

Final Report ICSB Project 99-15
Australian Component

Genetic diversity within Sugarcane yellow leaf virus

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EXECUTIVE SUMMARY

Sugarcane yellow leaf virus (SCYLV) is widespread in many sugarcane growing countries of the world. The aim of this study was to determine the extent of genomic variation in SCYLV isolates from various countries. Isolates were obtained from Mauritius, Reunion, South Africa, Australia, Papua New Guinea, Hawaii, U.S.A. and Brazil.

Four regions of the SCYLV genome (ORF 1, Replicase, Coat Protein and Readthrough) were analysed for variation using both RFLP analysis and sequence comparisons. Of the fifty isolates used, several did not produce RT-PCR amplicons in one or more of the regions covered, suggesting variation in regions where the primers bind. Of the amplicons produced across the four regions studied, RFLP analysis and sequencing results revealed the Coat Protein (CP) region to be the most conserved, followed by the Replicase (REP) region. These areas should be targeted for diagnosis of SCYLV and for use in viral mediated transgenic resistance in sugarcane varieties.

Phylogenetic studies of the nucleotide and protein sequences of the four regions covered were performed using eighteen isolates. Representative isolates from each country were used where possible. In a second round of phylogenetic studies, covering the REP and CP regions, nine isolates from North, South and Central America, sequenced by our American collaborators on this project, were included. Variation in nucleotide and protein sequences revealed that many haplotypes of SCYLV exist across the countries tested. Most isolates from the various countries are very closely related across all four regions. Phylograms produced from REP and CP sequences in Phylogeny study #2 revealed that isolates from Hawaii and Australia tend to group together as do isolates from Mauritius and Reunion. Phylogenetic analyses on the sequences used in this study have not identified any significant variants of SCYLV.

In conclusion, we recommend that the YLS111 and 462 RT-PCR primers originally developed by Mike Irey and colleagues continue to be used for routine SCYLV diagnosis. Also, the viral coat protein and replicase regions being the most conserved, should be targeted in research to genetically engineer resistance to SCYLV.

INTRODUCTION

A leaf-yellowing symptom of sugarcane (*Saccharum* L. interspecific hybrids) was first noted in Hawaii in 1988 (Schenck, 1990). Yellow leaf syndrome (YLS) has since been reported from Brazil, other countries of Central and South America, mainland USA, Australia, Mauritius, Reunion and various countries on the African continent (1,2,3,4,5,6,7,8,9).

Although a phytoplasma has been associated with YLS symptoms (9), the association of these symptoms with a virus, referred to as Sugarcane yellow leaf virus (SCYLV) has been more widely studied. SCYLV particles have been isolated from plants with YLS. Subsequent aphid transmission of these virus particles to YLS free plants resulted in the newly infected plants showing YLS symptoms (10).

SCYLV appears to be a new member of the family *Luteoviridae* that probably evolved by inter-species recombination between polerovirus, luteovirus and enamovirus members (11,12). To date, there has been no identification of strains of this virus, with only two isolates of SCYLV extensively studied. One is an isolate found in variety CP65-357 from Florida, which has been fully sequenced by two independent laboratories (11,12). The other is an isolate from Brazil infecting cultivar SP71-6163 (13), for which full genomic sequence is not available.

There is variation in the nature of YLS symptoms observed in SCYLV-infected sugarcane plants at a wide range of locales. Whether this variation in symptoms is due to genomic variation of the virus or variation in sugarcane varieties and/or farming practices is unknown (14). The aim of this study was to determine the extent of genomic variation in SCYLV isolates from various countries.

Areas of the SCYLV genome targeted for examination in this survey were the RNA-dependant RNA polymerase, also known as the replicase (REP), Coat Protein-Readthrough (CP-RT), ORF1 (possible Protease) and ORF5 (Readthrough protein, RT). Our American collaborators also examined the untranslated region between the REP and CP-RT(15). The replicase and coat protein regions are often used in the production of virus resistant plants (16). The efficacy of viral mediated resistance (VMR) could be reduced if extensive genetic variation occurs in either of these regions of SCYLV isolates. The ORF1 and ORF5 regions were also studied because they are long open reading frames enabling substantial comparisons between nucleotide sequences and their translated protein products.

MATERIALS AND METHODS

Sampling and RNA Extraction

Varieties collected for this study were primarily from 'Old World' countries (Table 1), though samples from the USA and Hawaii were also included. The basal portion of the oldest unfurled leaf whorl was sampled and RNA extracted from 100mg of fresh tissue using the Qiagen RNeasy Plant Kit as per the manufacturers instructions.

SCYLV Screening by RT-PCR

SCYLV specific primers YLS 111 and YLS 462 (17) were used in a RT-PCR assay. These primers bind in the coat protein region of SCYLV and enable the amplification of a 352bp product in RT-PCR. The Titan one tube RT-PCR System (Roche Diagnostics) was used for the RT-PCR mix with 0.5µL RNA extract added to each 25µL reaction.

Cycling Parameters used with YLS111/YLS462 primers:

50°C/30mins,94°C/2mins	x1
94°C/30secs,55°C/30secs,68°C/45secs(+ 5 secs/cycle)	x40
94°C/30secs,55°C/30secs,68°C/10mins	x1
4°C soak	

Amplification of other areas of the SCYLV genome

A selection of SCYLV positive varieties were used for RFLP analysis (Table 2). All RT-PCRs' were performed in duplicate using the Titan One Tube RT-PCR System. One microlitre of RNA extract was used per 50µL RT-PCR reaction. Primers for each region were designed from the complete sequence of SCYLV (11,12). The binding position of each primer refers to the position in the complete SCYLV genome.

ORF1 (1621bp product):

Forward (242): ORF1START 5'-ATG GCC CCA ACA CTC CCG TTT ACA-3'
Reverse(1862): 160R640R 5'-GAA TCA ACT GCG AGA CGA TG-3'

Cycling Parameters:

54°C/60mins,94°C/2mins	x1
94°C/15secs,61°C/2mins,68°C/2mins	x30
94°C/15secs,61°C/2mins,68°C/10mins	x1
4°C soak	

REPLICASE (1212bp product):

Forward (1518): OFM323 5'-CAG ACA TTG CTG ATT AC-3'
Reverse (2729): OFM359 5'-GCT CTC CAC AAA GCT ATC T-3'

Cycling Parameters:

50°C/60mins,94°C/2mins	x1
94°C/15secs,52°C/2mins,68°C/2mins	x30
94°C/15secs,52°C/2mins,68°C/10mins	x1
4°C Soak	

COAT PROTEIN-READTHROUGH (686bp product):

Forward (3667): OFM336 5'-GCT CAC GAA GGA ATG TCA G-3'
Reverse (4352): OFM361zb 5'-TGT TTT CAC GAT GTA GTT C-3'
not used OFM361 G

(note: OFM361zb has one base change compared to OFM361. This is marked above)

Cycling Parameters:

53°C/60mins,94°C/2mins	x1
94°C/15secs,59°C/2mins, 68°C/2mins	x30
94°C/15secs,59°C/2mins, 68°C/10mins	x1
4°C Soak	

READTHROUGH (1300bp product):

Forward (4367): 104R613R	5'-ATA TCT AGA TGT GGG TCC GC-3'
Reverse (5666): 3Prime2R	5'-GGA GGA GGA AGA TTT CGG TG-3'

Cycling Parameters:

50°C/30mins,94°C/2mins	x1
94°C/30secs,59°C/30secs,68°C/45secs(+5secs/cycle)	x40
94°C/30secs,59°C/30secs,68°C/10mins	x1
4°C Soak	

Analysis and Preparation of RT-PCR products:

The various RT-PCR reactions were fractionated by agarose gel electrophoresis, stained with ethidium bromide and detected by transillumination with UV light.

The amplicons were gel purified (Qiagen Mini-Elute columns or Ultrafree-DA columns from Millipore) as per manufacturers instructions.

Restriction enzyme digest of amplicons:

The gel purified amplicons were digested with the following enzymes:

ORF1:	Hha1
Replicase:	Sau3A1 and Taq1 in separate single digests
Coat Protein:	Hae111
Replicase:	Hae111

The digested amplicons were fractionated by electrophoresis through 2.5% agarose gels. Digest bands were visualised by transillumination with UV light after staining with Ethidium Bromide.

Cloning and Sequencing:

Gel cleaned amplicons were sequenced directly or cloned into either the PCR2.1 vector (Invitrogen) or pGEM-T Easy vector (Promega). SCYLV RT-PCR products were amplified from 18 SCYLV infected sugarcane varieties (Table 3a). These amplicons were sequenced and subjected to further phylogenetic analysis.

Due to the large size of the amplicon products, internal sequencing primers were designed to allow sequence to be obtained across the full length of the amplicons (see Figure 1).

Big Dye Terminator (Perkin Elmer) chemistry was used in the sequencing reactions. The sequence reactions were analysed on either ABI 377, 3700 or MD Mega BACE (capillary) automatic DNA sequencers at the Australian Genomic Research Facility.

Sequence analyses was performed using the Vector NTI suite (Informax).

Phylogenetic analysis:

Consensus sequences of each isolate were uploaded into ANGIS (Australian National Genomic Information Service) for subsequent phylogenetic analysis (Phylogeny study #1). Nine consensus sequences (covering the Replicase and CP-RT regions) from the Final Report from the Mirkov Lab (ICSB Project 99-15) were also uploaded into the ANGIS file for this project (Table 3b). Studies using these sequences in conjunction with the sequences from Phylogeny study #1 are referred to as Phylogeny study #2. Consensus sequences from each region were edited so that only coding regions were used in all the phylogenetic analysis (Figure 2).

ClustalW multiple sequence alignments (using 1000 multiple data sets) were performed on both the DNA and their respective Protein sequences.

These multiple sequence alignments were bootstrapped (1000 multiple data sets) using the program Eseqboot.

Bootstrapped sequences were entered into the following phylogeny inference programs (1000 multiple data sets used in each):

Maximum Parsimony Programs: EDNAPARS AND EPROTPARS

Distance Program: EDNADIST(Jukes-Cantor Model)
EPROTDIST(Dayhoff PAM matrix)

Resulting trees from the EDNAPARS AND EPROTPARS programs were entered directly into the program ECONSENSE to obtain a consensus tree file showing the most likely tree supported by the data.

The matrix outputs from the EDNADIST and EPROTDIST programs were entered into a neighbour joining algorithm, ENEIGHBOR (1000 multiple data sets used). Resulting trees from this were entered into the program ECONSENSE as mentioned above.

Consensus trees were drawn using the program TreeView-Win32 (18).

The four multiple sequence alignments (produced by the ClustalW program) from Phylogeny study #2 were also entered into a simple distance program (in the ANGIS suite) as follows:

DISTANCE: Nucleic Acid used the Jukes-Cantor model.
Protein used the Kimura model (similar to the Dayhoff model used in EPROTDIST).

The results from the DISTANCE program above were entered into the “treegrowing” program GROWTREE (Neighbour joining algorithm). The resulting phylogram trees were viewed using the TreeView-Win32 program mentioned above.

RESULTS

SCYLV screening by RT-PCR:

The result of SCYLV screening of varieties collected from various locales is listed in Table 1. Of the many positives that were identified, a selection were not used in further studies due to either the poor quality of the sample or the fact that the RT-PCR products were too weak to be useful in RFLP or sequence analysis. SCYLV positives not included in RFLP or sequence analysis are 69 = Unknown variety from Thailand, 74 = Pseudo Pokkah Boeng , 75 = RP193-67 and 76 = Q124. A breakdown of the number of positives versus the number of samples tested for each country is listed in Table 6. Note that SCYLV positives from Australia used in this diversity study were already known to be positive from previous projects. Weather hampered the collection of more varieties of canes throughout Australia at the commencement of this project. The number of positives in Table 6 refers to how many were used in the RFLP analysis.

Amplicons for RFLP Analysis:

Various isolates did not produce amplicons in one or more of the RT-PCR areas covered (Table 2). Other amplicons, marked “Yw” in Table 2, were repetitively produced in very low concentrations and were hence not able to be used in RFLP or sequence analysis.

There was variation in the number of amplicons produced in each RT-PCR region. Out of the total of 50 (Table 2), the most amplicons produced were in the CP-RT region, with 47 isolates amplifying the desired 686bp product. The ORF1 and REP regions produced 41 and 42 amplicon products respectively. The RT section had the most RT-PCR negatives, with only 38 amplicon products detected.

RFLP analysis:

The RFLP patterns obtained from each isolate in each of the four RT-PCR regions covered are listed in Table 4. RFLP patterns have been numbered so that pattern 1 is always the pattern given by the fully sequenced isolate #49(CP65-357). The countries the isolates are from, and the RFLP patterns they produced are summarised in Table 5a-5e. The number of patterns reads across the table, the countries read down the columns. Shaded cells are where the country had an isolate which produced the corresponding RFLP pattern. It is important to note that although the isolates from the USA showed a lot of variation in most regions, there were considerably more isolates from this area used in the RFLP analysis than any other country (Table 6) ie. 16 from USA compared to 7 from Hawaii, 6 from Reunion and Taiwan etc.

Least variation in isolates occurred in the CP-RT region with only 3 patterns produced from the 43 amplicons used. Of these, 40 isolates showed RFLP pattern #1. One isolate from the USA (10=CP89-2143) produced a unique RFLP pattern #2. RFLP pattern#3 was shared by one isolate from the USA (12=CP92-1641) and the only South African isolate (35=N30). It is interesting to note that isolate 10 which produced the unique RFLP pattern #2 in the CP-RT region, also produced unique RFLP patterns in both the Sau3AI and TaqI digests of the REP region and did not produce any amplicons in both the ORF1 and RT regions. The USA isolate #12 which shows RFLP pattern #3 in the CP-RT region has grouped in with the USA isolate 49 (fully sequenced isolate Mirkov) in all the other amplicon areas (Table 4).

The REP region was the only region to undergo two separate enzyme digests, with 12 patterns produced from the Sau3A1 digest and 13 from the Taq1 digest. The pattern groupings resulting from these digests were different for each enzyme. For example, isolates 1,2,3 & 5 grouped with #49 (ie RFLP pattern#1) in the Sau3AI digest, but did not group with #49 in the Taq1 digest. Isolate #20 (H78-3606) gave two patterns from duplicate RT-PCR's (20a & 20b) in the Sau3AI digest, but these duplicates only produced one pattern in the Taq1 digest. The opposite occurred with isolate #22 (H83-7206), which produced only one pattern in the Sau3A1 digest, but two in the Taq1 digest. As mentioned in the material and methods, each gel cleaned RT-PCR product was split in two with one aliquot used for the Sau3AI digest and the other for the TaqI digest.

The ORF1 and RT regions displayed 13 and 9 RFLP patterns respectively. In each case, as indeed across all the amplicon areas, most isolates grouped with the fully sequenced USA isolate #49. Several unique patterns were produced in both areas. There was no one isolate that produced a unique pattern in both the ORF1 and the RT regions. Some isolates grouped with others in both regions (Table 4). One such group contains isolates 20,21,22,23 & 24 which stayed together in the ORF1, CP and RT regions, but differed in both digests in the REP region. The only isolates that grouped together across all four amplicon regions and all five digestions were isolates #13,14 & 49 (CP88-1508, CP88-1540 & CP65-357 respectively).

Sequencing and Phylogeny:

Isolates sequenced and used in subsequent phylogeny studies are listed in Tables 3a & 3b. Most consensus sequences obtained covered the full length of the amplicons. Two deletions were found in the consensus sequences. One is a 48bp (16 amino acid) deletion in the ORF1 region of isolate 49 (CP65-357, sequencing reference: CPam1b). This deletion corresponds to position 1686-1733 in the total SCYLV sequence. The other deletion is in the RT section of isolate #6 (CP88-1409, sequencing reference: USA2b) which covers 84bp (28 amino acids) and corresponds to position 5138-5221 in the total SCYLV sequence. These deletions are not seen in the other consensus sequences obtained from each isolate (ie. Cpam1a and USA2b).

Phylogeny Study #1

The multiple sequence alignments (Appendix A) of both the DNA and protein sequences were used to ascertain the overall sequence variation in each region (Table 7). Least variation was seen in the CP-RT region followed by the REP region. The CP-RT region showed 94.2% similarity in the nucleotide sequence and 91.6% similarity in the protein sequence (92.41% without conserved amino acid changes). The REP region exhibited 91.01% similarity in the nucleotide sequence and 88.40% similarity in the protein sequence (91.54% without conserved amino acid changes). More sequence variation was shown in the ORF1 region, with the RT section showing the most variation across the four areas covered (Table 7). It is evident from the percentage similarity differences that many of the nucleotide changes are not silent mutations, but result in an altered amino acid sequence. Many of these amino acid changes are however conserved changes. This is particularly evident in the RT area, which showed 85.14% similarity in the peptide sequence which converted to 91.74% when conserved amino acid changes were not included in the calculations.

As can be seen in Table 3a, 22 sequences from the ORF1 region, 16 from the REP region, 17 from the CP-RT region and 17 from the RT region were used in the first phylogenetic analysis. Four individual consensus trees were produced for each amplicon area covered as follows:

Maximum Parsimony Programs: DNA and Protein

Distance/Neighbour Joining Programs: DNA and Protein

Unrooted consensus trees produced within each RT-PCR region using either phylogeny method mentioned above were comparable, therefore I have included one representative tree for each nucleotide and protein sequence (Figures. 3-10).

Note that these trees only include the probabilities of a branch occurring at a particular spot. Lengths of the branches are not related to the degree of sequence variation between particular isolates. Branching values of less than ~700 are not considered to be statistically significant. Groupings, which continue from branches with values of less than 700, are not necessarily valid representations of the data. Nonetheless, some general observations can be made from the unrooted trees generated.

The ORF 1 region shows 3 main groups in the nucleotide and protein sequences as follows:

Group1: isolates from Hawaii, Australia & USA (Haw1, Haw2, Aus1, Aus2, CPam1b)

Group2: isolates from Mauritius and Reunion (Maur1, Maur2, Reun1, Reun2)

Group3: remaining isolates from USA, Brazil, Taiwan, South Africa (USA1, USA2, CPaus1, CPam1, Braz1, Braz2, Taiw1, Taiw2, SA1)

This is also true in the nucleotide consensus trees in the REP and CP-RT regions. The only difference being that the USA isolate (CPam1b) from Group1 in the ORF1 region now clusters with Group3 in both the REP and CP-RT regions. Note too that only one isolate from Mauritius (Maur2) was available for use in the REP region compared to two isolates in the other regions. The three groupings are not as evident in the REP and CP-RT protein consensus trees.

The RT region nucleotide consensus tree produced four groupings. Group1 contains the isolates from Hawaii and Australia like Group1 previously mentioned. Group2 consists of the isolates from Mauritius and one Reunion isolate, Reun1. Reunion isolate Reun2 has grouped with isolates which were in Group3 in the previously mentioned amplicon regions. A new group, Group4, consists of three isolates, Cpm1, Cpaus1, USA2a & USA2b which previously clustered with Group3. The protein consensus tree for the RT has not got this fourth grouping. Instead a grouping which matches Group 3 of the Orf1, REP and CP-RT regions is produced. The only difference here is that the isolate Reun2 is found within this Group3, not Group2 as before.

Phylogeny Study #2

The nine American isolates in Table 3b (sequences from our American collaborators) were included in a second round of phylogeny studies of the REP and CP-RT regions. For ease of comparisons, these will be called REP₂ and CP-RT₂ respectively. Four

individual consensus trees were produced for each region as before i.e.2 methods used on both the nucleotide and protein sequences. In the REP region, the results were not the same between the methods, therefore we have included all four unrooted consensus trees (Figures 11-14). Results between the two methods were comparable in the CP-RT region, so only 1 consensus tree for the nucleotide and protein sequence respectively are included (Figures 15 & 16). Again, many of the branchings are not statistically significant (ie. values less than 700), hence the following observations are speculative only.

In the nucleotide sequence consensus trees of the REP₂ and CP-RT₂, there are still three main groupings as listed above, though the branchings are not as clear as those seen in the first phylogeny study of these regions (Figures 5 & 7). Any groupings are very obscure in all protein consensus trees of the Replicase₂ and CP-RT₂ alignments (Figures 13,14 & 16).

The four phylogenetic trees produced from the DISTANCES/GROWTREE method can be seen in Figures 17-20. Unlike the consensus trees produced from the other programs, the branch lengths of these trees reflect the calculated distances of the isolate sequences. The tree representing the nucleotide sequences of the REP region shows that most isolates are very closely related with isolates from Australia and Hawaii forming a slightly removed cluster and isolates from Mauritius and Reunion clustering in a group a little more distant again. These clusters reflect the three groupings observed in the REP nucleotide consensus trees. The distance of these clusters are reduced in the REP protein phylogenetic tree (Figure 18). Note that the C3 isolate (Colombia) is quite distant to the rest of the isolates, even further removed than the Mauritius/Reunion cluster.

This C3 isolate is also the most distant in both the CP-RT nucleotide and protein phylogenetic trees. The Australia/Hawaii cluster remains together in both these trees, though the Mauritius/Reunion cluster merges with the other isolates in the CP-RT protein phylogenetic tree (Figure 20).

DISCUSSION

SCYLV appears to be widespread throughout sugarcane growing countries of the world. We found SCYLV positive varieties from each country tested in this survey (Table 1). Variation in the amplifiable regions for each isolate (Table 2) and differences in the RFLP patterns of the amplicons chosen for further analysis (Table 2, 4) showed that genomic variation was present in SCYLV isolates. Many RFLP patterns from the various amplicon regions were shared by isolates from different countries (Table 5a-e). Unique patterns from individual isolates within each amplicon region were also obtained. These isolates may be useful for further studies into SCYLV variation. The use of RFLP analysis to detect variability in isolates has its limitations as restriction enzymes target only a few nucleotides of a larger sequence area. Depending on the enzyme used, results obtained can be quite different. For example, the replicase amplicons in this survey were digested with both Sau3AI and TaqI. producing different isolate patterns and groupings (Table 4). RFLP analysis is useful when comparing a new isolate to a set standard or standards with known patterns. As more sequence information is gathered from additional isolates,

restriction enzymes other than the ones used here may be more useful for identifying variation in regions of interest.

The CP-RT region showed the least variation in RFLP patterns (Table 5d). This region also produced the most amplicons from the SCYLV samples used (Table 2). The coat protein region is known to remain quite conserved in the *Luteoviridae* (19). This region remains the area of choice for detection of SCYLV isolates.

Sequence comparisons of the isolates chosen in each amplicon area showed there was variation evident at both the nucleotide and protein level (Table 7). Many of the nucleotide changes were not silent mutations, resulting in corresponding amino acid changes. Many of these amino acid changes were conserved changes which, it is assumed, are not significantly deleterious to the functioning of the proteins. Phylogenetic studies of the nucleotide and protein sequences of the four amplicon regions covered revealed that although many haplotypes of SCYLV were detected, no significant variation in SCYLV isolates could be identified by our analysis. As mentioned at length in the discussion of the final report of our American collaborators (15), RNA viruses are thought to naturally occur as “quasispecies”. That is, any one viral clone consists of a dynamic population of viral mutants. Differences in RFLP patterns from duplicate amplicons of the same isolate could be due to variations of that isolate within the plant. The possibility of errors introduced by the RT-PCR procedure should not be discounted (the Titan RT-PCR system used in this study contains the Pwo polymerase enzymes which has proofreading capabilities which should minimise this problem) nor should variations observed in duplicate nucleotide and protein sequences caused by a dynamic isolate population. Large deletions like that seen in the ORF1 region (48bp) and RT (84bp) could reflect a replicative moment frozen in time or a true genetic variation in individual virions of the isolate. Of course, in all the above scenarios there is also the possibility of more than one viral isolate infecting a plant at any one time (16).

Although our consensus trees (Figures 3-16) have few statistically significant branching values (ie. over 700), some speculative general observations can be made. Groupings appear across the four amplicon regions of the isolates tested in the first phylogeny study. These groupings are more evident from the nucleotide sequence than from the corresponding protein sequences. Group 1 consists of isolates from Hawaii and Australia, Group 2 of isolates from Mauritius and Reunion and Group 3 of isolates from the other countries tested.

In the second phylogeny study, which included the nine REP and CP-RT sequences analysed by our American collaborators (Table 3b), the groupings were less apparent. Phylogenetic trees in phylogeny study #2 (Figures 17-20) showed that isolates from Australia and Hawaii (Group 1) were slightly distant to the main body of isolates (corresponding to Group 3 above) and isolates from Mauritius and Reunion (Group 2) were further distant again. The C3 isolate (from Colombia; 15), branching out near isolates from Mauritius and Reunion, is most distant from all other isolates in both the nucleotide and protein phylograms of the CP-RT region, and in the protein phylogram of the REP region. This isolate would be useful in further SCYLV phylogeny studies, as would isolates from Mauritius and Reunion as they represent the most distant group of isolates identified to date. We did not find that the C-population mentioned in our collaborators final report grouped out independently of

the other isolates. The increased number of isolates used in our REP and CP-RT phylogeny study #2 (25 & 26 respectively) compared to our collaborators (9 for each) has shown that with an increased sample population the borders between sub and superpopulations are merged. Though more phylogenetic analysis is required on the sequences used in this study (and on other sequences in the future), it appears from the data available at this point in time that the population of SCYLV isolates tested represent variable but not significantly different genotypes.

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TABLE 1: VARIETIES TESTED FOR SCYLV BY RT-PCR

Ref #	ORIGIN	VARIETY	YLS111-462
1	Brazil	SP77-5181	positive
2	Brazil	SP79-2233	negative
3	Brazil	SP80-1816	negative
4	Brazil	SP80-1836	negative
5	Brazil	SP80-1842	negative
6	Brazil	SP80-185	negative
7	Brazil	SP80-3280	negative
8	Brazil	SP81-1763	positive
9	Brazil	SP81-3250	positive
10	Brazil	SP83-5073	positive
11	USA	CP81-1405	positive
12	USA	CP88-1409	positive
13	USA	CP88-1508	positive
14	USA	CP88-1540	positive
15	USA	CP88-1762	positive
16	USA	CP89-2143	positive
17	USA	CP92-1213	positive
18	USA	CP92-1641	positive
19	USA	CP92-1666	positive
20	USA	HCP85-845	inconclusive
21	USA	HCP91-555	positive
22	USA	LCP85-384	positive
23	USA	LCP86-454	positive
24	USA	TCP87-3388	positive
25	USA	TCP89-2377	positive
26	Hawaii	H78-3567	positive
27	Hawaii	H78-3606	positive
28	Hawaii	H78-7750	positive
29	Hawaii	H83-7206	positive
30	Hawaii	H84-0778	positive
31	Hawaii	H85-7362	positive
32	Hawaii	H87-4094	positive
33	Hawaii	H87-4319	negative
34	Mauritius	M1176-77	negative
35	Mauritius	M1551-80	negative
36	Mauritius	M1658-78	positive
37	Mauritius	M2350-79	positive
38	Mauritius	M261-78	negative
39	Mauritius	M52-78	positive
40	Reunion	R84-0075	positive

Ref #	ORIGIN	VARIETY	YLS111-462
41	Reunion	R84-0408	positive
42	Reunion	R84-0472	positive
43	Reunion	R85-0252	positive
44	Reunion	R85-0348	positive
45	Reunion	R85-0449	negative
46	Reunion	R85-0579	negative
47	Reunion	R85-0699	negative
48	Reunion	R85-0991	negative
49	Reunion	R85-1102	positive
50	Reunion	R85-1157	negative
51	Reunion	R85-1238	negative
52	Reunion	R85-1334	positive
53	South Africa	N23	positive
54	South Africa	N24	negative
55	South Africa	N25	negative
56	South Africa	N26	negative
57	South Africa	N28	negative
58	South Africa	N29	negative
59	South Africa	N30	positive
60	South Africa	N31	negative
61	Taiwan	ROC11	positive
62	Taiwan	ROC12	positive
63	Taiwan	ROC13	positive
64	Taiwan	ROC14	positive
65	Taiwan	ROC15	positive
66	Taiwan	ROC16	positive
67	Taiwan	ROC17	negative
68	PNG	Q146	positive
69	Thailand	unknown	positive
70	NC Hawaii ¹	Braz3381	positive
71	NC Hawaii ¹	H38	positive
72	NC Hawaii ¹	BSM ²	positive
73	NC Hawaii ¹	IJ76-361	positive
74	Australia	PPB ³	positive
75	Australia	RP193-67	positive
76	Australia	Q124	positive
77 ⁴	Australia	VMC71-238	positive
78 ⁴	Australia	VMC71-238	positive
79 ⁵	USA	CP65-357	positive
80 ⁵	USA	CP65-357	positive

1. NC Hawaii = Noble canes from Hawaii

3. PPB = Pseudo Pokkah Boeng

5. Isolate used in complete sequencing of SCYLV (11,12)

2.BSM = Brash Stripe Mutant

4.Same variety collected at different time and place

TABLE 2: RT-PCR RESULTS OF SCYLV POSITIVE SAMPLES USED IN SURVEY

No.	VARIETY	ORF1 (242-1862) ORF1START/ 160R640R 1621bp	REP (1518-2729) OFM359/ OFM323 1212bp	CP-RT (3667-4352) OFM336/ OFM361 686bp	RT (4367-5666) 104R613R/ 3PRIME2REV 1300bp
1	SP77-5181	Y	Y	Y	Y
2	SP81-1763	Y	Y	Y	Y
3	SP81-3250	Y	Y	Y	Y
4	SP83-5073	Y	Y	Y	Y
5	CP81-1405	Y	Y	Y	NP
6	CP88-1409	Y	Y	Y	Y
7	CP88-1508	Y	Y	Y	Y
8	CP88-1540	NP	NP	Yw	NP
9	CP88-1762	Y	Y	Y	Y
10	CP89-2143	NP	Y	Y	NP
11	CP92-1213	Y	Y	Y	Y
12	CP92-1641	Y	Y	Y	Y
13	CP92-1666	Y	Y	Y	Y
14	HCP91-555	Y	Y	Y	Y
15	LCP85-384	Y	Y	Y	NP
16	CLP86-454	NP	NP	Yw	NP
17	TCP87-3388	NP	NP	Y	NP
18	TCP89-2377	NP	NP	Yw	NP
19	H78-3567	NP	NP	NP	NP
20	H78-3606	Y	Y	Y	Y
21	H78-7750	Y	Y	Y	Y
22	H83-7206	Y	Y	Y	Y
23	H84-0778	Y	Y	Y	Y
24	H85-7362	Y	Y	Y	Y
25	H87-4094	Y	Y	Y	Y
26	M1658-78	Y	Y	Y	Y
27	M2350-79	Y	NP	Y	Y
28	M52-78	NP	NP	NP	NP
29	R84-0075	Y	Y	Y	Y
30	R84-0408	Y	Y	Y	NP
31	R84-0472	Y	Y	Y	Y
32	R85-0252	Y	Y	Y	Y
33	R85-0348	Y	Y	Y	Y
34	R85-1102	Y	Y	Y	Y
35	N30	Y	Y	Y	Y

NP = no product amplified

Y = product amplified

Yw = weak product amplified

No.	VARIETY	ORF1 (242-1862) ORF1START/ 160R640R 1621bp	REP (1518-2729) OFM359/ OFM323 1212bp	CP-RT (3667-4352) OFM336/ OFM361 686bp	RT (4367-5666) 104R613R/ 3PRIME2REV 1300bp
36	ROC11	Y	Y	Y	Y
37	ROC12	Y	Y	Y	Y
38	ROC13	Y	Y	Y	Y
39	ROC14	Y	Y	Y	Y
40	ROC15	Y	Y	Y	Y
41	ROC16	Y	Y	Y	Y
42	2203A (PNG)	NP	NP	NP	NP
43	Braz3381	NP	Yw	Yw	NP
44	H38	Y	Y	Y	Y
45	Brash Stripe Mutant	Y	Y	Y	Y
46	IJ76-361	Y	Y	Y	Y
47	VMC71-238(OLD)	Y	Y	Y	Y
48	VMC71-238(NEW)	Y	Y	Y	Y
49	(CP65-357)FLA-TX	Y	Y	Y	Y
50	(CP65-357)SCYLV	Y	Y	Y	Y

NP = no product amplified

Y = product amplified

Yw = weak product amplified

TABLE 3a: VARIETIES USED IN PHYLOGENY STUDY #1

RT-PCR Ref.	VARIETY	Sequencing Ref.	ORF1	REP	CP-RT	RT
1	SP77-5181	Braz1	Y	Y	Y	Y
4	SP83-5073	Braz2	Y	Y	Y	Y
5	CP81-1405	USA1	YY	Y	Y	NC
6	CP88-1409	USA2	YY	Y	Y	YY
20	H78-3606	Haw1	Y	Y	Y	Y
25	H87-4094	Haw2	Y	Y	Y	Y
21	H78-7750	Haw3	Y	N	N	N
26	M1658-78	Maur1	YY	Y	Y	Y
27	M2350-79	Maur2	Y	N	Y	Y
30	R84-0408	Reun1	Y	Y	Y	Y
34	R85-1102	Reun2	Y	Y	Y	Y
35	N30	SA1	Y	Y	Y	Y
36	ROC11	Taiw1	Y	Y	Y	Y
37	ROC12	Taiw2	Y	Y	Y	Y
50	CP65-357	CPaus1	Y	Y	Y	Y
49	CP65-357	Cpam1	YY	Y	Y	Y
48	VMC71-238	Aus1	Y	Y	Y	Y
47	VMC71-238	Aus2	Y	Y	Y	Y

Y = consensus sequence obtained in this region

N = no amplification product available for sequencing in this region

NC = full consensus sequence not obtained

Sequencing Ref. = name given to the consensus sequence in the phylogeny study

TABLE 3b: SEQUENCES USED IN PHYLOGENY STUDY #2

VARIETY	Sequencing Ref.	REP	CP-RT
CP65-357	T6	Y	Y
CP65-357	F1	Y	Y
SP71-6163	B1	Y	Y
CP92-1654	G2	Y	Y
Q136	N6	Y	Y
Lho83-153	L1	Y	Y
SP71-6163	C1	Y	Y
CC84-75	C3	Y	Y
CC85-964	C4	Y	Y

note: T6 & F1 are the isolate fully sequenced in America and Australia respectively

TABLE 4: ISOLATE RFLP PATTERNS DISPLAYED IN EACH AMPLICON AREA

ORF1		Sau3A1		REP	Taq1	CP-RT		RT	
RFLP#	Varieties with Pattern	RFLP#	Varieties with Pattern	RFLP#	Varieties with Pattern	RFLP#	Varieties with Pattern	RFLP #	Varieties with Pattern
1	12,13,14,26,27,29, 30,32,33,35,36,49	1	1,2,3,5,6,7,9,11, 12,13,14,15,49,50	1	7,9,11,12,13,14,15, 22a, 49,50	1	1,2,3,4,5,6,7,9,11, 13,14,15,17,20,21, 22,23,24,25,26,27, 29,3,31,32,33,34, 36,37,38,39,40,41, 44,45,46,47,48,49,50	1	5,7,9,11,25,13,14, 26,27,29,33,34,49
2	50	2	21,22a,24,25	2	47,48			2	50
3	20,21,22,23,24,31,47	3	4	3	1,2,3,4,5,20,24,25			3	47,48
4	44,46,48	4	10	4	6	2	10	4	1,2,3,4,35,36, 38,39,40,41
5	1,2,3,4,5	5	20a,26,29	5	10	3	12,35	5	6
6	7,39	6	20b	6	21			6	20,21,22,23,24,25,46
7	9	7	23	7	22b			7	31
8	11	8	30,31,32,33,34	8	23			8	37
9	15	9	35,36,37,40,41	9	26,30,31,32,33,34			9	44,45
10	25,38	10	38	10	29				
11	34	11	39	11	35,36,37,38,39,40,46				
12	37, 40, 41	12	44,45,46	12	41				
13	45			13	44,45				

All RFLP digests performed on duplicate amplicons. In the REP, 20a and 20b refer to the two individual digests from the two individual RT-PCR's of the one isolate. This is the case for 22a and 22b also.

TABLE 5: ORF-RESTRICTION ENZYME DIGESTION PATTERNS

**TABLE 5a: ORF 1 Hha1 digest patterns
#RFLP Patterns Generated**

COUNTRIES	1	2	3	4	5	6	7	8	9	10	11	12	13
U.S.A	■	■			■	■	■	■	■				
Brazil					■								
Hawaii			■										
NC from Hawaii				■						■			■
Australia			■	■									
Taiwan	■					■				■		■	
South Africa	■												
Mauritius	■												
Reunion	■		■								■		

**TABLE 5b: REPLICASE Sau3AI digest patterns
#RFLP Patterns Generated**

COUNTRIES	1	2	3	4	5	6	7	8	9	10	11	12
U.S.A	■			■								
Brazil	■		■									
Hawaii		■			■	■	■					
NC from Hawaii												■
Australia		■										
Taiwan									■	■	■	
South Africa									■			
Mauritius					■							
Reunion					■			■				

**TABLE 5c: REPLICASE Taq1 digest patterns
#RFLP Patterns Generated**

COUNTRIES	1	2	3	4	5	6	7	8	9	10	11	12	13
U.S.A	■		■	■	■								
Brazil			■										
Hawaii	■		■			■	■	■					
NC for Hawaii											■		■
Australia		■											
Taiwan											■	■	
South Africa											■		
Mauritius									■				
Reunion									■	■			

The amplicon area digested and the restriction enzyme used in the digest head each table. Reading across the table shows the total number of RFLP patterns generated by amplicons. Reading down the columns, the coloured cells show which countries had isolates which produced that RFLP pattern. (eg. In the ORF1/HhaI digest, a total of 13 RFLP patterns were recognised. The U.S.A., Taiwan, South Africa, Mauritius and Reunion all had isolates which gave RFLP pattern #1)

**TABLE 5d: COAT PROTEIN- READTHROUGH HaeIII digest patterns
#RFLP Patterns Generated**

COUNTRIES	1	2	3
U.S.A			
Brazil			
Hawaii			
NC for Hawaii			
Australia			
Taiwan			
South Africa			
Mauritius			
Reunion			

**TABLE 5e: READTHROUGH HAEIII digest patterns
#RFLP Patterns Generated**

COUNTRIES	1	2	3	4	5	6	7	8	9
U.S.A									
Brazil									
Hawaii									
NC for Hawaii									
Australia									
Taiwan									
South Africa									
Mauritius									
Reunion									

The amplicon area digested and the restriction enzyme used in the digest head each table. Reading across the table shows the total number of RFLP patterns generated by amplicons. Reading down the columns, the coloured cells show which countries had isolates which produced that RFLP pattern. (eg. In the ORF1/HhaI digest, a total of 13 RFLP patterns were recognised. The U.S.A., Taiwan, South Africa, Mauritius and Reunion all had isolates which gave RFLP pattern #1)

TABLE 6: NUMBER OF SCYLV POSITIVE SAMPLES FROM EACH COUNTRY USED IN RFLP ANALYSIS

COUNTRY	NUMBER TESTED	NUMBER SCYLV +VE
Brazil	10	4
America	15	14 ¹
Hawaii	8	7
Mauritius	6	3
Reunion	13	6
South Africa	8	1
Taiwan	7	6
Noble Canes from Hawaii	4	4
Papua New Guinea	1	1
Thailand	1	1
Australia	see note ²	2

1. This value does not include the CP65-357 samples (American isolate) which are included in the RFLP and sequencing analysis. note: this is the fully sequenced SCYLV isolate (11,12).
2. SCYLV positives from Australia used in this diversity study were already known to be positive from previous projects. Only 2 of these were used in RFLP analysis.

TABLE 7: PERCENTAGE SIMILARITY OF SCYLV NUCLEOTIDE SEQUENCES IN EACH AMPLICON

Amplicon Region	% Sim DNA	% Sim Proteins	%Sim Proteins not conserved
ORF1	87.85	86.85	89.81
REP	91.01	88.40	91.54
CP-RT	94.2	91.96	92.41
RT	84.59	85.14	91.74

FIGURE 1: PRIMERS USED IN SEQUENCING VARIOUS AMPLICONS

The names of the primers or the value in the brackets refer to where they bind in the complete SCYLV genome.

F = Forward, R = Reverse.

