = e-179 Identities = 327/329 (99%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|12343|emb|X62117.1|CHTAHSRA
SSH1-7 d12	429	Expect = 0.098 Identities = 32/35 (91%)	Platonia esculenta ribulose-1,5-bisphosphate carboxylase large subunit (rbcL) gene, partial cds; plastid gene or plastid product gi|22003627|gb|AF518394.1|
SSH1-7 e02	629	Expect = 6e-010 Identities = 49/53 (92%)	Platycodon grandiflorus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|50262289|gb|AY655156.1|
SSH1-7 h10	718	Expect = e-148 Identities = 293/301 (97%)	Australopyrum calcis subsp. calcis ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493523|gb|AY691636.1|
SSH1-8 a07	852	Expect = 2e-084 Identities = 276/314 (87%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-8 b03	466	Expect = 0.11 Identities = 62/75 (82%)	Amphibromus fluitans ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493513|gb|AY691631.1|
SSH1-8 b04	660	Expect = 3e-018 Identities = 153/187 (81%)	Trisetum youngii ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493543|gb|AY691646.1|
SSH1-8 c01	641	Expect = 2e-071 Identities = 226/257 (87%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-8 c03	823	Expect = 2e-059 Identities = 230/269 (85%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|12343|emb|X62117.1|CHTAHSRA
SSH1-8 c11	354	Expect = 0.005 Identities = 31/33 (93%)	Auxenochlorella protothecoides chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, strain SAG 211-7a gi|115430262|emb|AM260440.1|
SSH1-8 d11	554	Expect = 0.002 Identities = 89/110 (80%)	Elymus solanderi ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493535|gb|AY691642.1|
SSH1-8 f08	372	Expect = 1e-009 Identities = 99/120 (82%)	Trisetum youngii ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493543|gb|AY691646.1|

SSH1-8 g05	296	Expect = 3e-016 Identities = 107/127 (84%)	Agrostis magellanica ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493511|gb|AY691630.1|
SSH1-9 c06	357	Expect = 0.001 Identities = 29/30 (96%)	Selaginella wightii ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit-like (rbcL) gene, partial sequence; chloroplast gene for chloroplast product gi|27448369|gb|AF419062.1|
SSH1-9 c11	393	Expect = 2e-009 Identities = 36/36 (100%)	Ensete ventricosum ribulose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast gene for chloroplast product gi|336915|gb|L05448.1|ENVCPRBCL
SSH1-9 d06	343	Expect = 0.077 Identities = 29/31 (93%)	Trisetum flavescens ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|41056444|gb|AY395565.1|
SSH1-9 e04	915	Expect = e-160 Identities = 314/322 (97%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein gi|12343|emb|X62117.1|CHTAHSRA
SSH1-9 e09	697	Expect = 2e-016 Identities = 93/108 (86%)	Dactylis glomerata ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|41056392|gb|AY395535.1|
SSH1-9 f04	263	Expect = 1e-009 Identities = 36/36 (100%)	Tofieldia glutinosa ribulose-1,5-bisphosphate carboxylase large subunit (rbcL) gene, partial cds; chloroplast gi|81230680|gb|DQ182340.1|
SSH1-9 f08	612	Expect = 5e-035 Identities = 118/131 (90%)	Melica cupanii ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gi|54303881|gb|AY632365.1|
SSH1-9 h10	877	Expect = 2e-026 Identities = 95/105 (90%)	Elymus solanderi ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493535|gb|AY691642.1|
SSH1-10 b10	346	Expect = 1e-015 Identities = 74/82 (90%),	Polygonella fimbriata var. robusta ribulose-1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast gene for chloroplast product gi|25053461|gb|AF297132.1|
SSH1-10 c10	243	Expect = 4e-009 Identities = 47/51 (92%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-10 f11	506	Expect = 8e-012 Identities = 76/88 (86%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-11 a02	515	Expect = 1.9 Identities = 27/29 (93%)	Chenopodium sanctae-clarae ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|34576564|gb|AY270043.1|
SSH1-11 c05	653	Expect = 0.15 Identities = 95/119 (79%)	Zoysia sp. JID-2004 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gi|54303901|gb|AY632375.1|
SSH1-11 c08	840	Expect = e-150 Identities = 294/301 (97%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-11 d01	474	Expect = 2e-018 Identities = 117/139 (84%)	Triticum aestivum rbcS gene for ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit, complete cds, clone:p9-1 gi|11990896|dbj|AB042066.1|
SSH1-11 e03	272	Expect = 1e-012 Identities = 143/177 (80%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-11 f03	364	Expect = 5.1 Identities = 26/28 (92%)	Chlorophytum comosum ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|37722379|gb|AY149375.1|
SSH1-11 f07	457	Expect = 7e-006 Identities = 115/148 (77%)	Amphibromus fluitans ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493513|gb|AY691631.1|
SSH1-11 f11	286	Expect = 2e-072 Identities = 150/153 (98%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-12 a12	488	Expect = 5e-041 Identities = 233/281 (82%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|12343|emb|X62117.1|CHTAHSRA
SSH1-12 b08	506	Expect = 8e-012 Identities = 49/52 (94%)	Wheat (T. aestivum) chloroplast ribulosebisphosphate carboxylase small subunit mRNA, clone pTS406, 3' end gi|170760|gb|K02324.1|WHTRBCC
SSH1-12 c03	381	Expect = 0.001 Identities = 26/26 (100%)	wheat putative xylanase inhibitor mRNA, partial cds gi|77702556|gb|DQ219479.1|
		Expect = 0.022 Identities = 24/24 (100%)	Uniola paniculata ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gi|54303897|gb|AY632373.1|
SSH1-12 c12	667	Expect = 8e-025 Identities = 125/146 (85%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-12 d12	376	Expect = 2e-036 Identities = 223/269 (82%)	Australopyrum calcis subsp. calcis ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493523|gb|AY691636.1|
SSH1-12 e09	277	Expect = 0.016 Identities = 27/28 (96%)	Cortaderia selloana ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|66802798|gb|DQ005609.1|
SSH1-12 h11	51	Expect = 0.46 Identities = 26/28 (92%)	Leptopteris superba ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|113910739|gb|DQ646004.1|
SSH1-13 c10	389	Expect = 1.4 Identities = 36/41 (87%)	Wheat mRNA fragment for small subunit precursor of RuBPCase (EC 4.1.1.39) (ribulosebisphosphate carboxylase, clone 512) gi|21865|emb|X00234.1|TARUB1
		Expect = 5.5 Identities = 20/20 (100%)	Crimean-Congo hemorrhagic fever virus isolate BA66019 envelope glycoprotein precursor, gene, complete cds gi|14029591|gb|AF350448.1|
SSH1-13 c11	357	Expect = 0.005 Identities = 37/41 (90%)	Melica cupanii ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gi|54303881|gb|AY632365.1|
SSH1-13 d02	541	Expect = 7e-068 Identities = 210/234 (89%)	Wheat mRNA fragment for small subunit precursor of RuBPCase (EC 4.1.1.39 ribulosebisphosphate carboxylase) clones 234 and 406 gi|21867|emb|X00235.1|TARUB2
SSH1-13 d03	191	Expect = 7e-004 Identities = 51/58 (87%)	Wheat mRNA fragment for small subunit precursor of RuBPCase (EC 4.1.1.39) (ribulosebisphosphate carboxylase, clone 512) gi|21865|emb|X00234.1|TARUB1
SSH1-13 d09	473	Expect = 2e-021 Identities = 149/180 (82%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-13 d11	59	Expect = 0.15 Identities = 27/29 (93%)	Polytrichum juniperinum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|113910705|gb|DQ645987.1|
SSH1-13 e11	609	Expect = 2e-016 Identities = 63/68 (92%)	Hordeum vulgare carbonic anhydrase mRNA, complete cds gi|558498|gb|L36959.1|BLYCA
		Expect = 0.56 Identities = 28/30 (93%)	Takakia ceratophylla ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|113910731|gb|DQ646000.1|
SSH1-13 e12	269	Expect = 4e-006 Identities = 39/42 (92%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-13 f05	361	Expect = 0.001 Identities = 35/38 (92%)	Pentastemona sumatrana ribulose-1,5-bisphosphate carboxylase large subunit (rbcL) gene, partial sequence; chloroplast gene for chloroplast product gi|17224675|gb|AF307490.1|AF307490
SSH1-13 f07	281	Expect = 1e-021 Identities = 83/92 (90%)	Gossypium hirsutum ribulose-1,5-bisphosphate carboxylase/oxygenase activase alpha 2 mRNA, complete cds gi|78100211|gb|DQ233255.1|
SSH1-13 f11	581	Expect = 0.53 Identities = 22/22 (100%)	Frullania dilatata ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|113910689|gb|DQ645979.1|
SSH1-13 h04	355	Expect = 3e-020 Identities = 76/82 (92%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-13 h07	210	Expect = 2e-019 Identities = 52/52 (100%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-13 h08	604	Expect = e-117 Identities = 243/254 (95%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-13 h10	350	Expect = 2e-014 Identities = 122/148 (82%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-13 h12	338	Expect = 1e-022 Identities = 145/174 (83%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-14 a09	372	Expect = 1e-006	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA,

		Identities = 37/39 (94%)	complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-14 a12	481	Expect = 6e-025 Identities = 110/126 (87%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-14 b06	382	Expect = 1e-025 Identities = 176/211 (83%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|12343|emb|X62117.1|CHTAHSRA
SSH1-14 b10	731	Expect = 2e-047 Identities = 172/199 (86%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-14 c08	365	Expect = 6e-012 Identities = 67/76 (88%)	Wheat (T. aestivum) chloroplast ribulosebisphosphate carboxylase small subunit mRNA, clone pTS406, 3' end gi|170760|gb|K02324.1|WHTRBCC
SSH1-14 c12	269	Expect = 0.060 Identities = 26/27 (96%)	Aquilegia ecalcarata ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|63103256|gb|AY954495.1|
SSH1-14 d04	366	Expect = 1e-037 Identities = 182/215 (84%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-14 d06	868	Expect = 3e-019 Identities = 174/214 (81%),	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-14 d10	825	Expect = 4e-052 Identities = 183/209 (87%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-14 d12	354	Expect = 0.32 Identities = 22/22 (100%)	Astelia pumila ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gene for chloroplast product gi|11323476|gb|AF307906.1|
SSH1-14 f09	832	Expect = 2e-010 Identities = 47/50 (94%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-14 h07	390	Expect = 4e-007 Identities = 62/72 (86%)	Parrotia persica chloroplast partial rbcL gene for ribulose 1,5-bisphosphate carboxilase/oxigenase large subunit gi|115564968|emb|AM183411.1|
SSH1-15 a06	392	Expect = 2e-009 Identities = 42/44 (95%)	Ecdeiocolea monostachya ribulose-1,5-bisphosphate carboxylase/oxygenase (rbcL) gene, partial cds;chloroplast gi|5737777|gb|AF148773.1|
SSH1-15 c01	124	Expect = 0.39 Identities = 21/21 (100%)	Phaenosperma globosa ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gi|54303891|gb|AY632370.1|
SSH1-15 c03	302	Expect = 0.001 Identities = 29/30 (96%)	Danthoniopsis petiolata ribulose 1,5-bisphosphate carboxylase large subunit gene, partial cds; chloroplast gi|51572275|gb|AY618661.1|
SSH1-15 d12	125	Expect = 6.1 Identities = 19/19 (100%)	Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730010J01 product:6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2,6-bisphosphate 2-phosphatase (EC 3.1.3.46),hepatic homolog [Homo sapiens], full insert sequence gi|26093783|dbj|AK050073.1|
SSH1-15 e01	188	Expect = 9.8 Identities = 28/31 (90%)	Pharus parvifolius chloroplast partial rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit gi|21684954|emb|AJ419950.1|PPA419950
SSH1-15 f03	178	Expect = 0.15 Identities = 34/38 (89%)	Didymocistus chrysadenius ribulose 1,5-bisphosphate carboxylase large subunit (rbcL) gene, partial cds; chloroplast gi|55792670|gb|AY663581.1|
SSH1-15 f10	601	Expect = 2e-010 Identities = 83/98 (84%)	Hordeum vulgare subsp. vulgare ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene,complete cds; chloroplast gene for chloroplast product gi|31087908|gb|AY137456.1|
SSH1-15 h05	345	Expect = 5e-006 Identities = 59/66 (89%)	Micraira subulifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid
SSH1-16 a02	860	Expect = 9e-013 Identities = 134/166 (80%)	Wheat (T. aestivum) chloroplast ribulosebisphosphate carboxylase small subunit mRNA, clone pTS406, 3' end gi|170760|gb|K02324.1|WHTRBCC
SSH1-16 b04	294	Expect = 3e-007 Identities = 50/56 (89%)	Piptatherum miliaceum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast gi|51511894|gb|AY622898.1|
SSH1-16 b08	356	Expect = e-100 Identities = 239/257 (92%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-16 b11	790	Expect = 5e-005 Identities = 35/37 (94%)	Triticum aestivum rbcS gene for ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit, complete cds, clone:p9-1 gi|11990896|dbj|AB042066.1|
SSH1-16 c07	836	Expect = e-146 Identities = 310/327 (94%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate gi|12343|emb|X62117.1|CHTAHSRA
SSH1-16 c08	627	Expect = e-167 Identities = 322/329 (97%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|12343|emb|X62117.1|CHTAHSRA
SSH1-16 d11	849	Expect = 2e-023 Identities = 96/108 (88%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-16 d12	824	Expect = 0.19 Identities = 59/71 (83%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|170770|gb|M37477.1|WHTRUBIAB
SSH1-16 e11	719	Expect = e-107 Identities = 234/245 (95%)	Wheat mRNA fragment for small subunit precursor of RuBPCase (EC 4.1.1.39 ribulosebisphosphate carboxylase) clones 234 and 406 carboxylase/oxygenase and apoprotein I gi|21865|emb|X00234.1|TARUB1
SSH1-16 g02	303	Expect = 3e-010 Identities = 49/53 (92%)	Micraira subulifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gi|54303883|gb|AY632366.1|
SSH1-16 g11	342	Expect = 5e-083 Identities = 209/223 (93%),	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|

Rubisco

Contigs

CONTIG 1	(4 clones)		
SSH1-10 a12	379	Expect = e-157 Identities = 319/331 (96%)	Triticum aestivum partial mRNA for putative fructose 1-,6-biphosphate aldolase (ald gene) gi|18496064|emb|AJ420778.1|TAE420778
SSH1-10 a06 In SSH1-10 a12	353	Expect = e-120 Identities = 284/305 (93%)	Triticum aestivum partial mRNA for putative fructose 1-,6- biphosphate aldolase (ald gene) gi|18496064|emb|AJ420778.1|TAE420778
SSH1-10 b06	379	Expect = e-143 Identities = 311/328 (94%)	Triticum aestivum partial mRNA for putative fructose 1-,6-biphosphate aldolase (ald gene) gi|18496064|emb|AJ420778.1|TAE420778
SSH1-10 c06 In SSH1-10 b06	380	Expect = e-135 Identities = 310/331 (93%)	Triticum aestivum partial mRNA for putative fructose 1-,6-biphosphate aldolase (ald gene) gi|18496064|emb|AJ420778.1|TAE420778
CONTIG 35	(2 clones)		
SSH1-9 h08	313	Expect = 4e-022 Identities = 96/109 (88%)	Oryza sativa S-phase-specific ribosomal protein (RSPSP94) mRNA,complete cds gi|4079799|gb|AF052503.1|AF052503
		Expect = 2e-085 Identities = 163/163 (100%)	Triticum aestivum 40S ribosomal protein mRNA, partial cds gi|32400860|gb|AF479043.1|

SSH1-9 g05	308	Expect = 4e-071 Identities = 157/163 (96%)	Triticum aestivum 40S ribosomal protein mRNA, partial cds gi|32400860|gb|AF479043.1|
		Expect = 2e-017 Identities = 91/105 (86%)	Oryza sativa S-phase-specific ribosomal protein (RSPSP94) mRNA,complete cds gi|4079799|gb|AF052503.1|AF052503
SSH1-12 b01 In SSH1-10 e11	302	Expect = 4e-099 Identities = 233/251 (92%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-10 d01 In SSH1-10 e11	292	Expect = 2e-088 Identities = 197/209 (94%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
CONTIG 36	(100 clones)		
REPRESENTATIVE			
SSH1-12 b01 In SSH1-10 e11	302	Expect = 4e-099 Identities = 233/251 (92%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-10 d01 In SSH1-10 e11	292	Expect = 2e-088 Identities = 197/209 (94%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
CONTIG 38	(148 clones)		
REPRESENTATIVE			
SSH1-11 b01	509	Expect = e-115 Identities = 279/303 (92%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-10 g12	401	Expect = e-158 Identities = 295/298 (98%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-11 d06	884	Expect = e-165 Identities = 300/301 (99%)	Bromus arenarius ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493515|gb|AY691632.1|
SSH1-12 e05	347	Expect = e-117 Identities = 281/301 (93%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-13 b05	356	Expect = e-113 Identities = 270/290 (93%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-10 a04	426	Expect = e-139 Identities = 281/290 (96%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
CONTIG 39	(17 clones)		
REPRESENTATIVE			
SSH1-11 b12	320	Expect = 6e-064 Identities = 166/179 (92%)	Wheat mRNA fragment for small subunit precursor of RuBPCase (EC 4.1.1.39 ribulosebisphosphate carboxylase) clones 234 and 406 gi|21867|emb|X00235.1|TARUB2
SSH1-8 g04	292	Expect = e-131 Identities = 245/247 (99%)	Wheat mRNA fragment for small subunit precursor of RuBPCase (EC 4.1.1.39 ribulosebisphosphate carboxylase) clones 234 and 406 gi|21867|emb|X00235.1|TARUB2
SSH1-16 a06	854	Expect = 1e-082 Identities = 225/247 (91%)	Wheat mRNA fragment for small subunit precursor of RuBPCase (EC 4.1.1.39 ribulosebisphosphate carboxylase) clones 234 and 406 gi|21867|emb|X00235.1|TARUB2
CONTIG 40	(2 clones)		
SSH1-11 c12	243	Expect = 1e-058 Identities = 163/178 (91%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase activase precursor RNA, partial cds; nuclear gene for chloroplast product gi|37783282|gb|AY206372.1|
SSH1-7 c06	236	Expect = 3e-068 Identities = 167/178 (93%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase activase precursor RNA, partial cds; nuclear gene for chloroplast product gi|37783282|gb|AY206372.1|
CONTIG 41	(80 clones)		
REPRESENTATIVE			
SSH1-11 d05	269	Expect = e-121 Identities = 223/223 (100%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-11 h08	817	Expect = e-111 Identities = 220/223 (98%)	Elymus solanderi ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493535|gb|AY691642.1|
SSH1-15 f11	278	Expect = e-108 Identities = 213/217 (98%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
CONTIG 43	(81 clones)		
REPRESENTATIVE			
SSH1-11 e11	414	Expect = e-172 Identities = 324/329 (98%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|12343|emb|X62117.1|CHTAHSRA
SSH1-13 e10	522	Expect = e-160 Identities = 320/329 (97%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|12343|emb|X62117.1|CHTAHSRA
SSH1-14 b04	862	Expect = e-146 Identities = 309/326 (94%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|12343|emb|X62117.1|CHTAHSRA
SSH1-8 h05	812	Expect = 0.0 Identities = 329/329 (100%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|12343|emb|X62117.1|CHTAHSRA
SSH1-13 e09	905	Expect = e-180 Identities = 325/326 (99%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|12343|emb|X62117.1|CHTAHSRA
CONTIG 50	(9 clones)		
REPRESENTATIVE			

SSH1-16 e05	303	Expect = 1e-027 Identities = 111/126 (88%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-16 e04	302	Expect = 1e-009 Identities = 78/92 (84%)	H.brachyantherum chloroplast rbcL gene for ribulosebiphosphate carboxylase gi|1488585|emb|Z49844.1|HBCHRBPCX
CONTIG 53	(13 clones)		
REPRESENTATIVE			
SSH1-16 h08	374	Expect = 3e-069 Identities = 148/152 (97%)	Wheat mRNA fragment for small subunit precursor of RuBPCase (EC4.1.1.39) (ribulosebisphosphate carboxylase, clone 512) gi|21865|emb|X00234.1|TARUB1
SSH1-15 c08	368	Expect = e-119 Identities = 286/308 (92%)	Wheat mRNA fragment for small subunit precursor of RuBPCase (EC 4.1.1.39 ribulosebisphosphate carboxylase) clones 234 and 406 gi|21867|emb|X00235.1|TARUB2
SSH1-11 a09	443	Expect = 1e-096 Identities = 257/282 (91%)	Wheat (T. aestivum) chloroplast ribulosebisphosphate carboxylase small subunit mRNA, clone pTS406, 3' end gi|170760|gb|K02324.1|WHTRBCC
CONTIG 55	(7 clones)		
REPRESENTATIVE			
SSH1-2 e12	404	Expect = e-108 Identities = 223/230 (96%)	Stenostachys laevis ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493531|gb|AY691640.1|
SSH1-1 b09	478	Expect = 1e-093 Identities = 208/217 (95%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
CONTIG 58	(10 clones)		
REPRESENTATIVE			
SSH1-5 d04	524	Expect = e-118 Identities = 237/243 (97%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-1 a06	284	Expect = e-131 Identities = 243/244 (99%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-8 h12	357	Expect = e-125 Identities = 239/242 (98%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH1-11 b05	519	Expect = e-107 Identities = 227/236 (96%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
CONTIG 59	(8 clones)		
REPRESENTATIVE			
SSH1-7 d05	342	Expect = 0.001 Identities = 47/54 (87%)	Megastylis latissimus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|39655274|gb|AY381125.1|
SSH1-7 f09	345	Expect = 0.31 Identities = 22/22 (100%)	Homo sapiens BAC clone RP13-582L3 from 4, complete sequence gi|24080763|gb|AC116612.5|
SSH1-7 g09	349	Expect = 4.9 Identities = 50/60 (83%)	Molinia caerulea ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gi|54303885|gb|AY632367.1|
SSH1-7 h09	509	Expect = 0.002 Identities = 50/58 (86%)	Piptatherum miliaceum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast gi|51511894|gb|AY622898.1|
CONTIG 60	(2 clones)		
SSH1-7 e10	330	Expect = 0.005 Identities = 34/37 (91%)	Cortaderia selloana ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|66802798|gb|DQ005609.1|
SSH1-7 f10	324	Expect = 4e-022 Identities = 99/113 (87%)	Distichlis spicata ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gi|54303877|gb|AY632363.1|
CONTIG 62	(3 clones)		
SSH1-8 a04	537	Expect = 5e-004 Identities = 48/55 (87%)	Equisetum pratense ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gene for chloroplast product gi|31324658|gb|AY226137.1|
SSH1-8 a06 In SSH1-8 a04	417	Expect = 0.38 Identities = 46/54 (85%)	Equisetum pratense ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gene for chloroplast product gi|31324658|gb|AY226137.1|
		Expect = 0.002 Identities = 29/30 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
		Expect = 0.38 Identities = 25/26 (96%)	Photobacterium damselae subsp. piscicida trpB gene for putative transposase, clone pRDA16 gi|57635366|emb|AJ749797.1|
SSH1-8 a05	806	Expect = 0.012 Identities = 43/49 (87%)	Tylimanthus saccatus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|113910681|gb|DQ645975.1|
CONTIG 64	(32 clones)		
REPRESENTATIVE			
SSH1-8 c08	809		EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions
SSH1-12 b02	813	Expect = e-153 Identities = 280/281 (99%)	Wheat mRNA fragment for small subunit precursor of RuBPCase (EC 4.1.1.39 ribulosebisphosphate carboxylase) clones 234 and 406 gi|21867|emb|X00235.1|TARUB2
SSH1-11 h11	670	Expect = e-149 Identities = 277/279 (99%)	Triticum aestivum rbcS gene for ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit, complete cds, clone:p9-1 gi|11990896|dbj|AB042066.1|
SSH1-9 f02	671	Expect = e-179 Identities = 388/407 (95%)	Hordeum vulgare ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds gi|1167947|gb|U43493.1|HVU43493
SSH1-11 a02	515	Expect = 1.9 Identities = 27/29 (93%)	Chenopodium sanctae-clarae ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|34576564|gb|AY270043.1|

Chlorophyll A/B Binding Protein

Singletons

SSH1-1 a12	178	Expect = 0.59 Identities = 42/49 (85%)	Triticum aestivum chlorophyll a/b-binding protein WCAB precursor(Wcab) mRNA, complete cds gi|1657858|gb|U73218.1|TAU73218
SSH1-1 e10	444	Expect = 5e-025 Identities = 167/202 (82%)	Hordeum vulgare gene for CP29 precursor for **core chlorophyll a/b binding (CAB) protein** of photosystem II (PSII) gi|18957|emb|X63052.1|HVCP29
SSH1-2 a08	470	Expect = 7e-006 Identities = 107/132 (81%)	Wheat major **chlorophyll a/b-binding protein** gene, complete cds gi|170673|gb|M10144.1|WHTCAB
SSH1-4 f09	271	Expect = 3e-053 Identities = 148/161 (91%)	Maize cab-1 gene for chlorophyll a/b-binding protein gi|22223|emb|X14794.1|ZMCAB1
SSH1-4 g12	440	Expect = 1e-053 Identities = 152/166 (91%)	Maize cab-1 gene for chlorophyll a/b-binding protein gi|22223|emb|X14794.1|ZMCAB1
SSH1-5 c09	625	Expect = 2.3 Identities = 27/29 (93%)	Lemna gibba chlorophyll a/b apoprotein gene, complete cds gi|168289|gb|M12152.1|LGIAB19A
SSH1-8 f12	626	Expect = 0.002 Identities = 53/62 (85%)	Tabacco Cab50 mRNA for major chlorophyll a/b binding protein gi|19832|emb|X52742.1|NTCAB50
SSH1-8 g02	793	Expect = 1e-005 Identities = 46/50 (92%)	Zoysia sp. JID-2004 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gi|54303901|gb|AY632375.1|
SSH1-8 g12	772	Expect = 1e-045 Identities = 235/281 (83%)	Triticum aestivum chlorophyll a/b-binding protein WCAB precursor (Wcab) mRNA, complete cds gi|1657858|gb|U73218.1|TAU73218
SSH1-11 b08	444	Expect = 6e-031 Identities = 195/236 (82%)	Oryza sativa (japonica cultivar-group) Os03g0235700 (Os03g0235700)mRNA, complete cds
		Expect = 4e-004 Identities = 57/67 (85%)	Zea mays chlorophyll a/b-binding apoprotein CP26 (Lhcb5-2) mRNA,complete cds gi|733455|gb|U23189.1|ZMU23189
SSH1-11 g05	483	Expect = 4e-004 Identities = 42/47 (89%)	Oryza sativa (indica cultivar-group) putative soluble starch synthase IV-1 gene, complete cds gi|21429219|gb|AY100470.1|
SSH1-12 e12	452	Expect = 0.007 Identities = 31/33 (93%)	C.moewusii cab mRNA for chlorophyll a/b binding protein gi|18062|emb|X54856.1|CMCAB
SSH1-12 f04	477	Expect = 7e-006 Identities = 85/102 (83%)	Hordeum vulgare chlorophyll a/b-binding protein precursor (Lhca4) mRNA, partial cds; nuclear gene for chloroplast product gi|9624494|gb|AF287276.1|AF287276
SSH1-12 f10	646	Expect = 0.59 Identities = 37/42 (88%)	Oryza sativa chlorophyll a/b binding protein (kcdl895) mRNA,complete cds gi|1661159|gb|U74295.1|OSU74295
SSH1-12 h04	478	Expect = 2e-009 Identities = 45/48 (93%)	Hordeum vulgare chlorophyll a/b-binding protein precursor (Lhca4)mRNA, partial cds; nuclear gene for chloroplast product gi|9624494|gb|AF287276.1|AF287276
SSH1-12 h08	382	Expect = 2e-012 Identities = 65/73 (89%)	Sorghum bicolor putative chloroplast chlorophyll A-B binding protein type I mRNA, partial cds; nuclear gene for chloroplast product gi|77799147|gb|DQ185891.1|
SSH1-13 c01	212	Expect = 0.012 Identities = 39/44 (88%)	Hordeum vulgare gene for CP29 precursor for core chlorophyll a/b binding (CAB) protein of photosystem II (PSII) gi|18957|emb|X63052.1|HVCP29
SSH1-14 c03	717	Expect = 8e-016 Identities = 83/95 (87%)	Z.mays mRNA for type II light-harvesting chlorophyll a/b-binding protein gi|452340|emb|X68682.1|ZMLHCB
SSH1-14 f03	861	Expect = 3.2 Identities = 24/25 (96%)	Chlamydomonas incerta chloroplast light-harvesting chlorophyll-a/b binding protein (LhcII-1.3) mRNA, complete cds; nuclear gene for chloroplast product gi|74272670|gb|DQ122900.1|
SSH1-16 d08	375	Expect = 1e-083 Identities = 166/168 (98%)	Rice cab2R gene for light harvesting chlorophyll a/b-binding protein gi|20181|emb|X13909.1|OSCABR2
SSH1-16 e12	809	Expect = 2e-066 Identities = 237/272 (87%)	Maize cab-1 gene for chlorophyll a/b-binding protein gi|22223|emb|X14794.1|ZMCAB1

Chlorophyll A/B Binding Protein

Singletons

CONTIG 37	(2 clones)		
SSH1-10 h09	408	Expect = 4e-050 Identities = 167/188 (88%)	Zea mays chlorophyll a/b-binding apoprotein CP24 (Lhcb6-1) mRNA,complete cds gi|733457|gb|U23190.1|ZMU23190
SSH1-13 e04 In SSH1-10 h09	404	Expect = 6e-043 Identities = 170/196 (86%)	Zea mays chlorophyll a/b-binding apoprotein CP24 (Lhcb6-1) mRNA,complete cds gi|733457|gb|U23190.1|ZMU23190
CONTIG 44	(4 clones)		
REPRESENTATIVE			
SSH1-12 a04	416	Expect = e-109 Identities = 326/367 (88%)	Wheat major chlorophyll a/b-binding protein gene, complete cds gi|170673|gb|M10144.1|WHTCAB
SSH1-11 f12	270	Expect = 2e-054 Identities = 195/223 (87%)	Maize mRNA for light-harvesting chlorophyll a/b binding protein LHCP gi|22356|emb|Y00379.1|ZMLHCP
CONTIG 46	(11 clones)		
REPRESENTATIVE			
SSH1-7 a05	400	Expect = 2e-024 Identities = 79/85 (92%)	Triticum aestivum chlorophyll a/b-binding protein WCAB precursor(Wcab) mRNA, complete cds gi|1657858|gb|U73218.1|TAU73218
SSH1-12 f07	402	Expect = 3e-066 Identities = 242/279 (86%)	Oryza sativa chlorophyll a/b binding protein (kcdl895) mRNA,complete cds gi|1661159|gb|U74295.1|OSU74295
CONTIG 47	(3 clones)		
SSH1-12 g04	487	Expect = 0.0 Identities = 373/379 (98%)	Hordeum vulgare chlorophyll a/b-binding protein precursor (Lhca4)mRNA, partial cds; nuclear gene for chloroplast product gi|9624494|gb|AF287276.1|AF287276
SSH1-8 h07	812	Expect = 0.0 Identities = 373/379 (98%)	Hordeum vulgare chlorophyll a/b-binding protein precursor (Lhca4) mRNA, partial cds; nuclear gene for chloroplast product gi|9624494|gb|AF287276.1|AF287276
SSH1-12 c09 In SSH1-8 h07	324	Expect = e-111 Identities = 227/234 (97%)	Hordeum vulgare chlorophyll a/b-binding protein precursor (Lhca4) mRNA, partial cds; nuclear gene for chloroplast product gi|9624494|gb|AF287276.1|AF287276

CONTIG 49	(12 clones)		
REPRESENTATIVE			
SSH1-14 f06	490	Expect = 0.11 Identities = 50/59 (84%)	Hordeum vulgare gene for CP29 precursor for core chlorophyll a/b binding (CAB) protein of photosystem II (PSII) gi|18957|emb|X63052.1|HVCP29
SSH1-1 d10	443	Expect = e-167 Identities = 358/377 (94%)	Hordeum vulgare gene for CP29 precursor for core chlorophyll a/b binding (CAB) protein of photosystem II (PSII) gi|18957|emb|X63052.1|HVCP29
SSH1-13 c02	437	Expect = e-174 Identities = 361/377 (95%)	Hordeum vulgare gene for CP29 precursor for core chlorophyll a/b binding (CAB) protein of photosystem II (PSII) gi|18957|emb|X63052.1|HVCP29
SSH1-11 b06	443	Expect = e-162 Identities = 356/377 (94%)	Hordeum vulgare gene for CP29 precursor for core chlorophyll a/b binding (CAB) protein of photosystem II (PSII) gi|18957|emb|X63052.1|HVCP29
SSH1-4 e10	502	Expect = e-164 Identities = 357/377 (94%)	Hordeum vulgare gene for CP29 precursor for core chlorophyll a/b binding (CAB) protein of photosystem II (PSII) gi|18957|emb|X63052.1|HVCP29
CONTIG 61	(9 clones)		
REPRESENTATIVE			
SSH1-7 h12	502	Expect = 0.0 Identities = 400/418 (95%)	H.vulgare lhbC mRNA for **type III LHCII CAB** precursor protein gi|19022|emb|X63197.1|HVLHBC
SSH1-6 c09	433	Expect = 4e-072 Identities = 317/373 (84%)	Oryza sativa chlorophyll a-b binding protein mRNA, complete cds gi|2570510|gb|AF022738.1|AF022738
SSH1-10 a03	386	Expect = 3e-097 Identities = 309/351 (88%)	Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds gi|3126853|gb|AF061577.1|AF061577
SSH1-9 e10	682	Expect = 0.0 Identities = 530/591 (89%)	Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA, nuclear gene encoding chloroplast protein, complete cds gi|3126853|gb|AF061577.1|AF061577
SSH1-14 c04	697	Expect = e-144 Identities = 443/503 (88%)	Oryza sativa chlorophyll a/b binding protein (RCABP89) mRNA,nuclear gene encoding chloroplast protein, complete cds gi|3126853|gb|AF061577.1|AF061577
CONTIG 66	(2 clones)		
SSH1-9 g09	416	Expect = e-177 Identities = 338/345 (97%)	Hordeum vulgare partial mRNA for chlorophyll a/b-binding protein gi|3153150|emb|AJ006296.1|HVU6296
SSH1-4 e08	531	Expect = 0.0 Identities = 406/430 (94%)	Hordeum vulgare partial mRNA for chlorophyll a/b-binding protein gi|3153150|emb|AJ006296.1|HVU6296

Ribosomal RNA

Singletons

SSH1-1 b11	139	Expect = 0.11 Identities = 25/26 (96%)	Uncultured archaeon clone MD2896-3m.89 16S **ribosomal RNA** gene, partial sequence gi|115499558|gb|DQ984874.1|
SSH1-9 h05	376	Expect = 7e-024 Identities = 147/172 (85%)	Triticum aestivum 28S ribosomal RNA gene, partial sequence gi|15982657|gb|AY049041.1|
SSH1-12 d11	454	Expect = 0.41 Identities = 22/22 (100%)	Pythium longisporangium strain F-1200 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence gi|38373210|gb|AY455693.1|
SSH1-12 e07	233	Expect = 0.80 Identities = 24/25 (96%)	Uncultured Campylobacter sp. clone BES1 16S ribosomal RNA gene,partial sequence gi|75709287|gb|DQ184691.1|

SSH Adaptors

Singletons

SSH1-1 c06	72	Expect = 0.20 Identities = 24/25 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483162|emb|CT989710.1|
SSH1-1 h08	308	Expect = 3e-004 Identities = 27/27 (100%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103482641|emb|CT989025.1|
SSH1-2 d09	367	Expect = 0.005 Identities = 25/25 (100%)	Sesbania drummondii clone SSH-36_01_A09_T3 mRNA sequence gi|99126040|gb|DQ465789.1|
SSH1-2 f09	359	Expect = 2e-005 Identities = 29/29 (100%)	Synthetic construct RLS (RLS) gene, complete cds gi|64213751|gb|AY972077.1|
		Expect = 0.001 Identities = 29/30 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH1-3 b05	119	Expect = 5.8 Identities = 19/19 (100%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6986_7036_etc genomic sequence gi|109390343|gb|DQ518958.1|
SSH1-3 c10	350	Expect = 0.079 Identities = 23/23 (100%)	EST from a microgravity versus gravity **subtracted library** from Eucalyptus globulus seedlings grown under 14, 28 and 45days of clinostat conditions gi|103484081|emb|CT989434.1|
SSH1-3 f02	87	Expect = 0.98 Identities = 20/20 (100%)	Bordetella parapertussis strain Bpp5 **subtractive hybridization** product 6908 genomic sequence gi|109390333|gb|DQ518948.1|
SSH1-3 g09	20	Expect = 1.8 Identities = 17/17 (100%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103482030|emb|CT988166.1|
SSH1-4 a05	360	Expect = 8e-005 Identities = 31/32 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
		Expect = 2e-005 Identities = 29/29 (100%)	Photobacterium damselae subsp. piscicida trpB gene for putative transposase, clone pRDA16 gi|57635379|emb|AJ749803.1|
SSH1-4 b05	352	Expect = 8e-005 Identities = 31/32 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH1-4 c08	269	Expect = 0.001	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown

		Identities = 29/30 (96%)	under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH1-4 c10	398	Expect = 2e-005 Identities = 29/29 (100%)	Photobacterium damselae subsp. piscicida trpA gene for putative transposase, clone pRDA8 gi|57635379|emb|AJ749803.1|
SSH1-4 c11	515	Expect = 1e-004 Identities = 28/28 (100%)	Photobacterium damselae subsp. piscicida trpB gene for putative transposase, clone pRDA16 gi|57635379|emb|AJ749803.1|
SSH1-4 d07	640	Expect = 0.15 Identities = 23/23 (100%)	EST from a gravity versus microgravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103472242|emb|CT978757.1|
SSH1-4 e04	205	Expect = 7e-004 Identities = 29/30 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH1-4 e12	284	Expect = 0.99 Identities = 21/21 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45days of clinostat conditions gi|103484081|emb|CT989434.1|
SSH1-4 f03	385	Expect = 0.001 Identities = 26/26 (100%)	Photobacterium damselae subsp. piscicida trpA gene for putative transposase, clone pRDA33 gi|57635393|emb|AJ749809.1|
SSH1-4 g02	310	Expect = 0.018 Identities = 24/24 (100%)	Sesbania drummondii clone SSH-40_01_C12_T3 mRNA sequence gi|99126125|gb|DQ465793.1|
SSH1-4 g04	210	Expect = 1e-005 Identities = 29/29 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-5 a08	507	Expect = 0.030 Identities = 30/32 (93%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH1-5 a09	537	Expect = 1.9 Identities = 21/21 (100%)	EST from a gravity versus microgravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103472242|emb|CT978757.1|
SSH1-5 a10	731	Expect = 0.17 Identities = 23/23 (100%)	EST from a gravity versus microgravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103472242|emb|CT978757.1|
SSH1-5 b08	544	Expect = 1e-004 Identities = 31/32 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH1-5 c01	322	Expect = 1.1 Identities = 21/21 (100%)	EST from a gravity versus microgravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103472242|emb|CT978757.1|
SSH1-5 d07	345	Expect = 1.2 Identities = 21/21 (100%)	EST from a gravity versus microgravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103472242|emb|CT978757.1|
SSH1-5 d09	356	Expect = 0.081 Identities = 23/23 (100%)	EST from a gravity versus microgravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103472242|emb|CT978757.1|
SSH1-5 d11	527	Expect = 0.12 Identities = 23/23 (100%)	EST from a gravity versus microgravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103472242|emb|CT978757.1|
SSH1-6 f07	117	Expect = 4e-004 Identities = 26/26 (100%)	Photobacterium damselae subsp. piscicida partial coi genes for putative cytochrome C oxidase proteins, clone pRDA19 gi|57635379|emb|AJ749803.1|
SSH1-6 f09	313	Expect = 0.001 Identities = 26/26 (100%)	Photobacterium damselae subsp. piscicida trpA gene for putative transposase, clone pRDA8 gi|57635379|emb|AJ749803.1|
SSH1-6 g04	132	Expect = 0.11 Identities = 25/26 (96%)	Rhodococcus sp. RHA1, complete genome gi|110816552|gb|CP000431.1|
		Expect = 1.7 Identities = 20/20 (100%)	Sesbania drummondii clone SSH-57_01_G12_T3 mRNA sequence gi|99126419|gb|DQ465810.1|
SSH1-7 f03	582	Expect = 0.002 Identities = 26/26 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-8 b05	689	Expect = 7e-004 Identities = 27/27 (100%)	Pleurotus sapidus partial mRNA for putative versatile peroxidase gi|67763583|emb|AM039632.1|
SSH1-8 c09	487	Expect = 3e-005 Identities = 29/29 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-8 c10	710	Expect = 0.003 Identities = 29/30 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH1-8 c12	681	Expect = 0.003 Identities = 29/30 (96%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-8 d01	555	Expect = 5e-004 Identities = 27/27 (100%)	Pleurotus sapidus partial mRNA for putative versatile peroxidase gi|67763583|emb|AM039632.1|
SSH1-8 d03	382	Expect = 6e-006 Identities = 30/30 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-8 d12	759	Expect = 1e-005 Identities = 30/30 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-8 e08	509	Expect = 0.008 Identities = 25/25 (100%)	Pleurotus sapidus partial mRNA for putative versatile peroxidase gi|67763583|emb|AM039632.1|
SSH1-8 e10	420	Expect = 3e-005 Identities = 29/29 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-8 e11	515	Expect = 0.008 Identities = 28/29 (96%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-8 f01	331	Expect = 3e-004 Identities = 27/27 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-8 f11	624	Expect = 4e-005 Identities = 29/29 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-9 c08	521	Expect = 0.002 Identities = 26/26 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-9 d10	23	Expect = 0.019 Identities = 21/21 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-10 f05	321	Expect = 0.001 Identities = 26/26 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-10 h07	233	Expect = 8e-004 Identities = 26/26 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483534|emb|CT990082.1|
SSH1-11 a06	860	Expect = 0.003 Identities = 29/30 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483637|emb|CT990185.1|
SSH1-12 a07	833	Expect = 0.013 Identities = 28/29 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH1-12 a08	406	Expect = 0.006 Identities = 28/29 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH1-12 a11	354	Expect = 0.001 Identities = 29/30 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH1-12 b06	800	Expect = 0.74 Identities = 25/26 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH1-12 c06	396	Expect = 0.006 Identities = 28/29 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH1-12 c07	395	Expect = 0.023 Identities = 27/28 (96%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103482205|emb|CT988615.1|
SSH1-12 d04	465	Expect = 0.007 Identities = 25/25 (100%)	Photobacterium damselae subsp. piscicida partial coi genes for putative cytochrome C oxidase proteins, clone pRDA19 gi|57635372|emb|AJ749800.1|
SSH1-12 d10	358	Expect = 2e-005 Identities = 29/29 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|

SSH1-12 f05	339	Expect = 0.019 Identities = 24/24 (100%)	Agaricus bisporus partial mRNA for putative myosin heavy chain kinase (mhck gene), clone pm31 gi|26984416|emb|AJ534351.1|ABI534351
		Expect = 0.076 Identities = 23/23 (100%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6908 genomic sequence gi|109390333|gb|DQ518948.1|
SSH1-13 c06	319	Expect = 0.005 Identities = 25/25 (100%)	Photobacterium damselae subsp. piscicida partial coi genes for putative cytochrome C oxidase proteins, clone pRDA19 gi|57635372|emb|AJ749800.1|
SSH1-13 d01	197	Expect = 0.17 Identities = 25/26 (96%)	Arachis hypogaea clone Gsi52 trans caffeoyl CoA -3-o methyl transferase mRNA, partial sequence gi|53830011|gb|AY725194.1|
SSH1-13 d08	361	Expect = 0.001 Identities = 26/26 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-13 d10	473	Expect = 1.7 Identities = 24/25 (96%)	Sesbania drummondii clone SSH-40_01_C12_T3 mRNA sequence gi|99126125|gb|DQ465793.1|
SSH1-13 g04	613	Expect = 0.009 Identities = 28/29 (96%)	Pleurotus sapidus partial mRNA for putative versatile peroxidase gi|67763583|emb|AM039632.1|
SSH1-14 e09	310	Expect = 1.1 Identities = 21/21 (100%)	partial cDNA sequence from a Lambda ZAP II normalized full-length cDNA library of differentiating xylem from Eucalyptus gunnii gi|103479316|emb|CT985548.1|
SSH1-14 h04	426	Expect = 6.0 Identities = 23/24 (95%)	Pleurotus sapidus partial mRNA for putative versatile peroxidase gi|67763583|emb|AM039632.1|
SSH1-14 h09	100	Expect = 0.005 Identities = 30/32 (93%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH1-15 b10	214	Expect = 2.9 Identities = 20/20 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-15 c12	101	Expect = 0.076 Identities = 22/22 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-16 g03	302	Expect = 0.001 Identities = 29/30 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|

SSH Adaptors

Contigs

CONTIG 42	(4 clones)		
SSH1-11 d10	408	Expect = 2e-005 Identities = 29/29 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483637|emb|CT990185.1|
SSH1-3 f11 In SSH1-11 d10	392	Expect = 0.35 Identities = 22/22 (100%)	Mus musculus BAC clone RP23-274C16 from 1, complete sequence gi|23462966|gb|AC123955.5|
SSH1-2 e04 In SSH1-11 d10	411	Expect = 0.094 Identities = 23/23 (100%)	Zebrafish DNA sequence from clone DKEY-65B13 in linkage group 20,complete sequence gi|32400114|emb|AL929220.13|
		Expect = 0.37 Identities = 22/22 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions ADAPTOR gi|103483574|emb|CT990122.1|
SSH1-11 e06 In SSH1-11 d10	408	Expect = 2e-005 Identities = 29/29 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483637|emb|CT990185.1|
CONTIG 45	(2 clones)		
SSH1-12 b12	541	Expect = 0.13 Identities = 26/27 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH1-11 f06 In SSH1-12 b12	438	Expect = 4e-007 Identities = 48/52 (92%)	Triticum aestivum gi|109450933|emb|CT009735.1|
		Expect = 4e-004 Identities = 27/27 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483522|emb|CT990070.1|
CONTIG 48	(3 clones)		
SSH1-13 f10	552	Expect = 3e-005 Identities = 29/29 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
		Expect = 1e-004 Identities = 28/28 (100%)	Photobacterium damselae subsp. piscicida partial coi genes for putative cytochrome C oxidase proteins, clone pRDA19 gi|57635372|emb|AJ749800.1|
SSH1-3 g01 In SSH1-13 f10	434	Expect = 0.39 Identities = 28/30 (93%)	Pleurotus sapidus partial mRNA for putative versatile peroxidase gi|67763583|emb|AM039632.1|
		Expect = 1.6 Identities = 21/21 (100%)	PREDICTED: Rattus norvegicus similar to ADP-ribosylation factor guanine nucleotide factor 6 isoform a (predicted)(RGD1559968_predicted), mRNA gi|109504039|ref|XM_001070777.1|
SSH1-14 g04	829	Expect = 8e-004 Identities = 33/35 (94%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483637|emb|CT990185.1|
CONTIG 54	(3 clones)		
SSH1-2 b03	207	Expect = 1e-005 Identities = 29/29 (100%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103482566|emb|CT988924.1|
SSH1-2 a01	202	Expect = 0.003 Identities = 25/25 (100%)	EST from a gravity versus microgravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 gi|103472891|emb|CT979275.1|

SSH1-2 c03 In SSH1-2 a01	202	Expect = 1e-005 Identities = 29/29 (100%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103482566|emb|CT988924.1|
CONTIG 57	(3 clones)		
SSH1-4 b02	413	Expect = 3e-008 Identities = 50/54 (92%)	Medicago sativa clone C43 putative splicing factor Prp8 mRNA,partial cds gi|71534915|gb|DQ122784.1|
		Expect = 4e-007 Identities = 38/40 (95%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103482186|emb|CT988596.1|
SSH1-4 b03 In SSH1-4 b02	261	Expect = 2e-005 Identities = 29/29 (100%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103482186|emb|CT988596.1|
		Expect = 6e-005 Identities = 28/28 (100%)	Photobacterium damselae subsp. piscicida trpB gene for putative transposase, clone pRDA16 gi|57635366|emb|AJ749797.1|
SSH1-4 b08 In SSH1-4 b03	191	Expect = 1e-005 Identities = 29/29 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
		Expect = 2e-004 Identities = 27/27 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483838|emb|CT990386.1|
CONTIG 63	(2 clones)		
SSH1-8 b07	504	Expect = 3e-005 Identities = 29/29 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH1-8 b08	818	Expect = 5e-005 Identities = 29/29 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|

Vector Sequences

Singletons

SSH1-2 g11	633	Expect = 6e-038 Identities = 96/100 (96%)	Uncultured soil fungus partial ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene region, clone ITS11 (S2) gi|86604440|emb|AM229065.1|
		Expect = 9e-037 Identities = 97/102 (95%)	Cloning vector psiLentGene Hygromycin, complete sequence gi|45655413|gb|AY508734.1|
SSH1-8 c02	799	Expect = e-159 Identities = 384/414 (92%)	Uncultured soil fungus partial 18S rRNA gene, clone F47 (S2) gi|86604434|emb|AM229059.1|
		Expect = e-158 Identities = 368/394 (93%)	Cloning vector pGEM-WIZ, complete sequence gi|114846943|gb|DQ917671.1|
SSH1-10 c05	125	Expect = 3e-011 Identities = 38/38 (100%)	Cloning vector psiLentGene Hygromycin, complete sequence gi|45655413|gb|AY508734.1|
		Expect = 1e-010 Identities = 37/37 (100%)	Theobroma grandiflorum putative 21 kDa trypsin inhibitor gene, complete cds gi|55139087|gb|AY753564.1|
SSH1-11 c10	266	Expect = 4e-009 Identities = 35/35 (100%)	Uncultured Symphyonemopsis sp. clone TRK35 16S ribosomal RNA gene, partial sequence gi|58618861|gb|AY876902.1|
		Expect = 2e-008 Identities = 94/114 (82%)	Cloning vector pGEM-S1, complete sequence gi|114846943|gb|DQ917671.1|
SSH1-13 b03	117	Expect = 3e-011 Identities = 45/46 (97%)	Cloning vector psiLentGene Hygromycin, complete sequence gi|45655413|gb|AY508734.1|
SSH1-16 g10	837	Expect = 0.0 Identities = 519/539 (96%)	Cloning vector psiLentGene Basic, complete sequence gi|45655410|gb|AY508731.1|

Vector Sequences

Contigs

CONTIG 33	(2 clones)		
SSH1-8 f06	801	Expect = 2e-075 Identities = 199/207 (96%)	Cloning vector psiLentGene Hygromycin, complete sequence gi|45655413|gb|AY508734.1|
SSH1-9 h09 In SSH1-8 f06	780	Expect = 2e-026 Identities = 99/109 (90%)	Uncultured soil fungus partial ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene region, clone ITS11 (S2) gi|86604440|emb|AM229065.1|
		Expect = 2e-025 Identities = 100/111 (90%)	Cloning vector psiLentGene Hygromycin, complete sequence gi|45655413|gb|AY508734.1|
		Expect = 2e-025 Identities = 97/107 (90%)	Photobacterium damselae subsp. piscicida partial coi genes for putative cytochrome C oxidase proteins, clone pRDA19 gi|57635372|emb|AJ749800.1|
CONTIG 56	(2 clones)		
SSH1-2 h10	284	Expect = 2e-005 Identities = 29/29 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
		Expect = 0.001	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings

		Identities = 29/30 (96%)	grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH1-2 d11	589	Expect = e-105 Identities = 250/261 (95%)	Uncultured soil fungus partial 18S rRNA gene, clone F47 (S2) VECTOR gi|86604434|emb|AM229059.1|
		Expect = 1e-094 Identities = 232/243 (95%)	Cloning vector pGEM-WIZ, complete sequence gi|114846943|gb|DQ917671.1|

APPENDIX H

Detailed display of Blast N analysis results of SSH2 (R-D) classified according to function or origin categories.

