

Supplementary material for:

An ER-localised, extensive, essential and immunogenic glycoprotein family in trypanosomes

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Figure legends

Figure S1: Bioinformatic filters for identification of predicted type I *trans*-membrane domain surface membrane proteins. Firstly, the TREU927 proteome was downloaded from TriTrypDB (<http://tritrypdb.org/tritrypdb/>). All protein sequences were entered into SignalP HMM (<http://www.cbs.dtu.dk/services/SignalP-2.0/>) and those protein sequences containing predicted signal peptides and signal anchors were retained, whilst all others were discarded. Mitprot (<http://ihg.gsf.de/ihg/mitoprot.html>), Predotar (<http://www.hs-ls.pitt.edu/obrc/index.php?page=URL1043959648>) and TargetP (<http://www.cbs.dtu.dk/services/TargetP/>) were then used to remove predicted mitochondrial proteins. Using the output from SignalP HMM, signal sequences were removed and thus the mature protein sequence was generated for all retained protein sequences. These sequences were then entered into TMHMM (<http://www.cbs.dtu.dk/services/TMHMM/>). Finally, GPI-SOM (<http://gpi.unibe.ch>) and big-PI (http://mendel.imp.ac.at/gpi/gpi_server.html) were both used to remove all predicted GPI-anchored proteins. Only one GPI-anchored protein was found in this final output; Tb09.v4.0204. The final cohort of 208 protein IDs was parsed through the publicly available web-based mitochondrial proteome database (www.TrypsProteome.org), to check for the absence of mitochondrial-targeted proteins. Accession numbers and details for these sequences are available in Table S2.

Figure S2: Phylogenetic identification of the IGP family. (A) A neighbour joining tree was generated using ClustalW2. Adenylate cyclases are highlighted in pink, ISG and ISG-like proteins are highlighted in blue and light blue respectively. Those proteins which do not form clusters are highlighted in yellow and referred to as singletons. A family of 20 proteins, invariant glycoproteins (IGPs) are highlighted in green. (B) Phylogenetic analysis of IGPs and ISGs, which demonstrates the distinct nature of these two gene families. The IGP family is further divided into three subfamilies, designated IGP34 (two genes), IGP40 (ten genes) and IGP48 (eight genes), based on molecular weight, presence in all Salivarian trypanosomes and *T. cruzi* and also on possession of N-glycosylation sites.

Sequences from the nearest set of genes from the closer analysis in panel A were used as an out group. (C) Phylogenetic analysis of all retrieved IGP orthologs from a range of kinetoplastid genomes (see methods). *Leishmania* and related species are colour-coded in shades of green, African trypanosomes in shades of red/ochre and south American trypanosomes in shades of blue.

Figure S3: ClustalW alignment of IGP homologues. Panel A: Single representatives of the IGP34, 40 and 48 families are shown to illustrate the homology within the N-terminal region. Panel B: Eighty IGP family sequences, from *T. brucei brucei*, *T. brucei gambiense*, *T. vivax*, *T. congolense* and *T. cruzi* were aligned using ClustalW. The alignment was used for building the phylogeny shown in Figure S2C.

Figure S4: IGP48 is a tomato lectin-binding protein. 1×10^7 BSF cells over-expressing IGP48 full-length protein, IGP48 ectodomain, dTRIM or wild type cells (negative control) were lysed and HA-tagged proteins immunoprecipitated with anti-HA antibody and Dynabeads® Protein G (Life technologies). This was carried out under both native and denaturing conditions (addition of detergent and heating to 95°C). Samples were separated by SDS-PAGE followed by Western blot with TL-biotin conjugate (1:10,000, Vector Laboratories) and streptavidin-HRP (1:10,000, Sigma Aldrich). Membranes were stripped and re-probed with mouse anti-HA monoclonal antibody. Antibody light (~25kDa) and heavy chains (~50kDa) can be seen for all blots. Bands corresponding to HA-tagged proteins are also seen at the correct molecular weight when probed with mouse anti-HA to verify the immunoprecipitation of HA-tagged proteins. To confirm the specificity of immunoprecipitation, wild type BSF cells were lysed and incubated with mouse anti-HA and then Dynabeads under native and denaturing conditions. Following SDS-PAGE, membrane was probed with rabbit polyclonal antibodies against the highly N-glycosylated VSG221. A protein band corresponding to VSG221 was present in the whole cell sample, and no band was observed in the native or denaturing immunoprecipitated samples, indicating that only HA-tagged constructs were isolated in the immunoprecipitation process. The addition of chitin hydrolysate was used to check the carbohydrate specificity of tomato lectin for proteins containing poly-LacNAc units.