ORF1:

ORF1START(242)F: 5'-ATG GCC CCA ACA CTC CCG TTT ACA-3'
 729F: 5'-CTG TCT CTT GGT CGT CCT TAC-3'
 1465F: 5'-TGT GTA TGA GTC TCC GTC TC-3'
 933R: 5'-GGT GGT GAC ATG GGG ACG GC-3'
 1552R: 5'-CTC ATA CAC CTC CTC GGC G-3'
 160R640R(1862)R: 5'-GAA TCA ACT GCG AGA CGA TG-3'

Replicase:

OFM323(1518)F: 5'-CAG ACA TTG CTG ATT AC-3'
 1929F: 5'-AAC AGC AGC AGA ACG GAG GG-3'
 2309F: 5'-ATG CCC CAC ACA CCA GCT C-3'
 2077R: 5'-TTG GGG GAT GGT ATA GCG CGG-3'
 2488R: 5'-ATC GCG TCA GGA GCG GCA G-3'
 OFM359(2729)R: 5'-GCT CTC CAC AAA GCT ATC T-3'

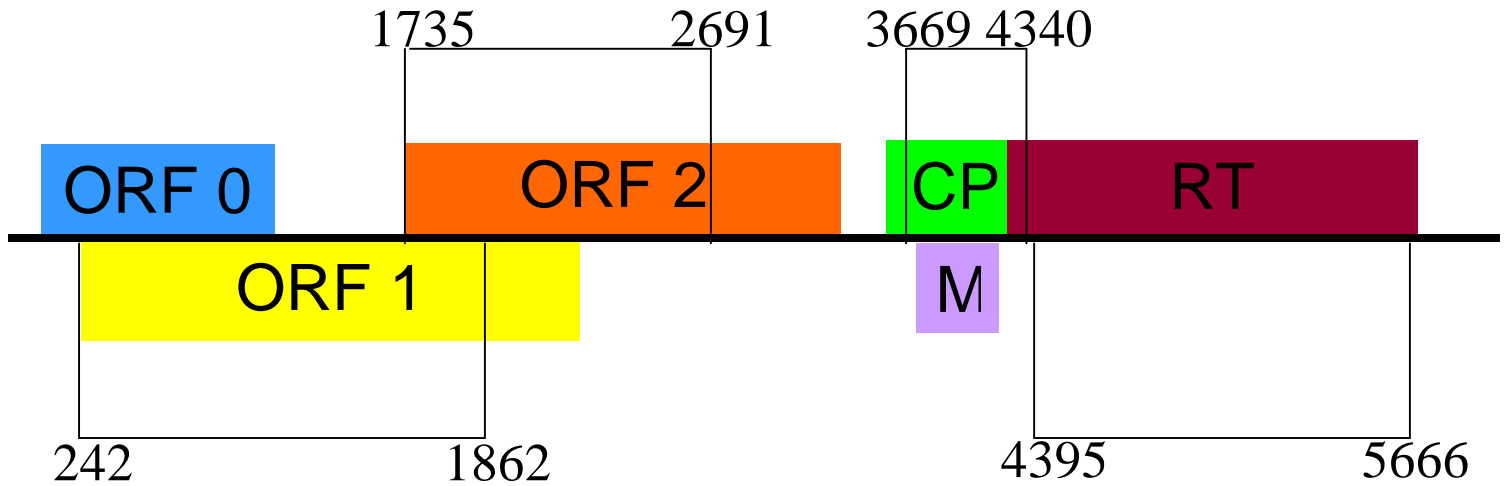
Coat Protein:

OFM336(3667)F: 5'-GCT CAC GAA GGA ATG TCA G-3'
 3897F: 5'-CAG TAC GCA GCG TTC AAC AAT GG-3'
 4114R: 5'-CTG ATG AAG GGG GCC GGG AAG-3'
 OFM361zb(4352)R: 5'-TGT TTT CAC GAT GTA GTT C-3'

Readthrough:

104R613R(4367)F: 5'-ATA TCT AGA TGT GGG TCC GC-3'
 4800F: 5'-GAG GCC CCA CCC ATT GAA AAG AG-3'
 5283F: 5'-GCT CTC ATG GCT AAC GCT TC-3'
 5033R: 5'-GTT AGT CGG TTG TTC AGG TGC-3'
 5469R: 5'-CGG ACT TAC AGA ACG GGG AG-3'
 3Prime2R(5666)R: 5'-GGA GGA GGA AGA TTT CGG TG-3'

FIGURE 2: AREAS OF SCYLV GENOME USED IN PHYLOGENETIC ANALYSIS



Amplicon Region	Reading frame of sequence used	Region covered	Number of nucleotide bases	Number of amino acid bases
ORF1	ORF1	242-1862	1621	540
REPLICASE	ORF2	1735-2691	957	319
CP-RT	CP	3669-4340	672	242
RT	READTHROUGH	4395-5666	1272	424

FIGURE 3: REPRESENTATIVE CONSENSUS TREE FOR ORF 1 NUCLEOTIDE

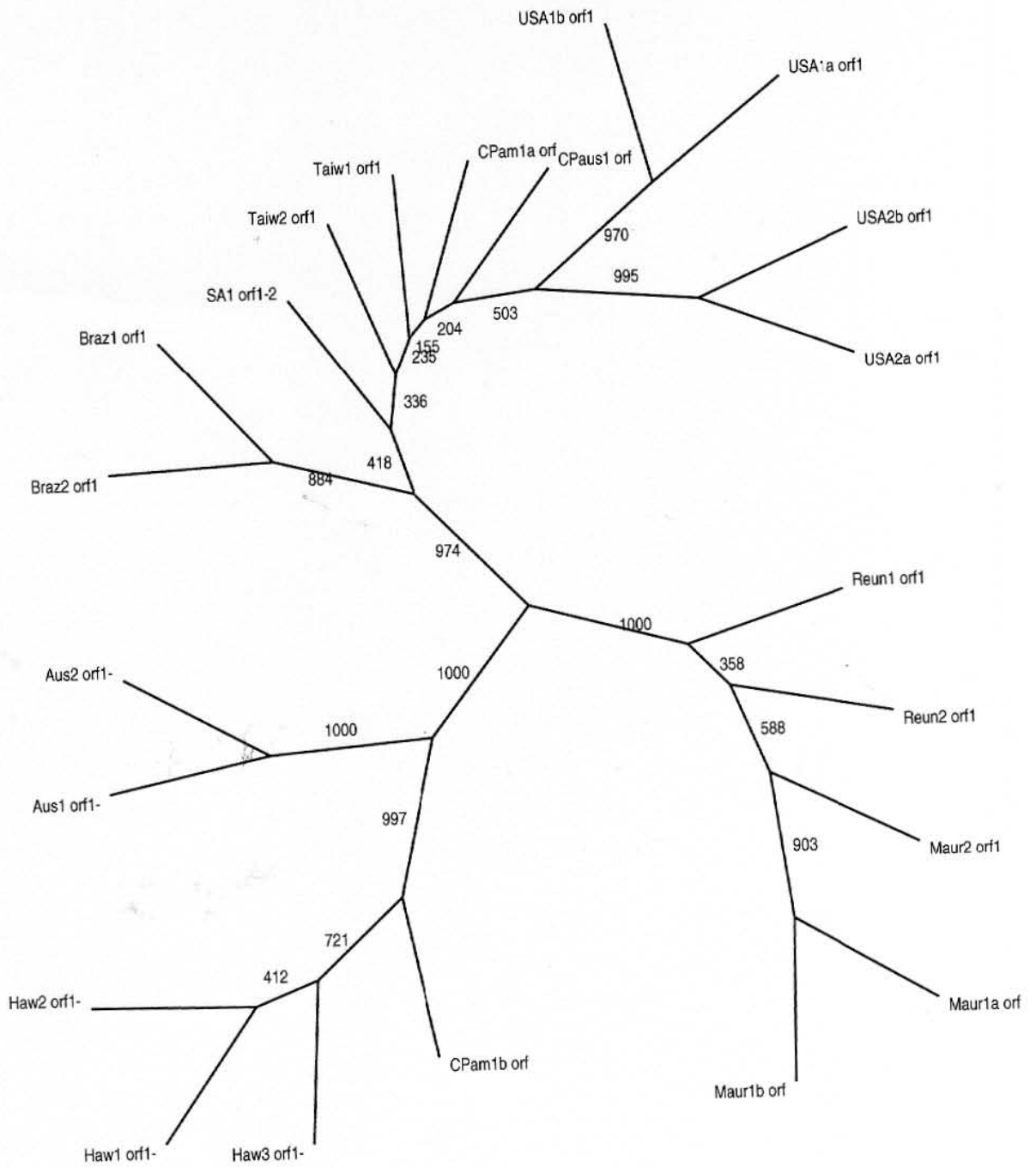


FIGURE 4: REPRESENTATIVE CONSENSUS TREE FOR ORF1 PROTEIN

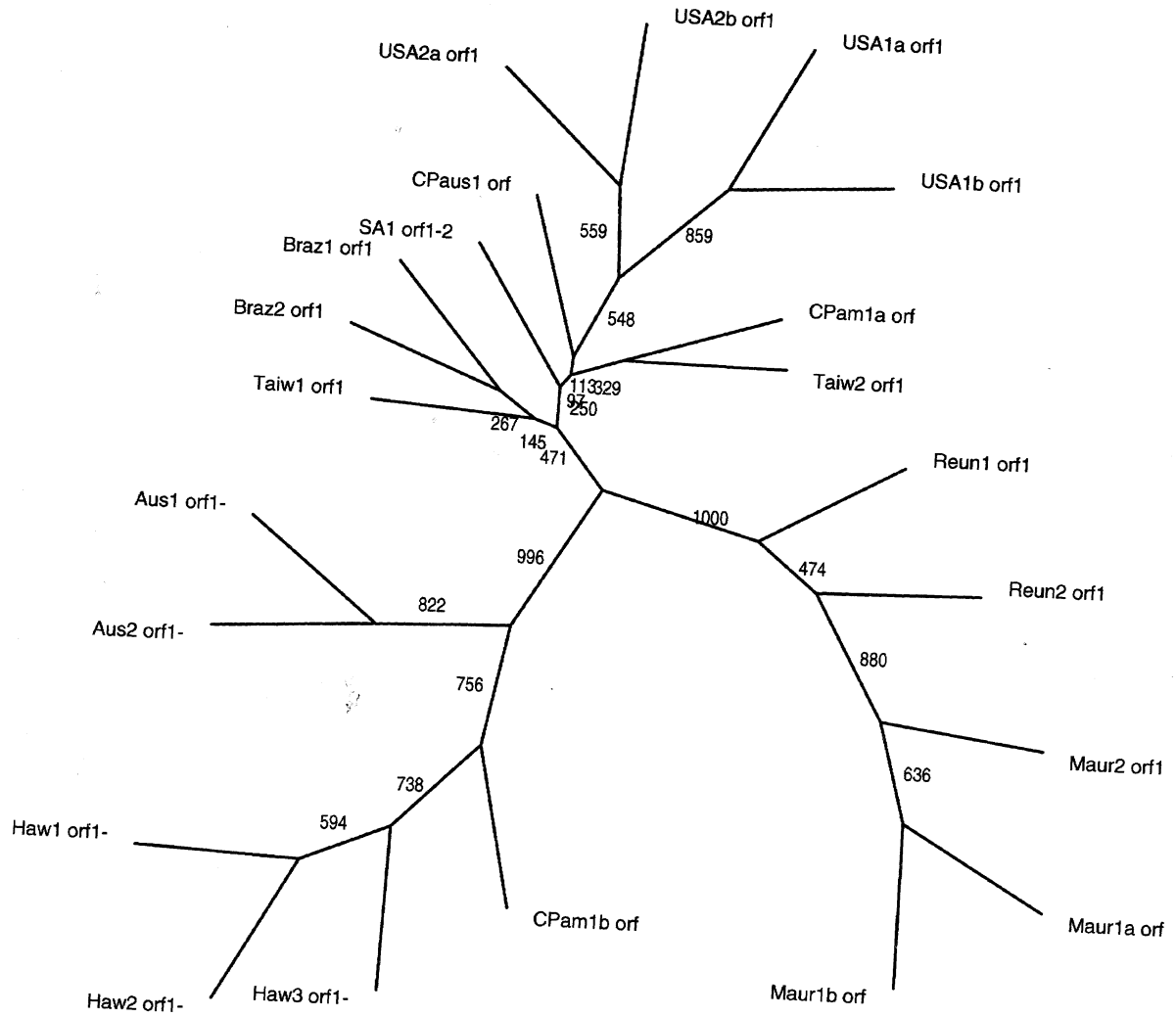


FIGURE 5: REPRESENTATIVE CONSENSUS TREE FOR REP NUCLEOTIDE

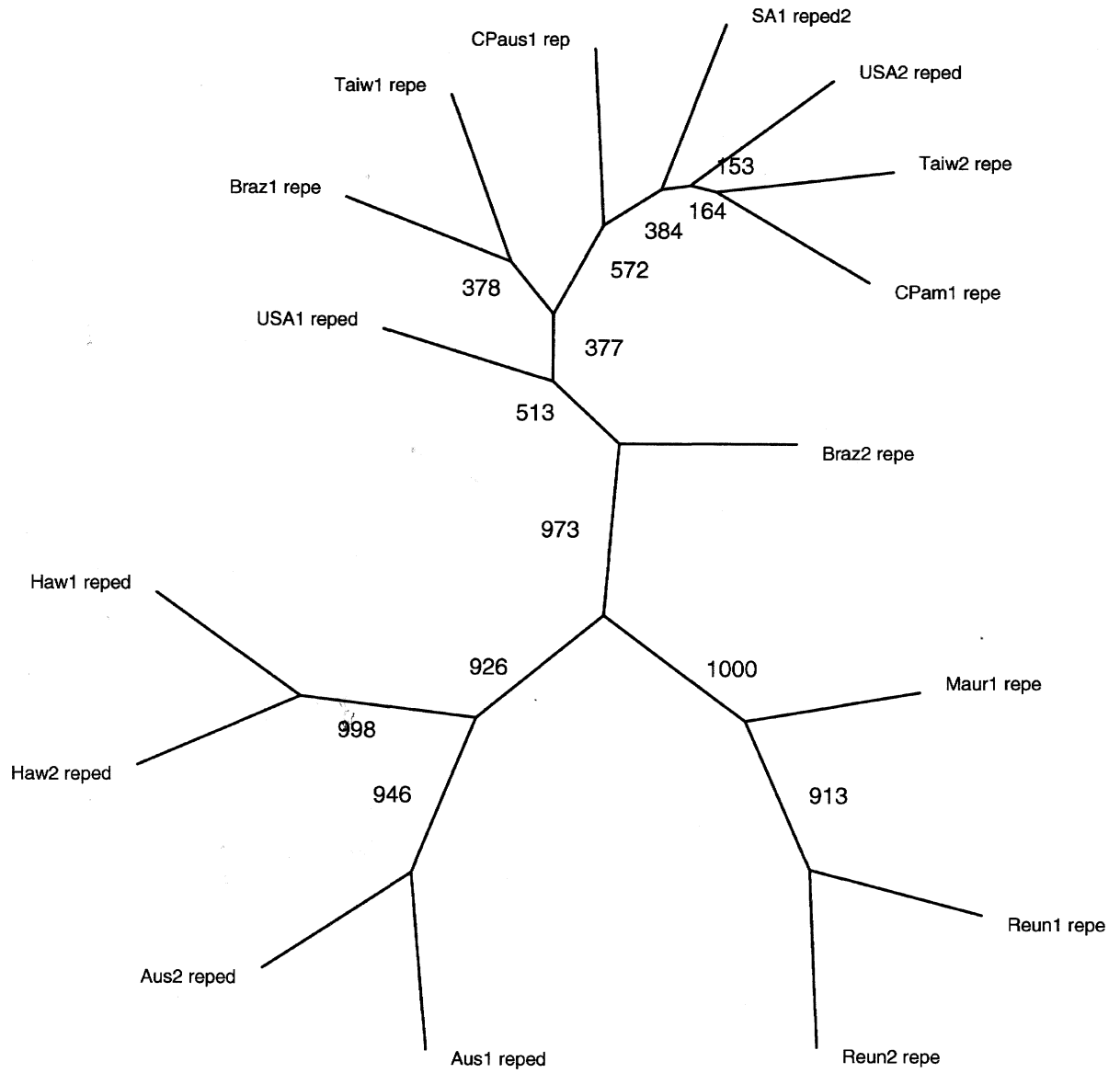


FIGURE 6: REPRESENTATIVE CONSENSUS TREE FOR REP PROTEIN

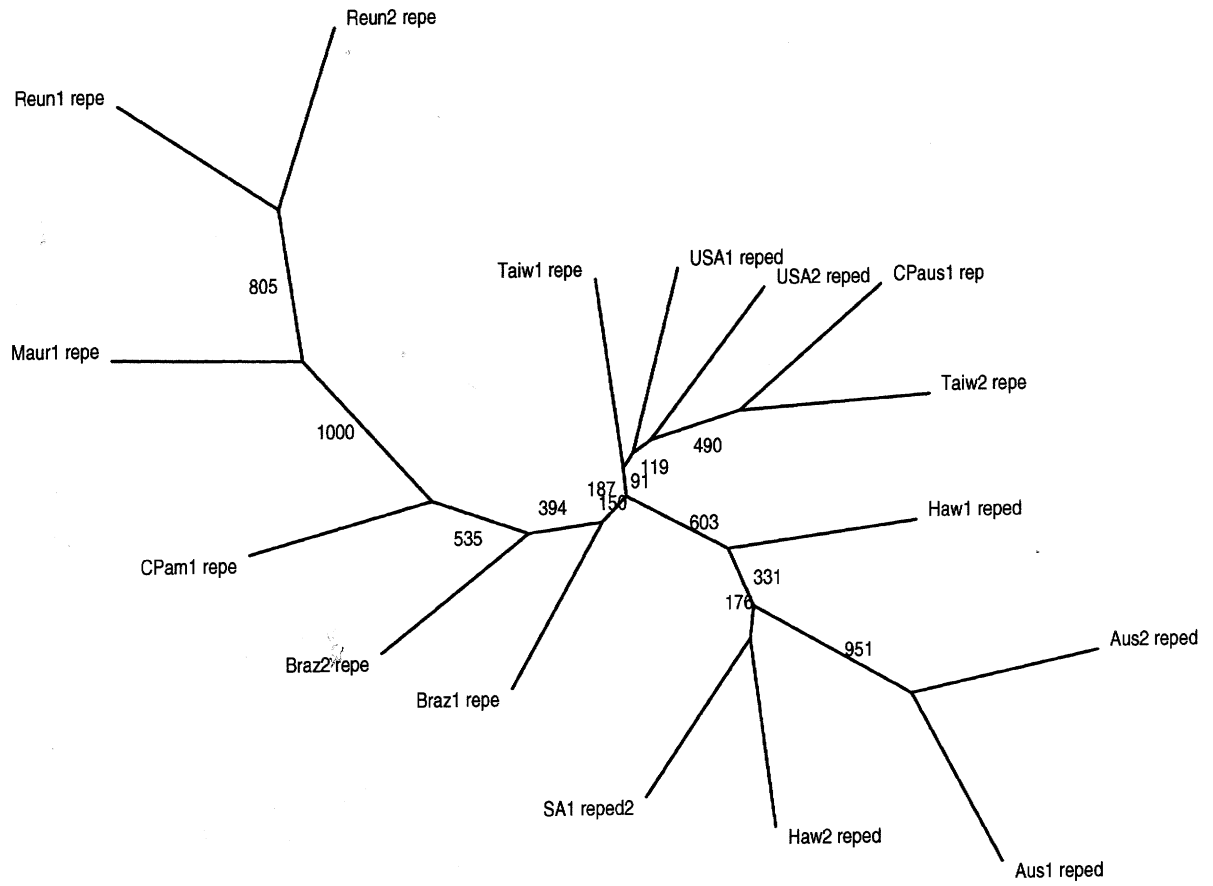


FIGURE 7: REPRESENTATIVE CONSENSUS TREE FOR CP NUCLEOTIDE

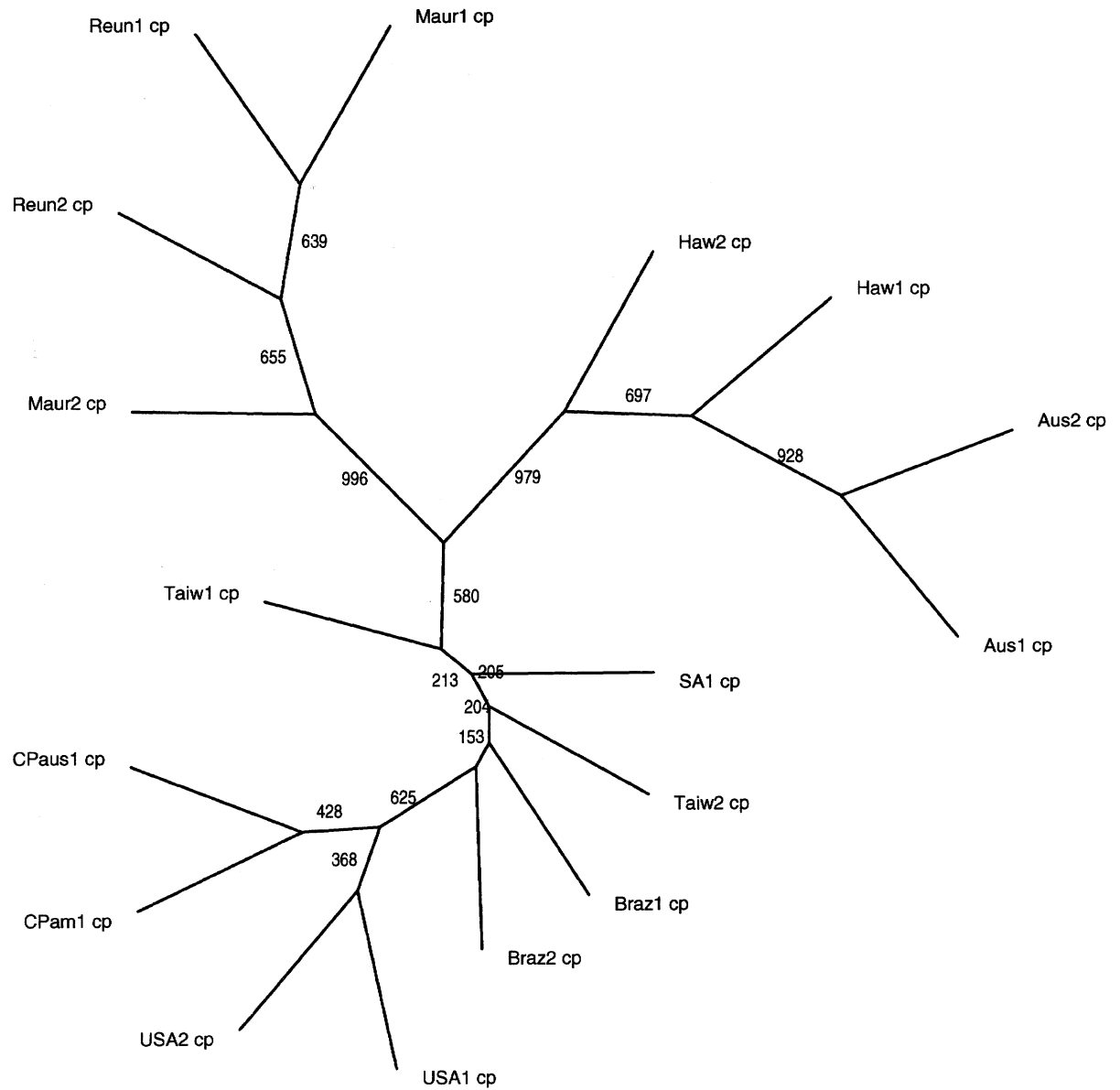


FIGURE 8: REPRESENTATIVE CONSENSUS TREE FOR CP PROTEIN

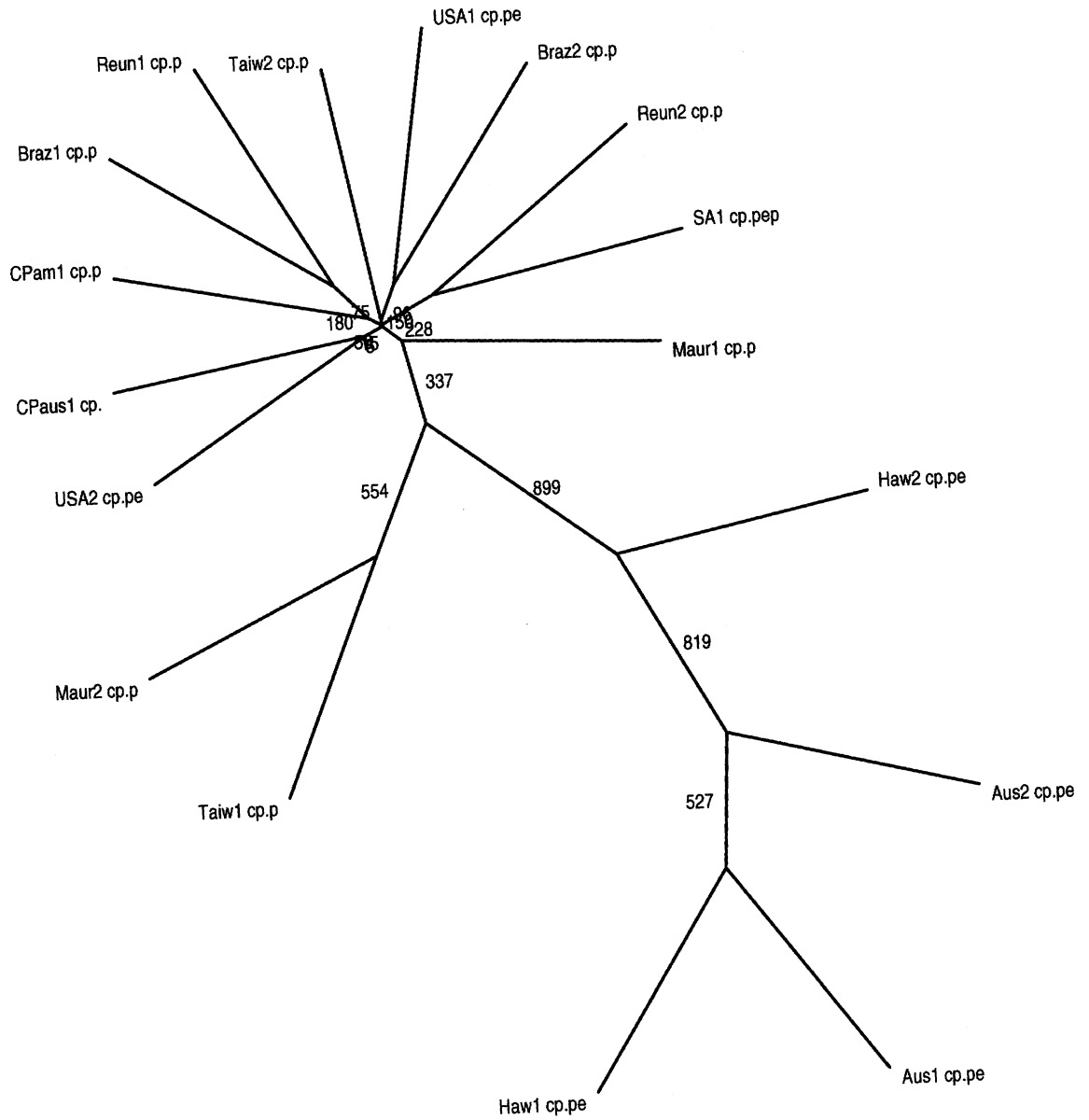


FIGURE 9: REPRESENTATIVE CONSENSUS TREE FOR RT NUCLEOTIDE

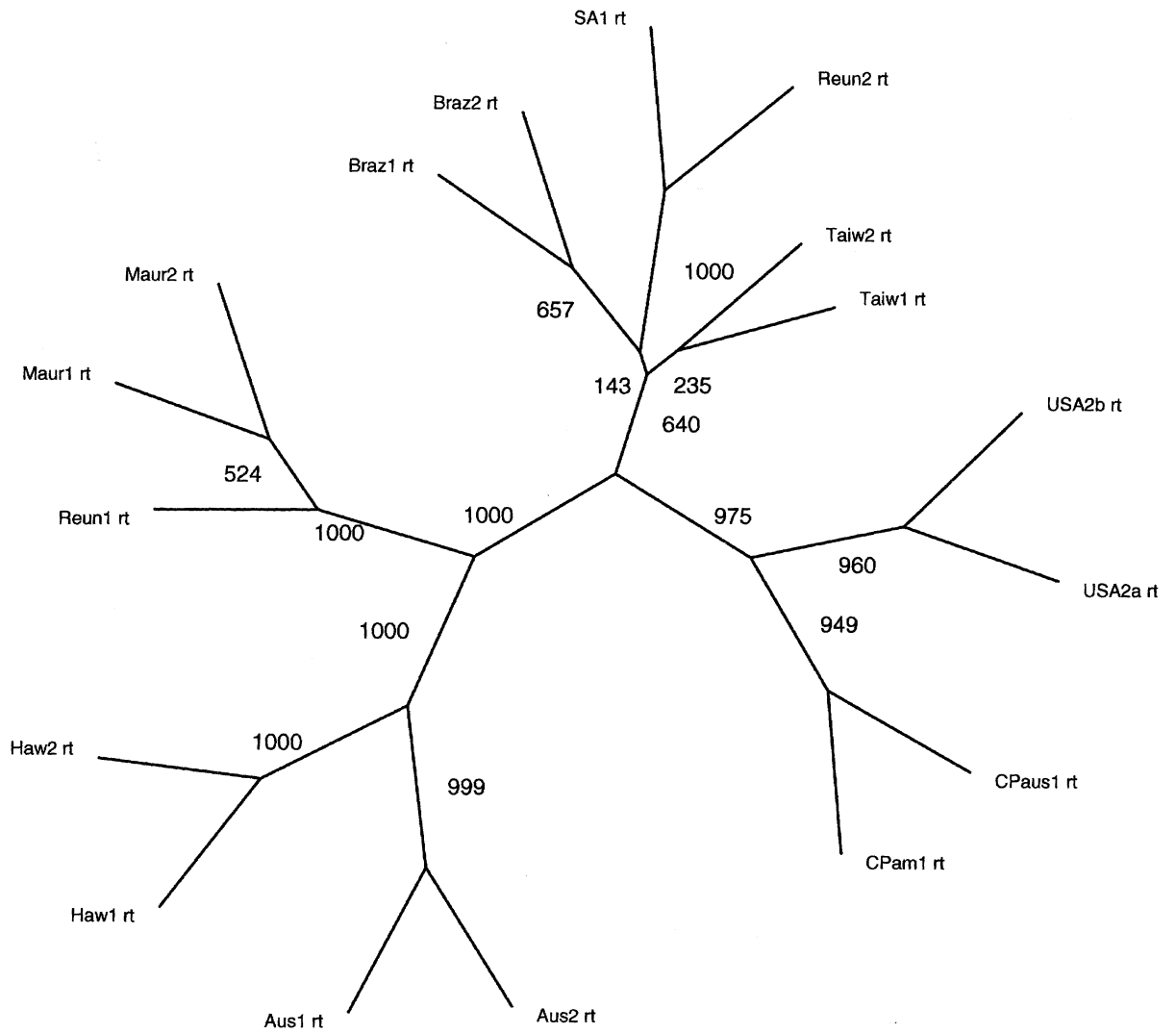


FIGURE 10: REPRESENTATIVE CONSENSUS TREE FOR RT PROTEIN

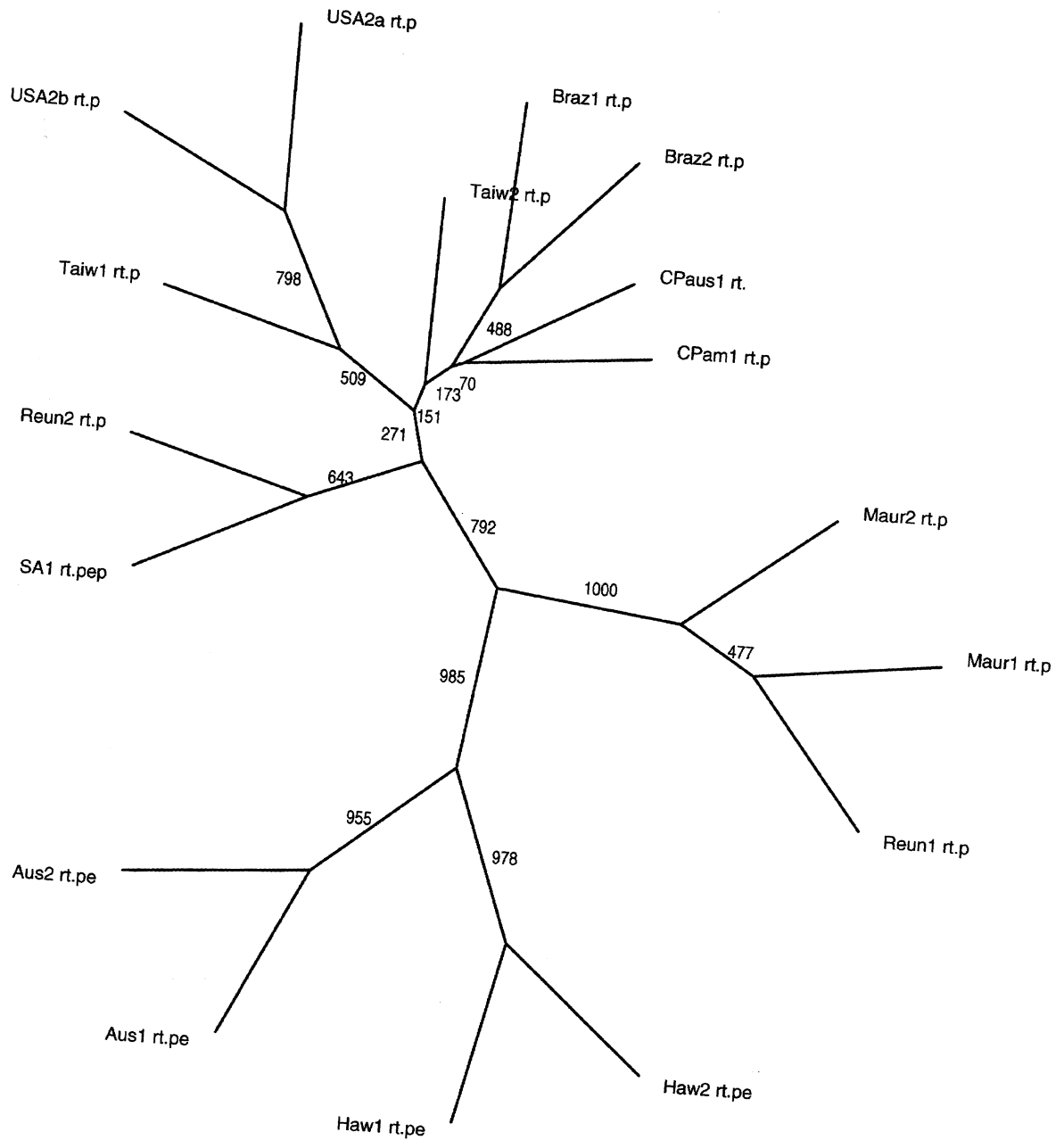


FIGURE 11: CONSENSUS TREE PRODUCED USING DISTANCE PROGRAM FOR REP NUCLEOTIDE PHYLOGENY STUDY #2

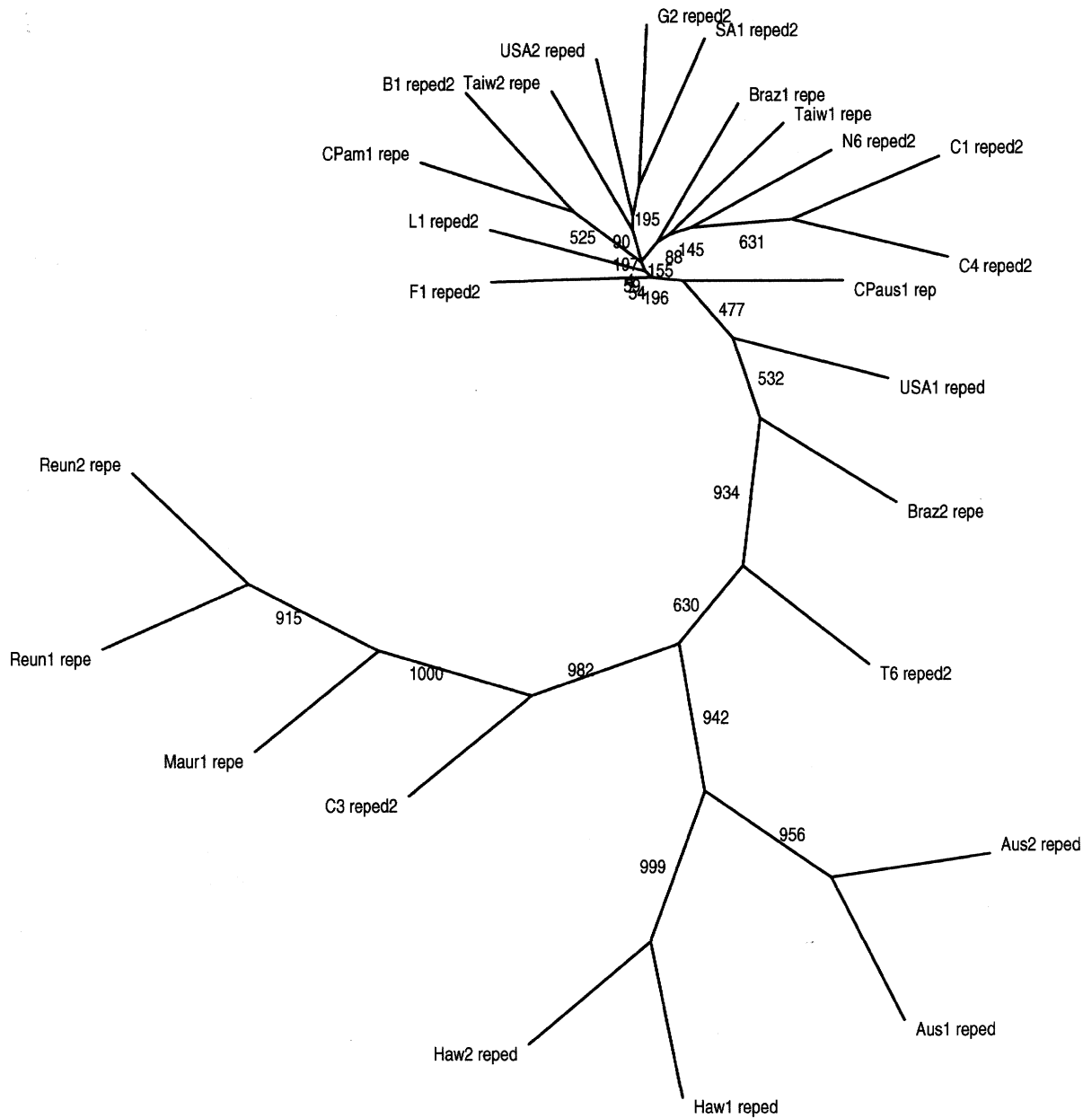
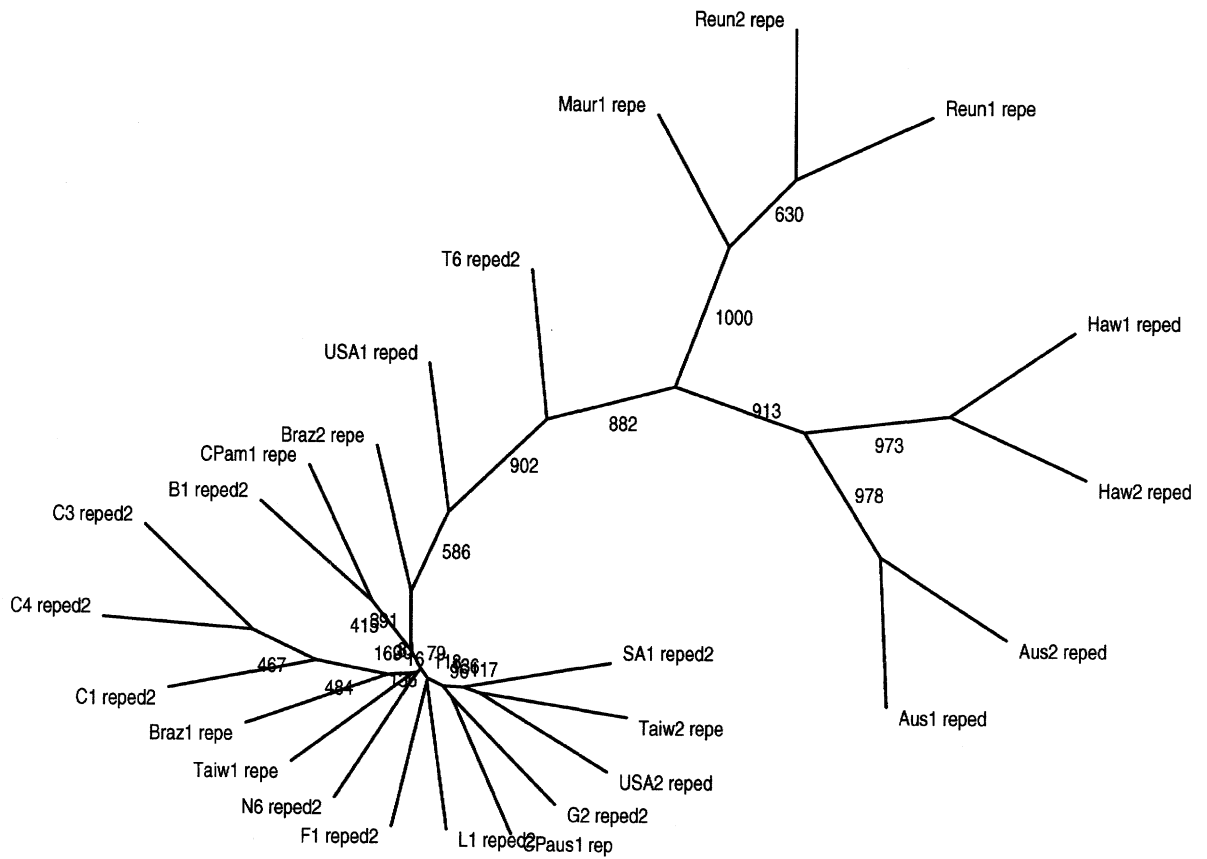