The singletons and contigs are presented in separate tables.

The contig assembly program Cap 3 detected that some sequences were within some other sequences. These cases are indicated under the clone numbers of these sequences, (as "In SSH...").

First coloumn shows the clone number, second coloumn shows the length of read sequence (after sequencing), third coloumn indicates E-Value and identity and the fourth coloumn displays Blast N Homology Result.

"Representative" is used to indicate that not all clones representing a particular contig are shown.

Metabolism and Energy

Singletons

SSH2-1 b03	379	Expect = 9e-005 Identities = 43/48 (89%)	Hordeum vulgare mRNA for mitochondrial aldehyde dehydrogenase ALDH2, complete cds gi|15128579|dbj|AB055519.1|
SSH2-1 b05	19	Expect = 7.3 Identities = 16/16 (100%)	PREDICTED: Mus musculus similar to 3-phosphoglycerate dehydrogenase(LOC670122), mRNA gi|94371072|ref|XM_979269.1|
SSH2-1 c02	367	Expect = 1.3 Identities = 21/21 (100%)	Aspergillus flavus isolate BN008 aflatoxin biosynthesis gene cluster,complete sequence gi|46370460|gb|AY510452.1|
		Expect = 5.1 Identities = 23/24 (95%)	Homo sapiens MHC class II antigen (HLA-DQB1) gene, HLA-DQB1*03 allele, exon 2 and partial cds gi|95116739|gb|DQ503572.1|
SSH2-1 d05	59	Expect = 9.1 Identities = 21/22 (95%)	C.curvatus strain CBS 570 Ole1 gene gi|1783356|emb|Y10422.1|CCCBSOLE1
SSH2-1 d06	263	Expect = 0.001 Identities = 32/34 (94%)	Oryza sativa (japonica cultivar-group) Os01g0208700 (Os01g0208700) mRNA, complete cds gi|115435199|ref|NM_001048893.1|
		Expect = 3.6 Identities = 20/20 (100%)	Setaria italica putative C4 phosphoenolpyruvate carboxylase (ppc) mRNA, complete cds gi|20257596|gb|AF495586.1|
SSH2-1 d07	159	Expect = 0.52 Identities = 21/21 (100%)	Salmonella typhimurium LT2 colanic acid locus, partial sequence gi|10946229|gb|AF285085.1|AF285084S2
		Expect = 8.1 Identities = 19/19 (100%)	Lactobacillus gasseri strain 4B2 Apf1 (apf1) and Apf2 (apf2) genes, complete cds gi|29725571|gb|AY245438.1|
SSH2-1 d09	310	Expect = 1.1 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-95H8 on chromosome 9 Contains a pseudogene similar to part of 6-pyruvoyltetrahydropterin synthase (PTS), a novel gene similar to c9orf36, two novel genes and a novel pseudogene, complete sequence gi|38143417|emb|BX664726.5|
SSH2-1 e01	68	Expect = 2.8 Identities = 19/19 (100%)	Streptomyces aizunensis strain NRRL B-11277 glycosyltransferase, polyketide synthase type Is, acyl transferase, membrane protein, ABC transporter, sugar dehydratase/epimerase,sugar epimerase, sugar nucleotidyltransferase, sugar dehydratase/epimerase, thioesterase, acyl CoA ligase,amine oxidase, phosphopantetheinyl transferase,transcriptional regulator,carboxylase/carboxyltransferase, amidinohydrolase, amide synthetase, 5-aminolevulinate synthase, and acyl CoA ligase genes, complete cds; and unknown gene gi|62737766|gb|AY899214.1|
SSH2-1 e06	190	Expect = 0.64 Identities = 21/21 (100%)	Uncultured bacterium clone 30.115 NifH-like (nifH) gene, partial sequence gi|89279359|gb|DQ426509.1|
SSH2-1 e07	87	Expect = 3.9 Identities = 22/23 (95%)	Pedomicrobium sp. ACM 3067 manganese oxidation operon gi|82940266|emb|AM049177.1|
SSH2-1 f09	56	Expect = 8.4 Identities = 18/18 (100%)	Aspergillus niger strain VanTieghem glucoamylase (gluA-A) mRNA,complete cds gi|49615614|gb|AY652617.1|
		Expect = 8.4 Identities = 18/18 (100%)	Aspergillus nidulans FGSC A4 N-(5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valine synthase (AN2621.2), mRNA gi|67524326|ref|XM_655133.1|
		Expect = 8.4 Identities = 18/18 (100%)	Emericella nidulans acv synthetase (acvA) gene, partial cds gi|232729|gb|S40247.1|AH000059S2
SSH2-1 g01	373	Expect = 0.085 Identities = 35/39 (89%)	Hordeum vulgare mRNA for mitochondrial aldehyde dehydrogenase ALDH2,complete cds gi|15128579|dbj|AB055519.1|
		Expect = 0.33 Identities = 37/42 (88%)	Zea mays T cytoplasm male sterility restorer factor 2 (rf2a) gene, rf2a-B73 allele, complete cds gi|41393748|gb|AF215823.2|
SSH2-1 g09	162	Expect = 8.3 Identities = 22/23 (95%)	Mus musculus lysyl oxidase-like 2, mRNA (cDNA clone MGC:102220 IMAGE:30605240), complete cds gi|56270560|gb|BC086801.1|
		Expect = 8.3 Identities = 19/19 (100%)	Rattus norvegicus corticotropin releasing hormone (Crh), mRNA gi|13591919|ref|NM_031019.1|
SSH2-1 h01	216	Expect = 0.012 Identities = 60/72 (83%)	Oryza sativa (japonica cultivar-group) Os07g0108300 (Os07g0108300) mRNA, complete cds gi|115470234|ref|NM_001065251.1|
		Expect = 2.9 Identities = 20/20 (100%)	Aspergillus terreus NIH2624 L-asparaginase precursor (ATEG_01943) mRNA, complete cds gi|115387230|ref|XM_001211121.1|
SSH2-2 a03	216	Expect = 2.9	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1

		Identities = 23/24 (95%)	gi|58530787|dbj|AP008207.1|
		Expect = 2.9 Identities = 20/20 (100%)	Setosphaeria turcica cryptochrome-type photoreceptor (Cry1) mRNA, partial cds gi|56236495|gb|AY805205.1|
SSH2-2 a05	431	Expect = 6.1 Identities = 20/20 (100%)	L.cuprina mRNA for PC2-like prohormone convertase, 3007bp gi|1620967|emb|Y08899.1|LCY08899
SSH2-2 a06	309	Expect = 8e-011 Identities = 83/98 (84%)	Oryza sativa (japonica cultivar-group) Os02g0622400 (Os02g0622400) mRNA, complete cds gi|115447376|ref|NM_001054003.1|
		Expect = 0.069 Identities = 23/23 (100%)	Neurospora crassa OR74A related to mitochondrial phenylalanyl-tRNA synthetase (MSF1) [MIPS] (NCU01512.1) partial mRNA gi|85082667|ref|XM_951868.1|
		Expect = 1.1 Identities = 21/21 (100%)	Cyamus ovalis isolate osSA1b12 (T44) cytochrome oxidase subunit I(COI) gene, complete cds; tRNA-Leu gene, complete sequence; cytochrome oxidase subunit II (COII) gene, complete cds; tRNA-Lys and tRNA-Asp genes, complete sequence; ATPase 8 (ATP8), ATPase 6 (ATP6), and cytochrome oxidase subunit III (COIII) genes, complete cds; and NADH dehydrogenase subunit 3 (ND3) gene, partial cds; mitochondrial gi|70610940|gb|DQ095017.1|
SSH2-2 a07	470	Expect = 9e-061 Identities = 221/254 (87%)	Oryza sativa mRNA for S-adenosylmethionine decarboxylase 2 (adometDC2 gene) gi|6646867|emb|AJ251899.1|OSA251899
SSH2-2 a08	460	Expect = 6.5 Identities = 20/20 (100%)	Trypanosoma cruzi exopolyphosphatase mRNA, complete cds gi|33333526|gb|AF545106.1|
SSH2-2 b04	179	Expect = 9.3 Identities = 19/19 (100%)	Pedetes capensis surdaster cytochrome b (cyt b) gene, mitochondrial gene encoding mitochondrial protein, partial cds gi|1911229|gb|U59178.1|PCU59178
SSH2-2 c06	61	Expect = 9.5 Identities = 18/18 (100%)	Hynobius amjiensis NADH dehydrogenase subunit 1 (ND1) gene,complete cds; mitochondrial gi|51891051|gb|AY593148.1|
SSH2-2 c09	180	Expect = 9.4 Identities = 19/19 (100%)	Daucus carota ATP1 (atp1) gene, atp1-N1 allele, complete cds; mitochondrial gene for mitochondrial product gi|15429017|gb|AF301604.1|
		Expect = 9.4 Identities = 19/19 (100%)	PREDICTED: Gallus gallus similar to semaphorin 3D; collapsin 2(LOC415932), mRNA gi|50754182|ref|XM_414276.1|
SSH2-2 d04	63	Expect = 10.0 Identities = 21/22 (95%)	Pseudomonas saccharophila sucrose phosphorylase gene, complete cds gi|5114443|gb|AF158367.1|
		Expect = 10.0 Identities = 18/18 (100%)	Pseudomonas sp. B10 L-ornithine N5-hydroxylase (psbA) gene,complete cds gi|11037216|gb|AF230494.1|AF230494
		Expect = 10.0 Identities = 18/18 (100%)	Nicotiana tabacum gene for extensin, complete cds gi|505143|dbj|D13951.1|TOBEXTS
SSH2-2 d08	141	Expect = 7.1 Identities = 19/19 (100%)	PREDICTED: Pan troglodytes kinesin family member 1C, transcript variant 2 (KIF1C), mRNA gi|114665904|ref|XM_511296.2|
		Expect = 7.1 Identities = 19/19 (100%)	Pyrus communis cultivar Conference flavanon 3 beta-hydroxylase mRNA, complete cds gi|62632854|gb|AY965342.1|
SSH2-2 d10	61	Expect = 9.5 Identities = 18/18 (100%)	Streptomyces hygroscopicus mannopeptimycin biosynthetic gene cluster, complete sequence gi|52222852|gb|AY735112.1|
SSH2-2 e04	54	Expect = 0.51 Identities = 20/20 (100%)	Triticum monococcum phosphatidylserine decarboxylase, ZCCT2, ZCCT1, and SNF2P genes, complete cds; nucellin pseudogene, complete sequence; putative transposase, phosphatidylinositol phosphatidylcholine transfer protein sec14 cytosolic-like protein, and phytochrome P450-like protein genes, complete cds; and unknown genes gi|45357051|gb|AY485644.1|
SSH2-2 e05	182	Expect = 2.4 Identities = 20/20 (100%)	Mus musculus blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:I1C0030N15 product:hypothetical Amino acid/polyamine transporter II containing protein, full insert sequence gi|74188964|dbj|AK167098.1|
SSH2-2 e07	65	Expect = 2.6 Identities = 19/19 (100%)	PREDICTED: Danio rerio similar to glucose-fructose oxidoreductase domain containing 1 (LOC556899), mRNA gi|68354263|ref|XM_679833.1|
SSH2-2 g07	188	Expect = 9.8 Identities = 19/19 (100%)	Oryza sativa (japonica cultivar-group) Os07g0678600 (Os07g0678600) mRNA, complete cds gi|115474074|ref|NM_001067171.1|
		Expect = 9.8 Identities = 22/23 (95%)	Xanthoceras sorbifolium ATP synthase beta subunit (atpB) gene,partial cds; chloroplast gene for chloroplast product gi|14718264|gb|AF209697.1|
		Expect = 9.8 Identities = 22/23 (95%)	Acer saccharum ATP synthase beta subunit (atpB) gene, chloroplast gene encoding chloroplast protein, partial cds gi|4063521|gb|AF035893.1|
SSH2-2 g08	186	Expect = 0.62 Identities = 21/21 (100%)	Mus musculus c222389 pseudogene, complete sequence; nuclear receptor 2E1(Nr2e1) and sorting nexin 3 (Snx3) genes, complete cds; and lactation elevated 1 (Lace1) gene, partial cds gi|21668100|gb|AF520420.1|
		Expect = 0.62 Identities = 21/21 (100%)	Homo sapiens methionine sulfoxide reductase gene, complete cds,alternatively spliced gi|62868462|gb|AY958432.1|
SSH2-2 h02	81	Expect = 3.6 Identities = 22/23 (95%)	Aspergillus nomius isolate AN13137 aflatoxin biosynthesis gene cluster, complete sequence gi|46370510|gb|AY510454.1|
SSH2-3 b05	190	Expect = 2.5 Identities = 20/20 (100%)	Homo sapiens carbamylphosphate synthetase 1 gene, complete cds; nuclear gene for mitochondrial product gi|25992605|gb|AF536523.1|
		Expect = 9.9 Identities = 22/23 (95%)	Homo sapiens metalloproteinase-disintegrin (ADAM22) gene, partial cds gi|5882226|gb|AF158642.1|AF158642
SSH2-3 c07	614	Expect = 2.2 Identities = 21/21 (100%)	Homo sapiens HLCS gene for holocarboxylase synthetase, complete cds gi|15823776|dbj|AB063285.1|
SSH2-3 d07	389	Expect = 5.5 Identities = 20/20 (100%)	Arabidopsis thaliana FK506 binding / peptidyl-prolyl cis-trans isomerase (AT1G73655) mRNA, complete cds gi|30698955|ref|NM_106024.2|
SSH2-3 d08	218	Expect = 2.9 Identities = 20/20 (100%)	Boloria eunomia voucher TS11 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gi|115493914|gb|DQ922869.1|
		Expect = 2.9 Identities = 20/20 (100%)	PREDICTED: Pan troglodytes DNA cytosine methyltransferase 3 alpha, transcript variant 4 (DNMT3A), mRNA gi|114576487|ref|XM_001148658.1|
SSH2-3 e09	536	Expect = 7.7 Identities = 20/20 (100%)	Mus musculus diadenosine triphosphate hydrolase (Fhit) gene, exons 6 through 10 and partial cds gi|38327334|gb|AY363103.1|AY363102S2
SSH2-3 f12	316	Expect = 8e-014 Identities = 79/91 (86%)	H.chilense x T.turgidum conv. durum (Tritordeum) mRNA for S-adenosylmethionine decarboxylase gi|1403043|emb|X83881.1|HCTTSAMDC
SSH2-3 g04	355	Expect = 2e-082 Identities = 230/254 (90%)	Oryza sativa (japonica cultivar-group) enolase (Eno1) mRNA,complete cds gi|33113258|gb|AY335488.1|
		Expect = 2e-054 Identities = 204/235 (86%)	Cynodon dactylon pollen 2-phosphoglycerate dehydrogenase 2 precursor, mRNA, complete cds gi|37222050|gb|AY344113.2|
SSH2-4 a04	531	Expect = 7.6 Identities = 20/20 (100%)	Arabidopsis thaliana catalytic/ glutamate 5-kinase/ glutamate-5-semialdehyde dehydrogenase (AT3G55610) mRNA, complete cds gi|30694278|ref|NM_115419.3|
		Expect = 7.6 Identities = 20/20 (100%)	Arabidopsis thaliana mRNA for delta-1-pyrroline-5-carboxylate synthetase, partial cds, clone: RAFL22-44-G03 gi|62319127|dbj|AK220885.1|
		Expect = 7.6 Identities = 23/24 (95%)	Sus scrofa alpha-1,2-fucosyltransferase (FUT2) gene, 5'UTR gi|7328565|gb|AF136897.1|AF136897
SSH2-4 g09	633	Expect = 0.0 Identities = 521/549 (94%)	Triticum aestivum clone wlk4.pk0010.d11:fis, full insert mRNA sequence gi|32128806|gb|BT009255.1|
		Expect = 4e-045 Identities = 321/396 (81%)	Oryza sativa (japonica cultivar-group) glutathione S-transferase 2 mRNA, complete cds gi|112385745|gb|DQ859020.1|
SSH2-4 h08	113	Expect = 5.4 Identities = 19/19 (100%)	Macaca silenus mitochondrial DNA for NADH dehydrogenase subunit 4, subunit 5, partial cds gi|1619808|dbj|D85286.1|

SSH2-5 a12	323	Expect = 8e-048 Identities = 148/164 (90%)	Hordeum vulgare subsp. vulgare partial mRNA for putative carotenoid cleavage dioxygenase 1 (ccd1 gene) gi|51035341|emb|AJ784279.1|
SSH2-5 c04	194	Expect = 2.6 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-156I14 on chromosome 6 Contains the 5' end of the B3GAT2 gene for beta-1,3-glucuronyltransferase 2 (glucuronosyltransferas S) (GLCATS, KIAA1963) and a CpG island, complete sequence gi|12329487|emb|AL450320.4|
SSH2-5 d11	359	Expect = 1e-025 Identities = 78/83 (93%)	Hordeum vulgare putative cellulose synthase catalytic subunit (CesA2) mRNA, complete cds gi|39726028|gb|AY483152.1|
SSH2-5 e09	372	Expect = 1e-096 Identities = 290/326 (88%)	Oryza sativa mRNA for ferrochelatase, partial cds gi|2429617|dbj|AB007120.1|
SSH2-5 g06	397	Expect = e-105 Identities = 205/208 (98%)	Hordeum vulgare photosystem I subunit C (PsaC) gene, complete cds;NADH dehydrogenase (ndhD) gene, complete cds gi|167037|gb|L06607.1|BLYDLPSAC
SSH2-5 g10	596	Expect = e-100 Identities = 237/253 (93%)	Triticum aestivum mRNA for catalase, complete cds gi|1408511|dbj|D86327.1|
SSH2-5 h09	347	Expect = 4.8 Identities = 20/20 (100%)	PREDICTED: Pan troglodytes leucine aminopeptidase 3, transcript variant 4 (LAP3), mRNA gi|114593295|ref|XM_517119.2|
SSH2-6 c01	326	Expect = e-142 Identities = 274/279 (98%)	Triticum aestivum acetyl-coenzyme A carboxylase mRNA, complete cds, nuclear gene encoding plastid protein gi|2827149|gb|AF029895.1|
SSH2-6 c02	499	Expect = 7.1 Identities = 20/20 (100%)	Brevibacillus brevis lgrA, lgrB, lgrC, lgrD and lgrT genes for gramicidin biosynthesis, strain ATCC 8185 gi|42820776|emb|AJ566197.1|BBR566197
SSH2-6 d01	270	Expect = 5e-095 Identities = 200/207 (96%)	Wheat gstA2 gene for glutathione-S-transferase gi|21789|emb|X56004.1|TAGSTAGST
SSH2-6 d07	822	Expect = 6e-051 Identities = 286/346 (82%)	Zea mays dihydrolipoamide S-acetyltransferase mRNA, complete cds; nuclear gene for mitochondrial product gi|5669870|gb|AF135014.1|AF135014
SSH2-6 e03	102	Expect = 4.8 Identities = 19/19 (100%)	Homo sapiens methionyl aminopeptidase 2 (METAP2), mRNA gi|111160875|ref|NM_006838.3|
SSH2-7 b09	479	Expect = 1.7 Identities = 70/85 (82%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28710) mRNA, complete cds gi|30689308|ref|NM_113791.2
SSH2-7 b10	149	Expect = 1.9 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-74E24 on chromosome 6 Contains a KIAA0663 pseudogene and part of the gene for a novel EGF-like domain containing protein, complete sequence gi|11878443|emb|AL365217.10|
		Expect = 7.5 Identities = 19/19 (100%)	Arabidopsis thaliana EMB1047/FTSH12; ATP-dependent peptidase/ ATPase/ metallopeptidase (EMB1047/FTSH12) mRNA, complete cds gi|30699431|ref|NM_106604.2|
SSH2-7 c04	859	Expect = 1e-033 Identities = 155/181 (85%)	Hordeum vulgare vacuolar ATPase B subunit isoform mRNA, complete cds gi|167107|gb|L11862.1|BLYVATP57A
SSH2-7 c10	515	Expect = 2e-009 Identities = 87/104 (83%)	Lupinus albus mRNA for ATP citrate lyase b-subunit (aclb gene) gi|15919088|emb|AJ344108.1|LAL344108
SSH2-7 h06	751	Expect = 0.0 Identities = 691/705 (98%)	Triticum aestivum methylmalonate semialdehyde dehydrogenase mRNA, partial cds; nuclear gene for mitochondrial product gi|30144413|gb|AY255673.1|
SSH2-8 b09	55	Expect = 8.1 Identities = 18/18 (100%)	Methylocella silvestris soluble methane monooxygenase operon (smmo genes) gi|74381908|emb|AM072757.1|
SSH2-8 b10	59	Expect = 0.15 Identities = 21/21 (100%)	Rattus norvegicus alpha 1,3-galactosyltransferase 2 (isoglobotriaosylceramide synthase), mRNA (cDNA clone MGC:72309 IMAGE:5598151), complete cds gi|38197639|gb|BC061714.1|
		Expect = 2.3 Identities = 22/23 (95%)	Danio rerio mRNA for ornithine decarboxylase antizyme, complete cds gi|4239975|dbj|AB017117.1|
SSH2-8 b12	76	Expect = 0.83 Identities = 20/20 (100%)	Anthopleura elegantissima ATP synthase subunit 6 gene, partial cds; mitochondrial gene for mitochondrial product gi|19387514|gb|AF480930.1|
SSH2-8 c01	28	Expect = 8.3 Identities = 17/17 (100%)	Methylobacterium extorquens methanol oxidation genes, mxaE, mxaH,mxaB, and pmi-like genes, complete cds gi|2394385|gb|AF017434.1|AF017434
SSH2-8 f11	385	Expect = e-129 Identities = 295/313 (94%)	Triticum aestivum plasma membrane H+-ATPase (ha1) mRNA, complete cds gi|45268532|gb|AY543630.1|
SSH2-8 g01	378	Expect = 5.3 Identities = 20/20 (100%)	Mus musculus nuclear receptor subfamily 2, group F, member 1(Nr2f1), mRNA gi|111185901|ref|NM_010151.2|
		Expect = 5.3 Identities = 26/28 (92%)	PREDICTED: Macaca mulatta ribonuclease/angiogenin inhibitor (RNH1),mRNA gi|109104850|ref|XM_001116618.1|
		Expect = 5.3 Identities = 20/20 (100%)	Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4731413G05 product:similar to DJ137F1.2(NOVEL MEMBER OF THE POTASSIUM CHANNEL SUBFAMILY K) [Homo sapiens], full insert sequence gi|12852597|dbj|AK014626.1|
SSH2-8 g02	180	Expect = 2.4 Identities = 20/20 (100%)	Mouse DNA sequence from clone RP23-42C15 on chromosome 4 Contains mitochondrial NADH dehydrogenase 5 and 6 (mt-Nd5, mt-Nd6) pseudogenes and a mitochondrial cytochrome b (Cytb)pseudogene, complete sequence gi|46406383|emb|AL773519.5|
SSH2-8 h12	100	Expect = 1.2 Identities = 20/20 (100%)	Rhizobium leguminosarum bv. trifolii plasmid pR1eW14-2c rhamnose catabolism gene locus, complete sequence gi|37528956|gb|AF085687.2|
SSH2-9 b11	516	Expect = 7.4 Identities = 23/24 (95%)	Gossypium hirsutum monofunctional lysine-ketoglutarate reductase 1 mRNA, complete cds gi|23193175|gb|AF264147.1|
		Expect = 7.4 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-402P6 on chromosome X Contains five novel genes, five NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa (NDUFA4) pseudogenes and two CpG islands, complete sequence gi|29372487|emb|BX276092.9|
SSH2-9 e02	479	Expect = 6.8 Identities = 20/20 (100%)	Rana grylio virus 9506 3beta-hydroxysteroid dehydrogenase gene,complete cds gi|113720220|gb|DQ887345.1|
SSH2-9 e04	133	Expect = 6.6 Identities = 19/19 (100%)	Mouse DNA sequence from clone RP23-174M12 on chromosome 11 Contains the 3' end of a novel gene, the Mnt gene for max binding protein, two novel genes, the Srr gene for serine racemase, the 5' end of a novel gene and five CpG islands, complete sequence gi|19571943|emb|AL604066.9|
		Expect = 6.6 Identities = 19/19 (100%)	Hordeum vulgare mRNA for methionine synthase 2 enzyme (ms2 gene) gi|68655499|emb|AM039905.1|
SSH2-9 e08	389	Expect = 1e-040 Identities = 249/300 (83%)	Triticum aestivum glucose-6-phosphate isomerase (GPI) mRNA, complete cds gi|91694276|gb|DQ456872.1|
SSH2-9 e09	378	Expect = 6e-006 Identities = 36/38 (94%)	Zea mays ferredoxin-dependent glutamate synthase mRNA, complete cds gi|168476|gb|M59190.1|MZEFEGLU
SSH2-10 b06	820	Expect = 3.0 Identities = 21/21 (100%)	Streptococcus mutans galactokinase, galactose-1-P-uridyl transferase and UDP-galactose 4-epimerase genes, complete cds gi|1877421|gb|U21942.1|SMU21942
SSH2-10 b11	319	Expect = 0.018 Identities = 24/24 (100%)	Mus musculus lysyl oxidase-like 2, mRNA (cDNA clone MGC:102220 IMAGE:30605240), complete cds gi|56270560|gb|BC086801.1|
SSH2-10 d01	363	Expect = e-142 Identities = 299/311 (96%)	Wheat PsbP mRNA for 23 kDa oxygen evolving protein of photosystem II gi|21836|emb|X57407.1|TAPPSBP
SSH2-10 d11	839	Expect = 5e-005 Identities = 125/157 (79%)	Hordeum vulgare mRNA for mitochondrial aldehyde dehydrogenase ALDH2 complete cds gi|15128579|dbj|AB055519.1|
SSH2-10 f09	27	Expect = 0.12 Identities = 23/24 (95%)	Homo sapiens DNA for O6-methylguanine-DNA-methyltransferase promoter gi|34556|emb|X61657.1|HSMETDMET
SSH2-10 g03	59	Expect = 9.1 Identities = 18/18 (100%)	Chlamydomonas reinhardtii protein disulfide isomerase mRNA, nuclear gene encoding chloroplast protein, complete cds gi|4104540|gb|AF036939.1|AF036939
SSH2-10 h04	337	Expect = 4.7 Identities = 20/20 (100%)	Penicillium chrysogenum phl gene for phenylacetyl-CoA ligase, exons 1-6 gi|77019263|emb|AM048877.1|

SSH2-10 h09	892	Expect = e-149 Identities = 324/342 (94%)	Hordeum vulgare mRNA for hordeum vulgare (barley) ribophorin I,partial gi|5918186|emb|AJ133278.1|HVU133278
		Expect = e-132 Identities = 365/392 (93%)	Cloning vector psiLentGene Basic, complete sequence gi|45655410|gb|AY508731.1|
SSH2-10 h10	626	Expect = 0.0 Identities = 491/498 (98%)	X Tritordeum sp. glycine decarboxylase P subunit mRNA, complete cds gi|2565304|gb|AF024589.1|
SSH2-11 b10	308	Expect = 4.3 Identities = 20/20 (100%)	Candida parapsilosis cpr-c2 gene for conjugated polyketone reductase C2, complete cds gi|38423523|dbj|AB084516.1|
		Expect = 4.3 Identities = 23/24 (95%)	Streptomyces noursei ATCC 11455 nystatin biosynthetic gene cluster,complete sequence gi|8050835|gb|AF263912.1|AF263912
SSH2-11 b11	491	Expect = 7.0 Identities = 20/20 (100%)	Rattus norvegicus H-K-ATPase alpha 2b subunit (HKalpha2b) mRNA,complete cds gi|2735427|gb|U94913.1|RNU94913
SSH2-11 d09	602	Expect = 8.6 Identities = 20/20 (100%)	Zea mays pyruvate decarboxylase (pdc2) gene, complete cds gi|19851519|gb|AF370004.1|
		Expect = 8.6 Identities = 20/20 (100%)	Human DNA sequence from clone RP1-104A17 on chromosome 6q12-13 Contains the 3' end of the gene for stromal membrane-associated protein SMAP1A and the 3' end of the B3GAT2 gene for beta-1,3-glucuronyltransferase 2 (glucuronosyltransferase S) (GLCATS, KIAA1963), complete sequence gi|8894647|emb|AL121961.8|HSJ104A17
SSH2-11 e08	428	Expect = 1.5 Identities = 21/21 (100%)	Human DNA sequence from clone RP4-585I14 on chromosome 20 Contains the 3' end of the C20orf13 gene for chromosome 20 open reading frame 13 and the GAPDP2 gene for glyceraldehyde-3-phosphate dehydrogenase pseudogene 2, complete sequence gi|6456831|emb|AL121782.9|HSJ585I14
SSH2-11 e09	354	Expect = 4.9 Identities = 20/20 (100%)	Bactericera cockerelli cytochrome b (cytB) gene, partial cds; tRNA-Ser gene, complete sequence; NADH dehydrogenase subunit 1 (nd1) gene, complete cds; tRNA-Leu, large subunit ribosomal RNA, and tRNA-Val genes, complete sequence; and small subunit ribosomal RNA gene, partial sequence; mitochondrial gi|51243163|gb|AY601890.1|
SSH2-11 f11	527	Expect = 2e-080 Identities = 312/363 (85%)	Hordeum vulgare Hv-MMT1 mRNA for S-adenosyl-L-methionine: L-methionine S-methyltransferase, complete cds gi|7634679|dbj|AB028870.1|
SSH2-12 a06	266	Expect = e-103 Identities = 202/205 (98%)	Triticum monococcum peroxidase 6 (POX6) mRNA, complete cds gi|57635156|gb|AY857760.1|
SSH2-12 a09	581	Expect = 2e-087 Identities = 327/383 (85%)	Oryza sativa (japonica cultivar-group) Os07g0187400 (Os07g0187400) mRNA, complete cds gi|115470954|ref|NM_001065611.1|
		Expect = 2e-016 Identities = 114/136 (83%)	Arabidopsis thaliana ATP binding / nucleoside-triphosphatase/nucleotide binding (AT3G10420) mRNA, complete cds
SSH2-12 b01	849	Expect = e-162 Identities = 334/348 (95%)	Secale cereale ALDH2b mRNA for mitochondrial aldehyde dehydrogenase,complete cds gi|20530126|dbj|AB084896.1|
SSH2-12 b09	536	Expect = 7.7 Identities = 20/20 (100%)	Homo sapiens membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME), transcript variant 1,mRNA gi|6042205|ref|NM_000902.2|
		Expect = 7.7 Identities = 20/20 (100%)	Candida utilis beta-1,3 glucan transferase Bgl2p (BGL2) gene, partial cds gi|3661544|gb|AF091241.1|AF091241
SSH2-12 e11	533	Expect = 7.6 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-154C3 on chromosome 13 Contains a cytochrome c oxidase subunit IV pseudogene, a novel gene,an aldo-keto reductase family 1, member B10 (aldose reductase) (AKR1B10) pseudogene, a novel gene, similar to RIKEN cDNA 1700086N05 and CpG island, complete sequence gi|15147683|emb|AL139320.18|
SSH2-12 f12	625	Expect = 9.0 Identities = 20/20 (100%)	Zea mays chloroplast phytoene synthase (Y1) gene, complete cds; nuclear gene for chloroplast product gi|39842608|gb|AY455286.1|
SSH2-12 g01	303	Expect = 3e-019 Identities = 73/80 (91%)	Triticum aestivum mRNA for glycosyltransferase (a3b gene) gi|56409855|emb|AJ867399.1|

Metabolism and Energy

Contigs

CONTIG 4	(2 clones)		
SSH2-11 f03	470	Expect = 5e-013 Identities = 60/66 (90%)	Wheat gstA1 gene for glutathione-S-transferase gi|21787|emb|X56012.1|TAGSTA1
SSH2-5 c11 In SSH2-11 f03	151	Expect = 1e-010 Identities = 70/81 (86%)	Triticum aestivum mRNA for glutathione transferase (gstf6b gene) gi|23572871|emb|AJ441055.1|TAE441055
CONTIG 5	(3 clones)		
SSH2-11 g02	149	Expect = 3e-030 Identities = 94/102 (92%)	Zea mays ferredoxin-dependent glutamate synthase mRNA, complete cds gi|168476|gb|M59190.1|MZEFEGLU
SSH2-11 h04 In SSH2-11 g02	145	Expect = 0.030 Identities = 63/75 (84%)	Zea mays ferredoxin-dependent glutamate synthase mRNA, complete cds gi|168476|gb|M59190.1|MZEFEGLU
		Expect = 0.12 Identities = 22/22 (100%)	Zebrafish DNA sequence from clone RP71-1D10 in linkage group 14 Contains two novel genes similar to MATR3 (matrin 3), a novel gene similar to PDE6A (cGMP-specific phosphodiesterase 6A alpha (rod)), a novel gene similar to PERC (PGC-1-related estrogen receptor alpha coactivator) and two CpG islands, complete sequence gi|22552779|emb|AL645792.7|
		Expect = 7.3 Identities = 19/19 (100%)	Aspergillus terreus NIH2624 GTP-binding protein 1 (ATEG_02011)mRNA, complete cds gi|115387366|ref|XM_001211189.1|
SSH2-11 h01 In SSH2-11 g02	143	Expect = 6e-028 Identities = 93/102 (91%)	Zea mays ferredoxin-dependent glutamate synthase mRNA, complete cds gi|168476|gb|M59190.1|MZEFEGLU
CONTIG 6	(6 clones)		
SSH2-11 h07	484	Expect = 0.007 Identities = 25/25 (100%)	Arachis hypogaea clone Gsi115 alcohol dehydrodenase mRNA, partial cds gi|54306361|gb|AY725189.1|
SSH2-5 e02 In SSH2-11 h07	452	Expect = 0.10 Identities = 23/23 (100%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6653_6821_etc genomic sequence gi|109390341|gb|DQ518956.1|
SSH2-5 c01 In SSH2-11 h07	408	Expect = 4e-004 Identities = 27/27 (100%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103482051|emb|CT988187.1|
SSH2-11 h08 In SSH2-11 h07	410	Expect = 1e-004 Identities = 28/28 (100%)	Arachis hypogaea clone Gsi115 alcohol dehydrodenase mRNA, partial cds gi|54306361|gb|AY725189.1|
SSH2-1 g12	360	Expect = 0.32 Identities = 22/22 (100%)	Paralichthys olivaceus ctrlr mRNA for calcitonin receptor-like receptor, complete cds gi|7262546|dbj|AB035315.1|
		Expect = 5.0	Hansenula polymorpha beta-isopropylmalate dehydrogenase (LEU2) gene,complete cds

		Identities = 20/20 (100%)	gi|392892|gb|U00889.1|U00889
SSH2-1 f11 In SSH2-11 h08	434	Expect = 0.39 Identities = 22/22 (100%)	Paralichthys olivaceus ctrlr mRNA for calcitonin receptor-like receptor, complete cds gi|7262546|dbj|AB035315.1|
		Expect = 1.6 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-385F7 on chromosome 6 Contains the 5' end of the CD2AP gene for CD2-associated protein and three CpG islands, complete sequence gi|13991969|emb|AL355353.23|
		Expect = 6.1 Identities = 23/24 (95%)	Solanum pimpinellifolium haplotype D fruit vacuolar invertase gene, intron 2 gi|34099922|gb|AY294248.1|
CONTIG 8	(2 clones)		
SSH2-12 a04	307	Expect = 1.1 Identities = 30/33 (90%)	Medicago truncatula clone mth2-15c20, complete sequence gi|32189458|gb|AC126009.22|
SSH2-12 a05	377	Expect = 0.086 Identities = 26/27 (96%)	Solanum tuberosum methionine synthase (MS) mRNA, complete cds gi|8439544|gb|AF082893.1|
		Expect = 1.3 Identities = 33/37 (89%)	Sorghum bicolor clone SBTXS_0032H17 putative cytochrome P450-like protein, putative DNA-binding protein homolog, TATA-binding protein, hypothetical protein M3E9.200, 3-glucanase, K-exchanger-like protein, small heat shock-like protein, methionine synthase protein, putative far-red impaired response protein, and putative vegetative storage protein genes, complete cds gi|18483227|gb|AF466201.1|
CONTIG 10	(3 clones)		
SSH2-12 c05	299	Expect = 1e-049 Identities = 139/151 (92%)	Hordeum vulgare HvMS mRNA for methionine synthase, complete cds gi|50897037|dbj|AB164396.1|
SSH2-5 b11 In SSH2-12 c05	298	Expect = e-123 Identities = 251/259 (96%)	Hordeum vulgare HvMS mRNA for methionine synthase, complete cds gi|50897037|dbj|AB164396.1|
SSH2-12 b04	311	Expect = 3e-013 Identities = 92/111 (82%)	Hordeum vulgare HvMS mRNA for methionine synthase, complete cds gi|50897037|dbj|AB164396.1|
		Expect = 4.3 Identities = 20/20 (100%)	Baboon herpesvirus 2 strain OU1-76 glycoprotein G (US4) gene,partial cds; glycoprotein gJ (US5) gene, complete cds;and glycoprotein gD (US6) gene, partial cds gi|3514049|gb|AF082809.1|
CONTIG 11	(2 clones)		
SSH2-1 a02	395	Expect = 2e-080 Identities = 251/283 (88%)	Oryza sativa fructose-6-phosphate-2-kinase/fructose-2, 6-bisphosphatase mRNA, complete cds gi|18251458|gb|AF456329.1|AF456329
SSH2-1 h08 In SSH2-1 a02	357	Expect = 1e-046 Identities = 245/294 (83%)	Oryza sativa fructose-6-phosphate-2-kinase/fructose-2, 6-bisphosphatase mRNA, complete cds gi|18251458|gb|AF456329.1|AF456329
CONTIG 15	(4 clones)		
SSH2-3 a08	564	Expect = 0.0 Identities = 482/517 (93%),	Wheat mRNA for chloroplast phosphoglycerate kinase (EC 2.7.2.3)
SSH2-3 e06	464	Expect = 0.0 Identities = 436/446 (97%)	Wheat mRNA for chloroplast phosphoglycerate kinase (EC 2.7.2.3) gi|21832|emb|X15233.1|TAPGKCHL
SSH2-9 d05 In SSH2-3 e06	464	Expect = 0.0 Identities = 423/439 (96%)	Wheat mRNA for chloroplast phosphoglycerate kinase (EC 2.7.2.3) gi|21832|emb|X15233.1|TAPGKCHL
SSH2-3 a07	755	Expect = 3e-080 Identities = 300/347 (86%),	Wheat mRNA for chloroplast phosphoglycerate kinase (EC 2.7.2.3) gi|21832|emb|X15233.1|TAPGKCHL
CONTIG 16	(4 clones)		
SSH2-3 f04	122	Expect = 1.5 Identities = 20/20 (100%)	Aspergillus nidulans FGSC A4 hypothetical protein (AN5843.2), mRNA gi|67539345|ref|XM_658355.1|
SSH2-9 b04 In SSH2-3 f04	122	Expect = 0.38 Identities = 21/21 (100%)	Oryza sativa (japonica cultivar-group) chromosome 10 clone B1107B01, complete sequence gi|37700282|gb|AC146893.1|
SSH2-3 g01 In SSH2-3 f04	122	Expect = 0.024 Identities = 47/55 (85%)	Oryza sativa (japonica cultivar-group) Os03g0108500 (Os03g0108500)mRNA, complete cds gi|115450200|ref|NM_001055236.1|
		Expect = 1.5 Identities = 23/24 (95%)	Homo sapiens CDC45 cell division cycle 45-like (S. cerevisiae) (CDC45L)gene, complete cds gi|45505187|gb|AY572790.1|
		Expect = 5.9 Identities = 19/19 (100%)	Human DNA sequence from clone RP3-395P12 on chromosome 1q24-25 Contains a glutamic-oxaloacetic transaminase 2, mitochondrial(aspartate aminotransferase 2)(GOT2) pseudogene, a novel gene and the TNFSF4 gene for tumor necrosis factor(ligand) superfamily, member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa), complete sequence gi|3646083|emb|AL022310.1|HS395P12
SSH2-3 f02	210	Expect = 0.046 Identities = 23/23 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483394|emb|CT989942.1|
CONTIG 30	(3 clones)		
SSH2-6 f08	183	Expect = 1e-051 Identities = 129/139 (92%)	Triticum aestivum clone wlk8.pk0011.e10:fis, full insert mRNA sequence gi|32128823|gb|BT009272.1|
SSH2-6 g05 In SSH2-6 f08	183	Expect = 3e-006 Identities = 51/58 (87%)	Pisum sativum serine hydroxymethyltransferase mRNA, complete cds gi|169157|gb|M87649.1|PEASHMTA
SSH2-6 g06	186	Expect = 3e-040 Identities = 108/115 (93%)	Triticum aestivum clone wlk8.pk0011.e10:fis, full insert mRNA sequence gi|32128823|gb|BT009272.1|
CONTIG 32	(2 clones)		
SSH2-6 g01	305	Expect = e-128 Identities = 253/259 (97%)	Triticum aestivum sucrose-phosphate synthase 7 mRNA, partial cds gi|33341092|gb|AF347069.1|
SSH2-6 g02 In SSH2-6 g01	305	Expect = e-128 Identities = 253/259 (97%)	Triticum aestivum sucrose-phosphate synthase 7 mRNA, partial cds gi|33341092|gb|AF347069.1|
CONTIG 39	(3 clones)		
SSH2-9 b05	353	Expect = 3e-026 Identities = 144/168 (85%)	Hordeum vulgare arabinoxylan arabinofuranohydrolase isoenzyme AXAH-II mRNA, complete cds gi|13398413|gb|AF320325.1|AF320325
SSH2-9 a04	555	Expect = e-128 Identities = 269/276 (97%)	Cloning vector psiLentGene Hygromycin, complete sequence gi|45655413|gb|AY508734.1|
SSH2-9 a05 In SSH2-9 a04	283	Expect = 5e-092 Identities = 213/226 (94%)	Hordeum vulgare arabinoxylan arabinofuranohydrolase isoenzyme AXAH-II mRNA, complete cds gi|13398413|gb|AF320325.1|AF320325
CONTIG 44	(11 clones)		
SSH2-11 b02	439	Expect = 1e-010 Identities = 74/86 (86%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28710) mRNA, complete cds gi|30689308|ref|NM_113791.2|
		Expect = 1e-010 Identities = 74/86 (86%)	Arabidopsis thaliana putative adenosine triphosphatase (At3g28710)mRNA, complete cds gi|23297056|gb|AY142622.1|
SSH2-11 d01	642	Expect = 3e-018	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-

In SSH2-11 b02		Identities = 162/199 (81%)	transporting ATPase, rotational mechanism (AT3G28715) mRNA, complete cds gi|18405896|ref|NM_113792.1|
SSH2-11 c02	600	Expect = 4e-011 Identities = 157/199 (78%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28715) mRNA, complete cds gi|18405896|ref|NM_113792.1|
SSH2-11 c03 In SSH2-11 c02	457	Expect = 0.007 Identities = 61/73 (83%)	Oryza sativa (japonica cultivar-group) Os01g0587000 (Os01g0587000) mRNA, complete cds gi|115437983|ref|NM_001049964.1|
		Expect = 6.5 Identities = 23/24 (95%)	Canis familiaris masticatory myosin heavy chain 2M gene, complete cds gi|83026773|gb|DQ227287.1|
SSH2-11 b03 In SSH2-11 c02	207	Expect = 0.70 Identities = 24/25 (96%)	Homo sapiens BAC clone CTD-2507I16 from 2, complete sequence gi|18098555|gb|AC079896.6|
		Expect = 2.8 Identities = 20/20 (100%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6895 genomic sequence gi|109390326|gb|DQ518941.1|
SSH2-11 a02	467	Expect = 3e-011 Identities = 72/83 (86%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28715) mRNA, complete cds gi|18405896|ref|NM_113792.1|
		Expect = 1.7 Identities = 24/25 (96%)	Arabidopsis thaliana putative protein kinase (At3g23310) mRNA,complete cds gi|17381025|gb|AY063969.1|
SSH2-11 e02	444	Expect = 3e-017 Identities = 106/125 (84%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28710) mRNA, complete cds gi|30689308|ref|NM_113791.2|
SSH2-11 d02	636	Expect = 7e-010 Identities = 146/185 (78%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28715) mRNA, complete cds gi|18405896|ref|NM_113792.1|
SSH2-11 c01 In SSH2-11 c02	474	Expect = 3e-011 Identities = 157/199 (78%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28715) mRNA, complete cds gi|18405896|ref|NM_113792.1|
SSH2-11 e01	833	Expect = 0.77 Identities = 28/30 (93%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28710) mRNA, complete cds gi|30689308|ref|NM_113791.2|
SSH2-11 a03 In SSH2-11 e01	605	Expect = 0.002 Identities = 44/50 (88%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28715) mRNA, complete cds gi|18405896|ref|NM_113792.1|