Figure S5: Effects of IGP RNAi on cell cycle progression. Uninduced and cells that have been induced for 24 hrs were fixed and stained with DAPI. Representative images were taken for cells with normal nuclei and kinetoplast content (1K:1N, 2K:1N, 2K:2N), as well as for cells with abnormal DNA content (0K:1N, 1K:0N, 1K:2N, 0K:2N, K:N $n > 2$). The percentage of cells with this type of DNA content out of 200 cells is indicated for induced and uninduced cells beside each image. All images were captured at the same magnification and scale bar represents 2µm.

Figure S6: Induction of IGP48 expression in stumpy and stumpy-like cells. BSF cells ectopically over-expressing HA epitope tagged IGP48 at the C-terminus were incubated at 37°C, 20°C (cold-shock), or in the presence of pCPT-cAMP for 12 hours. A Western blot of

endogenous IGP48 expression levels using rabbit anti-IGP48 antibody (1:100) is shown. Blots were stripped and re-probed with anti-ISG75 whose levels remained unchanged. IGP48 protein levels were determined by densitometry using ImageJ and quantified by normalisation to ISG75. Blots were probed for p67, which is up-regulated in cells treated with pCPT-cAMP and PAD2 (protein associated with differentiation 2), which is under thermoregulated control.

Figure S7: Visualisation of IGP48 by confocal microscopy. Cells were fixed and membranes remained intact (not permeabilised), so that incubation with anti-HA antibody stained only HA epitope-tagged proteins on the surface of the cell, if present. A representative image is shown for each condition of a single optical z-section. Confocal z sections were acquired using an SP2-visible inverted confocal microscope (Leica Microsystems GmbH, Germany). Scale bar is 2µm.

Figure S8: Analysis of glycosylation defects on IGP knockdown. (A) Whole cell lysates were prepared from p2T7 IGP48 RNAi cell lines cultured in the presence (induced) or absence (uninduced) of tetracycline for 24 hrs and proteins separated by NuPAGE® Bis-Tris Gel System (Invitrogen) using 4-12% gradient acrylamide gels, allowing high resolution separation of proteins. Analysis of protein abundance and molecular weight was carried out using ImageJ, and a line profile plot of grey value (the sum of the grey values of all the pixels in the selection) against distance from top to bottom of the blot was generated. (B) Samples were separated by SDS-PAGE and lectin blots were carried out with *Erythrina cristigalli* (EC; 1:1000) or *Ricinus communis* (RC; 1:1000) lectins conjugated to biotin and then incubated with streptavidin-HRP. A line profile plot, using ImageJ, was generated for each blot. Protein gels were also stained with Coomassie blue stain, to show equal protein loading. Each experiment was performed in duplicate with a representative experiment shown here.

Figure S9: Analysis of intracellular compartment morphology in IGP48 knockdown cells. (Left) Visualisation of ER structure and morphology of cells in *T. brucei* stained with TbBiP. (Centre and right) Distribution of VSG221 in permeabilised cells (intracellular VSG, centre) and non-permeabilised cells (surface VSG, right). Intracellular staining with BiP and VSG was visualised with confocal microscopy. Numbers on the panels indicate the period after induction when cells were taken for analysis. Scale bar, 2µm.

Figure S10: IGP48 knockdown does not induce ATG8-dependant autophagy. BSF IGP48 RNAi cells transfected with YFP-ATG8.2::GL2166. Cells were induced with tetracycline for 48 hours and fixed, permeabilised and stained with anti-GFP. The number of ATG8-positive puncta were counted for induced and uninduced cells (n = 20) and plotted as a bar graph. Error bars denote standard error of the mean. Knockdown of IGP48 is verified by Western blot, using anti-IGP48 antibody and anti-tubulin as a loading control. A Western blot probed with anti-GFP to verify molecular weight of YFP-ATG8 as 41kDa.

Table S1: Primer sequences for the verification of RNAi knockdown and localisation studies. The epitope tag is underlined and restriction sites are shown in bold. Primers are shown in 5' to 3' direction. Designation of primers is shown to the left and restriction sites and epitope tags used are given on the right.