FIGURE 12: CONSENSUS TREE PRODUCED USING MAXIMUM PARSIMONY PROGRAM FOR REP NUCLEOTIDE PHYLOGENY STUDY #2



**FIGURE 13: CONSENSUS TREE PRODUCED USING DISTANCE PROGRAM FOR
REP PROTEIN
PYLOGENY STUDY #2**

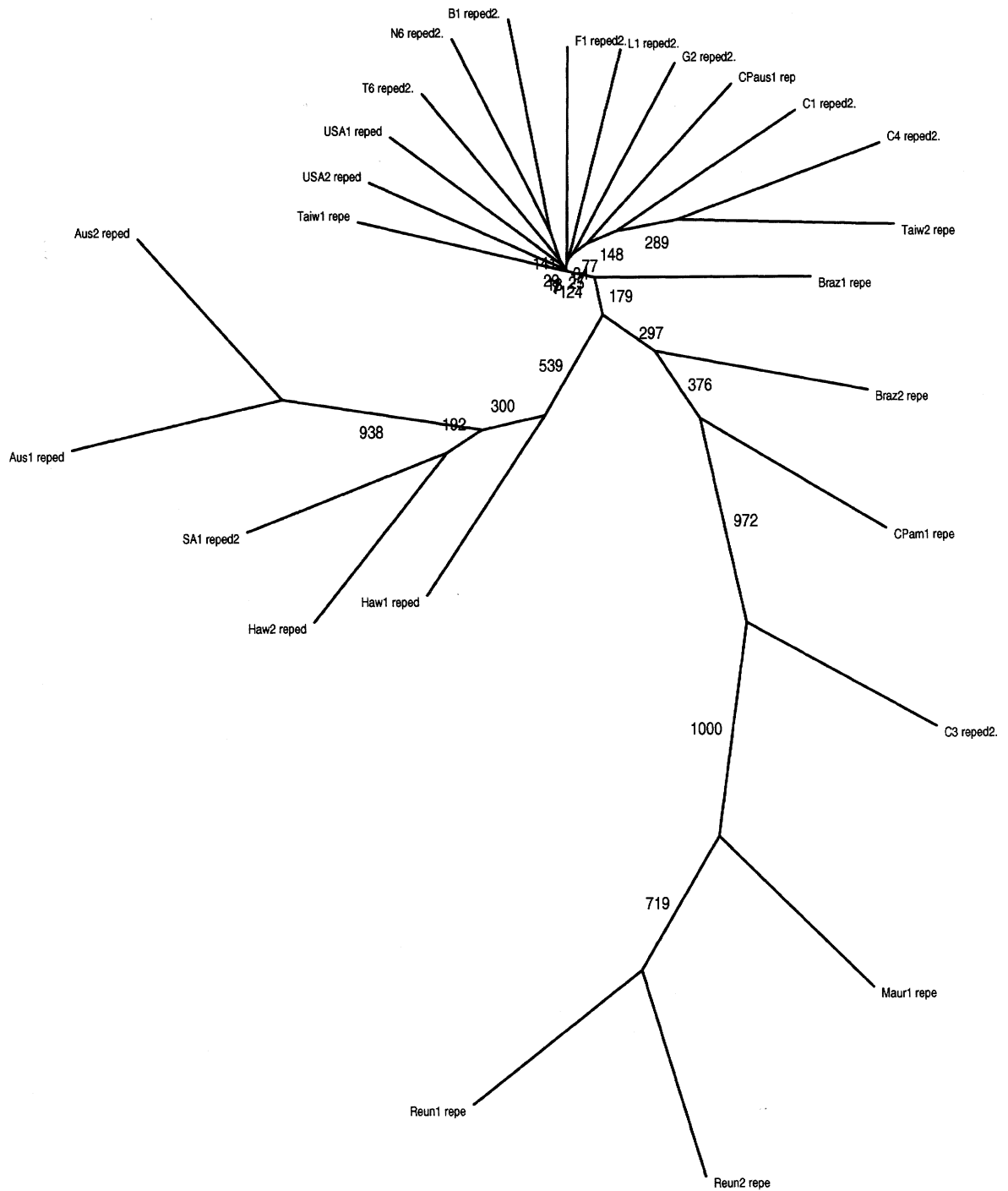


FIGURE 14: CONSENSUS TREE PRODUCED USING MAXIMUM PARSIMONY PROGRAMS FOR REP PROTEIN PHYLOGENY STUDY #2

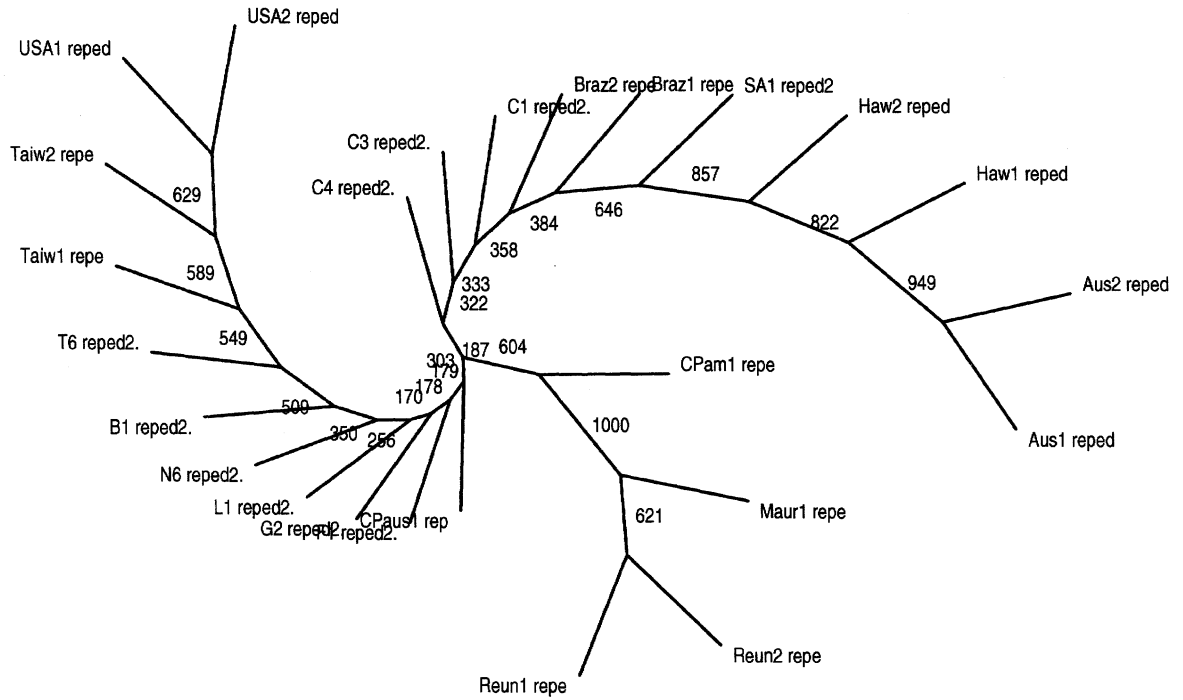


FIGURE 15: REPRESENTATIVE CONSENSUS TREE FOR CP-RT NUCLEOTIDE PHYLOGENY STUDY #2

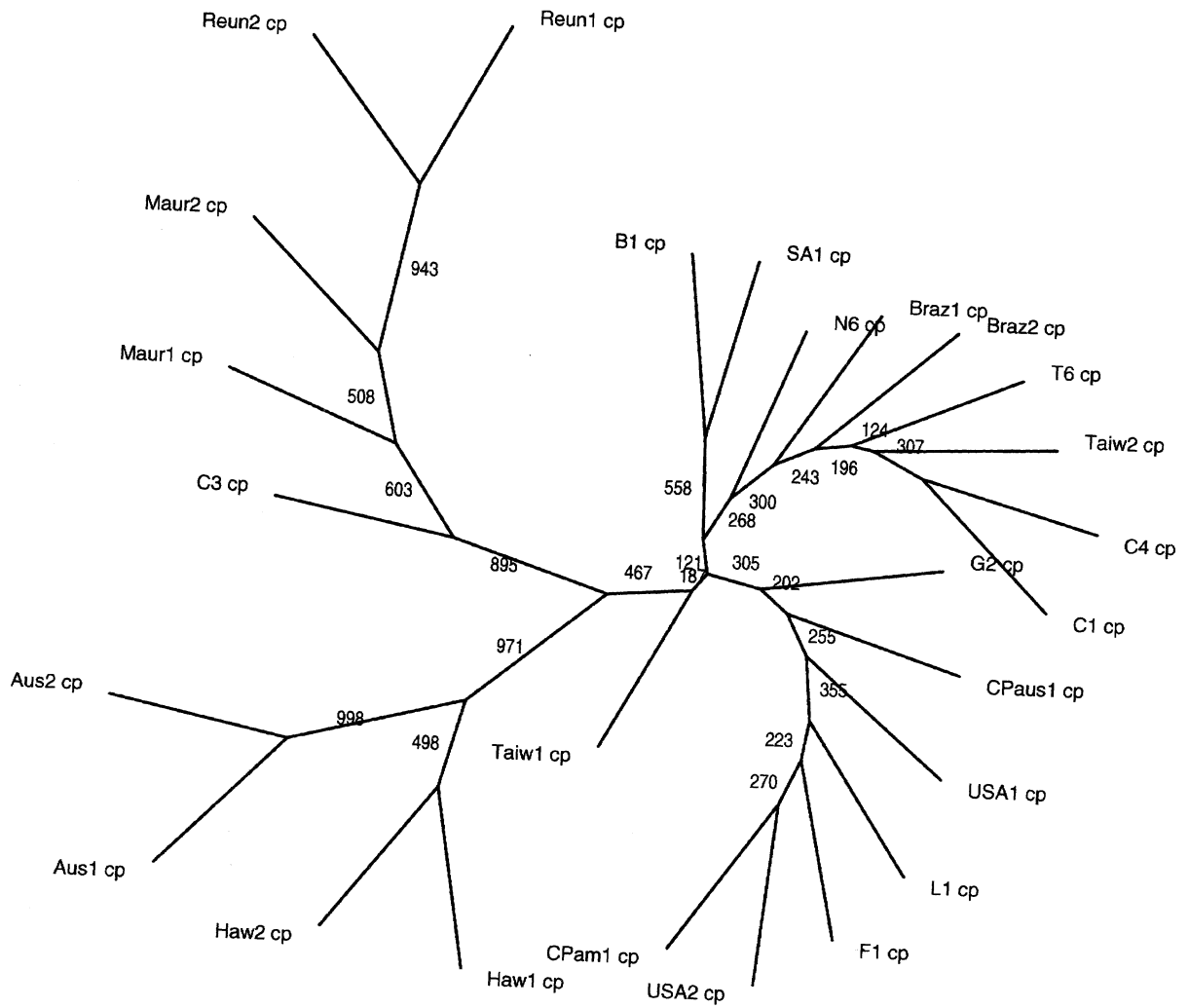
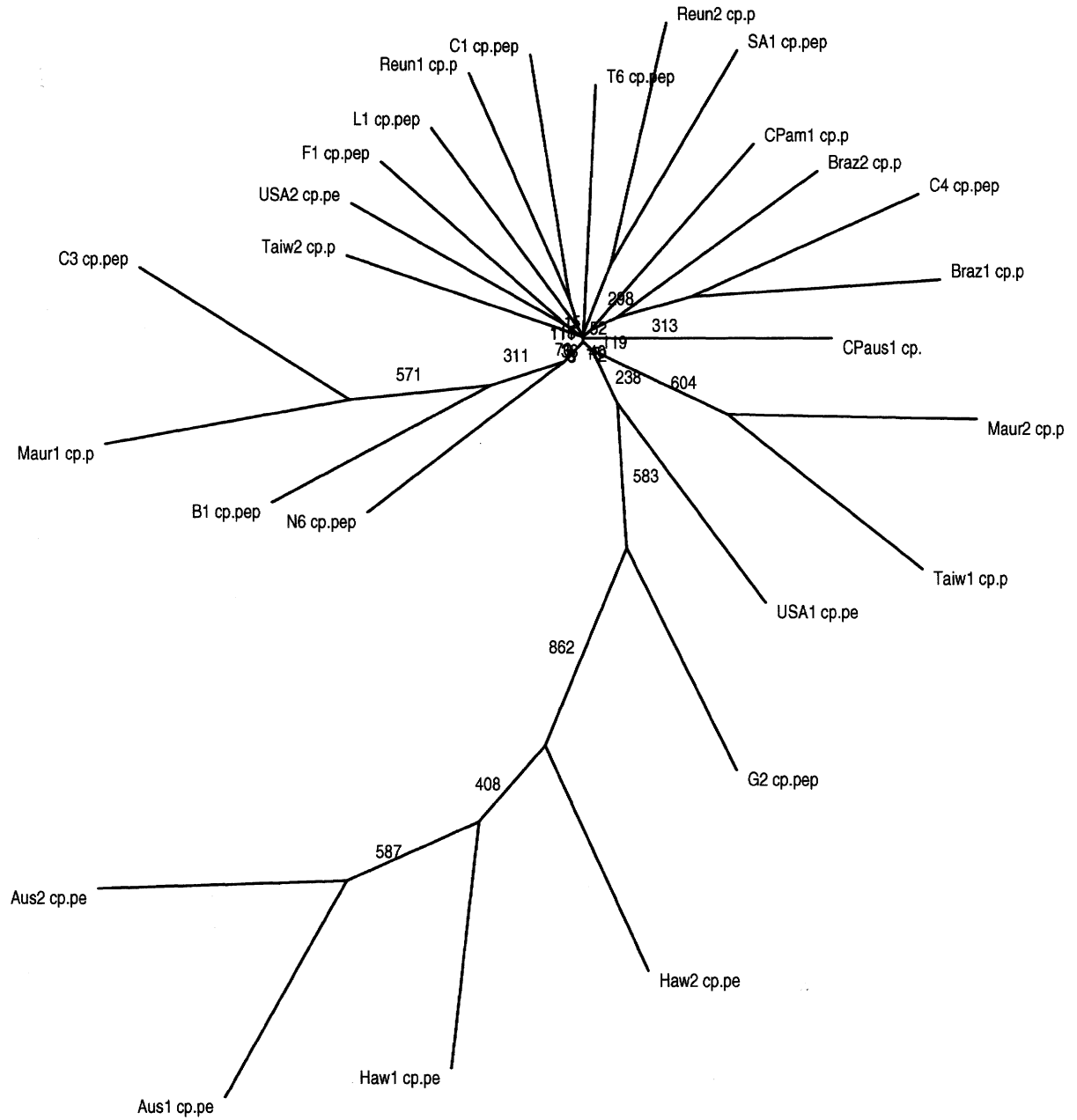
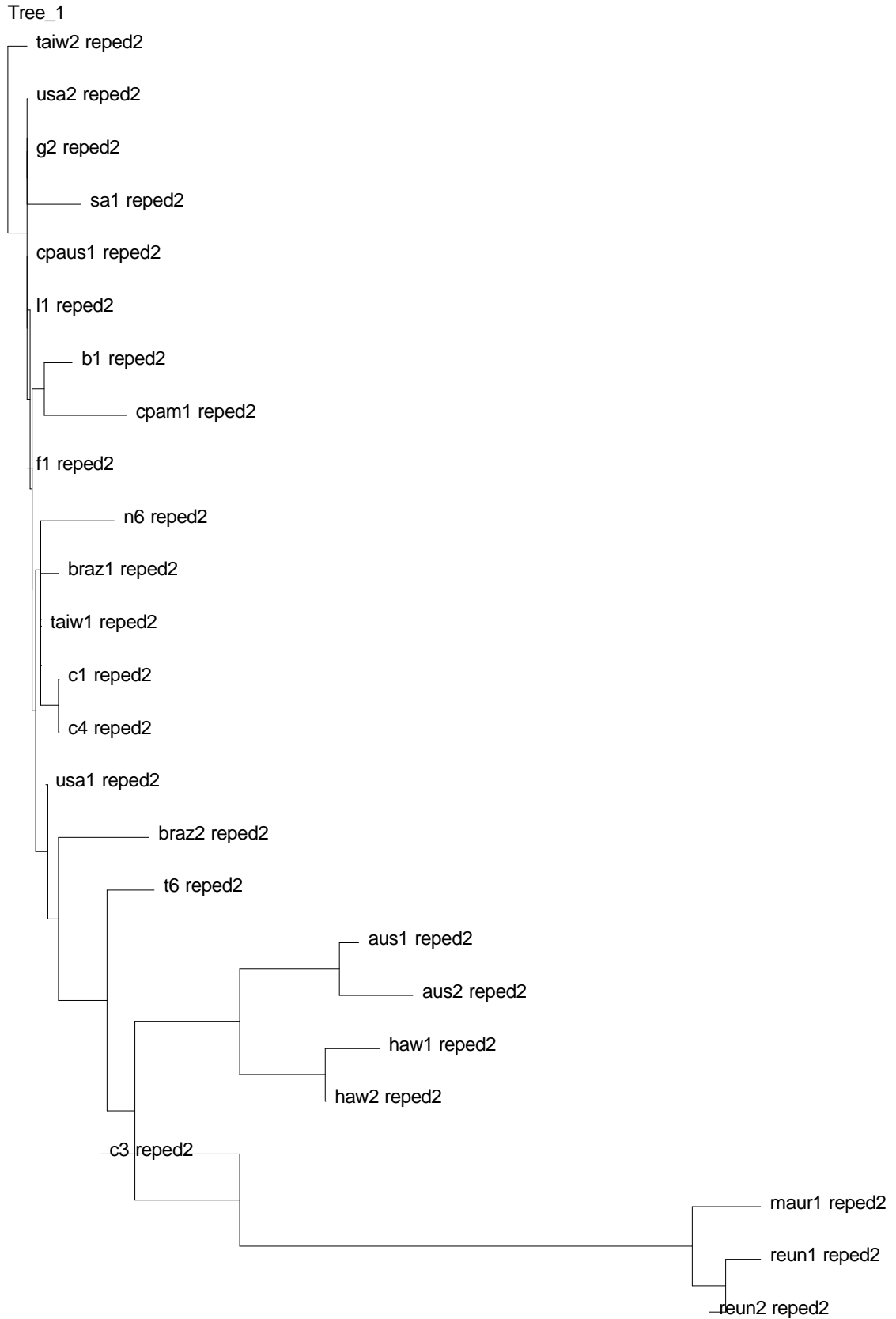


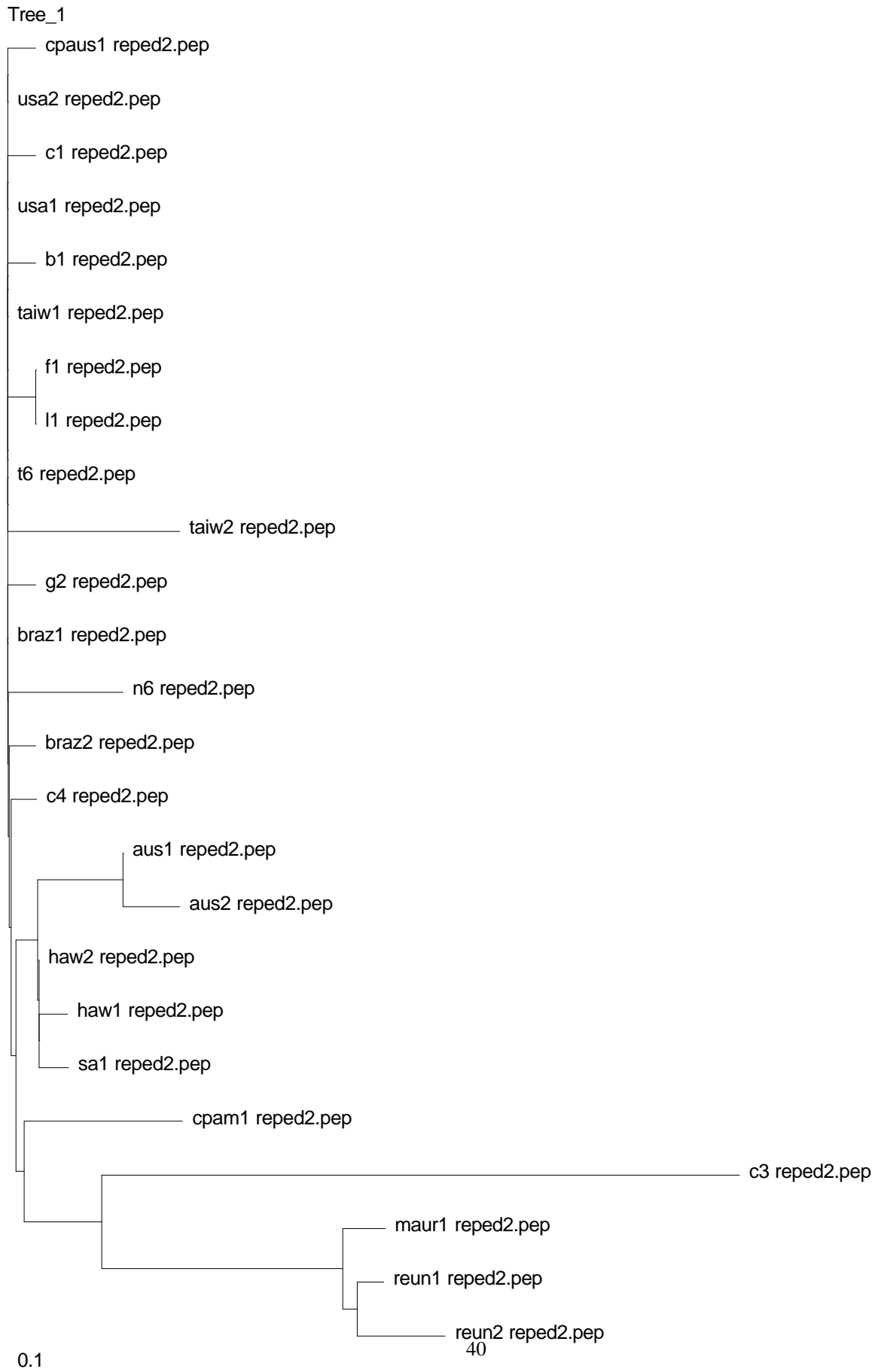
FIGURE 16: REPRESENTATIVE CONSENSUS TREE FOR CP-RT PROTEIN PHYLOGENY STUDY #2



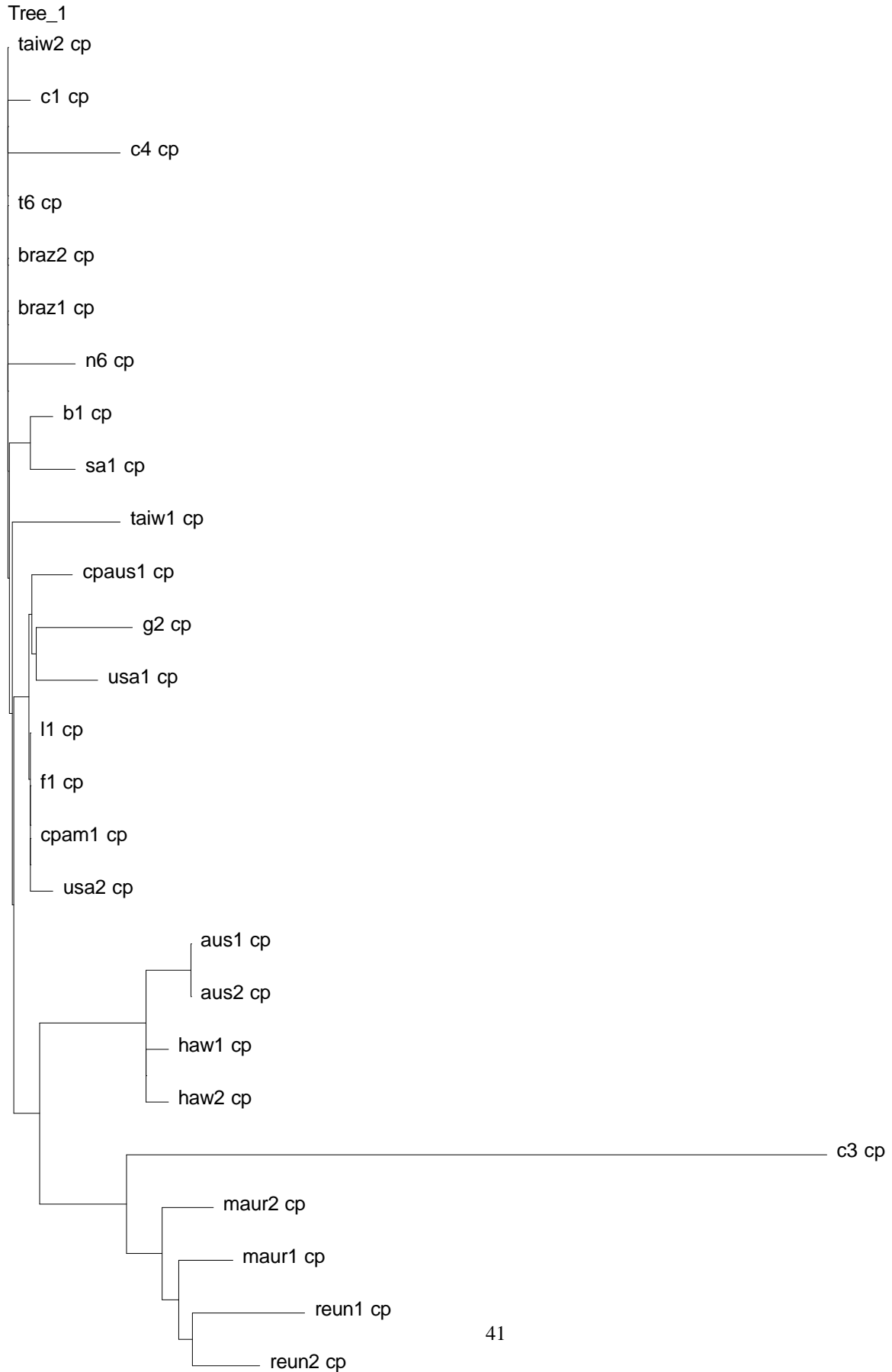
**FIGURE 17: PHYLOGRAM OF REP NUCLEOTIDE SEQUENCES
PHYLOGENY STUDY #2**



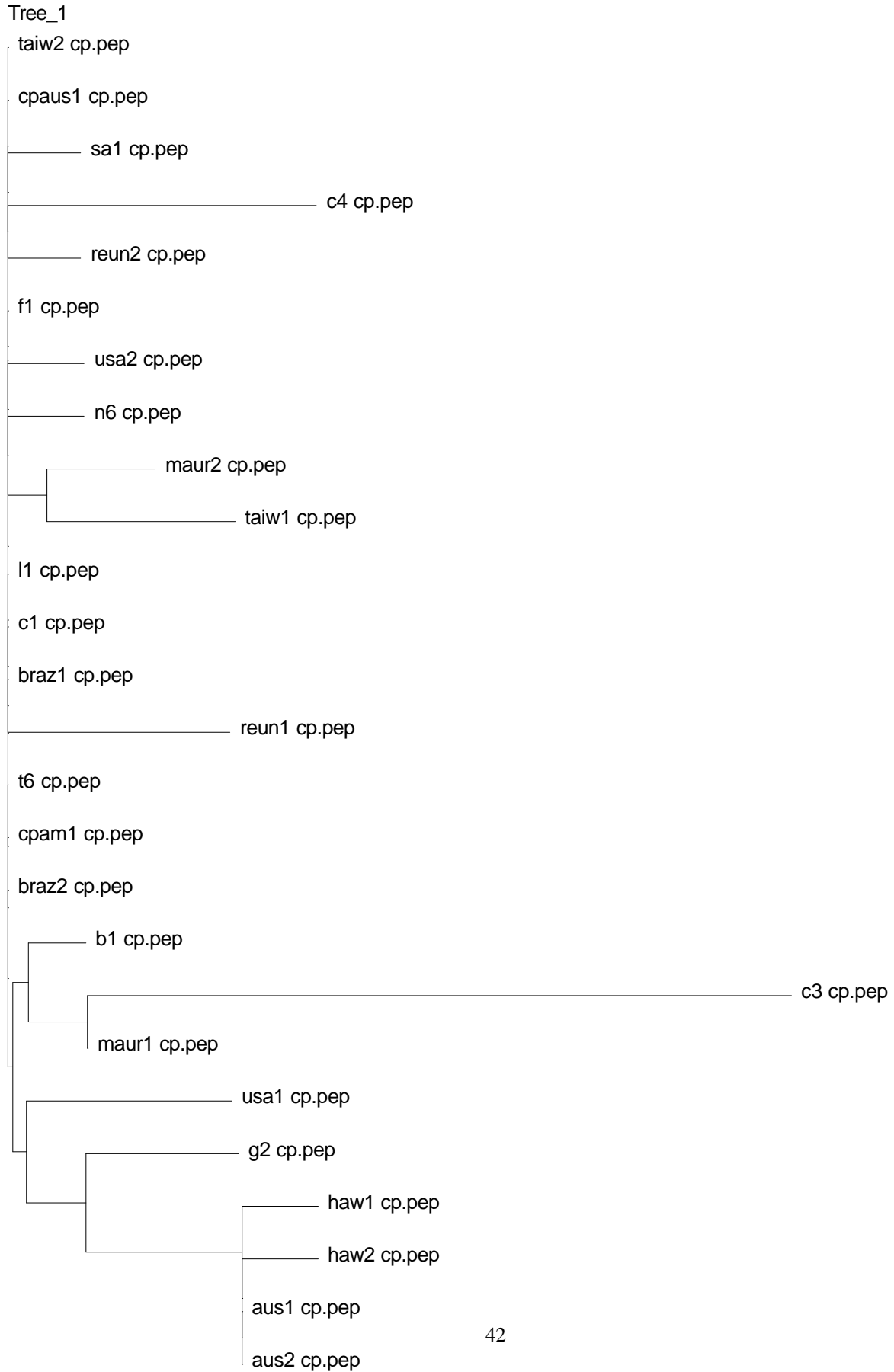
**FIGURE 18: PHYLOGRAM OF REP PROTEIN SEQUENCES
PHYLOGENY STUDY #2**



**FIGURE 19: PHYLOGRAM OF CP-RT NUCLEOTIDE SEQUENCES
PHYLOGENY STUDY #2**



**FIGURE 20: PHYLOGRAM OF CP-RT PROTEIN SEQUENCES
PHYLOGENY STUDY #2**



APPENDIX: MULTIPLE SEQUENCE ALIGNMENTS FOR PHYLOGENY STUDY #1**ORF1 nucleotide**

eclustalw August 2, 19101 10:32

of: @fil_5414.tmp

aus1_orf1	ck: 3298	from:	1	to:	1621	Length:	1621
aus2_orf1	ck: 3566	from:	1	to:	1621	Length:	1621
braz1_orf1	ck: 4153	from:	1	to:	1621	Length:	1621
braz2_orf1	ck: 1953	from:	1	to:	1621	Length:	1621
cpamla_orf1	ck: 321	from:	1	to:	1621	Length:	1621
cpamlb_orf1	ck: 7181	from:	1	to:	1573	Length:	1573
cpaus1_orf1	ck: 2856	from:	1	to:	1621	Length:	1621
haw1_orf1	ck: 8910	from:	1	to:	1621	Length:	1621
haw2_orf1	ck: 5201	from:	1	to:	1621	Length:	1621
haw3_orf1	ck: 5334	from:	1	to:	1621	Length:	1621
maurla_orf1	ck: 8253	from:	1	to:	1621	Length:	1621
maurlb_orf1	ck: 4866	from:	1	to:	1621	Length:	1621
maur2_orf1	ck: 9098	from:	1	to:	1621	Length:	1621
reun1_orf1	ck: 2032	from:	1	to:	1621	Length:	1621
reun2_orf1	ck: 7859	from:	1	to:	1621	Length:	1621
sal_orf1	ck: 355	from:	1	to:	1621	Length:	1621
taiw1_orf1	ck: 5281	from:	1	to:	1621	Length:	1621
taiw2_orf1	ck: 1539	from:	1	to:	1621	Length:	1621
usala_orf1	ck: 2366	from:	1	to:	1621	Length:	1621
usalb_orf1	ck: 2498	from:	1	to:	1621	Length:	1621
usa2a_orf1	ck: 2105	from:	1	to:	1621	Length:	1621
usa2b_orf1	ck: 1204	from:	1	to:	1621	Length:	1621

Pairwise similarity parameter:

K-Tuple length:	2
Gap Penalty:	5
Number of diagonals:	4
Diagonal window size:	4
Scoring Method:	Percentage

Multiple alignment parameter:

Gap Penalty (fixed):	10.00
Gap Penalty (varying):	5.00
Gap separation penalty range:	8
Percent. identity for delay:	40%
List of hydrophilic residue:	GPSNDQEKR
Transitions:	Weighted

Used Sequences:

1	/home/bses00/Za (1621) Aus\1a\orf
2	/home/bses00/Za (1621) Aus\1b\orf
3	/home/bses00/Za (1621) Braz\1orf1
4	/home/bses00/Za (1621) Braz\2orf1
5	/home/bses00/Za (1621) CP\amla\or
6	/home/bses00/Za (1573) CP\amlb\or
7	/home/bses00/Za (1621) CP\auslorf
8	/home/bses00/Za (1621) Haw\1orf1
9	/home/bses00/Za (1621) Haw\2orf1
10	/home/bses00/Za (1621) Haw\3orf1
11	/home/bses00/Za (1621) Maur\1a\or
12	/home/bses00/Za (1621) Maur\1b\or
13	/home/bses00/Za (1621) Maur\2orf1
14	/home/bses00/Za (1621) Reun\1orf1

- 15 /home/bses00/Za (1621) Reun\2orf1
- 16 /home/bses00/Za (1621) SA\1orf1-2
- 17 /home/bses00/Za (1621) Taiw\1orf1
- 18 /home/bses00/Za (1621) Taiw\2orf1
- 19 /home/bses00/Za (1621) USA\1a\orf
- 20 /home/bses00/Za (1621) USA\1b\orf
- 21 /home/bses00/Za (1621) USA\2a\orf
- 22 /home/bses00/Za (1621) USA\2b\orf

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	10	20	30	40	50	60
Aus1_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATACGCCTT	TATTGTTGTCACTA			
Aus2_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATACGCCTT	TATTGTTGTCACTA			
Braz1_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATTTCGCCTT	TATTGTTGTCACTA			
Braz2_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATTTCGCCTT	TATTGTTGTCACTA			
CPam1a_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATTTCGCCTT	TATCGTTGTCACTA			
CPam1b_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACGTACGCCTT	TATTGTTGTCACTA			
CPaus1_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATACGCCTT	TATTGTTGTCACTA			
Haw1_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATACGCCTT	TATTGTTGTCACTA			
Haw2_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATACGCCTT	TATTGTTGTCACTA			
Haw3_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATACGNCTT	TATTGTTGTCACTA			
Maur1a_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATTTCGCCTT	TATTGTTGCTACTA			
Maur1b_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATTTCGCCTT	TATTGTTGCTACTA			
Maur2_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATTTCGCCTT	TATTGTTGTTACTA			
Reun1_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCATATTTCGCCTT	TATTGTTGTTACTA			
Reun2_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATTTCGCCTT	TATTGTTGTTACTA			
SA1_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCATATTTCGCCTT	TATTGTTGTCACTA			
Taiw1_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATTTCGCCTT	TATTGTTGTCACTA			
Taiw2_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGGGCACATACGCCTT	TATTGTTGTCACTA			
USA1a_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATACGCCTT	TATTGTTGTCACTA			
USA1b_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATACGCCTT	TATTGTTGTCACTA			
USA2a_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATACGCCTT	ACTGTTGTCACTA			
USA2b_orf1	ATGGCCCCAACACTCCCGTTTACA	ACTGGCTGGAGCACATACGCCTT	ACTGTTGTCACTA			

***** ** * ** * ** * ** *

Aus1_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
Aus2_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
Braz1_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
Braz2_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
CPam1a_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
CPam1b_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
CPaus1_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
Haw1_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACAGCATATCCATATTAAGAGAC
Haw2_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
Haw3_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
Maur1a_orf1	TGGTACCAATTCTGCTCCTGCCAGACACAACCATTGGACAGCACATCCATATTAAGAGAC
Maur1b_orf1	TGGTACCAATTCTGCTCCTGCCAGACACAACCATTGGACAGCACATCCATATTAAGAGAC
Maur2_orf1	TGGTACCAATTCTGCTCCTGCCAGACACAACCATTGGACAGCACATCCATATTAAGAGAC
Reun1_orf1	TGGTACCAATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
Reun2_orf1	TGGTACCAATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
SA1_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACAGCACATCCATATTAAGAGAC
Taiw1_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
Taiw2_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
USA1a_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
USA1b_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
USA2a_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC
USA2b_orf1	TGGTGCCTATTCTGCTCCTGCCAGACACAACCATTGGACGGCACATCCATATTAAGAGAC

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Aus1_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
Aus2_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
Braz1_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
Braz2_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
CPam1a_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
CPam1b_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
CPaus1_orf1 AGTACCTCAAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
Haw1_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
Haw2_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
Haw3_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
Maur1a_orf1 AGTACCTCAAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
Maur1b_orf1 AGTACCTCAAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
Maur2_orf1 AGTACCTCAAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
Reun1_orf1 AGTACCTCAAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
Reun2_orf1 AGTACCTCAAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
SA1_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
Taiw1_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGTAACAAACTCTTCTATAGAGTTAAGA
Taiw2_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
USA1a_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
USA1b_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
USA2a_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA
USA2b_orf1 AGTACCTCCAGTCTGTCCTTTTATGGCTTGCCCGCAACAAACTCTACTATAGAGTTAAGA

Aus1_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
Aus2_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
Braz1_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
Braz2_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
CPam1a_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
CPam1b_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
CPaus1_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
Haw1_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
Haw2_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
Haw3_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
Maur1a_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
Maur1b_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
Maur2_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
Reun1_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
Reun2_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
SA1_orf1 GATGCCGTTCCAAGCGGTTTGTGCTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
Taiw1_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
Taiw2_orf1 GATGCCGTTCCAACCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
USA1a_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
USA1b_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
USA2a_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA
USA2b_orf1 GATGCCGTTCCAAGCGGTTTGTACTCGAGCAAGATCACATCGGCCCCGAAC TTTTCCGAA