Signal Transduction

Singletons

SSH2-1 b12	343	Expect = 0.020 Identities = 54/64 (84%)	Triticum aestivum chloroplast-localized Ptr ToxA-binding protein1(TaThf1) mRNA, complete cds; nuclear gene for chloroplast product gi|38570260|gb|AY377991.1|
		Expect = 0.020 Identities = 54/64 (84%)	Triticum aestivum chloroplast inositol phosphatase-like protein mRNA, complete cds; nuclear gene for chloroplast product gi|52548245|gb|AY736122.1|
		Expect = 0.31 Identities = 31/34 (91%)	Hordeum vulgare lt101.1 gene for putative membrane protein gi|13751166|emb|AJ310994.1|HVU310994
SSH2-1 c12	272	Expect = 2e-069 Identities = 159/169 (94%)	Triticum aestivum chloroplast-localized Ptr ToxA-binding protein1(TaThf1) mRNA, complete cds; nuclear gene for chloroplast product gi|38570260|gb|AY377991.1|
		Expect = 2e-069 Identities = 159/169 (94%)	Triticum aestivum chloroplast inositol phosphatase-like protein mRNA, complete cds; nuclear gene for chloroplast product gi|52548245|gb|AY736122.1|
SSH2-1 d02	158	Expect = 2.0 Identities = 20/20 (100%)	Mus musculus Rho GTPase activating protein 6 (Arhgap6), transcript variant 1, mRNA gi|87252723|ref|NM_009707.2|
SSH2-1 f03	148	Expect = 7.5 Identities = 19/19 (100%)	Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa)(CDC42) gene, complete cds gi|50234980|gb|AY673602.1|
		Expect = 7.5 Identities = 19/19 (100%)	Rattus sp. mRNA for wee1 tyrosine kinase, complete cds gi|500609|dbj|D31838.1|RATWEE1
SSH2-1 f06	539	Expect = 0.008 Identities = 43/49 (87%)	Oryza sativa (japonica cultivar-group) cDNA, clone: J100090E08, full insert sequence gi|116013042|dbj|AK243677.1|
		Expect = 7.7 Identities = 23/24 (95%)	Human DNA sequence from clone RP11-466G24 on chromosome 10 Contains the 5' end of the gene for Rho-GTPase activating protein 10(ARHGAP10) and a CpG island, complete sequence gi|15626404|emb|AL355979.11|
		Expect = 7.7 Identities = 20/20 (100%)	Oropouche virus strain IQT7085 small segment nucleoprotein gene,partial cds; and non-structural protein (NSs) gene, complete cds gi|7329054|gb|AF164554.1|AF164554
SSH2-1 h11	265	Expect = 3.6 Identities = 20/20 (100%)	Carassius auratus signal transducer and activator of transcription 1 (STAT1) mRNA, complete cds gi|29540611|gb|AY242386.1|
SSH2-2 b01	387	Expect = 1.4 Identities = 21/21 (100%)	PREDICTED: Macaca mulatta similar to olfactory receptor, family 1,subfamily F, member 1 (LOC703023), mRNA gi|109127390|ref|XM_001091333.1|
SSH2-2 b10	231	Expect = 3.1 Identities = 20/20 (100%)	Mus musculus toll-like receptor 7, mRNA (cDNA clone MGC:155833 IMAGE:40129519), complete cds gi|111308750|gb|BC120596.1|
		Expect = 3.1 Identities = 20/20 (100%)	PREDICTED: Gallus gallus similar to crystallin, zeta-like 1 isoform a; quinone reductase-like 1 (LOC418505), mRNA gi|50729938|ref|XM_416714.1|
		Expect = 3.1 Identities = 20/20 (100%)	Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630110O18 product:toll-like receptor 7, full insert sequence gi|74191946|dbj|AK154906.1|
		Expect = 3.1 Identities = 20/20 (100%)	Mouse DNA sequence from clone RP23-339O7 on chromosome 11 Contains part of a novel gene and the Nmu2r gene for neuromedin U receptor 2, complete sequence gi|29367465|emb|AL671969.39|
		Expect = 3.1 Identities = 20/20 (100%)	Mouse DNA sequence from clone RP23-20C9 on chromosome 11 Contains the Igfbp1 and Igfbp3 genes for insulin-like growth factor binding protein 1, a novel gene and a CpG island, complete sequence gi|20145926|emb|AL607124.15|
SSH2-2 b11	384	Expect = 5.4 Identities = 20/20 (100%)	PREDICTED: Danio rerio similar to GEM-interacting protein (GMIP)(LOC565801), mRNA gi|68357133|ref|XM_689070.1|
SSH2-2 b12	166	Expect = 2.2 Identities = 20/20 (100%)	Human DNA sequence from clone RP3-438L4 on chromosome 1p36.2-36.3 Contains part of the CAMTA1 gene for calmodulin binding transcription activator 1, complete sequence gi|4835272|emb|Z97635.10|HS438L4
SSH2-2 c12	349	Expect = 1.2 Identities = 21/21 (100%)	PREDICTED: Mus musculus BAT2 domain containing 1, transcript variant 6 (Bat2d), mRNA gi|94364478|ref|XM_976536.1|
		Expect = 1.2 Identities = 21/21 (100%)	PREDICTED: Danio rerio similar to adenylyl cyclase type V (LOC568654), mRNA gi|68382818|ref|XM_691996.1|

		Expect = 1.2 Identities = 24/25 (96%)	Mus musculus strain C57BL/6J cytokine gene cluster, partial sequence gi|27960533|gb|AF463670.1|
SSH2-2 d02	137	Expect = 0.44 Identities = 21/21 (100%)	Homo sapiens cDNA FLJ16738 fis, clone BRACE2007640, weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 gi|34528431|dbj|AK122984.1|
		Expect = 0.44 Identities = 21/21 (100%)	Homo sapiens mRNA for epidermal growth factor receptor pathway substrate 8-like protein 2 variant, clone: HRC04418 gi|62897364|dbj|AK222903.1|
SSH2-2 e01	179	Expect = 2.4 Identities = 20/20 (100%)	PREDICTED: Rattus norvegicus similar to putative pheromone receptor (Go-VN4) (LOC292510), mRNA gi|109460952|ref|XR_007939.1|
		Expect = 9.3 Identities = 19/19 (100%)	Candida albicans SC5314 putative protein kinase (CaO19_7388), mRNA gi|68478720|ref|XM_711536.1|
		Expect = 9.3 Identities = 19/19 (100%)	Homo sapiens DNA repair protein (XRCC1), partial sequence gi|21624595|gb|L34079.2|HUMXRCC1G
SSH2-2 e02	63	Expect = 10.0 Identities = 18/18 (100%)	Triticum aestivum partial cdc2l2 gene for cell division cycle 2-like 2 kinase gi|86438612|emb|AM072968.1|
SSH2-2 e11	388	Expect = 0.35 Identities = 28/30 (93%)	Agaricus bisporus partial mRNA for putative inorganic phosphate transporter (ipt gene), clone pm8 gi|26984428|emb|AJ534357.1|ABI534357
		Expect = 1.4 Identities = 21/21 (100%)	Drosophila melanogaster MAP kinase kinase 4 CG9738-RA (Mkk4), mRNA gi|24645101|ref|NM_058005.3|
SSH2-2 f01	106	Expect = 5.0 Identities = 19/19 (100%)	PREDICTED: Danio rerio similar to Neurobeachin protein (Lysosomal trafficking regulator 2) (BCL8B protein) (LOC559130), partial mRNA gi|68368042|ref|XM_682445.1|
		Expect = 5.0 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-313L9 on chromosome 13 Contains a novel gene, the IRS2 gene for insulin receptor substrate 2 and two CpG islands, complete sequence gi|14329908|emb|AL162497.20|
SSH2-2 f06	140	Expect = 7.0 Identities = 19/19 (100%)	Arabidopsis thaliana ATP binding (AT4G35520) mRNA, complete cds gi|30690397|ref|NM_119717.2|
		Expect = 7.0 Identities = 19/19 (100%)	Oryza sativa S-locus receptor-like kinase RLK11 (RLK11) mRNA, complete cds gi|22086625|gb|AF403128.1|
SSH2-2 f09	151	Expect = 1.9 Identities = 20/20 (100%)	Mus musculus solute carrier family 45, member 1 (Slc45a1), mRNA gi|75709221|ref|NM_173774.3|
		Expect = 7.6 Identities = 19/19 (100%)	PREDICTED: Gallus gallus similar to calcium-independent phospholipase A2 (LOC417785), mRNA gi|50728197|ref|XM_416028.1|
SSH2-2 g09	187	Expect = 9.8 Identities = 19/19 (100%)	Homo sapiens dopamine receptor D1 (DRD1), mRNA gi|88758587|ref|NM_000794.3|
SSH2-3 b02	44	Expect = 5.6 Identities = 18/18 (100%)	Mouse DNA sequence from clone RP23-338M9 on chromosome 11 Contains the 3' end of the Gas7 gene for growth arrest specific 7, the Rcvrn gene for recoverin, the Glp2r gene for glucagon-like peptide 2 receptor, a novel gene and the gene for a novel protein (1110001P11Rik), complete sequence gi|25045225|emb|AL646097.25|
SSH2-3 b06	158	Expect = 8.1 Identities = 22/23 (95%)	PREDICTED: Tribolium castaneum similar to G protein beta subunit-like (LOC661740), mRNA gi|91089924|ref|XM_967886.1|
		Expect = 8.1 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-153I24 on chromosome 13q33.1-34 Contains the LIG4 gene for ligase IV, DNA, ATP-dependent, a novel gene (FLJ14906), the TNFSF13B gene for tumor necrosis factor (ligand) superfamily, member 13b and a CpG island, complete sequence gi|15020854|emb|AL157762.13|
SSH2-3 b08	517	Expect = 5e-010 Identities = 85/101 (84%)	Oryza sativa (japonica cultivar-group) Os10g0511900 (Os10g0511900) mRNA, complete cds gi|115482897|ref|NM_001071577.1|
		Expect = 1.9 Identities = 21/21 (100%)	Trypanosoma danilewskyi alpha-tubulin mRNA, complete cds gi|74229923|gb|DQ080027.1|
		Expect = 1.9 Identities = 27/29 (93%)	Caenorhabditis elegans PhosphoLipase C family member (plc-3) (plc-3) mRNA, complete cds gi|71994160|ref|NM_063804.2|
SSH2-3 c02	511	Expect = 1.8 Identities = 21/21 (100%)	Human DNA sequence from clone RP4-658I14 on chromosome 1p33-34.3 Contains the 3' end of the MPRP-1 gene for metalloprotease related protein 1, complete sequence gi|9581793|emb|AL109845.8|HSJ658I14
		Expect = 7.3 Identities = 23/24 (95%)	Homo sapiens estrogen-related receptor gamma (ESRRG) gene, complete cds gi|41324139|gb|AY528719.1|
		Expect = 7.3 Identities = 20/20 (100%)	PREDICTED: Canis familiaris similar to vascular endothelial zinc finger 1, transcript variant 1 (LOC491106), mRNA gi|73966535|ref|XM_548226.2|
		Expect = 7.3 Identities = 23/24 (95%)	Mouse DNA sequence from clone RP24-316B1 on chromosome 4 Contains the 5' end of a variant of the Ptprd gene for receptor type protein tyrosine phosphatase D and a CpG island, complete sequence gi|27899682|emb|AL929553.6|
SSH2-3 d04	115	Expect = 5.5 Identities = 19/19 (100%)	Pleurodeles waltl transcription factor HoxC12 mRNA, complete cds gi|24637175|gb|AF434200.1|
		Expect = 5.5 Identities = 22/23 (95%)	Tetraodon fluviatilis JAK1 tyrosine kinase (JAK1) gene, complete cds gi|59276133|gb|AC148151.3|
SSH2-4 a09	175	Expect = 7e-013 Identities = 104/125 (83%)	Oryza sativa chromosome 3 BAC clone OSJNBb0024J17, complete sequence gi|33667149|gb|AC133340.4|
		Expect = 9.1 Identities = 19/19 (100%)	Canis familiaris isolate cOR5H12 olfactory receptor family 5 subfamily H-like gene, partial sequence gi|39655851|gb|AY355870.1|
		Expect = 9.1 Identities = 19/19 (100%)	Synthetic bovine rhodopsin gene, complete cds gi|208048|gb|M12689.1|SYNBOVRDPA
SSH2-4 a10	306	Expect = 1.1 Identities = 21/21 (100%)	Human DNA sequence from clone RP3-419C19 on chromosome 1q31 Contains the RGS2 gene for regulator of G-protein signalling 2, 24kDa, an unprocessed pseudogene similar to a hypothetical protein (FLJ10996), a processed pseudogene similar to integrin beta 1 binding protein 1 (ITGB1BP1) and a CpG island, complete sequence gi|5805139|emb|AL035407.15|HS419C19
SSH2-4 d01	604	Expect = 8.7 Identities = 20/20 (100%)	Danio rerio phospholipase C gamma 1 (plcg1) mRNA, complete cds gi|27883902|gb|AY163168.1|
		Expect = 8.7 Identities = 32/36 (88%)	Triticum aestivum chlorophyll a/b-binding protein WCAB precursor(Wcab) mRNA, complete cds gi|1657858|gb|U73218.1|TAU73218
SSH2-4 d05	188	Expect = 9.8 Identities = 19/19 (100%)	Mus musculus endothelial differentiation sphingolipid G-protein-coupled receptor 1, mRNA (cDNA clone MGC:61190 IMAGE:6415920), complete cds gi|29145074|gb|BC049094.1|
		Expect = 9.8 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-122K13 on chromosome 10 Contains the 5' end of the TUBGCP2 gene for tubulin gamma complex associated protein 2, the gene for a novel protein, the gene for calcyon D1 dopamine receptor-interacting protein(CALCYON), an autointegration factor (BANF1) pseudogene, a novel gene, the gene for uterine-specific proline-rich acidic protein (UPA), gene FLJ34392, the ECHS1 gene for enoyl Coenzyme A hydratase, short chain, 1, mitachondrial, the gene for peroxisomal N1-acetyl-spermine/spermidine oxidase (PAO), a novel gene, the 5' end of a novel gene (LOC92170) and ten CpG islands, complete sequence gi|21211719|emb|AL360181.37|
SSH2-4 d09	384	Expect = 5.4 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-81F11 on chromosome 13 Contains a gene for a novel protein similar to RhoGAP, complete sequence gi|11061969|emb|AL139187.19|
SSH2-4 e11	477	Expect = 6.8 Identities = 20/20 (100%)	Homo sapiens RAS protein activator like 2, mRNA (cDNA clone MGC:129919 IMAGE:40028914), complete cds gi|115528556|gb|BC110611.2|

SSH2-4 e12	305	Expect = 4.2 Identities = 20/20 (100%)	PREDICTED: Danio rerio similar to Receptor-type tyrosine-protein phosphatase-like N precursor (R-PTP-N) (105 kDa islet cell antigen) (ICA105) (PTP IA-2) (PTPLP) (Brain-enriched membrane-associated protein tyrosine phosphatase) (BEM-3) (LOC564351), mRNA gi|68362003|ref|XM_687691.1|
SSH2-4 f02	372	Expect = 5.2 Identities = 23/24 (95%)	Takifugu rubripes platelet-derived growth factor receptor beta 2(PDGFRbeta2) gene, partial cds; colony stimulating factor 1 receptor 2 (CSF1R2) gene, complete cds; and enteropeptidase precursor, gene, partial cds gi|17980235|gb|AF411927.1|
		Expect = 5.2 Identities = 20/20 (100%)	Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C630003C14 product:similar to CDNA FLJ30794 FIS, CLONE FEBRA2001093, WEAKLY SIMILAR TO MONOCARBOXYLATE TRANSPORTER 4 [Homo sapiens], full insert sequence gi|26340581|dbj|AK049846.1|
SSH2-4 g03	459	Expect = 6.5 Identities = 20/20 (100%)	Photobacterium phosphoreum hdc gene for histidine decarboxylase, complete cds, strain: NBRC 13896 gi|95113532|dbj|AB259287.1|
		Expect = 6.5 Identities = 26/28 (92%)	Mus musculus RAB2B, member RAS oncogene family, mRNA (cDNA clone IMAGE:5367910), complete cds gi|38181925|gb|BC061513.1|
SSH2-4 g06	486	Expect = 1.7 Identities = 24/25 (96%)	Homo sapiens plasminogen activator, urokinase receptor (PLAUR) gene, complete cds gi|27357206|gb|AY194849.1|
		Expect = 6.9 Identities = 20/20 (100%)	Danio rerio UDP-N-acteylglucosamine pyrophosphorylase 1, like 1,mRNA (cDNA clone MGC:56509 IMAGE:5913623), complete cds gi|29436947|gb|BC049467.1|
SSH2-6 a10	319	Expect = 1.1 Identities = 21/21 (100%)	Entamoeba histolytica HM-1:IMSS protein kinase (131.t00015) partial mRNA gi|67472666|ref|XM_647033.1|
		Expect = 1.1 Identities = 24/25 (96%)	Human DNA sequence from clone RP3-455E7 on chromosome 6 Contains a pseudogene similar to part of hormonally upregulated Neu-associated kinase (HUNK), complete sequence gi|9588501|emb|AL139806.7|
SSH2-6 e01	385	Expect = 1e-034 Identities = 258/318 (81%)	Oryza sativa (japonica cultivar-group) Os04g0321800 (Os04g0321800)mRNA, complete cds gi|115457729|ref|NM_001059000.1|
		Expect = 0.35 Identities = 22/22 (100%)	Arabidopsis thaliana catalytic/ protein phosphatase type 2C (AT1G79630) mRNA, complete cds gi|42572178|ref|NM_202451.1|
SSH2-6 e10	626	Expect = 9.0 Identities = 20/20 (100%)	Mus musculus phosphatidylinositol 4-kinase, catalytic, alpha polypeptide, mRNA (cDNA clone MGC:100009 IMAGE:6856662),complete cds gi|49523335|gb|BC075629.1|
SSH2-6 h01	250	Expect = 7e-020 Identities = 104/121 (85%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1 gi|58530787|dbj|AP008207.1|
		Expect = 3.4 Identities = 20/20 (100%)	PREDICTED: Mus musculus similar to vomeronasal 1 receptor, D14(LOC673193), mRNA gi|94419973|ref|XR_004153.1|
SSH2-7 b07	849	Expect = 3.1 Identities = 21/21 (100%)	Petunia x hybrida cysteine proteinase inhibitor (CPI1) mRNA, complete cds gi|52546927|gb|AY662997.1|
		Expect = 3.1 Identities = 21/21 (100%)	Human DNA sequence from clone RP3-516C23 on chromosome 6q12 Contains the 5' end of the KHDRBS2 gene for KH domain containing RNA binding signal transduction associated protein 2, complete sequence gi|4539080|emb|Z93021.2|HS516C23
		Expect = 3.1 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-3N15 on chromosome 10 Contains part of the gene for a novel protein (possible ortholog of mouse phosphoinositide-3-kinase adaptor protein 1 (Pik3ap1)), complete sequence gi|14670332|emb|AL591364.3|
SSH2-7 b08	834	Expect = 3.1 Identities = 24/25 (96%)	Rat DNA for phospholipase A2 (EC 3.1.1.4) gi|56894|emb|X52613.1|RNPHLPA2
SSH2-7 d04	620	Expect = 0.57 Identities = 22/22 (100%)	Apis mellifera mRNA for IP3phosphatase, complete cds gi|18265365|dbj|AB072429.1|
SSH2-7 d05	619	Expect = 2.2 Identities = 21/21 (100%)	PREDICTED: Apis mellifera similar to SNF4/AMP-activated protein kinase gamma subunit CG17299-PC, isoform C (LOC411717),mRNA gi|110757750|ref|XM_395185.3|
SSH2-7 e01	143	Expect = 1.8 Identities = 20/20 (100%)	Arabidopsis thaliana ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase(AT5G63370) mRNA, complete cds gi|30697829|ref|NM_125732.2|
SSH2-7 e09	173	Expect = 8.9 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-394A14 on chromosome 13 Contains a protein phosphatase 1, regulatory (inhibitor) subunit 2(PPP1R2) pseudogene, a novel gene and an olfactory receptor pseudogene, complete sequence gi|16972978|emb|AL445238.12|
SSH2-8 a05	186	Expect = 2.5 Identities = 20/20 (100%)	Homo sapiens protein kinase D1 (PRKD1) gene, complete cds gi|92918936|gb|DQ485452.1|
SSH2-8 a08	141	Expect = 1.8 Identities = 20/20 (100%)	Human DNA sequence from clone XXbac-147D4 on chromosome 6 contains the OR5U1 gene for olfactory receptor, family 5, subfamily U,member 1, the OR2H4P, OR2G1P, OR2U1P, OR2U2P, OR2B4P pseudogenes for olfactory receptor, family 2, subfamily H, member 4, subfamily G, member 1, subfamily U, member 1, subfamily U, member 2, subfamily B, member 4 and a DEAD/H(Asp-Glu-Ala-Asp) box polypeptide 6 (DDX6) (RNA helicase,54 kD) pseudogene, complete sequence gi|18121532|emb|AL662857.3|
SSH2-8 a09	92	Expect = 4.2 Identities = 22/23 (95%)	PREDICTED: Pan troglodytes regulator of G-protein signalling 19 interacting protein 1 (GIPC1), mRNA gi|114675663|ref|XM_001157869.1|
SSH2-8 d01	47	Expect = 6.3 Identities = 18/18 (100%)	Human DNA sequence from clone RP11-486G15 on chromosome 1 Contains the 5' end of the PRKACB gene for cAMP-dependent catalytic protein kinase beta, a thioredoxin 2 (TXN2) pseudogene and a CpG island, complete sequence gi|20068411|emb|AL359504.29|
		Expect = 6.3 Identities = 18/18 (100%)	Human DNA sequence from clone RP1-46C2 on chromosome 6p22.2-23 Contains the 5' end of the E2F3 gene for E2F transcription factor 3 (E2F-3, KIAA0075) and two CpG islands, complete sequence gi|10800863|emb|AL132775.29|HSDJ46C2
SSH2-8 d06	265	Expect = 3.6 Identities = 20/20 (100%)	Danio rerio cyclin-dependent kinase inhibitor 1C (p57, Kip2), mRNA(cDNA clone MGC:86618 IMAGE:6892669), complete cds gi|47937851|gb|BC071317.1|
SSH2-8 e09	270	Expect = 3.7 Identities = 23/24 (95%)	PREDICTED: Rattus norvegicus NCK-associated protein 1 (Nckap1), mRNA
SSH2-8 e12	154	Expect = 7.8 Identities = 19/19 (100%)	PREDICTED: Pan troglodytes MAP/microtubule affinity-regulating kinase 4 (MARK4), mRNA gi|114677739|ref|XM_512745.2|
		Expect = 7.8 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-184B22 on chromosome 9 Contains the 3' end of a gene for DKFZP434C212 protein (DKFZP434C212), a methylation-controlled J protein (MCJ) pseudogene, and CpG island, complete sequence gi|20145936|emb|AL627223.23|
SSH2-9 a10	675	Expect = 0.62 Identities = 40/46 (86%)	Triticum aestivum small Ras-related GTP-binding protein mRNA,complete cds gi|16903081|gb|AF433653.1|AF433653
		Expect = 2.5 Identities = 21/21 (100%)	Campylobacter lari CLA0934, flaC genes for probable integral membrane protein Cj0721c, flagellin, partial and complete cds, strain: NCTC12893 gi|113734910|dbj|AB266777.1|
SSH2-9 b01	323	Expect = 1.1 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-211A18 on chromosome 1 Contains the 5' end of the CDC42BPA gene for CDC42 binding protein kinase alpha (DMPK-like), a cathepsin B (CTSB) pseudogene,a novel pseudogene and a CpG island, complete sequence gi|21655335|emb|AL627308.20|
SSH2-9 b03	501	Expect = 7.1 Identities = 20/20 (100%)	Human DNA sequence from clone RP4-534N18 on chromosome 1p34.2-35.3 Contains the PTP4A2 gene for tyrosine phosphatase type IVA, a novel gene and a CpG island, complete sequence gi|24430222|emb|AL136115.21|
SSH2-9 g08	435	Expect = 0.006 Identities = 25/25 (100%)	Dictyostelium discoideum AX4 sphingosine kinase (sgkB) mRNA, complete cds gi|66809634|ref|XM_633448.1|
SSH2-10 a03	622	Expect = 2e-013	Antrodia camphorata partial mnsod gene for manganese superoxide dismutase, exons 1-3, strain

		Identities = 43/43 (100%)	B85 gi|33186703|emb|AJ496411.1|ACA496411
		Expect = 3e-009 Identities = 36/36 (100%)	Schistosoma mansoni CD36-like class B scavenger receptor mRNA, complete cds gi|78893614|gb|DQ249305.1|
SSH2-10 b04	770	Expect = 0.003 Identities = 32/34 (94%)	Oryza sativa (japonica cultivar-group) mRNA for putative mitogen-activated protein kinase wjumk1 (wjumk1 gene) gi|24412849|emb|AJ512643.1|OSA512643
SSH2-10 b10	73	Expect = 3.1 Identities = 19/19 (100%)	Rattus norvegicus alcium/calmodulin-dependent protein gene, 5' end gi|310086|gb|L16999.1|RATCCDPK
SSH2-10 c10	249	Expect = 0.86 Identities = 21/21 (100%)	PREDICTED: Bos taurus similar to Plexin B2 precursor (MM1),transcript variant 6 (LOC508175), mRNA gi|76617280|ref|XM_882686.1|
SSH2-10 f07	114	Expect = 5.5 Identities = 19/19 (100%)	PREDICTED: Mus musculus similar to Serine/threonine-protein kinase Kist (Kinase interacting with stathmin) (U2AF homology motif kinase 1) (PAM COOH-terminal interactor protein 2)(P- CIP2) (LOC622708), mRNA gi|94364510|ref|XM_887157.2|
SSH2-11 f05	499	Expect = 7.1 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-433N2 on chromosome 1 Contains the 5' end of the PDE4B gene for phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog,Drosophila), complete sequence gi|16973039|emb|AL513493.11|

Signal Transduction

Contigs

CONTIG 2	(2 clones)		
SSH2-10 g12	477	Expect = 2e-058 Identities = 304/366 (83%)	Oryza sativa (japonica cultivar-group) Os02g0195500 (Os02g0195500)mRNA, complete cds gi|115444810|ref|NM_001052720.1|
SSH2-10 h01 In SSH2-10 g12	281	Expect = 3.9 Identities = 20/20 (100%)	TPA_exp: Homo sapiens S100 calcium binding protein A7-like gene duplications, clone RP1- 128L15, chromosome 1q21.1-21.3 gi|57547667|tpd|BR000043.1|
CONTIG 22	(5 clones)		
SSH2-5 e03	282	Expect = 5e-089 Identities = 232/253 (91%)	Oryza sativa (japonica cultivar-group) Os04g0660500 (Os04g0660500) mRNA, complete cds gi|115461087|ref|NM_001060679.1|
SSH2-10 g10	582	Expect = 6e-016 Identities = 158/195 (81%)	Arabidopsis thaliana MAPKKK6; ATP binding / kinase/ protein kinase/protein serine/threonine kinase/ protein-tyrosine kinase (MAPKKK6) mRNA, complete cds gi|42563746|ref|NM_111677.3|
SSH2-12 a10 In SSH2-10 g10	580	Expect = e-111 Identities = 453/532 (85%)	Oryza sativa (japonica cultivar-group) Os04g0660500 (Os04g0660500)mRNA, complete cds gi|115461087|ref|NM_001060679.1|
		Expect = 9e-006 Identities = 51/58 (87%)	Arabidopsis thaliana MAPKKK6; ATP binding / kinase/ protein kinase/protein serine/threonine kinase/ protein-tyrosine kinase(MAPKKK6) mRNA, complete cds gi|42563746|ref|NM_111677.3|
SSH2-5 g05 In SSH2-10 g10	517	Expect = 6e-016 Identities = 158/195 (81%)	Arabidopsis thaliana MAPKKK6; ATP binding / kinase/ protein kinase/protein serine/threonine kinase/ protein-tyrosine kinase (MAPKKK6) mRNA, complete cds gi|42563746|ref|NM_111677.3|
SSH2-10 f11	734	Expect = 5e-011 Identities = 78/91 (85%)	Zea mays clone EL01N0524D03.d mRNA sequence gi|54653543|gb|BT018762.1|
CONTIG 29	(4 clones)		
SSH2-6 e07	550	Expect = 2e-009 Identities = 63/72 (87%)	Arabidopsis thaliana CPL3; CTD phosphatase (CPL3) mRNA, complete cds gi|30685743|ref|NM_128914.2|
SSH2-6 e09 In SSH2-6 e07	458	Expect = 9e-067 Identities = 267/312 (85%)	Oryza sativa (japonica cultivar-group) Os11g0521900 (Os11g0521900) mRNA, complete cds gi|115485680|ref|NM_001074516.1|
		Expect = 8e-012 Identities = 64/72 (88%)	Arabidopsis thaliana CPL3; CTD phosphatase (CPL3) mRNA, complete cds gi|30685743|ref|NM_128914.2|
		Expect = 7e-006 Identities = 39/42 (92%)	Medicago sativa clone C43 putative splicing factor Prp8 mRNA, partial cds gi|71534915|gb|DQ122784.1|
SSH2-3 h02 In SSH2-6 e09	359	Expect = 3e-029 Identities = 207/253 (81%)	Oryza sativa (japonica cultivar-group) Os11g0521900 (Os11g0521900) mRNA, complete cds gi|115485680|ref|NM_001074516.1|
SSH2-6 b10 In SSH2-6 e09	355	Expect = 4e-050 Identities = 260/312 (83%)	Oryza sativa (japonica cultivar-group) Os11g0521900 (Os11g0521900) mRNA, complete cds gi|115485680|ref|NM_001074516.1|
		Expect = 0.020 Identities = 57/68 (83%)	Arabidopsis thaliana CTD phosphatase-like 3 (CPL3) mRNA, complete cds gi|22212704|gb|AF486633.1|
CONTIG 47	(2 clones)		
SSH2-12 e02	866	Expect = 2e-013 Identities = 76/86 (88%)	Nyctotherus ovalis partial gene for GTP-binding protein YPT1 gi|60417389|emb|AJ871359.1|
SSH2-12 e01 In SSH2-12 e02	570	Expect = 2.1 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-613M10 on chromosome 9 Contains part of a novel gene, the FBXO10 gene (FBX10) for F-box only protein 10, two novel genes, a RAB1B (member RAS oncogene family) pseudogene the 5' end of a novel gene (KIAA0967) and three CpG islands, complete sequence gi|15591280|emb|AL513165.12|
		Expect = 8.2 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-74N20 on chromosome 1 Contains the 5'end of the NMNAT2 gene for nicotinamide nucleotide adenylyltransferase 2, a novel transcript, the 5' end of the C1orf16 gene for chromosome 1 open reading frame 16 and a CpG island, complete sequence gi|11863459|emb|AL449223.7|
CONTIG 60	(7 clones)		
SSH2-9 c12	378	Expect = e-136 Identities = 310/333 (93%)	Triticum aestivum small Ras-related GTP-binding protein mRNA,complete cds gi|16903081|gb|AF433653.1|AF433653
SSH2-3 f03 In SSH2-9 c12	373	Expect = e-158 Identities = 322/334 (96%)	Triticum aestivum small Ras-related GTP-binding protein mRNA, complete cds gi|16903081|gb|AF433653.1|AF433653
SSH2-7 f10 In SSH2-9 c12	383	Expect = e-165 Identities = 330/341 (96%)	Triticum aestivum small Ras-related GTP-binding protein mRNA, complete cds gi|16903081|gb|AF433653.1|AF433653
SSH2-9 a12	396	Expect = 5e-065	Triticum aestivum small Ras-related GTP-binding protein mRNA,complete cds

In SSH2-7 f10		Identities = 284/333 (85%)	gi|16903081|gb|AF433653.1|AF433653
SSH2-9 b12	519	Expect = e-139 Identities = 313/333 (93%)	Triticum aestivum small Ras-related GTP-binding protein mRNA,complete cds gi|16903081|gb|AF433653.1|AF433653
SSH2-9 c11	557	Expect = e-145 Identities = 318/336 (94%)	Triticum aestivum small Ras-related GTP-binding protein mRNA, complete cds gi|16903081|gb|AF433653.1|AF433653
SSH2-9 a11 In SSH2-9 c11	267	Expect = 1e-021 Identities = 150/180 (83%)	Triticum aestivum small Ras-related GTP-binding protein mRNA, complete cds gi|16903081|gb|AF433653.1|AF433653

Defence Related

Singletons

SSH2-1 c06	230	Expect = 6e-020 Identities = 96/109 (88%)	Triticum aestivum cyclophilin mRNA, partial cds gi|32401383|gb|AF542973.1|
		Expect = 6e-020 Identities = 96/109 (88%)	Triticum aestivum cyclophilin mRNA, partial sequence gi|32351007|gb|AY290733.1|
SSH2-1 h05	341	Expect = 0.001 Identities = 38/42 (90%)	Triticum aestivum cyclophilin mRNA, partial cds gi|32401383|gb|AF542973.1|
SSH2-2 a10	391	Expect = 0.35 Identities = 28/30 (93%)	Triticum aestivum pore-forming toxin-like protein Hfr-2 mRNA,complete cds gi|57233443|gb|AY587018.1|
SSH2-2 c10	375	Expect = 2e-008 Identities = 68/78 (87%)	Triticum aestivum pore-forming toxin-like protein Hfr-2 mRNA,complete cds gi|57233443|gb|AY587018.1|
		Expect = 1.3 Identities = 21/21 (100%)	Oryza sativa centromeric satellite and non-functional centromere-specific retrotransposon sequences gi|23428944|gb|AY101510.1|
SSH2-2 g12	179	Expect = 2.4 Identities = 20/20 (100%)	Triticum urartu ER-localized cyclophilin (CYP23-b) gene, partial cds gi|83700351|gb|DQ270193.1|
		Expect = 2.4 Identities = 20/20 (100%)	Triticum aestivum cyclophilin (CYP23-d) gene, partial cds gi|82547213|gb|DQ265735.1|
SSH2-6 h07	398	Expect = 1.4 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-305L7 on chromosome 9 Contains four novel genes, a peptidylpolyl isomerase A (cyclophilin A) (PPIA) pseudogene, the 3' end of the AUH gene for AU RNA binding protein/enoyl-Coenzyme A hydratase and three CpG islands, complete sequence gi|17939692|emb|AL158071.23|
SSH2-10 a11	589	Expect = 2.1 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-291L19 on chromosome 1 Contains the5' end of the TESK2 gene for testis-specific kinase 2, a peptidylprolyl isomerase A (cyclophilin A) (PPIA)pseudogene, a novel gene, a novel gene (DKFZP564I122) and the 3' end of the PRDX1 gene for peroxiredoxin 1, complete sequence gi|17939718|emb|AL451136.11|
SSH2-12 f01	308	Expect = 0.27 Identities = 22/22 (100%)	Arabidopsis thaliana ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase(AT3G15220) mRNA, complete cds gi|30683507|ref|NM_112385.2|

Defence Related

Contigs

CONTIG 25	(2 clones)		
SSH2-5 h12	471	Expect = 0.0 Identities = 384/400 (96%)	Triticum aestivum cyclophilin mRNA, partial cds gi|32401383|gb|AF542973.1|
SSH2-11 a07	546	Expect = 3e-079 Identities = 310/360 (86%),	Triticum aestivum cyclophilin mRNA, partial cds gi|32401383|gb|AF542973.1|

Stress Related

Singletons

SSH2-1 c04	84	Expect = 0.061 Identities = 22/22 (100%)	Micropogonias undulatus hypoxia-inducible factor 2 alpha mRNA, complete cds gi|87204422|gb|DQ363932.1|
SSH2-2 b06	348	Expect = 0.079 Identities = 23/23 (100%)	Human DNA sequence from clone RP3-471M13 on chromosome 1q24 Contains a small inducible cytokine subfamily E, member 1(endothelial monocyte-activating) (SCYE1) pseudogene and a novel transcript, complete sequence gi|3169111|emb|Z97198.1|HS471M13
		Expect = 1.2 Identities = 39/45 (86%)	Lophopyrum elongatum salt-stress induced hydrophobic peptide (ESI3) gi|392943|gb|U00966.1|U00966
		Expect = 1.2 Identities = 21/21 (100%)	Bacteroides thetaiotaomicron neopullulanase (susA) and alpha-glucosidase (susB) genes, complete cds gi|1519524|gb|U66897.1|BTU66897
SSH2-2 c04	346	Expect = 4.8 Identities = 20/20 (100%)	Chlamys farreri heat shock protein 90 mRNA, complete cds gi|38146756|gb|AY362761.1|
		Expect = 4.8 Identities = 20/20 (100%)	Aspergillus oryzae RIB40 genomic DNA, SC003 gi|83767101|dbj|AP007155.1|
SSH2-3 d09	147	Expect = 7.4 Identities = 19/19 (100%)	PREDICTED: Rattus norvegicus similar to Myb proto-oncogene protein(C-myb) (predicted) (RGD1560020_predicted), mRNA gi|109460386|ref|XM_001061499.1|
		Expect = 7.4	Phoma betae PbGGS, ACS, PbP450-1, PbTP, PbP450-2, PbTF genes for

		Identities = 19/19 (100%)	geranylgeranyldiphosphate synthase, aphidicolan-16b-ol synthase, P450 monooxygenase 1, transporter protein, P450 monooxygenase 2, transcription factor, complete cds gi|50355630|dbj|AB114137.1|
SSH2-4 f12	80	Expect = 0.23 Identities = 21/21 (100%)	Oryza sativa (indica cultivar-group) multiple stress-associated zinc-finger protein (OSISAP1) gene, complete cds gi|37548822|gb|AY137590.1|
		Expect = 0.89 Identities = 20/20 (100%)	PREDICTED: Apis mellifera similar to ubiquitin specific protease 34(LOC410109), mRNA gi|110756660|ref|XM_393596.3|
SSH2-6 c09	399	Expect = 1e-013 Identities = 43/43 (100%)	Antrodia camphorata partial mnsod gene for manganese superoxide dismutase, exons 1-3, strain B85 gi|33186703|emb|AJ496411.1|ACA496411
SSH2-8 d10	61	Expect = 9.5 Identities = 18/18 (100%)	Bradyrhizobium japonicum USDA 110 cytochrome P-450 BJ-2 (CYP115P) pseudogene, cytochrome P-450 BJ-1 (CYP112) gene, cytochrome P-450 BJ-3 (CYP114) gene, putative ferredoxin gene, putative sterol dehydrogenase-like enzyme gene, cytochrome P-450 BJ-4 (CYP117) gene, and putative dimethylallyltranstransferase gene, complete cds gi|529961|gb|U12678.1|BJU12678
SSH2-9 f05	551	Expect = 0.0 Identities = 501/522 (95%)	Triticum aestivum mRNA for cytochrome P450 reductase (r2 gene) gi|18103932|emb|AJ303373.1|TAE303373
SSH2-10 b05	631	Expect = 9.1 Identities = 20/20 (100%)	PREDICTED: Macaca mulatta similar to Egl nine homolog 3, mitochondrial precursor (Hypoxia-inducible factor prolyl hydroxylase 3) (HIF-prolyl hydroxylase 3) (HIF-PH3) (SM-20) (LOC717342), mRNA gi|109083260|ref|XM_001108734.1|
SSH2-10 c04	235	Expect = 3.2 Identities = 20/20 (100%)	Caenorhabditis elegans heavy metal tolerance factor 1 (hmt-1) gene complete cds gi|20977858|gb|AF497514.1|

Stress Related

Contigs

CONTIG 1	(2 clones)		
SSH2-10 f06	646	Expect = 1e-011 Identities = 40/40 (100%)	Antrodia camphorata partial mnsod gene for manganese superoxide dismutase, exons 1-3, strain B85 gi|33186703|emb|AJ496411.1|ACA496411
		Expect = 3e-009 Identities = 36/36 (100%)	Cucumis sativus C-repeat/DRE binding factor 1 (cbf1) mRNA,complete cds gi|109693569|gb|DQ776899.1|
SSH2-12 e12	603	Expect = e-162 Identities = 478/540 (88%)	Oryza sativa (japonica cultivar-group) Os08g0288200 (Os08g0288200) mRNA, complete cds gi|115475715|ref|NM_001067989.1|

Protein Degradation and Ubiquitinylation

Singletons

SSH2-1 b11	421	Expect = 1.5 Identities = 21/21 (100%)	PREDICTED: Macaca mulatta similar to protease inhibitor 15 preproprotein, transcript variant 2 (LOC697375), mRNA gi|109086723|ref|XM_001087254.1|
SSH2-1 d11	353	Expect = 4.9 Identities = 20/20 (100%)	PREDICTED: Bos taurus similar to Smad ubiquitination regulatory factor 1 (Ubiquitin--protein ligase SMURF1)(Smad-specific E3 ubiquitin ligase 1) (hSMURF1) (LOC513902), mRNA gi|76654269|ref|XM_591663.2|
SSH2-2 d06	134	Expect = 2e-006 Identities = 42/46 (91%)	Oryza sativa (japonica cultivar-group) mRNA for homologue of Tat binding protein, complete cds gi|556557|dbj|D17789.1|RICHTBP2
		Expect = 7e-006 Identities = 41/45 (91%)	Oryza sativa (japonica cultivar-group) OsRPT2b mRNA for 26S proteasome regulatory particle triple-A ATPase subunit2b, complete cds gi|17297986|dbj|AB037154.1|
		Expect = 0.11 Identities = 22/22 (100%)	Macaca mulatta genes, MHC class I region, partial and complete cds gi|55700762|dbj|AB128049.1|
		86	partial cDNA sequence from a Lambda ZAP II normalized full-length cDNA library of differentiating xylem from Eucalyptus gunnii
		110	Pisum sativum partial mRNA for putative cysteine protease (plp gene)
		71	Arabidopsis thaliana calcium ion binding (AT5G04170) mRNA, complete cds
SSH2-3 a02	198	Expect = 5e-051 Identities = 141/153 (92%)	Triticum aestivum 20S proteasome beta 7 subunit mRNA, complete cds
SSH2-4 c04	88	Expect = 1.00 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-667B21 on chromosome 13 Contains the 3' end of the gene for a novel protein similar to ubiquitin specific protease 12 (LOC219333), complete sequence gi|15391097|emb|AL355473.20|
SSH2-4 e07	305	Expect = 4.2 Identities = 23/24 (95%)	Xenopus laevis similar to methionyl aminopeptidase 1, mRNA (cDNA clone MGC:80018 IMAGE:3401285), complete cds gi|47124678|gb|BC070567.1|
SSH2-4 f08	137	Expect = 0.11 Identities = 25/26 (96%)	Human DNA sequence from clone RP1-237J2 on chromosome 20q12-13.13 Contains part of the NCOA3 gene for nuclear receptor coactivator 3 and a CpG island, complete sequence gi|11493113|emb|AL021394.10|HS237J2
		Expect = 0.44 Identities = 24/25 (96%)	Mus musculus gene for U-box-type ubiquitin ligase UFD2a, complete cds gi|60683924|dbj|AB083274.2|
SSH2-6 g04	206	Expect = 4e-030 Identities = 121/138 (87%)	Oryza sativa (japonica cultivar-group) OsRPT1b mRNA for 26S proteasome regulatory particle triple-A ATPase subunit1b, partial cds gi|17298142|dbj|AB070252.1|
SSH2-7 h01	505	Expect = 7.2 Identities = 20/20 (100%)	Xenopus laevis isopeptidase T (IsoT) mRNA, partial cds gi|36939184|gb|AY376839.1|
SSH2-9 a08	237	Expect = 8e-004 Identities = 29/30 (96%)	Oryza sativa (japonica cultivar-group) OsRPT3 mRNA for 26S proteasome regulatory particle triple-A ATPase subunit3, partial cds gi|17298144|dbj|AB070253.1|
SSH2-10 f12	455	Expect = 1e-013 Identities = 109/131 (83%)	Triticum aestivum mRNA for triticain alpha, complete cds gi|111073714|dbj|AB267407.1|
		Expect = 3e-005 Identities = 32/33 (96%)	Zea mays mRNA for cysteine protease component of protease-inhibitor complex, complete cds gi|6682828|dbj|AB020961.1|

SSH2-12 e08	663	Expect = 5e-023 Identities = 131/155 (84%)	Oryza sativa mRNA, partial homologous to ATP-dependent protease gene gi|474004|dbj|D29692.1|RICYK4
SSH2-12 h07	850	Expect = 0.0 Identities = 341/346 (98%)	Triticum aestivum mRNA for triticain gamma, complete cds gi|111073718|dbj|AB267409.1|
		Expect = 6e-048 Identities = 137/149 (91%)	Lolium multiflorum mRNA for cysteine protease (see1 gene) gi|6851029|emb|AJ249847.1|LMU249847
		98	Arabidopsis thaliana AALP; cysteine-type endopeptidase/ cysteine-type peptidase (AALP) mRNA, complete cds