Table S2: Accession numbers of predicted type I proteins in *T. brucei*. The accession numbers of all 208 proteins resulting from the bioinformatics search outlined in Fig. S1 are shown in the table.

Table S3: Serum immunoglobulin responses to IGP48 in *T. b. rhodesiense* patients. Immunoglobulin G and M responses to recombinant IGP48 detected by Western blotting are recorded as either positive (+) or negative (-). For each patient, disease stage, age and thick film parasitaemia (i.e. Number of Giemsa stained parasites observed per 10 fields, at 400x magnification) are recorded.

Trypanosoma brucei predicted proteome (TREU 927)

Tritypdb

11,412



Identification of signal peptide- and signal anchor-containing proteins

SignalP HMM



8,681

2,731

Removal of predicted mitochondrial proteins

Mitoprot, Predotar and TargetP



867

1,864

Generation of mature protein sequences using signal peptide predictions



Topology prediction and selection for type I TMD proteins

TMHMM



1,655

209

Removal of predicted GPI-anchored proteins

GPI-SOM and Big-PI

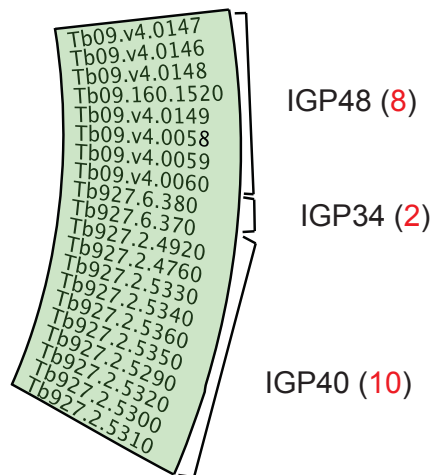
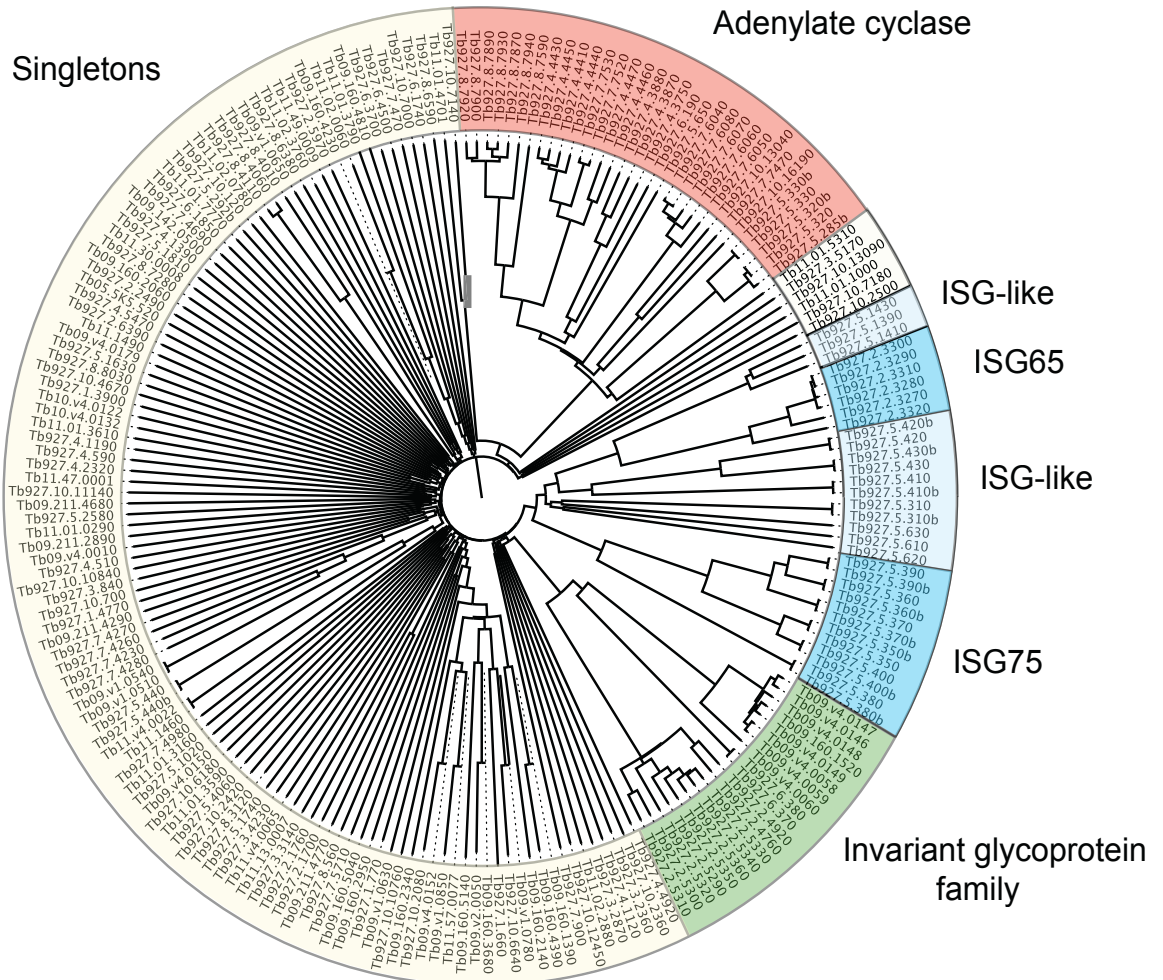