Aus1_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGATTTTTCAAATGTGGCTCGATTGCAAAACC
Aus2_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGATTTTTCAAATGTGGCTCGATTGCAAAACC
Braz1_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
Braz2_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
CPam1a_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
CPam1b_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAATGTGGCTCGATTGCAAGACA
CPaus1_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
Haw1_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAATGTGGCTCGATTGCAAGACA
Haw2_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAATGTGGCTCGATTGCAAGACA
Haw3_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAATGTGGCTCGATTGCAAGACA
Maur1a_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
Maur1b_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
Maur2_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
Reun1_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
Reun2_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
SA1_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
Taiw1_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
Taiw2_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
USA1a_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
USA1b_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
USA2a_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
USA2b_orf1 CTCAGCTACTCCAGTATGCTGGGTTGGATGTTTTTCAAGATGTGGCTCGATTGCAAGACT
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Aus1_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTTCACCTTCTCGAACACG
Aus2_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTTCACCTTCTCGAACACG
Braz1_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTACACCTTCTCGAACACG
Braz2_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTACACCTTCTCGAACACG
CPam1a_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTTCACCTTCTCGAACACG
CPam1b_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTACACCTTCTCGAACACG
CPaus1_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTACACCTTCTCGAACACG
Haw1_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTACACCTTCTCGAACACG
Haw2_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTACACCTTCTCGAACACG
Haw3_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTACACCTTCTCGAACACG
Maur1a_orf1 TTCTCGAGAGAGGCTACGACTCTTTCCGATCGGTTCTTGGAGTACATCTTCTCGAACACG
Maur1b_orf1 TTCTCGAGAGAGGCTACGACTCTTTCCGATCGGTTCTTGGAGTACATCTTCTCGAACACG
Maur2_orf1 TTCTCGAGAGAGGCTACGACTCTTTCCGATCGGTTCTTGGAGTTCATCTTCTCGAACACG
Reun1_orf1 TTCTCGAGAGAGGCTACGACTCTTTCCGATCGGTTCTTGGAGTACACCTTCTCGAACACG
Reun2_orf1 TTCTCGAGAGAGGCTACGACTCTTTCCGATCGGTTCTTGGAGTACACCTTCTCGAACACG
SA1_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTACACCTTCTCGAACACG
Taiw1_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTACACCTTCTCGAACACG
Taiw2_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTACACCTTCTCGAACACG
USA1a_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTACACCTTCTCGAACACG
USA1b_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTACACCTTCTCGAACACG
USA2a_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTTCACCTTCTCGAACACG
USA2b_orf1 TTCTCGAGAGAGGCTACGACACTTTCCGATCGGTTCTTGGAGTTCACCTTCTCGAACACG
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Aus1_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTATTATGGAACCTGATCAAGCTGTACGTT
Aus2_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTATTATGGAACCTGATCAAGCTGTACGTT
Braz1_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTGTTGTGGAACCTGATCAAGCTGTACGTT
Braz2_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTGTTATGGAACCTGATCAAGCTGTACGTT
CPam1a_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTGTTATGGAACCTGATCAAGCTGTACGTT
CPam1b_orf1 AAAGGTTTGTAGTCGAATCCTTGAACAACCTATTATGGAACCTGATCAAGCTGTACGTT
CPaus1_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTGTTATGGAACCTGATCAAGCTGTACGTT
Haw1_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTATTATGGAGCCTGATCAAGCTGTACGTT
Haw2_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTATTATGGAACCTGATCAAGCTGTACGTC
Haw3_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTATTATGGAACCTGATCAAGCTGTACGTT
Maur1a_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTATTATGGAACCTGATCAGGCTGTACGTT
Maur1b_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTATTATGGAACCTGATCAGGCTGTACGTT
Maur2_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTATTATGGAACCTGATCAGGCTGTACGTT
Reun1_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTATTATGGAACCTGATCAGGCTGTACGTT
Reun2_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTATTATGGAACCTGATCAGGCTGTACGTT
SA1_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTGTTATGGAACCTGATCAAGCTGTACGTT
Taiw1_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTATTATGGAACCTGATCAAGCTGTACGTT
Taiw2_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTGTTATGGAACCTGATCAAGCTGTACGTT
USA1a_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTGTTATGGAACCTGATCAAGCTGTACGTT
USA1b_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTGTTATGGAACCTGATCAAGCTGTACGTT
USA2a_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTGTTATGGAACCTGATCAAGCTGTACGTC
USA2b_orf1 AAAGGTTTGTAGTCGAATTCTTGAACAACCTGTTATGGAACCTGATCAAGCTGTACGTT
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Aus1_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAGACCG
Aus2_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAGACCG
Braz1_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
Braz2_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
CPam1a_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
CPam1b_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
CPaus1_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
Haw1_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAGACCG
Haw2_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAGACCG
Haw3_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
Maur1a_orf1 TGTGCTTTCACTATCACAATGCGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
Maur1b_orf1 TGTGCTTTCACTATCACAATGCGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
Maur2_orf1 TGTGCTTTCACTATCACAATGCGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
Reun1_orf1 TGTGCTTTCACTATCACAATGCGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
Reun2_orf1 TGTGCTTTCACTATCACAATGCGCTTGATCATGACAATGACGATTCTGGCCTGGAAACCG
SA1_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
Taiw1_orf1 TATGCTTTCACTATCATAATGCGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
Taiw2_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
USA1a_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
USA1b_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
USA2a_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
USA2b_orf1 TATGCTTTCACTATCATAACACGCTTGATCATGACGATGACGATTCTGGCCTGGAAACCG
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Aus1_orf1      ATTTTAATAATCTGTCTCTTGGTCGTCCTTACATCGATGGTCTACCACCTAATGAGAAAA
Aus2_orf1      ATTTTAATAATCTGTCTCTTGGTCGTCCTTACATCGATGGTCTACCACCTAATGAGAAAA
Braz1_orf1     ATTTTGATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
Braz2_orf1     ATTTTAATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
CPam1a_orf1   ATTTTGATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
CPam1b_orf1   ATTTTAATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
CPaus1_orf1   ATTTTGATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
Haw1_orf1     ATTTTAATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
Haw2_orf1     ATTTTAATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
Haw3_orf1     ATTTTAATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
Maur1a_orf1   ATTTTAATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
Maur1b_orf1   ATTTTAACAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTGATGAGAAAA
Maur2_orf1    ATTTTAACAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTGATGAGAAAA
Reun1_orf1    ATTTTAATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTGATGAGAAAA
Reun2_orf1    ATTTTAATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTGACGAGAAAA
SA1_orf1      ATTTTGATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
Taiw1_orf1    ATTTTGATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
Taiw2_orf1    ATTTTGATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
USA1a_orf1    ATTTTGATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
USA1b_orf1    ATTTTGATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
USA2a_orf1    ATTTTGATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
USA2b_orf1    ATTTTGATAATCTGTCTCTTGGTCGTCCTTACATCAATGGTCTACCACCTAATGAGAAAA
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Aus1_orf1      TTATTTTCATTCATTCAAATTTGGTGGGTCGTGGCCCTCTTCTCATGATATATAGGACC
Aus2_orf1      TTATTTTCATTCATTCAAATTTGGTGGGTCNTGNCCCTCTTCTCATGATATATAGGACC
Braz1_orf1     TTATTTTCATTCATTCAAATTTGGTGGGTCGTAGCACCTATTCTCATGATATATAGGACC
Braz2_orf1     TTATTTTCATTCATTCAAATTTGGTGGGTCGNAGCACCTATTCTCATGATATATAGGACC
CPam1a_orf1   TTATTTTCATTCATTCAAATTTGGTGGGTCGTAGCACCTATTCTCATGATATATAGGACC
CPam1b_orf1   TTATTTTCATTCATTCAAATTTGGTGGGTTATGGCCCTCTTCTCATGATATATAGGACC
CPaus1_orf1   TTATTTTCATTCATTCAAATTTGGTGGGTCGTAGCACCTATTCTCATGATATATAGGACC
Haw1_orf1     TTATTTTCATTCATTCAAATTTGGTGGGTTATGGCCCTCTTCTCATGATATATAGGACC
Haw2_orf1     TTATTTTCATTCATTCAAATTTGGTGGGTCATGGCCCTCTTCTCATGATATATAGGACC
Haw3_orf1     TTATTTTCATTCATTCAAATTTGGTGGGTTATGGCCCTCTTCTCATGATATATAGGACC
Maur1a_orf1   TTATTTTCATTCATTCAAATCTGGTGGGTCATAGCACCTGTTCTCATGATATATAGGACC
Maur1b_orf1   TTATTTTCATTCATTCAAATCCGGTGGGTCATAGCACCTATTCTCATGATATATAGGACC
Maur2_orf1    TTATTTTCATTCATTCAAATCTGGTGGGTCATAGCACCTATTCTCATGATATATAGGACC
Reun1_orf1    TTATTTTCATTCATTCAAATCTGGTGGGTCATAGCACCTATTCTCATGATATATAGGACC
Reun2_orf1    TTATTTTCATTCATTCAAATCTGGTGGGTCATAGCACCTATTCTCATGATATATAGGACC
SA1_orf1      TTATTTTCATTCATTCAAATTTGGTGGGTCGTAGCACCTATTCTCATGATATATAGGACC
Taiw1_orf1    TTATTTTCATTCATTCAAATTTGGTGGGTCGTAGCACCTATTCTCATGATATATAGGACC
Taiw2_orf1    TTATTTTCATTCATTCAAATTTGGTGGGTCGTAGCACCTATTCTCATGATATATAGGACC
USA1a_orf1    TTATTTTCATTCATTCAAATTTGTTGGGTCGTAGCACCAATTCTCATGATATATAGGACC
USA1b_orf1    TTATTTTCATTCATTCAAATTTGTTGGGTCGTAGCACCAATTCTCATGATATATAGGACC
USA2a_orf1    TTATTTTCATTCATTCAAATTTATTGGGTCGTAGCACCAATTCTCATGATATATAGGACC
USA2b_orf1    TTATTTTCATTCATTCAAATTTATTGGGTCGTAGCACCAATTCTCATGATATATAGGACC
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Aus1_orf1      GTCATGTGGATTACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGC
Aus2_orf1      GTCATGTGGATTACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGC
Braz1_orf1     GTCACGTACATCCACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGT
Braz2_orf1     GTCACGTACATCCACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGT
CPam1a_orf1    GTCACGTACATTCACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGT
CPam1b_orf1    GTCATGTGGATTACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGT
CPaus1_orf1    GTCACGTACATTCACAGGAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGT
Haw1_orf1      GTCATGTGGATTACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGT
Haw2_orf1      GTCATGTGGATTACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGT
Haw3_orf1      GTCATGTGGATTACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGT
Maur1a_orf1    GTCATATGCATTACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGC
Maur1b_orf1    GTCATATGCATTACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGC
Maur2_orf1     GTCATCTGCATTACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGC
Reun1_orf1     GTCATATGCATTACAGGAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGC
Reun2_orf1     GTCATATGCATTACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGC
SA1_orf1       GTCACGTACATTCACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGT
Taiw1_orf1     GTCACGTACATTCACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGT
Taiw2_orf1     GTCACGTACATTCACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGT
USA1a_orf1     GTCACGTACATTCACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGT
USA1b_orf1     GTCACGTACATTCACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGT
USA2a_orf1     GTCACGTACATTCACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGT
USA2b_orf1     GTCACGTACATTCACAGAAAGGTTGTTTCGCTTCACGTGGGGACGAGAAAATGGTCCAAGGT
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Aus1_orf1      TTCAAAAGTTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
Aus2_orf1      TTCAAAAGTTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
Braz1_orf1     TTCAAAAGCTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
Braz2_orf1     TTCAAAAGCTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
CPam1a_orf1    TTCAAAAGCTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
CPam1b_orf1    TTCAAAAGTTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
CPaus1_orf1    TTCAAAAGCTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
Haw1_orf1      TTCAAAAGTTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
Haw2_orf1      TTCAAAAGTTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
Haw3_orf1      TTCAAAAGTTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
Maur1a_orf1    TTTAAGAGCTTCGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
Maur1b_orf1    TTTAAGAGCTTCGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
Maur2_orf1     TTTAAGAGCTTCGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
Reun1_orf1     TTTAAGAGCTTCGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
Reun2_orf1     TTTAAGAGCTTCGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
SA1_orf1       TTCAAAAGCTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
Taiw1_orf1     TTCAAAAGCTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
Taiw2_orf1     TTCAAAAGCTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
USA1a_orf1     TTCAAAAGCTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
USA1b_orf1     TTCAAAAGCTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
USA2a_orf1     TTCAAAAGCTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
USA2b_orf1     TTCAAAAGCTTTGCCGTCCCCATGTCACCACCAGGACACTCAGTGCTTGAGATAGTACAC
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Aus1_orf1 CCTGATGGTTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAGAACGGGGAAGAGGGT
Aus2_orf1 CCTGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAGAACGGGGAAGAGGCT
Braz1_orf1 CCCGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAAAACGGGGAAGAGGCT
Braz2_orf1 CCCGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAAAACGGGGAAGAGGCT
CPam1a_orf1 CCCGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAAAACGGGGAAGAGGCT
CPam1b_orf1 CCTGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAAAACGGGGAAGAGGCT
CPaus1_orf1 CCCGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAAAACGGGGAAGAGGCT
Haw1_orf1 CCTGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAAAACGGGGAAGAGGCT
Haw2_orf1 CCTGATGATTCTCACATGGGGTATGCATCCTGTGTTTCGATTGAAAAACGGGGAAGAGGCT
Haw3_orf1 CCTGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAAAACGGGGAAGAGGCT
Maur1a_orf1 CCCGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAGAACGGGGAAGAGGCT
Maur1b_orf1 CCCGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAGAACGGGGAAGAGGCT
Maur2_orf1 CCCGATGATTCCCACATGGGATATGCATCCTGTGTTTCGATTGAAGGACGGGGAAGAGGCT
Reun1_orf1 CCCGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAGAACGGGGAAGAGGCT
Reun2_orf1 CCCGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAGAACGGGGAAGAGGCT
SA1_orf1 CCCGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAAAACGGGGAAGAGGCT
Taiw1_orf1 CCCGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAAAACGGGGAAGAGGCT
Taiw2_orf1 CCCGATGATTCTCACATGAGATATGCATCCTGTGTTTCGATTGAAAAACGGGGAAGAGGCT
USA1a_orf1 CCCGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAAAACGGGGAAGAGGCT
USA1b_orf1 CCCGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAAAACGGGGAAGAGGCT
USA2a_orf1 CCCGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAGAACGGGGAAGAGGCT
USA2b_orf1 CCCGATGATTCTCACATGGGATATGCATCCTGTGTTTCGATTGAAGAACGGGGAAGAGGCT
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Aus1_orf1 CTCATGACATCTGTTCACTGTATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
Aus2_orf1 CTCATGACATCTGTTCACTGTATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
Braz1_orf1 CTCATGACATCCGTTCACTGCATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
Braz2_orf1 CTCATGACATCCGTTCACTGCATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
CPam1a_orf1 CTCATGACATCCGTTCACTGTATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
CPam1b_orf1 CTCATGACATCCGTTCACTGCATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
CPaus1_orf1 CTCATGACATCCGTTCACTGCATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
Haw1_orf1 CTCATGACATCCGTTCACTGCATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
Haw2_orf1 CTCATGACATCCGTTCACTGCATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
Haw3_orf1 CTCATGACATCCGTTCACTGCATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
Maur1a_orf1 CTCATGACTTCCGTACTGCATAAGCGATGCTTTCAAAGTTCGCTCGTTTCAGAAACGGA
Maur1b_orf1 CTCATGACTTCCGTACTGCATAAGCGATGCTTTCAAAGTTCGCTCGTTTCAGAAACGGA
Maur2_orf1 CTTATGACTTCCGTACTGCATAAGCGATGCTTTCAAAGTTCGCTCATTCAGAAACGGA
Reun1_orf1 CTCATGACTTCCGTACTGCATAAGCGATACTTTCAAAGTTCGCTCGTTTCAGAAACGGA
Reun2_orf1 CTCATGACTTCCGTACTGTATAAGCGATGCTTTCAAAGTTCGCTCGTTTCAGAAACGGA
SA1_orf1 CTCATGACATCCGTTCACTGCATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
Taiw1_orf1 CTCATGACATCCGTTCACTGCATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
Taiw2_orf1 CTCATGACATCCGTTCACTGCATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
USA1a_orf1 CTCATGACATCCGTTCACTGCATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
USA1b_orf1 CTCATGACATCCGTTCACTGCATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
USA2a_orf1 CTCATGACATCCGTTCACTGCATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
USA2b_orf1 CTCATGACATCCGTTCACTGCATAAGCGATTCTTTCAAAGTTCGCTCGTTTCAGGAATGGT
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Aus1_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTGTTGCCCGCCAATGTGATGGATATCGTT
Aus2_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTGTTGCCCGCCAATGCGATGGATATCGTT
Braz1_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTGTTGCCCGCCAATGCGATGGACATTGTT
Braz2_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTGTTGCCCGCCAATGCGATGGACATCGTT
CPam1a_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTACTGTTGCCCGCCAATGCGATGGACATTGTT
CPam1b_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTGTTGCCCGCCAATGTGATGGATATTGTT
CPaus1_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTACTGTTGCCCGCCAATGCGATGGACATTGTT
Haw1_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTGTTGCCCGCCAATGTGATGGATATCGTT
Haw2_orf1 ATCAAAATCCCTCTAACGGAATTC AAGTGCTGTTGCCCGCCAATGTGATGGATATCGTT
Haw3_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTGTTGCCCGCCAATGTGATGGATATCGTT
Maur1a_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTATTGCCCGCCAATGCGATGGACATTGTT
Maur1b_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTACTGCCCGCCAATGCGATGGACATTGTT
Maur2_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTACTGCCCGCCAATGCGATGGACATTGTT
Reun1_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTACTGCCCGCCAATGTGATGGACATTGTT
Reun2_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTACTGCCCGCCAATGCGATGGACATTGTT
SA1_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTGTTGCCCGCCAATGCGATGGACATTGTT
Taiw1_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTGTTGCCCGCCAATGCGATGGACATTGTT
Taiw2_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTGTTGCCCGCCAATGCGATGGACATTGTT
USA1a_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTGTTGCCCGCCAATGCGATGGACATTGTT
USA1b_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTGCTGTTGCCCGCCAATGCGATGGACATTGTT
USA2a_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTACTGTTGCCCGCCAATGCGATGGACATTGTT
USA2b_orf1 ATCAAGATCCCTCTAACGGAATTC AAGTACTGTTGCCCGCCAATGCGATGGACATTGTT
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Aus1_orf1 CTTCTTCGAGGCCACCCGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
Aus2_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
Braz1_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
Braz2_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
CPam1a_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
CPam1b_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
CPaus1_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
Haw1_orf1 CTTCTTCGAGGCCACCCGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
Haw2_orf1 CTTCTTCGAGGCCACCCGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
Haw3_orf1 CTTCTTCGAGGCCACCCGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
Maur1a_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
Maur1b_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
Maur2_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
Reun1_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
Reun2_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
SA1_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
Taiw1_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
Taiw2_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
USA1a_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
USA1b_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
USA2a_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
USA2b_orf1 CTTCTTCGAGGCCACCTGAGTGGAAATCCATCCTTGGAGCCAAAGCAGCCCATTTCACT
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Aus1_orf1      CCAGTCAACCAGCTCAACAAAGGAGCTGTGTCTTTCTTCATTTTCGACAAGGAGTGGATG
Aus2_orf1      CCAGTCAACCAGCTCAACAAAGGAGCTGTGTCTTTCTTCATTTTCGACAAGGAGTGGATG
Braz1_orf1     CCAGTCAACCAGCTCAACAAAGGAGCTGTGTCTTTCTTCATTTTCGACAAGGAGTGGATG
Braz2_orf1     CCAGTCAACCAGCTCAACAAAGGAGCTGTGTCTTTCTTCATTTTCGACAAGGAGTGGATG
CPam1a_orf1    CCAGTCAACCAGCTCAACAAAGGGGCTGTGTCTTTCTTCATTTTCGACAAGGAGTGGATG
CPam1b_orf1    CCAGTCAACCAGCTCAACAAAGGAGCTGTGTCTTTCTTCATTTTCGATAAAGGAGTGGATG
CPaus1_orf1    CCAGTCAACCAGCTCAACAAAGGGGCTGTGTCTTTCTTCATTTTGGACAAGGAGTGGATG
Haw1_orf1     CCAGTCAACCAGCTCAACAAAGGAGCTGTGTCTTTCTTCATTTTCGATAAAGGAGTGGATG
Haw2_orf1     CCAGTCAACCAGCTCAACAAAGGAGCTGTGTCTTTCTTCATTTTCGATAAAGGAGTGGATG
Haw3_orf1     CCAGTCAACCAGCTCAACAAAGGAGCTGTGTCTTTCTTCATTTTCGATAAAGGAGTGGATG
Maur1a_orf1    CCTGTCAACCAGCTCAACAAAGGAGCTGTTTCCTTCTTTATTTTGGACAAAGAGTGGATG
Maur1b_orf1    CCTGTCAACCAGCTCAACAAAGGAGCTGTTTCCTTCTTTATTTTGGACAAAGAGTGGATG
Maur2_orf1    CCTGTCAACCAGCTCAACAAAGGAGCTGTTTCCTTCTTTATTTTGGACAAAGAGTGGATG
Reun1_orf1    CCTGTCAACCAGCTCAACAAAGGAGCTGTTTCCTTCTTTATTTTGGACAAAGAGTGGATG
Reun2_orf1    CCTGTCAACCAGCTCAACAAAGGAGCTGTTTCCTTCTTTATTTTGGACAAAGAGTGGATG
SA1_orf1      CCAGTCAACCAGCTCAACAAAGGAGCTGTGTCTCTCTTCATTTTCGACAAGGAGTGGATG
Taiw1_orf1    CCAGTCAACCAGCTCAACAAAGGGGCTGTGTCTTTCTTCATCTTCGACAAGGAGTGGATG
Taiw2_orf1    CCAGTCAACCAGCTCAACAAAGGAGCTGTGTCTTTCTTCATTTTCGACAAGGAGTGGATG
USA1a_orf1    CCAGTCAACCAGCTCAACAAAGGGGCTGTGTCTTTCTTCATTTTCGACAAGGAGTGGATG
USA1b_orf1    CCAGTCAACCAGCTCAACAAAGGGGCTGTGTCTTTCTTCATTTTCGACAAGGAGTGGATG
USA2a_orf1    CCAGTCAACCAGCTCAACAAAGGGGCTGTGTCTTTCTTCATTTTCGACAAGGAGTGGATG
USA2b_orf1    CCAGTCAACCAGCTCAACAAAGGGGCTGTGTCTTTCTTCATTTTCGACAAGGAGTGGATG
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Aus1_orf1      ATGCACAATGCAAAGATTACAGGAAGCTGATGGCTTTTACGCCACAGTTCTTAGTAACACT
Aus2_orf1      ATGCACAATGCAAAGATTACAGGAAGCTGATGGCTTTTACGCCACAGTTCTTAGTAACACT
Braz1_orf1     ATGCACAATGCAAAAAGTACAGGAAGCTGATGGTTTTTATGCCACAGTTCTTAGTAACACT
Braz2_orf1     ATGCACAACGCAAAAAGTACAGGAAGCTGATGGTTTTTATGCCACAGTTCTTAGTAACACT
CPam1a_orf1    ATGCACAACGCAAAAAGTTACAGGAAGCTGATGGTTTTTATGCCACAGTTCTTAGTAACACT
CPam1b_orf1    ATGCACAATGCAAAGATTACAGGAAGCTGATGGTTTTTATGCCACAGTTCTTAGTAACACT
CPaus1_orf1    ATGCACAACGCAAAAAGTTACAGGAAGCTGATGGTTTTTATGCCACAGTTCTTAGTAACACT
Haw1_orf1     ATGCACAATGCAAAGATTACAGGAAGCTGATGGTTTTTATGCCACAGTTCTTAGTAACACT
Haw2_orf1     ATGCACAATGCAAAGATTACAGGAAGCTGATGGTTTTTATGCCACAGTTCTTAGTAACACT
Haw3_orf1     ATGCACAACGCAAAAAGTACAGGAAGCTGATGGTTTTTACGCCACAGTTCTTAGTAACACT
Maur1a_orf1    ATGCACAACGCAAAAAGTTACGGGAAGCTGATGGCTTTTATGCCACAGTTCTTAGCAACACC
Maur1b_orf1    ATGCACAACGCAAAAAGTTACGGGAAGCTGATGGCTTTTATGCCACAGTTCTTAGCAACACC
Maur2_orf1    ATGCACAACGCAAAAAGTTACGGGAACCGATGGCTTTTACGCCACAGTTCTTAGCAATACT
Reun1_orf1    ATGCACAATGCAAAAAGTTACGGGAACCGATGGTTTTTATGCCACAGTTCTTAGCAACACT
Reun2_orf1    ATGCACAACGCAAAAAGTTACGGGAACCGATGGTTTTTATGCCACAGTTCTTAGCAACACT
SA1_orf1      ATACACAACGCAAAAGTTACAGGAAGCTGATGGTTTTTACGCCACAGTTCTTAGTAACACT
Taiw1_orf1    ATGCACAACGCAAAAAGTTACAGGAAGCTGATGGTTTTTATGCCACAGTTCTTAGTAACACT
Taiw2_orf1    ATGCACAACGCAAAAAGTTACAGGAAGCTGATGGTTTTTATGCCACAGTTCTTAGTAACACT
USA1a_orf1    ATGCACAACGCAAAAAGTTACAGGAAGCTGATGGTTTTTATGCCACAGTTCTTAGTAACACT
USA1b_orf1    ATGCACAACGCGAAAAGTTACAGGAAGCTGATGGTTTTTATGCCACAGTTCTTAGTAACACT
USA2a_orf1    ATGCACAATGCAAAAAGTTACAGGAAGCTGATGGTTTTTATGCCACAGTTCTTAGTAACACT
USA2b_orf1    ATGCACAACGCAAAAAGTTACAGGAAGCTGATGGTTTTTATGCCACAGTTCTTAGTAACACT
** ***** ** ** * ** ***** ***** ***** ***** ***** ** **

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Aus1_orf1      GAGAAAGGCTACAGTGGCGCCCCCTACTGGAATGGGAAATCTATAGTAGGGGTACATAAA
Aus2_orf1      GAGAAAGGCTACAGTGGCGCCCCCTACTGGAATGGGAAATCTATAGTAGGGGTACATAAA
Braz1_orf1     GAGAAGGGCTACAGTGGCGCCCCCTACTGGAATGGGAAATCTATAGTAGGGGTGCATAAA
Braz2_orf1     GAGAAGGGCTACAGTGGCGCCCCCTACTGGAATGGNAAATCTATAGTAGGGGTGCATAAA
CPam1a_orf1    GAGAAGGGCTACAGTGGCGCCCCCTACTGGAATGGGAAATCTATAGTAGGGGTGCACAAA
CPam1b_orf1    GAGAAGGGCTACAGTGGCGCCCCCTATTGGAACGGGAAATCTATAGTAGGGGTGCATAAA
CPaus1_orf1    GAGAAGGGCTACAGTGGCGCCCCCTACTGGAATGGGAAATCTATAGTAGGGGTGCATAAA
Haw1_orf1     GAGAAGGGCTACAGTGGCGCCCCCTATTGGAACGGGAAATCTATAGTAGGGGTGCATAAA
Haw2_orf1     GAGAAGGGCTACAGTGGCGCCCCCTATTGGAACGGGAAATCTATAGTAGGGGTGCATAAA
Haw3_orf1     GAGAAGGGCTACAGTGGCGCCCCCTATTGGAACGGGAAATCTATAGTAGGGGTGCATAAA
Maur1a_orf1    GAAAAGGGCTACAGTGGCGCTCCCTACTGGAACGGTAAATCAATAGTGGGAGTTCATAAA
Maur1b_orf1    GAAAAGGGCTACAGTGGCGCTCCCTACTGGAACGGTAAATCCATAGTGGGAGTTCATAAA
Maur2_orf1     GAAAAGGGCTACAGTGGCGCTCCCTACTGGAACGGTAAATCCATAGTGGGAGTTCATAAA
Reun1_orf1     GAAAAGGGCTACAGTGGCGCTCCCTACTGGAACGGCAAATCAATAGTGGGAGTTCATAAA
Reun2_orf1     GAAAAGGGCTACAGTGGCGCTCCCTACTGGAACGGTAAATCCATAGTGGGAGTTCATAAA
SA1_orf1       GAGAAGGGCTACAGTGGCGCCCCCTACTGGAATGGGAAATCTATAGTAGGGGTGCATAAA
Taiw1_orf1    GAGAAGGGCTACAGTGGCGCCCCCTACTGGAATGGGAAATCTATAGTAGGGGTGCATAAA
Taiw2_orf1    GAGAAGGGCTACAGTGGCGCCCCCTACTGGAATGGGAAATCTATAGTAGGGGTACATAAA
USA1a_orf1    GAGAAGGGCTACAGTGGCGCCCCCTACTGGAATGGGAAATCTATAGTAGGGGTGCATAAA
USA1b_orf1    GAGAAGGGCTACAGTGGCGCCCCCTACTGGAATGGGAAATCTATAGTAGGGGTGCATAAA
USA2a_orf1    GAGAAGGGCTACAGTGGCGCCCCCTACTGGAATGGGAAATCTATAGTAGGGGTGCATAAA
USA2b_orf1    GAGAAGGGCTACAGTGGCGCCCCCTACTGGAATGGGAAATCTATAGTAGGGGTGCATAAA
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Aus1_orf1      GGGCATGTGTACGGAGACGATTCCAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
Aus2_orf1      GGGCATGTGTACGGAGACGATTCCAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
Braz1_orf1     GGGCACGTGTACGGAGACGATTCCAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
Braz2_orf1     GGGCACGTGTACGGAGACGATTCCAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
CPam1a_orf1    GGGCACGTGTACGGAGACGACTCCAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
CPam1b_orf1    GGGCATGTGTACGGAGACGATTCCAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
CPaus1_orf1    GGGCACGTGTACGGAGACGATTCCAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
Haw1_orf1     GGGCATGTGTACGGAGACGATTCTAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
Haw2_orf1     GGGCATGTGTACGGAGACGATTCCAAGAATTACAATCTTATGTGCGCCAATTCCCCCTGTC
Haw3_orf1     GGGCATGTGTACGGAGACGATTCCAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
Maur1a_orf1    GGGCACGTGTACGGAGACGACTCCAAGAATTACAATCTCATGTGCGCCAATACCCCTGTC
Maur1b_orf1    GGGCACGTGTACGGAGACGACTCCAAGAATTACAATCTCATGTGCGCCAATACCCCTGTC
Maur2_orf1     GGGCACGTGTACGGAGACGACTCCAAGAATTACAATCTTATGTGCGCCAATACCCCTGTC
Reun1_orf1     GGGCACGTGTACGGAGACGACTCCAAGAATTACAATCTCATGTGCGCCAATACCCCTGTC
Reun2_orf1     GGGCACGTGTACGGAGACGACTCCAAGAATTACAATCTCATGTGCGCCAATACCCCTGTC
SA1_orf1       GGGCACGTGTACGGAGACGATTCCAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
Taiw1_orf1    GGGCACGTGTACGGAGACGATTCCAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
Taiw2_orf1    GGGCACGTGTACGGAGACGATTCCAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
USA1a_orf1    GGGCACGTGTACGGAGACGATTCCAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
USA1b_orf1    GGGCACGTGTACGGAGACGATTCCAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
USA2a_orf1    GGGCACGTGTACGGAGACGATTCCAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
USA2b_orf1    GGGCACGTGTACGGAGACGATTCCAAGAATTACAATCTTATGTGCGCCGATTCCCCCTGTC
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Aus1_orf1 AAAGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
Aus2_orf1 AAAGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
Braz1_orf1 AAGGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
Braz2_orf1 AAGGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
CPam1a_orf1 AAGGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
CPam1b_orf1 AAGGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTACAAGGAGATGTCTTT
CPaus1_orf1 AAGGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
Haw1_orf1 AAGGGGTTAACGGCGCCTAATTTTGTGTATGANTCTCCGTCTCTACAAGGAGATGTCTTT
Haw2_orf1 AAGGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
Haw3_orf1 AAGGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTACAAGGAGATGTCTTT
Maur1a_orf1 AAGGGGTTGACAGCGCCTAATTTTGTGTACGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
Maur1b_orf1 AAGGGGTTGACAGCGCCTAATTTTGTGTACGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
Maur2_orf1 AAGGGGTTGACAGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
Reun1_orf1 AAGGGGTTGACAGCGCCTAATTTTGTGTACGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
Reun2_orf1 AAGGGGTTGACAGCGCCTAATTTTGTGTACGAGTCTCCGTCTCTTCAAGGAGATGTCTTT
SA1_orf1 AAGGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
Taiw1_orf1 AAGGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
Taiw2_orf1 AAGGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
USA1a_orf1 AAGGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
USA1b_orf1 AAGGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
USA2a_orf1 AAGGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
USA2b_orf1 AAGGGGTTAACGGCGCCTAATTTTGTGTATGAGTCTCCGTCTCTGCAAGGAGATGTCTTT
** ***** ** ***** *****

Aus1_orf1 AGCGACGCCGACGTTTTAGACATTGCTGATTACGCCGAGGAGGTGTATGAGAAAACCCCTT
Aus2_orf1 AGCGACGCCGACGTTTTAGACATTGCTGATTACGCCGAGGAGGTGTATGAGAAAACCCCTT
Braz1_orf1 AGCGACGCCGACGTTTTAGACATTGCTGATTACGCCGAGGAGGTGTATGAGAAANCCCNT
Braz2_orf1 AGCGACGCCGACGTTTTAGACATTGCTGATTACGCCGAAGAGGTGTATGAGAAAGCCCTT
CPam1a_orf1 AGCGACGCCGACGTTTTAGACATTGCTGATTACGCCGAGGAGGTGTATGAGAAAACCCCTT
CPam1b_orf1 AGCGACGCCGACGTTTTAGACATTGCTGATTACGCCGAGGAGGTGTATGAGAAAACCCCTT
CPaus1_orf1 AGCGACGCCGACGTTTTAGACATTGCTGATTACGCCGAGGAGGTGTATGAGAAAACCCCTT
Haw1_orf1 AGCGACGCCGACGTTTTAGACATTGCTGATTACGCCGAGGAGGTGTATGAGAAAACCCCTT
Haw2_orf1 AGCGATGCCGACGTTTTAGACATTGCTGATTACGCCGAGGAGGTGTATGAGAAAACCCCTT
Haw3_orf1 AGCGACGCCGACGTTTTAGACATTGCTGATTACGCCGAAGAGGTGTATGAGAAAACCCCTT
Maur1a_orf1 AGCGACGCCGACGTTTTAGACATTGCCGACTACGCTGAAGAAGTGTATGAGAAAACCCCTT
Maur1b_orf1 AGCGACGCCGACGTTTTAGACATTGCCGACTACGCTGAAGAAGTGCATGAGAAAACCCCTT
Maur2_orf1 AGCGACGCCGACGTTTTAGACATTGCCAACTACGCTGAAGAAGTGTATGAGAAAACCCCTT
Reun1_orf1 AGCGACGCCGACGTTTTAGACATTGCCGACTACGCTGAAGAAGTGTATGAGAAAACCCCTT
Reun2_orf1 AGCGACGCCGACGTTTTAGACATTGCCGACTACGCTGAAGAAGTGTATGAGAAAACCCCTT
SA1_orf1 AGCGACGCCGACGTTTTAGACATTGCTGATTACGCCGAGGAGGTGTATGAGAAAACCCCTT
Taiw1_orf1 AGCGACGCCGACGTTTTAGACATTGCTGATTACGCCGAGGAGGTGTATGAGAAAACCCCTT
Taiw2_orf1 AGCGACGCCGACGTTTTAGACATTACTGATTACGCCGAGGAGGTGTATGAGAAAACCCCTT
USA1a_orf1 AGCGACGCCGACGTTTTAGACATTGCTGATTACGCCGAGGAGGTGTATGAGAAAACCCCTT
USA1b_orf1 AGCGACGCCGACGTTTTAGACATTGCTGATTACGCCGAGGAGGTGTATGAGAAAACCCCTT
USA2a_orf1 AGCGACGCCGACGTTTTAGACATTGCTGATTACGCCGAGGAGGTGTATGAGAAAACCCCTT
USA2b_orf1 AGCGACGCCGACGTTTTAGACATTGCTGATTACGCCGAGGAGGTGTATGAGAAAACCCCTT
***** ***** * * ***** ** ** ** ***** ** *