Protein Degradation and Ubiquitinylation

Contigs

CONTIG 3	(2 clones)		
SSH2-11 b01	440	Expect = 4e-007 Identities = 65/76 (85%)	Arabidopsis thaliana cysteine-type peptidase (AT2G27350) mRNA,complete cds gi|42570942|ref|NM_201816.1|
		Expect = 1.6 Identities = 21/21 (100%)	Human DNA sequence from clone RP4-696P19 on chromosome 6p12.3-21.2 Contains the 3' end of the TFEB gene for transcription factor EB (TCFEB), a nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1) pseudogene, the MDF gene for MyoD family inhibitor, the 5' end of a novel gene and two CpG islands, complete sequence gi|5419648|emb|AL035588.21|HS696P19
		Expect = 6.2 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-88J11 on chromosome 13 Contains the 3' end of the CDK8 gene for cyclin-dependent kinase 8, complete sequence gi|13445322|emb|AL159159.21|
SSH2-6 f07 In SSH2-11 b01	440	Expect = 1e-004 Identities = 88/108 (81%)	Arabidopsis thaliana cysteine-type peptidase (AT2G27350) mRNA, complete cds gi|42570322|ref|NM_179768.2|
CONTIG 17	(7 clones)		
SSH2-3 f08	361	Expect = 3e-097 Identities = 276/307 (89%)	Oryza sativa (japonica cultivar-group) Os11g0140600 (Os11g0140600) mRNA, complete cds gi|115484098|ref|NM_001072243.1|
		Expect = 2e-015 Identities = 76/86 (88%)	partial cDNA sequence from a Lambda ZAP II normalized full-length cDNA library of differentiating xylem from Eucalyptus gunnii gi|103478802|emb|CT985186.1|
		Expect = 4e-013 Identities = 57/62 (91%)	Pisum sativum partial mRNA for putative cysteine protease (plp gene) gi|6624720|emb|AJ251828.1|PSA251828
		Expect = 6e-009 Identities = 62/71 (87%)	Arabidopsis thaliana calcium ion binding (AT5G04170) mRNA, complete cds gi|42567633|ref|NM_120499.4|
SSH2-3 e07 In SSH2-3 f08	394	Expect = 5e-071 Identities = 260/303 (85%)	Oryza sativa (japonica cultivar-group) Os12g0137100 (Os12g0137100)mRNA, complete cds gi|115487237|ref|NM_001072638.1|
		Expect = 9e-011 Identities = 74/86 (86%)	partial cDNA sequence from a Lambda ZAP II normalized full-length cDNA library of differentiating xylem from Eucalyptus gunnii gi|103478802|emb|CT985186.1|
		Expect = 2e-008 Identities = 91/110 (82%)	Pisum sativum partial mRNA for putative cysteine protease (plp gene) gi|6624720|emb|AJ251828.1|PSA251828
		Expect = 3e-004 Identities = 60/71 (84%)	Arabidopsis thaliana calcium ion binding (AT5G04170) mRNA, complete cds gi|42567633|ref|NM_120499.4|
SSH2-3 f07 In SSH2-3 f08	394	Expect = 9e-079 Identities = 263/300 (87%)	Oryza sativa (japonica cultivar-group) Os12g0137100 (Os12g0137100)mRNA, complete cds gi|115487237|ref|NM_001072638.1|
		Expect = 2e-008 Identities = 55/62 (88%)	Pisum sativum partial mRNA for putative cysteine protease (plp gene) gi|6624720|emb|AJ251828.1|PSA251828
		Expect = 4e-007 Identities = 44/48 (91%)	partial cDNA sequence from a Lambda ZAP II normalized full-length cDNA library of differentiating xylem from Eucalyptus gunnii gi|103478802|emb|CT985186.1|
		Expect = 0.006 Identities = 34/37 (91%)	Arabidopsis thaliana calcium ion binding (AT5G04170) mRNA, complete cds gi|42567633|ref|NM_120499.4|
		Expect = 0.35 Identities = 22/22 (100%)	Human DNA sequence from clone RP5-983F16 on chromosome 1p21.3-22.2 Contains a eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) pseudogene and a CpG island, complete sequence gi|8745060|emb|AL136325.6|
		Expect = 5.5 Identities = 20/20 (100%)	PREDICTED: Pan troglodytes polymerase (DNA directed) iota, transcript variant 4 (POLI), mRNA gi|114673198|ref|XM_512141.2|
SSH2-3 g07 In SSH2-3 f07	226	Expect = 5e-039 Identities = 133/149 (89%)	Oryza sativa (japonica cultivar-group) Os11g0140600 (Os11g0140600)mRNA, complete cds gi|115484098|ref|NM_001072243.1|
		Expect = 6e-011 Identities = 56/62 (90%)	Pisum sativum partial mRNA for putative cysteine protease (plp gene) gi|6624720|emb|AJ251828.1|PSA251828
		Expect = 3e-006 Identities = 45/50 (90%)	partial cDNA sequence from a Lambda ZAP II normalized full-length cDNA library of differentiating xylem from Eucalyptus gunnii gi|103475323|emb|CT981707.1|
		Expect = 0.20 Identities = 34/38 (89%)	Arabidopsis thaliana calcium ion binding (AT3G10300) mRNA, complete cds gi|42563948|ref|NM_111865.4|
SSH2-3 g02 In SSH2-3 f08	381	Expect = 4e-081 Identities = 264/300 (88%)	Oryza sativa (japonica cultivar-group) Os12g0137100 (Os12g0137100) mRNA, complete cds gi|115487237|ref|NM_001072638.1|
		Expect = 4e-013 Identities = 57/62 (91%)	Pisum sativum partial mRNA for putative cysteine protease (plp gene) gi|6624720|emb|AJ251828.1|PSA251828
		Expect = 0.006 Identities = 28/29 (96%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103482679|emb|CT989063.1|
SSH2-3 e08	558	Expect = 4e-088 Identities = 267/300 (89%)	Oryza sativa (japonica cultivar-group) Os11g0140600 (Os11g0140600) mRNA, complete cds gi|115484098|ref|NM_001072243.1|
CONTIG 24	(2 clones)		
SSH2-5 f04	401	Expect = 2e-005 Identities = 68/81 (83%)	Arabidopsis thaliana ZTL (ZEITLUPE); ubiquitin-protein ligase (ZTL) mRNA, complete cds gi|30696862|ref|NM_125119.2|
SSH2-5 g03 In SSH2-5 f04	362	Expect = 2e-005 Identities = 68/81 (83%)	Arabidopsis thaliana ZTL (ZEITLUPE); ubiquitin-protein ligase (ZTL) mRNA, complete cds gi|30696862|ref|NM_125119.2|
CONTIG 31	(4 clones)		
SSH2-6 f10	430	Expect = 7e-009 Identities = 65/75 (86%)	Oryza sativa (japonica cultivar-group) OsRPT2b mRNA for 26S proteasome regulatory particle triple-A ATPase subunit2b, complete cds gi|17297986|dbj|AB037154.1|
SSH2-1 b02	552	Expect = e-125 Identities = 344/382 (90%)	Oryza sativa (japonica cultivar-group) mRNA for homologue of Tat binding protein, complete cds gi|556557|dbj|D17789.1|RICHTBP2
		Expect = 1e-066	Oryza sativa (japonica cultivar-group) OsRPT2b mRNA for 26S proteasome regulatory

		Identities = 309/368 (83%)	particle triple-A ATPase subunit2b, complete cds gi|17297986|dbj|AB037154.1|
SSH2-1 d12 In SSH2-1 b02	437	Expect = 4e-081 Identities = 270/308 (87%)	Oryza sativa (japonica cultivar-group) mRNA for homologue of Tat binding protein, complete cds gi|556557|dbj|D17789.1|RICHTBP2
		Expect = 1e-044 Identities = 236/283 (83%)	Oryza sativa (japonica cultivar-group) OsRPT2b mRNA for 26S proteasome regulatory particle triple-A ATPase subunit2b, complete cds gi|17297986|dbj|AB037154.1|
SSH2-1 g08 In SSH2-1 b02	434	Expect = 1e-047 Identities = 256/308 (83%)	Oryza sativa (japonica cultivar-group) OsRPT2b mRNA for 26S proteasome regulatory particle triple-A ATPase subunit2b, complete cds gi|17297986|dbj|AB037154.1|
		Expect = 0.025 Identities = 33/36 (91%)	Arabidopsis thaliana FTSH7; ATP-dependent peptidase/ ATPase/metallopeptidase (FTSH7) mRNA, complete cds gi|30692800|ref|NM_114573.2|
CONTIG 45	(7 clones)		
SSH2-12 c07	679	Expect = e-103 Identities = 361/417 (86%)	Oryza sativa (japonica cultivar-group) Os04g0397100 (Os04g0397100) mRNA, partial cds gi|115458129|ref|NM_001059200.1|
		Expect = 9e-065 Identities = 165/177 (93%)	Oryza sativa mRNA, partial homologous to ATP-dependent protease gene gi|474004|dbj|D29692.1|RICYK4
SSH2-12 c08 In SSH2-12 c07	464	Expect = 6e-025 Identities = 252/314 (80%)	Tomato ATP-dependent protease (CD4B) gene, complete cds gi|170434|gb|M32604.1|TOMCD4B
		Expect = 3e-014 Identities = 258/328 (78%)	Pisum sativum (clone pCLp) nuclear encoded precursor to chloroplast protein mRNA, complete cds gi|169127|gb|L09547.1|PEAPCLP
SSH2-5 c03 In SSH2-12 c07	641	Expect = 8e-065 Identities = 165/177 (93%)	Oryza sativa mRNA, partial homologous to ATP-dependent protease gene gi|474004|dbj|D29692.1|RICYK4
		Expect = 1e-057 Identities = 342/417 (82%)	Spinacia oleracea ClpC protease (clpC) mRNA, chloroplast gene encoding chloroplast protein, complete cds gi|4105130|gb|AF043539.1|AF043539
SSH2-4 c09 In SSH2-5 c03	432	Expect = 7e-006 Identities = 72/86 (83%)	Oryza sativa (japonica cultivar-group) Os04g0397100 (Os04g0397100) mRNA, partial cds gi|115458129|ref|NM_001059200.1|
		Expect = 7e-006 Identities = 57/66 (86%)	Tomato ATP-dependent protease (CD4B) gene, complete cds gi|170434|gb|M32604.1|TOMCD4B
		Expect = 0.025 Identities = 54/64 (84%)	Spinacia oleracea ClpC protease (clpC) mRNA, chloroplast gene encoding chloroplast protein, complete cds gi|4105130|gb|AF043539.1|AF043539
SSH2-5 d03 In SSH2-5 c03	473	Expect = 3e-045 Identities = 144/160 (90%)	Oryza sativa mRNA, partial homologous to ATP-dependent protease gene gi|474004|dbj|D29692.1|RICYK4
		Expect = 2e-021 Identities = 267/336 (79%)	Spinacia oleracea ClpC protease (clpC) mRNA, chloroplast gene encoding chloroplast protein, complete cds gi|4105130|gb|AF043539.1|AF043539
SSH2-5 e01 In SSH2-5 c03	434	Expect = 8e-061 Identities = 275/326 (84%)	Tomato ATP-dependent protease (CD4B) gene, complete cds gi|170434|gb|M32604.1|TOMCD4B
		Expect = 3e-042 Identities = 298/367 (81%)	Spinacia oleracea ClpC protease (clpC) mRNA, chloroplast gene encoding chloroplast protein, complete cds gi|4105130|gb|AF043539.1|AF043539
SSH2-5 d02 In SSH2-5 c03	458	Expect = 2e-061 Identities = 276/327 (84%)	Tomato ATP-dependent protease (CD4A) gene, complete cds gi|170432|gb|M32603.1|TOMCD4A
		Expect = 3e-060 Identities = 343/417 (82%)	Spinacia oleracea ClpC protease (clpC) mRNA, chloroplast gene encoding chloroplast protein, complete cds gi|4105130|gb|AF043539.1|AF043539
CONTIG 50	(4 clones)		
SSH2-3 c05	312	Expect = e-102 Identities = 222/232 (95%)	Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds gi|170784|gb|M62720.1|WHTUCP1A
		Expect = 4e-065 Identities = 171/185 (92%)	Oryza sativa (japonica cultivar-group) OsRad6 mRNA for Rad6,complete cds gi|18844989|dbj|AB079798.1|
		Expect = 4e-031 Identities = 159/188 (84%)	partial cDNA sequence from a Lambda ZAP II normalized full-length cDNA library of differentiating xylem from Eucalyptus gunnii gi|103479914|emb|CT986395.1|
SSH2-9 d04	279	Expect = e-130 Identities = 241/242 (99%)	Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds gi|170784|gb|M62720.1|WHTUCP1A
SSH2-9 c04	279	Expect = e-132 Identities = 242/242 (100%)	Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds gi|170784|gb|M62720.1|WHTUCP1A
SSH2-8 h07	267	Expect = 3e-062 Identities = 203/228 (89%),	Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds gi|170784|gb|M62720.1|WHTUCP1A

Transcription and Translation

Singletons

SSH2-1 b07	366	Expect = 5.1 Identities = 20/20 (100%)	Homo sapiens estrogen-related receptor gamma (ESRRG) gene, complete cds gi|41324139|gb|AY528719.1|
SSH2-1 b10	427	Expect = 6.0 Identities = 23/24 (95%)	Drosophila melanogaster LIM homeobox protein (islet) mRNA, complete cds gi|1895061|gb|U89385.1|DMU89385
SSH2-1 e05	95	Expect = 0.28 Identities = 21/21 (100%)	Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730020E23 product:inferred: chromodomain helicase DNA binding protein 1 / putative [Mus musculus], full insert sequence gi|26089236|dbj|AK042739.1|
SSH2-1 e12	78		PREDICTED: Rattus norvegicus splicing factor 3b, subunit 3 (predicted) (Sf3b3_predicted), mRNA
SSH2-1 f02	56	Expect = 8.4 Identities = 21/22 (95%)	Oscillatoria sp. CCAP 1459/26 clone 4 non-ribosomal peptide synthetase gene cluster, partial sequence gi|60116512|gb|AY768447.1|
SSH2-1 f10	276	Expect = 0.96 Identities = 21/21 (100%)	Human DNA sequence from clone RP1-72A23 on chromosome 6 Contains an adaptor-related (clathrin-associated) protein complex 4,sigma 1 subunit (AP4A1) pseudogene, a novel pseudogene,the 5' end of the RNGTT gene for RNA guanylyltransferase and 5'-phosphatase (mRNA capping enzyme, CAP1A) and two CpG islands, complete sequence gi|6018784|emb|AL079342.17|HSDJ72A23
		Expect = 0.96 Identities = 21/21 (100%)	Simian type D virus 1, partial proviral genome gi|2246463|gb|U85506.1|STU85506
SSH2-2 a01	421	20	PREDICTED: Rattus norvegicus doublesex and mab-3 related transcription factor like family A1 (predicted) (Dmrta1_predicted), mRNA
		Expect = 5.9 Identities = 20/20 (100%)	Soochong virus-4 isolate SC-4 nucleocapsid protein mRNA, complete cds gi|50541930|gb|AY675352.1|
SSH2-2 a09	202	Expect = 2.7 Identities = 20/20 (100%)	Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130308L17 product:TRANSCRIPTION FACTOR HES-2 (HAIRY AND ENHANCER OF SPLIT 2), full insert Sequence gi|26343736|dbj|AK053792.1|
		Expect = 2.7 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-129K24 on chromosome 6 Contains the 5' end of a variant of the BPAG1 gene for bullous pemphigoid antigen 1 (230/240kD), the 5' end of a novel

			gene, a novel pseudogene, a ferritin heavy polypeptide 1(FTH1) pseudogene and a CpG island, complete sequence gi|14456363|emb|AL590037.7|
SSH2-2 c05	507	Expect = 8e-077 Identities = 337/397 (84%)	Oryza sativa (japonica cultivar-group) Os01g0896500 (Os01g0896500)mRNA, complete cds gi|115441602|ref|NM_001051616.1|
		Expect = 7.2 Identities = 20/20 (100%)	Takifugu rubripes HoxAa gene cluster, complete sequence gi|94482748|gb|DQ481663.1|
		Expect = 7.2 Identities = 20/20 (100%)	Dictyostelium discoideum AX4 DNA topoisomerase II (topB) mRNA, complete cds gi|66826862|ref|XM_641694.1|
SSH2-3 b10	257	Expect = 3.5 Identities = 20/20 (100%)	Homo sapiens eukaryotic initiation factor 4AI (EIF4A1) gene, partial cds gi|6969997|gb|AF175325.1|
SSH2-3 d02	284	Expect = 3e-081 Identities = 213/232 (91%)	Wheat translation elongation factor 1 alpha-subunit (TEF1) mRNA,complete cds gi|170775|gb|M90077.1|WHTTEF1X
		Expect = 7e-079 Identities = 215/236 (91%)	Oryza sativa translation elongation factor-1 alpha mRNA, complete cds gi|2996095|gb|AF030517.1|AF030517
SSH2-5 a08	468	Expect = 2e-071 Identities = 298/353 (84%)	Peperomia caperata RNA polymerase II second largest subunit (RPB2) mRNA, partial cds gi|3002938|gb|AF043426.1|AF043426
SSH2-5 c07	467	Expect = 6.6 Identities = 23/24 (95%)	PREDICTED: Macaca mulatta similar to transcription elongation factor A (SII), 2 (LOC711362), mRNA gi|109129942|ref|XM_001096593.1|
		Expect = 6.6 Identities = 23/24 (95%)	Cryptosporidium parvum Iowa II RecQ SF II RNA helicase, DEXDc+HELICc(cgd3_390), partial mRNA gi|66358891|ref|XM_626624.1|
SSH2-6 c10	21	Expect = 0.70 Identities = 18/18 (100%)	PREDICTED: Pan troglodytes Mix-like homeobox protein 1 (MIXL1),mRNA gi|114572950|ref|XM_001140733.1|
SSH2-7 e04	430	Expect = 1.5 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-544L8 on chromosome 6 Contains the 3' end of the HDAC2 gene for histone deacetylase 2 (human transcriptional regulator homolog RPD3, YAF1) and a putative novel gene, complete sequence gi|18642416|emb|AL671967.1|
		Expect = 6.1 Identities = 20/20 (100%)	Arabidopsis thaliana putative transcription factor (MYB50) mRNA,partial cds gi|3941463|gb|AF062886.1|AF062886
SSH2-8 e06	201	Expect = 2.7 Identities = 20/20 (100%)	PREDICTED: Bos taurus similar to transcription elongation factor A(SII)-like 4 (LOC513987), mRNA gi|76672568|ref|XM_591765.2|
		Expect = 2.7 Identities = 20/20 (100%)	Caenorhabditis elegans GEX Interacting protein family member (gei-14)(gei-14) mRNA, complete cds gi|71991580|ref|NM_063344.2|
SSH2-9 a01	353	Expect = 1.2 Identities = 21/21 (100%)	Picea glauca genotype 81115 homeobox transcription factor KN2 (KN2)gene, KN2-2 allele, partial cds gi|82911501|gb|DQ259459.1|
SSH2-11 e12	455	Expect = 0.41 Identities = 22/22 (100%)	Mouse DNA sequence from clone RP23-338K15 on chromosome 11 Contains a eukaryotic translation elongation factor 2 (Eef2) pseudogene, complete sequence gi|57975582|emb|AL645843.14|

Transcription and Translation

Contigs

CONTIG 37	(3 clones)		
SSH2-7 d11	214	Expect = 0.047 Identities = 38/43 (88%)	Oryza sativa (indica cultivar-group) partial mRNA for putative IAA8 auxin regulated transcriptional repressor (IAA8 gene) gi|62120057|emb|AJ627256.1|
SSH2-10 a12	218	Expect = 5e-005 Identities = 40/44 (90%)	Oryza sativa (indica cultivar-group) partial mRNA for putative IAA8 auxin regulated transcriptional repressor (IAA8 gene) gi|62120057|emb|AJ627256.1|
SSH2-10 a10	872	Expect = 4e-015 Identities = 52/54 (96%)	Arabidopsis thaliana IAA9; transcription factor (IAA9) mRNA, complete ds gi|30698144|ref|NM_125965.2|
		Expect = 4e-012 Identities = 56/61 (91%)	Arabidopsis thaliana clone C00020 (e) auxin-regulated protein IAA13(At2g33310) mRNA, complete cds gi|12083207|gb|AF332399.1|

Cellular Organization

Singletons

SSH2-1 a08	434	Expect = 0.39 Identities = 22/22 (100%)	Cyprinus carpio zinc exporter 5 mRNA, partial cds gi|52078204|gb|AY695928.1|
SSH2-1 a09	553	Expect = 7.9 Identities = 23/24 (95%)	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette,sub-family G (WHITE), member 1), complete cds gi|10280531|dbj|AB038161.1|
SSH2-1 a11	412	Expect = 5.8 Identities = 20/20 (100%)	Homo sapiens cadherin 2, type 1, N-cadherin (neuronal), mRNA (cDNA clone MGC:41765 IMAGE:5264944), complete cds gi|22209069|gb|BC036470.1|
		Expect = 5.8 Identities = 20/20 (100%)	Mouse DNA sequence from clone RP23-343C18 on chromosome 11 Contains the gene for a novel helix-loop-helix DNA-binding domain containing protein, a novel gene, the Gosr1 gene for golgi SNAP receptor complex member 1 and a CpG island, complete sequence gi|27552284|emb|BX000359.7|
SSH2-1 a07	459	Expect = 0.42 Identities = 22/22 (100%)	Homo sapiens partial TTN gene for titin gi|17066103|emb|AJ277892.2|HSA277892
		Expect = 6.5 Identities = 23/24 (95%)	Homo sapiens complement system membrane cofactor protein CD46(CD46) gene, promoter region and partial cds gi|115393873|gb|DQ912494.1|
SSH2-1 c03	545	Expect = 7.8 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-96C4 on chromosome 10 Contains part of the ANK3 gene for ankyrin 3, node of Ranvier (ankyrin G), complete sequence gi|16972922|emb|AL359377.18|
SSH2-1 h09	250	Expect = 0.86 Identities = 21/21 (100%)	Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1) gene,complete cds gi|62945798|gb|DQ015919.1|
SSH2-2 g01	256	Expect = 0.89 Identities = 21/21 (100%)	PREDICTED: Mus musculus kinesin family member 14 (Kif14), mRNA Length = 8952 gi|94364272|ref|XM_989909.1|
		Expect = 3.5	Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBa0043L24,complete sequence

		Identities = 20/20 (100%)	gi|32489509|emb|AL662969.3|OSJN00169
SSH2-2 g03	254	Expect = 0.88 Identities = 21/21 (100%)	Human DNA sequence from clone RP4-689N3 on chromosome Xp11.1-11.4 Contains the 5' end of the RP2 gene for retinitis pigmentosa 2 (X-linked recessive), the 5' end of the SLC9A7 gene for solute carrier family 9 (sodium/hydrogen exchanger), isoform 7 (NHE7), and two CpG Islands, complete sequence gi|6562569|emb|AL050307.13|HSDJ689N3
SSH2-3 c03	139	Expect = 6.9 Identities = 19/19 (100%)	Caenorhabditis elegans Na/Ca eXchangers family member (ncx-1) (ncx-1) mRNA, complete cds gi|115533321|ref|NM_001047718.1|
SSH2-3 c06	646	Expect = 2.4 Identities = 21/21 (100%)	PREDICTED: Gallus gallus similar to Potassium voltage-gated channel subfamily B member 2 (Voltage-gated potassium channel subunit Kv2.2) (LOC431181), partial mRNA gi|50804811|ref|XM_428730.1|
SSH2-3 h06	334	Expect = 5e-071 Identities = 166/175 (94%)	Oryza sativa (japonica cultivar-group) mrp1 gene for MRP-like ABC transporter, exons 1-28 gi|27263147|emb|AJ535215.1|OSA535215
		Expect = 6e-018 Identities = 143/174 (82%)	Arabidopsis thaliana ATMRP1; xenobiotic-transporting ATPase (ATMRP1) mRNA, complete cds gi|79318956|ref|NM_001036039.1|
SSH2-5 a04	187	Expect = 2.5 Identities = 20/20 (100%)	Caenorhabditis elegans potassium channel, KvQLT family member (kqt-1) (kqt-1) mRNA, complete cds gi|71984029|ref|NM_171710.2|
SSH2-6 a02	501	Expect = 9e-015 Identities = 124/149 (83%)	Triticum aestivum putative calcium channel mRNA, complete cds gi|34391394|gb|AY114121.1|
SSH2-7 a04	811	Expect = 3.0 Identities = 21/21 (100%)	Human DNA sequence from clone RP13-130D24 on chromosome Xq21.31-22.1 Contains a karyopherin (importin) beta 1 (KPNB1)pseudogene, complete sequence gi|10732488|emb|AL391666.5|
SSH2-7 e03	149	Expect = 7.5 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-31J20 on chromosome 9 Contains part of the ABCA1 gene for ATP-binding cassette sub-family A(ABC1) member 1, complete sequence gi|14329534|emb|AL353685.23|
SSH2-7 e11	390	Expect = 5.5 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-255G4 on chromosome 1 Contains part of the KCNH1 gene for a potassium voltage-gated channel, subfamily H (eag-related), member, complete sequence gi|15617296|emb|AL590132.7|
SSH2-8 b01	102	Expect = 4.8 Identities = 19/19 (100%)	Arabidopsis thaliana mRNA for D-xylose-H+ symporter - like protein,complete cds, clone: RAFL04-15-M01 gi|110740546|dbj|AK226214.1|
SSH2-8 b11	63	Expect = 10.0 Identities = 18/18 (100%)	Naegleria gruberi alpha-tubulin TUBA4 (TUBA4) gene, partial cds gi|15082213|gb|AF401641.1|
SSH2-8 e05	179	Expect = 9.3 Identities = 19/19 (100%)	Giardia lamblia ATCC 50803 ABC transporter (GLP_623_62539_67263) partial mRNA gi|71078370|ref|XM_766602.1|
SSH2-9 e03	210	Expect = 0.046 Identities = 23/23 (100%)	Klebsiella pneumoniae partial YC04 gene for putative capsule polysaccharide export protein precursor, contig region pSL001 gi|9909732|emb|AJ293853.1|KPN293853
SSH2-11 a04	462	Expect = 1.7 Identities = 21/21 (100%)	Mus musculus sperm-specific sodium proton exchanger mRNA, complete cds gi|37089352|gb|AY368685.1|

Other

Singletons

SSH2-1 a12	473	Expect = 1.7 Identities = 24/25 (96%)	Zebrafish DNA sequence from clone CH211-8G12 in linkage group 21,complete sequence gi|49065289|emb|BX470244.6|
		Expect = 6.7 Identities = 23/24 (95%)	Human DNA sequence from clone RP5-1009H6 on chromosome 20 Contains the 3' end of the NFATC2 gene for cytoplasmic calcineurin-dependent (2) nuclear factor of activated T-cells, complete sequence gi|5596686|emb|AL035682.16|HS1009H6
SSH2-1 c05	82	Expect = 3.6 Identities = 19/19 (100%)	TPA_exp: Homo sapiens RING finger protein COP1 gene, complete cds gi|28394260|tpg|BK000438.1|
SSH2-1 g05	348	Expect = 8e-008 Identities = 48/53 (90%)	Hordeum vulgare rubisco activase (RcaA2) mRNA, complete cds gi|167090|gb|M55447.1|BLYRCAA2
SSH2-1 h10	44	Expect = 5.6 Identities = 18/18 (100%)	Mus musculus membrane-associated ring finger (C3HC4) 3, mRNA (cDNA clone MGC:130167 IMAGE:40052073), complete cds gi|76827382|gb|BC107232.1|
SSH2-2 a02	429	Expect = 1.5 Identities = 24/25 (96%)	Human DNA sequence from clone GS1-304P7 on chromosome 1q25.1-31.1 Contains a zinc-finger protein pseudogene and a novel pseudogene, complete sequence gi|6010162|emb|AL096803.8|HSBG304P7
SSH2-2 c01	310	Expect = 0.069 Identities = 23/23 (100%)	Gallus gallus prkdc gene for DNA-dependent protein kinase catalytic subunit, complete cds gi|20334954|dbj|AB028136.1|
SSH2-2 c03	305	Expect = 0.27 Identities = 22/22 (100%)	PREDICTED: Rattus norvegicus antigen identified by monoclonal antibody Ki-67 (predicted) (Mki67_predicted), mRNA gi|109463072|ref|XM_001056221.1|
SSH2-2 c08	379	Expect = 5.3 Identities = 23/24 (95%)	Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230071K24 product:similar to RIBONUCLEASE P PROTEIN SUBUNIT P40 (EC 3.1.26.5) (RNASEP PROTEIN P40) (RNASE P SUBUNIT 1) [Homo sapiens], full insert sequence gi|26339587|dbj|AK048810.1|
		Expect = 5.3 Identities = 20/20 (100%)	Arabidopsis thaliana mitochondrial genome gi|49256807|emb|Y08501.2|MIATGENA
		Expect = 5.3 Identities = 20/20 (100%)	Sus scrofa PPAR gamma coactivator 1 (PPARGC1) gene, exon 2 and partial cds gi|45544853|gb|AY484495.1|AY484494S2
SSH2-2 d11	45	Expect = 1.5 Identities = 19/19 (100%)	PREDICTED: Pan troglodytes ring finger and WD repeat domain 1,transcript variant 1 (TRAF7), mRNA gi|114660447|ref|XM_001162280.1|
		Expect = 1.5 Identities = 19/19 (100%)	Homo sapiens TNF receptor-associated factor 7 (TRAF7), transcript variant 1, mRNA gi|45594311|ref|NM_032271.2|
		Expect = 5.8 Identities = 18/18 (100%)	PREDICTED: Danio rerio similar to intercellular signalling molecule Notch6 (LOC569815), mRNA gi|68432652|ref|XM_693223.1|
SSH2-2 e08	144	Expect = 1.8 Identities = 20/20 (100%)	Theileria annulata strain Ankara 40S ribosomal protein S6 (TA13460) partial mRNA gi|84995011|ref|XM_947135.1|
SSH2-2 f03	225	Expect = 0.19 Identities = 22/22 (100%)	Trichodesmium erythraeum IMS101, complete genome gi|110164990|gb|CP000393.1|
		Expect = 3.0 Identities = 20/20 (100%)	Homo sapiens Goodpasture antigen-binding protein (COL4A3BP) gene,partial cds gi|11967332|gb|AF232935.1|AF232935
		Expect = 0.30 Identities = 22/22 (100%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries (ORTADA) gi|103482547|emb|CT988905.1|
		Expect = 1.2 Identities = 24/25 (96%)	HIV-1 isolate 00CMNYU360 from Cameroon envelope glycoprotein (env) gene, partial cds gi|21306485|gb|AF509521.1|
SSH2-2 h03	40	Expect = 4.7	Fowl adenovirus 10 major late promoter and bipartite leader sequence and pre-terminal protein gene,

		Identities = 18/18 (100%)	complete cds gi|2674063|gb|AF007577.1|AF007577
SSH2-2 h09		Expect = 0.070 Identities = 23/23 (100%)	Carpodacus mexicanus Came-DAB1 and serine-threonine kinase genes,complete sequence gi|10281551|gb|AF205032.1|AF205032
		Expect = 1.1 Identities = 21/21 (100%)	Mus musculus UDP-glucose ceramide glucosyltransferase-like 2, mRNA(cDNA clone IMAGE:5368593), containing frame-shift errors gi|22749732|gb|BC032274.1|
		Expect = 4.3 Identities = 23/24 (95%)	Arabidopsis thaliana unknown protein (AT2G46150) mRNA, complete cds i|30690241|ref|NM_130177.2|
SSH2-3 a12	338	25	Zebrafish DNA sequence from clone CH211-8G12 in linkage group 21,complete sequence
		24	Human DNA sequence from clone RP5-1009H6 on chromosome 20 Contains the 3' end of the NFATC2 gene for cytoplasmic calcineurin-dependent (2) nuclear factor of activated T-cells, complete sequence
SSH2-3 b03	739	Expect = 2e-028 Identities = 119/136 (87%)	H.vulgare mRNA for Hv14-3-3b gi|1070353|emb|X93170.1|HV1433B
		Expect = 0.044 Identities = 27/28 (96%)	Zea mays regulatory protein GF14-12 mRNA, complete cds gi|168602|gb|M96856.1|MZEREGP
		Expect = 2.7 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-248G5 on chromosome 13q14.3-21.1 Contains the 5' end of the ATP7B gene for ATPase, Cu++ transporting, beta polypeptide (Wilson disease), four novel genes, the NEK3 gene for NIMA (never in mitosis gene a)-related kinase 3, the 3' end of a novel gene and five CpG islands, complete sequence gi|12227312|emb|AL139082.18|
SSH2-3 b11	187	Expect = 0.63 Identities = 21/21 (100%)	Pseudomonas aeruginosa PA14 pathogenicity island PAPI-1, complete sequence gi|32481613|gb|AY273869.1|
		Expect = 2.5 Identities = 20/20 (100%)	Oryza sativa (japonica cultivar-group) aos mRNA for allene oxide synthase, complete cds gi|41351506|dbj|AB116527.1|
		Expect = 9.8 Identities = 19/19 (100%)	PREDICTED: Pan troglodytes Yeast Sps1/Ste20-related kinase 4 (YSK4),mRNA gi|114581129|ref|XM_525928.2|
		Expect = 9.8 Identities = 19/19 (100%)	Trichoderma reesei creA gene for DNA-binding protein, complete cds gi|940428|dbj|D63514.1|TRRCREA
SSH2-3 b12	152	Expect = 7.7 Identities = 22/23 (95%)	Brugia malayi microfilarial sheath protein SHP3a (Bmshp3a) and microfilarial sheath protein SHP3 precursor (Bmshp3) genes, complete cds gi|2642218|gb|AF030944.1|
SSH2-3 c04	471	Expect = 6.7 Identities = 20/20 (100%)	Xenopus tropicalis annexin A7, mRNA (cDNA clone MGC:79834 IMAGE:6987252), complete cds gi|49899003|gb|BC076713.1|
		Expect = 6.7 Identities = 20/20 (100%)	Human DNA sequence from clone RP1-120G22 on chromosome 1p36.21-36.33 Contains the 5' end of the CHD5 gene for chromodomain helicase DNA binding protein 5, the RPL22 gene for ribosomal protein L22, eight novel genes, the ICMT gene for isoprenylcysteine carboxyl methyltransferase, possible ortholog of rodent transcription factor HES-3, the 3' end of the gene for brain acyl-CoA hydrolase (BACH) and seven CpG islands, complete sequence gi|9369286|emb|AL031847.17|HS120G22
SSH2-3 c10	255	Expect = 0.88 Identities = 21/21 (100%)	Mouse DNA sequence from clone RP23-327K3 on chromosome 11 Contains a cyclic AMP phosphoprotein (Arpp19) pseudogene, a heat shock protein (Hsp) pseudogene and a ribosomal protein S6 (Rps6) pseudogene, complete sequence gi|21627926|emb|AL669825.10|
SSH2-3 c12	304	Expect = 1.1 Identities = 21/21 (100%)	Bordetella holmesii strain B2739 30S ribosomal protein S15 (rpsO) and genes, partial cdspolyribonucleotide nucleotidyltransferase (pnp) gi|89888172|gb|DQ420098.1|
		Expect = 1.1 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-481A12 on chromosome 10 Contains a receptor coactivator 4, the TIMM23 gene for translocase ofpseudogene similar to part of ral guanine nucleotide dissociation stimulator (RALGDS), the MSMB gene for microseminoprotein beta, the NCOA4 gene for nuclear inner mitochondrial membrane 23, a poly (ADP-ribose) glycohydrolase (PARG) pseudogene, a ribosomal protein L35a (RPL35A) pseudogene and three CpG islands, complete Sequence gi|21436511|emb|AL450342.16|
		Expect = 4.2 Identities = 20/20 (100%)	Xanthomonas campestris pv. campestris putative NTPase VagA (vagA) gene, complete cds gi|13936892|gb|AF360374.1|AF360374
SSH2-3 d01	762	Expect = 2.8 Identities = 21/21 (100%)	Mouse DNA sequence from clone RP23-20G7 on chromosome 1 Contains a cytochrome c oxidase subunit Vb (Cox5b) pseudogene, a ribosomal protein S2 (Rps2) pseudogene, the 5' end of the Nrp2 gene for neuropilin 2, the 3' end of the gene for an ortholog of human amyotrophic lateral sclerosis 2 (juvenile) chromosome region candidate 19 (ALS2CR19) and two CpG islands, complete sequence gi|21537461|emb|AL645727.16|
SSH2-3 d03	290	Expect = 4.0 Identities = 20/20 (100%)	Human DNA sequence from clone RP1-66H14 on chromosome 6q21-22 Contains the 3' end of the FYN gene for the FYN oncogene related to SRC, FGR, YES and the 5' end of the C6orf5 gene for chromosome 6 open reading frame 5 (NFkB-activating protein ACT1, connection to IKK and SAPK/JNK, chromosome 6 open reading frame 6) (C6orf5)(ACT1, CIKS, C6ORF6, DKFZP586G0522)(contains FLJ22949), complete sequence gi|2760549|emb|Z97989.1|HS66H14
SSH2-3 d06	108	Expect = 5.1 Identities = 19/19 (100%)	Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes gi|7768311|emb|AJ249895.1|MMU249895
		Expect = 5.1 Identities = 19/19 (100%)	Ganoderma formosanum manganese peroxidase (mnp0109) gene, complete cds gi|82470013|gb|DQ267752.1|
SSH2-3 d10	575	Expect = 0.53 Identities = 22/22 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2, BAC clone:OJ1149_C12 gi|48716388|dbj|AP004082.3|
		Expect = 8.2 Identities = 20/20 (100%)	Aedes aegypti clone AE-3223 HHYHHH motif-containing secreted protein mRNA, complete cds gi|94468491|gb|DQ440062.1|
		Expect = 8.2 Identities = 20/20 (100%)	Oryctolagus cuniculus interleukin-10 mRNA, complete cds gi|3242895|gb|AF068058.1|AF068058
		Expect = 5.4 Identities = 19/19 (100%)	Trypanosoma cruzi strain CL Brener protein kinase (Tc00.1047053509105.120) partial mRNA gi|71652467|ref|XM_809797.1|
		Expect = 5.4 Identities = 22/23 (95%)	Human DNA sequence from clone RP11-224P11 on chromosome 10 Contains a single-stranded DNA binding protein (SSBP1)(SSBP) pseudogene, complete sequence gi|16943977|emb|AL353093.18|
		Expect = 1e-056 Identities = 248/291 (85%),	Oryza sativa (japonica cultivar-group) Os03g0835400 (Os03g0835400) mRNA, complete cds gi|115456434|ref|NM_001058353.1|
		Expect = 0.35 Identities = 34/38 (89%)	Danio rerio clone RK140A1B05 electron-transfer-flavoprotein, alpha polypeptide (ETFA) mRNA, complete cds gi|37681798|gb|AY398344.1|
		Expect = 1.4 Identities = 21/21 (100%)	PREDICTED: Danio rerio similar to solute carrier family 16 (monocarboxylic acid transporters), member 6 (LOC564872), mRNA gi|68393837|ref|XM_688196.1|
SSH2-3 e02	263	Expect = 7e-017 Identities = 78/88 (88%)	Triticum aestivum J-domain protein (J3) mRNA, complete cds gi|110617799|gb|DQ789026.1|
		Expect = 0.91 Identities = 21/21 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103484029|emb|CT989382.1|
SSH2-3 e05	324	Expect = 4.5 Identities = 23/24 (95%)	Arabidopsis thaliana ATFER1; ferric iron binding (ATFER1) mRNA,complete cds gi|42567569|ref|NM_120238.3|
SSH2-3 g09	188	Expect = 9.8 Identities = 25/27 (92%)	Penicillium chrysogenum virus segment 1 RNA-dependent RNA polymerase gene, complete cds gi|22324502|gb|AF296439.1|
		Expect = 9.8 Identities = 19/19 (100%)	Homo sapiens mRNA for Syntaxin binding protein 1 variant protein gi|62087939|dbj|AB209180.1|

		Expect = 9.8 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-56D16 on chromosome 9 Contains the STXBP1 gene for syntaxin binding protein 1(UNC18,hUNC18,MUNC18-1), two novel genes, a novel gene (LOC138428), the gene for a novel protien (LOC286207), the gene for anovel protein (FLJ32780), the TOR2A gene for torsin family 2, member A (FLJ14771), the 3' end of the SH2D3C gene for SH2 domain containing 3C (CHAT,NSP3) and five CpG islands, complete sequence gi|13624960|emb|AL162426.20|
SSH2-3 h03	126	Expect = 6.2 Identities = 19/19 (100%)	Aspergillus fumigatus Af293 MFS transporter (Afu1g05010) partial mRNA gi|70990801|ref|XM_745157.1|
SSH2-3 h09	210	Expect = 2.8 Identities = 20/20 (100%)	Mouse DNA sequence from clone RP23-64E17 on chromosome 11 Cntains the 3' end of the Nipsnap1 gene for 4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans), a novel gene, a ribosomal protein L17 (Rpl17) pseudogene, the Nefh gene for neurofilament heavy polypeptide, the Ap1b1 gene for adaptor protein complex AP-1 beta 1 subunit, the gene for the ortholog of human RAS-related protein on chromosome 22, the gene for the ortholog of human growth arrest-specific 2 like 1 GAS2L1 and six CpG islands, complete sequence gi|20135754|emb|AL645522.12|
SSH2-4 a02	434	Expect = 6.1 Identities = 20/20 (100%)	Osmerus mordax type II antifreeze protein gene, partial cds gi|66934580|gb|DQ004949.1|
		Expect = 6.1 Identities = 20/20 (100%)	Campylobacter jejuni serotype HS:36 possible polysaccharide modification protein gene, partial cds; putative adenylylsulfate kinase, putative sugar nucleotidyltransferase, putative pyruvate kinase, putative methyltransferases, putative glycosyltransferase, putative D-glycero-D-manno-heptose 1-phosphate guanosyltransferase, putative sedoheptulose 7-phosphate isomerase, putative D-glycero-D-manno-heptose 7-phosphate kinase, putative UDP-glucose 4-epimerase, putative GDP-mannoheptose-4,6 dehydratase, putative GDP-fucose synthase, putative dTDP-4-dehydro rhamnose 3,5-epimerase, and putative glycosyltransferases genes, complete cds; and unknown genes gi|37719569|gb|AY332624.1|
		Expect = 6.1 Identities = 20/20 (100%)	Campylobacter jejuni subsp. jejuni 81-176 putative glycosyl transferases, putative glycosyl transferase (CjB1442c), and KpsF (kpsF) genes, complete cds gi|62754287|gb|AY934867.1|
SSH2-4 a06	133	Expect = 6.6 Identities = 19/19 (100%)	PREDICTED: Mus musculus similar to Histone acetyltransferase MYST4(MYST protein 4) (MOZ, YBF2/SAS3, SAS2 and TIP60 protein 4) (Querkopf protein) (LOC673600), mRNA gi|94419176|ref|XR_004275.1|
		Expect = 6.6 Identities = 19/19 (100%)	Sorghum bicolor putative protein kinase gene, partial cds; putative Cf-2,fertilization-independent endosperm proteins, hypothetical protein, putative non-LTR retroelement reverse transcriptase, OCL5 protein, tryptophan synthase beta-subunit, hypothetical proteins, putative AP endonuclease, putative RNA polymerase II complex component SRB7, putative beta-1,3-glucanase, hypothetical protein, TNP2-like protein, hypothetical protein, putative phosphate/phosphoenolpyruvate translocator, putative protein, hypothetical proteins, putative galactosyltransferase family, hypothetical protein, putative cytochrome P450 family, putative lipid transfer protein, putative photoreceptor-interacting protein, and hypothetical protein genes, complete cds; and hypothetical protein gene, partial cds gi|46200512|gb|AF466200.2|
SSH2-4 a07	92	Expect = 4.2 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-354P17 on chromosome 9 Contains the IFNA6 gene for interferon, alpha 6, the IFNA13 gene for interferon, alpha 13, the IFNA2 gene for interferon, alpha 2, the IFNA8 gene for interferon, alpha 8, an interferon, omega 1 (IFNW1) pseudogene, the IFNA1 gene for interferon, alpha 1, 4 interferon pseudogenes, the 3' end of a novel gene and a CpG island, complete sequence gi|11414526|emb|AL353732.14|
SSH2-4 a11	386	Expect = 5.4 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-472K17 on chromosome 13 Contains a novel gene, the 3' end of the COL4A1 gene for collagen type IV alpha 1 and a CpG island, complete sequence gi|9864606|emb|AL390755.5|
		Expect = 5.4 Identities = 26/28 (92%)	Mus musculus alpha(1,2)fucosyltransferase gene, complete cds i|1906006|gb|U90553.1|MMU90553
SSH2-4 b01	405	Expect = 1.4 Identities = 21/21 (100%)	Homo sapiens fatty acid amide hydrolase (FAAH) gene, complete cds gi|56410856|gb|AY842444.1|
		Expect = 1.4 Identities = 21/21 (100%)	Human DNA sequence from clone RP4-603I14 on chromosome 1p31.3-33 Contains the 5' end of the gene for MUF1 protein (MUF1), the UQCRH gene for ubiquinol-cytochrome c reductase hinge protein, gene MGC22960 (FLJ40205, FLJ32858, FLJ46186), the FAAH gene for fatty acid amide hydrolase and a CpG island,complete sequence gi|9588441|emb|AL122001.32|HSJ603I14
SSH2-4 b03	264	Expect = 3.6 Identities = 20/20 (100%)	Mus musculus more than blood (Mtb) mRNA, complete cds gi|38489965|gb|AY455829.1|
SSH2-4 b06	466	Expect = 6.6 Identities = 20/20 (100%)	PREDICTED: Strongylocentrotus purpuratus similar to acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)(LOC584928), partial mRNA gi|115746767|ref|XM_784772.2|
		Expect = 6.6 Identities = 20/20 (100%)	PREDICTED: Pan troglodytes solute carrier family 35, member C2,transcript variant 1 (SLC35C2), mRNA gi|114682364|ref|XM_001161443.1|
SSH2-4 b07	538	Expect = 1.9 Identities = 21/21 (100%)	Entamoeba histolytica HM-1:IMSS BspA-like leucine rich repeat protein (385.t00004) partial mRNA gi|67465276|ref|XM_643731.1|
		Expect = 7.7 Identities = 20/20 (100%)	PREDICTED: Danio rerio similar to neuropeptide Y receptor Y1(LOC556478), mRNA gi|68441328|ref|XM_679294.1|
		Expect = 7.7 Identities = 20/20 (100%)	Sus scrofa CC chemokine receptor genes (CCR2, CCR5, CCRL2, LTF, TMEM7,LRRC2), complete cds, clone: 0475A03 gi|41688294|dbj|AP006185.1|
		Expect = 7.7 Identities = 23/24 (95%)	Entamoeba histolytica HM-1:IMSS RNA-binding protein (57.t00015) partial mRNA gi|67477715|ref|XM_649208.1|
SSH2-4 b08	183	Expect = 9.5 Identities = 19/19 (100%)	Human DNA sequence from clone RP5-823D19 on chromosome 1q42.11-4 Contains the 5' end of the SIPA1L2 gene for signal-induced proliferation-associated 1 like 2, complete sequence gi|15131205|emb|AL157409.16|
		Expect = 9.5 Identities = 22/23 (95%)	Actinobacillus pleuropneumoniae hypothetical protein gene, partial cds; and ApxIIC (apxIIC) gene, complete cds gi|60476781|gb|AY795601.1|
		Expect = 9.5 Identities = 19/19 (100%)	E.coli glyV alpha,beta and gamma genes for tRNA-Gly gi|43151|emb|X53236.1|ECTRNAG3
SSH2-4 b10	542	Expect = 2.0 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-239B6 on chromosome 1 Contains the 3' end of the EIF2C4 gene for eukaryotic translation initiation factor 2C, 4, complete sequence gi|21955470|emb|AL359186.15|
		Expect = 7.7 Identities = 20/20 (100%)	PREDICTED: Homo sapiens similar to golgi autoantigen, golgin subfamily a-like, transcript variant 1 (LOC642346), mRNA gi|113425486|ref|XM_928707.2|
SSH2-4 b11	513	Expect = 7.3 Identities = 20/20 (100%)	Lepeophtheirus salmonis T-complex protein 1 gamma subunit (Cctg) mRNA, partial cds g i|6318664|gb|AF167366.1|AF167366
SSH2-4 b12	511	Expect = 7.3 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-408E5 on chromosome 13q11-12.2 Contains an FSH primary respone homolog 1 (FSHPRH1)pseudogene, a paraspeckle protein 1 alpha pseudogene,a novel gene, the TUBA2 gene for tubulin alpha 2, two novel pseudogenes and a gene for a novel protein similar to DMPK-like CDC42-binding protein kinase beta (CDC42BPB), complete sequence gi|9187183|emb|AL139327.18|
SSH2-4 c01	530	Expect = 1.9 Identities = 21/21 (100%)	PREDICTED: Gallus gallus similar to tumor suppressor candidate 3 isoform b (LOC422738), mRNA gi|50746954|ref|XM_420692.1|
		Expect = 7.6 Identities = 20/20 (100%)	Homo sapiens UDP glucuronosyltransferase 2 family, polypeptide B4 (UGT2B4) gene, complete cds gi|94717611|gb|DQ520733.1|
		Expect = 7.6	PREDICTED: Gallus gallus similar to importin alpha Q2 (LOC418870),mRNA