1 Tb09.v4.0204

208

Figure S1

Figure S2A



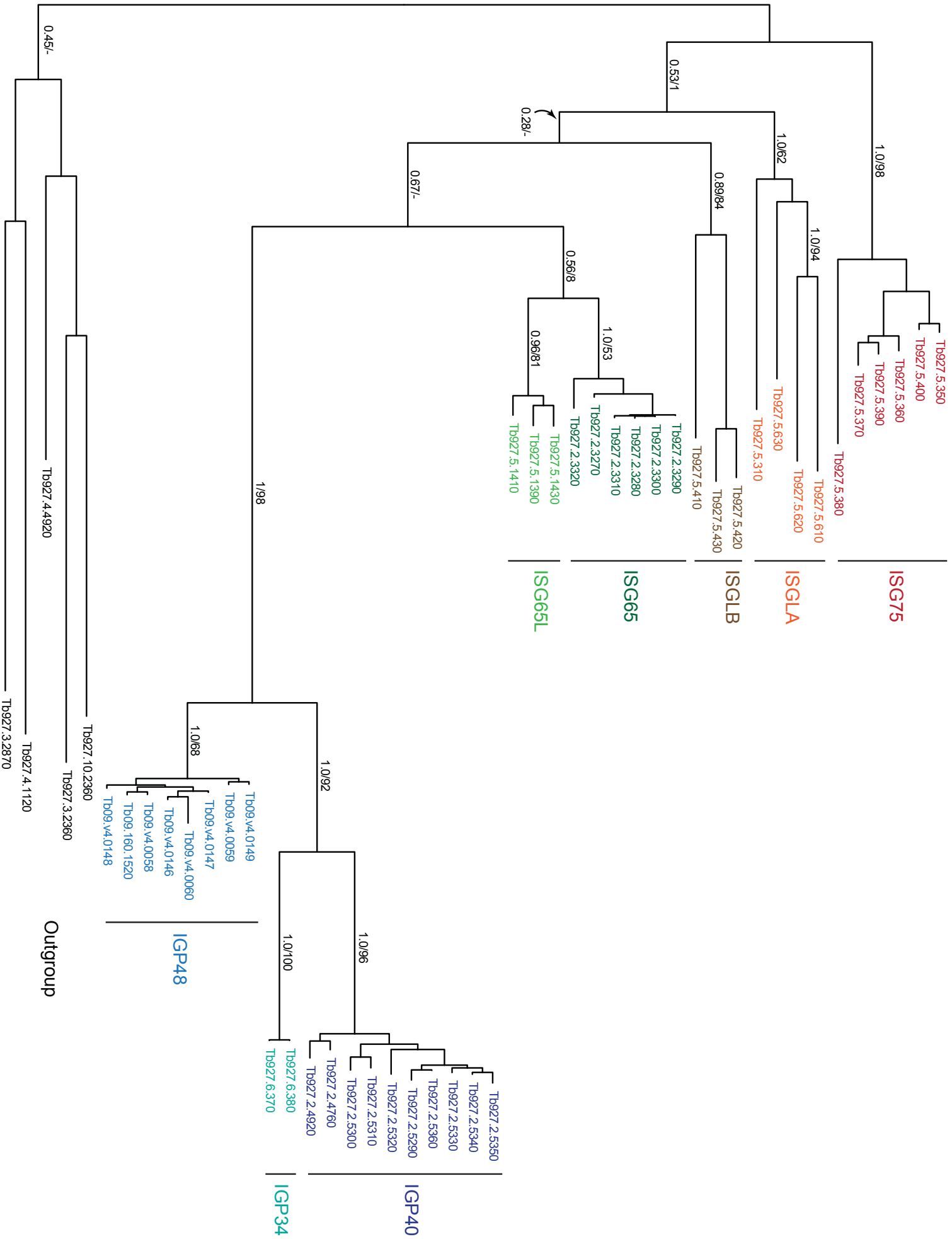


Figure S2B



Species	Strain
<i>Angomonas culicis</i>	
<i>Strigomonas culicis</i>	
<i>Phytomonas EM</i>	
<i>Phytomonas HART</i>	
<i>Phytomonas serpens</i>	
<i>Leishmania donovani</i>	
<i>Leishmania infantum</i>	
<i>Leishmania major</i>	
<i>Leishmania mexicana</i>	
<i>Leishmania braziliensis</i>	
<i>Leishmania tarentolae</i>	
<i>Leptomonas pyrthocoris</i>	
<i>Typanosoma gambiense</i>	
<i>Typanosoma brucei</i>	
<i>Typanosoma congolense</i>	
<i>Typanosoma vivax</i>	
<i>Typanosoma cruzi marinkellei</i>	B7
<i>Typanosoma cruzi</i>	TSyVio
<i>Typanosoma cruzi</i>	CL Brener Esmeraldo like
<i>Typanosoma cruzi</i>	ICL Brener Non-Esmeraldo like