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Aus1_orf1 GCAGAGCCTAAAGTGTGGAAACCTGCCAGCGGCAAATACTGGTGGGAAATGGCTGAAGAA
Aus2_orf1 GCAGAGCCTAAAGTGTGGAAACCTGCCAGCGGCAAATACTGGTGGGAAATGGCTGAAGAA
Braz1_orf1 GCAGAGCCTAAAGTGTGGAAACCTGCCAGCGGTAAATACTGGTGGGAAATGGCTGAAGAA
Braz2_orf1 GCAGAGCCTAAAGTGTGGAAACCTGCCAGCGGTAAATACTGGTGGGAAATGGCTGAAGAA
CPam1a_orf1 GCAGAGCCTAAAGTGTGGAAACCTGCCAGCGGTAAATACTGGTGGGAAATGGCTGAAGAA
CPam1b_orf1 GCAGAGCCTAAAGTGTGGAAACCCGCCAGCGGCAAATACTGGTGGGAGATGGCCGAAGAA
CPaus1_orf1 GCAGAGCCTAAAGTGTGGAAACCTGCCAGCGGTAAATACTGGTGGGAAATGGCTGAAGAA
Haw1_orf1 GCAGAGCCTAAAGTGTGGAAACCCGCCAGCGGCAAATACTGGTGGGAGATGGCCGAAGAA
Haw2_orf1 GCAGAGCCTAAAGTGTGGAAACCCGCCAGCGGCAAATACTGGTGGGAGATGGCCGAAGAA
Haw3_orf1 GCAGAGCCTAAAGTGTGGAAACCCGCCAGCGGCAAATACTGGTGGGAGATGGCCGAAGAA
Maur1a_orf1 GCAGAGCCCAAAGTGTGGAAACCCGCCAGCGGCAAATACTGGTGGGAAATGGCTGAAGAA
Maur1b_orf1 GCAGAGCCCAAAGTGTGGAAACCCGCCAGCGGCAAATACTGGTGGGAAATGGCTGAAGAA
Maur2_orf1 GCAGAGCCCAAAGTGTGGAAACCCGCCAGCGGCAAATACTGGTGGGAAATGGCTGAAGAA
Reun1_orf1 GCAGAGCCCAAAGTGTGGAAACCCGCCAGCGGCAAATACTGGTGGGAAATGGCTGAAGAA
Reun2_orf1 GCAGAGCCCAAAGTGTGGAAACCCGCCAGCGGCAAATACTGGTGGGAAATGGCTGAAGAA
SA1_orf1 GCAGAGCCTAAAGTGTGGAAACCTGCCAGCGGCAAATACTGGTGGGAAATGGCTGAAGAA
Taiw1_orf1 GCAGAGCCTAAAGTGTGGAAACCTGCCAGCGGTAAATACTGGTGGGAAATGGCTGAAGAA
Taiw2_orf1 GCAGAGCCTAAAGTGTGGAAACCTGCCAGCGGTAAATACTGGTGGGAAATGGCTGAAGAA
USA1a_orf1 GCAGAGCCTAAAGTGTGGAAACCTGCCAGCGGTAAATACTGGTGGGAAATGGCTGAAGAA
USA1b_orf1 GCAGAGCCTAAAGTGTGGAAACCTGCCAGCGGTAAATACTGGTGGGAAATGGCTGAAGAA
USA2a_orf1 GCAGAGCCTAAAGTGTGGAAACCTGCCAGCGGTAAATACTGGTGGGAAATGGCTGAAGAA
USA2b_orf1 GCAGAGCCTAAAGTGTGGAAACCTGCCAGCGGTAAATACTGGTGGGAAATGGCTGAAGAA
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Aus1_orf1 GAGGATGATTTTGTCTGTTGAGGCAAATTCACCCCTCCCTGATAAACCTGTTGAGAACGCT
Aus2_orf1 GAGGATGATTTTGTCTGTTGAGGCAAATTCACCCCTCCCTGATAAACCTGTTGAGAACGCT
Braz1_orf1 GAGGATGATTTTGTCTGTTGAGGCAAAGTACCTCCCCCTGATAAACCTGTTGAGAACGCT
Braz2_orf1 GAGGATGATTTTGTCTGTTGAGGCAAAGTACCTCCCCCTGATAAACCTGTTGAGAACGCT
CPam1a_orf1 GAGGATGATTTTGTCTGTTGAGGCAAAGTTACCTCCCCCTGATAAACCTGTTGAGAACGCT
CPam1b_orf1 GAGGATGATTTTGTCTGTTGAGGCAAATTCACCTCCCCCTGATAAACCTGTTGAGAACGCT
CPaus1_orf1 GAGGATGATTTTGTCTGTTGAGGCAAAGTACCTCCCCCTGATAAACCTGTTGAGAACGCT
Haw1_orf1 GAGGATGATTTTGTCTGTTGAGGCAAATTCACCTCTCCCTGATAAACCTGTTGAGAACGCT
Haw2_orf1 GAGGATGATTTTGTCTGTTGAGGCAAATTCACCTCCCCCTGATAAACCTGTTGAGAACGCT
Haw3_orf1 GAGGATGATTTTGTCTGTTGAGGCAAATTCACCTCCCCCTGATAAACCTGTTGAGAACGCT
Maur1a_orf1 GAGGATGATTTTGTCTGTTGAGGCTAATCTTCTCCCCCTGATAAACCTGTTGAGAACTCT
Maur1b_orf1 GAGGATGATTTTGTCTGTTGAGGCTAATCTTCTCCCCCTGATAAACCTGTTGAGAACTCT
Maur2_orf1 GAGGATGATTTTGTCTGTTGAGGCTAATCTTCTCCCCCTGGTAAACCTGTTGAGAACTCC
Reun1_orf1 GAGGATGATTTTGTCTGTTGAGGCTAATCTTCTCCCCCTGATAAACCTGTTGAGAACTCT
Reun2_orf1 GAGGATGATTTTGTCTGTTGAGGCTAATCTTCTCCCCCTGATAAACCTGTTGAGAACTCT
SA1_orf1 GAGGATGATTTTGTCTGTTGAGGCAAAGTACCTCCCCCTGATAAACCTGTTGAGAACGCT
Taiw1_orf1 GAGGATGATTTTGTCTGTTGAGGCAAAGTACCTCCCCCTGATAAACCTGTTGAGAACGCT
Taiw2_orf1 GAGGATGATTTTGTCTGTTGAGGCAAAGTACCTCCCCCTGATAAACCTGTTGAGAACGCT
USA1a_orf1 GAGGATGATTTTGTCTGTTGAGGCAAAGTACCTCCCCCTGATAAACCTGTTGAGAACGCT
USA1b_orf1 GAGGATGATTTTGTCTGTTGAGGCAAAGTACCTCCCCCTGATAAACCTGTTGAGAACGCT
USA2a_orf1 GAGGATGATTTTGTCTGTTGAGGCAAAGTACCTCCCCCTGATAAACCTGTTGAGAACGCT
USA2b_orf1 GAGGATGATTTTGTCTGTTGAGGCAAAGTACCTCCCCCTGATAAACCTGTTGAGAACGCT
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Aus1_orf1 ACAGCAAAGAGCAGACTCCAGCTTCGACTGTGCGAGAAAGCTATGGTTGCTGATAAGCCG
Aus2_orf1 ATAGCAAAGAGCAGACTCCAGCTTCGACTGTGCGAGAAAGCTACGGTTGCTGATAAGCCG
Braz1_orf1 ACAGCAAAGAGCAGACTCCAGCTNCGACTGTGCGAGAAAGCTATGGTTGCTGATCAGCNG
Braz2_orf1 ACAGCAAAGAGCAGACTCCAGCTTCGACTGTGCGAGAAAGCTATGGTTGCTGGTCAGCCG
CPam1a_orf1 ACAGCAAAGAGCAGACTCCAGCTCCGACTGTGCGAGAAAGCTATGGTTGCTGATCAGCCG
CPam1b_orf1 ACAG-----ATAAGCCG
CPaus1_orf1 ACAGCAAAGAGCAGACTCCAGCTCCGACTGTGCGAGAAAGCTATGGTTGCTGATCAGCCG
Haw1_orf1 ACAGCAAAGAGCAGACTCCAGTTTTGACTGTGCGAGAAAGCTACGGTTGCTGATAAGCCG
Haw2_orf1 ACAGCAAAGAGCAGACTCCAGTTTTGACTGTGCGAGAAAGCTACGGTTGCTGATAAGCCG
Haw3_orf1 ACAGCAAAGAGCAGACTCCAGCTTTGACTGTGCGAGAAAGCTACGGTTGCTGATAAGCCG
Maur1a_orf1 ACGGCAAAGAGCAGACTCCAGCTTCGACTGTTGAGAAAGCTACAGNTGCCGGTCAGATG
Maur1b_orf1 ACGGCAAAGAGCAGACTCCAGCTTCGACTGTTGAGAAAGCTACAGTTGCCGGTCAGATG
Maur2_orf1 ACGGCAAAGAGCAGACTCCAGCTTCGACTGTTGAGAAAGCTACAGTTGCCGGTCAGATG
Reun1_orf1 ACGGCAAAGAGCAGACTCCAGCTTCGACTGTTGAGAAAGCTACAGTTGCCGGTCAGATG
Reun2_orf1 ACGGCAAAGAGCAGACTCCAGCTTCGACTGTTGAGAAAGCTACAGTTGCCGGTCAGATG
SA1_orf1 ACAGCAAAGAGCAGACTCCAGCTCCGACTGTGCGAGAAAGCTATGGTTGCTGATCAGCCG
Taiw1_orf1 ACAGCAAAGAGCAGACTCCAGCTTCGACTGTGCGAGAAAGCTATGGTTGCTGATCAGCCG
Taiw2_orf1 ACAGCAAAGAGCAGACTCCAGCTCCGACTGTGCGAGAAAGCTATGGTTGCTGATCAGCCG
USA1a_orf1 ACAGCAAAGAGCAGACTCCAGCTCCGACTGTGCGAGAAAGCTATGGTTGCTGATCAGCCG
USA1b_orf1 ACAGCAAAGAGCAGACTCCAGCTCCGACTGTGCGAGAAAGCTATGGTTGCTGATCAGCCG
USA2a_orf1 ACAGCAAAGAGCAGACTCCAGCTTTGACTGTGCGAGAAAGCTATGGTTGCTGATCAGCCG
USA2b_orf1 ACAGCAAAGAGCAGACTCCAGCTCCGACTGTGCGAGAAAGCTATGGTTGCTGATCAGCCG
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Aus1_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
Aus2_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
Braz1_orf1 ACTCCAGACCAGGGAAACGAGCCNAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
Braz2_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
CPam1a_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
CPam1b_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
CPaus1_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAATACCGGAATCCACC
Haw1_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
Haw2_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
Haw3_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
Maur1a_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
Maur1b_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACGCGGAATCCACC
Maur2_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
Reun1_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
Reun2_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
SA1_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
Taiw1_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
Taiw2_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
USA1a_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
USA1b_orf1 ACTCCAGACCAGGGAAACGAGCCGAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
USA2a_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
USA2b_orf1 ACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGAATCCACC
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Aus1_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
Aus2_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
Braz1_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
Braz2_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
CPam1a_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
CPam1b_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
CPaus1_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
Haw1_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
Haw2_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
Haw3_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
Maur1a_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
Maur1b_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
Maur2_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
Reun1_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
Reun2_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
SA1_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
Taiw1_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
Taiw2_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
USA1a_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
USA1b_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
USA2a_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
USA2b_orf1 CCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCAGTTGATT
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Aus1_orf1 C
Aus2_orf1 C
Braz1_orf1 C
Braz2_orf1 C
CPam1a_orf1 C
CPam1b_orf1 C
CPaus1_orf1 C
Haw1_orf1 C
Haw2_orf1 C
Haw3_orf1 C
Maur1a_orf1 C
Maur1b_orf1 C
Maur2_orf1 C
Reun1_orf1 C
Reun2_orf1 C
SA1_orf1 C
Taiw1_orf1 C
Taiw2_orf1 C
USA1a_orf1 C
USA1b_orf1 C
USA2a_orf1 C
USA2b_orf1 C
*

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ORF1 Protein

eclustalw August 2, 19101 14:16

of: @fil_12024.tmp

aus1_orf1.pep	ck: 584	from: 1	to: 540	Length: 540
aus2_orf1.pep	ck: 637	from: 1	to: 540	Length: 540
braz1_orf1.pep	ck: 916	from: 1	to: 540	Length: 540
braz2_orf1.pep	ck: 9405	from: 1	to: 540	Length: 540
cpamla_orf1.pep	ck: 9902	from: 1	to: 540	Length: 540
cpamlb_orf1.pep	ck: 7756	from: 1	to: 524	Length: 524
cpaus1_orf1.pep	ck: 133	from: 1	to: 540	Length: 540
haw1_orf1.pep	ck: 921	from: 1	to: 540	Length: 540
haw2_orf1.pep	ck: 1096	from: 1	to: 540	Length: 540
haw3_orf1.pep	ck: 892	from: 1	to: 540	Length: 540
maurla_orf1.pep	ck: 9071	from: 1	to: 540	Length: 540
maurlb_orf1.pep	ck: 7362	from: 1	to: 540	Length: 540
maur2_orf1.pep	ck: 9435	from: 1	to: 540	Length: 540
reun1_orf1.pep	ck: 197	from: 1	to: 540	Length: 540
reun2_orf1.pep	ck: 8664	from: 1	to: 540	Length: 540
sal_orf1.pep	ck: 155	from: 1	to: 540	Length: 540
taiw1_orf1.pep	ck: 758	from: 1	to: 540	Length: 540
taiw2_orf1.pep	ck: 663	from: 1	to: 540	Length: 540
usala_orf1.pep	ck: 463	from: 1	to: 540	Length: 540
usalb_orf1.pep	ck: 267	from: 1	to: 540	Length: 540
usa2a_orf1.pep	ck: 49	from: 1	to: 540	Length: 540
usa2b_orf1.pep	ck: 389	from: 1	to: 540	Length: 540

Pairwise similarity parameter:

K-Tuple length:	1
Gap Penalty:	3
Number of diagonals:	5
Diagonal window size:	5
Scoring Method:	Percentage

Multiple alignment parameter:

Gap Penalty (fixed):	10.00
Gap Penalty (varying):	0.05
Gap separation penalty range:	8
Percent. identity for delay:	40%
List of hydrophilic residue:	GPSNDQEKR
Protein Weight Matrix:	blosum

Used Sequences:

- 1 /home/bses00/Za (540) Aus1_orf1.pep
- 2 /home/bses00/Za (540) Aus2_orf1.pep
- 3 /home/bses00/Za (540) Braz1_orf1.pep
- 4 /home/bses00/Za (540) Braz2_orf1.pep
- 5 /home/bses00/Za (540) CPamla_orf1.pep
- 6 /home/bses00/Za (524) CPamlb_orf1.pep
- 7 /home/bses00/Za (540) CPaus1_orf1.pep
- 8 /home/bses00/Za (540) Haw1_orf1.pep
- 9 /home/bses00/Za (540) Haw2_orf1.pep
- 10 /home/bses00/Za (540) Haw3_orf1.pep
- 11 /home/bses00/Za (540) Maurla_orf1.pep
- 12 /home/bses00/Za (540) Maurlb_orf1.pep
- 13 /home/bses00/Za (540) Maur2_orf1.pep
- 14 /home/bses00/Za (540) Reun1_orf1.pep
- 15 /home/bses00/Za (540) Reun2_orf1.pep

- 16 /home/bses00/Za (540) SA1_orf1.pep
- 17 /home/bses00/Za (540) Taiw1_orf1.pep
- 18 /home/bses00/Za (540) Taiw2_orf1.pep
- 19 /home/bses00/Za (540) USA1a_orf1.pep
- 20 /home/bses00/Za (540) USA1b_orf1.pep
- 21 /home/bses00/Za (540) USA2a_orf1.pep
- 22 /home/bses00/Za (540) USA2b_orf1.pep

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	10	20	30	40	50	60
Aus1_orf1.pep	MAPTLPFTTGWSTYALLLSLWCLFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
Aus2_orf1.pep	MAPTLPFTTGWSTYALLLSLWCLFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
Braz1_orf1.pep	MAPTLPFTTGWSTFALLLSLWCLFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
Braz2_orf1.pep	MAPTLPFTTGWSTFALLLSLWCLFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
CPam1a_orf1.pep	MAPTLPFTTGWSTFALSLSLWCLFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
CPam1b_orf1.pep	MAPTLPFTTGWSTYALLLSLWCLFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
CPaus1_orf1.pep	MAPTLPFTTGWSTYALLLSLWCLFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
Haw1_orf1.pep	MAPTLPFTTGWSTYALLLSLWCLFCSCQTQPLDSISILRDSTSSLSFYGLPATNSTIELR					
Haw2_orf1.pep	MAPTLPFTTGWSTYALLLSLWCLFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
Haw3_orf1.pep	MAPTLPFTTGWSTYXLLLSLWCLFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
Maur1a_orf1.pep	MAPTLPFTTGWSTFALLLLLWYQFCSCQTQPLDSTSILRDSTSSLSFYGLHATNSTIELR					
Maur1b_orf1.pep	MAPTLPFTTGWSTFALLLLLWYQFCSCQTQPLDSTSILRDSTSSLSFYGLHATNSTIELR					
Maur2_orf1.pep	MAPTLPFTTGWSTFALLLLLWYQFCSCQTQPLDSTSILRDSTSSLSFYGLPATNSTIELR					
Reun1_orf1.pep	MAPTLPFTTGWSTFALLLLLWYQFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
Reun2_orf1.pep	MAPTLPFTTGWSTFALLLLLWYQFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
SA1_orf1.pep	MAPTLPFTTGWSTFALLLSLWCLFCSCQTQPLDSTSILRDSTSSLSFYGLPATNSTIELR					
Taiw1_orf1.pep	MAPTLPFTTGWSTFALLLSLWCLFCSCQTQPLDGTSILRDSTSSLSFYGLPVTNSSIELR					
Taiw2_orf1.pep	MAPTLPFTTGWSTYALLLSLWCLFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
USA1a_orf1.pep	MAPTLPFTTGWSTYALLLSLWCLFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
USA1b_orf1.pep	MAPTLPFTTGWSTYALLLSLWCLFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
USA2a_orf1.pep	MAPTLPFTTGWSTYALLLSLWCLFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
USA2b_orf1.pep	MAPTLPFTTGWSTYALLLSLWCLFCSCQTQPLDGTSILRDSTSSLSFYGLPATNSTIELR					
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Aus1_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMIFKMWLDCKTFSREATTLSDRFLEFTFSNT
Aus2_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMIFKMWLDCKTFSREATTLSDRFLEFTFSNT
Braz1_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYTFSNT
Braz2_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYTFSNT
CPam1a_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEFTFSNT
CPam1b_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYTFSNT
CPaus1_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYTFSNT
Haw1_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYTFSNT
Haw2_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYTFSNT
Haw3_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYTFSNT
Maur1a_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYIFSNT
Maur1b_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYIFSNT
Maur2_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYIFSNT
Reun1_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYTFSNT
Reun2_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYTFSNT
SA1_orf1.pep	DAVPSGLCSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYTFSNT
Taiw1_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYTFSNT
Taiw2_orf1.pep	DAVPNGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYTFSNT
USA1a_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYTFSNT
USA1b_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEYTFSNT
USA2a_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEFTFSNT
USA2b_orf1.pep	DAVPSGLYSSKITSAPNFSELSYSSMLGWMFFKMWLDCKTFSREATTLSDRFLEFTFSNT
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Aus1_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWRPILIIICLLVVLTSMVYHLMRK
 Aus2_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWRPILIIICLLVVLTSMVYHLMRK
 Braz1_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWKPILIIICLLVVLTSMVYHLMRK
 Braz2_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWKPILIIICLLVVLTSMVYHLMRK
 CPamla_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWKPILIIICLLVVLTSMVYHLMRK
 CPamlb_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWKPILIIICLLVVLTSMVYHLMRK
 CPaus1_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWKPILIIICLLVVLTSMVYHLMRK
 Haw1_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWRPILIIICLLVVLTSMVYHLMRK
 Haw2_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWRPILIIICLLVVLTSMVYHLMRK
 Haw3_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWKPILIIICLLVVLTSMVYHLMRK
 Maurla_orf1.pep KGLLVEFLNLLWNLIRLYVCAFTITMRLIMTMTILAWKPILIIICLLVVLTSMVYHLMRK
 Maurlb_orf1.pep KGLLVEFLNLLWNLIRLYVCAFTITMRLIMTMTILAWKPILIIICLLVVLTSMVYHLMRK
 Maur2_orf1.pep KGLLVEFLNLLWNLIRLYVCAFTITMRLIMTMTILAWKPILIIICLLVVLTSMVYHLMRK
 Reun1_orf1.pep KGLLVEFLNLLWNLIRLYVCAFTITMRLIMTMTILAWKPILIIICLLVVLTSMVYHLMRK
 Reun2_orf1.pep KGLLVEFLNLLWNLIRLYVCAFTITMRLIMTMTILAWKPILIIICLLVVLTSMVYHLMRK
 SA1_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWKPILIIICLLVVLTSMVYHLMRK
 Taiw1_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITMRLIMTMTILAWKPILIIICLLVVLTSMVYHLMRK
 Taiw2_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWKPILIIICLLVVLTSMVYHLMRK
 USA1a_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWKPILVICLLVVLTSMVYHLMRK
 USA1b_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWKPILVICLLVVLTSMVYHLMRK
 USA2a_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWKPILIIICLLVVLTSMVYHLMRK
 USA2b_orf1.pep KGLLVEFLNLLWNLIKLYVYAFTIITRLIMTMTILAWKPILIIICPLVVLTSMVYHLMRK
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Aus1_orf1.pep LFSFIQIWWVVAPLLMIYRTVMWIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 Aus2_orf1.pep LFSFIQIWWVXXPLLMYRTVMWIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 Braz1_orf1.pep LFSFIQIWWVVAPILMIYRTVTYIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 Braz2_orf1.pep LFSFIQIWWVXAPILMIYRTVTYIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 CPamla_orf1.pep LFSFIQIWWVVAPILMIYRTVTYIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 CPamlb_orf1.pep LFSFIQIWWVMAPLLMIYRTVMWIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 CPaus1_orf1.pep LFSFIQIWWVVAPILMIYRTVTYIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 Haw1_orf1.pep LFSFIQIWWVMAPLLMIYRTVMWIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 Haw2_orf1.pep LFSFIQIWWVMAPLLMIYRTVMWIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 Haw3_orf1.pep LFSFIQIWWVMAPLLMIYRTVMWIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 Maurla_orf1.pep LFSFIQIWWVIAPVLMYRTVICIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 Maurlb_orf1.pep LFSFIQIRWVIAPILMIYRTVICIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 Maur2_orf1.pep LFSFIQIWWVIAPILMIYRTVICIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 Reun1_orf1.pep LFSFIQIWWVIAPILMIYRTVICIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 Reun2_orf1.pep LFSFIQIWWVIAPILMIYRTVICIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 SA1_orf1.pep LFSFIQIWWVVAPILMIYRTVTYIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 Taiw1_orf1.pep LFSFIQIWWVVAPILMIYRTVTYIHRRLFASRGDEKLVQGFKSFAVPMSPPGHSVLEIVH
 Taiw2_orf1.pep LFSFIQIWWVVAPILMIYRTVTYIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 USA1a_orf1.pep LFSFIQICWVVAPILMIYRTVTYIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 USA1b_orf1.pep LFSFIQICWVVAPILMIYKTVTYIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 USA2a_orf1.pep LFSFIQIYWVVAPILMIYRTVTYIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
 USA2b_orf1.pep LFSFIQIYWVVAPILMIYRTVTYIHRRLFASRGDEKMQGFKSFAVPMSPPGHSVLEIVH
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Aus1_orf1.pep PDGSHMGYASCVRLKNGEEGLMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANVMDIV
Aus2_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANAMDIV
Braz1_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANAMDIV
Braz2_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANAMDIV
CPamla_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANAMDIV
CPamlb_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANVMDIV
CPaus1_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANAMDIV
Haw1_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANVMDIV
Haw2_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANVMDIV
Haw3_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANVMDIV
Maur1a_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDAFKVRSFRNGIKIPLTEFQVLLPANAMDIV
Maur1b_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDAFKVRSFRNGIKIPLTEFQVLLPANAMDIV
Maur2_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDAFKVRSFRNGIKIPLTEFQVLLPANAMDIV
Reun1_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDTFKVRSFRNGIKIPLTEFQVLLPANVMDIV
Reun2_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDAFKVRSFRNGIKIPLTEFQVLLPANAMDIV
SA1_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANAMDIV
Taiw1_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANAMDIV
Taiw2_orf1.pep PDDSHMRYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANAMDIV
USA1a_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANAMDIV
USA1b_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANAMDIV
USA2a_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANAMDIV
USA2b_orf1.pep PDDSHMGYASCVRLKNGEEALMTSVHCISDSFKVRSFRNGIKIPLTEFQVLLPANAMDIV

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Aus1_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKITGTDGFYATVLSNT
Aus2_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKITGTDGFYATVLSNT
Braz1_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKVTTGTDGFYATVLSNT
Braz2_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKVTTGTDGFYATVLSNT
CPamla_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKVTTGTDGFYATVLSNT
CPamlb_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKITGTDGFYATVLSNT
CPaus1_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKVTTGTDGFYATVLSNT
Haw1_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKITGTDGFYATVLSNT
Haw2_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKITGTDGFYATVLSNT
Haw3_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKITGTDGFYATVLSNT
Maur1a_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKVTTGTDGFYATVLSNT
Maur1b_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKVTTGTDGFYATVLSNT
Maur2_orf1.pep LLRGPEWKFILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKVTTGTDGFYATVLSNT
Reun1_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKVTTGTDGFYATVLSNT
Reun2_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKVTTGTDGFYATVLSNT
SA1_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSLFIFDKEWMIHNAKVTTGTDGFYATVLSNT
Taiw1_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKVTTGTDGFYATVLSNT
Taiw2_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKVTTGTDGFYATVLSNT
USA1a_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKVTTGTDGFYATVLSNT
USA1b_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKVTTGTDGFYATVLSNT
USA2a_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKVTTGTDGFYATVLSNT
USA2b_orf1.pep LLRGPEWKSILGAKAAHFTPVNQLNKGAVSFFIFDKEWMMHNAKVTTGTDGFYATVLSNT

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Aus1_orf1.pep  EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
Aus2_orf1.pep  EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
Braz1_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
Braz2_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
CPamla_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
CPamlb_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
CPaus1_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
Haw1_orf1.pep  EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
Haw2_orf1.pep  EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
Haw3_orf1.pep  EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
Maur1a_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
Maur1b_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
Maur2_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
Reun1_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
Reun2_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
SA1_orf1.pep   EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
Taiw1_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
Taiw2_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
USA1a_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
USA1b_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
USA2a_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
USA2b_orf1.pep EKGYSGAPYWNGKSI VGVHKGHVYGDSDSKNYNLMSP I PPVKGLTAPNFVYESP SLQGDVF
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Aus1_orf1.pep  SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEANSPLDPKPVENA
Aus2_orf1.pep  SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEANSPLDPKPVENA
Braz1_orf1.pep SDADVSDIADYAE EVYEKXXAEPKVWKPASGKYWWE MAEEEDDFVVEAKSPPDPKPVENA
Braz2_orf1.pep SDADVSDIADYAE EVYEKALAEPAEPKVWKPASGKYWWE MAEEEDDFVVEAKLPPDPKPVENA
CPamla_orf1.pep SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEAKLPPDPKPVENA
CPamlb_orf1.pep SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVGANSPPDPKPVENA
CPaus1_orf1.pep SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEAKSPPDPKPVENA
Haw1_orf1.pep  SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEANSPLDPKPVENA
Haw2_orf1.pep  SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEANSPPDPKPVENA
Haw3_orf1.pep  SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEANSPPDPKPVENA
Maur1a_orf1.pep SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEANLPPDPKPVENS
Maur1b_orf1.pep SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEANLPPDPKPVENS
Maur2_orf1.pep  SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEANPPPPGKPVENS
Reun1_orf1.pep  SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEANLPPDPKPVENS
Reun2_orf1.pep  SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEANLPPDPKPVENS
SA1_orf1.pep   SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEAKSPPDPKPVENA
Taiw1_orf1.pep  SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEAKSPPDPKPVENA
Taiw2_orf1.pep  SDADVSDITDYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEAKLPPDPKPVENA
USA1a_orf1.pep  SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEAKSPPDPKPVENA
USA1b_orf1.pep  SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEAKSPPDPKPVENA
USA2a_orf1.pep  SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEAKSPPDPKPVENA
USA2b_orf1.pep  SDADVSDIADYAE EVYEKTLAEPKVWKPASGKYWWE MAEEEDDFVVEAKSPPDPKPVENA
*****. ***** ** *****

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Aus1_orf1.pep TAKEQTPASTVEKAMVADKPTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
Aus2_orf1.pep IAKEQTPASTVEKATVADKPTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
Braz1_orf1.pep TAKEQTPAXTVEKAMVADQXTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
Braz2_orf1.pep TAKEQTPASTVEKAMVAGQPTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
CPam1a_orf1.pep TAKEQTPAPTVEKAMVADQPTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
CPam1b_orf1.pep T-----DKPTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
CPaus1_orf1.pep TAKEQTPAPTVEKAMVADQPTPDQGNESGADHLKIPESTPLKQDESTKELLNIVSQLI
Haw1_orf1.pep TAKEQTPVLTVEKATVADKPTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
Haw2_orf1.pep TAKEQTPVLTVEKATVADKPTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
Haw3_orf1.pep TAKEQTPVLTVEKATVADKPTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
Maur1a_orf1.pep TAKEQTPASTVEKATXAGQMTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
Maur1b_orf1.pep TAKEQTPASTVEKATVAGQMTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
Maur2_orf1.pep TAKEQTPASTVEKATVAGQMTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
Reun1_orf1.pep TAKEQTPASTVEKATVAGQMTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
Reun2_orf1.pep TAKEQTPAPTVEKATVAGQMTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
SA1_orf1.pep TAKEQTPAPTVEKAMVADQPTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
Taiw1_orf1.pep TAKEQTPASTVEKAMVADQPTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
Taiw2_orf1.pep TAKEQTPAPTVEKAMVADQPTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
USA1a_orf1.pep TAKEQTPAPTVEKAMVADQPTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
USA1b_orf1.pep TAKEQTPAPTVEKAMVADQPTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
USA2a_orf1.pep TAKEQTPALTVEKAMVADQPTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
USA2b_orf1.pep TAKEQTPAPTVEKAMVADQPTPDQGNESGADHLKTPESTPLKQDESTKELLNIVSQLI
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Replicase Nucleotide

eclustalw August 3, 19101 13:15

of: @fil_8605.tmp

aus1_reped2	ck: 9132	from:	1	to:	957	Length:	957
aus2_reped2	ck: 8580	from:	1	to:	957	Length:	957
braz1_reped2	ck: 8934	from:	1	to:	957	Length:	957
braz2_reped2	ck: 8488	from:	1	to:	957	Length:	957
cpam1_reped2	ck: 1306	from:	1	to:	957	Length:	957
cpaus1_reped2	ck: 9505	from:	1	to:	957	Length:	957
haw1_reped2	ck: 8173	from:	1	to:	957	Length:	957
haw2_reped2	ck: 8258	from:	1	to:	957	Length:	957
maur1_reped2	ck: 382	from:	1	to:	957	Length:	957
reun1_reped2	ck: 170	from:	1	to:	957	Length:	957
reun2_reped2	ck: 2241	from:	1	to:	957	Length:	957
sal_reped2	ck: 7859	from:	1	to:	957	Length:	957
taiw1_reped2	ck: 8832	from:	1	to:	957	Length:	957
taiw2_reped2	ck: 1502	from:	1	to:	957	Length:	957
usa1_reped2	ck: 9258	from:	1	to:	957	Length:	957
usa2_reped2	ck: 8910	from:	1	to:	957	Length:	957

Pairwise similarity parameter:

K-Tuple length:	2
Gap Penalty:	5
Number of diagonals:	4
Diagonal window size:	4
Scoring Method:	Percentage

Multiple alignment parameter:

Gap Penalty (fixed):	10.00
Gap Penalty (varying):	5.00
Gap separation penalty range:	8
Percent. identity for delay:	40%
List of hydrophilic residue:	GPSNDQEKR
Transitions:	Weighted

Used Sequences:

- 1 /home/bses00/Za (957) Aus\1a\rep
- 2 /home/bses00/Za (957) Aus\1b\rep
- 3 /home/bses00/Za (957) Braz\1rep
- 4 /home/bses00/Za (957) Braz_2rep.rev
- 5 /home/bses00/Za (957) CP\amlrep
- 6 /home/bses00/Za (957) CP\aus1rep
- 7 /home/bses00/Za (957) Haw\1rep
- 8 /home/bses00/Za (957) Haw\2rep
- 9 /home/bses00/Za (957) Maur\1rep
- 10 /home/bses00/Za (957) Reun\1rep
- 11 /home/bses00/Za (957) Reun\2rep
- 12 /home/bses00/Za (957) SA\1rep
- 13 /home/bses00/Za (957) Taiw\1rep
- 14 /home/bses00/Za (957) Taiw\2rep
- 15 /home/bses00/Za (957) USA\1rep
- 16 /home/bses00/Za (957) USA\2rep

..