		Identities = 20/20 (100%)	gi|50730888|ref|XM_417065.1|
		Expect = 7.6 Identities = 20/20 (100%)	Human DNA sequence from clone RP1-154K9 on chromosome Xp11.3-11.4 Contains the 3' end of a novel gene, the gene for type 1 protein phosphatase inhibitor (I-4) and one CpG island,complete sequence gi|2578060|emb|Z94277.1|HS154K9
SSH2-4 c02	575	Expect = 2.1 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-107L7 on chromosome 10 Contains the 3'end of the gene forVPS10 domain receptor protein SORCS 3 (SORCS3), complete sequence gi|16304992|emb|AL596118.6|
SSH2-4 c03	325	Expect = 4.5 Identities = 20/20 (100%)	Human DNA sequence from clone RP1-68D18 on chromosome 11p12-13 Contains part of the SLC1A2 gene for three variants of solute carrier family 1 (glial high affinity glutamate transporter) member 2 and part of the CD44 gene for CD44 antigen (homing function and Indian blood group system)with five variants, complete sequence gi|9650514|emb|AL133330.14|
		Expect = 4.5 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-108P5 on chromosome 13q14.12-21.1 Contains the CYSLTR2 gene for cysteinyl leukotriene receptor 2 (CYSLT2, CYSLT2R), complete sequence gi|11034480|emb|AL137118.20|
SSH2-4 c05	80	Expect = 0.89 Identities = 20/20 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1 gi|58530787|dbj|AP008207.1|
		Expect = 3.5 Identities = 22/23 (95%)	PREDICTED: Danio rerio similar to plakophilin 2 (LOC568060), mRNA gi|68359073|ref|XM_691368.1|
SSH2-4 c07	139	Expect = 1.8 Identities = 20/20 (100%)	Bacillus sp. Y proYK gene for protease, complete cds gi|51338930|dbj|AB100359.1|
		Expect = 1.8 Identities = 20/20 (100%)	Mesocricetus auratus delta sarcoglycan mRNA, alternative exon 1b gi|2051976|gb|U94389.1|MAU94389
		Expect = 6.9 Identities = 22/23 (95%)	Arabidopsis thaliana MBD9; DNA binding (MBD9) mRNA, complete cds gi|30678340|ref|NM_111012.2|
		Expect = 6.9 Identities = 19/19 (100%)	Mouse DNA sequence from clone RP23-413O19 on chromosome 11 Contains a laminin receptor 1 (ribosomal protein SA) (Lamr1) pseudogene, a novel gene, the 3' end of the Fgf18 gene for fibroblast growth factor 18 and a CpG island, complete sequence gi|22265445|emb|AL732390.10|
SSH2-4 c10	347	Expect = 1.2 Identities = 21/21 (100%)	Bartonella quintana citrate synthase (gltA) gene, partial cds gi|21322253|gb|AY035823.1|
		Expect = 4.8 Identities = 23/24 (95%)	Mus musculus nuclear transport factor 2-like export factor 2, mRNA(cDNA clone MGC:144847 IMAGE:40106658), complete cds gi|111599891|gb|BC118503.1|
		Expect = 4.8 Identities = 23/24 (95%)	Mus musculus 21 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:G630029H06 product:NTF2-related export protein 2, full insert sequence gi|74188403|dbj|AK144349.1|
SSH2-4 c11	195	Expect = 0.17 Identities = 22/22 (100%)	PREDICTED: Bos taurus similar to E74-like factor 1 (ets domain transcription factor), transcript variant 2 (LOC505251),mRNA gi|76631277|ref|XM_871587.1|
		Expect = 2.6 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-2P5 on chromosome 13 Contains the 5' end of a novel gene, the gene for suppressor of G2 allele of SKP1, S. cerevisiae, the 5' end of a gene similar to TPTE and PTEN homologous inositol lipid phosphatase (TPIP), a pseudogene similar to part of regulator of G-protein signalling 17 (RGS17), the WBP4 gene for WW domain binding protein 4 (formin binding protein 21) and 4 CpG islands, complete sequence gi|11414487|emb|AL157877.11|
		Expect = 2.6 Identities = 20/20 (100%)	Oncorhynchus mykiss recombination activating protein (RAG-1) gene, complete cds gi|558917|gb|U15663.1|OMU15663
		Expect = 2.6 Identities = 20/20 (100%)	Human cis-acting sequence gi|180551|gb|M82882.1|HUMCIS
SSH2-4 c12	376	Expect = 0.34 Identities = 22/22 (100%)	PREDICTED: Pan troglodytes similar to synaptojanin 2 (SYNJ2), mRNA gi|114610013|ref|XR_023281.1|
		Expect = 0.34 Identities = 22/22 (100%)	TPA_exp: Homo sapiens neuregulin 1 isoform (NRG1) gene, alternatively spliced, complete cds gi|22004070|tpg|BK000383.1|
		Expect = 0.34 Identities = 22/22 (100%)	Human DNA sequence from clone RP11-266C7 on chromosome 6q25.2-26 Contains the SYNJ2 gene for synaptojanin 2 (inositol phosphate 5'-phosphatase 2, INPP5H) (contains FLJ23714 and DKFZp761E1512), a novel gene and the 3' end of the SNX9 gene for sorting nexin 9 (SH3 and PX domain-containing protein (SH3PX1, SDP1), FLJ22984). Contains two CpG islands, complete sequence gi|13398696|emb|AL139330.17|
SSH2-4 d04	483	Expect = 0.44 Identities = 22/22 (100%)	Mus musculus matn3 gene for matrilin-3 (partial), exon 4 i|6912032|emb|AJ242932.1|MMU242932
		Expect = 1.7 Identities = 21/21 (100%)	Caenorhabditis elegans COLlagen family member (col-2) (col-2) mRNA,complete cds gi|71994876|ref|NM_069428.2|
		Expect = 1.7 Identities = 21/21 (100%)	Human DNA sequence from clone RP13-444K19 on chromosome X Contains a mitochondrial ribosomal protein S18C (MRPS18C) pseudogene, the 3' end of the gene for a novel protein similar to PHD finger protein 2 PHF2 and a CpG island, complete sequence gi|23476649|emb|AL732374.14|
		Expect = 1.7 Identities = 21/21 (100%)	Human DNA sequence from clone RP5-1125N11 on chromosome 1p34.2-35.3 Contains the 5' end of the gene for Lysosomal-associated multispanning membrane protein-5 (LAPTM5), a novel gene and the 5' end of a novel gene, complete sequence gi|18307331|emb|AL137027.17|
		Expect = 1.7 Identities = 21/21 (100%)	Mus musculus poly (ADP-ribose) polymerase 2 (Parp2) gene, complete cds gi|13160479|gb|AF191547.1|AF191547
		Expect = 1.7 Identities = 21/21 (100%)	Caenorhabditis elegans gene Col-2 coding for a collagen gi|6683|emb|V00148.1|CECOL2
SSH2-4 d06	175	Expect = 0.15 Identities = 22/22 (100%)	PREDICTED: Macaca mulatta similar to ring finger protein 166(LOC711056), mRNA gi|109129499|ref|XM_001099780.1|
		Expect = 2.3 Identities = 20/20 (100%)	Mus musculus FGF15 (Fgf15) gene, complete cds; BC1 scRNA gene, complete sequence; hypothetical protein and cyclin D1 (Ccnd1) genes, complete cds gi|27448227|gb|AF384675.1|
		Expect = 9.1 Identities = 19/19 (100%)	Homo sapiens SOST gene, 3' UTR, MEOX1 gene, 5' UTR, and SOST/MEOX1 intergenic region gi|19880618|gb|AF397423.1|
		Expect = 9.1 Identities = 19/19 (100%)	Human DNA sequence from clone GS1-165F21 on chromosome 10 Contains the 5'end of the PAX2 gene for paired box gene 2 and fifteen CpG islands, complete sequence gi|21425225|emb|AL589862.28|
SSH2-4 d07	184	Expect = 2.4 Identities = 23/24 (95%)	Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4733401E02 product:Keratin-associated protein PMG2, full insert sequence gi|74208965|dbj|AK132534.1|
		Expect = 2.4 Identities = 20/20 (100%)	Streptococcus pneumoniae serotype 6A capsular polysaccharide locus, partial sequence gi|18376696|gb|AF246898.1|
		Expect = 2.4 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-56P10 on chromosome 9q31.3-33.3 Contains the 3' end of the gene for a novel C2H2 type zinc finger protein, the AMBP gene for alpha-1-microglobulin/bikunin precursor, the gene for a novel protein similar to mouse kinesin 12 (LOC113220) and two CpG islands, complete sequence gi|14575073|emb|AL137850.12|
		Expect = 9.6	Amblystegium humile clone beta adenosine kinase-like gene, partial sequence

		Identities = 22/23 (95%)	gi|27463012|gb|AF465105.1|
SSH2-4 d08	179	Expect = 9.3 Identities = 19/19 (100%)	Gallus gallus PC4 and SFRS1 interacting protein 1 (PSIP1), mRNA gi|71896262|ref|NM_001031610.1|
SSH2-4 d10	323	Expect = 0.29 Identities = 22/22 (100%)	Human metabotropic glutamate receptor 6 (mGluR6) gene, complete cds gi|2231437|gb|U82083.1|HSU82083
		Expect = 4.5 Identities = 20/20 (100%)	Human DNA sequence from clone RP4-560B9 on chromosome 1q24-25 Contains three processed pseudogenes and the VAMP4 gene for vesicle-associated membrane protein 4, complete sequence gi|2814366|emb|Z98751.1|HS560B9
SSH2-4 d12	68	Expect = 2.8 Identities = 19/19 (100%)	Trypanosoma brucei TREU927 glycosyl hydrolase-like protein (Tb11.01.2140) partial mRNA gi|74025069|ref|XM_824008.1|
		Expect = 2.8 Identities = 19/19 (100%)	PREDICTED: Danio rerio similar to cyclic nucleotide gated channel beta 3 (LOC566867), mRNA gi|68437328|ref|XM_690154.1|
		Expect = 2.8 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-103A2 on chromosome 10 Contains the HTR7 gene for 5-hydroxytryptamine receptor 7 (adenylate cyclase-coupled) and a CpG island, complete sequence gi|14547262|emb|AL360011.19|
SSH2-4 e01	567	Expect = 0.52 Identities = 22/22 (100%)	Homo sapiens DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae)(DCLRE1A) gene, complete cds gi|15591647|emb|AL592546.7|
		Expect = 0.52 Identities = 22/22 (100%)	Human DNA sequence from clone RP11-211N11 on chromosome 10 Contains the 3' end of the CASP7 gene for caspase 7 apoptosis-related cysteine protease, a novel gene (FLJ23537), the DCLRE1A gene for DNA cross-link repair 1A (PSO2 homolog S. cerevisiae), the 5' end of the gene for a novel NHL repeat domain containing protein (FLJ33312), a novel gene and a CpG island, complete sequence gi|15591647|emb|AL592546.7|
		Expect = 2.1 Identities = 21/21 (100%)	Human DNA sequence from clone RP1-192P9 on chromosome Xp11.23-11.4 Contains a transmembrane 4 superfamily member 11(plasmolipin) (PMLP) pseudogene and a CpG island, complete gi|4539519|emb|AL020989.2|HS192P9
SSH2-4 e02	453	Expect = 0.41 Identities = 22/22 (100%)	Mus musculus cDNA, RIKEN full-length enriched library, clone:M5C1081D17 product:weakly similar to YY1 associated protein [Homo sapiens], full insert sequence gi|74184822|dbj|AK147575.1|
		Expect = 0.41 Identities = 22/22 (100%)	Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610100B20 product:hypothetical Myb DNA binding domain containing protein, full insert gi|12848117|dbj|AK011779.1|
		Expect = 1.6 Identities = 24/25 (96%)	Solanum tuberosum nematode resistance-like protein (Gro1-2) gene, Gro1-2-P40 allele, complete cds gi|37781279|gb|AY196153.1|
		Expect = 6.4 Identities = 20/20 (100%)	Oryza sativa phospholipase D beta 2 (PLDbeta2) gene, complete cds gi|18765899|gb|AF411221.1|
SSH2-4 e06	308	Expect = 1.1 Identities = 21/21 (100%)	PREDICTED: Homo sapiens similar to oocyte-specific histone H1(LOC652297), mRNA gi|113415095|ref|XR_019321.1|
		Expect = 1.1 Identities = 21/21 (100%)	PREDICTED: Homo sapiens hypothetical LOC642487 (LOC642487), mRNA gi|113414532|ref|XR_016158.1|
SSH2-4 e08	60	Expect = 2.4 Identities = 19/19 (100%)	Escherichia coli hemolysin operon, serotype O83:K24:H31 gi|94480742|emb|AM261284.1|
SSH2-4 f05	418	Expect = 1.5 Identities = 21/21 (100%)	PREDICTED: Macaca mulatta similar to F-box/WD-repeat protein 2 (F-box and WD-40 domain protein 2) (MD6 protein), transcript variant 2 (LOC700958), mRNA gi|109110428|ref|XM_001096189.1|
SSH2-4 f09	698	Expect = 2.5 Identities = 21/21 (100%)	Mouse DNA sequence from clone RP24-371A24 on chromosome 4 Contains a ribosomal protein S2 (Rps2) pseudogene, complete sequence gi|37652274|emb|BX649539.6|
SSH2-4 f11	183	Expect = 9.5 Identities = 19/19 (100%)	Human DNA sequence from clone RP3-382I10 on chromosome 6q14.3-15 Contains a novel gene, a TAF13 RNA polymerase II, TATA box binding protei (TBP)-associated factor (TAF13) (TAF2K) pseudogene, an S-adenosylmethionine decarboxylase 1 (AMD1) pseudogene, a suppression of tumorigenicity 13 (colon carcinoma) (Hsp70-interacting protein) (ST13) (HIP) pseudogene, the SLC35A1 gene for solute carrier family 35(CMP-sialic acid transporter) member 1, the 3' end of the gene for a novel protein similar to arginyl-tRNA synthetase (arginine-tRNA ligase, EC 6.1.1.19) and two CpG islands, complete sequence gi|6456830|emb|AL049697.9|HSJ382I10
SSH2-4 g01	639	Expect = 9.2 Identities = 20/20 (100%)	Caenorhabditis elegans ForKHead transcription factor family member(fkh-2) (fkh-2) mRNA, complete cds gi|71996543|ref|NM_076243.2|
		Expect = 9.2 Identities = 20/20 (100%)	Human DNA sequence from clone RP4-616B8 on chromosome 20q11.22-12 Contains the DDX35 gene for DEAD/H box polypeptide 35, the NPM1P19 gene for nucleophosmin 1 (nucleolar phosphoprotein B23, numatrin) pseudogene 19, the C20orf129 gene for chromosome 20 open reading frame 129, the 3' end of the PPP1R16B gene for protein phosphatase 1 regulatory (inhibitory) subunit 16B and four CpG islands, complete sequence gi|9408726|emb|AL023803.3|HS616B8
SSH2-4 g02	459	Expect = 0.42 Identities = 22/22 (100%)	Arabidopsis thaliana nickel ion transporter (AT2G16800) mRNA,complete cds gi|30679766|ref|NM_127232.2|
		Expect = 1.6 Identities = 21/21 (100%)	Triticum aestivum fasciclin-like protein FLA25 mRNA, complete cds gi|115349933|gb|DQ872398.1|
SSH2-4 g04	649	Expect = 2.4 Identities = 30/33 (90%)	Oryza sativa (japonica cultivar-group) Os03g0227800 (Os03g0227800) mRNA, partial cds gi|115451694|ref|NM_001055983.1|
		Expect = 2.4 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-313J2 on chromosome 10 Contains a zinc finger protein pseudogene and a CpG island, complete sequence gi|29539158|emb|BX322639.2|
SSH2-4 g05	455	Expect = 1.6 Identities = 21/21 (100%)	Ceratitis pinax tRNA-Thr gene, partial sequence; tRNA-Pro gene, complete sequence; and NADH dehydrogenase 6 gene, partial cds; mitochondrial gi|62001035|gb|AY790573.1|
		Expect = 6.4 Identities = 20/20 (100%)	Mouse DNA sequence from clone RP23-191E3 on chromosome 11 Contains four novel genes, an eukaryotic translation elongation factor 2(Eef2) pseudogene, a Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (Fau) pseudogene, the Eif4enif1 gene for eukaryotic translation initiation factor 4E nuclear import factor 1, the Drg1 gene for developmentally regulated GTP binding protein 1, the Zfp278 gene for zinc finger protein 278, the 3' end of the Limk2 gene LIM motif-containing protein kinase 2 and five CpG islands, complete sequence gi|24414663|emb|AL671968.17|
SSH2-4 g07	440	Expect = 6.2 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-122C9 on chromosome 1p21.2-22.1 Contains a ribosomal protein L7 (RPL7) pseudogene, the PTBP2 gene for polypyrimidine tract binding protein 2 and a CpG island, complete sequence gi|9714912|emb|AL357150.7|
SSH2-4 h01	234	Expect = 0.80 Identities = 21/21 (100%)	PREDICTED: Rattus norvegicus similar to Peptidylprolyl isomerase-like 5 (LRR-repeat protein 1) (LRR-1) (4-1BB-mediated signaling molecule) (4-1BBlrr) (LOC687175), mRNA gi|109479303|ref|XM_001076561.1|
		Expect = 0.80 Identities = 24/25 (96%)	Mouse DNA sequence from clone RP23-19L22 on chromosome 11 Contains the Actr2 gene for ARP2 actin-related protein 2 homolog (yeast), a small nuclear ribonucleoprotein polypeptide G (Snrpg) pseudogene, two novel genes, the Rab1 gene for RAB1, member RAS oncogene family and three CpG islands, complete sequence gi|20792609|emb|AL606522.6|
		Expect = 3.2 Identities = 23/24 (95%)	Human DNA sequence from clone RP1-125N5 on chromosome 6q26-27 Contains the 3' end of a variant of the gene for smooth muscle cell associated protein 2 (SMAP2) or secreted modular calcium binding protein 2 (SMOC2), a novel gene and a CpG island, complete sequence gi|3820992|emb|AL008728.1|HS125N5
SSH2-4 h03	76	Expect = 3.3 Identities = 22/23 (95%)	Heterorhabditis sp. strain SJ6 NADH dehydrogenase subunit 4 (ND4) gene, mitochondrial gene encoding mitochondrial protein, partial cds gi|3192844|gb|AF066884.1|AF066884

		Expect = 3.3 Identities = 19/19 (100%)	Entamoeba histolytica HM-1:IMSS DNA mismatch repair protein mutL(117.t00008) partial mRNA gi|67473434|ref|XM_647392.1|
		Expect = 3.3 Identities = 19/19 (100%)	Oryza sativa subsp. indica putative ethylene receptor gene, complete cds gi|15054445|gb|AY043031.1|
		Expect = 3.3 Identities = 19/19 (100%)	Homo sapiens mitogen-activated protein kinase kinase 4 (MAP2K4) gene,complete cds gi|62945792|gb|DQ015703.1|
		Expect = 3.3 Identities = 19/19 (100%)	Plasmodium berghei strain ANKA protein phosphatase 2c-like protein(PB000526.03.0) partial mRNA gi|68071090|ref|XM_672367.1|
SSH2-4 h04	100	Expect = 1.2 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-472K17 on chromosome 13 Contains a novel gene, the 3' end of the COL4A1 gene for collagen type IV alpha 1 and a CpG island, complete sequence gi|9864606|emb|AL390755.5|
		Expect = 4.6 Identities = 19/19 (100%)	PREDICTED: Bos taurus similar to protocadherin gamma subfamily C, 3 isoform 3, transcript variant 10 (LOC520024), mRNA gi|76623279|ref|XM_881641.1|
		Expect = 4.6 Identities = 19/19 (100%)	Homo sapiens T-cell gamma receptor locus, complete sequence gi|5566238|gb|AF159056.1|AF159056
SSH2-4 h05	136	Expect = 6.8 Identities = 19/19 (100%)	Aphanius danfordii isolate A.dan27637 16S ribosomal RNA gene, partial sequence; tRNA-Leu gene, complete sequence; NADH dehydrogenase subunit 1 gene, complete cds; tRNA-Ile, tRNA-Gln, and tRNA-Met genes, complete sequence; NADH dehydrogenase subunit 2 gene, complete cds; tRNA-Trp, tRNA-Ala, tRNA-Asn, tRNA-Cys, and tRNA-Tyr genes,complete sequence; and cytochrome oxidase subunit 1 gene, partial cds; mitochondrial genes for mitochondrial products gi|23664167|gb|AF451655.1|
SSH2-4 h07	53	Expect = 7.7 Identities = 18/18 (100%)	Human DNA sequence from clone RP11-4E23 on chromosome 9 Contains the 5' end of the MLLT3 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 (AF9), a novel gene, the 5' end of a novel gene (FLJ2035, KIAA1797) and two CpG islands, complete sequence gi|15546079|emb|AL354879.12|
SSH2-4 h10	299	Expect = 1.0 Identities = 24/25 (96%)	Human DNA sequence from clone RP1-179N16 on chromosome 6p21.1-21.33 Contains the MAPK13 and MAPK14 genes for mitogen-activated protein kinase 13 and 14 , a nudix type 5 motif (nudt5) pseudogene, the 5' end of the SLC26A8 gene for solute carrier family 26 member 8 and two CpG islands, complete sequence gi|3036773|emb|Z95152.1|HS179N16
SSH2-5 a07	718	Expect = 0.66 Identities = 25/26 (96%)	TPA_exp: Mus musculus immunoglobulin heavy chain variable region locus,strain C57BL/6 gi|90704841|tpe|BN000872.1|
SSH2-5 b05	348	Expect = 4.9 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-569D9 on chromosome 13 Contains the CDC16 gene for CDC16 cell division cycle 16 homolog (S. cerevisiae), the gene for similar to yeast Upf3, variant A(UPF3A, HUPF3A, RENT3A), a Charot-Leyden crystal protein(CLC) pseudogene, the 5' end of the gene for a novel protein (KIAA1802) and 6 CpG islands, complete sequence gi|19335754|emb|AL160396.33|
SSH2-5 b06	331	Expect = 4.6 Identities = 23/24 (95%)	PREDICTED: Pan troglodytes zinc binding alcohol dehydrogenase, domain containing 2, transcript variant 1 (ZADH2), mRNA gi|114673602|ref|XM_001138011.1|
		Expect = 4.6 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-413N19 on chromosome 13 Contains FABP3P2 for fatty acid binding protein 3 pseudogene 2(FABP3P, FABP3-PS), complete sequence gi|13785012|emb|AL138703.10|
SSH2-5 b09	358	Expect = 0.021 Identities = 57/68 (83%)	Hordeum vulgare mRNA for mitochondrial aldehyde dehydrogenase ALDH2,complete cds gi|15128579|dbj|AB055519.1|
		Expect = 5.0 Identities = 20/20 (100%)	PREDICTED: Bos taurus similar to protocadherin 7 isoform b precursor, transcript variant 1 (LOC514537), mRNA gi|76673980|ref|XM_592405.2|
SSH2-5 c06	765	Expect = 2.8 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-113A10 on chromosome 9 Contains three seven transmembrane helix receptor pseudogenes, a pseudogene similar to part of a seven transmembrane helix receptor, the RECK gene for reversion-inducing-cysteine-rich protein with kazal motifs (ST15, hRECK) and a CpG island, complete sequence gi|14494868|emb|AL138834.28|
SSH2-5 d04	437	Expect = 3e-020 Identities = 69/74 (93%)	Medicago sativa clone C43 putative splicing factor Prp8 mRNA, partial cds gi|71534915|gb|DQ122784.1|
		Expect = 2e-012 Identities = 53/57 (92%)	Antrodia camphorata partial mnsod gene for manganese superoxide dismutase, exons 1-3, strain B85 gi|33186703|emb|AJ496411.1|ACA496411
		Expect = 1e-010 Identities = 50/54 (92%)	Triticum aestivum MADS-box transcription factor TaAGL29 (AGL29)mRNA, complete cds gi|95981889|gb|DQ512346.1|
		Expect = 1e-010 Identities = 50/54 (92%)	Solanum tuberosum calcium-dependent protein kinase 2 mRNA, complete cds gi|89202790|gb|AF418563.3|
SSH2-5 d07	339	Expect = 1.2 Identities = 21/21 (100%)	PREDICTED: Pan troglodytes zinc finger protein 484, transcript variant 2 (ZNF484), mRNA gi|114625577|ref|XM_001147475.1|
		Expect = 1.2 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-526D8 on chromosome 9 Contains the 5' end of the gene for coiled-coil protein (BICD2) (KIAA0699),a novel gene, a eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D) pseudogene, the gene for a novel KRAB box-containing C2H2 type zinc finger protein, a novel gene, a pseudogene similar to part of sorting nexin associated golgi protein 1(SNAG1), a novel pseudogene, a melanoma antigen pseudogene and three CpG islands, complete sequence gi|9621476|emb|AL136981.22|
SSH2-5 e04	134	Expect = 1.7 Identities = 20/20 (100%)	PREDICTED: Pan troglodytes similar to transmembrane protein 16A(LOC451719), mRNA gi|114639021|ref|XR_025296.1|
		Expect = 6.6 Identities = 19/19 (100%)	PREDICTED: Macaca mulatta similar to zinc finger protein 12 (KOX 3)(LOC705346), mRNA gi|109065946|ref|XM_001092802.1|
SSH2-5 e05	485	Expect = 3e-014 Identities = 103/122 (84%)	Oryza sativa (japonica cultivar-group) Os03g0797700 (Os03g0797700) mRNA, complete cds gi|115455926|ref|NM_001058099.1|
		Expect = 0.44 Identities = 22/22 (100%)	Homo sapiens low density lipoprotein receptor-related protein 5 (LRP5) gene, exons 1 through 9 gi|14028616|gb|AF283320.1|AF283320S1
		Expect = 6.9 Identities = 20/20 (100%)	Neosinocalamus affinis clone Na-1 transposon mariner-like transposase gene, partial cds gi|108861636|gb|DQ528684.1|
		Expect = 6.9 Identities = 20/20 (100%)	PREDICTED: Danio rerio similar to zinc finger protein 206 (LOC562114), mRNA gi|68392611|ref|XM_685511.1|
SSH2-5 f06	402	Expect = 3e-060 Identities = 181/201 (90%)	Triticum aestivum J-domain protein (J3) mRNA, complete cds gi|110617799|gb|DQ789026.1|
		Expect = 1e-041 Identities = 132/146 (90%)	Glycine max seed maturation protein PM37 (PM37) mRNA, complete cds gi|5802243|gb|AF169022.1|AF169022
SSH2-5 g02	394	Expect = 1.4 Identities = 21/21 (100%)	Saccharomyces cerevisiae aminonitrophenyl propanediol (ANP1), UV excision repair protein (RAD23), cytochrome c isozyme(CYC7) genes, complete cds gi|347496|gb|L22173.1|YSCRAD23CY
		Expect = 5.5 Identities = 20/20 (100%)	Myzopoda aurita partial stat5A gene for putative Signal Transducer and Activator of Transcription, exon 16 gi|66990256|emb|AJ865410.1|
		Expect = 5.5 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-520F24 on chromosome 13 Contains an HNRPA1 (heterogenous nuclear ribonucleoprotein A1) pseudogene, an ELL-related RNA polymerase II, elongation factor (ELL2) pseudogene and a ribosomal protein L37 (RPL37) pseudogene, complete sequence gi|12225422|emb|AL356954.16|
SSH2-5 h08	413	Expect = 2e-018 Identities = 91/103 (88%)	Triticum sp. mRNA for GRAB2 protein gi|4218536|emb|AJ010830.1|TSP010830
		Expect = 3e-017	X Tritordeum sp. glycine decarboxylase P subunit mRNA, complete cds gi|2565304|gb|AF024589.1|

		Identities = 49/49 (100%)	
SSH2-5 h10	632	Expect = 2e-016 Identities = 60/64 (93%)	Oryza sativa (japonica cultivar-group) isolate 29042 fibrillin-like protein mRNA, complete cds gi|29367474|gb|AY224474.1|
		Expect = 0.002 Identities = 44/50 (88%)	Lycopersicon esculentum plastid lipid associated protein CHRC (ChrC) mRNA, complete cds; nuclear gene for plastid Product gi|83743300|gb|DQ310151.1|
SSH2-6 a01	267	Expect = 1e-006 Identities = 71/83 (85%)	Oryza sativa (japonica cultivar-group) Os09g0133600 (Os09g0133600) mRNA, complete cds gi|115478071|ref|NM_001069166.1|
		Expect = 3.6 Identities = 20/20 (100%)	PREDICTED: Mus musculus similar to regulating synaptic membrane exocytosis 1 (LOC669030), mRNA gi|94364875|ref|XM_972621.1|
SSH2-6 a03	468	Expect = 1.7 Identities = 24/25 (96%)	Legionella pneumophila clone pA39C putative cobalt/magnesium uptake transporter (corA) and aresenite efflux membrane component-like protein (lrsB) genes, complete cds; and unknown gene gi|19881010|gb|AF480913.1|
		Expect = 6.6 Identities = 20/20 (100%)	Xenopus laevis lipoprotein receptor-related protein 6 mRNA, complete cds gi|22854903|gb|AF508961.1|
		Expect = 6.6 Identities = 23/24 (95%)	Zebrafish DNA sequence from clone DKEY-8O19 in linkage group 20 Contains the gene for a novel protein (zgc:63746), the gene for a novel protein (zgc:55614), the gene for the 5' end of a novel protein similar to mouse and human cyclin-dependent kinase (CDC2-like) 11 (CDK11), the gene for a novel protein similar to vertebrate mitogen-activated protein kinase kinase kinase 5 (MAP3K5), a novel gene and eleven CpG islands, complete sequence gi|54649958|emb|BX545848.23|
SSH2-6 a07	730	Expect = e-114 Identities = 484/570 (84%)	Oryza sativa (japonica cultivar-group) Os07g0658300 (Os07g0658300) mRNA, complete cds gi|115473840|ref|NM_001067054.1|
		Expect = 2.7 Identities = 24/25 (96%)	Mus musculus cryopyrin (Cias1) gene, exon 2 gi|37791069|gb|AY337301.1|AY337300S2
SSH2-6 a09	486	Expect = 6.9 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-332L8 on chromosome 1 Contains an H+ transporting ATPase lysosomal accessory protein 2 (ATP6AP2) pseudogene, the 5' end o the CRB1 gene for crumbs homolog 1(Drosophila) and a mitochondrial ribosomal protein S21(MRPS21) pseudogene, complete sequence gi|16944085|emb|AL513325.13|
		Expect = 6.9 Identities = 20/20 (100%)	Nicotiana tabacum EF-1-alpha-related GTP-binding protein (SUP1)mRNA, complete cds gi|1009231|gb|L38828.1|TOBSUP1NT
SSH2-6 b03	577	Expect = 2.1 Identities = 24/25 (96%)	Zebrafish DNA sequence from clone DKEY-70P6 in linkage group 17 Contains two novel genes, a novel gene similar to human and mouse URKL1 (uridine kinase-like 1), a novel gene similar to vertebrate SYP (synaptophysin), a novel gene similar to vertebrate CACNA1 (voltage-dependent calcium channel P/Q type alpha 1 subunit), a novel pseudogene similar to human and mouse EMILIN2 (elastin microfibril interfacer 2) and a CpG island, complete sequence gi|23557096|emb|AL831748.7|
		Expect = 8.3 Identities = 20/20 (100%)	PREDICTED: Tribolium castaneum similar to Alpha-fetoprotein enhancer-binding protein (AT motif-binding factor) (AT-binding transcription factor 1) (LOC657717), mRNA gi|91079813|ref|XM_964159.1|
SSH2-6 b05	270	Expect = 3.7 Identities = 20/20 (100%)	Ehrlichia canis major outer membrane protein P30 multigene cluster 1, complete sequence gi|13512584|gb|AF078553.2|
SSH2-6 b09	59	Expect = 2.3 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-137M6 on chromosome 13q21.33-22.3 Contains the SCEL gene for sciellin, a novel gene and a CpG island, complete sequence gi|12963897|emb|AL137140.12|
SSH2-6 c03	390	Expect = 5.5 Identities = 20/20 (100%)	Mouse DNA sequence from clone RP23-316C11 on chromosome 11 Contains the Cct6b gene for chaperonin subunit 6b (zeta), a barrier to autointegration factor 1 (Banf1) pseudogene, a GTP binding protein 3 (Gtpbp3) pseudogene, a ribosomal protein S20 (Rps20) pseudogene, three novel genes, the Lig3 gene for ATP-dependent DNA ligase III,, complete sequence gi|18375861|emb|AL645594.9|
SSH2-6 d04	760	Expect = 2.8 Identities = 24/25 (96%)	Human DNA sequence from clone RP5-862K6 on chromosome 20q12-13.13 Contains the 5' end of the L3MBTL gene for l(3)mbt-like (Drosophila), the SFRS6 gene for arginine/serine-rich splicing factor 6, the EIF4EBP2P gene for eukaryotic translation initiation factor 4E binding protein 2 pseudogene, a pseudogene similar to part of nucleotide binding protein (NBP) and two CpG islands, complete sequence gi|11323332|emb|AL031681.16|HS862K6
SSH2-6 d09	404	Expect = 3e-029 Identities = 134/153 (87%)	Triticum aestivum HOTR mRNA, partial cds gi|32400755|gb|AF469493.1|
SSH2-6 d11	764	Expect = 2.8 Identities = 21/21 (100%)	Mouse DNA sequence from clone RP23-326P7 on chromosome 11 Contains the Gp1ba gene for glycoprotein 1b alpha polypeptide, the Slc25a11 gene for solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier) member 11, the gene for a novel PA domain and C3HC4 type zinc finger (RING finger) containing protein, the Pfn1 gene for profilin 1, five novel genes, the Eno3 gene for muscle enolase 3 beta, the Spag7 gene for sperm associated antigen 7, the Kif1c gene for kinesin family member 1C, a ribosomal protein 37A (Rpl37a) pseudogene, the gene for a novel zinc finger protein and six CpG islands, complete sequence gi|18151499|emb|AL596117.19|
SSH2-6 e12	432	Expect = 6.1 Identities = 23/24 (95%)	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds gi|8650408|gb|AF217490.1|AF217491S3
SSH2-6 f01	114	Expect = 0.35 Identities = 24/25 (96%)	Danio rerio partial mRNA for intermediate form of collagen XVIII alpha 1 chain (col18a1i gene) gi|84617866|emb|AJ967005.1|
SSH2-6 f09	458	Expect = 1.6 Identities = 21/21 (100%)	Eremothecium gossypii dynein heavy chain 1 (DHC1) gene, complete cds gi|13374276|gb|AF287477.1|AF287477
SSH2-6 g11	376	Expect = 5.3 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-247A12 on chromosome 9 Contains the CRAT gene for carnitine acetyltransferase (CAT1), the PPP2R4 gene for protein phosphatase 2A, regulatory subunit B' (PR 53) (PTPA), the IER5L gene for immediate early response 5-like, a novel gene and three CpG islands, complete sequence gi|14626056|emb|AL158151.16|
SSH2-6 h03	241	Expect = 3.3 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-10O23 on chromosome 13 Contains a hepatocyte nuclear factor 4 alpha (HNF4A) pseudogene, complete sequence http://en.wikipedia.org/wiki/Hepatocyte_nuclear_factor_4 gi|11340233|emb|AL138997.18|
SSH2-6 h05	315	Expect = 1.1 Identities = 21/21 (100%)	Zebrafish DNA sequence from clone RP71-80D13 in linkage group 3 Contains part of the IgH locus (annotation by J. Bussmann, Steiner lab), a novel gene similar to X. laevis RAP74(transcription initiation factor IIF, alpha subunit), a novel gene and a CpG island, complete sequence gi|38524380|emb|BX510335.6|
SSH2-6 h10	381	Expect = 5.3 Identities = 36/40 (90%)	Triticum aestivum putative Rieske Fe-S precursor protein mRNA, complete cds gi|32394643|gb|AY123422.1|
		Expect = 5.3 Identities = 20/20 (100%)	Human DNA sequence from clone RP4-569M23 on chromosome 20q12-13.1 Contains the PRKCBP1 gene for protein kinase C binding protein 1, a putative novel gene, ESTs, STSs and GSSs, complete sequence gi|13677197|emb|AL031666.6|HS569M23
SSH2-6 h11	774	Expect = 2.8 Identities = 21/21 (100%)	Chloranthus brachystachys maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product gi|33333435|gb|AF543733.1|
SSH2-6 h12	283	Expect = 0.98 Identities = 24/25 (96%)	Macaca mulatta Major Histocompatibility Complex BAC MMU222I18, complete sequence gi|46358471|gb|AC148689.1|
SSH2-7 a01	450	Expect = 6.4	Homo sapiens cell division cycle 25B (CDC25B) gene, complete cds

		Identities = 20/20 (100%)	gi|38679289|gb|AY494082.1|
		Expect = 6.4 Identities = 20/20 (100%)	Homo sapiens cdc25B phosphatase (CDC25B) gene, alternatively spliced, partial cds gi|2739198|gb|AF036233.1|AF036233
SSH2-7 a03	782	Expect = 5e-014 Identities = 143/176 (81%)	Oryza sativa (japonica cultivar-group) Os04g0687900 (Os04g0687900) mRNA, complete cds gi|115461469|ref|NM_001060870.1|
		Expect = 2.9 Identities = 21/21 (100%)	Zebrafish DNA sequence from clone CH211-276E8 in linkage group 20 Contains the 5' end of the gene for a novel protein similar to vertebrate ring finger protein 144 (RNF144), the gene for a novel radical SAM superfamily protein, the gene for a novel protein similar to mouse thymidylate kinase family LPS-inducible member (Tyki) and a CpG island, complete sequence gi|42516963|emb|BX571665.6|
SSH2-7 a05	36	Expect = 4.0 Identities = 18/18 (100%)	Streptomyces granaticolor pkg4, pkg3 genes and ORF1 gi|3618204|emb|AJ223176.1|SGAJ3176
SSH2-7 a06	42	Expect = 0.33 Identities = 20/20 (100%)	Mus musculus jumping translocation breakpoint, mRNA (cDNA clone MGC:5746 IMAGE:3582930), complete cds gi|14198163|gb|BC008139.1|
SSH2-7 a08	844	Expect = 3.1 Identities = 21/21 (100%)	Human DNA sequence from clone RP1-109F14 on chromosome 6p21.2-21.3 Contains the TEAD3 gene for TEA domain family member 3, the RPL10A gene for ribosomal protein RPL10a, the FANCE gene for Fanconi anemia, complementation group E, the PPARD gene for peroxisome proliferative activated receptor delta, the MKRNP2 pseudogene (a makorin ring finger protein pseudogene 2) and six CpG islands, complete sequence gi|3367610|emb|AL022721.1|HS109F14
SSH2-7 a09	366	Expect = 0.33 Identities = 22/22 (100%)	Human DNA sequence from clone RP1-253B10 on chromosome 6q14.3-16.1 Contains a ribosomal protein L29 (RPL29) pseudogene and a novel pseudogene, complete sequence gi|9650540|emb|AL353133.7|
SSH2-7 b05	565	Expect = 8.1 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-328N1 on chromosome 1 Contains the 3' end of a novel gene and the 5' end of the DNAH14 gene for dynein (axonemal) heavy polypeptide 14, complete sequence gi|14018273|emb|AL357912.10|
SSH2-7 b12	534	Expect = 1.9 Identities = 21/21 (100%)	TPA_exp: Mus musculus immunoglobulin heavy chain variable region locus, strain C57BL/6 gi|90704841|tpe|BN000872.1|
SSH2-7 c07	597	Expect = 2.2 Identities = 21/21 (100%)	Human DNA sequence from clone RP3-468O1 on chromosome 20 Contains the 3' end of the ITCH gene for itchy homolog E3 ubiquitin protein ligase (mouse), a ferredoxin 1 (FDX1) pseudogene, the 5' end of the DNCL2A gene for cytoplasmic dynein light polypeptide 2A, two novel genes and two CpG islands, complete sequence gi|8894632|emb|AL109923.29|HSDJ468O1
SSH2-7 c12	314	Expect = 7e-036 Identities = 140/160 (87%)	Oryza sativa (japonica cultivar-group) Os09g0464000 (Os09g0464000) mRNA, complete cds gi|115479630|ref|NM_001069944.1|
		Expect = 0.070 Identities = 26/27 (96%)	Arachis hypogaea clone Gsi115 alcohol dehydrodenase mRNA, partial cds gi|54306361|gb|AY725189.1|
		Expect = 0.070 Identities = 23/23 (100%)	Oryza sativa OsNIF2 mRNA for bZIP transcription factor, complete cds gi|17025919|dbj|AB051295.1|
SSH2-7 d01	306	Expect = 1.1 Identities = 21/21 (100%)	Danio rerio myb binding protein (P160) 1a-like mRNA, complete cds gi|49618954|gb|AY648744.1|
		Expect = 1.1 Identities = 21/21 (100%)	Chlamydomonas reinhardtii class II DNA photolyase (PHR2) gene,complete cds gi|5081540|gb|AF129458.1|AF129458
SSH2-7 d03	495	Expect = 1.8 Identities = 21/21 (100%)	Mouse DNA sequence from clone RP23-340E18 on chromosome 11 Contains the Mylc2a gene for myosin light chain, regulatory A, the Gck gene for glucokinase, a novel gene, the gene for prenylated SNARE protein (Ykt6), the Camk2d gene for calcium/calmodulin-dependent protein kinase II delta and two CpG islands, complete sequence gi|21211964|emb|AL645469.18|
		Expect = 7.0 Identities = 20/20 (100%)	Homo sapiens angiotensin I converting enzyme precursor (DCP1) gene, alternative splice products, complete cds gi|4732025|gb|AF118569.1|
SSH2-7 d07	487	Expect = 6.9 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-461H3 on chromosome 6 Contains the 5' end of the UST gene for uronyl-2-sulfotransferase, a laminin receptor 1 (ribosomal protein SA, 67 kDa) (LAMR1)pseudogene and a CpG island, complete sequence gi|22138729|emb|AL807246.11|
		Expect = 6.9 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-13J16 on chromosome 6 Contains the gene for winged helix/forkhead transcription factor (HFH1) and two CpG islands, complete sequence gi|17973944|emb|AL499606.18|
SSH2-7 d08	580	Expect = 8.3 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-455C19 on chromosome 1 Contains the 5' end of the BCAR3 gene for breast cancer anti-estrogen resistance 3 and a CpG island, complete sequence gi|22531392|emb|AL359820.12|
		Expect = 8.3 Identities = 20/20 (100%)	Pseudoeurycea sp. nov. GGB-1 clone e15.11 NADH dehydrogenase subunit 4 (ND4) gene, partial cds; mitochondrial gene for mitochondrial product gi|14719064|gb|AF379674.1|AF379674
SSH2-7 e05	575	Expect = 2.1 Identities = 21/21 (100%)	PREDICTED: Pan troglodytes golgi autoantigen, golgin subfamily b,macrogolgin (with transmembrane signal), 1, transcript variant 1 (GOLGB1), mRNA gi|114588769|ref|XM_001165627.1|
		Expect = 2.1 Identities = 21/21 (100%)	PREDICTED: Pan troglodytes leucine rich repeat (in FLII)interacting protein 2, transcript variant 4 (LRRFIP2), mRNA gi|114585996|ref|XM_001170711.1|
SSH2-7 e06	350	Expect = 4.9 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-175D17 on chromosome 9 Contains the 5' end of the NR6A1 gene for nuclear receptor (subfamily 6, group A) member 1, three novel genes, the RPL35 gene for ribosomal protein L35, the gene for a hypothetical protein similar to actin related protein 2/3 complex subunit 5 (MGC3038), the 3' end of the GOLGA1 gene for golgi autoantigen (golgin subfamily a, 1) and six CpG islands, complete sequence gi|12214304|emb|AL354928.9|
		Expect = 4.9 Identities = 20/20 (100%)	Human DNA sequence from clone RP3-519P24 on chromosome Xq22.1-23 Contains part of the IL1RAPL2 gene for interleukin 1 receptor accessory protein-like 2 and a prohibitin (PHB)pseudogene, complete sequence gi|5262435|emb|AL050401.5|HSJ519P24
SSH2-7 e07	269	Expect = 3.7 Identities = 23/24 (95%)	Mouse DNA sequence from clone RP23-462P2 on chromosome 13 Contains the 3' end of the Slc17a1 gene for solute carrier family 17 vesicular glutamate transporter) member 1, the gene for a novel solute carrier family 17 (Slc17a) member, a U1 small nuclear ribonucleoprotein 1C (Snrp1c) pseudogene, a H2B histone family (H2b) pseudogene, the gene for a novel H2A histone family (H2a) member, a novel gene, the gene for the ortholog of human secretagogin, EF-hand calcium binding protein SCGN and the 3' end of a novel gene, complete sequence gi|16073721|emb|AL606464.11|
SSH2-7 e10	813	Expect = 8e-004 Identities = 48/55 (87%)	Oryza sativa (japonica cultivar-group) Os08g0531100 (Os08g0531100)mRNA, complete cds gi|115477470|ref|NM_001068866.1|
		Expect = 3.0 Identities = 24/25 (96%)	Human DNA sequence from clone RP11-517D11 on chromosome X Contains the 3' end of a aldo-keto reductase family 1 member B1(aldose reductase) (AKR1B1) pseudogene, a apoptosis inhibitor 5 (API5) pseudogene and the AGTR2 gene for type 2 angiotensin II receptor, complete sequence gi|32451319|emb|AL732602.5|
SSH2-7 f04	635	Expect = 2.3 Identities = 21/21 (100%)	Human DNA sequence from clone RP5-1090M5 on chromosome 1p34.1-34.3 Contains the 5' end of the GRIK3 gene for glutamate receptor ionotropic kainate 3 and a CpG island, complete sequence gi|10443430|emb|AL355386.9|
		Expect = 9.1 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-23I7 on chromosome 1q32.1-32.3 Contains the 5' end of the LRRN5 gene for leucine rich repeat neuronal 5 and a novel gene, complete sequence gi|12830397|emb|AL161793.9|

		Expect = 9.1 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-54K22 on chromosome 9q34.11-34.2 Contains a NADH dehydrogenase 3, mitochondrial (MTND3) pseudogene, complete sequence gi|6967346|emb|AL133413.5|
SSH2-7 f05	485	Expect = 6.9 Identities = 23/24 (95%)	Human DNA sequence from clone RP4-705F19 on chromosome 1p32.2-34.2 Contains the 5' end of the SSBP3 gene for single stranded DNA binding protein 3, two novel genes and a CpG island, complete sequence gi|6522966|emb|AL035415.22|HS705F19
SSH2-7 f06	343	Expect = 0.077 Identities = 29/31 (93%)	Human DNA sequence from clone RP11-327P2 on chromosome 13 Contains 3 novel genes, a meningioma-expressed antigen 6/11 (MEA6)(MEA11) pseudogene and the 3' end of the ATP7B gene for ATPase, Cu++ transporting, beta polypeptide (Wilson disease), complete sequence gi|11121388|emb|AL162377.10|
		Expect = 4.8 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-33E24 on chromosome 6 Contains a ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3) pseudogene, two novel genes, a pseudogene similar to part of heat shock 90kD protein 1, beta (HSPCB) and a CpG island, complete sequence gi|12584709|emb|AL355615.12|
SSH2-7 f08	460	Expect = 1.7 Identities = 34/37 (91%)	Zea mays 22 kDa alpha zein gene cluster, complete sequence gi|13606087|gb|AF090447.2|
SSH2-7 g01	98	Expect = 4.5 Identities = 19/19 (100%)	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41 gi|6453350|emb|Y11107.3|HSA011107
SSH2-7 g05	475	Expect = 6.7 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-36D19 on chromosome 10 Contains part of a pseudogene similar to nuclear pore complex interacting proteins (NPIP), a eukaryotic translation initiation factor 5A (EIF5A) pseudogene, the MAT1A gene for methionine adenosyltransferase I alpha, a novel zinc finger protein pseudogene, three novel genes, the 5' end of the gene for a novel protein (MGC4248) and three CpG islands, complete sequence gi|16073659|emb|AL359195.24|
		Expect = 6.7 Identities = 23/24 (95%)	Canis familiaris DRD4 gene for dopamine receptor D4, intron 2,complete sequence, allele:DRD4-Q gi|47522547|dbj|AB126591.1|
SSH2-7 g06	269	Expect = 0.93 Identities = 21/21 (100%)	Ustilago maydis GABA aminotransferase-like protein (ugatA) gene,complete cds gi|881561|gb|U28655.1|
		Expect = 0.93 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-545A16 on chromosome 1q25.1-31.1 Contains the 3' end of a novel gene, a novel gene, the NPHS2 gene for idiopathic steroid-resistant nephrosis 2 protein (podocin), a centaurin gamma 2 (CENTG2) pseudogene and the 5' end of a novel gene, complete sequence gi|17384054|emb|AL160286.16|
SSH2-7 g08	159	Expect = 2.1 Identities = 26/28 (92%)	Human DNA sequence from clone RP11-139D23 on chromosome 1 Contains two novel genes (FLJ37964), the gene for C-terminal modulator protein (CTMP), a keratin 8 (KRT8) pseudogene, the S100A10 gene for S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)), the 5' end of a novel gene, a novel pseudogene and a CpG island, complete sequence gi|18375805|emb|AL450992.17|
		Expect = 2.1 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-463J7 on chromosome 1q31.1-31.3 Contains a coronin actin binding protein 1C (CORO1C) pseudogene, the 3' end of a novel gene and a glycine cleavage system protein H (aminomethyl carrier) (GCSH)pseudogene, complete sequence gi|17976561|emb|AL139135.15|
SSH2-7 g11	637	Expect = 0.0 Identities = 434/463 (93%)	Hordeum vulgare methyljasmonate-inducible lipoxygenase 2 mRNA, complete cds gi|1777960|gb|U56406.1|HVU56406
SSH2-7 h03	88	Expect = 3.9 Identities = 19/19 (100%)	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130056P17 product:sparc/osteonectin, cwcv and kazal-like domains proteoglycan 3, full insert sequence gi|74216628|dbj|AK164338.1|
SSH2-7 h08	283	Expect = 3.9 Identities = 23/24 (95%)	Human DNA sequence from clone RP1-28F12 on chromosome 20q11.22-12 Contains the 5' end of the PPP1R16B gene for protein phosphatase 1 regulatory (inhibitory) subunit 16B and a CpG island, complete sequence gi|11544571|emb|AL031657.5|HS28F12
SSH2-8 a04	141	Expect = 0.45 Identities = 24/25 (96%)	Homo sapiens protein kinase, DNA-activated, catalytic polypeptide (PRKDC) gene, complete cds gi|32140472|gb|AY316117.1|
SSH2-8 a07	153	Expect = 2.0 Identities = 23/24 (95%)	Human DNA sequence from clone RP11-147H23 on chromosome 13 Contains the 3' end of gene for a novel protein similar to phosphoinositide-binding protein and the 3' end of a novel gene for a novel protein similar to oxidoreductase, complete sequence gi|13751890|emb|AL136525.17|
		Expect = 2.0 Identities = 23/24 (95%)	Human DNA sequence from clone RP1-198G23 on chromosome Xq21.1-21.33 Contains a nonhistone chromosomal protein (HMG-14) pseudogene and a ubiquitin-conjugating enzyme E2 (UBE2V1)pseudogene, complete sequence gi|17065906|emb|AL022150.2|HS198G23
SSH2-8 a12	38	Expect = 1.1 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-710A11 on chromosome 10 Contains the 3' end for a novel gene (KIAA1274), the PRF1 gene forperforin 1 (pore forming protein), the 5' end of the ADAMTS14 gene for a disintegrin-like and metalloprotease(reprolysin type) with thrombospondin type 1 motif 14, and one CpG island, complete sequence gi|21738358|emb|AL355344.20|
		Expect = 4.2 Identities = 18/18 (100%)	Neisseria gonorrhoeae putative ATP-binding protein (abcZ) gene,abcZ-7 allele, partial cds gi|47132397|gb|AY601815.1|
		Expect = 4.2 Identities = 18/18 (100%)	Neisseria meningitidis strain 2601400 putative ABC transporter (abcZ) gene, partial cds gi|22858258|gb|AY120029.1|
SSH2-8 b02	59	Expect = 2.3 Identities = 19/19 (100%)	Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11 gi|4003380|dbj|AB020860.1|
SSH2-8 b04	420	Expect = 5.9 Identities = 23/24 (95%)	Human DNA sequence from clone RP11-232D9 on chromosome X Contains two pseudogenes similar to part of solute carrier family 6(neurotransmitter transporter) member 14 (SLC6A14) and a novel gene, complete sequence gi|28193290|emb|BX119904.4|
SSH2-8 b05	366	Expect = 1.3 Identities = 21/21 (100%)	Dictyostelium discoideum AX4 CHD gene family protein containing chromodomain, helicase domain, and DNA-binding domain(DDB_0220644) mRNA, complete cds gi|66813907|ref|XM_636041.1|
SSH2-8 b07	175	Expect = 9.1 Identities = 19/19 (100%)	Human DNA sequence from clone RP5-1042I8 on chromosome 1p11-13.2 Contains the REG4 gene for regenerating islet-derived family member 4, a novel pseudogene, a profilin 1 (PFN1) pseudogene, the ADAM30 gene for a disintegrin and metalloproteinase domain 30 and the 3' end of the NOTCH2 gene for Notch homolog 2 (Drosophila), complete sequence gi|13443418|emb|AL359752.11|
SSH2-8 c02	279	Expect = 3.8 Identities = 20/20 (100%)	Nasua nasua beta-fibrinogen gene, intron 7 gi|63014864|gb|AY882047.1|
SSH2-8 c04	478	Expect = 1.7 Identities = 24/25 (96%)	Lycopersicon esculentum mutant FLORICAULA/LEAFY-like protein(FALSIFLORA) mRNA, FALSIFLORA-fa allele, complete cds gi|7658234|gb|AF197935.1|AF197935
SSH2-8 c05	64	Expect = 2.6 Identities = 19/19 (100%)	Arabidopsis thaliana nucleoside-triphosphatase/ nucleotide binding(AT4G18820) mRNA, complete cds gi|30684539|ref|NM_117998.2|
		Expect = 2.6 Identities = 19/19 (100%)	Mouse DNA sequence from clone RP23-9N7 on chromosome 11 Contains the 5' end of a novel gene, a novel gene, the Clk4 gene for CDC like kinase 4, the 5' end of the Col23a1 gene for procollagen (type XXIII, alpha 1) and two CpG islands, complete sequence gi|20145332|emb|AL645907.9|
SSH2-8 d03	186	Expect = 9.7 Identities = 19/19 (100%)	Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530039B03 product:matrix metalloproteinase 17, full insert sequence gi|26098355|dbj|AK079221.1|
		Expect = 9.7 Identities = 19/19 (100%)	Human DNA sequence from clone RP1-163G9 on chromosome 1p36.2-36.3 Contains two novel genes, the 5' end of the PRDM16 gene for PR domain containing 16 and two CpG islands, complete sequence gi|6635876|emb|AL008733.10|HS163G9