Figure S2C


```
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2
3
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6 Tb927.2.5290 MSM DTRMVNFGFTRAALLCG-LLLLLTAVCPLHVTAADNGRVIVNVKSYFSMDNFAFAHR
7 : * . .*:* . * ** . : : . . .*.* : * :
8
9 Tb09.v4.0147 GVYNVDYVNSERVCRAEGMNLATDHSEATNSLIYKLLKPKNKLGYLYAYLGGDAKYSASS
10 Tb927.6.380 GDYLVVDYSNSVHICREAGGTLATDHSQATNERLTAYHLGVADGPFiYSYLGGDATYSASA
11 Tb927.2.5290 GNYFVSYKNAAYCGDNGAVLPADQTEAAHQSLQSAIKRVITGSDAFSYLGGDAVYSSGE
12 * * *.* * : * * * .:*:::*::: : :***** **:.
13
14 Tb09.v4.0147 VHEEKDRCKVGD LASSLNCVYRWNTGLFAPATPDDNGVAFWRGSYYEVTGAGSMNDYPSF
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26 Tb927.2.5290 STTTTTTTTTTTTTTTTTTAAPASGEVPEP-----
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31 Tb927.2.5290 -----TVTKDEEVTVT-----TVSLEERSNWHIILIA-----
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42
43
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Figure S3B

CLUSTAL W (1.8) multiple sequence alignment

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Tbg97223350 ---MSMDTRMVNFGFTR---AALLCG-----LLLLLTAVCPLHVT---AAADD---NG
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TcIL3000027940 RKKEISKQAKISKTTMSSGRNALFACGAILRAVVA-LLLLQCVGRPLCLTASAT-----E
TcIL3000001110 RKKEISKTKISKTTMSPGRNALFSCGTILRAVVALLLLLQCVGRPLCLTASAT-----E
TcIL3000033420 RKKEISKKAKISKTTMSPGRNALFACGAILRAVVA-LLLLQCVGRPLCLTASAD-----E
Tb9276380 ----MGTEISMTACGFAR---MVLVFT-----ALL-QCLSGSSHLFAFGK-----V
Tbg972630 ----MGTEISMTACGFAR---MVLVFT-----ALL-QCLSGSSHLFAFGK-----V
Tb9276370 ----MGTEISMTACGFAR---MVLVFT-----ALL-QCLSGSSHLFAFGK-----V
TcIL3000050510 -----
TcIL3000050500 -----MSKGTHA---APYALV-----LAL-LCVVHPLQVAVVAQ-----P
TcIL3000016620 -----MSKGTHA---APYALV-----LVL-LCVVHPLQVAVVAQ-----P
TcIL3000016630 -----MSKGTHA---TPCALV-----LVL-LCVVHPLQMAVSAK-----E
TcIL3000047260 -----MSKGTHA---VPHVLV-----MAL-LCVVHPLQVAASAK-----E

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Tbg97291270 PVTAAKSYAIYTHEVFENNGVYVNDYVNSERVCR AEGMNLATDHSEATNSLIYKLLKPK
Tbg97291300 PVTAAKSYAIYTHEVFENNGVYVNDYVNSERVCR AEGMNLATDHSEATNSLIYKLLKPK
Tb09v40146 PVTAAKSYAVYPHEVFENNGVYVNDYVNSERVCR AEGMNLATDHSEATNSLIYKLLKPK
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Tbg97223390 RVIVNVKEYFSMPNRAFIRDGEYHVSYN ANAYCGDNGAVLPADQTEAAHQSLQDAMKRV
Tbg97223430 RVIVNVKEYFSMPNRAFIRDGEYHVSYN ANAYCGDNGAVLPADQTEAAHQSLQDAMKRV
Tbg97223760 RVIVNVKEYFSMPNRAFIRDGEYHVSYN ANAYCGDNGAVLPADQTEAAHQSLQDAMKRV
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Tbg97223680 RVIVNVKEYFSMPNRAFIRDGEYHVSYN ANAYCGDNGAVLPADQTEAAHQSLQDAMKRV