10 20 30 40 50 60

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Aus1_reped2 TAAGCCGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTAAAAACACCGGA
Aus2_reped2 TAAGCCGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTAAAAACACCGGA
Braz1_reped2 TCAGCTGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTAAAAACACCGGA
Braz2_reped2 TCAGCCGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTAAAAACACCGGA
CPam1_reped2 TCAGCCGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTANAAACACCGGA
CPaus1_reped2 TCAGCCGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTAAAAACACCGGA
Haw1_reped2 TAAGCCGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTAAAAACACCGGA
Haw2_reped2 TAAGCCGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTAAAAACACCGGA
Maur1_reped2 TCAGATGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTAAAAACACCGGA
Reun1_reped2 TCAGATGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTAAAAACACCGGA
Reun2_reped2 TCAGATGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTAAAAACACCGGA
SA1_reped2 TCAGCCGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTAAAAACACCGGA
Taiw1_reped2 TCAGCCGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTAAAAACACCGGA
Taiw2_reped2 TCAGCCGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTAAAAACACCGGA
USA1_reped2 TCAGCCGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTAAAAACACCGGA
USA2_reped2 TCAGCCGACTCCAGACCAGGGAAACGAGCCAAGTGGCGCCGACCACTTAAAAACACCGGA
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Aus1_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
Aus2_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
Braz1_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
Braz2_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
CPam1_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
CPaus1_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
Haw1_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
Haw2_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
Maur1_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
Reun1_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
Reun2_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
SA1_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
Taiw1_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
Taiw2_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
USA1_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
USA2_reped2 ATCCACCCCGCTCAAGCAAGACGAATCTACAAAAGAGTTGCTCAACAACATCGTCTCGCA
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Aus1_reped2 GTTGATCCAAAAGATCGACCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCG
Aus2_reped2 GTTGATCCAAAAGATCGACCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCG
Braz1_reped2 GTTGATTCAAAGATCGACCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCG
Braz2_reped2 GTTGATTCAAAGATCGACCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCG
CPam1_reped2 GTTGATTCAAAGATCGACCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCG
CPaus1_reped2 GTTGATTCAAAGATCGACCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCG
Haw1_reped2 GTTGATTCAAAGATCGACCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCG
Haw2_reped2 GTTGATTCAAAGATCGATCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCA
Maur1_reped2 ATTGATTCAAAGATCGATCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCA
Reun1_reped2 ATTGATTCAAAGATCGATCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCA
Reun2_reped2 ATTGATTCAAAGATCGATCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCA
SA1_reped2 GTTGATTCAAAGATCGACCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCG
Taiw1_reped2 GTTGATTCAAAGATCGACCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCG
Taiw2_reped2 GTTGATTCAAAGATCGACCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCG
USA1_reped2 GTTGATTCAAAGATCGACCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCG
USA2_reped2 GTTGATTCAAAGATCGACCTGAGCTCCATTGCAACGAGGGTGGAGGAGAAAAGTCTGCG
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Aus1_reped2 TCAGGCCCGAGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTCACCCAGAAAACGCAAGAC
Aus2_reped2 TCAGGCCCGAGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTCACCCAGAAAACGCAAGAC
Braz1_reped2 TCAGGCCCGAGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTCGCCCAGAAAACGCAAGAC
Braz2_reped2 TCAGGCTCAGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTCGCCCAGAAAACGCAAGAC
CPam1_reped2 TCAAGGCCCGAGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTCGCCCAGAAAACGCAAGAC
CPaus1_reped2 TCAGGCCCGAGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTCGCCCAGAAAACGCAAGAC
Haw1_reped2 TCAGGCCCGAGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTCACCCAGAAAACGCAAGAC
Haw2_reped2 TCAGGCCCGAGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTCACCCAGAAAACGCAAGAC
Maur1_reped2 TCAAGCACGGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTTGCCAGAAAACGCAAGAC
Reun1_reped2 TCAAGCACGGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTCGCCCAGAAAACGCAAGAC
Reun2_reped2 TCAAGCACGGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTCGCCCAGAAAACGCAAGAC
SA1_reped2 TCAGGCCCGAGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTCACCCAGAAAACACAAGAC
Taiw1_reped2 TCAGGCCCGAGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTCGCCCAGAAAACGCAAGAC
Taiw2_reped2 TCAGGCCCGAGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTCGCCCAGAAAACGCAAGAC
USA1_reped2 TCAGGCCCGAGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTCGCCCAGAAAACGCAAGAC
USA2_reped2 TCAGGCCCGAGAACAACAGCAGCAGAGAACGGAGGGAAGAAGTCGCCCAGAAAACGCAAGAC
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Aus1_reped2 CTCGAACGCTTCTTCCAAGCCGCATACAAATGGGAAGAGTCCACCAGCGACATCCCAGGA
Aus2_reped2 CTCGAACGCTTCTTCCAAGCCGCATACAAATGGGAAGAGTCCACCAGCGACATCCCAGGA
Braz1_reped2 CTCGAACACTTCTTCCAAGCCGCATACAAATGGGAAGAGTCCACCAGTGACATCCCAGGG
Braz2_reped2 CTCGAACACTTCTTCCAAGCCGCATACAAATGGGAAGAGTCCACCAGTGACATCCCAGGG
CPam1_reped2 CTCGAACACTTCTTCCAAGCCGCATACAAATGGGAAGAGTCCACCAGTGACATCCCAGGG
CPaus1_reped2 CTCGAACACTTCTTCCAAGCCGCATACAAATGGGAAGAGTCCACCAGTGACATCCCAGGG
Haw1_reped2 CTCGAACACTTCTTCCAAGCCGCATACAAATGGGAAGAGTCCACCAGCGACATCTCAGGA
Haw2_reped2 CTCGAACACTTCTTCCAAGCCGCATACAAATGGGAAGAGTCCACCAGCGACATCCCAGGA
Maur1_reped2 CTCGAACACTTCTTCCAAGCCGCATATAAATGGGAAGAGTCCACCAGTGACATCCCCGGG
Reun1_reped2 CTCGAACACTTCTTCCAAGCCGCATACAAATGGGAAGAGTCCACCAGTGACATCCCCGGG
Reun2_reped2 CTCGAACACTTCTTCCAAGCCGCATACAAATGGGAAGAGTCCACCAGTGACATCCCCGGG
SA1_reped2 CTCGAACACTTCTTCCAAGCCGCATACAAATGGGAAGAGTCCACCAGTGACATCCCAGGG
Taiw1_reped2 CTCGAACACTTCTTCCAAGCCGCATACAAATGGGAAGAGTCCACCAGTGACATCCCAGGG
Taiw2_reped2 CTCGAACACTTCTTCCAAGCCGCATACAAATGGGAAGAGTCCACCAGTGACATCCCAGGG
USA1_reped2 CTCGAACACTTCTTCCAAGCCGCATACAAATGGGAAGAGTCCACCAGTGACATCCCAGGG
USA2_reped2 CTCGAACACTTCTTCCAAGCCGCATACAAATGGGAAGAGTCCACCAGTGACATCCCAGGG
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Aus1_reped2 TTCAGGAAATGCGGNAAACTCCCCGCGCTATACCATCCCCAAAACCGAAGAGCACACAA
Aus2_reped2 TTCAGGAAATGCGGCAAACTCCCCGCGCTATACCATCCCCAAAACCGAAGAGCACACAA
Braz1_reped2 TTCAGGAAATGCGGCAAACTCCCCGCGCTATACCATCCCCAAAACCGAAGAGCACACAA
Braz2_reped2 TTCAGGAAATGCGGCAAACTCCCCGCGCTATACCATCCCCAAAACCGAAGAGCACACAA
CPam1_reped2 TTCAGGAAATGCGGCAAACTCCCCGCGCTATACCATCCCCAAAACCGAAGAGCACACAA
CPaus1_reped2 TTCAGGAAATGCGGCAAACTCCCCGCGCTATACCATCCCCAAAACCGAAGAGCACACAA
Haw1_reped2 TTCAGGAAATGCGGTAAACTCCCCGCGCTATACCATCCCCAAAACCGAAGAGCACACAA
Haw2_reped2 TTCAGGAAATGCGGTAAACTCCCCGCGCTATACCATCCCCAAAACCGAAGAGCACACAA
Maur1_reped2 TTCAGGAAATGCGGCAAACTCCCCGCGCTATACCATCCCCAAAACCGAAGAGCACACAA
Reun1_reped2 TTCAGGAAATGCGGCAAACTCCCCGCGCTATACCATCCCCAAAACCGAAGAGCACACAA
Reun2_reped2 TTCAGGAAATGCGGCAAACTCCCCGCGCTATACCATCCCCAAAACCGAAGAGCACACAA
SA1_reped2 TTCAGGAAATGCGGCAAACTCCCCGCGCTATACCATCCCCAAAACCGAAGAGCACACAA
Taiw1_reped2 TTCAGGAAATGCGGCAAACTCCCCGCGCTATACCATCCCCAAAACCGAAGAGCACACAA
Taiw2_reped2 TTCAGGAAATGCGGCAAACTCNCCGCGCTATACCATCCCCAAAACCGAAGAGCNCACAA
USA1_reped2 TTCAGGAAATGCGGCAAACTCCCCGCGCTATACCATCCCCAAAACCGAAGAGCACACAA
USA2_reped2 TTCAGGAAATGCGGCAAACTCCCCGCGCTATACCATCCCCAAAACCGAAGAGCACACAA
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Aus1_reped2      TGGGGGGAGCGCATCATCTCAGAACACCCAGAAATGGCGTCCAAAGTCGCCGGTTTCGGG
Aus2_reped2      TGGGGGGAGCGCATCATCTCAGAACACCCAGAAATGGCGTCCAAAGTCGCCGGTTTCGGG
Braz1_reped2     TGGGGGAGAGCGCATCATCTCAGAGCACCCAGAAATGGCGTCCAAAGTCGCCGGTTTCGGG
Braz2_reped2     TGGGGGAGAGCGCATCATCTCAGAGCACCCAGAAATGGCGTCCAAAGTCGCCGGTTTCGGG
CPam1_reped2    TGGGGGAGAGCGCATCATCTCAGAGCACCCAGAAATGGCGTCCAAAGTCGCCGGTTTCGGG
CPaus1_reped2   TGGGGGAGAGCGCATCATCTCAGAGCACCCAGAAATGGCGTCCAAAGTCGCCGGTTTCGGG
Haw1_reped2     TGGGGGAGAGCGCATCATCTCAGAACACCCAGAAATGGCGTCCAAAGTCGCCGGTTTCGGG
Haw2_reped2     TGGGGGAGAGCGCATCATCTCAGAACACCCAGAAATGGCGTCCAAAGTCGCCGGTTTCGGG
Maur1_reped2    TGGGGGGAGCGCATCATCTCAGAACACCCAGAGATGGCGGCCAAAGTCGCCGGTTTCGGG
Reun1_reped2    TGGGGGGAGCGCATCATCTCAGAACACCCAGAGATGGCGGCCAAAGTCGCCGGTTTCGGG
Reun2_reped2    TGGGGGGAGCGCATCATCTCAGAACACCCAGAGATGGCGGCCAAAGTCGCCGGTTTCGGG
SA1_reped2      TGGGGGAGAGCGCATCATCTCAGAGCACCCAGAAATGGCGTCCAAAGTCGCCGGTTTCGGG
Taiw1_reped2    TGGGGGAGAGCGCATCATCTCAGAGCACCCAGAAATGGCGTCCAAAGTCGCCGGTTTCGGG
Taiw2_reped2    TGGGGGAGAGCGCATCATCTCAGAGCACCCAGAAATGGCGTCCAAAGTCGCCGGTTTCGGG
USA1_reped2     TGGGGGAGAGCGCATCATCTCAGAGCACCCAGAAATGGCGTCCAAAGTCGCCGGTTTCGGG
USA2_reped2     TGGGGGAGAGCGCATCATCTCAGAGCACCCAGAAATGGCGTCCAAAGTCGCCGGTTTCGGG
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Aus1_reped2      TGGCCCTCCTTCGGCGCCCAAGCCGAGGAGACAAGTCTGAGACTCCAAGCGGCACGCTGG
Aus2_reped2      TGGCCCTCCTTCGGCGCCCAAGCCGAAGAGACAAGTCTGAGACTCCAAGCGGCACGCTGG
Braz1_reped2     TGGCCCTCCTTCGGCGCCCAAGCCGAAGAGACAAGTCTGAGACTCCAAGCGGCACGCTGG
Braz2_reped2     TGGCCCTCCTTCGGCGCCCAAGCCGAAGAGACAAGTCTGAGACTCCAAGCGGCACGCTGG
CPam1_reped2    TGGCCCTCCTTCGGCGCCCAAGCCGAAGAGACAAGTCTGAGACTCCAAGCGGCACGCTGG
CPaus1_reped2   TGGCCCTCCTTCGGCGCCCAAGCCGAAGAGACAAGTCTGAGACTCCAAGCGGCACGCTGG
Haw1_reped2     TGGCCTCCTTCGGCGCCCAAGCCGAGGAGACAAGTCTGAGACTCCAAGCGGCACGCTGG
Haw2_reped2     TGGCCTCCTTCGGCGCCCAAGCCGAGGAGACAAGTCTGAGACTCCAAGCGGCACGCTGG
Maur1_reped2    TGGCCTCCTTCGGCGCCCAAGCCGAGGAGACAAGTCTGAGACTCCAAGCGGCACGCTGG
Reun1_reped2    TGGCCTCCTTCGGCGCCCAAGCCGAGGAGACAAGTCTGAGACTCCAAGCGGCACGCTGG
Reun2_reped2    TGGCCTCCTTCGGCGCCCAAGCCGAGGAGACAAGTCTGAGACTCCAAGCGGCACGCTGG
SA1_reped2      TGGCCTCCTTCGGCGCCCAAGCCGAAGAGACAAGTCTGAGACTCCAAGCGGCACGCTGG
Taiw1_reped2    TGGCCTCCTTCGGCGCCCAAGCCGAAGAGACAAGTCTGAGACTCCAAGCGGCACGCTGG
Taiw2_reped2    TGGCCTCCTTCGGCGCCCAAGCCGAAGAGACAAGTNTGAGGCTCCAAGCGGCACGCTGG
USA1_reped2     TGGCCTCCTTCGGCGCCCAAGCCGAAGAGACAAGTCTGAGACTCCAAGCGGCACGCTGG
USA2_reped2     TGGCCTCCTTCGGCGCCCAAGCCGAAGAGACAAGTCTGAGACTCCAAGCGGCACGCTGG
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Aus1_reped2      CTTAAACGAGCTGAGTCAGCGGAAAAGCCGACAGAAAAACAACGCAAGCTCGTCATTGAT
Aus2_reped2      CTTAAACGAGCTGAGTCAGCGGAAAAGCCGACAGAAAAACAACGCAAGCTCGTCATTGAT
Braz1_reped2     CTTAAACGAGCTGAGTCAGCGGAAAAGCCGACAGAAAAACAACGCAAGCTCGTCATTGAT
Braz2_reped2     CTTAAACGAGCTGAGTCAGCGGAAAAGCCGACAGAAAAACAACGCAAGCTCGTCATTGAT
CPam1_reped2    CTTAAACGAGCTGAGTCAGCGGAAAAGCCGACAGAAAAACAACGCAAGCTCGTCATTGAT
CPaus1_reped2   CTTAAACGAGCTGAGTCAGCGGAAAAGCCGACAGAAAAACAACGCAAGCTCGTCATTGAT
Haw1_reped2     CTTAAACGAGCTGAGTCAGCGGAGAAGCCGACAGAAAAACAACGCAAGCTCGTCATTGAT
Haw2_reped2     CTTAAACGAGCTGAGTCAGCGGAGAAGCCGACAGAAAAACAACGCAAGCTCGTCATTGAT
Maur1_reped2    CTCAAACGAGCTGAGTCAGCGGAAAAGCCGACCGCAGCACAACGCAAGCTCGTCATTGAT
Reun1_reped2    CTCAAACGAGCTGAGTCAGCGGAAAAGCCGACCGCAGCACAACGCAAGCTCGTCATTGAT
Reun2_reped2    CTCAAACGAGCTGAGTCAGCNGANANGCCGACCGCAGCACAACGCAAGCTCGTCATTGAT
SA1_reped2      CTTAAACGAGCTGAGTCAGCGGAAAAGCCGACAGAAAAACAACGCAAGCTCGTCATTGAT
Taiw1_reped2    CTTAAACGAGCTGAGTCAGCGGAAAAGCCGACAGAAAAACAACGCAAGCTCGTCATTGAT
Taiw2_reped2    CTTAAACGAGNTGAGTCAGCGGAAAAGCCGACAGAAAAACAACGCAAGCTCGTCATTGAT
USA1_reped2     CTTAAACGAGCTGAGTCAGCGGAAAAGCCGACAGAAAAACAACGCAAGCTCGTCATTGAT
USA2_reped2     CTTAAACGAGCTGAGTCAGCGGAAAAGCCGACAGAAAAACAACGCAAGCTCGTCATTGAT
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Aus1_reped2      CGTGTGGTTAAGGCATATGAACCGTGTAGAACCAATGCCCCACACACCAGCTCCTCTGGC
Aus2_reped2      CGTGTGGTTAAGGCATATGAACCGTGTAGAACCAATGCCCCACACACCAGCTCCTCTGGC
Braz1_reped2     CGTGTGGTCAAGGCATATGAACCGTGTAGAACCAATGCCCCACACACCAGCTCCTCTGGC
Braz2_reped2     CGTGTGGTTAAGGCATATGAACCGTGTAGAACCAATGCCCCACACACCAGCTCCTCTGGC
CPam1_reped2     CGTGTGGTCAAGGCATATGAACCGTATAGAATAATGCCCCACACACCAGCTCCTCTGGC
CPaus1_reped2    CGTGTGGTCAAGGCATATGAACCGTGTAGAATAATGCCCCACACACCAGCTCCTCTGGC
Haw1_reped2      CGTGTGGTCAAGGCATATGAACCGTGTAGAACCAATGCCCCACACACCAGCTCCTCTGGC
Haw2_reped2      CGTGTGGTCAAGGCATATGAACCGTGTAGAACCAATGCCCCACACACCAGCTCCTCTGGC
Maur1_reped2     CGTGTGGTCAAGGCATATGAACCGTGTAAAACCAATGCCCCACACACCAGCTCCTCTGGC
Reun1_reped2     CGTGTGGTCAAGGCATATGAACCGTGTAAAACCAATGCCCCACACACCAGCTCCTCTGGC
Reun2_reped2     CGTGTGGTCAAGGCATATGAACCGTGTAAAACCAATGCCCCACACACCAGCTCCTCTGGC
SA1_reped2       CGTGTGGTCAAGGCATATGAACCGTGTAGAATAATGCCCCACACACCAGCTCCTCTGGC
Taiw1_reped2     CGTGTGGTCAAGGCATATGAACCGTGTAGAACCAATGCCCCACACACCAGCTCCTCTGGC
Taiw2_reped2     CGTGTGGTCAAGGCATATGAACCGTGTAGAATAATGCCCCACACACCAGCTCCTCTGGC
USA1_reped2      CGTGTGGTCAAGGCATATGAACCGTGTAGAACNAATGCCCCACACACCAGCTCCTCTGGC
USA2_reped2      CGTGTGGTCAAGGCATATGAACCGTGTAGAATAATGCCCCACACACCAGCTCCTCTGGC
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Aus1_reped2      AGCCTCATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTAGAACTT
Aus2_reped2      AGCCTCATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTAGAACTT
Braz1_reped2     AGCCTCATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTAGAACTC
Braz2_reped2     AGCCTCATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTAGAACTC
CPam1_reped2     AGCCTCATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTAGAACTC
CPaus1_reped2    AGCCTCATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTANAACTC
Haw1_reped2      AGCCTCATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTAGAACTC
Haw2_reped2      AGCCTCATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTAGAACTC
Maur1_reped2     AGCCTCATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTAGAACTT
Reun1_reped2     AGCCTCATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTAGAACTT
Reun2_reped2     AGCCTCATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTAGAACTT
SA1_reped2       AGCCTCATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTAGAACTC
Taiw1_reped2     AGCCTCATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTAGAACTC
Taiw2_reped2     AGCCTTATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTAGAACTC
USA1_reped2      AGCCTCATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTAGAACTC
USA2_reped2      AGCCTCATCTGGTCCGACTTCTTGAAAGATTTCAAGGAGGCTGTCAACTCACTAGAACTC
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Aus1_reped2      GACGCAGGAATAGGTCTCCCATACAAACTTCTTCGCAAAGACACTCACCGTCAGATGGTT
Aus2_reped2      GATGCAGGAATAGGTCTCCCATACAAACTTCTTCGCAAAGACACTCACCGTCAGATGGTT
Braz1_reped2     GATGCAGGAATAGGTCTCCCATACAAAGCTTCTTCACAAAGACACTCATCGTCAGATGGTT
Braz2_reped2     GACGCAGGAATAGGTCTCCCATACAAGCTTCTTCACAAAGACACTCATCGTCAGATGGTT
CPam1_reped2     NATGCANGAATAGGTCTCCCATACAAGCTTCTTCACAAAGACACTCATCGTCAGATGGTT
CPaus1_reped2    GATGCAGGAATAGGTCTCCCATACAAGCTTCTTCACAAAGACACTCATCGTCAGATGGTT
Haw1_reped2      GACGCAGGAATAGGTCTCCCATACAAACTTCTTCACAAAGACACCCACCGTCAGATGGTT
Haw2_reped2      GACGCAGGAATAGGTCTCCCATACAAACTTCTTCACAAAGACACCCACCGTCAGATGGTT
Maur1_reped2     GACGCAGGAATAGGTCTCCCATACAAACTTCTTCACAAAGACACTCATCGTCAAATGGTA
Reun1_reped2     GACGCAGGAATAGGTCTCCCATACAAACTTCTCAACAAAGACACTCATCGTCAAATGGTA
Reun2_reped2     GACGCAGGAATAGGTCTCCCATACAANCTTCTCAACAAAGACACTCATCGTCAAATGGTA
SA1_reped2       GATGCAGGAATAGGTCTCCCATACAAGCTTCTTCACAAAGACACTCATCGTCAGATGGTT
Taiw1_reped2     GATGCAGGAATAGGTCTCCCATACAAGCTTCTTCACAAAGACACTCATCGTCAGATGGTT
Taiw2_reped2     GATGCAGGAATAGGTCTCCCATACAAGCTTCTTCACAAAGACACTCATCGTCAGATGGTT
USA1_reped2      GANGCAGGAATAGGTCTCCCATACAAGCTTCTTCACAAAGACACTCATCGTCAGATGGTT
USA2_reped2      GATGCAGGAATAGGTCTCCCATACAAGCTTCTTCACAAAGACACTCATCGTCAGATGGTT
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Aus1_reped2 GAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG
Aus2_reped2 GAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG
Braz1_reped2 GAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG
Braz2_reped2 GAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG
CPam1_reped2 GAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG
CPaus1_reped2 GAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG
Haw1_reped2 GAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG
Haw2_reped2 GAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG
Maur1_reped2 GAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG
Reun1_reped2 GAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG
Reun2_reped2 NAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG
SA1_reped2 GAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG
Taiw1_reped2 GAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG
Taiw2_reped2 GAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG
USA1_reped2 GAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG
USA2_reped2 GAAGACCCCAAATTCCTGCCGCTCCTGACGCGATTGACCTGGAACCGTTTACAGAAGATG

Aus1_reped2 TCCCAGGTNGACTTCCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAT
Aus2_reped2 TCCCAGGTGACTTCCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAT
Braz1_reped2 TCCCAGGTGACTTCCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAT
Braz2_reped2 TCCCAGGTGACTTCCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAT
CPam1_reped2 TCCCAGGTGACTTCCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAT
CPaus1_reped2 TCCCAGGTGACTTCCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAT
Haw1_reped2 TCCCAGGTGATTTCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAC
Haw2_reped2 TCCCAGGTGATTTCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAT
Maur1_reped2 TCCCAGGTGATTTCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAC
Reun1_reped2 TCCCAGGTGATTTCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAC
Reun2_reped2 TCCCAGGTGATTTCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAC
SA1_reped2 TCCCAGGTGACTTCCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAT
Taiw1_reped2 TCCCAGGTGACTTCCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAT
Taiw2_reped2 TCCCAGGTGACTTCCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAT
USA1_reped2 TCCCAGGTGACTTCCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAT
USA2_reped2 TCCCAGGTGACTTCCAGGAGATGACTCCTGAACAACACTAGTGAGAGAAGGATTGTGCGAT

Aus1_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC
Aus2_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC
Braz1_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC
Braz2_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC
CPam1_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC
CPaus1_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC
Haw1_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC
Haw2_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC
Maur1_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC
Reun1_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC
Reun2_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC
SA1_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC
Taiw1_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC
Taiw2_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC
USA1_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC
USA2_reped2 CCGATTCGTTTGTTCGTCAAAGGAGAACCGCACAAAGCAGGCGAAGCTTGATGAAGGGCGC

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Aus1_reped2      TACCGCCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCCCCGGGTTTTGTTC
Aus2_reped2      TACCGCCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCCCCGGGTTTTGTTC
Braz1_reped2     TACCGCCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCCCCGGGTTTTGTTC
Braz2_reped2     TACCGCCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCGAGGGTTCGTTC
CPam1_reped2    TACCGTCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCCCCGGGTTTTGTTC
CPaus1_reped2   TACCGCCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCCCCGGGTTTTGTTC
Haw1_reped2     TACCGCCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCCCCGGGTTTTGTTC
Haw2_reped2     TACCGCCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCCCCGGGTTTTGTTC
Maur1_reped2    TACCGCCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCCCCGGGTTTTGTTC
Reun1_reped2    TACCGCCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCCCCGGGTTTTGTTC
Reun2_reped2    TACCGCCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCCCCGGGTTTTGTTC
SA1_reped2      TACCGCCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCCCCGGGTTTTGTTC
Taiw1_reped2    TACCGCCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCCCCGGGTTTTGTTC
Taiw2_reped2    TACCGCCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCCCCGGGTTTTGTTC
USA1_reped2     TACCGCCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCCCCGGGTTTTGTTC
USA2_reped2     TACCGCCTCATCATGTTCAGTCTCGCTGGTAGATCAACTGGTAGCCCCGGGTTTTGTTC
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Replicase Protein

eclustalw August 3, 19101 14:02

of: @fil_9094.tmp

aus1_reped2.pep	ck: 1883	from: 1	to: 319	Length: 319
aus2_reped2.pep	ck: 423	from: 1	to: 319	Length: 319
braz1_reped2.pep	ck: 1411	from: 1	to: 319	Length: 319
braz2_reped2.pep	ck: 1429	from: 1	to: 319	Length: 319
cpam1_reped2.pep	ck: 3708	from: 1	to: 319	Length: 319
cpaus1_reped2.pep	ck: 2323	from: 1	to: 319	Length: 319
haw1_reped2.pep	ck: 1838	from: 1	to: 319	Length: 319
haw2_reped2.pep	ck: 1712	from: 1	to: 319	Length: 319
maur1_reped2.pep	ck: 994	from: 1	to: 319	Length: 319
reun1_reped2.pep	ck: 575	from: 1	to: 319	Length: 319
reun2_reped2.pep	ck: 2247	from: 1	to: 319	Length: 319
sal_reped2.pep	ck: 2345	from: 1	to: 319	Length: 319
taiw1_reped2.pep	ck: 1411	from: 1	to: 319	Length: 319
taiw2_reped2.pep	ck: 4786	from: 1	to: 319	Length: 319
usal_reped2.pep	ck: 1411	from: 1	to: 319	Length: 319
usa2_reped2.pep	ck: 1411	from: 1	to: 319	Length: 319

Pairwise similarity parameter:

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K-Tuple length:      1
Gap Penalty:         3
Number of diagonals: 5
Diagonal window size: 5
Scoring Method:      Percentage
    
```

Multiple alignment parameter:

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Gap Penalty (fixed):      10.00
Gap Penalty (varying):    0.05
Gap separation penalty range: 8
Percent. identity for delay: 40%
List of hydrophilic residue: GPSNDQEKR
Protein Weight Matrix:    blosum
    
```

Used Sequences:

- 1 /home/bses00/Za (319) Aus1_reped2.pep
- 2 /home/bses00/Za (319) Aus2_reped2.pep

- 3 /home/bses00/Za (319) Braz1_reped2.pep
- 4 /home/bses00/Za (319) Braz2_reped2.pep
- 5 /home/bses00/Za (319) CPam1_reped2.pep
- 6 /home/bses00/Za (319) CPaus1_reped2.pep
- 7 /home/bses00/Za (319) Haw1_reped2.pep
- 8 /home/bses00/Za (319) Haw2_reped2.pep
- 9 /home/bses00/Za (319) Maur1_reped2.pep
- 10 /home/bses00/Za (319) Reun1_reped2.pep
- 11 /home/bses00/Za (319) Reun2_reped2.pep
- 12 /home/bses00/Za (319) SA1_reped2.pep
- 13 /home/bses00/Za (319) Taiw_reped2.pep
- 14 /home/bses00/Za (319) Taiw2_reped2.pep
- 15 /home/bses00/Za (319) USA1_reped2.pep
- 16 /home/bses00/Za (319) USA2_reped2.pep

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10 20 30 40 50 60

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Aus1_reped2.pep -ADSRPGKRAKWRRLKNTGIHPAQARRIYKRVAQQHRLAVDPKDRPELHCNEGGGETAA
Aus2_reped2.pep -ADSRPGKRAKWRRLKNTGIHPAQARRIYKRVAQQHRLAVDPKDRPELHCNEGGGETAA
Braz1_reped2.pep SADSRPGKRAKWRRLKNTGIHPAQARRIYKRVAQQHRLAVDSKDRPELHCNEGGGETAA
Braz2_reped2.pep SADSRPGKRAKWRRLKNTGIHPAQARRIYKRVAQQHRLAVDSKDRPELHCNEGGGETAA
CPam1_reped2.pep SADSRPGKRAKWRRLXNTGIHPAQARRIYKRVAQQHRLAVDSEDRPELHCNEGGGETAA
CPaus1_reped2.pep SADSRPGKRAKWRRLKNTGIHPAQARRIYKRVAQQHRLAVDSKDRPELHCNEGGGETAA
Haw1_reped2.pep -ADSRPGKRAKWRRLKNTGIHPAQARRIYKRVAQQHRLAVDSKDRPELHCNEGGGETAA
Haw2_reped2.pep -ADSRPGKRAKWRRLKNTGIHPAQARRIYKRVAQQHRLAVDSKDRPELHCNEGGGETAA
Maur1_reped2.pep SDDSRPGKRAKWRRLKNTGIHPAQARRIYKRVAQQHRLAIDSKDRSELHCNEGGGETAA
Reun1_reped2.pep SDDSRPGKRAKWRRLKNTGIHPAQARRIYKRVAQQHRLAIDSKDRSELHCNEGGGETAA
Reun2_reped2.pep SDDSRPGKRAKWRRLKNTGIHPAQARRIYKRVAQQHRLAIDSKDRSELHCNEGGGETAA
SA1_reped2.pep SADSRPGKRAKWRRLKNTGIHPAQARRIYKRVAQQHRLAVDSKDRPELHCNEGGGETAA
Taiw1_reped2.pep SADSRPGKRAKWRRLKNTGIHPAQARRIYKRVAQQHRLAVDSKDRPELHCNEGGGETAA
Taiw2_reped2.pep SADSRPGKRAKWRRLKNTGIHPAQARRIYKRVAQQHRLAVDSKDRPELHCNEGGGETAA
USA1_reped2.pep SADSRPGKRAKWRRLKNTGIHPAQARRIYKRVAQQHRLAVDSKDRPELHCNEGGGETAA
USA2_reped2.pep SADSRPGKRAKWRRLKNTGIHPAQARRIYKRVAQQHRLAVDSKDRPELHCNEGGGETAA
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Aus1_reped2.pep SGPEQTAAERREEVTQKTQDLERFFQAAYKWEESTSDIPGFRKCGKLPALYHPPKPKSTQ
Aus2_reped2.pep SGPEQTAAERREEVTQKTQDLERFFQAAYKWEESTSDIPGFRKCGKLPALYHPPKPKSTQ
Braz1_reped2.pep SGPEQTAAERREEVAQKTQDLEHFFQAAYKWEESTSDIPGFRKCGKLPALYHPPKPKSTQ
Braz2_reped2.pep SGSEQTAAERREEVAQKTQDLEHFFQAAYKWEESTSDIPGFRKCGKLPALYHPPKPKSTQ
CPam1_reped2.pep SSPEQTAAERREEVAQKTQDLEHFFQAAYKWEESTSDIPGFRKCGKLPALYHPPKPKSTQ
CPaus1_reped2.pep SGPEQTAAERREEVAQKTQDLEHFFQAAYKWEESTSDIPGFRKCGKLPALYHPPKPKSTQ
Haw1_reped2.pep SGPEQTAAERREEVTQKTQDLEHFFQAAYKWEESTSDIPGFRKCGKLPALYHPPKPKSTQ
Haw2_reped2.pep SGPEQTAAERREEVTQKTQDLEHFFQAAYKWEESTSDIPGFRKCGKLPALYHPPKPKSTQ
Maur1_reped2.pep SSTEQTAAERREEVAQKTQDLEHFFQAAYKWEESTSDIPGFRKCGRLPALYHPPKPKSTQ
Reun1_reped2.pep SSTEQTAAERREEVAQKTQDLEHFFQAAYKWEESSDIPGFRKCGKLPALYHPPKPKSTQ
Reun2_reped2.pep SSTEQTAAERREEVAQKTQDLEHFFQAAYKWEESTSDIPGFRKCGKLPALYHPPKPKSTQ
SA1_reped2.pep SGPEQTAAERREEVTQKTQDLEHFFQAAYKWEESTSDIPGFRKCGKLPALYHPPKPKSTQ
Taiw1_reped2.pep SGPEQTAAERREEVAQKTQDLEHFFQAAYKWEESTSDIPGFRKCGKLPALYHPPKPKSTQ
Taiw2_reped2.pep SGPEQTAAERREEVAQKTQDLEHFFQAAYKWEESTSDIPGFRKCGKLPALYHPPKPKSXQ
USA1_reped2.pep SGPEQTAAERREEVAQKTQDLEHFFQAAYKWEESTSDIPGFRKCGKLPALYHPPKPKSTQ
USA2_reped2.pep SGPEQTAAERREEVAQKTQDLEHFFQAAYKWEESTSDIPGFRKCGKLPALYHPPKPKSTQ
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Aus1_reped2.pep WGERI ISEHPMASKVAGFGWPSFGAQAEETSLRLQAARWLKRAESAIEKPTQKRLVID
Aus2_reped2.pep WGERI ISEHPMASKVAGFGWPFSGAQAEETSLRLQAARWLKRAESAIEKPAEKQKRLVID
Braz1_reped2.pep WGERI ISEHPMASKVAGFGWPSFGAQAEETSLRLQAARWLKRAESAIEKPTQKRLVID
Braz2_reped2.pep WGERI ISEHPMASKVAGFGWPSFGAQAEETSLRLQAARWLKRAESAIEKPTQKRLVID
CPam1_reped2.pep WGERI ISEHPMASKVAGFGWPSFGAQAEETSLRLQAARWLKRAESAIEKPTQKRLVID
CPaus1_reped2.pep WGERI ISEHPMASKVAGFGWPSFGAQAEETSLRLQAARWLKRAESAIEKPTQKRLVID
Haw1_reped2.pep WGERI ISEHPMASKVAGFGWPSFGAQAEETSLRLQAARWLKRAESAIEKPTQKRLVID
Haw2_reped2.pep WGERI ISEHPMASKVAGFGWPSFGAQAEETSLRLQAARWLKRAESAIEKPTQKRLVID
Maur1_reped2.pep WGERI ISEHPMAAKVAGFGWPSFGAQAEETSLRLQAARWLKRAESAIEKPTATQKRLVID
Reun1_reped2.pep WGERI ISEHPMAAKVAGFGWPSFGAQAEETSLRLQAARWLKRAESAIEKPTAAQKRLVID
Reun2_reped2.pep WGERI ISEHPMAAKVAGFGWPSFGAQAEETSLRLQAARWLKRAESAIEKPTAAQKRLVID
SA1_reped2.pep WGERI ISEHPMAAKVAGFGWPSFGAQAEETSLRLQAARWLKRAESAIEKPTQKRLVID
Taiw1_reped2.pep WGERI ISEHPMASKVAGFGWPSFGAQAEETSLRLQAARWLKRAESAIEKPTQKRLVID
Taiw2_reped2.pep WGERI ISEHPMASKVXGFGWPSFGAQAEETSXRLQAARWLKRXESAIEKPTQKRLVID
USA1_reped2.pep WGERI ISEHPMASKVAGFGWPSFGAQAEETSLRLQAARWLKRAESAIEKPTQKRLVID
USA2_reped2.pep WGERI ISEHPMASKVAGFGWPSFGAQAEETSLRLQAARWLKRAESAIEKPTQKRLVID
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Aus1_reped2.pep RVVKAYEPCRTNAPHTSSSGSLIWSDFLKDFKEAVNSLELDAGIGLPYKLLRKDTHRQMV
Aus2_reped2.pep RVVKAYEPCRTNAPHTSSSGSLIWSDFLKDFKEAVNSLELDAGIGLPYKLLRKDTHRQMV
Braz1_reped2.pep RVVKAYEPCRTNAPHTSSSGSLIWSDFLKDFKEAVNSLELDAGIGLPYKLLHKDTHRQMV
Braz2_reped2.pep RVVKAYEPCRTNAPHTSSSGSLIWSDFLKDFKEAVNSLELDAGIGLPYKLLHKDTHRQMV
CPam1_reped2.pep RVVKAYEPYRTNAPHTSSSGSLIWSDFLKDFKEAVNSLELXAXIGLPYKLLHKDTHRQMV
CPaus1_reped2.pep RVVKAYEPCRTNAPHTSSSGSLIWSDFLKDFKEAVNSLXLDAIGLPYKLLHKDTHRQMV
Haw1_reped2.pep RVVKAYEPCRTNAPHTSSSGSLIWSDFLKDFKEAVNSLELDAGIGLPYKLLHKDTHRQMV
Haw2_reped2.pep RVVKAYEPCRTNAPHTSSSGSLIWSDFLKDFKEAVNSLELDAGIGLPYKLLHKDTHRQMV
Maur1_reped2.pep RVVKAYEPCRTNAPHTSSSGSLIWSDFLKDFKEAVNSLELDAGIGLPYKLLNKDTHRQMV
Reun1_reped2.pep RVVKAYEPCRTNAPHTSSSGSLIWSDFLKDFKEAVNSLELDAGIGLPYKLLNKDTHRQMV
Reun2_reped2.pep RVVKAYEPCRTNAPHTSSSGSLIWSDFLKDFKEAVNSLELDAGIGLPYKLLNKDTHRQMV
SA1_reped2.pep RVVKAYEPCRTNAPHTSSSGSLIWSDFLKDFKEAVNSLELDAGIGLPYKLLHKDTHRQMV
Taiw1_reped2.pep RVVKAYEPCRTNAPHTSSSGSLIWSDFLKDFKEAVNSLELDAGIGLPYKLLHKDTHRQMV
Taiw2_reped2.pep RVVKAYEPCRTNAPHTSSSGSLIWSDFLKDFKEAVNSLELDAGIGLPYKLLHKDTHRQMV
USA1_reped2.pep RVVKAYEPCRTNAPHTSSSGSLIWSDFLKDFKEAVNSLELDAGIGLPYKLLHKDTHRQMV
USA2_reped2.pep RVVKAYEPCRTNAPHTSSSGSLIWSDFLKDFKEAVNSLELDAGIGLPYKLLHKDTHRQMV
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```

Aus1_reped2.pep EDPKFLPLLTRLTWNRLQKMSQVDFQEMTPEQLVREGLCDP IRLFVKGEPHKQAKLDEGR
Aus2_reped2.pep EDPKFLPLLTRLTWNRLQKMSQVDFQEMTPEQLVREGLCDP IRLFVKGEPHKQAKLDEGR
Braz1_reped2.pep EDPKFLPLLTRLTWNRLQKMSQVDFQEMTPEQLVREGLCDP IRLFVKGEPHKQAKLDEGR
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CPaus1_reped2.pep EDPKFLPLLTRLTWNRLQKMSQVDFQEMTPEQLVREGLCDP IRLFVKGEPHKQAKLDEGR
Haw1_reped2.pep EDPKFLPLLTRLTWNRLQKMSQVDFQEMTPEQLVREGLCDP IRLFVKGEPHKQAKLDEGR
Haw2_reped2.pep EDPKFLPLLTRLTWNRLQKMSQVDFQEMTPEQLVREGLCDP IRLFVKGEPHKQAKLDEGR
Maur1_reped2.pep EDPKFLPLLTRLTWNRLQKMSQVDFREMSPEQLVREGLCDP IRLFVKGEPHKQAKLDEGR
Reun1_reped2.pep EDPKFLPLLTRLTWNRLQKMSQVDFREMSPEQLVREGLCDP IRLFVKGEPHKQAKLDEGR
Reun2_reped2.pep XDPKFLPLLTRLTWNRLQKMSQVDFREMSPEQLVREGLCDP IRLFVKGEPHKQAKLDEGR
SA1_reped2.pep EDPKFLPLLTRLTWNRLQKMSQVDFQEMTPEQLVREGLCDP IRLFVKGEPHKQAKLDEGR
Taiw1_reped2.pep EDPKFLPLLTRLTWNRLQKMSQVDFQEMTPEQLVREGLCDP IRLFVKGEPHKQAKLDEGR
Taiw2_reped2.pep EDPKFLPLLTRLTWNRLQKMSQVDFQEMTPEQLVREGLCDP IRLFVKGEPHKQAKLDEGR
USA1_reped2.pep EDPKFLPLLTRLTWNRLQKMSQVDFQEMTPEQLVREGLCDP IRLFVKGEPHKQAKLDEGR
USA2_reped2.pep EDPKFLPLLTRLTWNRLQKMSQVDFQEMTPEQLVREGLCDP IRLFVKGEPHKQAKLDEGR
***** . ** ***** ***** ***** *****

```

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Aus1_reped2.pep  YRLIMSVSLVDQLVARVLF
Aus2_reped2.pep  YRLIMSVSLVDQLVARVLF
Braz1_reped2.pep YRLIMSVSLVDQLVARVLF
Braz2_reped2.pep YRLIMSVSLVDQLVARVLF
CPam1_reped2.pep YRLIMSVSLVDQLVARVLF
CPaus1_reped2.pep YRLIMSVSLVDQLVARVLF
Haw1_reped2.pep  YRLIMSVSLVDQLVARVLF
Haw2_reped2.pep  YRLIMSVSLVDQLVARVLF
Maur1_reped2.pep YRLIMSVSLVDQLVARVLF
Reun1_reped2.pep YRLIMSVSLVDQLVARVLF
Reun2_reped2.pep YRLIMSVSLVDQLVARVLF
SA1_reped2.pep   YRLIMSVSLVDQLVARVLF
Taiw1_reped2.pep YRLIMSVSLVDQLVARVLF
Taiw2_reped2.pep YRLIMSVSLVDQLVARVLF
USA1_reped2.pep  YRLIMSVSLVDQLVARVLF
USA2_reped2.pep  YRLIMSVSLVDQLVARVLF
*****
    
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Coat-Protein Nucleotide

eclustalw August 2, 19101 12:20

of: @fil_20497.tmp

aus1_cp	ck: 6328	from:	1	to:	672	Length:	672
aus2_cp	ck: 6328	from:	1	to:	672	Length:	672
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braz2_cp	ck: 7095	from:	1	to:	672	Length:	672
cpam1_cp	ck: 7860	from:	1	to:	672	Length:	672
cpaus1_cp	ck: 8088	from:	1	to:	672	Length:	672
haw1_cp	ck: 7139	from:	1	to:	672	Length:	672
haw2_cp	ck: 6783	from:	1	to:	672	Length:	672
maur1_cp	ck: 7898	from:	1	to:	672	Length:	672
maur2_cp	ck: 7819	from:	1	to:	672	Length:	672
reun1_cp	ck: 9545	from:	1	to:	672	Length:	672
reun2_cp	ck: 7530	from:	1	to:	672	Length:	672
sa1_cp	ck: 7244	from:	1	to:	672	Length:	672
taiw1_cp	ck: 8113	from:	1	to:	672	Length:	672
taiw2_cp	ck: 7095	from:	1	to:	672	Length:	672
usa1_cp	ck: 9830	from:	1	to:	672	Length:	672
usa2_cp	ck: 7180	from:	1	to:	672	Length:	672

Pairwise similarity parameter:

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K-Tuple length:      2
Gap Penalty:         5
Number of diagonals: 4
Diagonal window size: 4
Scoring Method:      Percentage
    
```

Multiple alignment parameter:

```

Gap Penalty (fixed):      10.00
Gap Penalty (varying):    5.00
Gap separation penalty range: 8
Percent. identity for delay: 40%
List of hydrophilic residue: GPSNDQEKR
Transitions:              Weighted
    
```

Used Sequences:

```

1 /home/bses00/Za ( 672) Aus\1a\cp
2 /home/bses00/Za ( 672) Aus\1b\cp
    
```

- 3 /home/bses00/Za (672) Braz\1cp
- 4 /home/bses00/Za (672) Braz\2cp
- 5 /home/bses00/Za (672) CP\am1cp
- 6 /home/bses00/Za (672) CP\aus1cp
- 7 /home/bses00/Za (672) Haw\1cp
- 8 /home/bses00/Za (672) Haw\2cp
- 9 /home/bses00/Za (672) Maur\1cp
- 10 /home/bses00/Za (672) Maur\2cp
- 11 /home/bses00/Za (672) Reun\1cp
- 12 /home/bses00/Za (672) Reun\2cp
- 13 /home/bses00/Za (672) SA\1cp
- 14 /home/bses00/Za (672) Taiw\1cp
- 15 /home/bses00/Za (672) Taiw\2cp
- 16 /home/bses00/Za (672) USA\1cp
- 17 /home/bses00/Za (672) USA\2cp

..