SSH2-8 d07	158	Expect = 8.1 Identities = 22/23 (95%)	Plasmodium chabaudi chabaudi CIR protein (PC106789.00.0) partial mRNA gi|70941848|ref|XM_736069.1|
SSH2-8 d08	309	Expect = 0.069 Identities = 23/23 (100%)	Thermococcus kodakaraensis Tk-Dac gene for diacetylchitobiose deacetylase, complete cds gi|50284477|dbj|AB125969.1|
		Expect = 0.27 Identities = 22/22 (100%)	Human DNA sequence from clone RP11-208C17 on chromosome 10 Contains the CYP2C9 gene for cytochrome P450 family 2 subfamily C polypeptide 9, a mitochondrial NADH dehydrogenase 4 (MTND4) pseudogene, a pseudogene similar to part of cytochrome P450 family 2 subfamily C, a novel pseudogene and the CYP2C8 gene for cytochrome P450 family 2 subfamily C polypeptide 8, complete sequence gi|16751347|emb|AL359672.19|
SSH2-8 d09	315	Expect = 1.1 Identities = 21/21 (100%)	PREDICTED: Rattus norvegicus bromodomain adjacent to zinc finger domain, 2A (predicted) (Baz2a_predicted), mRNA gi|109481420|ref|XM_001070233.1|
		20	PREDICTED: Bos taurus similar to translocation protein 1, transcript variant 3 (LOC538938), mRNA
SSH2-8 d11	67	Expect = 0.18 Identities = 21/21 (100%)	Triticum aestivum endotransglucosylase/hydrolase XTH3 mRNA, complete cds gi|51039059|gb|AY589587.1|
		Expect = 2.8 Identities = 19/19 (100%)	Arabidopsis thaliana DNA binding / protein binding / zinc ion binding (AT1G77250) mRNA, complete cds gi|42563279|ref|NM_106374.2|
		Expect = 2.8 Identities = 19/19 (100%)	Danio rerio myosin VIb (myo6b) mRNA, complete cds gi|51011626|gb|AY691328.1|
SSH2-8 e01	344	Expect = 1.2 Identities = 21/21 (100%)	Human DNA sequence from clone XXbac-294E21 on chromosome 6 contains the gene for a novel protein similar to lysophospholipase II(LYPLA2), the KNSL2 gene for kinesin-like 2, the PHF1 gene for PHD finger protein 1, the gene for divalent cation tolerant protein CUTA, the SYNGAP1 gene for synaptic Ras GTPase activating protein 1 homolog and five CpG islands, complete sequence gi|21212026|emb|AL662799.16|
SSH2-8 e03	190	Expect = 9.9 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-426A6 on chromosome 9 Contains the OBP2A gene for odorant-binding protein 2A, the LCN1 gene for lipocalin 1, the MRPS2 gene for mitochondrial ribosomal protein S2, gene MGC29761, a novel gene, gene KIAA0649, a novel gene, a novel gene, a suppressor of cytokine signaling 5 (SOCS5) pseudogene and two CpG islands, complete sequence gi|14272254|emb|AL161452.19|
SSH2-8 f02	69	Expect = 2.9 Identities = 19/19 (100%)	Pseudomonas aeruginosa fliS, orf4, and regulatory protein (orf5) genes, complete cds, regulatory protein (orf6) and flagellum cap protein (fliD) genes, partial cds gi|1311636|gb|L43064.1|PSEFLID
SSH2-8 f07	123	Expect = 0.38 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-86L19 on chromosome 9 Contains the 3' end of the SMC2L1 gene for SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (CAPE, CAP-E, hCAP-E), a novel pseudogene and a CpG island, complete sequence gi|14625559|emb|AL354938.12|
		Expect = 6.0 Identities = 19/19 (100%)	Sus scrofa transforming growth factor beta type 1 receptor (TGFBR1) gene, complete cds gi|108755893|gb|DQ519377.1|
SSH2-8 f08	69	Expect = 2.9 Identities = 19/19 (100%)	Hemicentrotus pulcherrimus mRNA for ryanodine receptor, complete cds gi|18656154|dbj|AB051576.1|
SSH2-8 f09	175	Expect = 2.3 Identities = 20/20 (100%)	Human DNA sequence from clone RP3-451B15 on chromosome 6p24 Contains the 3' end of the HIVEP1 gene for human immunodeficiency virus type I enhancer-binding protein 1, the EDN1 gene for endothelin 1 (ET1) and a SMT3 suppressor of mif two 3 homolog 1 (yeast) (SMT3H1) pseudogene, complete sequence gi|2791272|emb|Z98050.1|HS451B15
		Expect = 9.1 Identities = 22/23 (95%)	PREDICTED: Homo sapiens similar to eukaryotic translation elongation factor 1 alpha 2 (LOC647167), mRNA gi|113411610|ref|XR_017690.1|
SSH2-8 g03	50	Expect = 7.0 Identities = 18/18 (100%)	X.laevis mRNA for myelin proteolipid protein (PLP) gi|64985|emb|Z19522.1|XLPLPA
SSH2-8 g05	168	Expect = 8.6 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-34F20 on chromosome 13 Contains the 3' end of the RFP2 gene for ret finger protein 2, the DLEU2 gene for deleted in lymphocytic leukemia 2 (LEU2 BCMSUN), the 5' end of the DLEU1 gene for deleted in lymphocytic leukemia 1 (BCMS LEU1), a ribosomal protein L18 (RPL18) pseudogene, a novel gene and four CpG islands, complete sequence gi|11120982|emb|AL137060.13|
SSH2-8 g06	146	Expect = 7.4 Identities = 19/19 (100%)	Oryza sativa (japonica cultivar-group) chromosome 5 clone OJ1675_H07,complete sequence gi|49658587|gb|AC105320.2|
		Expect = 7.4 Identities = 19/19 (100%)	Human DNA sequence from clone RP4-562D20 on chromosome 11 Contains the FSHB gene for follicle stimulating hormone beta polypeptide, ESTs, STSs and GSSs, complete sequence gi|14272299|emb|AL358944.12|
SSH2-8 g07	60	Expect = 9.3 Identities = 18/18 (100%)	PREDICTED: Strongylocentrotus purpuratus similar to PDZ domain containing RING finger protein 3 (Semaphorin cytoplasmic domain-associated protein 3) (SEMACAP3 protein)(LOC591153), partial mRNA gi|72076330|ref|XM_790731.1|
		Expect = 9.3 Identities = 21/22 (95%)	Human DNA sequence from clone RP11-525O21 on chromosome 6 Contains the 3' end of the F13A1 gene for coagulation factor XIII, A1 polypeptide, complete sequence gi|11121004|emb|AL157775.15|
		Expect = 9.3 Identities = 18/18 (100%)	Human DNA sequence from clone RP5-995J12 on chromosome 20q12 Contains the 5' end of the GDAP1L1 gene for ganglioside-induced differentiation-associated protein 1-like 1, the 3' end of a novel gene and a CpG island, complete sequence gi|11323328|emb|AL035462.21|HS995J12
SSH2-8 g08	145	Expect = 0.47 Identities = 24/25 (96%)	Dictyostelium discoideum ABC transporter ABCA.9 (abca9) gene, partial cds gi|19110831|gb|AF465311.1|
		Expect = 1.8 Identities = 20/20 (100%)	Human DNA sequence from clone RP1-54B20 on chromosome Xp11.1-11.3 Contains the 5' end of the SSX6 gene for synovial sarcoma X breakpoint 6, two novel genes similar to a C2H2 type zinc finger protein, a novel gene, a novel gene similar to lysozyme C (1,4-beta-N-acetylmuramidase), the ZNF81 gene for zinc finger protein 81 (HFZ20) and three CpG islands, complete sequence gi|3980429|emb|Z98304.1|HS54B20
		Expect = 7.3 Identities = 22/23 (95%)	Homo sapiens protein tyrosine kinase non catalytic form (NTRK2) mRNA, complete cds gi|21886727|gb|AF508964.1|
SSH2-8 g09	157	Expect = 0.13 Identities = 22/22 (100%)	Zea mays cytokinin oxidase (ckx1) gene, complete cds gi|3341977|gb|AF044603.1|AF044603
SSH2-8 g12	75	Expect = 3.2 Identities = 19/19 (100%)	Human DNA sequence from clone RP3-425P12 on chromosome 6p21.33-22.3 Contains 3 novel genes, a nucleoporin 50kD (NUP50) (NPAP60 NPAP60L) pseudogene and the CMAH gene for cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) (CSAH), complete gi|12597029|emb|AL133268.15|
SSH2-8 h01	316	Expect = 4.4 Identities = 20/20 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 8 gi|58531195|dbj|AP008214.1|
		Expect = 4.4 Identities = 20/20 (100%)	Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 1/11 gi|4003378|dbj|AB020858.1|
SSH2-8 h02	130	Expect = 0.41 Identities = 21/21 (100%)	Human DNA sequence from clone RP3-473J16 on chromosome 6q25.3-26 Contains 3' end of the MAP3K4 gene for mitogen-activated protein kinase kinase kinase 4 (MTK1, MEKK4, MAPKKK4, KIAA0213, homolog of yeast SSK2/SSK22 MAP kinase kinase kinase), the gene for lysophosphatidic acid acyltransferase-delta (LPAAT-delta) (FLJ23628, contains mRNA DKFZp434M038) and the gene for hypothetical protein FLJ23112 (DKFZP566E2324), complete sequence gi|8894643|emb|AL109942.13|HSJ473J16
		Expect = 6.4	Salmo salar taurine transporter mRNA, complete cds gi|22086692|gb|AF428143.1|

		Identities = 22/23 (95%)	
		Expect = 6.4 Identities = 22/23 (95%)	Rattus norvegicus chromosome 20, major histocompatibility complex,assembled from 40 BACs, strain Brown Norway (BN/ssNHsd),RT1n haplotype; segment 5/11 gi|46237620|emb|BX883046.1|
SSH2-9 a03	185	Expect = 9.6 Identities = 19/19 (100%)	Human DNA sequence from clone RP3-503G16 on chromosome 6p23 Contains the 5' end of the RANBP9 gene for RAN binding protein 9(RanBPM) and three CpG islands, complete sequence gi|3288048|emb|Z93020.1|HS503G16
		Expect = 9.6 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-271B5 on chromosome 13 Contains the FGF9 gene for fibroblast growth factor 9 (glia-activating factor (GAF, HBFG-9)), a ribosomal protein S7 (40S ribosomal protein S7) (RPS7) pseudogene and two CpG islands, complete sequence gi|8247510|emb|AL139378.15|
SSH2-9 a09	625	Expect = 0.57 Identities = 28/30 (93%)	Human DNA sequence from clone RP11-300B2 on chromosome 10 Contains the 5' end of the MGMT gene for O-6-methylguanine-DNA methyltransferase, complete sequence gi|21694356|emb|AL355531.16|
		Expect = 2.3 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-543N17 on chromosome 10 Contains the 3' end of a novel gene (FLJ20445) and a MAP/microtubule affinity-regulating kinase 2 (MARK2) pseudogene, complete sequence gi|16972804|emb|AL161652.25|
SSH2-9 b06	657	Expect = 2.4 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-181K3 on chromosome 1 Contains the 3' end of the LAMC1 for laminin, gamma 1 (formerly LAMB2), the LAMC2 gene for laminin, gamma 2 and the 3' end of the NMNAT2 gene for nicotinamide nucleotide adenylyltransferase 2, complete sequence gi|16973821|emb|AL354953.16|
SSH2-9 b08	508	Expect = 1.8 Identities = 21/21 (100%)	PREDICTED: Canis familiaris similar to KH domain containing, RNA binding, signal transduction associated 3, transcript variant 6 (LOC475106), mRNA gi|73974651|ref|XM_850841.1|
		Expect = 7.2 Identities = 23/24 (95%)	Homo sapiens interleukin 9 receptor (IL9Rps) pseudogene, complete sequence; and DNA-directed RNA polymerases III 12.5 kDa polypeptide (POLR3K), U11/U12 snRNP 25 kDa protein(C16orf33), RHBDG1 (C16orf8), DNA-3-methyladenine glycosylase (MPG), -14 gene protein (C16orf35), hemoglobin zeta subunit (HBZ), HBD (HBD), alpha globin (HBA2), alpha globin (HBA1), theta globin (HBQ1), and putative RNA-binding protein Luc7-like 1 (LUC7L) genes, complete cds gi|90653001|gb|DQ431198.1|
SSH2-9 b09	175	Expect = 9.1 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-29E12 on chromosome 1 Contains part of the ELTD1 gene for EGF latrophilin and seven transmembrane domain containing 1, complete sequence gi|16973151|emb|AL596269.6|
		Expect = 9.1 Identities = 22/23 (95%)	Human DNA sequence from clone RP4-609B14 on chromosome 1q42.11-42.3 Contains the gene for a novel protein (DKFZp547B1713), the 5' end of the GNPAT gene for glyceronephosphate O-acyltransferase and a CpG island, complete sequence gi|21211626|emb|AL137801.11|
SSH2-9 b10	468	Expect = 1.7 Identities = 21/21 (100%)	PREDICTED: Strongylocentrotus purpuratus similar to BRAP2 (LOC584009), mRNA gi|115617603|ref|XR_025943.1|
		Expect = 1.7 Identities = 21/21 (100%)	Human DNA sequence from clone RP5-1018D12 on chromosome 20q11.1-11.22 Contains part of a CDK5 regulatory subunit associated protein 3 (CDK5RAP3) pseudogene, the RPL31P3 gene for ribosomal protein L31 pseudogene 3, a novel pseudogene,the DEFB118 gene for defensin beta 118 and the 3' end of the the DEFB119 gene for defensin beta 119, complete sequence gi|13277283|emb|AL031650.22|HS1018D12
SSH2-9 c05	1015	Expect = 3.7 Identities = 24/25 (96%)	Human DNA sequence from clone RP11-114G1 on chromosome 13q31.3-33.1 contains a Sp3 transcription factor (SP3) pseudogene and a novel gene, complete sequence gi|9800736|emb|AL163533.14|
SSH2-9 c09	353	Expect = 4.9 Identities = 23/24 (95%)	Danio rerio homeodomain leucine zipper gene, mRNA (cDNA clone MGC:136423 IMAGE:7405668), complete cds gi|108742138|gb|BC117599.1|
SSH2-9 c10	365	Expect = 1.3 Identities = 21/21 (100%)	Human DNA sequence from clone RP3-322L4 on chromosome 6 Contains the SOX4 gene for SRY (sex determining region Y)-box 4, a novel pseudogene and CpG islands, complete sequence gi|8649149|emb|AL136179.15|
SSH2-9 d01	317	Expect = 4.4 Identities = 20/20 (100%)	Human DNA sequence from clone RP3-353H6 on chromosome Xq25-26.2 Contains the 3' end of the SMARCA1 gene for SWI/SNF related, matrix associated, actin dependent regulator of chromatin (subfamily a, member 1) and aribosomal protein S26 (RPS26) pseudogene, complete sequence gi|3550044|emb|AL022577.1|HS353H6
SSH2-9 d02	53	Expect = 1.9 Identities = 22/23 (95%)	PREDICTED: Strongylocentrotus purpuratus similar to solute carrier family 35, member F4 (LOC761063), mRNA gi|115932121|ref|XM_001190628.1|
		Expect = 7.7 Identities = 18/18 (100%)	Arabidopsis thaliana pyruvate kinase (AT3G25960) mRNA, complete cds gi|18404742|ref|NM_113500.1|
SSH2-9 d06	127	Expect = 6.2 Identities = 19/19 (100%)	PREDICTED: Macaca mulatta similar to UV excision repair protein RAD23 homolog A (mHR23A) (LOC720675), mRNA gi|109126537|ref|XM_001116344.1|
SSH2-9 d09	55	Expect = 2.1 Identities = 19/19 (100%)	Zea mays small basic membrane integral protein ZmSIP1-1 mRNA,complete cds gi|13447812|gb|AF326497.1|AF326497
SSH2-9 f10	128	Expect = 0.40 Identities = 21/21 (100%)	Homo sapiens zinc finger protein 749 (ZNF749), mRNA gi|66472887|ref|NM_001023561.1|
		Expect = 1.6 Identities = 20/20 (100%)	PREDICTED: Canis familiaris similar to hedgehog-interacting protein, transcript variant 1 (LOC475452), mRNA gi|73977793|ref|XM_532677.2|
SSH2-9 g01	395	Expect = 5.6 Identities = 20/20 (100%)	Zea mays cultivar (LG11) ROA mRNA for replication origin activator protein, MCM3 homolog gi|114049618|emb|Z29368.2|
		Expect = 5.6 Identities = 20/20 (100%)	PREDICTED: Gallus gallus similar to fasting-induced adipose factor(LOC420064), mRNA gi|50760925|ref|XM_418184.1|
SSH2-9 g02	563	Expect = 8.1 Identities = 20/20 (100%)	TPA_exp: Homo sapiens transcriptional regulator (NIPBL) mRNA,complete cds gi|47458030|tpg|BK005151.1|
		Expect = 8.1 Identities = 20/20 (100%)	PREDICTED: Macaca mulatta similar to delangin isoform A, transcript variant 2 (LOC701209), mRNA gi|109077002|ref|XM_001096346.1|
SSH2-9 g07	666	Expect = 9.6 Identities = 20/20 (100%)	Bos taurus large conductance calcium-activated potassium channel alpha subunit mRNA, partial cds gi|34333801|gb|AF026000.2|
SSH2-9 g09	344	Expect = 1.2 Identities = 21/21 (100%)	Zebrafish DNA sequence from clone CH211-156N3 in linkage group 5 Contains a gene for a novel protein with ATPase domain,complete sequence gi|22204559|emb|AL772163.7|
SSH2-9 h02	690	Expect = 0.64 Identities = 22/22 (100%)	Human DNA sequence from clone RP11-365K22 on chromosome 13 Contains a novel gene similar to ribosomal protein L13a (RPL13A),complete sequence gi|13277089|emb|AL356120.10|
SSH2-10 a01	518	Expect = 7.4 Identities = 20/20 (100%)	Mus musculus slc43a2 mRNA for L-type amino acid transporter 4,complete cds gi|61287128|dbj|AB120363.1|
		Expect = 7.4 Identities = 20/20 (100%)	Nostoc punctiforme lipid-A-disaccharide synthase, cytosine-specific DNA methyltransferase (dmtC), and putative oxidoreductase genes, complete cds gi|14594712|gb|AY037295.1|
SSH2-10 a02	513	Expect = 1.8 Identities = 21/21 (100%)	Human DNA sequence from clone RP3-429K2 on chromosome 1p35.3-36.1 Contains the 5' end of the PTAFR gene for platelet-activating factor receptor and the 3' end of the DNAJC8 gene for DnaJ (Hsp40) homolog, subfamily C, member 8, complete sequence gi|20152630|emb|AL353354.36|
		Expect = 7.3 Identities = 20/20 (100%)	Mus musculus signal transducer and activator of transcription 1, mRNA (cDNA clone MGC:6411 IMAGE:3587831), complete cds gi|13435935|gb|BC004808.1|
		Expect = 7.3 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-280I16 on chromosome 9 Contains the 5' end of the SLC1A1 gene for solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter

			system Xag) member 1 (EAAC1 EAAT3), the 3' end of a novel gene (FLJ10058) and a CpG island, complete sequence gi|12584692|emb|AL162587.20|
SSH2-10 a07	498	Expect = 0.45 Identities = 22/22 (100%)	PREDICTED: Rattus norvegicus similar to spindlin (LOC682571), mRNA gi|109466443|ref|XM_001062077.1|
SSH2-10 a09	474	Expect = 6.7 Identities = 20/20 (100%)	Dictyostelium discoideum AX4 leucine-rich repeat-containing protein(LRR) (DDB_0232387) mRNA, complete cds gi|66823968|ref|XM_640247.1|
SSH2-10 b01	171	Expect = 2.2 Identities = 20/20 (100%)	Human DNA sequence from clone RP13-469O16 on chromosome 6 Contains a nucleophosmin (nucleolar phosphoprotein B23, numatrin) (NPM1)(B23, NPM) pseudogene and a CpG island, complete sequence gi|14018308|emb|AL589796.7|
		Expect = 2.2 Identities = 20/20 (100%)	Human DNA sequence from clone RP13-469O16 on chromosome 6 Contains a nucleophosmin (nucleolar phosphoprotein B23, numatrin)(NPM1)(B23, NPM) pseudogene and a CpG island, complete sequence gi|14018308|emb|AL589796.7|
SSH2-10 c11	409	Expect = 1.5 Identities = 24/25 (96%)	PREDICTED: Pan troglodytes similar to factor activating exoenzyme S(LOC459589), mRNA gi|114580763|ref|XR_022945.1|
		Expect = 5.8 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-540N4 on chromosome X Contains the 3' end of the PRPS1 gene for phosphoribosyl pyrophosphate synthetase 1 (PRSI), complete sequence gi|21738687|emb|AL772400.3|
SSH2-10 c12	180	Expect = 2.4 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-428O18 on chromosome 13 Contains the RPL21 gene for ribosomal protein L21 (60S ribosomal protein L21, L21), a novel gene for a Ras family protein similar to 1110065D03RIK, a novel gene, the 5' end of novel gene and two CpG islands, complete sequence gi|11022597|emb|AL159977.10|
		Expect = 9.4 Identities = 19/19 (100%)	Entamoeba histolytica HM-1:IMSS DNA-directed RNA polymerase III largest subunit (73.t00023) partial mRNA gi|67476289|ref|XM_648656.1|
SSH2-10 d03	131	Expect = 1.6 Identities = 23/24 (95%)	Human DNA sequence from clone RP1-293L6 on chromosome 22 Contains the first exon of the CACNG2 gene for voltage-dependent calcium channel gamma subunit 2, ESTs, STSs, GSSs and a putative CpG island, complete sequence gi|6580415|emb|AL049749.2|HS293L6
		Expect = 6.5 Identities = 19/19 (100%)	PREDICTED: Pan troglodytes regulator of chromosome condensation 1, transcript variant 4 (RCC1), mRNA gi|114555100|ref|XM_001152723.1|
SSH2-10 d10	450	Expect = 1.6 Identities = 21/21 (100%)	Artemia franciscana artemin (Artn) mRNA, complete cds gi|18071493|gb|AY062896.1|
		Expect = 6.4 Identities = 20/20 (100%)	Toxoplasma gondii Rop2 protein (Rop2) mRNA, partial cds gi|115299637|gb|DQ923323.1|
SSH2-10 e03	908	Expect = 3.3 Identities = 21/21 (100%)	Plasmodium falciparum isolate WR87 sequence Var2csa_DBL1x_DBL2x_seq1 erythrocyte membrane protein 1 (var2csa) gene, partial cds gi|90193490|gb|DQ408087.1|
SSH2-10 e11	463	Expect = 0.11 Identities = 23/23 (100%)	Human DNA sequence from clone RP11-195O1 on chromosome 10 Contains the 3' end of a novel gene novel protein (FLJ32762) (FLJ25419), a nuclear DNA-binding protein (C1D) pseudogene, the 5' end of a novel gene (FLJ13031) and two CpG islands, complete sequence gi|10715924|emb|AL354750.12|
		Expect = 0.11 Identities = 23/23 (100%)	Human DNA sequence from clone RP11-188P8 on chromosome 10 Contains the 3' end of a novel gene, a NADH dehydrogenase 2 (MTND2) pseudogene, the 5' end of the gene for tumor endothelial marker 7-related precursor (TEM7R) (FLJ14623) and a CpG island, complete sequence gi|15209407|emb|AL353147.10|
		Expect = 1.7 Identities = 24/25 (96%)	Ancistrocladus abbreviatus trnK gene, partial sequence; and maturase K (matK) gene, complete cds; chloroplast genes for chloroplast products gi|14193652|gb|AF315939.1|AF315939
SSH2-10 f10	811	Expect = 0.19 Identities = 23/23 (100%)	Sus scrofa cyclin G1 (CCNG1) mRNA, complete cds gi|62526590|gb|AY974246.1|
		Expect = 3.0 Identities = 24/25 (96%)	Mus musculus 14 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:I530028O16 product:ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase) 1, full insert sequence gi|74198525|dbj|AK167699.1|
SSH2-10 g02	398	Expect = 0.023 Identities = 24/24 (100%)	Trypanosoma cruzi strain CL Brener mucin-associated surface protein gi|71421213|ref|XM_806644.1|
		Expect = 0.091 Identities = 23/23 (100%)	Human DNA sequence from clone RP11-281B1 on chromosome Xp21.3-22.12 Contains part of a novel gene, an arginine/serine-rich splicing factor 2 (SFRS2) pseudogene and a CpG island, complete sequence gi|15858979|emb|AL592043.7|
SSH2-10 g09	639	Expect = 1e-035 Identities = 212/256 (82%)	Oryza sativa (japonica cultivar-group) Os03g0652100 (Os03g0652100) mRNA, complete cds gi|115454388|ref|NM_001057330.1|
		Expect = 2.3 Identities = 21/21 (100%)	Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) gene,alternatively spliced, complete cds gi|32261244|gb|AY129950.1|
		Expect = 9.2 Identities = 20/20 (100%)	PREDICTED: Canis familiaris similar to zinc finger protein (C2H2 type) 277 (LOC475289), mRNA gi|73976613|ref|XM_532521.2|
		Expect = 9.2 Identities = 20/20 (100%)	Nierembergia caerulea mRNA for Na H-antiportor, complete cds gi|14211575|dbj|AB051818.1|
SSH2-10 g11	867	Expect = 4e-012 Identities = 47/49 (95%)	Oryza sativa (japonica cultivar-group) Os04g0660500 (Os04g0660500) mRNA, complete cds gi|115461087|ref|NM_001060679.1|
		Expect = 0.81 Identities = 22/22 (100%)	Ciona intestinalis mRNA for transcription factor protein, complete cds, clone: cidg847h10 gi|70570319|dbj|AB210573.1|
SSH2-10 h06	272	Expect = 0.94 Identities = 21/21 (100%)	Rattus norvegicus tachykinin receptor 1 (Tacr1), mRNA gi|6981627|ref|NM_012667.1|
		Expect = 0.94 Identities = 21/21 (100%)	Rat substance P receptor (SPR) gene, exon 1 gi|207053|gb|M64232.1|RATSPR01
		Expect = 3.7 Identities = 20/20 (100%)	Mus musculus ATP-binding cassette 1, sub-family A, member 1 (Abca1) gene, complete cds gi|11611824|gb|AF287263.1|AF287263
SSH2-10 h12	54	Expect = 7.9 Identities = 18/18 (100%)	Psilotum nudum RNA polymerase III large subunit (rpc1) mRNA, partial cds gi|45935352|gb|AY490564.1|
SSH2-11 a05	639	Expect = 2.3 Identities = 24/25 (96%)	Mesocricetus auratus beta-myosin heavy chain gene, complete cds gi|402371|gb|L12104.1|HAMBMHC
SSH2-11 a08	452	Expect = 1.6 Identities = 30/33 (90%)	Arabidopsis thaliana long chain acyl-CoA synthetase 5 (LACS5) mRNA,complete cds gi|20805870|gb|AF503755.1|
		Expect = 1.6 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-563J2 on chromosome 10 Contains the 3' end of the PRKCQ gene for protein kinase C, theta and a CpG island, complete sequence gi|9581557|emb|AL137145.13|
		Expect = 6.4 Identities = 20/20 (100%)	Arabidopsis thaliana SIGE; DNA binding / DNA-directed RNA polymerase/ sigma factor/ transcription factor (SIGE) mRNA, complete cds gi|30689284|ref|NM_122317.2|
SSH2-11 a10	459	Expect = 6.5 Identities = 23/24 (95%)	PREDICTED: Apis mellifera similar to Guanine nucleotide Exchange factor DBS (DBLs big sister) (MCF2 transforming sequence-like protein) (LOC409217), mRNA gi|110759505|ref|XM_392741.3|
SSH2-11 b04	473	Expect = 0.43 Identities = 25/26 (96%)	Arabidopsis thaliana hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPase, rotational mechanism (AT3G28715) mRNA, complete cds gi|18405896|ref|NM_113792.1|
		Expect = 1.7 Identities = 21/21 (100%)	PREDICTED: Pan troglodytes similar to RNA binding motif protein, Y-linked, family 1, member F (LOC736159), mRNA gi|114691690|ref|XR_019801.1|
SSH2-11 b05	495	Expect = 1.8 Identities = 24/25 (96%)	Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cds gi|1817732|gb|U63834.1|HSU63834

		Expect = 7.0 Identities = 20/20 (100%)	Arabidopsis thaliana ATP binding / ATP-dependent helicase/helicase/ nucleic acid binding (AT1G33390) mRNA, complete cds gi|30692859|ref|NM_103064.2|
SSH2-11 b07	545	Expect = 0.13 Identities = 23/23 (100%)	Human DNA sequence from clone RP11-4E23 on chromosome 9 Contains the 5' end of the MLLT3 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 (AF9), a novel gene, the 5' end of a novel gene (FLJ2035, KIAA1797) and two CpG islands, complete sequence gi|15546079|emb|AL354879.12|
SSH2-11 b08	348	Expect = 4.9 Identities = 20/20 (100%)	Homo sapiens cDNA FLJ46866 fis, clone UTERU3011837, moderately similar to NG-CAM related cell adhesion molecule precursor gi|34536207|dbj|AK128699.1|
		Expect = 4.9 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-494K3 on chromosome 1 Contains the 3' end of the gene for neurofascin (NFASC) and a ribosomal protein L13a (RPL13A) pseudogene, complete sequence gi|16972965|emb|AL391822.12|
SSH2-11 b09	420	Expect = 5.9 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-293A10 on chromosome 1 Contains the 3' end of a novel gene (FLJ10330), a novel gene(FLJ35838), the 5' end of the STXBP3 gene for syntaxin binding protein 3, a novel gene and a chromosome 20 open reading frame 147 (C20orf147) pseudogene, complete sequence gi|14530314|emb|AL591719.8|
		Expect = 5.9 Identities = 26/28 (92%)	Fontinalis antipyretica chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gi|11230630|emb|AJ275183.1|FAN275183
SSH2-11 c04	470	Expect = 6.7 Identities = 20/20 (100%)	Mus musculus strain C57BL/6J cytokine gene cluster, partial sequence gi|27960627|gb|AF463736.1|
		Expect = 6.7 Identities = 20/20 (100%)	Klebsiella pneumoniae partial YC04 gene for putative capsule polysaccharide export protein precursor, contig region pSL001 gi|9909732|emb|AJ293853.1|KPN293853
SSH2-11 c05	438	Expect = 6.2 Identities = 20/20 (100%)	Lycopersicon esculentum cultivar Ailsa Craig leucine-rich repeat family protein, putative polyprotein, auxin repressed/dormancy associated protein, putative zinc finger protein, putative protease/hydrolase, mitochondrial amino acid carrier, squamosa promoter binding-like protein, putative retroelement pol polyprotein, and Dof zinc finger protein genes, complete cds gi|111183160|gb|DQ672601.1|
		Expect = 6.2 Identities = 20/20 (100%)	Sphoeroides nephelus immune-type receptor 1-5, 7 and 9-26 genes,complete cds and immune-type receptor 6 and 8, pseudogenes, complete sequence gi|6840825|gb|AF094698.1|AF094698
		Expect = 3.9 Identities = 19/19 (100%)	Streptomyces chartreusis HKI-249 chartreusin biosynthesis gene cluster A gi|68146464|emb|AJ786382.1|
SSH2-11 c06	88	Expect = 3.9 Identities = 22/23 (95%)	Human DNA sequence from clone RP1-150O5 on chromosome 1p36.13-36.22 Contains the 5' end of the gene for up-regulated in liver cancer 1 (UPLC1) (FLJ34972), the E2F2 gene for E2F transcription factor 2, the ID3 gene for inhibitor of DNA binding 3 dominant negative helix-loop-helix protein, a novel gene and two CpG islands, complete sequence gi|3219576|emb|AL021154.1|HS150O5
		Expect = 2.5 Identities = 26/28 (92%)	Human DNA sequence from clone RP11-263F15 on chromosome 6 Contains a keratin 19 (KRT19) pseudogene and a CpG island, complete sequence gi|10862758|emb|AL354933.8|
SSH2-11 c07	190	Expect = 9.9 Identities = 19/19 (100%)	Human DNA sequence from clone RP5-1077K16 on chromosome 1 Contains the gene for protein arginine N-methyltransferase 6 (PRMT6) and a CpG island, complete sequence gi|21530886|emb|AL355539.18|
		Expect = 8.1 Identities = 20/20 (100%)	PREDICTED: Pan troglodytes class I alcohol dehydrogenase, alpha subunit (ADH1A), mRNA gi|114595309|ref|XM_001166683.1|
SSH2-11 c08	567	Expect = 8.1 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-264C14 on chromosome 10 Contains the 5' end of the gene for a novel protein (MGC10848), the ITIH2 gene for inter-alpha (globulin) inhibitor, H2 polypeptide (H2P), the KIN gene for KIN, antigenic determinant of recA protein homolog (mouse), the 3' end of the ATP5C1 gene for ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1(ATP5C,ATP5CL1), a novel gene and two CpG islands, complete sequence gi|16214543|emb|AL158044.17|
		Expect = 0.032 Identities = 24/24 (100%)	Human DNA sequence from clone RP11-202C2 on chromosome 10 Contains part of the gene for VPS10 domain receptor protein SORCS 3 (SORCS3), complete sequence gi|15282141|emb|AL353900.14|
SSH2-11 c09	553	Expect = 2.0 Identities = 24/25 (96%)	Mus musculus adenylate kinase 1, mRNA (cDNA clone MGC:62584 IMAGE:5346232), complete cds gi|32449847|gb|BC054366.1|
		Expect = 8.8 Identities = 20/20 (100%)	PREDICTED: Strongylocentrotus purpuratus similar to predicted CDS, peptidase family A16 and RNA-directed DNA polymerase and Integrase, catalytic domain and Zn-finger, CCHC type(XC382) (LOC593649), mRNA gi|72041676|ref|XM_793119.1|
SSH2-11 c11	612	Expect = 8.8 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-133M9 on chromosome 9q13-21.33 Contains the 3' end of the RORB gene for RAR-related orphan receptor B protein (RZRB, ROR-BETA), complete sequence gi|14141220|emb|AL137018.9|
SSH2-11 d04	615	Expect = 8.9 Identities = 23/24 (95%)	Nicotiana tabacum NtpolI-like2 mRNA for DNA polymerase, complete cds gi|76880151|dbj|AB174899.1|
SSH2-11 d08	623	Expect = 5.0 Identities = 20/20 (100%)	Mus musculus 0 day neonate cortex cDNA, RIKEN full-length enriched library, clone:G630008M14 product:Neuronal transmembrane protein Slitrk1, full insert sequence gi|74188319|dbj|AK144290.1|
SSH2-11 d10	361	Expect = 7.7 Identities = 20/20 (100%)	PREDICTED: Macaca mulatta similar to transmembrane emp24 protein transport domain containing 9, transcript variant 1 gi|109079977|ref|XM_001093602.1|
SSH2-11 d12	537	Expect = 7.7 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-280O24 on chromosome 9 Contains a ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d (ATP5H) (ATPQ, ATP5JD) pseudogene, the 3' end of the NFIB gene for nuclear factor I/B (NFIB2, NFIB3, NFI-RED) and a ribosomal protein L7a (RPL7A) pseudogene,complete sequence gi|12963957|emb|AL441963.7|
		Expect = 7.7 Identities = 20/20 (100%)	Homo sapiens SULT1C sulfotransferase (SULT1C) mRNA, complete cds gi|3649607|gb|AF055584.1|AF055584
		Expect = 7.3 Identities = 20/20 (100%)	Human DNA sequence from clone RP1-223H12 on chromosome 1q25.1-25.3 Contains the GLUL gene for glutamate-ammonia ligase (glutamine synthase), the gene for putative membrane protein HE9 (HE9), a novel gene (LOC388719), a membrane protein family pseudogene, the RGSL2 gene for regulator of G-protein signalling like 2, the 5' end of the RGSL1 gene for regulator of G-protein signalling like 1 and a CpG island, complete sequence gi|17907186|emb|AL139344.24|
SSH2-11 e06	509	Expect = 7.3 Identities = 20/20 (100%)	Human DNA sequence from clone RP3-452M16 on chromosome Xq21.1-21.33 Contains a capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2) pseudogene, complete sequence gi|3288439|emb|AL024493.1|HS452M16
		Expect = 7.3 Identities = 20/20 (100%)	Homo sapiens glutamine synthetase gene, complete cds gi|45331254|gb|AY486123.1|
		Expect = 0.45 Identities = 22/22 (100%)	Homo sapiens calcium-sensing receptor (hypocalciuric hypercalcemia 1, severe neonatal hyperparathyroidism) (CASR) gene, complete cds gi|67515426|gb|DQ088967.1|
SSH2-11 e07	499	Expect = 7.1 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-234P3 on chromosome X Contains the IMAGED1 gene for melanoma antigen, family D, 1, a pseudogene similar to part of PFKFB1 (6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1), a pseudogene similar to part of IPO7 (importin 7), a ubiquinol-cytochrome c reductase complex (7.2 kD)(HSPC051) pseudogene and a thiopurine S-methyltransferase (TMPT) pseudogene, complete sequence gi|24940061|emb|AL929410.7|

		Expect = 2.5 Identities = 24/25 (96%)	Human DNA sequence from clone RP11-69L16 on chromosome 6 Contains the 3' end of the RREB1 gene for ras responsive element binding protein 1, part of a novel gene, the SSR1 gene for signal sequence receptor alpha (translocon-associated protein alpha), the ATP5GP1 pseudogene (ATPsynthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9)), a ribosomal protein S3 pseudogene, the CAGE1 gene for cancer antigen 1, the 5' end of the RIOK1 gene for RIO kinase 1 (yeast) and three CpG islands, complete sequence gi|10944540|emb|AL139095.15|
SSH2-11 e10	698	Expect = 4.7 Identities = 20/20 (100%)	Homo sapiens mitochondrial ribosomal protein L27 (MRPL27), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA gi|22547130|ref|NM_148571.1|
SSH2-11 e11	337	Expect = 4.7 Identities = 20/20 (100%)	Human DNA sequence from clone RP4-676J13 on chromosome 6q14 Contains the 3' end of the gene for flavohemoprotein B5+B5R and a novel gene, complete sequence gi|6911927|emb|AL034347.23|HS676J13
		Expect = 5.7 Identities = 20/20 (100%)	Bovine elastin gene, exon 1 gi|163023|gb|M58652.1|BOVELAS
SSH2-11 f06	405	Expect = 5.4 Identities = 23/24 (95%)	Cucumis melo clone M6-L12 orf124, orf118, tRNA-Met, and atp9 genes, complete sequence; and atp6 pseudogene, partial sequence; mitochondrial gi|37896205|gb|AY305264.1|
SSH2-11 f08	388	Expect = 5.4 Identities = 20/20 (100%)	Homo sapiens integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) (ITGA2) gene, complete cds gi|21105794|gb|AF512556.1|
		Expect = 5.4 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-12A2 on chromosome 6 Contains a DnaJ (Hsp40) homolog subfamily C member 7 (DNAJC7) pseudogene, the CITED2 gene for Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 2 (MRG1, P35SRJ) and a putative novel gene. Contains two CpG islands, complete sequence gi|17384496|emb|AL592429.6|
		Expect = 0.31 Identities = 25/26 (96%)	Human DNA sequence from clone RP1-306F2 on chromosome 6p12.1-21.1 Contains RBMXP1 for RNA binding motif protein (X chromosome) pseudogene 1, complete sequence gi|12964239|emb|AL121573.15|HSDJ306F2
SSH2-11 f09	349	Expect = 4.9 Identities = 23/24 (95%)	Arabidopsis thaliana clone U20118 putative arabinogalactan-protein(AGP17) (At2g23130) mRNA, complete cds gi|30793948|gb|BT008601.1|
		Expect = 2.1 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-328N1 on chromosome 1 Contains the 3' end of a novel gene and the 5' end of the DNAH14 gene for dynein (axonemal) heavy polypeptide 14, complete sequence gi|14018273|emb|AL357912.10|
SSH2-11 f10	570	Expect = 0.006 Identities = 24/24 (100%)	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene,partial cds; 55kd erythrocyte membrane protein (P55),synaptic vesicle-associated integral membrane protein(VAMP-1), procollagen C-proteinase enhancer protein(PCOLCE) genes, complete cds; and glucose repression mediator protein (GRMP) gene, partial cds gi|2736067|gb|AF016494.1|
SSH2-11 g03	116	Expect = 0.023 Identities = 64/75 (85%)	Wheat gstA1 gene for glutathione-S-transferase gi|21787|emb|X56012.1|TAGSTA1
		Expect = 9.1 Identities = 20/20 (100%)	PREDICTED: Pan troglodytes nucleoporin 153kDa, transcript variant 7(NUP153), mRNA gi|114605627|ref|XM_518255.2|
SSH2-11 g05	632	Expect = 9.1 Identities = 20/20 (100%)	Morus serrator ATPase 8 and ATPase 6 genes, partial cds; mitochondrial genes for mitochondrial products gi|12382963|gb|AY009345.1|
		Expect = 5.5 Identities = 20/20 (100%)	Klebsiella pneumoniae partial YC04 gene for putative capsule polysaccharide export protein precursor, contig region pSL001 gi|9909732|emb|AJ293853.1|KPN293853
SSH2-11 g06	389	Expect = 0.49 Identities = 22/22 (100%)	Encephalitozoon cuniculi GB-M1 DNA REPLICATION FACTOR C (ACTIVATOR 1) SUBUNIT (ECU02_0290) partial mRNA gi|107770625|ref|NM_001040745.1|
SSH2-11 g07	537	Expect = 0.42 Identities = 22/22 (100%)	Human DNA sequence from clone RP11-64J21 on chromosome 13 Contains part of a novel gene similar to tumour-associated hydroquinone(NADH) oxidase TNOX, a ribosomal protein L36 (RPL36)pseudogene and a CpG island, complete sequence gi|11137628|emb|AL138823.14|
SSH2-11 g08	464	Expect = 1.7 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-223J15 on chromosome 1 Contains a novel gene (MDS2), a eukaryotic translation elongation factor 1 alpha 2 (EEF1A2) pseudogene and the RPL11 gene for ribosomal protein L11, complete sequence gi|16751359|emb|AL451000.16|
		Expect = 6.6 Identities = 20/20 (100%)	Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130046B08 product:channel-interacting PDZ domain protein, full insert sequence gi|26086039|dbj|AK037743.1|
		Expect = 0.43 Identities = 22/22 (100%)	Anopheles gambiae putative odorant receptor Or5 gene, complete cds gi|21307826|gb|AY062432.1|
SSH2-11 g10	476	Expect = 0.54 Identities = 24/25 (96%)	PREDICTED: Pan troglodytes X-linked neuroligin 4, transcript variant 1 (NLGN4X), mRNA gi|114687617|ref|XM_001138211.1|
SSH2-12 a02	165	Expect = 2.1 Identities = 23/24 (95%)	Human DNA sequence from clone RP11-669M2 on chromosome 1 Contains the 3' end of a novel gene and apolipoprotein L 3 (APOL3) pseudogene, complete sequence gi|30523816|emb|AL929288.4|
		Expect = 8.5 Identities = 19/19 (100%)	Human DNA sequence from clone RP11-536C5 on chromosome 1q23.1-24.1 Contains the 5' end of the KCNJ10 gene for potassium inwardly-rectifying channel subfamily J member 10, a novel gene, the KCNJ9 gene for potassium inwardly-rectifying channel subfamily J member 9, the IGSF8 gene for immunoglobulin superfamily member 8, the ATP1A2 gene for Na+/K+ transporting ATPase alpha 2 (+) polypeptide, the ATP1A4 gene for Na+/K+ transporting ATPase alpha 4 (+) polypeptide, the CASQ1 gene for calsequestrin 1 (fast-twitch, skeletal muscle), a novel gene, the PEA15 gene for phosphoprotein enriched in astrocytes 15 and four CpG islands, complete sequence gi|25137136|emb|AL121987.34|HSBA536C5
		Expect = 7.0 Identities = 26/28 (92%)	Zebrafish DNA sequence from clone RP71-1D10 in linkage group 14 Contains two novel genes similar to MATR3 (matrin 3), a novel gene similar to PDE6A (cGMP-specific phosphodiesterase 6A alpha (rod)), a novel gene similar to PERC (PGC-1-related estrogen receptor alpha coactivator) and two CpG islands, complete sequence gi|22552779|emb|AL645792.7|
SSH2-12 a08	494	Expect = 0.31 Identities = 22/22 (100%)	Human DNA sequence from clone RP11-85A1 on chromosome 10 Contains the NKX2-3 gene for NK2 transcription factor related, locus 3(Drosophila), the gene for putative mitochondrial solute carrier (MRS3/4) and five CpG islands, complete sequence gi|15787725|emb|AL353719.10|
SSH2-12 b08	351	Expect = 4.9 Identities = 20/20 (100%)	Mouse DNA sequence from clone RP23-396K15 on chromosome 11 Contains the 5' end of the Gabrg2 gene for gamma-aminobutyric acid(GABA-A) receptor, subunit gamma 2, the 3' end of the Gabra1 gene for gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 1 and the 3' end of a novel gene, complete sequence gi|21211995|emb|AL645751.12|
		Expect = 0.13 Identities = 23/23 (100%)	Homo sapiens polymerase (DNA directed), mu (POLM) gene, complete cds gi|58102202|gb|AY899911.1|
SSH2-12 b12	547	Expect = 7.8 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-88I18 on chromosome 9 Contains part of the PGM5 gene for phosphoglucomutase 5 and 2 novel genes, complete sequence gi|16304894|emb|AL161457.13|
		Expect = 1.0 Identities = 21/21 (100%)	Human DNA sequence from clone RP4-570L12 on chromosome Xq13.1-21.1 Contains the PGK1 gene for phosphoglycerate kinase 1, the TAF9L gene for TAF9-like RNA polymerase II TATA box binding protein (TBP)-associated factor 31kDa, a novel pseudogene and a CpG island, complete sequence gi|5679567|emb|AL049589.15|HSJ570L12
SSH2-12 c04	299	Expect = 0.090 Identities = 23/23 (100%)	Human DNA sequence from clone RP11-341A19 on chromosome 10 Contains the 3' end of the MRF2 gene for modulator recognition factor 2, complete sequence gi|21911536|emb|AL671972.8|