	10	20	30	40	50	60
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Aus2_cp	TCACGAAGGAATGTCAGAAGACGCGCTA	AACCGTCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT
Braz1_cp	TCACGAAGGAATGTCAGAAGACGCGCTA	AACCGTCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT
Braz2_cp	TCACGAAGGAATGTCAGAAGACGCGCTA	AACCGTCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT
CPam1_cp	TCACGAAGGAATGTCAGAAGACGCGCTA	AACCGTCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT
CPaus1_cp	TCACGAAGGAATGTCAGAAGACGCGCTA	AACCGTCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT
Haw1_cp	TCACGAAGGAATGTCAGAAGACGCGCTA	AACCGTCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT
Haw2_cp	TCACGAAGGAATGTCAGAAGACGCGCTA	AACCGTCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT
Maur1_cp	TCACGAAGGAATGTCAGAAGACGCGCTA	AACCGTCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT
Maur2_cp	TCACGAAGGAATGTCAGAAGACGCGCTA	AACCGTCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT
Reun1_cp	TCACGAAGGAATGTCAGAAGACGCGCTA	AACCGTCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT
Reun2_cp	TCACGAAGGAATGTCAGAAGACGCGCTA	AACCGTCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT
SA1_cp	TCACGAAGGAATGTCAGAAGACGCGCTA	AACCGTCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT
Taiw1_cp	TCACGAAGGAATGTCAGAAGACGCGCTA	AACCGTCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT
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USA1_cp	TCACGAAGGAATGTCAGAAGACGCGCTA	AACCGTCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT
USA2_cp	TCACGAAGGAATGTCAGAAGACGCGCTA	AACCGTCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT	TCGTAGACAGACTCGGCCAGTGGT

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Reun1_cp	GTCCGGGCTCCCCAGGACCTANACGAGTACGACGACGTAGAGCACGTGTTGGAGGAAAC
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Aus1_cp TTTTGGTTGCTGTACAAAGGGAATGGAGACTCGAGCCTAGCAGGACAGTTCGTTTGCCGA

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Aus2_cp      TTTTGGTTGCTGTACAAAGGGAATGGAGACTCGAGCCTAGCAGGACAGTTTCGTTTGCCGA
Braz1_cp     TTTTGGTTGCTGTACAAAGGGAATGGAGACTCGAGCCTAGCAGGACAATTCGTCTGCCGA
Braz2_cp     TTTTGGTTGCTGTACAAAGGGAATGGAGACTCGAGCCTAGCAGGACAATTCGTCTGCCGA
CPam1_cp     TTTTGGTTGCTGTACAAAGGGAATGGAGACTCGAGCCTAGCAGGACAATTCGTCTGCCGA
CPaus1_cp    TTTTGGTTGCTGTACAAAGGGAATGGAGACTCGAGCCTAGCAGGACAATTCGTCTGCCGA
Haw1_cp      TTTTGGTTGCTGTACAAAGGGAATGGAGACTCGAGCCTAGCAGGACAATTCGTTTGCCGA
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USA2_cp      TTTTGGTTGCTGTACAAAGGGAATGGAGACTCGAGCCTAGCAGGACAATTCGTCTGCCGA
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```

Aus1_cp      TTTGAATGCCTTTTCCAGAATCCCAAATAGGTAAGCGACGCTCCCCAACACCCACCCCA
Aus2_cp      TTTGAATGCCTTTTCCAGAATCCCAAATAGGTAAGCGACGCTCCCCAACACCCACCCCA
Braz1_cp     TTTGAATGCCTTTTCCAGAATCCCAAATAGGTAGGCGACGCTCCCCAACACCCACCCCA
Braz2_cp     TTTGAATGCCTTTTCCAGAATCCCAAATAGGTAGGCGACGCTCCCCAACACCCACCCCA
CPam1_cp     TTTGAATGCCTTTTCCAGAATCCCAAATAGGTAGGCGACGCTCCCCAACACCCACCCCA
CPaus1_cp    TTTGAATGCCTTTTCCAGAATCCCAAATAGGTAGGCGACGCTCCCCAACACCCACCCCA
Haw1_cp      TTTGAATGCCTTTTCCAGAATCCCAAATAGGTAAGCGACGCTCCCCAACACCCACCCCA
Haw2_cp      TTTGAATGCCTTTTCCAGAATCCCAAATAGGTAAGCGACGCTCCCCAACACCCACCCCA
Maur1_cp     TTTGAATGTTTATTCCAGAATCCCAAATAGGTAGGCGACGCTCCCCAACACCCACACCA
Maur2_cp     TTTGAATGTTTATTCCAGAATCCCAAATAGGTAGGCGACGCTCCCCAACACCCACACCA
Reun1_cp     TTTGAATGTTTATTCCAGAATCCCAAATAGGTAGGCGACGCTCCCCAACACCCACACCA
Reun2_cp     TTTGAATGTTTATTCCAGAATCCCAAATAGGTAGGCGACGCTCCCCAACACCCACACCA
SA1_cp       TTTGAATGCCTTTTCCAGAATCCCAAATAGGTAGGCGACGCTCCCCAACACCCACCCCA
Taiw1_cp     TTTGAATGCCTTTTCCAGAATCCCAAATAGGTAGGCGACGCTCCCCAACACCCACCCCA
Taiw2_cp     TTTGAATGCCTTTTCCAGAATCCCAAATAGGTAGGCGACGCTCCCCAACACCCACCCCA
USA1_cp      TTTGAATGCCTTTTCCAGAATCCCAAATAGGTAGGCGACGCTCCCCAACACCCACCCCA
USA2_cp      TTTGAATGCCTTTTCCAGAATCCCAAATAGGTAGGCGACGCTCCCCAACACCCACCCCA
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Aus1_cp      ACACCAACCCACCCGCTCCGACCCCGGCACCGGCTTCTAAGTATCTCGGATACCAAGGA
Aus2_cp      ACACCAACCCACCCGCTCCGACCCCGGCACCGGCTTCTAAGTATCTCGGATACCAAGGA
Braz1_cp     ACACCAACCCACCCGCTCCGACCCCGGCACCGGCTCCCAAGTATTTTGGATACCAAGGA
Braz2_cp     ACACCAACCCACCCGCTCCGACCCCGGCACCGGCTCCCAAGTATTTTGGATACCAAGGA
CPam1_cp     ACACCAACCCACCTGCTCCGACCCCGGCACCGGCTCCCAAGTATTTTGGATACCAAGGA
CPaus1_cp    ACACCAACCCACCTGCTCCGACCCCGGCACCGGCTCCCAAGTATTTTGGATACCAAGGA
Haw1_cp      ATACCAACCCACCCGCTCCGACCCCGGCACCGGCTTCTAAGTATCTTGGATACCAAGGA
Haw2_cp      ACACCAACCCACCCGCTCCGACCCCGGCACCGGCTTCTAAGTATCTTGGATACCAAGGA
Maur1_cp     ACACCAACCCACCCGCTCCGACCCCGGCACCGGCTCCTAAGTATTTTGGATACCAAGGA
Maur2_cp     ACACCAACCCACCCGCTCCGACCCCGGCACCGGCTCCTAAGTATTTTGGATACCAAGGA
Reun1_cp     ACACCAACCCACCCGCTCCGACCCCGGCACCGGCTCCTAAGTATTTTGGATACCAAGGA
Reun2_cp     ACACCAACCCACCCGCTCCGACCCCGGCACCGGCTCCTAAGTATTTTGGATACCAAGGA
SA1_cp       ACACCAACCCACCCGCTCCGACCCCGGCACCGGCTCCCAAGTATTTTGGATACCAAGGA
Taiw1_cp     ACACCAACCCACCCGNTCCGACCCCGGCACCGGTTCCCAAGTATTTTGGATACCAAGGA
Taiw2_cp     ACACCAACCCACCCGCTCCGACCCCGGCACCGGCTCCCAAGTATTTTGGATACCAAGGA
USA1_cp      ACACCAACCCACNTGCTCCGACCCCGGCACCGGCTCCCAAGTCTTTTGGATACCAAGGA
USA2_cp      ACACCAACCCACCTGCTCCGACCCCGGCACCGGCTCCCAAGTATTTTGGATACCAAGGA
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Aus1_cp      GTGCCGAACAAC

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Aus2_cp      GTGCCGAACAAC
Braz1_cp     GTGCCGAACAAC
Braz2_cp     GTGCCGAACAAC
CPam1_cp    GTGCCGAACAAC
CPaus1_cp   GTGCCGAACAAC
Haw1_cp     GTGCCGAACAAC
Haw2_cp     GTGCCGAACAAC
Maur1_cp    GTGCCGAACAAC
Maur2_cp    GTGCCGAACAAC
Reun1_cp    GTGCCGAACAAC
Reun2_cp    GTGCCGAACAAC
SA1_cp      GTGCCGAACAAC
Taiw1_cp    GTGCCGAACAAC
Taiw2_cp    GTGCCGAACAAC
USA1_cp     GTGCCGAACAAC
USA2_cp     GTGCCGAACAAC
*****

```

Coat-Protein Protein

eclustalw August 2, 19101 12:22

of: @fil_21108.tmp

aus1_cp.pep	ck: 2850	from: 1	to: 224	Length: 224
aus2_cp.pep	ck: 2850	from: 1	to: 224	Length: 224
braz1_cp.pep	ck: 2202	from: 1	to: 224	Length: 224
braz2_cp.pep	ck: 2202	from: 1	to: 224	Length: 224
cpam1_cp.pep	ck: 2202	from: 1	to: 224	Length: 224
cpaus1_cp.pep	ck: 2202	from: 1	to: 224	Length: 224
haw1_cp.pep	ck: 2520	from: 1	to: 224	Length: 224
haw2_cp.pep	ck: 3060	from: 1	to: 224	Length: 224
maur1_cp.pep	ck: 2189	from: 1	to: 224	Length: 224
maur2_cp.pep	ck: 2538	from: 1	to: 224	Length: 224
reun1_cp.pep	ck: 2430	from: 1	to: 224	Length: 224
reun2_cp.pep	ck: 2397	from: 1	to: 224	Length: 224
sa1_cp.pep	ck: 2447	from: 1	to: 224	Length: 224
taiw1_cp.pep	ck: 3940	from: 1	to: 224	Length: 224
taiw2_cp.pep	ck: 2202	from: 1	to: 224	Length: 224
usa1_cp.pep	ck: 2495	from: 1	to: 224	Length: 224
usa2_cp.pep	ck: 2400	from: 1	to: 224	Length: 224

Pairwise similarity parameter:

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K-Tuple length:      1
Gap Penalty:         3
Number of diagonals: 5
Diagonal window size: 5
Scoring Method:      Percentage

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Multiple alignment parameter:

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Gap Penalty (fixed):      10.00
Gap Penalty (varying):    0.05
Gap separation penalty range: 8
Percent. identity for delay: 40%
List of hydrophilic residue: GPSNDQEKR
Protein Weight Matrix:    blosum

```

Used Sequences:

- 1 /home/bses00/Za (224) Aus_1a_cp.pep
- 2 /home/bses00/Za (224) Aus_1b_cp.pep
- 3 /home/bses00/Za (224) Braz_1cp.pep
- 4 /home/bses00/Za (224) Braz_2cp.pep
- 5 /home/bses00/Za (224) CP_amlcp.pep
- 6 /home/bses00/Za (224) CP_aus1cp.pep
- 7 /home/bses00/Za (224) Haw_1cp.pep
- 8 /home/bses00/Za (224) Haw_2cp.pep
- 9 /home/bses00/Za (224) Maur_1cp.pep
- 10 /home/bses00/Za (224) Maur_2cp.pep
- 11 /home/bses00/Za (224) Reun_1cp.pep
- 12 /home/bses00/Za (224) Reun_2cp.pep
- 13 /home/bses00/Za (224) SA_1cp.pep
- 14 /home/bses00/Za (224) Taiw_1cp.pep
- 15 /home/bses00/Za (224) Taiw_2cp.pep
- 16 /home/bses00/Za (224) USA_1cp.pep
- 17 /home/bses00/Za (224) USA_2cp.pep

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10 20 30 40 50 60

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Aus1_cp.pep      SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
Aus2_cp.pep      SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
Braz1_cp.pep     SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
Braz2_cp.pep     SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
CPam1_cp.pep     SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
CPaus1_cp.pep   SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
Haw1_cp.pep     SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
Haw2_cp.pep     SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
Maur1_cp.pep    SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
Maur2_cp.pep    SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
Reun1_cp.pep    SLRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
Reun2_cp.pep    SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
SA1_cp.pep      SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
Taiw1_cp.pep    SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
Taiw2_cp.pep    SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
USA1_cp.pep     SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
USA2_cp.pep     SRRNVRRRANRRRQTRPVVVVRAPPGPRRVRRRRARVGGNAVRGPGGRSNRDVLTFTVDD
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Aus1_cp.pep      LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
Aus2_cp.pep      LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
Braz1_cp.pep     LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
Braz2_cp.pep     LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
CPam1_cp.pep     LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
CPaus1_cp.pep   LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
Haw1_cp.pep     LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
Haw2_cp.pep     LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
Maur1_cp.pep    LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
Maur2_cp.pep    LKANSTGIXKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
Reun1_cp.pep    LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
Reun2_cp.pep    LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITXLTIQYNSCSDATPGAIALEVDT
SA1_cp.pep      LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
Taiw1_cp.pep    LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
Taiw2_cp.pep    LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
USA1_cp.pep     LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
USA2_cp.pep     LKANSTGILKFGPNLSQYAAFNNGLLKAYHEYKITSLSLTIQYNSCSDATPGAIALEVDT
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Aus1_cp.pep      CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
Aus2_cp.pep      CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
Braz1_cp.pep     CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
Braz2_cp.pep     CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
CPam1_cp.pep     CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
CPaus1_cp.pep   CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
Haw1_cp.pep      CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
Haw2_cp.pep      CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
Maur1_cp.pep     CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
Maur2_cp.pep     CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
Reun1_cp.pep     CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
Reun2_cp.pep     CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
SA1_cp.pep       CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
Taiw1_cp.pep     CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
Taiw2_cp.pep     CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
USA1_cp.pep      CSQTTTGSKITSFVVKRNAAKVFPPAPFIRGKDFMTTSDAQFWLLYKNGDXSLAGQFVCR
USA2_cp.pep      CSQTTTGSKITSFVVKRNAAKVFPPAPLIIRGKDFMTTSDAQFWLLYKNGDSSLAGQFVCR
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Aus1_cp.pep      FECLFQNPQ-VSDAPPTPTPTPPAPTAPASKYLGYQGVPNN
Aus2_cp.pep      FECLFQNPQ-VSDAPPTPTPTPPAPTAPASKYLGYQGVPNN
Braz1_cp.pep     FECLFQNPQ-VGDAPPTPTPTPPAPTAPAPKYFGYQGVPNN
Braz2_cp.pep     FECLFQNPQ-VGDAPPTPTPTPPAPTAPAPKYFGYQGVPNN
CPam1_cp.pep     FECLFQNPQ-VGDAPPTPTPTPPAPTAPAPKYFGYQGVPNN
CPaus1_cp.pep   FECLFQNPQ-VGDAPPTPTPTPPAPTAPAPKYFGYQGVPNN
Haw1_cp.pep      FECLFQNPQ-VSDAPPTPTPTPTPPAPTAPASKYLGYQGVPNN
Haw2_cp.pep      FECLFQNPQ-VSDAPPTPTPTPTPPGPTAPASKYLGYQGVPNN
Maur1_cp.pep     FECLFQNPQ-VGDAPPTPTPTPPAPTAPAPKYFGYQGVPNN
Maur2_cp.pep     FECLFQNPQ-VGDAXPTPTPTPPAPTAPAPKYFGYQGVPNN
Reun1_cp.pep     FECLFQNPQ-VGDAPPTPTPTPTPPAPTAPAPKYFGYQGVPNN
Reun2_cp.pep     FECLFQNPQ-VGDAPPTPTPTPTPPAPTAPAPKYFGYQGVPNN
SA1_cp.pep       FECLFQNPQ-VGDAPPTPTPTPTPPAPTAPAPKYFGYQGVPNN
Taiw1_cp.pep     FECLFQNPQ-VGDASPTPTPTPTPPXPTAPVPKYFGYQGVPNN
Taiw2_cp.pep     FECLFQNPQ-VGDAPPTPTPTPTPPAPTAPAPKYFGYQGVPNN
USA1_cp.pep      FECLFQNPQ-VGDAPPTPTPTPTPXAPTAPAPKSFYQGVPNN
USA2_cp.pep      FECLFQNPQ-VGDAPPTPTPTPTPPAPTAPAPKYFGYQGVPNN
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Readthrough Nucleotide

eclustalw August 3, 19101 16:44

of: @fil_29928.tmp

aus1_rt	ck: 2392	from:	1	to:	1272	Length:	1272
aus2_rt	ck: 5222	from:	1	to:	1272	Length:	1272
braz1_rt	ck: 5850	from:	1	to:	1272	Length:	1272
braz2_rt	ck: 6149	from:	1	to:	1272	Length:	1272
cpam1_rt	ck: 5112	from:	1	to:	1272	Length:	1272
cpaus1_rt	ck: 5095	from:	1	to:	1272	Length:	1272
haw1_rt	ck: 5036	from:	1	to:	1272	Length:	1272
haw2_rt	ck: 7075	from:	1	to:	1272	Length:	1272
maur1_rt	ck: 8187	from:	1	to:	1272	Length:	1272
maur2_rt	ck: 8762	from:	1	to:	1272	Length:	1272
reun1_rt	ck: 7602	from:	1	to:	1272	Length:	1272
reun2_rt	ck: 6271	from:	1	to:	1272	Length:	1272
sal_rt	ck: 6733	from:	1	to:	1272	Length:	1272
taiw1_rt	ck: 5309	from:	1	to:	1272	Length:	1272
taiw2_rt	ck: 6452	from:	1	to:	1272	Length:	1272
usa2a_rt	ck: 6613	from:	1	to:	1272	Length:	1272
usa2b_rt	ck: 3756	from:	1	to:	1188	Length:	1188

Pairwise similarity parameter:

K-Tuple length: 2
 Gap Penalty: 5
 Number of diagonals: 4
 Diagonal window size: 4
 Scoring Method: Percentage

Multiple alignment parameter:

Gap Penalty (fixed): 10.00
 Gap Penalty (varying): 5.00
 Gap separation penalty range: 8
 Percent. identity for delay: 40%
 List of hydrophilic residue: GPSNDQEKR
 Transitions: Weighted

Used Sequences:

- 1 /home/bses00/Za (1272) Aus\1a\rt
- 2 /home/bses00/Za (1272) Aus\1b\rt
- 3 /home/bses00/Za (1272) Braz\1rt
- 4 /home/bses00/Za (1272) Braz\2rt
- 5 /home/bses00/Za (1272) CP\amlrt
- 6 /home/bses00/Za (1272) CP\auslrt
- 7 /home/bses00/Za (1272) Haw_1rt.rev
- 8 /home/bses00/Za (1272) Haw\2rt
- 9 /home/bses00/Za (1272) Maur\1rt
- 10 /home/bses00/Za (1272) Maur\2rt
- 11 /home/bses00/Za (1272) Reun\1rt
- 12 /home/bses00/Za (1272) Reun\2rt
- 13 /home/bses00/Za (1272) SA\1rt
- 14 /home/bses00/Za (1272) Taiw\1rt
- 15 /home/bses00/Za (1272) Taiw\2rt
- 16 /home/bses00/Za (1272) USA\2a\rt
- 17 /home/bses00/Za (1188) USA\2b\rt

..

	10	20	30	40	50	60
Aus1_rt	GTGACCATGTATCTCTGGAAAGACGAATCGTGGAGCATTGAGCAACTGTCAGCCGGATAT					
Aus2_rt	GTAACCATGTATCTTTGGAAAGACGAATCGTGGAGCATTGAGCAACTGTCAGCCGGATAT					
Braz1_rt	GTGACCATGTATCTTTGGAAAGACGAATCGTGGAGCATTGAGCAACTGTCAGCCGGATAT					
Braz2_rt	GTGACCATGTATCTTTGGAAAGATGAATCGTGGAGCATTGAGCAACTGTCAGCCGGATAT					
CPaml_rt	GTGACCATGTATCTTTGGAAAGACGAATCGTGGAGCATTGAGCAACTGTCAGCCGGATAT					
CPausl_rt	GTGACCATGTATCTTTGGAAAGACGAATCGTGGAGCATTGAGCAACTGTCAGCCGGATAT					
Haw1_rt	GTAACCATGTATCTCTGGCAAGACGAATCGTGGAGCATCGAGCAACTGTCAGCCGGATAT					
Haw2_rt	GTAACCATGTATCTCTGGCAAGATGAATCGTGGAGCATCGAGCAACTGTCAGCCGGATAT					
Maur1_rt	GTGACCATGTACCTCTGGAAAGACGAATCGTGGAGCATCGAGCAACTGTCAGCCGGATAT					
Maur2_rt	GTGACCATGTACCTCTGGAAAGACGAATCGTGGAGCATCGAGCAACTGTCAGCCGGATAT					
Reun1_rt	GTGACCATGTACCTCTGGAAAGACGAATCGTGGAGCATCGAGCAACTGCCAGCCGGATAT					
Reun2_rt	GTGACCATGTATCTTTGGAAAGACGAATCGTGGAGCATTGAGCAACTGTCAGCCGGATAT					
SA1_rt	GTGACCATGTATCTTTGGAAAGACGAATCGTGGAGCATTGAGCAACTGTCAGCCGGATAT					
Taiw1_rt	GTGACCATGTATCTTTGGAAAGACGAATCGTGGAGCATTGAGCAACTGTCAGCCGGATAT					
Taiw2_rt	GTGACCATGTATCTTTGGAAAGACGAATCGTGGAGCATTGAGCAACTGTCAGCCGGATAT					
USA2a_rt	GTGACCATGTATCTTTGGAAAGACGAATCGTGGAGCATTGAGCAACTGTCAGCCGGATAT					
USA2b_rt	GTGACCATGTATCTTTGGAAAGATGAATCGTGGAGCATTGAGCAACTGTCAGCCGGATAT					
	** ***** ** ** * ** * ***** ***** ***** *****					
Aus1_rt	CGCGTCAACAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCAGTGGATAAAGGCAAA					
Aus2_rt	CGCGTCAACAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCAGTGGATAAAGGCAAA					

Braz1_rt CGCGTTAACAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCAGTGGATAAAAGGCAAG
 Braz2_rt CGCGTTAACAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCAGTGGATAAAAGGCAAG
 CPam1_rt CGCGTTAACAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCAGTGGATAAAAGGTA
 CPaus1_rt CGCGTTAACAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCAGTGGATAAAAGGTA
 Haw1_rt CGCGTTAACAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCAGTGGATAAAAGGCA
 Haw2_rt CGCGTTAATAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCAGTGGATAAAAGGCA
 Maur1_rt CGCGTGAATAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCCAATAGACAAAGGCA
 Maur2_rt CGCGTGAATAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCAGTAGACAAAGGCAG
 Reun1_rt CGCGTAAATAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCAGTAGACAAAGGCAG
 Reun2_rt CGCGTTAACAATCGAGAACGTGCCATAACCCTCTGTCTCTTTCCAGTTGATAAAAGGCA
 SA1_rt CGCGTTAACAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCAGTGGATAAAAGGCA
 Taiw1_rt CGCGTTAACAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCAGTGGATAAAAGGCA
 Taiw2_rt CGCGTTAACAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCAGTGGATAAAAGGCA
 USA2a_rt CGCGTTAACAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCAGTGGATAAAAGGCA
 USA2b_rt CGCGTTAACAATCGAGAACGTGCCATAACCCTTTGTCCTCTTTCCAGTGGATAAAAGGCA
 ***** ** ***** ** * ** ***** *

Aus1_rt TACTCCGTGTTTCATACAATGTGAGGGCTTTAAGGCAGCTAAAGCCAAAGGAGGCACGAAC
 Aus2_rt TACTCCGTGTTTCATACAATGTGAGGGCTTTAAGGCAGTTAAAGCCAAAGGAGGCACGAAC
 Braz1_rt TACTCCGTGTTTATACAATGTGAGGGCTTTAAGGCAGTTAAAGCCAAAGGAGGCACGAAC
 Braz2_rt TACTCCGTGTTTATACAATGTGAGGGCTTTAAGGCAGTTAAAGCCAAAGGAGGCACGAAC
 CPam1_rt TACTCCGTGTTTATACAATGTGAGGGCTTTAAGGCAGTTAAAGCCAAAGGAGGCACGAAC
 CPaus1_rt TACTCCGTGTTTATACAATGTGAGGGCTTTAAGGCAGTTAAAGCCAAAGGAGGCACGAAC
 Haw1_rt TACTCTGTGTTTCATACAATGCGAGGGCTTTAAGGCAGTTAAAGCCAAAGGAGGCACGAAC
 Haw2_rt TACTCTGTGTTTCATACAATGTGAGGGCTTTAAGGCAGTTAAAGCCAAAGGAGGCACGAAC
 Maur1_rt TACTCCGTGTTTATACAATGTGAGGGCTTTAAGGCAGTTAAAGCAAAGGAGGCACGAAC
 Maur2_rt TACTCCGTGTTTATACAATGTGAGGGCTTTAAGGCAGTTAAAGCAAAGGAGGCACGAAC
 Reun1_rt TACTCCGTGTTTATACAATGTGAGGGCTTTAAGGCAGTTAAAGCAAAGGAGGCACGAAC
 Reun2_rt TACTCCGTGTTTATACAATGTGAGGGCTTTAAGGCAGTTAAAGCAAAGGAGGCACGAAC
 SA1_rt TACTCCGTGTTTATACAATGTGAGGGCTTTAAGGCAGTTAAAGCCAAAGGAGGCACGAAC
 Taiw1_rt TACTCCGTGTTTATACAATGTGAGGGCTTTAAGGCAGTTAAAGCCAAAGGAGGCACGAAC
 Taiw2_rt TACTCCGTGTTTCATACAATGTGAGGGCTTTAAGGCAGTTAAAGCCAAAGGAGGCACGAAC
 USA2a_rt TACTCCGTGTTTATACAATGTGAGGGCTTTAAGGCAGTTAAAGCCAAAGGAGGCACGAAC
 USA2b_rt TACTCCGTGTTTATACAATGTGAGGGCTTTAAGGCAGTTAAAGCCAAAGGAGGCACGAAC
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Aus1_rt GACGGCAAGATGAGCGGGTTTCTTTGTGACAATGCAAATCTCGCGGGTTGGCGAGCATAAC
 Aus2_rt GACGGCAAGATGAGCGGGTTTCTTTGTGACAATGCAAATCTCGCGGGTTGGCGAGCATAAC
 Braz1_rt GACGGCAAGATGAGCGGGTTTCTTTGTGACAATGCAAATCTCGCGGGTTGGCGAGCATAAC
 Braz2_rt GACGGCAAGATGAGCGGGTTTCTTTGTGACAATGCAAATCTCGCGGGTTGGCGAGCATAAC
 CPam1_rt GACGGCAAGATGAGCGGGTTTCTTTGTGACAATGCAAATCTCGCGGGTTGGCGAGCATAAC
 CPaus1_rt GACGGCAAGATGAGCGGGTTTCTTTGTGACAATGCAAATCTCGCGGGTTGGCGAGCATAAC
 Haw1_rt GATGGCAAGATGAGCGGGTTTCTCTGTGANAATGCAAATCTCGCGGGTTGGCGAGCATAAC
 Haw2_rt GACGGCAAGATGAGCGGGTTTCTCTGTGACAATGCAAATCTTGCAGGGTTGGCGAGCATAAC
 Maur1_rt GACGGCAAAATGAGCGGGTTTCTCTGTGACAATGCAAATCTCGCGGGTTGGCGAGCATAAC
 Maur2_rt GACGGCAAGATGAGCGGGTTTCTCTGTGACAATGCAAATCTCGCGGGTTGGCGAGCATAAC
 Reun1_rt GACGGCAAAATGAGCGGGTTTCTCTGTGACAATGCAAATCTCGCGGGTTGGCGAGCATAAC
 Reun2_rt GACGGCAAAATGAGCGGGTTTCTTTGTGACAATGCAAATCTTGCAGGGTTGGCGAGCATAAC
 SA1_rt GACGGCAAAATGAGCGGGTTTCTTTGTGACAATGCAAATCTTGCAGGGTTGGCGAGCATAAC
 Taiw1_rt GACGGCAAGATGAGCGGGTTTCTTTGTGACAATGCAAATCTCGCGGGTTGGCGAGCATAAC
 Taiw2_rt GACGGCAAGATGAGCGGGTTTCTCTGTGACAATGCAAATCTCGCGGGTTGGCGAGCATAAC
 USA2a_rt GACGGCAAGATGAGCGGGTTTCTTTGTGACAATGCAAATCTCGCGGGTTGGCGAGCATAAC
 USA2b_rt GACGGCAAGATGAGCGGGTTTCTTTGTGACAATGCAAATCTCGCGGGTTGGCGAGCATAAC
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Aus1_rt GCATACAGTGGGTGTACAATCTCTAATTATAGAACATCAGACTCTAATGACCCTGGCCAT
 Aus2_rt GCATACAGTGGGTGTACAATCTCTAATTATAGAACATCAGACTCTAATGTCCCTGGCCAT

Braz1_rt GCATATAGTGGGTGTACAATCTCTAATTATAGAACATCGGACTCCAATGTTCCCTGGTCAT
 Braz2_rt GCATATAGTGGGTGTTCAATCTCTAATTATAGAACATCGGACTCTAATGTTCCCTGGTCAT
 CPam1_rt GCATATAGTGGGTGTACAATCTCTAATTATAGAACATCGGACTCTAATGTTCCCTGGTCAT
 CPaus1_rt GCATATAGTGGGTGTACAATCTCTAATTATAGAACATCGGACTCTAATGTTCCCTGGTCAT
 Haw1_rt GCATACAGTGGGTGCACAATCTCTAATTATAAAACATCAGACTCCAATGTCCCTGGTCAT
 Haw2_rt GCATACAGTGGGTGTACAATCTCTAATTATAAAACATCAGACTCCAATGTCCCTGGTCAC
 Maur1_rt GCATATAGTGGGTGTACAGTCTCTAATTACAGAACATCAGACTCAAATGTCCCTGGTCAT
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 Reun1_rt GCATATAGTGGGTGTACAGTCTCTAATTATAGAACATCAGACTCAAATGTTCCCTGGTCAT
 Reun2_rt GCATATAGTGGGTGTACAGTCTCTAATTATAGAACATCAGACTCTAATGTTCCCTGGTCAT
 SA1_rt GCATATAGTGGGTGTACAATCTCTAATTATAGAACATCAGACTCTAATGTTCCCTGGTCAT
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 USA2b_rt GCATATAGTGGGTGTACAATCTCTAATTATAGAACATCGGACTCTAATGTTCCCTGGCCAT
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Aus1_rt CCAGACATGAAAGTCAATGGTGGATCTATTACCGACCAGTTGGTTGAGAGAGATTTTTCT
 Aus2_rt CCAGACATGAAAGTCAATGGTGGATCTTTTACCAACCAGTTGGTTGAGAGAGATTTTTCT
 Braz1_rt CCGGACATGAAAGTCAATGGTGGATCTTTTACCGACCAATTGGTCGAGAGAGATTTTTCT
 Braz2_rt CCGGACATGAAAGTCAATGGTGGATCTTTTACCGACCAATTGGTCGAGAGAGATTTTTCT
 CPam1_rt CCGGACATGAAAGTCAATGGTGGATCTTTTACCGACCAATTGGTCGAGAGAGATTTTTCT
 CPaus1_rt CCGGACATGAAAGTCAATGGTGGATCTTTTACCGACCAATTGGTCGAGAGAGATTTTTCT
 Haw1_rt CCAGACATGAAAGTCAATGGTGGATCTTTTACCGACCAGTTGGTTGAGAGAGATTTTTCT
 Haw2_rt CCAGACATGAAAGTCAATGGTGGATCTTTTACCGACCAGTTGGTTGAGAGAGATTTTTCT
 Maur1_rt CCGGACATGAAAGTCAATGGTGGATCTTTTACCGACCAATTGGTCGAGAGAGACTTTTTCT
 Maur2_rt CCGGATATGAAAGTCAATGGTGGATCTTTTACCGACCAATTGGTCGAGAGAGACTTTTTCT
 Reun1_rt CCGGACATGAAAGTCAACGGTGGATCTTTTACCGACCAATTGGTCGAGAGAGACTTTTTCT
 Reun2_rt CCGGACATGAAAGTCAATGGTGGATCTTTTACCGACCAATTGGTCGAGAGAGATTTTTCT
 SA1_rt CCGGACATGAAAGTCAATGGTGGATCTTTTACCGACCAATTGGTCGAGAGAGATTTTTCT
 Taiw1_rt CCGGACATGAAAGTCAATGGTGGATCTTTTACCGACCAATTGGTCGAGAGAGATTTTTCT
 Taiw2_rt CCGGACATGAAAGTCAATGGTGGATCTTTTACCGACCAATTGGTCGAGAGAGATTTTTCT
 USA2a_rt CCGGACATGAAAGTCAATGGTGGATCTTTTACCGACCAATTGGTCGAGAGAGATTTTTCT
 USA2b_rt CCGNACATGAAAGTCAATGGTGGATCTTTTACCGACCAATTGGTCGAGAGAGATTTTTCT
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Aus1_rt TGTTCAATTACACCTCGAGGTGCCTCAACAAGGCTATTTTGGCCTAGAGGCCCCACCCATT
 Aus2_rt TGTTCATTTTACCTCGAGGTGCCTCAACAAGGCTATTTTGGCCTAGAGGCCCCACCCATT
 Braz1_rt TGTTCAATTTACCTTGAGGTGCCTCAACAAGGCTATTTTGGCCTAGAGGCCCCACCCATT
 Braz2_rt TGTTCAATTTACCTTGAGGTGCCTCAACAAGGCTATTTTGGCCTAGAGGCCCCACCCATT
 CPam1_rt TGTTCAATTTACCTTGAGGTGCCTCAACAAGGCTATTTTGGCCTAGAGGCCCCACCCATT
 CPaus1_rt TGTTCAATTTACCTTGAGGTGCCTCAACAAGGCTATTTTGGCCTAGAGGCCCCACCCATT
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 Haw2_rt TGTTCAATTTACCTCGAGGTGCCTCAACAAGGTTATTTTAGCCTAGAGGCCCCACCCATT
 Maur1_rt TGTTCAATTTACCTCGAGGTGCCTCAACAAGGCTACTTTGGCCTTGAGGCCCCACCCATT
 Maur2_rt TGTTCAATTTACCTCGAGGTGCCTCAACAAGGCTACTTTGGCCTTGAGGCCCCACCCATT
 Reun1_rt TGTTCAATTTACCTCGAGGTGCCTCAACAAGGCTACTTTGGCCTTGAGGCCCCACCCATT
 Reun2_rt TGTTCAATTTACCTTGAGGTGCCTCAACAAGGCTATTTTGGCCTAGAGGCCCCACCCATT
 SA1_rt TGTTCAATTTACCTTGAGGTGCCTCAACAAGGCTATTTTGGCCTAGAGGCCCCACCCATT
 Taiw1_rt TGTTCAATTTACCTTGAGGTGCCTCAACAAGGCTATTTTGGCCTAGAGGCCCCACCCATT
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 USA2a_rt TGTTCAATTTACCTTGAGGTGCCTCAACAAGGCTATTTTGGCCTAGAGGCCCCACCCATT
 USA2b_rt TGTTCAATTTACCTTGAGGTGCCTCAACAAGGCTATTTTGGCCTAGAGGCCCCACCCATT
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Aus1_rt GAAAAGAGTGATCATTTCATTTAGTGGTGTACATACGCTAACTTCACTGATAAAATCCTG
 Aus2_rt GAAAAGAGTGATCATTTCATTTTGTGGTGTCTCACGCTAACTTCACTGATAAAATCCTG

Braz1_rt GAAAAGAGTGATCATTTCATTTTTGTGGTGTCTTACGCTAACTTCACTGATAAAAATCCTG
 Braz2_rt GAAAAGAGTGATCATTTCATTTTTGTGGTGTCTCAGCTAACTTCACTGATAAAAATCCTG
 CPam1_rt GAAAAGAGTGATCATTTCATTTTTGTGGTGTCTTACGCTAACTTCACTGATAAAAATCCTG
 CPaus1_rt GAAAAGAGTGATCATTTCATTTTTGTGGTGTCTTACGCTAACTTCACTGATAAAAATCCTG
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 SA1_rt GAAAAGAGTGATCATTTCATTTTTGTGGTGTCTTACGCTAACTTCACTGATAAAAATCCTG
 Taiw1_rt GAAAAGAGTGATCATTTCATTTTTGTGGTGTCTTACGCTAACTTCACTGATAAAAATCCTG
 Taiw2_rt GAAAAGAGTGATCATTTCATTTTTGTGGTGTCTTACGCTAACTTCACTGATAAAAATCCTG
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Aus1_rt GAATGGGGTTCAATCTCCGTAGCGATAGACGAGGTAAATGACGGAGCGTATAGCAGATCA
 Aus2_rt GAATGGGGTTCAATCTCCGTAGCGATAGACGAGGTAAATGACGGAGCGTATAACAGATCA
 Braz1_rt GAATGGGGTTCAATCTCCGTAGCGATAGACGAGGTGAATGACGGAGCGTATAGTAGATCA
 Braz2_rt GAATGGGGTTCAATCTCCGTAGCGATAGACGAGGTGAATGACGGAGCGTATAGTAGATCA
 CPam1_rt GAATGGGGTTCAATCTCTGTAGCGATAGACGAGGTGAATGACGGAGCGTATAGTAGATCA
 CPaus1_rt GAATGGGGTTCAATCTCTGTAGCGATAGACGAGGTGAATGACGGAGCGTATAGTAGATCA
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 Maur2_rt GAATGGGGTTCAATCTCCGTAGCGGTAGACGAGGTGAATGACGGAGCGTATAGTAGATCA
 Reun1_rt GAATGGGGTTCAATCTCCGTAGCGATAGACGAGGTGAATGACGGAGCGTATAGTAGATCA
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 SA1_rt GAATGGGGTTCAATCTCCGTAGCGATAGACGAGGTGAATGACGGAGCGTATAGTAGATCA
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 USA2a_rt GAATGGGGTTCAATCTCTGTAGCGATAGACGAGGTGAATGACGGAGCGTATAGTAGATCA
 USA2b_rt GAATGGGGTTCAATCTCTGTAGCGATAGACGAGGTGAATGACGGAGCGTATAGTAGATCA

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 Braz1_rt AAATGGGATAAGACTACTGCAATGAGTGCTCGTTTGCCGACTCAGGTGAGCGCCCCCTTCT
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 CPam1_rt AAATGGGATAAGACTACTGCAATGAGTGCTCGTTTGCCGACTCAGGTGAGCGCCCCCTCT
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 Haw1_rt AAATGGGATAAGACTGCTGCAATGAGTGCTCGTTTGCCGACTCAGGTGAGCGCCCCCTTCT
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 SA1_rt AAATGGGATAAGACTACTGCAATGAGTGCTCGTTTGCCGACTCAGGTGAGCGCCCCCTCT
 Taiw1_rt AAATGGGATAAGACTACTGCAATGAGTGCTCGTTTGCCGACTCAGGTGAGCGCCCCCTCT
 Taiw2_rt AAATGGGATAAGACTACTGCAATGAGTGCTCGTTTGCCGACTCAGGTGAGCGCCCCCTCT
 USA2a_rt AAATGGGATAAGACTACTGCAATGAGTGCTCGTTTGCCGGCTCAGGTGAGCGCCCCCTCT
 USA2b_rt AAATGGGATAAGACTACTGCAATGAGTGCTCGTTTGCCGGCTCAGGTGAGCGCCCCCTCT

Aus1_rt GAGGTTTACACCCCGAAACACCTGAACAACCGACTGACGAAGGGACGGAGAGTATGCCT
 Aus2_rt GAGGTTTACACCCCGAAACACCTGAACAACCGACTGACGAAGGGACGGAGAGTATGCCT

Braz1_rt GAGGTTTACACCCC GGAAGCACCTGAGCAACCGACTAACGAAGGGACGGAGAGTATGCCT
 Braz2_rt GAGGTTTACACCCC GGAAGCACCTGAGCAACCGACTAACGAAGGGACGGAGAGTATGCCT
 CPam1_rt GAGGTTTACACCCC GGAAGCACCTGAACAACCGACTAACGAAGGGACGGAGAGTATGCCT
 CPaus1_rt GAGGTTTACACCCC GGAAGCACCTGAACAACCGACTAACGAAGGGACGGAGAGTATGCCT
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 Haw2_rt GAGGTTTACACCCC GGAACACCTGAACAACCGACTGACGAAGGGACGGAGAGTATGCCT
 Maur1_rt GAGGTTTATAACCCC GGAACACCTGAGGAATCGGAAAACGAAGGGACGGAGAGTACGCCT
 Maur2_rt GAGGTTTTTAACCCC GGAACACCTGAGGAATCGAAAAACGAAGGGACGGAGAGTACGCCT
 Reun1_rt GAGGTTTATAACCCC GGAACACCTGAGGAATCGGAAAACGAAGGGACGGAGAGTACGCCT
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 SA1_rt GAGGTTTACACCCC GGAAGCACCTGAGCAACCGACTAACGAAGGGACGGAGAGTATGCCT
 Taiw1_rt GAGGTTTACACCCC GGAAGCACCTGAGCAACCGACTAACGAAGGGACGGAGAGTATGCCT
 Taiw2_rt GAGGTTTACACCCC GGAAGCACCTGAGCAACCGACTAACGAAGGGACGGAGAGTATGCCT
 USA2a_rt GAGGTTTACACCCC GGAAGCACCTGAACAACCGACTAACGAAGGGACGGAGAGTATGCCT
 USA2b_rt GAGGTTTACACCCC GGAAGCACCTGAACAACCGACTAACGAAGGGACGGAGAGTATGCCT
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Aus1_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAACCCACGCCAAA
 Aus2_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAACCCACGCCAAA
 Braz1_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAACCCACGCCAAA
 Braz2_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAACCCACGCCAAA
 CPam1_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAACCCACGCCAAA
 CPaus1_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAACCCACGCCAAA
 Haw1_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAACCCACGTCCAAA
 Haw2_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAACCCACGCCAAA
 Maur1_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAGCCACGCCGAAA
 Maur2_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAGCCACGCCGAAA
 Reun1_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAGCCACGCCGAAA
 Reun2_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAACCCACGCCAAA
 SA1_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAACCCACGCCAAA
 Taiw1_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAACCCACGCCAAA
 Taiw2_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAACCCACGCCAAA
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 USA2b_rt CCAGCCCCGAACCC GGCACCTGGGACCCGGACAACCCAGCAACCAAAGAACCCACGCCAAA
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Aus1_rt ATCGTGGATAATCC G GACCCAAAGGTACTCAACTGGCTCAACAACCAGCGAGGATAAACCT
 Aus2_rt ATCGTGGATAATCC G GACCCAAAGGTACTCAACTGGCTCAACAACCAGCGAGATAAACCT
 Braz1_rt ATCGTGGATAATCC G GACCCGAAGGTACTCAACTGGCTCAACAACCAGCGAGATAAACCT
 Braz2_rt ATCGTGGATAATCC G GACCCGAAGGTACTCAACTGGCTCAACAACCAGCGAGATAAACCT
 CPam1_rt ATCGTGGATAATCC G GACCCAAAGGTACTCAACTGGCTTAACAACCAGCGAGATAAACCT
 CPaus1_rt ATCGTGGATAATCC G GACCCAAAGGTACTCAACTGGCTTAACAACCAGCGAGATAAACCT
 Haw1_rt ATCGTGGATAATCC G GACCCAAAGGTGCTCAACTGGCTCAACAACCAGCGAGATAAACCT
 Haw2_rt ATCGTGGATAATCC G GACCCAAAGGTGCTCAACTGGCTCAACAACCAGCGAGATAAACCT
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 Maur2_rt ATCGTGGACAATCC G GACCCGAAGGTGCTCAACTGGCTTAACAACCAGCGAGATAAACCT
 Reun1_rt ATCGTGGACAATCC G GACCCGAAGGTGCTCAACTGGCTTAACAACCAGCGAGACAAACCT
 Reun2_rt ATCGTGGATAATCC G GACCCAAAGGTACTCAACTGGCTCAACAACCAGCGAGATAAACCT
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 Taiw2_rt ATCGTGGATAATCC G GACCCAAAGGTACTCAACTGGCTCAACAACCAGCGAGATAAACCT
 USA2a_rt ATCGTGGATAATCC G GACCCAAAGGTACTCAACTGGCTCAACAACCAGCGAGATAAACCT
 USA2b_rt ATCGTGGATAATCC G GACCCAAA-----
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Aus1_rt GTGGTGAAGAGGTTTT GCGTGAATCTCCGATTTATGCTCCTCCACCCCCCGTCTCTA
 Aus2_rt GTGGTGAAGAGGTTTT GCGTGAATCTCCGATTTATGCTCCTCCACCCCCCGTCTCTA