SSH2-12 c09	396	Expect = 5.6 Identities = 23/24 (95%)	Human DNA sequence from clone RP4-792G4 on chromosome 1p31.2-32.2 Contains the 5' end of the ALG6 gene for asparagine-linked glycosylation 6 homolog (yeast alpha-1 3-glucosyltransferase), a DnaJ (Hsp40) homolog subfamily C member 7 (DNAJC7) pseudogene, the FOXD3 gene for forkhead box D3, a novel gene, the 5' end of a novel gene and a CpG island, complete sequence gi|11967799|emb|AL049636.22|HSDJ792G4
		Expect = 5.6 Identities = 20/20 (100%)	Rattus norvegicus acyl-CoA thioesterase 8, mRNA (cDNA clone MGC:93234 IMAGE:7114090), complete cds gi|50927580|gb|BC078751.1|
		Expect = 7.4 Identities = 20/20 (100%)	PREDICTED: Rattus norvegicus ATP-binding cassette, sub-family A(ABC1), member 15 (predicted) (Abca15_predicted), mRNA gi|109462763|ref|XM_001075753.1|
SSH2-12 c10	516	Expect = 7.4 Identities = 20/20 (100%)	Mesocricetus auratus 11 beta-hydroxysteroid dehydrogenase type 1 (Hsd11b1) mRNA, complete cds gi|41323485|gb|AY519498.1|
		Expect = 8.3 Identities = 26/28 (92%)	Human DNA sequence from clone RP11-80H5 on chromosome 10 Contains the PANK1 gene for pantothenate kinase 1, a pantothenate kinase 1 (PANK1) pseudogene, four novel genes, the 5' end of the MPHOSPH1 gene for M-phase phosphoprotein 1, a Homo sapiens miR-107-precursor-10 micro RNA and two CpG islands, complete sequence gi|14596274|emb|AL157400.8|
SSH2-12 d01	580	Expect = 6.9 Identities = 20/20 (100%)	Human DNA sequence from clone RP3-333A15 on chromosome 1p31.1-31.3 Contains the 5' end of the PTGER3 gene for prostaglandin E receptor 3 (subtype EP3), part of a novel gene and a CpG island, complete sequence gi|4775605|emb|AL031429.11|HS333A15
SSH2-12 d02	483	Expect = 2.4 Identities = 21/21 (100%)	Human DNA sequence from clone RP11-24B13 on chromosome 9 Contains the 3' end of the gene for a novel protein similar to contactin associated protein-like 3 (CNTNAP3) and an RNA binding motif protein 17 (RBM17) pseudogene, complete sequence gi|54262063|emb|CR788268.5|
SSH2-12 d06	665	Expect = 9.6 Identities = 20/20 (100%)	PREDICTED: Danio rerio similar to Proto-oncogene Serine/threonine-protein kinase Pim-1 (LOC567487), mRNA gi|68432928|ref|XM_690784.1|
		Expect = 9.6 Identities = 20/20 (100%)	Parainfluenza virus type 1 HT87 hemagglutinin-neuraminidase mRNA, complete cds gi|393060|gb|U01081.1|PVU01081
		Expect = 8.8 Identities = 20/20 (100%)	PREDICTED: Canis familiaris similar to SWI/SNF related, matrix associated, actin dependent regulator of chromatin subfamily d, member 2, transcript variant 3 (LOC480477), mRNA gi|73965202|ref|XM_856284.1|
SSH2-12 e06	615	Expect = 2.7 Identities = 21/21 (100%)	Human DNA sequence from clone RP13-24G8 on chromosome X Contains a novel gene, a delta sleep inducing peptide, immunoreactor (DSIPI) pseudogene, the PABPC5 gene for poly(A) binding protein, cytoplasmic 5 and a CpG island, complete sequence gi|18307358|emb|AL662874.9|
SSH2-12 e10	750	Expect = 5.6 Identities = 18/18 (100%)	Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length enriched library, clone:B430203J24 product:hypothetical Microbodies C-terminal targeting signal containing protein, full insert sequence gi|26348862|dbj|AK080904.1|
SSH2-12 f07	44	Expect = 5e-028 Identities = 169/203 (83%)	Arabidopsis thaliana ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding (AT5G11170) mRNA, gi|18416485|ref|NM_121155.1|
SSH2-12 f08	425	Expect = 0.18 Identities = 25/26 (96%)	Human DNA sequence from clone CTA-215D11 on chromosome 1p36.12-36.33 Contains the PARK7 gene for Parkinson disease (autosomal recessive, early onset) 7, a novel gene, gene 33/Mig-6(MIG-6), a ribosomal protein L7a (RPL7A) pseudogene, the 5' end of a novel gene (FLJ26758) and two CpG islands, complete sequence gi|5102616|emb|AL034417.14|HS215D11
SSH2-12 f11	213	Expect = 2.9 Identities = 20/20 (100%)	Hayhurstia atriplicis elongation factor 1 alpha (EF1a) gene, partial cds gi|66774461|gb|DQ005141.1|
		Expect = 1e-011 Identities = 42/43 (97%)	Wheat histone H3 gene gi|21796|emb|X00937.1|TAHI02
SSH2-12 h01	200	Expect = 1e-011 Identities = 42/43 (97%)	Wheat histone H3 gene gi|21796|emb|X00937.1|TAHI02

Other

Contigs

CONTIG 9	(3 clones)		
SSH2-12 a07	364	Expect = 6e-018 Identities = 146/178 (82%)	Oryza sativa (japonica cultivar-group) Os10g0492000 (Os10g0492000)mRNA, partial cds gi|115482671|ref|NM_001071464.1|
SSH2-12 b06 In SSH2-12 a07	362	Expect = 0.021 Identities = 42/48 (87%)	P.sativum mRNA for 110 kD chloroplast inner envelope protein IEP110 gi|1495767|emb|Z68506.1|PSIEP110
SSH2-12 b07 In SSH2-12 a07	364	Expect = 9e-005 Identities = 43/48 (89%)	P.sativum mRNA for 110 kD chloroplast inner envelope protein IEP110 gi|1495767|emb|Z68506.1|PSIEP110
CONTIG 14	(2 clones)		
SSH2-2 g06	215	Expect = 1e-011 Identities = 54/59 (91%)	Oryza sativa (japonica cultivar-group) Os03g0339900 (Os03g0339900) mRNA, complete cds gi|115452922|ref|NM_001056597.1|
		Expect = 0.73 Identities = 36/41 (87%)	Arabidopsis thaliana CIPK10 (CBL-INTERACTING PROTEIN KINASE 10);ATP binding / kinase/ protein kinase/ protein-E139 serine/threonine kinase/ protein-tyro> (CIPK10) mRNA, complete cds gi|30697057|ref|NM_125224.2|
		Expect = 0.73 Identities = 36/41 (87%)	Arabidopsis thaliana SOS2-like protein kinase PKS2 mRNA, complete cds gi|13448028|gb|AF339143.1|AF339143
		Expect = 0.73 Identities = 36/41 (87%)	Arabidopsis thaliana CBL-interacting protein kinase 10 (CIPK10) mRNA, complete cds gi|13249118|gb|AF295665.1|AF295665
SSH2-2 h06 In SSH2-2 g06	179	Expect = 2e-010 Identities = 55/61 (90%)	Oryza sativa (japonica cultivar-group) Os03g0339900 (Os03g0339900)mRNA, complete cds gi|115452922|ref|NM_001056597.1|
CONTIG 20	(2 clones)		
SSH2-5 c08	396	Expect = 8e-030 Identities = 112/126 (88%)	Oryza sativa (japonica cultivar-group) cDNA, clone: J090088O10, full insert sequence gi|116012316|dbj|AK242951.1|
		Expect = 0.001 Identities = 32/34 (94%)	Danio rerio MOB1, Mps One Binder kinase activator-like 1B (yeast), mRNA (cDNA clone MGC:76936 IMAGE:6524831), complete cds gi|46362542|gb|BC066567.1|
SSH2-5 c09 In SSH2-5 c08	394	Expect = 4e-004 Identities = 88/107 (82%)	Zea mays clone Contig41 mRNA sequence gi|54650989|gb|BT016208.1|
CONTIG 21	(2 clones)		
SSH2-5 c10	431	Expect = 5e-019 Identities = 140/168 (83%)	Zea mays PCO092396 mRNA sequence gi|21209387|gb|AY106309.1|
		Expect = 6.1 Identities = 35/40 (87%)	Arabidopsis thaliana mRNA for transporter like protein, complete cds, clone: RAFL14-02-D05 gi|110742894|dbj|AK227331.1|
		Expect = 6.1	Thermoanaerobacterium thermosulfurigenes pullulanase (amyB) maltose-binding protein (amyE),

		Identities = 23/24 (95%)	membrane proteins for maltose transport (amyD and amyC), and alpha-cyclodextrin glycosyltransferase (amyA) genes, complete cds gi|1235794|gb|M57692.1|TTPULSA
SSH2-5 c05	436	Expect = 2e-006 Identities = 88/107 (82%)	Oryza sativa (japonica cultivar-group) Os03g0797700 (Os03g0797700) mRNA, complete cds gi|115455926|ref|NM_001058099.1|
CONTIG 33	(2 clones)		
SSH2-6 g03	401	Expect = 0.001 Identities = 29/30 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-1 g04	394	Expect = 5.5 Identities = 20/20 (100%)	TPA_exp: Bos taurus X-ray radiation resistance associated 1 protein (Xrra1) mRNA, complete cds gi|33620424|tpg|BK000644.1|
CONTIG 34	(2 clones)		
SSH2-7 a12	524	Expect = 6e-013 Identities = 129/158 (81%)	Oryza sativa (indica cultivar-group) clone 7S11F33 mRNA sequence gi|69048902|gb|DQ083211.1|
		Expect = 7.5 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-2J18 on chromosome 6 Contains the 5' end of a ribosomal protein S15a (RPS15A) and part of the gene for BRG1-binding protein ELD/OSA1 (p250R KIAA1235)(FLJ00253, FLJ22292), complete sequence gi|11229090|emb|AL162578.13|
SSH2-10 a08	562	Expect = 2e-015 Identities = 125/150 (83%)	Oryza sativa (indica cultivar-group) clone 7S11F33 mRNA sequence gi|69048902|gb|DQ083211.1|
		Expect = 1e-004 Identities = 31/32 (96%)	Photobacterium damselae subsp. piscicida partial coi genes for putative cytochrome C oxidase proteins, clone pRDA19 gi|57635372|emb|AJ749800.1|
		Expect = 0.008 Identities = 25/25 (100%)	Phytophthora capsici clone Gsi21 mannose glucose binding lectin precursor, mRNA, partial cds gi|54306351|gb|AY725178.1|
CONTIG 35	(2 clones)		
SSH2-7 b02	283	Expect = 0.98 Identities = 27/29 (93%)	Mus musculus adenylyl cyclase type VII gene, partial cds gi|40647349|gb|AY494946.1|
		Expect = 0.98 Identities = 24/25 (96%)	Human DNA sequence from clone RP13-42E14 on chromosome Xq13.1-13.3 Contains the 3' end of the ABCB7 gene for ATP-binding cassette sub-family B (MDR/TAP) member 7, complete sequence gi|13897100|emb|AL359545.12|
		Expect = 3.9 Identities = 23/24 (95%)	Encephalitozoon cuniculi GB-M1 ER protein-translation complex subunit alpha (ECU09_0130) partial mRNA gi|85014138|ref|XM_950472.1|
SSH2-7 b03	843	Expect = 3.1 Identities = 21/21 (100%)	Gallus gallus embryonic alpha-type globin pi, adult alpha D globin, and adult alpha A globin genes, complete cds gi|20043262|gb|AF098919.2|
CONTIG 36	(3 clones)		
SSH2-7 d10	153	Expect = 6e-022 Identities = 104/120 (86%)	Oryza sativa (japonica cultivar-group) Os08g0531100 (Os08g0531100) mRNA, complete cds gi|115477470|ref|NM_001068866.1|
SSH2-10 e02	152	Expect = 2.0 Identities = 20/20 (100%)	PREDICTED: Bos taurus similar to protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform, transcript variant 3 (LOC534776), mRNA gi|76672790|ref|XM_865345.1|
		Expect = 7.7 Identities = 22/23 (95%)	Mus musculus 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930405B01 product:zinc finger protein 100, full insert sequence gi|74140948|dbj|AK134251.1|
SSH2-10 e05	927	Expect = 0.014 Identities = 34/37 (91%)	Nicotiana tabacum cDNA-AFLP-fragment BSTT2-44-390, cultivar Bright Yellow 2 gi|47970923|emb|AJ719155.1|
		Expect = 3.4 Identities = 21/21 (100%)	Dictyostelium discoideum AX4 putative protein serine/threonine kinase (ireA) mRNA, complete cds gi|66827674|ref|XM_642100.1|
CONTIG 41	(2 clones)		
SSH2-9 h10	312	Expect = 0.070 Identities = 26/27 (96%)	Mus musculus fibronectin 1, mRNA (cDNA clone IMAGE:6486803), complete cds gi|29835173|gb|BC051082.1|
SSH2-9 h09	352	Expect = 1.2 Identities = 21/21 (100%)	Triticum aestivum low molecular weight glutenin subunit LMW-Wan49 pseudogene, complete sequence gi|112363567|gb|DQ857250.1|
CONTIG 43	(2 clones)		
SSH2-10 h08	179	Expect = 3e-006 Identities = 66/78 (84%)	Arabidopsis thaliana 60S ribosomal protein L36-like protein(F5K20.4) mRNA, complete cds gi|20148500|gb|AY081579.1|
		Expect = 0.002 Identities = 25/25 (100%)	Agaricus bisporus partial mRNA for putative stress protein (sp gene) gi|26984412|emb|AJ534349.1|ABI534349
SSH2-10 h11 In SSH2-10 h08	181	Expect = 4e-014 Identities = 46/47 (97%)	Saccharum officinarum putative 60S ribosomal protein L36 mRNA,complete cds gi|56182367|gb|AY796052.1|
CONTIG 46	(7 clones)		
SSH2-12 d04	177	Expect = 7e-019 Identities = 105/123 (85%)	Zea mays clone EL01N0551D04.d mRNA sequence gi|54653612|gb|BT018831.1|
SSH2-12 d09 In SSH2-12 d04	177	Expect = 9.2 Identities = 22/23 (95%)	Human DNA sequence from clone RP11-341A19 on chromosome 10 Contains the 3' end of the MRF2 gene for modulator recognition factor 2, complete sequence gi|21911536|emb|AL671972.8|
SSH2-12 d08	574	Expect = e-107 Identities = 398/464 (85%)	Oryza sativa (japonica cultivar-group) Os10g0542200 (Os10g0542200) mRNA, complete cds gi|115483199|ref|NM_001071728.1|
SSH2-12 e04 In SSH2-12 d08	171	Expect = 2e-010 Identities = 46/49 (93%)	Oryza sativa (japonica cultivar-group) Os10g0542200 (Os10g0542200) mRNA, complete cds gi|115483199|ref|NM_001071728.1|
SSH2-12 c11 In SSH2-12 d08	174	Expect = 3e-009 Identities = 53/59 (89%)	Oryza sativa (japonica cultivar-group) Os10g0542200 (Os10g0542200)mRNA, complete cds gi|115483199|ref|NM_001071728.1|
		Expect = 0.037 Identities = 23/23 (100%)	Human DNA sequence from clone RP11-341A19 on chromosome 10 Contains the 3' end of the MRF2 gene for modulator recognition factor 2, complete sequence gi|21911536|emb|AL671972.8|
SSH2-12 d11 In SSH2-12 d08	177	Expect = 7e-010 Identities = 57/64 (89%)	Zea mays clone EL01N0551D04.d mRNA sequence gi|54653612|gb|BT018831.1|
SSH2-12 d10 In SSH2-12 d08	177	Expect = 2e-016 Identities = 77/87 (88%)	Oryza sativa (japonica cultivar-group) Os10g0542200 (Os10g0542200) mRNA, complete cds gi|115483199|ref|NM_001071728.1|

Unknown

Singletons

SSH2-1 a05	94	Expect = 4.3 Identities = 22/23 (95%)	Burkholderia cepacia AMMD chromosome 1, complete sequence gi|115280044|gb|CP000440.1|
SSH2-1 a10	491	Expect = 1.8 Identities = 21/21 (100%)	Zebrafish DNA sequence from clone CH211-263M11 in linkage group 22, complete sequence gi|49614033|emb|BX942822.5|
SSH2-1 b04	202	Expect = 2.7 Identities = 20/20 (100%)	Homo sapiens chromosome 5 clone CTC-316C21, complete sequence gi|18921277|gb|AC010232.10|
SSH2-1 b06	111	Expect = 0.022 Identities = 26/27 (96%)	Homo sapiens chromosome 16 clone CTD-2522B17, complete sequence gi|31745199|gb|AC136932.4|
SSH2-1 b08	223	Expect = 3.0 Identities = 20/20 (100%)	Oryza sativa (japonica cultivar-group), complete sequence gi|45598397|gb|AC134256.4|
SSH2-1 b09	249	Expect = 0.22 Identities = 22/22 (100%)	Mus musculus chromosome 6, clone RP23-367C6, complete sequence gi|35929172|gb|AC117667.9|
SSH2-1 c01	84	Expect = 0.95 Identities = 20/20 (100%)	Nitrosomonas eutropha C71, complete genome gi|114307050|gb|CP000450.1|
SSH2-1 c08	284	Expect = 3.9 Identities = 20/20 (100%)	Mus musculus BAC clone RP24-83P13 from chromosome 16, complete sequence gi|78190218|gb|AC166346.5|
SSH2-1 c09	37	Expect = 0.27 Identities = 20/20 (100%)	Leishmania major Friedlin chromosome 4, left end gi|15027087|emb|AL389894.4|LMFLCHR4A
SSH2-1 c11	336	Expect = 1.2 Identities = 21/21 (100%)	Human DNA sequence from clone RP1-148H17 on chromosome 20 Contains a novel gene, complete sequence gi|8655558|emb|AL109825.23|HSJ148H17
SSH2-1 d03	134	Expect = 6.6 Identities = 19/19 (100%)	Sus scrofa mRNA, clone:OVR010049C08, expressed in ovary gi|115546533|dbj|AK234371.1|
SSH2-1 d10	422	Expect = 1.5 Identities = 21/21 (100%)	Mus musculus chromosome 5, clone RP24-298D13, complete sequence gi|52077710|gb|AC102714.16|
SSH2-1 e03	50	Expect = 7.0 Identities = 18/18 (100%)	Mus musculus chromosome 8, clone RP24-484I6, complete sequence gi|54144536|gb|AC112997.10|
SSH2-1 f01	68	Expect = 2.8 Identities = 19/19 (100%)	Drosophila melanogaster genomic scaffold 211000022280790 gi|114329629|gb|CP000223.2|
SSH2-1 f05	154	Expect = 7.8 Identities = 25/27 (92%)	Gallus gallus BAC clone CH261-83E11 from chromosome z, complete sequence gi|113951797|gb|AC189034.2|
SSH2-1 f07	86	Expect = 3.9 Identities = 19/19 (100%)	Homo sapiens BAC clone RP11-42B7 from 7, complete sequence gi|13811918|gb|AC017000.5|
SSH2-1 f12	266	Expect = 3.6 Identities = 20/20 (100%)	Mus musculus chromosome 1, clone RP23-138J12, complete sequence gi|45736852|gb|AC112675.12|
SSH2-1 g03	173	Expect = 2.3 Identities = 20/20 (100%)	Caenorhabditis elegans cosmid F46H5, complete sequence gi|21106007|gb|U41543.2|
SSH2-1 g10	76	Expect = 0.83 Identities = 23/24 (95%)	Newcastle disease virus genome (strain D26) 3' end (2.6 kb) gi|4902844|emb|X04274.2|PANDV3E
SSH2-1 h02	209	Expect = 2.8 Identities = 20/20 (100%)	Mus musculus chromosome 7, clone RP23-134L4, complete sequence gi|74272045|gb|AC102547.8|
SSH2-1 h03	28	Expect = 2.1 Identities = 21/22 (95%)	Human DNA sequence from clone XX-HCC1954_31F14, complete sequence gi|90818870|emb|CT824641.5|
SSH2-2 a12	226	Expect = 0.77 Identities = 21/21 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 8 gi|58531195|dbj|AP008214.1|
SSH2-2 b02	303	Expect = 4.2 Identities = 20/20 (100%)	Oryza sativa (japonica cultivar-group) chromosome 5 clone P0663C08, complete sequence gi|37992242|gb|AC130728.2|
SSH2-2 b05	427	Expect = 1.5 Identities = 24/25 (96%)	Homo sapiens Chromosome 11q13 BAC Clone 18h3, complete sequence gi|6970735|gb|AC000353.27|
SSH2-2 b08	74	Expect = 3.2 Identities = 19/19 (100%)	Gibberella zeae PH-1 chromosome 2 hypothetical protein (FG08413.1) partial mRNA gi|46128070|ref|XM_388589.1|
SSH2-2 b09	214	Expect = 2.9 Identities = 20/20 (100%)	Human DNA sequence from clone RP1-155D22 on chromosome 6q27 Contains a novel gene, complete sequence gi|2827470|emb|Z97205.1|HS155D22
SSH2-2 c11	58	Expect = 2.2 Identities = 19/19 (100%)	Oryza sativa (japonica cultivar-group) Os04g0616400 (Os04g0616400) mRNA, partial cds gi|115460555|ref|NM_001060413.1|
SSH2-2 d01	152	Expect = 0.49 Identities = 21/21 (100%)	Mus musculus BAC clone RP23-186C6 from 9, complete sequence gi|21844689|gb|AC112521.4|
SSH2-2 d03	142	Expect = 1.8 Identities = 20/20 (100%)	Macaca mulatta chromosome UNK clone CH250-82H12, complete sequence gi|112984708|gb|AC190192.1|
SSH2-2 d05	63	Expect = 10.0 Identities = 18/18 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 7 gi|58531194|dbj|AP008213.1|
SSH2-2 d07	253	Expect = 3.5 Identities = 20/20 (100%)	Kuenenia stuttgartiensis genome fragment KUST_D (4 of 5) gi|91202367|emb|CT573072.1|
SSH2-2 d09	74	Expect = 3.2 Identities = 22/23 (95%)	Novosphingobium aromaticivorans DSM 12444, complete genome gi|87133707|gb|CP000248.1|
SSH2-2 d12	134	Expect = 1.7 Identities = 20/20 (100%)	Homo sapiens chromosome 8, clone RP11-55J5, complete sequence gi|15290886|gb|AC090811.5|
SSH2-2 e03	220	Expect = 3.0 Identities = 20/20 (100%)	Mus musculus BAC clone RP23-97M20 from chromosome 3, complete sequence gi|74013585|gb|AC164091.3|
SSH2-2 e06	304	Expect = 0.27 Identities = 22/22 (100%)	Mus musculus chromosome 3, clone RP24-176I19, complete sequence gi|42491492|gb|AC113454.8|
SSH2-2 e09	352	Expect = 1.2 Identities = 21/21 (100%)	Mouse DNA sequence from clone RP23-119O19 on chromosome 2, complete sequence gi|29466500|emb|AL845271.10|
SSH2-2 e10	142	Expect = 1.8 Identities = 20/20 (100%)	Nitrosospira multiformis ATCC 25196, complete genome gi|82409200|gb|CP000103.1|
SSH2-2 e12	106	Expect = 1.3 Identities = 20/20 (100%)	Mus musculus 6 BAC RP24-490O5 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence gi|62867821|gb|AC155841.6|
SSH2-2 f02	178	Expect = 0.59 Identities = 24/25 (96%)	Mus musculus BAC clone RP24-296C19 from 9, complete sequence gi|50839061|gb|AC122463.4|
SSH2-2 f04	261	Expect = 3.6 Identities = 23/24 (95%)	Glomus intraradices telomeric region, clone Telo2.1_i32 gi|115564865|emb|AJ851846.1|
		Expect = 3.6 Identities = 23/24 (95%)	Rattus norvegicus BAC CH230-224J5 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence gi|90855796|gb|AC103077.6|
SSH2-2 f05	267	Expect = 3.6 Identities = 20/20 (100%)	Oryza sativa (japonica cultivar-group) chromosome 5 clone OSJNBa0088M05, complete sequence gi|40556614|gb|AC136222.2|

SSH2-2 f07	147	Expect = 7.4 Identities = 19/19 (100%)	Mouse DNA sequence from clone RP23-353H5 on chromosome 2, complete sequence gi|27801664|emb|AL928586.10|
SSH2-2 f08	63	Expect = 10.0 Identities = 21/22 (95%)	Zea mays cultivar Mo17 locus 9002, complete sequence gi|55741081|gb|AY664417.1|
SSH2-2 f12	127	Expect = 1.6 Identities = 20/20 (100%)	Oryza sativa (japonica cultivar-group) cDNA clone:002-162-H09, full insert sequence gi|32995463|dbj|AK110254.1|
SSH2-2 g05	266	Expect = 3.6 Identities = 20/20 (100%)	Human DNA sequence from clone RP5-917C11 on chromosome 22 Contains ESTs, STS and GSSs, complete sequence gi|5579006|emb|AL078642.12|HSJ917C11
SSH2-1 g07	158	Expect = 2.0 Identities = 20/20 (100%)	Arabidopsis thaliana unknown protein (AT5G38020) mRNA, complete cds gi|30693189|ref|NM_123161.2|
SSH2-2 g10	192	Expect = 2.5 Identities = 20/20 (100%)	Homo sapiens chromosome 8, clone RP11-544H16, complete sequence gi|13958539|gb|AC020692.5|AC020692
SSH2-2 h04	250	Expect = 3e-019 Identities = 79/88 (89%)	Zea mays subsp. mays genotype CMS-T mitochondrion, complete genome gi|93116122|gb|DQ490953.1|
SSH2-2 h05	159	Expect = 8.1 Identities = 19/19 (100%)	Oryza sativa (japonica cultivar-group) Os02g0224800 (Os02g0224800)mRNA, complete cds gi|115445112|ref|NM_001052871.1|
SSH2-2 h07	194	Expect = 2.6 Identities = 23/24 (95%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 5 gi|58530791|dbj|AP008211.1|
SSH2-2 h08	265	Expect = 0.92 Identities = 21/21 (100%)	Sequence of BAC F19C14 from Arabidopsis thaliana chromosome 1, complete sequence gi|7462019|gb|AC008051.3|F19C14
SSH2-2 h10	187	Expect = 9.8 Identities = 19/19 (100%)	Mus musculus BAC clone RP23-224G24 from X, complete sequence gi|28016780|gb|AC115298.6|
SSH2-2 h11	27	Expect = 0.47 Identities = 19/19 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 4 gi|58530790|dbj|AP008210.1|
SSH2-3 a03	455	Expect = 0.41 Identities = 22/22 (100%)	Homo sapiens chromosome 11 clone RP11-61J24, complete sequence gi|13096043|gb|AC010583.5|AC010583
SSH2-3 a04	507	Expect = 0.46 Identities = 22/22 (100%)	Mus musculus strain C57BL6/J chromosome 5 clone RP23-434H17, complete sequence
SSH2-3 b09	576	Expect = 2.1 Identities = 21/21 (100%)	Onion yellows phytoplasma OY-M DNA, complete genome gi|39721595|dbj|AP006628.1|
		Expect = 8.2 Identities = 20/20 (100%)	Oryza sativa (japonica cultivar-group) Os09g0307300 (Os09g0307300) mRNA, complete cds gi|115478461|ref|NM_001069361.1|
SSH2-3 c08	486	Expect = 1.7 Identities = 24/25 (96%)	Human DNA sequence from clone RP11-237J7 on chromosome 10 Contains two CpG islands, complete sequence gi|16409246|emb|AL590411.7|
		Expect = 6.9 Identities = 20/20 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103482916|emb|CT989464.1|
SSH2-3 c11	714	Expect = 2.6 Identities = 24/25 (96%)	Oryza sativa (japonica cultivar-group) chromosome 3 clone B1339A06, complete sequence gi|42761480|gb|AC148339.1|
SSH2-3 e10	574	Expect = 2.1 Identities = 21/21 (100%)	Caenorhabditis briggsae embryonic nuclear protein (lin-14) gene, exons 4, 5, and 6 gi|11890739|gb|AF304862.1|AF304859S4
SSH2-3 e12	241	Expect = 3e-016 Identities = 101/119 (84%)	Oryza sativa (japonica cultivar-group) Os05g0272900 (Os05g0272900) mRNA, complete cds gi|115462934|ref|NM_001061602.1|
SSH2-3 g03	137	Expect = 0.11 Identities = 22/22 (100%)	Schizosaccharomyces pombe 972h- hypothetical protein (SPAC4G9.07),partial mRNA gi|67999739|ref|NM_001019121.1|
SSH2-3 g10	353	Expect = 3e-023 Identities = 143/171 (83%)	Oryza sativa (japonica cultivar-group) Os01g0896500 (Os01g0896500) mRNA, complete cds gi|115441602|ref|NM_001051616.1|
SSH2-3 h05	511	Expect = 8e-012 Identities = 58/64 (90%)	Oryza sativa (japonica cultivar-group) Os08g0537800 (Os08g0537800) mRNA, partial cds gi|115477542|ref|NM_001068902.1|
		Expect = 1e-004 Identities = 44/48 (91%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103482385|emb|CT988720.1|
SSH2-4 a01	88	Expect = 1.00 Identities = 20/20 (100%)	Homo sapiens cDNA FLJ35396 fis, clone SKNSH2003483 gi|21751378|dbj|AK092715.1|
SSH2-4 a03	311	Expect = 0.28 Identities = 22/22 (100%)	Homo sapiens 12 BAC RP11-25J3 (Roswell Park Cancer Institute Human BAC Library) complete sequence gi|14669923|gb|AC022507.26|
		Expect = 4.3 Identities = 20/20 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1 gi|58530787|dbj|AP008207.1|
SSH2-4 a05	128	Expect = 0.40 Identities = 21/21 (100%)	Homo sapiens 12 BAC RP11-424C20 (Roswell Park Cancer Institute Human BAC Library) complete sequence gi|21263149|gb|AC112777.7|
SSH2-4 a08	53	Expect = 7.7 Identities = 21/22 (95%)	Mouse DNA sequence from clone RP23-36H17 on chromosome 14, complete sequence gi|95136188|emb|CT573025.12|
SSH2-4 b02	59	Expect = 2.3 Identities = 19/19 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6,fosmid clone:OSJNOa230J22 gi|88193776|dbj|AP006854.2|
SSH2-4 b04	69	Expect = 0.18 Identities = 24/25 (96%)	Mus musculus BAC clone RP24-208D21 from chromosome 6, complete sequence gi|41386976|gb|AC121938.3|
SSH2-4 b05	450	Expect = 0.41 Identities = 22/22 (100%)	Zebrafish DNA sequence from clone DKEY-75M8 in linkage group 1, complete sequence gi|62954667|emb|CR388002.6|
SSH2-4 c08	325	Expect = 1.1 Identities = 21/21 (100%)	Mus musculus chromosome 17, clone RP23-89A3, complete sequence
SSH2-4 c06	74	Expect = 0.80 Identities = 20/20 (100%)	Mus musculus BAC clone RP23-427D2 from chromosome 5, complete sequence gi|74039326|gb|AC164103.5|
SSH2-4 d02	464	Expect = 6.6 Identities = 20/20 (100%)	Mus musculus chromosome 3, clone RP24-63C3, complete sequence gi|56404099|gb|AC121304.7|
		Expect = 6.6 Identities = 20/20 (100%)	Ligidium beieri isolate KEF3 16S ribosomal RNA gene, partial sequence; mitochondrial gi|83778143|gb|DQ183003.1|
SSH2-4 d03	67	Expect = 0.18 Identities = 21/21 (100%)	Agrobacterium tumefaciens str. C58 circular chromosome, section 128 of 256 of the complete sequence gi|17739830|gb|AE009102.1|
SSH2-4 d11	54	Expect = 7.9 Identities = 18/18 (100%)	Rhizobium sp. NGR234 megaplasmid 2 contig 1, complete sequence gi|36958823|gb|AY316747.1|
SSH2-4 e03	221	Expect = 3.0 Identities = 23/24 (95%)	Oryza sativa (japonica cultivar-group) Os09g0321200 (Os09g0321200)mRNA, complete cds gi|115478521|ref|NM_001069391.1|
SSH2-4 e04	65	Expect = 2.6 Identities = 19/19 (100%)	Zebrafish DNA sequence from clone DKEY-153N9 in linkage group 2, complete sequence gi|73853139|emb|CR392026.10|
SSH2-4 f01	151	Expect = 7.6 Identities = 22/23 (95%)	Drosophila melanogaster, chromosome 2L, region 38A5-38B4, BAC clone BACR48M05, complete sequence gi|14141717|gb|AC005719.2|AC005719
SSH2-4 f03	533	Expect = 1.9 Identities = 24/25 (96%)	Oryza sativa (japonica cultivar-group) Os04g0492400 (Os04g0492400) mRNA, complete cds gi|115459151|ref|NM_001059711.1|
SSH2-4 f04	61	Expect = 2.4 Identities = 19/19 (100%)	Oryza sativa (japonica cultivar-group) cDNA clone:002-162-B02, full insert sequence gi|32995406|dbj|AK110197.1|
SSH2-4 f06	152	Expect = 2.0 Identities = 20/20 (100%)	Mus musculus BAC clone RP24-1D8 from chromosome y, complete sequence gi|89941531|gb|AC163691.4|
SSH2-4 f07	257	Expect = 3.5 Identities = 26/28 (92%)	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 83 gi|7270470|emb|AL161587.2|ATCHRIV83
SSH2-4 g08	47	Expect = 6.3	Oryza sativa (japonica cultivar-group) chromosome 11 BAC clone B1356F10, complete

		Identities = 18/18 (100%)	sequence gi|35060965|gb|AC146334.2|
SSH2-4 g10	516	Expect = 8e-009 Identities = 114/139 (82%)	Oryza sativa (japonica cultivar-group) Os01g0815700 (Os01g0815700) mRNA, complete cds gi|115440668|ref|NM_001051149.1|
SSH2-4 h02	68	Expect = 2.8 Identities = 19/19 (100%)	Oryza sativa (japonica cultivar-group) chromosome 11 clone OSJNBb0026K20 map S10559, complete sequence gi|56159081|gb|AC133008.3|
SSH2-4 h06	220	Expect = 0.75 Identities = 21/21 (100%)	Drosophila melanogaster chromosome 3R, complete sequence gi|55380579|gb|AE014297.2|
SSH2-4 h09	56	Expect = 8.4 Identities = 18/18 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6 gi|58531193|dbj|AP008212.1|
SSH2-5 a03	194	Expect = 0.16 Identities = 22/22 (100%)	Mus musculus 6 BAC RP23-321M22 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence gi|76880508|gb|AC160400.12|
SSH2-5 b01	281	Expect = 6e-030 Identities = 145/170 (85%)	Oryza sativa (japonica cultivar-group) Os09g0548400 (Os09g0548400) mRNA, complete cds gi|115480522|ref|NM_001070390.1|
SSH2-5 b03	415	Expect = e-105 Identities = 334/380 (87%)	Oryza sativa (japonica cultivar-group) Os07g0588000 (Os07g0588000) mRNA, complete cds gi|115473080|ref|NM_001066674.1|
SSH2-5 b04	254	Expect = 3.5 Identities = 20/20 (100%)	Theileria annulata strain Ankara hypothetical protein (TA20160) partial mRNA gi|84998939|ref|XM_949098.1|
SSH2-5 d05	229	Expect = 3.1 Identities = 20/20 (100%)	Homo sapiens chromosome 16 clone RP11-29G3, complete sequence
SSH2-5 d12	365	Expect = 2e-092 Identities = 289/320 (90%)	Triticum aestivum clone wr1.pk0107.a5:fis, full insert mRNA sequence gi|32129074|gb|BT009523.1|
SSH2-5 g07	823	Expect = 3e-009 Identities = 105/128 (82%)	Oryza sativa (japonica cultivar-group) Os06g0335500 (Os06g0335500) mRNA, complete cds gi|115467909|ref|NM_001064089.1|
SSH2-5 h07	475	Expect = 3e-048 Identities = 255/305 (83%)	Oryza sativa (japonica cultivar-group) Os01g0712600 (Os01g0712600)mRNA, complete cds gi|115439540|ref|NM_001050585.1|
SSH2-6 b02	798	Expect = 0.047 Identities = 24/24 (100%)	Mus musculus BAC clone RP23-137D14 from 16, complete sequence gi|25141141|gb|AC122233.4|
SSH2-6 b04	826	Expect = 3.0 Identities = 21/21 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1 gi|58530787|dbj|AP008207.1|
SSH2-6 b07	160	Expect = 4e-008 Identities = 57/65 (87%)	Oryza sativa (japonica cultivar-group) Os06g0683200 (Os06g0683200) mRNA, complete cds gi|115469575|ref|NM_001064922.1|
SSH2-6 c12	590	Expect = 0.0 Identities = 507/518 (97%)	Oryza sativa (japonica cultivar-group) cultivar Nipponbare chloroplast,complete genome gi|42795537|gb|AY522330.1|
SSH2-6 d02	425	Expect = 6.0 Identities = 20/20 (100%)	Mus musculus BAC clone RP24-138O17 from chromosome 7, complete sequence gi|33187097|gb|AC133088.3|
SSH2-6 d05	252	Expect = 3.4 Identities = 20/20 (100%)	Mus musculus BAC clone RP23-146B12 from chromosome 14, complete sequence gi|73853595|gb|AC165163.2|
SSH2-6 d06	303	Expect = 1.1 Identities = 21/21 (100%)	Homo sapiens BAC clone RP11-473D12 from 4, complete sequence gi|19551194|gb|AC108149.4|
SSH2-6 d08	57	Expect = 6e-007 Identities = 36/38 (94%)	Zea mays PCO140702 mRNA sequence gi|21207232|gb|AY104154.1|
		Expect = 1e-004 Identities = 35/38 (92%)	Oryza sativa (japonica cultivar-group) Os04g0551800 (Os04g0551800)mRNA, complete cds gi|115459799|ref|NM_001060035.1|
SSH2-6 e02	753	Expect = 7e-004 Identities = 27/27 (100%)	Oryza sativa (japonica cultivar-group) Os06g0105400 (Os06g0105400) mRNA, complete cds gi|115465911|ref|NM_001063090.1|
SSH2-6 e04	832	Expect = 0.003 Identities = 35/38 (92%)	Oryza sativa (japonica cultivar-group) Os06g0105400 (Os06g0105400) mRNA, complete cds gi|115465911|ref|NM_001063090.1|
SSH2-6 e05	293	Expect = 4.0 Identities = 20/20 (100%)	Homo sapiens chromosome 15, clone RP11-30G8, complete sequence gi|18071435|gb|AC021979.6|
SSH2-6 e06	716	Expect = 0.66 Identities = 22/22 (100%)	Mus musculus chromosome 19, clone RP24-334K20, complete sequence gi|76362965|gb|AC162612.2|
SSH2-6 e08	120	Expect = 5.8 Identities = 37/43 (86%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 11 gi|58531198|dbj|AP008217.1|
SSH2-6 e11	461	Expect = 0.42 Identities = 28/30 (93%)	Medicago truncatula clone mth2-15c20, complete sequence gi|32189458|gb|AC126009.22|
SSH2-6 f04	54	Expect = 7.9 Identities = 24/26 (92%)	Mus musculus BAC clone CH36-45A22 from chromosome y, complete sequence gi|115334788|gb|AC190181.2|
SSH2-6 f11	179	Expect = 0.038 Identities = 23/23 (100%)	Human DNA sequence from clone RP1-273F20 on chromosome 6q16.1-16.3 Contains the gene for a novel protein and a CpG island,complete sequence i|4938279|emb|AL034371.16|HS273F20
SSH2-6 g12	447	Expect = 2e-018 Identities = 147/178 (82%)	Oryza sativa (japonica cultivar-group) Os01g0848900 (Os01g0848900) mRNA, partial cds gi|115441052|ref|NM_001051341.1|
SSH2-6 h02	257	Expect = 4e-012 Identities = 43/44 (97%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1 gi|58530787|dbj|AP008207.1|
SSH2-6 h06	317	Expect = 1e-015 Identities = 73/82 (89%)	Oryza sativa (japonica cultivar-group) Os05g0270200 (Os05g0270200) mRNA, complete cds gi|115462914|ref|NM_001061592.1|
SSH2-7 a02	739	Expect = 0.17 Identities = 23/23 (100%)	Human DNA sequence from clone RP11-271J19 on chromosome 6 Contains the 5' end of gene KIAA1320, complete sequence gi|14031111|emb|AL513472.9|
SSH2-7 a07	837	Expect = 0.78 Identities = 25/26 (96%)	Zebrafish DNA sequence from clone DKEY-267L16 in linkage group 9, complete sequence gi|56798094|emb|BX294387.11|
SSH2-7 a11	490	Expect = 2e-098 Identities = 363/421 (86%)	Oryza sativa (japonica cultivar-group) Os03g0182400 (Os03g0182400) mRNA, complete cds gi|115451144|ref|NM_001055708.1|
SSH2-7 b01	816	Expect = 0.048 Identities = 24/24 (100%)	Homo sapiens chromosome 4, clone RP11-634F16, complete sequence gi|19807874|gb|AC023772.22|
SSH2-7 b04	828	Expect = 0.77 Identities = 22/22 (100%)	Mus musculus BAC clone RP24-291H9 from chromosome 18, complete sequence gi|46395448|gb|AC132307.5|
SSH2-7 c01	703	Expect = 2.6 Identities = 21/21 (100%)	Rattus norvegicus BAC CH230-333G5 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence gi|104294894|gb|AC128583.4|
SSH2-7 c02	531	Expect = 1.9 Identities = 21/21 (100%)	Mus musculus BAC clone RP24-262O15 from chromosome 16, complete sequence gi|68268216|gb|AC154654.2|
SSH2-7 c03	103	Expect = 1.2 Identities = 20/20 (100%)	Mus musculus BAC clone RP24-487N2 from chromosome 8, complete sequence gi|89112041|gb|AC140227.7|
SSH2-7 c05	455	Expect = 0.41 Identities = 25/26 (96%)	Homo sapiens chromosome 5 clone CTD-2216N22, complete sequence gi|15887315|gb|AC026430.5|
SSH2-7 c06	818	Expect = 0.049 Identities = 27/28 (96%)	Mouse DNA sequence from clone RP23-27P11 on chromosome 11, complete sequence gi|32451340|emb|AL645934.7|
SSH2-7 c08	317	Expect = 0.071 Identities = 23/23 (100%)	Zebrafish DNA sequence from clone CH211-207M2 in linkage group 21, complete sequence gi|29165199|emb|AL928707.5|
SSH2-7 c09	772	Expect = 1e-005 Identities = 45/50 (90%)	Oryza sativa (japonica cultivar-group) Os01g0587000 (Os01g0587000) mRNA, complete cds gi|115437983|ref|NM_001049964.1|
SSH2-7 d02	823	Expect = 3.0 Identities = 21/21 (100%)	Mus musculus BAC clone RP24-388H18 from chromosome 9, complete sequence gi|30141987|gb|AC132580.2|

SSH2-7 d06	335	Expect = 4.7 Identities = 20/20 (100%)	M.truncatula DNA sequence from clone MTH2-87N3 on chromosome 3, complete sequence gi|112703117|emb|CT961059.9|
SSH2-7 d09	467	Expect = 0.007 Identities = 70/85 (82%)	Oryza sativa (japonica cultivar-group) Os01g0587000 (Os01g0587000)mRNA, complete cds gi|115437983|ref|NM_001049964.1|
SSH2-7 e02	492	Expect = 1.8 Identities = 21/21 (100%)	Human DNA sequence from clone RP5-976H15 on chromosome 1p34.1-35.3 Contains part of the CSMD2 gene for CUB and Sushi multiple domains 2, complete sequence gi|38568125|emb|AL161643.26|
SSH2-7 e08	462	Expect = 0.42 Identities = 22/22 (100%)	Pan troglodytes BAC clone CH251-295K11 from Y, complete sequence gi|39540585|gb|AC146214.2|
SSH2-7 f07	99	Expect = 4.6 Identities = 22/23 (95%)	Mus musculus chromosome 1, clone RP23-10C10, complete sequence gi|49406050|gb|AC084310.16|
SSH2-7 g03	60	Expect = 9.3 Identities = 21/22 (95%)	Drosophila melanogaster chromosome 2L, complete sequence gi|113194944|gb|AE014134.5|
SSH2-7 g04	812	Expect = 0.19 Identities = 26/27 (96%)	Zebrafish DNA sequence from clone DKEY-172F14 in linkage group 5,complete sequence gi|55734178|emb|CR759889.5|
SSH2-7 h10	435	Expect = 9e-070 Identities = 221/249 (88%)	Oryza sativa (japonica cultivar-group) Os07g0160400 (Os07g0160400)mRNA, complete cds gi|115470680|ref|NM_001065474.1|
SSH2-7 h11	324	Expect = 4e-068 Identities = 197/218 (90%)	Oryza sativa (japonica cultivar-group) cDNA, clone: J100012M17, full insert sequence gi|116012417|dbj|AK243052.1|
SSH2-8 b03	228	Expect = 3.1 Identities = 20/20 (100%)	Pan troglodytes BAC clone RP43-37K18 from 7, complete sequence gi|28850255|gb|AC140953.1|
SSH2-8 b06	152	Expect = 7.7 Identities = 22/23 (95%)	Populus trichocarpa clone Pop1-64B3, complete sequence gi|114158742|gb|AC184091.2|
SSH2-8 c03	300	Expect = 1.0 Identities = 21/21 (100%)	Gallus gallus BAC clone CH261-4A15 from chromosome z, complete sequence gi|111120398|gb|AC186857.2|
SSH2-8 c06	61	Expect = 2.4 Identities = 19/19 (100%)	Anabaena variabilis ATCC 29413 chromosome, complete sequence gi|75699950|gb|CP000117.1|
SSH2-8 c07	57	Expect = 2.2 Identities = 19/19 (100%)	Burkholderia xenovorans LB400 chromosome 3, complete sequence gi|91692731|gb|CP000272.1|
SSH2-8 c08	182	Expect = 9.5 Identities = 19/19 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 4 gi|58530790|dbj|AP008210.1|
SSH2-8 c09	82	Expect = 3.6 Identities = 19/19 (100%)	Oryza sativa chromosome 3 BAC clone OSJNBb0024J17, complete sequence gi|33667149|gb|AC133340.4|
SSH2-8 c10	63	Expect = 10.0 Identities = 27/30 (90%)	Agrobacterium tumefaciens str. C58 circular chromosome, section 221 of 256 of the complete sequence gi|17740971|gb|AE009195.1|
SSH2-8 c12	46	Expect = 6.0 Identities = 18/18 (100%)	Colwellia psychrerythraea 34H, complete genome gi|71143482|gb|CP000083.1|
SSH2-8 d04	305	Expect = 1.1 Identities = 21/21 (100%)	Drosophila melanogaster chromosome 3R, complete sequence gi|55380579|gb|AE014297.2|
SSH2-8 d05	344	Expect = 1.2 Identities = 24/25 (96%)	Cryptosporidium parvum Iowa II Brf1p like coiled coil protein(cgd2_2700), partial mRNA gi|66358585|ref|XM_626471.1|
SSH2-8 e02	234	Expect = 3.2 Identities = 20/20 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 3 gi|58530789|dbj|AP008209.1|
SSH2-8 e04	71	Expect = 0.76 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-478H13 on chromosome 10 Contains 3 novel genes and two CpG islands, complete sequence gi|14970797|emb|AL355376.6|
SSH2-8 e07	64	Expect = 2.6 Identities = 19/19 (100%)	Gallus gallus BAC clone CH261-18F10 from chromosome unknown, complete sequence gi|63147570|gb|AC159985.2|
SSH2-8 e08	230	Expect = 0.20 Identities = 22/22 (100%)	Plasmodium chabaudi chabaudi hypothetical protein (PC302089.00.0) partial mRNA gi|70915274|ref|XM_727024.1|
SSH2-8 f01	32	Expect = 3.0 Identities = 18/18 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC clone:OSJNBa0010K01 gi|13486858|dbj|AP003210.3|
SSH2-8 f03	266	Expect = 0.92 Identities = 21/21 (100%)	Schizosaccharomyces pombe 972h- hypothetical protein (SPAPB8E5.02c), partial mRNA gi|68005481|ref|NM_001020204.1|
SSH2-8 f04	179	Expect = 9.3 Identities = 19/19 (100%)	Pan troglodytes BAC clone CH251-454H3 from chromosome 7, complete sequence gi|113700390|gb|AC187522.3|
SSH2-8 f05	90	Expect = 0.26 Identities = 21/21 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 8 gi|58531195|dbj|AP008214.1|
SSH2-8 f06	67	Expect = 2.8 Identities = 19/19 (100%)	Loxodonta africana clone VMRC15-519D8, complete sequence gi|63094058|gb|AC153773.3|
SSH2-8 h05	71	Expect = 3.0 Identities = 22/23 (95%)	Homo sapiens chromosome 5 clone CTD-2009F3, complete sequence gi|19747179|gb|AC114277.2|
SSH2-8 h08	217	Expect = 2.9 Identities = 20/20 (100%)	Mus musculus chromosome 1, clone RP24-309N24, complete sequence gi|76362866|gb|AC162869.3|
SSH2-9 a02	855	Expect = 3.1 Identities = 21/21 (100%)	Mus musculus BAC clone RP24-369B15 from chromosome 3, complete sequence gi|37497217|gb|AC132259.3|
SSH2-9 a06	689	Expect = 2.5 Identities = 21/21 (100%)	Mus musculus chromosome 5, clone RP23-1N19, complete sequence gi|51988056|gb|AC137676.11|
SSH2-9 b02	818	Expect = 0.76 Identities = 22/22 (100%)	Mouse DNA sequence from clone RP23-332L17 on chromosome 11, complete sequence gi|20386856|emb|AL645647.8|
SSH2-9 b07	621	Expect = 0.57 Identities = 22/22 (100%)	Zebrafish DNA sequence from clone DKEY-31M5 in linkage group 2, complete sequence gi|48994230|emb|BX649508.10|
SSH2-9 c02	391	Expect = 5.5 Identities = 20/20 (100%)	Human DNA sequence from clone RP11-212B22 on chromosome Xq21.2-22.2 Contains the 3' end of the DIAPH2 gene for diaphanous(Drosophila, homolog) 2 and the 5' end of a novel gene(EPAG), complete sequence gi|11121082|emb|AL391821.7|
SSH2-9 c06	879	Expect = 0.82 Identities = 22/22 (100%)	Drosophila melanogaster, chromosome 3R, region 88E-88E, BAC clone BACR32A03, complete sequence gi|15451478|gb|AC009904.7|
SSH2-9 d07	211	Expect = 0.72 Identities = 21/21 (100%)	Zebrafish DNA sequence from clone CH211-90K4 in linkage group 5,complete sequence gi|72535113|emb|CR354390.16|
SSH2-9 d10	393	Expect = 0.35 Identities = 22/22 (100%)	Human DNA sequence from clone RP4-703F12 on chromosome 1p34.3-36.11,complete sequence gi|16973793|emb|AL139151.13|
SSH2-9 e01	147	Expect = 7.4 Identities = 19/19 (100%)	Platypus DNA sequence from clone CLM1-572A11, complete sequence gi|110625547|emb|CU041381.1|
SSH2-9 e05	378	Expect = 1e-028 Identities = 167/200 (83%)	Oryza sativa (japonica cultivar-group) Os02g0575500 (Os02g0575500) mRNA, complete cds gi|115446864|ref|NM_001053747.1|
SSH2-9 f02	355	Expect = 1.3 Identities = 24/25 (96%)	PREDICTED: Apis mellifera similar to CG33041-PA (LOC408824), mRNA gi|110756454|ref|XM_392356.3|
SSH2-9 f03	166	Expect = 0.55 Identities = 21/21 (100%)	Zea mays clone CH201-171E16, complete sequence gi|92087080|gb|AC165172.2|
SSH2-9 g06	323	Expect = 4.5 Identities = 20/20 (100%)	Homo sapiens chromosome 5 clone RP11-479O16, complete sequence gi|28416064|gb|AC016642.7|
SSH2-9 g10	337	Expect = 1.2 Identities = 21/21 (100%)	Homo sapiens genomic DNA, chromosome 11, clone:RP11-821O7, complete sequence gi|21327924|dbj|AP001201.7|

SSH2-9 h01	722	Expect = 0.17 Identities = 23/23 (100%)	Mus musculus BAC clone RP23-37D14 from chromosome 9, complete sequence gi|77020709|gb|AC160334.2|
SSH2-9 h03	141	Expect = 0.45 Identities = 24/25 (96%)	Toxoplasma gondii, strain RH, genomic DNA chromosome Ib gi|95007251|emb|AM055943.1|
SSH2-9 h06	146	Expect = 1.9 Identities = 20/20 (100%)	Mus musculus chromosome 2, clone ResGen-533P1 strain 129/Sv, complete sequence gi|57209577|emb|CR932806.1|
SSH2-9 h11	340	Expect = 4.7 Identities = 23/24 (95%)	Macaca mulatta chromosome UNK clone CH250-91H12, complete sequence gi|109809869|gb|AC188181.1|
SSH2-10 a04	839	Expect = 3.1 Identities = 21/21 (100%)	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130093L10 product:unclassifiable, full insert sequence gi|26101714|dbj|AK084108.1|
SSH2-10 b08	512	Expect = 0.47 Identities = 22/22 (100%)	Aster yellows witches'-broom phytoplasma AYWB, complete genome gi|84789385|gb|CP000061.1|
SSH2-10 b09	713	Expect = 0.66 Identities = 22/22 (100%)	Mus musculus BAC clone RP24-494I18 from chromosome 13, complete sequence gi|41351677|gb|AC134439.4|
SSH2-10 b12	313	Expect = 4.3 Identities = 23/24 (95%)	Mus musculus chromosome 13, clone RP23-104G24, complete sequence gi|46409704|gb|AC137691.7|
SSH2-10 c05	791	Expect = 0.73 Identities = 25/26 (96%)	Zebrafish DNA sequence from clone DKEY-48A22 in linkage group 16, complete sequence gi|111185865|emb|CR848729.10|
SSH2-10 c06	703	Expect = 0.16 Identities = 23/23 (100%)	Mus musculus chromosome 1, clone RP24-512M8, complete sequence gi|54697269|gb|AC102490.7|
SSH2-10 d09	484	Expect = 1.7 Identities = 21/21 (100%)	Homo sapiens chromosome 15, clone RP11-285I14, complete sequence gi|14589623|gb|AC011966.7|AC011966
SSH2-10 e04	85	Expect = 3.8 Identities = 22/23 (95%)	Triticum aestivum gi|109450933|emb|CT009735.1|
SSH2-10 e10	741	Expect = 0.17 Identities = 26/27 (96%)	Gallus gallus BAC clone CH261-68C18 from chromosome z, complete sequence gi|114431599|gb|AC188946.3|
SSH2-10 f03	192	Expect = 2.5 Identities = 23/24 (95%)	Mus musculus BAC clone RP24-212A21 from chromosome 13, complete sequence gi|66773672|gb|AC155303.2|
SSH2-10 g01	222	Expect = 3.0 Identities = 20/20 (100%)	Rubrobacter xylanophilus DSM 9941, complete genome gi|108764099|gb|CP000386.1|
SSH2-10 g08	426	Expect = 2e-012 Identities = 53/57 (92%)	Oryza sativa (japonica cultivar-group) Os02g0122300 (Os02g0122300) mRNA, complete cds gi|115443890|ref|NM_001052260.1|
SSH2-10 h03	74	Expect = 0.80 Identities = 20/20 (100%)	Pan troglodytes BAC clone CH251-115A24 from chromosome 7, complete sequence gi|115312584|gb|AC190256.3|
SSH2-10 h07	464	Expect = 5e-093 Identities = 344/398 (86%)	Oryza sativa (japonica cultivar-group) Os05g0310800 (Os05g0310800)mRNA, complete cds gi|115463118|ref|NM_001061694.1|
SSH2-11 a01	134	Expect = 6.6 Identities = 19/19 (100%)	Mus musculus BAC clone RP24-316G24 from chromosome 9, complete sequence gi|63028289|gb|AC160964.1|
SSH2-11 a12	705	Expect = 0.65 Identities = 22/22 (100%)	Homo sapiens chromosome 8, clone RP11-107M13, complete sequence gi|18464108|gb|AC084834.4|
SSH2-11 b06	664	Expect = 2.4 Identities = 21/21 (100%)	Mus musculus BAC clone RP23-428P21 from chromosome 10, complete sequence gi|68268194|gb|AC122360.4|
SSH2-11 b12	546	Expect = 2.0 Identities = 21/21 (100%)	Zebrafish DNA sequence from clone CH211-13I23, complete sequence gi|89994205|emb|CR376776.19|
SSH2-11 c10	474	Expect = 0.007 Identities = 25/25 (100%)	Homo sapiens chromosome 3 clone RP11-340I14, complete sequence gi|21954022|gb|AC122178.2|
SSH2-11 d05	539	Expect = 7.7 Identities = 20/20 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 12 gi|58531199|dbj|AP008218.1|
SSH2-11 d07	264	Expect = 0.91 Identities = 21/21 (100%)	Arabidopsis thaliana chromosome 2 clone T9F8 map mi310, complete sequence gi|20197405|gb|AC005561.3|
SSH2-11 d11	303	Expect = 4.2 Identities = 23/24 (95%)	Mus musculus chromosome 17, clone RP23-211H11, complete sequence gi|39841432|gb|AC120548.15|
SSH2-11 e03	468	Expect = 6.6 Identities = 23/24 (95%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P0458E05 gi|21902053|dbj|AP004365.3|
SSH2-11 e04	415	Expect = 5.9 Identities = 20/20 (100%)	Mus musculus chromosome 10, clone RP24-151B6, complete sequence gi|46359986|gb|AC131977.8|
SSH2-11 f01	160	Expect = 8.2 Identities = 19/19 (100%)	Callithrix jacchus chromosome UNK clone CH259-80H12, complete sequence gi|111120417|gb|AC189864.1|
SSH2-11 g09	348	Expect = 4.9 Identities = 23/24 (95%)	Zebrafish DNA sequence from clone DKEYP-10H11 in linkage group 1, complete sequence gi|71142798|emb|CR381708.8|
SSH2-11 g11	470	Expect = 0.11 Identities = 23/23 (100%)	Human DNA sequence from clone RP11-308P9 on chromosome 9 Contains a CpG island, complete sequence gi|16973842|emb|AL357872.23|
SSH2-11 g12	521	Expect = 1e-063 Identities = 266/311 (85%)	Oryza sativa (japonica cultivar-group) Os01g0281000 (Os01g0281000) mRNA, complete cds gi|115435995|ref|NM_001049291.1|
SSH2-12 a01	694	Expect = 2.5 Identities = 21/21 (100%)	Homo sapiens BAC clone RP11-416J17 from 7, complete sequence gi|16756355|gb|AC069288.7|
SSH2-12 a03	308	Expect = 1.1 Identities = 21/21 (100%)	Mus musculus chromosome 7, clone RP23-327E18, complete sequence gi|83035271|gb|AC162175.10|
SSH2-12 a12	510	Expect = 0.12 Identities = 23/23 (100%)	Canis Familiaris chromosome 11, clone XX-269B15, complete sequence gi|112181281|gb|AC188520.4|
SSH2-12 b02	58	Expect = 2.2 Identities = 25/27 (92%)	Oryza sativa (japonica cultivar-group) Os08g0531100 (Os08g0531100)mRNA, complete cds gi|115477470|ref|NM_001068866.1|
SSH2-12 b03	696	Expect = 2.5 Identities = 21/21 (100%)	Neurospora crassa OR74A hypothetical protein (NCU08265.1) partial mRNA gi|85089427|ref|XM_952854.1|
SSH2-12 b11	820	Expect = 3.0 Identities = 21/21 (100%)	Oryza sativa (japonica cultivar-group) chromosome 5 clone OSJNBa0075J06, complete sequence gi|50300534|gb|AC136220.3|
SSH2-12 c01	832	Expect = 0.20 Identities = 23/23 (100%)	Oryza sativa (japonica cultivar-group) Os08g0531100 (Os08g0531100) mRNA, complete cds gi|115477470|ref|NM_001068866.1|
SSH2-12 c06	409	Expect = 5.8 Identities = 20/20 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 4 gi|58530790|dbj|AP008210.1|
SSH2-12 c12	521	Expect = 3e-005 Identities = 29/29 (100%)	Homo sapiens chromosome 2 oral squamous cell carcinoma allelic imbalance region, genomic sequence gi|23194468|gb|AF539915.1|
		Expect = 5e-004 Identities = 37/39 (94%)	Antrodia camphorata partial ITS1, 5.8S rRNA gene and partial ITS2, strain #96 gi|33145938|emb|AJ496405.1|ACA496405
SSH2-12 d05	155	Expect = 7.9 Identities = 19/19 (100%)	Oryza sativa (japonica cultivar-group) Os06g0725900 (Os06g0725900) mRNA, complete cds gi|115470051|ref|NM_001065160.1|
SSH2-12 d07	515	Expect = 9e-055 Identities = 223/260 (85%)	Oryza sativa (japonica cultivar-group) Os02g0712000 (Os02g0712000) mRNA, complete cds gi|115448250|ref|NM_001054440.1|
SSH2-12 d12	831	Expect = 2e-004 Identities = 43/48 (89%)	Oryza sativa (japonica cultivar-group) Os10g0542200 (Os10g0542200) mRNA, complete cds gi|115483199|ref|NM_001071728.1|
SSH2-12 e05	602	Expect = 0.14 Identities = 23/23 (100%)	Sesbania drummondii clone SSH-40_01_C12_T3 mRNA sequence gi|99126125|gb|DQ465793.1|
SSH2-12 e07	708	Expect = 1e-005	Oryza sativa (japonica cultivar-group) Os10g0542200 (Os10g0542200) mRNA, complete cds

		Identities = 75/90 (83%)	gi|115483199|ref|NM_001071728.1|
SSH2-12 f05	478	Expect = 4e-023 Identities = 116/135 (85%)	Hordeum vulgare mRNA for hypothetical protein, clone RG98 gi|2695932|emb|AJ222780.1|HVJ222780
SSH2-12 h06	320	Expect = 2e-033 Identities = 118/132 (89%)	Oryza sativa (japonica cultivar-group) Os02g0817900 (Os02g0817900) mRNA, complete cds gi|115449680|ref|NM_001055061.1|

Unknown

Contigs

CONTIG 18	(2 clones)		
SSH2-5 a09	431	Expect = 2e-074 Identities = 339/397 (85%)	Oryza sativa (japonica cultivar-group) chromosome 10 clone OSJNAb0023M11, complete sequence
SSH2-5 a10	556	Expect = 0.0 Identities = 512/522 (98%)	Mus musculus chromosome 5, clone RP24-107D19, complete sequence Oryza sativa (japonica cultivar-group) cDNA clone:001-014-B08, full insert sequence
CONTIG 19	(2 clones)		
SSH2-5 a11	480	Expect = 4e-066 Identities = 233/267 (87%)	Oryza sativa (japonica cultivar-group) Os05g0404400 (Os05g0404400) mRNA, complete cds gi|115463806|ref|NM_001062038.1|
SSH2-11 h05 In SSH2-5 a11	463	Expect = 9e-064 Identities = 205/231 (88%)	Oryza sativa (japonica cultivar-group) Os05g0404400 (Os05g0404400) mRNA, complete cds gi|115463806|ref|NM_001062038.1|
		Expect = 3e-014 Identities = 110/132 (83%)	Arabidopsis thaliana unknown protein (AT2G48070) mRNA, complete cds gi|30690883|ref|NM_130374.2|
CONTIG 23	(3 clones)		
SSH2-5 e07	439	Expect = 2e-070 Identities = 237/270 (87%)	Oryza sativa (japonica cultivar-group) Os06g0683200 (Os06g0683200) mRNA, complete cds gi|115469575|ref|NM_001064922.1|
SSH2-3 h10 In SSH2-5 e07	475	Expect = 6e-022 Identities = 214/271 (78%)	Oryza sativa (japonica cultivar-group) Os06g0683200 (Os06g0683200) mRNA, complete cds gi|115469575|ref|NM_001064922.1|
SSH2-11 a11	700	Expect = 5e-054 Identities = 237/279 (84%)	Oryza sativa (japonica cultivar-group) Os06g0683200 (Os06g0683200)mRNA, complete cds gi|115469575|ref|NM_001064922.1|
CONTIG 26	(2 clones)		
SSH2-6 b08	593	Expect = 1e-078 Identities = 230/256 (89%)	Oryza sativa (japonica cultivar-group) cDNA, clone: J065011J02,full insert sequence gi|116013772|dbj|AK240821.1|
SSH2-2 b07 In SSH2-6 b08	471	Expect = 1e-019 Identities = 120/141 (85%)	Oryza sativa (japonica cultivar-group) cDNA, clone: J065011J02, full insert sequence gi|116013772|dbj|AK240821.1|
		Expect = 1.7 Identities = 21/21 (100%)	Human DNA sequence from clone RP5-823D19 on chromosome 1q42.11-43 Contains the 5' end of the SIPA1L2 gene for signal-induced proliferation-associated 1 like 2, complete sequence gi|15131205|emb|AL157409.16|
CONTIG 27	(6 clones)		
SSH2-6 c06	496	Expect = 0.0 Identities = 458/460 (99%)	Triticum aestivum chloroplast DNA, complete genome gi|13928184|dbj|AB042240.3|
SSH2-10 c03 In SSH2-6 c06	503	Expect = e-134 Identities = 355/394 (90%)	Triticum aestivum chloroplast DNA, complete genome gi|13928184|dbj|AB042240.3|
SSH2-6 c07	630	Expect = 0.0 Identities = 459/460 (99%)	Triticum aestivum chloroplast DNA, complete genome gi|13928184|dbj|AB042240.3|
SSH2-5 h06 In SSH2-6 c07	501	Expect = 0.0 Identities = 453/460 (98%)	Triticum aestivum chloroplast DNA, complete genome gi|13928184|dbj|AB042240.3|
SSH2-12 g07 In SSH2-6 c07	493	Expect = 0.0 Identities = 446/454 (98%)	Festuca arundinacea 23S ribosomal RNA gene, partial sequence; chloroplast gi|94959246|gb|DQ490949.1|
SSH2-3 a05 In SSH2-6 c07	508	Expect = 0.0 Identities = 454/461 (98%)	Festuca arundinacea 23S ribosomal RNA gene, partial sequence; chloroplast
CONTIG 38	(2 clones)		
SSH2-8 h09	273	Expect = 3.7 Identities = 20/20 (100%)	Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P0440D10 gi|15290189|dbj|AP003852.2|
SSH2-7 h04	743	Expect = 1e-005 Identities = 180/230 (78%)	Arabidopsis thaliana protein binding (AT5G49510) mRNA, complete cds gi|18423034|ref|NM_124328.1|

Rubisco

Singletons

SSH2-2 a04	373	Expect = 6e-012 Identities = 88/104 (84%)	Wheat (T. aestivum) chloroplast ribulosebisphosphate carboxylase small subunit mRNA, clone pTS406, 3' end gi|170760|gb|K02324.1|WHTRBCC
SSH2-2 g11	341	Expect = 1.2 Identities = 52/60 (86%)	Trisetum youngii ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493543|gb|AY691646.1|
SSH2-3 a09	269	Expect = 1e-009 Identities = 111/136 (81%)	Secale cereale mRNA for hypothetical protein, clone 9 gi|4090292|emb|AJ131738.1|SCE131738
SSH2-5 b07	250	Expect = 3e-019 Identities = 154/188 (81%)	Trisetum youngii ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493543|gb|AY691646.1|
SSH2-6 c04	414	Expect = 7e-009 Identities = 50/55 (90%)	Nardus stricta ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast gi|51511888|gb|AY622895.1|
SSH2-6 d10	627	Expect = 3e-061	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA,

		Identities = 174/191 (91%)	complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-6 g09	510	Expect = 0.002 Identities = 76/95 (80%)	Triticum urartu DNA for ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit, partial cds, clone Ura-B gi|4038712|dbj|AB020954.1|
SSH2-7 d12	784	Expect = e-127 Identities = 251/257 (97%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-9 a07	315	Expect = 1e-012 Identities = 88/104 (84%)	Psathyrostachys rupestris subsp. daghestanica voucher H6703 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51859668|gb|AY607058.1|
SSH2-9 c01	311	Expect = 0.28 Identities = 25/26 (96%)	Peperomia serpens ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|52082853|gb|AY572270.1|
SSH2-9 d12	435	Expect = 6e-040 Identities = 156/179 (87%)	Amphipogon strictus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, chloroplast gene encoding chloroplast protein, partial cds gi|2580528|gb|U88403.1|ASU88403
SSH2-9 f07	311	Expect = 8e-011 Identities = 78/92 (84%)	Triticum aestivum rbcS gene for ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit, complete cds, clone:p9-1 gi|11990896|dbj|AB042066.1|
SSH2-9 f12	320	Expect = 1e-006 Identities = 37/39 (94%)	Stachytarpheta dichotoma ribulose-1,5-biphosphate carboxylase/oxygenase large subunit (rbcL) gene, chloroplast gene encoding chloroplast protein, partial cds gi|1209045|gb|U32161.1|SDU32161
SSH2-9 g12	391	Expect = 6e-012 Identities = 73/84 (86%)	Oryza sativa chloroplast partial rbcL gene for ribulose bisphosphate carboxylase large chain gi|57283873|emb|AJ746297.1|
SSH2-10 b07	393	Expect = 0.023 Identities = 75/92 (81%)	Amphibromus fluitans ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493513|gb|AY691631.1|
SSH2-10 c08	635	Expect = 2e-010 Identities = 77/90 (85%)	Elymus sibiricus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) mRNA, complete cds; chloroplast gi|54401455|gb|AY772669.1|
SSH2-10 c09	898	Expect = 2e-004 Identities = 99/122 (81%)	Hordeum patagonicum subsp. mustersii ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, complete cds; chloroplast gene for chloroplast product gi|31087888|gb|AY137446.1|
SSH2-10 d04	383	Expect = 1e-016 Identities = 51/52 (98%)	Puccinellia stricta ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493537|gb|AY691643.1|
SSH2-10 d08	943	Expect = 2e-017 Identities = 126/150 (84%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-10 e07	745	Expect = 1e-088 Identities = 257/285 (90%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-10 e08	912	Expect = 2e-075 Identities = 231/259 (89%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-10 e09	612	Expect = 0.002 Identities = 35/38 (92%)	Brighamia insignis ribulose-1,5-bisphosphate carboxylase large subunit (rbcL) gene, partial cds; chloroplast gene for chloroplast product gi|6649967|gb|AF042664.1|AF042664
SSH2-10 e12	448	Expect = 7e-009 Identities = 35/35 (100%)	Elymus sibiricus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) mRNA, complete cds; chloroplast gi|54401455|gb|AY772669.1|
SSH2-10 f02	703	Expect = 1e-088 Identities = 223/246 (90%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-10 f05	915	Expect = 4e-018 Identities = 132/159 (83%)	Trisetum youngii ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493543|gb|AY691646.1|
SSH2-10 g04	682	Expect = 0.63 Identities = 34/38 (89%)	Micraira subulifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid gi|54303883|gb|AY632366.1|
SSH2-10 h02	666	Expect = 1e-029 Identities = 153/181 (84%)	Psathyrostachys rupestris subsp. daghestanica voucher H6703 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51859668|gb|AY607058.1|
SSH2-11 d03	130	Expect = 0.10 Identities = 28/30 (93%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-11 g04	478	Expect = 1e-047 Identities = 228/268 (85%)	Triticum aestivum rbcS gene for ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit, complete cds, clone:p9-1 gi|11990896|dbj|AB042066.1|
SSH2-12 c02	174	Expect = 1e-008 Identities = 90/111 (81%)	Puccinellia stricta ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493537|gb|AY691643.1|
SSH2-12 c03	356	Expect = e-118 Identities = 269/286 (94%)	Australopyrum calcis subsp. calcis ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493523|gb|AY691636.1|
SSH2-12 d03	621	Expect = 1e-029 Identities = 226/279 (81%),	Australopyrum calcis subsp. calcis ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|51493523|gb|AY691636.1|
SSH2-12 e03	661	Expect = 1e-035 Identities = 180/209 (86%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-12 f03	509	Expect = 4e-060 Identities = 236/279 (84%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-12 g12	619	Expect = 0.002 Identities = 38/42 (90%)	Cortaderia selloana ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast gi|66802798|gb|DQ005609.1|
SSH2-12 h10	846	Expect = e-124 Identities = 248/257 (96%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|

Rubisco

Contigs

CONTIG 42	(22 clones)		
REPRESENTATIVE			
SSH2-10 d05	262	Expect = 1e-043 Identities = 126/137 (91%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-5 b10	262	Expect = e-116 Identities = 222/223 (99%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-4 b09	515	Expect = 0.0 Identities = 466/473 (98%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-5 f10	295	Expect = e-129 Identities = 250/257 (97%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
CONTIG 48	(11 clones)		

REPRESENTATIVE			
SSH2-1 f04	512	Expect = e-172 Identities = 352/365 (96%)	Cloning vector psiLentGene Basic, complete sequence gi|45655410|gb|AY508731.1|
SSH2-12 a11	533	Expect = 0.0 Identities = 425/442 (96%)	Hordeum vulgare ribulose-1,5-bisphosphate carboxylase small subunit mRNA, complete cds gi|1167947|gb|U43493.1|HVU43493
SSH2-5 d09	441	Expect = e-151 Identities = 279/281 (99%)	Wheat mRNA fragment for small subunit precursor of RuBPCase (EC 4.1.1.39 ribulosebisphosphate carboxylase) clones 234 and 406 gi|21867|emb|X00235.1|TARUB2
SSH2-10 a05	796	Expect = 8e-081 Identities = 210/228 (92%)	Triticum aestivum rbcS gene for ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit, complete cds, clone:p9-1 gi|11990896|dbj|AB042066.1|
CONTIG 52	(17 clones)		
REPRESENTATIVE			
SSH2-3 g08	346	Expect = e-163 Identities = 297/298 (99%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-10 d06	582	Expect = e-132 Identities = 284/298 (95%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-10 e06	827	Expect = e-147 Identities = 286/292 (97%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
CONTIG 55	(5 clones)		
SSH2-5 d01	282	Expect = e-132 Identities = 242/242 (100%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-11 c12 In SSH2-5 d01	220	Expect = 1e-082 Identities = 179/186 (96%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-9 g11 In SSH2-5 d01	474	Expect = 9e-095 Identities = 224/239 (93%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-12 h03 In SSH2-5 d01	238	Expect = e-110 Identities = 208/209 (99%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
SSH2-9 f11	677	Expect = 7e-013 Identities = 166/206 (80%)	Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) mRNA, complete cds; chloroplast gene for chloroplast product gi|32966579|gb|AY328025.1|
CONTIG 56	(7 clones)		
REPRESENTATIVE			
SSH2-6 h04	541	Expect = 1e-047 Identities = 109/112 (97%)	Triticum aestivum rbcS gene for ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit, complete cds, clone:p9-1 gi|11990896|dbj|AB042066.1|
CONTIG 61	(17 clones)		
REPRESENTATIVE			
SSH2-9 g05	421	Expect = e-115 Identities = 296/323 (91%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|12343|emb|X62117.1|CHTAHSRA
SSH2-5 h01	373	Expect = e-178 Identities = 324/326 (99%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|12343|emb|X62117.1|CHTAHSRA
SSH2-5 g01	367	Expect = e-178 Identities = 324/326 (99%)	T.aestivum chloroplast genes rbcL, psaI, ORF 185 and ORF 230 for large subunit of ribulose 1,5 bisphosphate carboxylase/oxygenase and apoprotein I gi|12343|emb|X62117.1|CHTAHSRA
SSH2-11 a09	373	Expect = e-138 Identities = 305/323 (94%)	Triticum aestivum chloroplast gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (H-type), complete cds gi|344052|dbj|D00206.1|WHTCPRBCL
SSH2-5 h02	836	Expect = 0.0 Identities = 456/475 (96%),	Cloning vector psiLentGene Basic, complete sequence gi|45655410|gb|AY508731.1|
SSH2-7 h02	613	Expect = 0.0 Identities = 496/500 (99%)	Cloning vector pGEM-WIZ, complete sequence gi|114846943|gb|DQ917671.1|

Chlorophyll A/B Binding Protein

Singletons

SSH2-3 b01	579	Expect = 5e-026 Identities = 146/172 (84%)	Hordeum vulgare partial mRNA for chlorophyll a/b-binding protein gi|3153150|emb|AJ006296.1|HVU6296
		Expect = 2.1 Identities = 21/21 (100%)	Danio rerio RNA polymerase II CTD phosphatase mRNA, complete cds gi|49618914|gb|AY648724.1|
SSH2-3 f09	469	Expect = 1e-016 Identities = 91/104 (87%)	Hordeum vulgare partial mRNA for chlorophyll a/b-binding protein gi|3153150|emb|AJ006296.1|HVU6296
SSH2-6 b01	538	Expect = 0.032 Identities = 52/60 (86%)	Hordeum vulgare gene for CP29 precursor for core chlorophyll a/b binding (CAB) protein of photosystem II (PSII) gi|18957|emb|X63052.1|HVCP29
SSH2-6 f02	381	Expect = 5.3 Identities = 29/32 (90%)	Ginkgo biloba nuclear-encoded chloroplast chlorophyll a/b binding protein mRNA, complete cds gi|349442|gb|L23107.1|GBICABBP
SSH2-6 f03	378	Expect = 0.022 Identities = 30/32 (93%)	Triticum aestivum chlorophyll a/b-binding protein WCAB precursor(Wcab) mRNA, complete cds gi|1657858|gb|U73218.1|TAU73218
SSH2-7 f03	316	Expect = 1e-009 Identities = 133/164 (81%)	H.vulgare lhbC mRNA for type III LHCII CAB precursor protein gi|19022|emb|X63197.1|HVLHBC
SSH2-8 a06	184	Expect = 7e-010 Identities = 42/44 (95%)	Maize cab-1 gene for chlorophyll a/b-binding protein gi|22223|emb|X14794.1|ZMCAB1
SSH2-8 e10	388	Expect = e-127 Identities = 309/334 (92%)	Triticum aestivum chlorophyll a/b-binding protein WCAB precursor(Wcab) mRNA, complete cds gi|1657858|gb|U73218.1|TAU73218
SSH2-8 h04	82	Expect = 0.23 Identities = 21/21 (100%)	B.juncea mRNA for chlorophyll a/b-binding protein gi|1644288|emb|X95727.1|BJMCAB1GE

SSH2-9 d11	456	Expect = 0.10 Identities = 38/43 (88%)	H.vulgare lhbC mRNA for type III LHCII CAB precursor protein gi|19022|emb|X63197.1|HVLHBC
SSH2-12 h04	338	Expect = 0.019 Identities = 27/28 (96%)	Arabidopsis thaliana CAB1 (CHLOROPHYLL A/B BINDING PROTEIN 1);chlorophyll binding (CAB1) mRNA, complete cds gi|30690951|ref|NM_102733.2|
SSH2-12 h08	330	Expect = e-120 Identities = 231/234 (98%)	Hordeum vulgare chlorophyll a/b-binding protein precursor (Lhca4) mRNA, partial cds; nuclear gene for chloroplast product gi|9624494|gb|AF287276.1|AF287276
SSH2-12 h09	449	Expect = e-169 Identities = 362/379 (95%)	Hordeum vulgare gene for CP29 precursor for core chlorophyll a/b binding (CAB) protein of photosystem II (PSII) gi|18957|emb|X63052.1|HVCP29

Chlorophyll A/B Binding Protein

Contigs

CONTIG 28	(6 clones)		
SSH2-6 c11	561	Expect = e-111 Identities = 270/291 (92%)	Triticum aestivum chlorophyll a/b-binding protein WCAB precursor(Wcab) mRNA, complete cds gi|1657858|gb|U73218.1|TAU73218
SSH2-12 h05	341	Expect = 1e-071 Identities = 242/276 (87%)	Z.mays cab-m7 gene for light harvesting chlorophyll a/b binding protein gi|22229|emb|X53398.1|ZMCABM7
SSH2-9 f08 In SSH2-12 h05	245	Expect = 7e-020 Identities = 74/81 (91%)	Triticum aestivum chlorophyll a/b-binding protein WCAB precursor (Wcab) mRNA, complete cds gi|1657858|gb|U73218.1|TAU73218
SSH2-3 h12 In SSH2-12 h05	336	Expect = 4e-065 Identities = 219/249 (87%)	Triticum aestivum chlorophyll a/b-binding protein WCAB precursor (Wcab) mRNA, complete cds gi|1657858|gb|U73218.1|TAU73218
SSH2-12 g05 In SSH2-12 h05	417	Expect = 5e-062 Identities = 238/276 (86%)	Z.mays cab-m7 gene for light harvesting chlorophyll a/b binding protein gi|22229|emb|X53398.1|ZMCABM7
SSH2-12 g04	592	Expect = 1e-060 Identities = 201/222 (90%)	Hordeum vulgare vacuolar ATPase B subunit isoform mRNA, complete cds gi|167107|gb|L11862.1|BLYVATP57A
CONTIG 40	(2 clones)		
SSH2-9 c03	458	Expect = 1e-087 Identities = 355/415 (85%)	Oryza sativa chlorophyll a-b binding protein mRNA, complete cds gi|2570510|gb|AF022738.1|AF022738
SSH2-9 d08 In SSH2-9 c03	458	Expect = 3e-085 Identities = 345/403 (85%)	Oryza sativa chlorophyll a-b binding protein mRNA, complete cds gi|2570510|gb|AF022738.1|AF022738

Ribosomal RNA

Singletons

SSH2-1 b01	104	Expect = 0.079 Identities = 22/22 (100%)	Oryza eichingeri clone 2 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence gi|37778796|gb|AY188683.1|
SSH2-3 a01	655	Expect = e-117 Identities = 251/261 (96%),	Rye 26S rRNA 3' end and 18S rRNA, 5' end
SSH2-3 b04	192	Expect = 5e-023 Identities = 91/102 (89%)	Buxus sempervirens large subunit ribosomal RNA gene, partial sequence; chloroplast gi|109138876|gb|DQ629363.1|
		Expect = 1e-020 Identities = 84/94 (89%)	Lycopersicon esculentum complete chloroplast genome, cultivar IPA-6 gi|113531108|emb|AM087200.3|
		Expect = 1e-020 Identities = 84/94 (89%)	Zea mays subsp. mays genotype CMS-C mitochondrion, complete genome gi|102579626|gb|DQ645536.1|
SSH2-5 a06	341	Expect = 4e-031 Identities = 178/208 (85%)	Circaeaster agrestis 26S ribosomal RNA gene, partial sequence gi|22595019|gb|AF389246.1|
SSH2-6 a06	673	Expect = 3e-015 Identities = 103/122 (84%)	Rye 26S rRNA 3' end and 18S rRNA, 5' end gi|169834|gb|M37231.1|RYENORR1
SSH2-6 f05	460	Expect = 2e-074 Identities = 304/357 (85%)	Triticum aestivum 18S ribosomal RNA gene, partial sequence gi|15982656|gb|AY049040.1|
SSH2-7 f09	322	Expect = 3e-016 Identities = 68/75 (90%)	Drosophila testacea 28S large subunit ribosomal RNA gene, partial sequence gi|33338168|gb|AF184018.1|
SSH2-7 g07	461	Expect = 0.42 Identities = 25/26 (96%)	Oligonychus coffeae 28S ribosomal RNA gene, partial sequence gi|58760607|gb|AY750699.1|
SSH2-8 a01	188	Expect = 7e-007 Identities = 37/39 (94%)	Euphorbia milii var. splendens 25S ribosomal RNA gene, partial sequence gi|4102909|gb|AF017173.1|
SSH2-8 g10	229	Expect = 1e-011 Identities = 64/75 (85%)	Rana japonica 28S ribosomal RNA gene, partial sequence gi|90183528|gb|DQ283529.1|
SSH2-10 b02	511	Expect = e-166 Identities = 337/350 (96%)	Triticum aestivum mitochondrial DNA, complete genome gi|78675232|dbj|AP008982.1|
		Expect = e-166 Identities = 337/350 (96%)	T.aestivum mitochondrion rrn26 gene for rRNA large subunit (26S) gi|19560|emb|Z11889.1|MITTARRNG
SSH2-10 b03	500	Expect = 2e-021 Identities = 185/228 (81%)	Tofieldia calyculata large subunit ribosomal RNA gene, partial sequence; mitochondrial gi|66969404|gb|DQ008816.1|
SSH2-10 g05	498	Expect = 6e-028 Identities = 134/159 (84%)	Rye 26S rRNA 3' end and 18S rRNA, 5' end gi|169834|gb|M37231.1|RYENORR1

SSH2-11 f04	472	Expect = 5e-019 Identities = 134/160 (83%)	Triticum aestivum 28S ribosomal RNA gene, partial sequence gi|15982657|gb|AY049041.1|
SSH2-11 g01	664	Expect = 0.0 Identities = 620/626 (99%)	Rye 26S rRNA 3' end and 18S rRNA, 5' end gi|169834|gb|M37231.1|RYENORR1
SSH2-12 g08	566	Expect = 4e-026 Identities = 97/108 (89%)	Andreaea rupestris large subunit ribosomal RNA gene, partial sequence; chloroplast gi|109138747|gb|DQ629234.1|
SSH2-12 g09	469	Expect = 2e-006 Identities = 34/35 (97%)	Amborella trichopoda large subunit ribosomal RNA gene, partial sequence; chloroplast gi|109138849|gb|DQ629336.1|

Ribosomal RNA

Contigs

CONTIG 12	(2 clones)		
SSH2-1 h07	321	Expect = 6e-095 Identities = 240/257 (93%)	Triticum aestivum 28S ribosomal RNA gene, partial sequence gi|15982657|gb|AY049041.1|
SSH2-1 a01 In SSH2-1 h07	308	Expect = 1e-089 Identities = 201/210 (95%)	Triticum aestivum 28S ribosomal RNA gene, partial sequence gi|15982657|gb|AY049041.1|
SSH2-9 c08	351	Expect = 5e-077 Identities = 227/249 (91%)	Triticum aestivum 28S ribosomal RNA gene, partial sequence gi|15982657|gb|AY049041.1|
CONTIG 58	(15 clones)		
REPRESENTATIVE			
SSH2-7 h09	503	Expect = 0.0 Identities = 459/478 (96%)	Rye 26S rRNA 3' end and 18S rRNA, 5' end gi|169834|gb|M37231.1|RYENORR1
SSH2-10 c01	666	Expect = 0.0 Identities = 607/620 (97%)	Rye 26S rRNA 3' end and 18S rRNA, 5' end gi|169834|gb|M37231.1|RYENORR1
SSH2-7 b06	838	Expect = e-109 Identities = 376/432 (87%)	Rye 26S rRNA 3' end and 18S rRNA, 5' end gi|169834|gb|M37231.1|RYENORR1
CONTIG 59	(10 clones)		
REPRESENTATIVE			
SSH2-8 g11	344	Expect = e-150 Identities = 291/296 (98%)	Rye 26S rRNA 3' end and 18S rRNA, 5' end gi|169834|gb|M37231.1|RYENORR1
SSH2-6 g07	473	Expect = 0.0 Identities = 436/448 (97%)	Gunnera manicata 26S ribosomal RNA gene, partial sequence gi|22595023|gb|AF389250.1|

SSH Adaptors

Singletons

SSH2-1 a04	300	Expect = 0.27 Identities = 25/26 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-1 d08	180	Expect = 0.60 Identities = 24/25 (96%)	EST from a gravity versus microgravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103472935|emb|CT979319.1|
SSH2-1 e08	92	Expect = 0.068 Identities = 25/26 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-1 e09	311	Expect = 1.1 Identities = 24/25 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-1 e10	66	Expect = 0.69 Identities = 20/20 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103484086|emb|CT989439.1|
SSH2-1 g06	81	Expect = 0.91 Identities = 20/20 (100%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6908 genomic sequence gi|109390333|gb|DQ518948.1|
SSH2-1 g11	41	Expect = 0.079 Identities = 21/21 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483847|emb|CT990395.1|
SSH2-2 b03	390	Expect = 5.5 Identities = 20/20 (100%)	Sesbania drummondii clone SSH-51_01_C09_T3 mRNA sequence19 gi|99126314|gb|DQ465804.1|
SSH2-2 c02	203	Expect = 0.17 Identities = 25/26 (96%)	EST from a gravity versus microgravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103472935|emb|CT979319.1|
SSH2-2 f11	217	Expect = 2.9 Identities = 20/20 (100%)	Crassostrea gigas BAT1 homolog mRNA, complete cds gi|33337642|gb|AF075691.1|
SSH2-3 b07	273	Expect = 0.95 Identities = 24/25 (96%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6653_6821_etc genomic sequence gi|109390341|gb|DQ518956.1|
SSH2-3 h01	262	Expect = 0.058 Identities = 23/23 (100%)	Sesbania drummondii clone SSH-40_01_C12_T3 mRNA sequence gi|99126125|gb|DQ465793.1|
SSH2-3 h11	44	Expect = 0.36 Identities = 20/20 (100%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6908 genomic sequence gi|109390333|gb|DQ518948.1|
SSH2-5 b02	236	Expect = 0.81 Identities = 21/21 (100%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6908 genomic sequence gi|109390333|gb|DQ518948.1|
SSH2-5 c02	54	Expect = 3e-005 Identities = 48/54 (88%)	Sesbania drummondii clone SSH-31_01_B08_T3 mRNA sequence gi|99125943|gb|DQ465784.1|
SSH2-5 d06	85	Expect = 0.016 Identities = 23/23 (100%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6908 genomic sequence gi|109390333|gb|DQ518948.1|

SSH2-5 e06	458	Expect = 0.002 Identities = 29/30 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-5 e11	347	Expect = 0.078 Identities = 23/23 (100%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6908 genomic sequence gi|109390333|gb|DQ518948.1|
SSH2-5 e12	402	Expect = 0.001 Identities = 29/30 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-5 f12	214	Expect = 0.003 Identities = 25/25 (100%)	Sesbania drummondii clone SSH-51_01_C09_T3 mRNA sequence gi|99126314|gb|DQ465804.1|
SSH2-5 g04	375	Expect = 2e-005 Identities = 29/29 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483637|emb|CT990185.1|
SSH2-5 g08	428	Expect = 0.002 Identities = 29/30 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-5 h11	388	Expect = 0.006 Identities = 28/29 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-6 a11	537	Expect = 0.002 Identities = 29/30 (96%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103482887|emb|CT989239.1|
SSH2-6 a12	374	Expect = 0.001 Identities = 26/26 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103484083|emb|CT989436.1|
SSH2-6 b11	799	Expect = 3e-006 Identities = 43/47 (91%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103482303|emb|CT988638.1|
SSH2-6 b12	531	Expect = 3e-005 Identities = 29/29 (100%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483637|emb|CT990185.1|
SSH2-7 h12	380	Expect = 0.001 Identities = 32/34 (94%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103482819|emb|CT989203.1|
SSH2-11 a06	304	Expect = 0.068 Identities = 26/27 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-11 e05	380	Expect = 0.086 Identities = 26/27 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-11 f07	279	Expect = 0.001 Identities = 29/30 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-11 f12	251	Expect = 0.056 Identities = 26/27 (96%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103481894|emb|CT988228.1|
SSH2-11 h02	482	Expect = 3e-005 Identities = 29/29 (100%)	Eucalyptus globulus EST from juvenile versus mature wood and mature versus juvenile wood SSH libraries gi|103482308|emb|CT988643.1|
SSH2-11 h06	473	Expect = 1.7 Identities = 21/21 (100%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6908 genomic sequence gi|109390333|gb|DQ518948.1|
SSH2-11 h11	461	Expect = 0.027 Identities = 27/28 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-12 b10	219	Expect = 0.048 Identities = 23/23 (100%)	Sesbania drummondii clone SSH-40_01_C12_T3 mRNA sequence gi|99126125|gb|DQ465793.1|
SSH2-12 e09	453	Expect = 0.41 Identities = 25/26 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-12 f02	339	Expect = 0.001 Identities = 26/26 (100%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6653_6821_etc genomic sequence gi|109390341|gb|DQ518956.1|
SSH2-12 f04	598	Expect = 0.009 Identities = 28/29 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-12 f09	227	Expect = 0.003 Identities = 25/25 (100%)	Sesbania drummondii clone SSH-40_01_C12_T3 mRNA sequence gi|99126125|gb|DQ465793.1|
SSH2-12 f10	453	Expect = 0.007 Identities = 28/29 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-12 g02	516	Expect = 0.12 Identities = 26/27 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|

SSH Adaptors

Contigs

CONTIG 13	(2 clones)		
SSH2-2 c02	203	Expect = 0.17 Identities = 25/26 (96%)	EST from a gravity versus microgravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103472935|emb|CT979319.1|
SSH2-1 d01	453	Expect = 6.4 Identities = 20/20 (100%)	PREDICTED: Rattus norvegicus deoxyribonuclease 1-like 2 (predicted)(Dnase1l2_predicted), mRNA gi|109490312|ref|XM_001055139.1|

Vector Sequences

Singletons

SSH2-3 g12	440	Expect = 6e-068 Identities = 158/166 (95%)	Cloning vector psiLentGene Hygromycin, complete sequence gi|45655413|gb|AY508734.1|
SSH2-7 c11	791	Expect = e-131 Identities = 305/320 (95%)	Cloning vector psiLentGene Hygromycin, complete sequence gi|45655413|gb|AY508734.1|
SSH2-7 g10	811	Expect = 0.0 Identities = 506/532 (95%)	Cloning vector psiLentGene Basic, complete sequence gi|45655410|gb|AY508731.1|
SSH2-10 a06	895	Expect = 7e-094 Identities = 271/298 (90%)	Cloning vector psiLentGene Hygromycin, complete sequence gi|45655413|gb|AY508734.1|

Vector Sequences

Contigs

CONTIG 7	(3 clones)		
SSH2-11 h12	482	Expect = 0.007 Identities = 28/29 (96%)	EST from a microgravity versus gravity subtracted library from Eucalyptus globulus seedlings grown under 14, 28 and 45 days of clinostat conditions gi|103483277|emb|CT989825.1|
SSH2-11 h10 In SSH2-11 h12	464	Expect = 0.11 Identities = 23/23 (100%)	Bordetella parapertussis strain Bpp5 subtractive hybridization product 6653_6821_etc genomic sequence gi|109390341|gb|DQ518956.1|
SSH2-5 b12	788	Expect = 4e-030 Identities = 139/159 (87%)	Cloning vector psiLentGene Hygromycin, complete sequence gi|45655413|gb|AY508734.1|
CONTIG 57	(6 clones)		
REPRESENTATIVE			
SSH2-7 f11	721	Expect = e-170 Identities = 392/410 (95%)	Cloning vector psiLentGene Basic, complete sequence gi|45655410|gb|AY508731.1|