Braz1_rt	GTGGTGGGAAGAAGTTTTGCGTGAATCTCCGATTTATGCCCTCCACCCCCCGTCTCTA
Braz2_rt	GTGGTGGGAAGAAGTTTTGCGTGAATCTCCGATTTATGCTCCTCCACCCCCCGTCTCTA
CPam1_rt	GTGGTGGGAAGAGGTTTTGCGTGAATCTCCGATTTATGCTCCTCCACCCCCCGTCTCTA
CPaus1_rt	GTGGTGGGAAGAGGTTTTGCGTGAATCTCCGATTTATGCTCCTCCACCCCCCGTCTCTA
Haw1_rt	GTGGTGGGAAGAGGTTTTGCGTGAATCTCCGATTTATGCTCCTCCACCCCCCGTCTCTA
Haw2_rt	GTGGTGGGAAGAGGTTTTGCGTGAATCTCCGATTTATGCTCCTCCACCCCCCGTCTCTA
Maur1_rt	GTAGTGGGAAGAGGTTTTGCGTGAATCTCCGATTTATGCTCCTCCACCTCCCCCGTCTCTA
Maur2_rt	GTAGTGGGAAGAGGTTTTGCGTGAATCTCCGATTTATGCTCCTCCACCTCCCCCGTCTCTA
Reun1_rt	GTGGTGGGAAGAGGTTTTGCGTGAATCTCCGATTTATGCTCCTCCACCTCCCCCGTCTCTA
Reun2_rt	GTGGTGGGAAGAGGTTTTGCGTGAATCTCCGATTTATGCTCCTCCACCTCCCCCGTCTCTA
SA1_rt	GTGGTGGGAAGAGGTTTTGCGTGAATCTCCGATTTATGCTCCTCCACCCCCCGTCTCTA
Taiw1_rt	GTGGTGGGAAGAGGTTTTGCGTGAATCTCCGATTTATGCTCCTCCACCCCCCGTCTCTA
Taiw2_rt	GTGGTGGGAAGAGGTTTTGCGTGAATCTCCGATTTATGCCCTCCACCCCCCGTCTCTA
USA2a_rt	GTGGTGGGAAGAGGTTTTGCGTGAATCTCCGATTTATGCTCCTCCACCCCCCGTCTTTA
USA2b_rt	-----CCCCCGTCTCTA

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Aus1_rt	ACCCCGACTTCTGCCGACACTTTGAGACAGGCGGACAAGGTCCGGAGAGCTCTCATGGCT
Aus2_rt	ACCCCGACTTCTGCCGACACTTTGAGACAGGCGGACAAGGTCCGGAGAGCTCTCATGGCT
Braz1_rt	GTTCCGACTCATGCCGACACTTTAAGACAGGCGGATAAAGGTCCGGAGAGCTCTCATGGCT
Braz2_rt	GTTCCGACTCATGCCGACACTTTAAGACAGGCGGATAAAGGTCCGGAGAGCTCTCATGGCT
CPam1_rt	GTCCCGACTCATGCCGACACTTTAAGACAGGCGGATAAAGGTCCGGAGAGCTCTCATGGCT
CPaus1_rt	GTCCCGACTCATGCCGATACTTTAAGACAGGCGGATAAAGGTCCGGAGAGCTCTCATGGCT
Haw1_rt	ACCCCGACTTCTGCCGACACTTTGAGACAGGCGGATAAAGGTCCGGAGAGCTCTCATGGCT
Haw2_rt	ACCCCGACTTCTGCCGACACTTTGAGACAGGCGGATAAAGGTCCGGAGAGCTCTCATGGCT
Maur1_rt	ACCCCGACTTCTGCCGACACTTTGAGACAGGCGGATAAAGGTCCGGAGAGCTCTCATGGCT
Maur2_rt	ACCCCGACTTCTGCCGACACTTTGAGACAGGCGGATAAAGGTCCGGAGAGCTCTCATGGCT
Reun1_rt	ACCCCGACTTCTGCCGACACTTTGAGACAGGCGGATAAAGGTCCGGAGAGCTCTCATGGCT
Reun2_rt	GTTCCGACTCATGCCGACACTTTAAGACAGGCGGATAAAGGTCCGGAGAGCTCTCATGGCT
SA1_rt	GTTCCGACTCATGCCGACACTTTAAGACAGGCGGATAAAGGTCCGGAGAGCTCTCATGGCT
Taiw1_rt	GTCCCGACCCATGTCGACACTTTGAGACAGGCGGATAAAGGTCCGGAGAGCTCTCATGGCT
Taiw2_rt	GTTCCGACTCATGCCGACACTTTAAGACAGGCGGATAAAGGTCCGGAGAGCTCTCATGGCT
USA2a_rt	GTCCCGACTCATGCCGACACTTTAAGACAGGCGGATAAAGGTCCGGAGAGCTCTCATGGCT
USA2b_rt	GTCCCGACTCATGCCGACACTTTAAGACAGGCGGATAAAGGTCCGGAGAGCTCTCATGGCT

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Aus1_rt	AACGCTTCGCGTGCAGCCTCACCTCCCCCACGGCTACCGAAGTTCCTGTTCTTGAGGCC
Aus2_rt	AACGCTTCGCGTGCAGCCTCACCTCCCCCACGGCTACCGAAGTTCCTGTTCTTGAGGCC
Braz1_rt	AACGCTTCAGTTTCAGCCTCACCTCCCCCATGAATACCGAAGTTCCTGTTCTTGAGGCC
Braz2_rt	AACGCTTCAGTTTCAGCCTCACCTCCCCCTGTGAACACCGAAGTTCCTGTTCTTGAGGCC
CPam1_rt	AACGCTTCAGTTTCAGCCTCACCTCCCCCACGAACACCGAAGTTCCTGTTCTTGAGGCC
CPaus1_rt	AACGCTTCAGTTTCAGCCTCACCTCCCCCACGAACACCGAAGTTCCTGTTCTTGAGGCC
Haw1_rt	AACGCTTCGCGTGCAGCCTCACCTCCCCCACGACTGCCGAAGTTCCTATTCTTGAGGCC
Haw2_rt	AACGCTTCGCGTGCAGCCTCACCTCCCCCACGACTACCGAAGTTCCTGTTCTTGAGGCC
Maur1_rt	AACGCTTCGTTTCAGCTTCACCCCCCTCGACTACCGAAGTTCCTGTTCTTGAGGCC
Maur2_rt	AACGCTTCTCGTTTCAGCCTCACCCCCCTCGACTACCGAAGTTCCTGTTCTTGAGGCC
Reun1_rt	AACGCTTCTCGTTTCAGCCTCACCCCCCTCGACTACCGAAGTTCCTGTTCTTGAGGCC
Reun2_rt	AACGCTTCAGTTTCAGCCTCACCTCCCCCTACGAACACCGAAGTTCCTGTTCTTGAGGCC
SA1_rt	AACGCTTCAGTTTCAGCCTCACCTCCCCCTACGAACACCGAAGTTCCTGTTCTTGAGGCC
Taiw1_rt	AACGCTTCAGTTTCAGCCTCACCTCCCCCTACGAACACCGAAGTTCCTGTTCTTGAGGCC
Taiw2_rt	AACGCTTCTCGTTTCAGCCTCACCTCCCCCTACGAATACCGAGGTTTCCTGTTCTTGAGGCC
USA2a_rt	AACGCTTCATGTTTCAGCCTCACCTCCCCCACGAACACCGAAGTTCCTGTTCTTGAGGCC
USA2b_rt	AACGCTTCAGTTTCAGCCTCACCTCCCCCACGAACACCGAAGTTCCTGTTCTTGAGGCC

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Aus1_rt	NCTGACACCGCTTCTCTAAGTGGATCATTACGCGGTGGCTCCCTCAGAGGTAATTTGGGT
Aus2_rt	GCTGACACCGCTTCTCTAAGTGGATCTTTACGCGGTGGCTCCCTCAGAGGTAATTTGGGT
Braz1_rt	ACTGACTGCTTCTTGTAGTGGATCATTACGCGGTGGCTCCCTCAGAGGTAATTTGGGT

Braz2_rt ACTGACACTGCTTCTCTAAGTGGATCATTACGCGGTGGCTCCCTCAGAGGTAATTTGGGT
 CPam1_rt ACTGACACCGCTTCTCTTAGTGGATCATTACGCGGTGGCTCCCTCAGGGGTAATTTGGGT
 CPaus1_rt ACTGACACCGCTTCTCTTAGTGGATCATTACGCGGTGGCTCCCTCAGGGGTAATTTGGGT
 Haw1_rt NCTGACACCGCTTCTCTAAGTGGATCATTACGCGGTGGCTCCCTCAGAGGTAATTTGGGT
 Haw2_rt GNTGACACCGCTTCTCAAAGTGGATCATTACGCGGTGGCTCCCTCAGAGGTAATTTGGGT
 Maur1_rt ACTGACACCGCTTCTTTAAGTGGGTCATTACGCGGTGGCTCCCTCAGGGGTAATTTGGGT
 Maur2_rt ACTGACACCGCTTCTTTAAGTGGATCATTACGCGGTGGCTCCCTCAGGGGTAATCTGGGT
 Reun1_rt ACTGACACTGCTTCTTTAAGTGGATCATTACGCGGTGGCTCCCTCAGGGGTAATTTGGGT
 Reun2_rt ACTGACACTGCTTCTCTAAGTGGATCATTACGCGGTGGCTCCCTCAGAGGTAATTTGGGT
 SA1_rt ACTGACACTGCTTCTCTAAGTGGATCATTACGCGGTGGCTCCCTCAGAGGTAATTTGGGT
 Taiw1_rt ACTGACACTGCTTCTCTAAGTGGATCATTACGCGGTGGCTCCCTCAGAGGTAATTTGGGT
 Taiw2_rt ACTGACACCGCTTCTCTAAGTGGATCATTACGCGGTGGCTCCCTCAGAGGTAATTTGGGT
 USA2a_rt ACTGACACTGCTTCTCTTAGTGGATCATTACGCGGTGGCTCCCTCAGGGGTAATTTGGGT
 USA2b_rt ACTGACACTGCTTCCCTTAGTGGATCATTACGCGGTGGCTCCCTCAGGGGTAATTTGGGT
 ***** **

Aus1_rt TCTCGCCCCCTCCCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 Aus2_rt TCTCGCCCCCTCCCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 Braz1_rt TCCC GCCCTCTCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 Braz2_rt TCTCGCCCCCTCTCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 CPam1_rt TCTCGCCCCCTCTCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 CPaus1_rt TCTCGCCCCCTCTCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 Haw1_rt TCTCGCCCCCTCCCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 Haw2_rt TCTCGCCCCCTCCCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 Maur1_rt TCTCGCCCCCTCTCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 Maur2_rt TCTCGCCCCCTCTCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 Reun1_rt TCCC GCCCTCTCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 Reun2_rt TCTCGCCCCCTCTCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 SA1_rt TCTCGCCCCCTCTCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 Taiw1_rt TCTCGCCCCCTCTCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 Taiw2_rt TCTCGCCCCCTCTCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 USA2a_rt TCTCGCCCCCTCTCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 USA2b_rt TCTCGCCCCCTCTCTTCCGAGGGTTCGCTGACAGCCCTCCCCGTTCTGTAAAGTCCGGTTCGT
 ** ***** **

Aus1_rt TCTGAGACCAGTACTCTACAAGGCGGTTCTCTGAGTGGTGGTTCTTTGAGGGGTGGTAAC
 Aus2_rt TCTGAGACCAGTACTCTACAAGGCGGTTCTCTGAGTGGTGGTTCTTTGAGGGGTGGTAAC
 Braz1_rt TCTGAGACCAGTACTCTACAAGGCGGTTCTCTGAGCAGTGGTTCTTTGAGAGGTGGCAAC
 Braz2_rt TCCGAGACCAGTACTCTACAAGGCGGTTCTCTGAGCAGTGGTTCTTTGAGAGGTGGCAAC
 CPam1_rt TCCGAGACCAGTACTTTACAGGGCGGTTCCCTGAGCAGTGGTTCTTTGAGAGGTGGTAAC
 CPaus1_rt TCCGAGACCAGTACTTTACAGGGCGGTTCCCTGAGCAGTGGTTCTTTGAGAGGTGGTAAC
 Haw1_rt TCTGAGACCAGTACTCTACAAGGCGGTTCTCTGAGTGGTGGTTCTTTGAGGGGTGGTAAC
 Haw2_rt TCTGAAACCAGTACTCTACAAGGCGGTTCTCTGAGTGGTGGTTCTTTGAGGGGTGGTAAC
 Maur1_rt TCCGAGACCAGTACTTTACAAGGCGGTTCTTTGGGTGGTGGTTCGCTAAGGGGTGGTAAC
 Maur2_rt TCCGAGACCAGTACTCTACAAGGCGGTTCTTTGGGTGGTGGTTCGCTAAGGGGTGGTAAC
 Reun1_rt TCCGAAACCAGTACTCTACAAGGCGGTTCCCTGAGCAGTGGTTCTTTGAGAGGTGGCAAC
 Reun2_rt TCCGAAACCAGTACTCTACAAGGCGGTTCTCTGAGCAGTGGTTCTTTGAGAGGTGGCAAC
 SA1_rt TCCGAAACCAGTACTCTACAAGGCGGTTCTCTGAGCAGTGGTTCTTTGAGAGGTGGCAAC
 Taiw1_rt TCCGAGACCAGTACTCTACAAGGCGGTTCTCTGAGCAGTGGTTCTTTGAGAGGTGGCAAC
 Taiw2_rt TCCGAGACCAGTACTCTACAAGGCGGTTCTCTGAGCAGTGGTTCTTTGAGAGGTGGCAAC
 USA2a_rt TCCGAGACCAGTACTCTACAAGGCGGTTCCCTGAGCAGTGGTTCTTTGAGAGGTGGTAAC
 USA2b_rt TCCGAGACCAGTACTTTACAGGGCGGTTCCCTGAGCAGTGGTTCTTTGAGAGGTGGCAAC
 ** * ***** ** * ** ***** **

Aus1_rt CTTCGGGCTTTGCCTGAAGCCACAAGAGAGCAAAGGAGGGAATATGAACGTCTCAAGAAT
 Aus2_rt CTTCGGGCTTTGCCTGAGGCCACAAGAGAGCAAAGGAGGGAATATGAACGTCTCAAGAAT
 Braz1_rt CTCCAGGCTTTGCCTGAGGCCACAAGAGAGCAAAGGAGGGAATATGAACGTCTCAAGAAT


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Braz2_rt      CTCCAGGCTTTGCCTGAGGCCACGAGAGAGCAAAGGAGGGAATATGAACGTCTCAAGAAT
CPam1_rt     CTCCAGGCTTTGCCTGAGGCCACAAGAGAGCAAAGGAGGGAATATGAACGTCTCAAGAAT
CPaus1_rt    CTCCAGGCTTTGCCTGAGGCCACAAGAGAGCAAAGGAGGGAATATGAACGTCTCAAGAAT
Haw1_rt      CTTCGGGCTTTGCCTGAGGCCACAAGAGAGCAAAGGAGGGAATATGAACGTCTCAAGAAT
Haw2_rt      CTTCGGGCTTTGCCTGAGGCCACAAGAGAGCAAAGGAGGGAATATGAACGTCTCAAGAAT
Maur1_rt     CTCCAGGTTTTACCTGAGGCCACAAGAGAGCAGAGGAGGGAATATGAACGTCTTAAAAAT
Maur2_rt     CTCCAGGTTTTACCTGAGGCCACAAGAGAGCAGAGGAGGGAATATGAACGTCTCAAAAAAT
Reun1_rt     CTCCAGGTTTTACCTGAGGCCACAAGAGAGCAAAGGAGGGAATATGAACGTCTCAAAAAAT
Reun2_rt     CTCCAGGCTTTGCCTGAGGCCACAAGAGAGCAAAGGAGGGAATATGAACGTCTCAAGAAT
SA1_rt       CTCCAGGCTTTGCCTGAGGCCACAAGAGAGCAAAGGAGGGAATATGAACGTCTCAAGAAT
Taiw1_rt     CTCCAGGCTTTGCCTGAGGCCACAAGAGAGCAAAGGAGGGAATATGAACGTCTCAAGAAT
Taiw2_rt     CTCCAGGCTTTGCCTGAGGCCACAAGAGAGCAAAGGAGGGAATATGAACGTCTCAAGAAT
USA2a_rt     CTCCGGGCTTTGCCTGAGGCCACAAGAGAGCAAAGGAGGGAATATGAACGTCTCAAGAAT
USA2b_rt     CTCCGGGCTTTGCCTGAGGCCACAAGAGAGCAAAGGAGGGAATATGAACGTCTCAAGAAT
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Aus1_rt      TCACAAGNAAAGACGGTGGCGAAAGCCCATGCTCAAGAACACGGTTACAAACCACCGAAA
Aus2_rt      TCACAAGGAAGGACGGTGGCGAAAGCCCATGCTCAAGAACACGGTTACAAACCACCGAAA
Braz1_rt     TCACAAGGGAAGACGGTAGCAAAAGCCCATGCTAAAGAACATGGTTACAAACCACCGAAA
Braz2_rt     TCACAAGGGAAGACGGTAGCAAAAGCCCACGCTAAAGAACATGGTTACAAGCCACCGAAA
CPam1_rt     TCACAAGGGAAGACGGTAGCAAAAGCCCATGCTAAAGAACACGGTTACAAGCCACCGAAA
CPaus1_rt    TCACAAGGGAAGACGGTAGCAAAAGCCCATGCTAAAGAACACGGTTACAAGCCACCGAAA
Haw1_rt     TCACAAGGAAAGACGGTGGCAAAGCCCATGCTAAAGAACACGGTTACAAACCACCGAAA
Haw2_rt     TCACAAGGAAAGACGGTGGCAAAGCCCATGCTAAAGAACACGGTTATAAAACCACCGAAA
Maur1_rt     TCACAAGGGAAGACCGTGGCAGGAGCCCATGCTAGAGAACACGGTTACAAGCCACCGAAA
Maur2_rt     TCACAAGGGAAGACCGTGGCAGGAGCCCATGCTAAAGAACACGGTTACAAGCCACCGAAA
Reun1_rt     TCACAAGGGAAGACCGTGGCAGGAGCCCATGCTAGAGAACACGGTTACAAGCCACCGAAA
Reun2_rt     TCGCAAGGGAAGACGGTAGCAAGAGCCCATGCTAAAGAACACGGTTACAATCCACCGAAA
SA1_rt       TCGCAAGGGAAGACGGTAGCAAGAGCCCATGCTAAAGAACACGGTTACAATCCACCGAAA
Taiw1_rt     TCACAAGGGAAGACGGTAGCAAAAGCTCATGCTCAAGAACATGGTTACAAGCCACCGAAA
Taiw2_rt     TCACAAGGGAAGACGGTAGCAAAAGCTCATGCTAGAGAACATGGTTACAAGCCACCGAAA
USA2a_rt     TCACAAGGGAAGACGGCAGCAAAAGCCCACGCTAAAGAACATGGTTACAAGCCACCGAAA
USA2b_rt     TCACAAGGGAAGACGGTAGCAAAAGCCCACGCTAAAGAACATGGTTACAAGCCACCGAAA
** **** * ** * ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** * ** * ** * **

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Aus1_rt      TCTTCCTCCTCC
Aus2_rt      TCTTCCTCCTCC
Braz1_rt     TCTTCCTCCTCC
Braz2_rt     TCTTCCTCCTCC
CPam1_rt     TCTTCCTCCTCC
CPaus1_rt    TCTTCCTCCTCC
Haw1_rt     TCTTCCTCCTCC
Haw2_rt     TCTTCCTCCTCC
Maur1_rt     TCTTCCTCCTCC
Maur2_rt     TCTTCCTCCTCC
Reun1_rt     TCTTCCTCCTCC
Reun2_rt     TCTTCCTCCTCC
SA1_rt       TCTTCCTCCTCC
Taiw1_rt     TCTTCCTCCTCC
Taiw2_rt     TCTTCCTCCTCC
USA2a_rt     TCTTCCTCCTCC
USA2b_rt     TCTTCCTCCTCC
*****

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Readthrough Protein

eclustalw August 3, 19101 16:50

of: @fil_812.tmp
aus1_rt.pep

ck: 2076 from: 1 to: 424 Length: 424

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aus2_rt.pep      ck: 2580  from:    1 to:    424  Length:  424
braz1_rt.pep    ck: 2867  from:    1 to:    424  Length:  424
braz2_rt.pep    ck: 2426  from:    1 to:    424  Length:  424
cpam1_rt.pep    ck: 3049  from:    1 to:    424  Length:  424
cpaus1_rt.pep   ck: 3049  from:    1 to:    424  Length:  424
haw1_rt.pep     ck: 3010  from:    1 to:    424  Length:  424
haw2_rt.pep     ck: 3801  from:    1 to:    424  Length:  424
maur1_rt.pep    ck: 4892  from:    1 to:    424  Length:  424
maur2_rt.pep    ck: 4681  from:    1 to:    424  Length:  424
reun1_rt.pep    ck: 5459  from:    1 to:    424  Length:  424
reun2_rt.pep    ck: 3515  from:    1 to:    424  Length:  424
sal_rt.pep      ck: 3484  from:    1 to:    424  Length:  424
taiw1_rt.pep    ck: 4364  from:    1 to:    424  Length:  424
taiw2_rt.pep    ck: 2877  from:    1 to:    424  Length:  424
usa2a_rt.pep    ck: 2220  from:    1 to:    424  Length:  424
usa2b_rt.pep    ck: 5697  from:    1 to:    396  Length:  396
    
```

Pairwise similarity parameter:

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K-Tuple length:      1
Gap Penalty:         3
Number of diagonals: 5
Diagonal window size: 5
Scoring Method:      Percentage
    
```

Multiple alignment parameter:

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Gap Penalty (fixed):      10.00
Gap Penalty (varying):    0.05
Gap separation penalty range: 8
Percent. identity for delay: 40%
List of hydrophilic residue: GPSNDQEKR
Protein Weight Matrix:    blosum
    
```

Used Sequences:

- 1 /home/bses00/Za (424) Aus1_rt.pep
- 2 /home/bses00/Za (424) Aus2_rt.pep
- 3 /home/bses00/Za (424) Braz1_rt.pep
- 4 /home/bses00/Za (424) Braz2_rt.pep
- 5 /home/bses00/Za (424) CPam1_rt.pep
- 6 /home/bses00/Za (424) CPaus1_rt.pep
- 7 /home/bses00/Za (424) Haw1_rt.pep
- 8 /home/bses00/Za (424) Haw2_rt.pep
- 9 /home/bses00/Za (424) Maur1_rt.pep
- 10 /home/bses00/Za (424) Maur2_rt.pep
- 11 /home/bses00/Za (424) Reun1_rt.pep
- 12 /home/bses00/Za (424) Reun2_rt.pep
- 13 /home/bses00/Za (424) SA1_rt.pep
- 14 /home/bses00/Za (424) Taiw1_rt.pep
- 15 /home/bses00/Za (424) Taiw2_rt.pep
- 16 /home/bses00/Za (424) USA2a_rt.pep
- 17 /home/bses00/Za (396) USA2b_rt.pep

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                                     10      20      30      40      50      60
Aus1_rt.pep      VTMYLWKDESWSIEQLSAGYRVNNRERAI PFVLFPPVDKGGKYSVFIQCEGFKA AKAGG TN
Aus2_rt.pep      VTMYLWKDESWSIEQLSAGYRVNNRERAI PFVLFPPVDKGGKYSVFIQCEGFKA VKAKAGG TN
    
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Braz1_rt.pep	VTMYLWKDESWSIEQLSAGYRVNNRERAI PFVLF PVDPK GKYSVFI QCEGFKAVKAKGGTN
Braz2_rt.pep	VTMYLWKDESWSIEQLSAGYRVNNRERAI PFVLF PVDPK GKYSVFI QCEGFKAVKAKGGTN
CPaml_rt.pep	VTMYLWKDESWSIEQLSAGYRVNNRERAI PFVLF PVDPK GKYSVFI QCEGFKAVKAKGGTN
CPaus1_rt.pep	VTMYLWKDESWSIEQLSAGYRVNNRERAI PFVLF PVDPK GKYSVFI QCEGFKAVKAKGGTN
Haw1_rt.pep	VTMYLWQDESWSIEQLSAGYRVNNRERAI PFVLF PVDPK GKYSVFI QCEGFKAVKAKGGTN
Haw2_rt.pep	VTMYLWQDESWSIEQLSAGYRVNNRERAI PFVLF PVDPK GKYSVFI QCEGFKAVKAKGGTN
Maur1_rt.pep	VTMYLWKDESWSIEQLSAGYRVNNRERAI PFVLF PIDK GKYSVFI QCEGFKAVKAKGGTN
Maur2_rt.pep	VTMYLWKDESWSIEQLSAGYRVNNRERAI PFVLF PVDPK GRYSVFI QCEGFKAVKAKGGTN
Reun1_rt.pep	VTMYLWKDESWSIEQLPAGYRVNNRERAI PFVLF PVDPK GRYSVFI QCEGFKAVKAKGGTN
Reun2_rt.pep	VTMYLWKDESWSIEQLSAGYRVNNRERAI PSVLF PVDPK GKYSVFI QCEGFKAVKAKGGTN
SA1_rt.pep	VTMYLWKDESWSIEQLSAGYRVNNRERAI PFVLF PVDPK GKYSVFI QCEGFKAVKAKGGTN
Taiw1_rt.pep	VTMYLWKDESWSIEQLSAGYRVNNRERAI PFVLF PVDPK GKYSVFI QCEGFKAVKAKGGTN
Taiw2_rt.pep	VTMYLWKDESWSIEQLSAGYRVNNRERAI PFVLF PVDPK GKYSVFI QCEGFKAVKAKGGAN
USA2a_rt.pep	VTMYLWKDESWSIEQLSAGYRVNNRERAI PFVLF PVDPK GKYSVFI QCEGFKAVKAKGGTN
USA2b_rt.pep	VTMYLWKDESWSIEQLSAGYRVNNRERAI PFVLF PVDPK GKYSVFI QCEGFKAVKAKGGTN

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Aus1_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTI SNYRTSDSNDPGHPDMKVNGGSITDQLVERDFS
Aus2_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTI SNYRTSDSNVPGHPDMKVNGGSFTNQLVERDFS
Braz1_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTI SNYRTSDSNVPGHPDMKVNGGSFTDQLVERDFS
Braz2_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCSI SNYRTSDSNVPGHPDMKVNGGSFTDQLVERDFS
CPaml_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTI SNYRTSDSNVPGHPDMKVNGGSFTDQLVERDFS
CPaus1_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTI SNYRTSDSNVPGHPDMKVNGGSFTDQLVERDFS
Haw1_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTI SNYKTSDSNVPGHPDMKVNGGSFTDQLVERDFS
Haw2_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTI SNYKTSDSNVPGHPDMKVNGGSFTDQLVERDFS
Maur1_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTVSNYRTSDSNVPGHPDMKVNGGSFTDQLVERDFS
Maur2_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTVSNYRTSDSNVPGHPDMKVNGGSFTDQLVERDFS
Reun1_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTVSNYRTSDSNVPGHPDMKVNGGSFTDQLVERDFS
Reun2_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTI SNYRTSDSNVPGHPDMKVNGGSFTDQLVERDFS
SA1_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTI SNYRTSDSNVPGHPDMKVNGGSFTDQLVERDFS
Taiw1_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTI SNYRTSDSNVPGHPDMKVNGGSFTDQLVERDFS
Taiw2_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTI SNYRTSDSNVPGHPDMKVNGGSFTDQLVERDFS
USA2a_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTI SNYRTSDSNVPGHPDMKVNGGSFTDQLVERDFS
USA2b_rt.pep	DGKMSGFLCDNANLAGWRAYAYS GCTI SNYRTSDSNVPGHPXMKVNGGSFTDQLVERDFS

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Aus1_rt.pep	CSLHLEVPQQGYFGLEAPPIEKSDFHFNLVVSYANFTDKILEWGSISVAIDEVNDGAYSRS
Aus2_rt.pep	CSFYLEVPQQGYFGLEAPPIEKSDFHFN FVVSANFTDKILEWGSISVAIDEVNDGAYNRS
Braz1_rt.pep	CSFHLEVPQQGYFGLEAPPIEKSDFHFN FVVSANFTDKILEWGSISVAIDEVNDGAYSRS
Braz2_rt.pep	CSFHLEVPQQGYFGLEAPPIEKSDFHFN FVVSANFTDKILEWGSISVAIDEVNDGAYSRS
CPaml_rt.pep	CSFHLEVPQQGYFGLEAPPIEKSDFHFN FVVSANFTDKILEWGSISVAIDEVNDGAYSRS
CPaus1_rt.pep	CSFHLEVPQQGYFGLEAPPIEKSDFHFN FVVSANFTDKILEWGSISVAIDEVNDGAYSRS
Haw1_rt.pep	CSFHLEVPQQGYFSLEAPPIEKSDFHFN FVVSANFTDKILEWGSISVAIDEVNDGAYSRS
Haw2_rt.pep	CSFHLEVPQQGYFSLEAPPIEKSDFHFN FVVSANFTDKILEWGSISVAIDEVNDGAYSRS
Maur1_rt.pep	CSFHLEVPQQGYFGLEAPPIEKSDFHFN FVVSANFTDKIMEWGSISVAVDEVNDGAYSRS
Maur2_rt.pep	CSFHLEVPQQGYFGLEAPPIEKSDFHFN FVVSANFTDKIMEWGSISVAVDEVNDGAYSRS
Reun1_rt.pep	CSFHLEVPQQGYFGLEAPPIEKSDFHFN FVVSANFTDKIMEWGSISVAIDEVNDGAYSRS
Reun2_rt.pep	CSFHLEVPQQGYFGLEAPPIEKSDFHFN FVVSANFTDKILEWGSISVAIDEVNDGAYSRS
SA1_rt.pep	CSFHLEVPQQGYFGLEAPPIEKSDFHFN FVVSANITDKILEWGSISVAIDEVNDGAYSRS
Taiw1_rt.pep	CSFHLEVPQQGYFGLEAPPIEKSDFHFN FVVSANFTDKILEWGSISVAIDEVNDGAYSRS
Taiw2_rt.pep	CSFHLEVPQQGYFGLEAPPIEKSDFHFN FVVSANFTDKILEWGSISVAIDEVNDGAYSRS
USA2a_rt.pep	CSFHLEVPQQGYFGLEAPPIEKSDFHFN FVVSANFTDKILEWGSISVAIDEVNDGAYSRS
USA2b_rt.pep	CSFHLEVPQQGYFGLEAPPIEKSDFHFN FVVSANFTDKILEWGSISVAIDEVNDGAYSRS

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Aus1_rt.pep	KWDKTAAMSARLPTQVSALSEVYTPETPEQPTDEGTESMPAPNPALGPDNPATKEPTPK
Aus2_rt.pep	KWDKTAAMSARLPTQVSALSEVYTPETPEQPTDEGTESMPAPNPALGPDNPATKEPTPK
Braz1_rt.pep	KWDKTTAMSARLPTQVSAPSEVYTPEAPEQPTNEGTESMPAPNPALGPDNPATKEPTPK
Braz2_rt.pep	KWDKTTAMSARLPTQVSAPSEVYTPEAPEQPTNEGTESMPAPNPALGPDNPATKEPTPK

CPam1_rt.pep	KWDKTTAMSARLPTQVSAPSEVYTPPEAPEQPTNEGTE SMPPAPNPALGPDNPATKEPTPK
CPaus1_rt.pep	KWDKTTAMSARLPTQVSAPSEVYTPPEAPEQPTNEGTE SMPPAPNPALGPDNPATKEPTPK
Haw1_rt.pep	KWDKTAAMSARLPTQVSAPSEVYTPETPEQPTDEGTE SMPPAPNPALGPDNPATKEPTSK
Haw2_rt.pep	KWDKTAAMSARLPTQVSAPSEVYTPETPEQPTDEGTE SMPPAPNPALGPDNPATKEPTPK
Maur1_rt.pep	KWDKTTAMSARLPTQVSAPSEVYNPETPEESENEGTE STPPAPNPALGPDNPATKEPTPK
Maur2_rt.pep	KWDKTTAMSARLPTQVSAPSEVFNPETPEESKNEGTE STPPAPNPALGPDNPATKEPTPK
Reun1_rt.pep	KWDKTTAMSARLPTQVSAPSEVYNPETPEESENEGTE STPPAPNPALGPDNPATKEPTPK
Reun2_rt.pep	KWDKTTAMSARLPTQVSAPSEVYTPPEAPEQPTNEGTE SMPPAPNPALGPDNPATKEPTPK
SA1_rt.pep	KWDKTTAMSARLPTQVSAPSEVYTPPEAPEQPTNEGTE SMPPAPNPALGPDNPATKEPTPK
Taiw1_rt.pep	KWDKTTAMSARLPTQVSAPSEVYTPPEAPEQPTNEGTE SMPPAPNPALGPDNPATKEPTPK
Taiw2_rt.pep	KWDKTTAMSARLPTQVSAPSEVYTPPEAPEQPTNEGTE SMPPAPNPALGPDNPATKEPTPK
USA2a_rt.pep	KWDKTTAMSARLPAQVSAPSEVYTPPEAPEQPTNEGTE SMPPAPNPALGPDNPATKEPTPK
USA2b_rt.pep	KWDKTTAMSARLPAQVSAPSEVYTPPEAPEQPTNEGTE SMPPAPNPALGPDNPATKEPAPK
	*****.*****.***** ****.***.***.***** *****.*****.***** *

Aus1_rt.pep	IVDNPDPKVLNWLNNQRGKPVVEEVLRESPIYAPPPPSLTPTSADTLRQADKVRRALMA
Aus2_rt.pep	IVDNPDPKVLNWLNNQRDKPVVEEVLRESPIYAPPPPSLTPTSADTLRQADKVRRALMA
Braz1_rt.pep	IVDNPDPKVLNWLNNQRDKPVVEEVLRESPIYAPPPPSLVPTHADTLRQADKVRRALMA
Braz2_rt.pep	IVDNPDPKVLNWLNNQRDKPVVEEVLRESPIYAPPPPSLVPTHADTLRQADKVRRALMA
CPam1_rt.pep	IVDNPDPKVLNWLNNQRDKPVVEEVLRESPIYAPPPPSLVPTHADTLRQADKVRRALMA
CPaus1_rt.pep	IVDNPDPKVLNWLNNQRDKPVVEEVLRESPIYAPPPPSLVPTHADTLRQADKVRRALMA
Haw1_rt.pep	IVDNPDPKVLNWLNNQRDKPVVEEVLRESPIYAPPPPSLTPTSADTLRQADKVRRALMA
Haw2_rt.pep	IVDNPDPKVLNWLNNQRDKPVVEEVLRESPIYAPPPPSLTPTSADTLRQADKVRRALMA
Maur1_rt.pep	IVDNPDPKVLNWLNNQRDKPVVEEVLRESPIYAPPPPSLTPTSADTLRQADKVRRALMA
Maur2_rt.pep	IVDNPDPRVLNWLNNQRDKPVVEEVLRESPIYAPPPPSLTPTSADTLRQADKVRRALMA
Reun1_rt.pep	IVDNPDPKVLNWLNNQRDKPVVEEVLRESPIYAPPPPSLTPTSADTLRQADKVRRALMA
Reun2_rt.pep	IVDNPDPKVLNWLNNQRDKPVVEEVLRESPIYAPPPPSLVPTHADTLRQADKVRRALMA
SA1_rt.pep	IVDNPDPKVLNWLNNQRDKPVVEEVLRESPIYAPPPPSLVPTHADTLRQADKVRRALMA
Taiw1_rt.pep	IVDNPDPKVLNWLNNQRDKPVVEEVLRESPIYAPPPPSLVPTHADTLRQADKVRRALMA
Taiw2_rt.pep	IVDNPDPKVLNWLNNQRDKPVVEEVLRESPIYAPPPPSLVPTHADTLRQADKVRRALMA
USA2a_rt.pep	IVDNPDPKVLNWLNNQRDKPVVEEVLRESPIYAPPPPSLVPTHADTLRQADKVRRALMA
USA2b_rt.pep	IVDNPD-----NPPSLVPTHADTLRQADKVRRALMA
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Aus1_rt.pep	NASRAASPPPTATEVPVLGAXDTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPVR
Aus2_rt.pep	NASRAASPPPTATEVPVLGAADTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPVR
Braz1_rt.pep	NASRSASPPPMNTEVPVLGATDTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPAR
Braz2_rt.pep	NASRSASPPPVNTEVPVLGATDTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPAR
CPam1_rt.pep	NASRSASPPPTNTEVPVLGATDTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPAR
CPaus1_rt.pep	NASRSASPPPTNTEVPVLGATDTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPAR
Haw1_rt.pep	NASRAASPPPTTAEVPI LGAXDTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPVR
Haw2_rt.pep	NASRAASPPPTTTEVPVLGAXDTASQSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPVR
Maur1_rt.pep	NASRSASPPPSTTEVPVLGATDTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPAR
Maur2_rt.pep	NASRSASPPPSTTEVPVLGATDTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPAR
Reun1_rt.pep	NASRSASPPPSTTEVPVLGATDTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPAR
Reun2_rt.pep	NASRSASPPPTNTEVPVLGATDTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPAR
SA1_rt.pep	NASRSASPPPTNTEVPVLGATDTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPAR
Taiw1_rt.pep	NASRSASPPPTNTEVPVLGATDTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPAR
Taiw2_rt.pep	NASRSASPPPTNTEVPVLGATDTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPAR
USA2a_rt.pep	NASCSASPPPTNTEVPVLGATDTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPAR
USA2b_rt.pep	NASRSASPPPTNTEVPVLGATDTASLSGSLRGGSLRGNLGSRPSLPRVADSPPRS SVSPAR
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Aus1_rt.pep	SETSTLQGGSLSGGSLRGGNLRALPEATREQRREYERLKN SQXKTVAKAHAQEHGYKPPK
Aus2_rt.pep	SETSTLQGGSLSGGSLRGGNLRALPEATREQRREYERLKN SQGRTVAKAHAQEHGYKPPK
Braz1_rt.pep	SETSTLQGGSLSGGSLRGGNLRALPEATREQRREYERLKN SQGKTVAKAHAQEHGYKPPK
Braz2_rt.pep	SETSTLQGGSLSGGSLRGGNLRALPEATREQRREYERLKN SQGKTVAKAHAQEHGYKPPK

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CPam1_rt.pep      SETSTLQGGSLSGGSLRGGNLQALPEATREQRREYERLKNSQGKTVAKAHAKEHGYKPPK
CPaus1_rt.pep    SETSTLQGGSLSGGSLRGGNLQALPEATREQRREYERLKNSQGKTVAKAHAKEHGYKPPK
Haw1_rt.pep      SETSTLQGGSLSGGSLRGGNLRALPEATREQRREYERLKNSQGKTVAKAHAKEHGYKPPK
Haw2_rt.pep      SETSTLQGGSLSGGSLRGGNLRALPEATKEQRREYERLKNSQGKTVAKAHAKEHGYKPPK
Maur1_rt.pep     SETSTLQGGSLGGGSLRGGNLQVLPEATREQRREYERLKNSQGKTVARAHAREHGYKPPK
Maur2_rt.pep     SETSTLQGGSLGGGSLRGGNLQVLPEATREQRREYERLKNSQGKTVARAHAKEHGYKPPK
Reun1_rt.pep     SETSTLQGGSLGGGSLRGGNLQVLPEATREQRREYERLKNSQGKTVARAHAREHGYKPPK
Reun2_rt.pep     SETSTLQGGSLSGGSLRGGNLQALPEATREQRREYERLKNSQGKTVARAHAKEHGYKPPK
SA1_rt.pep       SETSTLQGGSLSGGSLRGGNLQALPEATREQRREYERLKNSQGKTVARAHAKEHGYNPPK
Taiw1_rt.pep     SETSTLQGGSLSGGSLRGGNLRALPEATREQRREYERLKNSQGKTVAKAHAQEHGYKPPK
Taiw2_rt.pep     SETSTLHGGSLSGGSLRGGNLQALPEATREQRREYERLKNSQGKTVAKAHAKEHGYKPPK
USA2a_rt.pep     SETSTLQGGSLSGGSLRGGNLRALPEATREQRREYERLKNSQGKTAKAHAKEHGYKPPK
USA2b_rt.pep     SETSTLQGGSLSGGSLRGGNLRALPEATREQRREYERLKNSQGKTVAKAHAKEHGYKPPK
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Aus1_rt.pep      SSSS
Aus2_rt.pep      SSSS
Braz1_rt.pep     SSSS
Braz2_rt.pep     SSSS
CPam1_rt.pep     SSSS
CPaus1_rt.pep    SSSS
Haw1_rt.pep      SSSS
Haw2_rt.pep      SSSS
Maur1_rt.pep     SSSS
Maur2_rt.pep     SSSS
Reun1_rt.pep     SSSS
Reun2_rt.pep     SSSS
SA1_rt.pep       SSSS
Taiw1_rt.pep     SSSS
Taiw2_rt.pep     SSSS
USA2a_rt.pep     SSSS
USA2b_rt.pep     SSSS
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