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Tbg97223370 RVIVNINTIISMVNRAFIRDGEYVSYN ANAYCGDNGAVLPADQTEAAHQSLQDAMKRV
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Tb091601520 NE--LGYLAYLGGDDAKYSASSVHEEKDRCKVGDlasslncVYRWNTGLFAPATPDDNGV
Tb09v40149 NK--LGYLAYLGGDDAKYSASSVHEEKDRCKVGDlasslncVYRWNTGLFAPATPDDNGV
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Tbg97222800 AFWRGSYVKYAFAPMNGYPSFWGSEYPKHGQLYTLWSYHEDDDVTTWYDGREASGT---
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TcIL3000016620 AFWRGSYRSTPGAGSMNDFPFRWIKDYPKFGFLYXISRHYRESKRTWFDDEYEDTGHEAA
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TcIL3000047260 AFWRGSYKRMPGAGSMNDFPFRWHPQFPGAGLLYVDSGYAKIFAGSVWFDKNE-TQOALI

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TcIL3000050510 YTVRAERPVGIFYVALCNIVVFTTSAPVPOPEST-----
TcIL3000050500 YTVRAERPVGIFYVALCNIVVFTTSAPVPOPEST-----
TcIL3000016620 HVVRKEKQVKNFVLLCNIVVPTTSAPVPOPESE-----
TcIL3000016630 -----
TcIL3000047260 YEVFRFRTHLILCQLQNKKPAPLPPSPGPATADNEELNGTDANETASEELNGTDANETA-----

Tbg97291330 -----
Tbg97291280 -----
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Tbg97291300 -----
Tb09v40146 -----
Tb09v40147 -----
Tb091601520 -----
Tb09v40149 -----
Tb09v40059 -----
Tb09v40058 -----
Tb09v40148 -----
Tbg97291380 -----
Tb09v40060 -----
Tbg97291360 -----
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Tc00104705350401180 -----
Tc001047053511859200 -----
Tc00104705350601110 -----
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Tc0010475350894510 -----
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Tc00104705351112960 -----
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Tc00104705351024930 -----
Tc00104705350735910 -----
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TvY486_0600050 -----
TvY486_0028480 -----
TvY486_0201850 -----
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Tbg97223660 -----
Tbg97223640 -----

Tb92725350 -----
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Tb92725290 -----
Tbg97223720 -----
Tb92725320 -----
Tbg97223350 -----
Tbg97223500 -----
Tb92725300 -----
Tb92725310 -----
Tbg97222800 -----
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Tbg97222940 -----
Tb92724920 -----
TcIL30002110 -----
TcIL3000013740 -----
TcIL3000027940 -----
TcIL3000001110 -----
TcIL3000033420 -----
Tb9276380 -----
Tbg972630 -----
Tb9276370 -----
TcIL3000050510 -----ETESEEHNGTNTNETESEELNGTNANETASEELNGTNVNETAGEELNGTN
TcIL3000050500 -----ETESEEHNGTNTNETASEELNGTNANETASEELNGTNVNETAGEELNGTN
TcIL3000016620 -----
TcIL3000016630 -----
TcIL3000047260 -----SEELNGTDANETASEELNGTNANETASEELNGTDANETASEELNGTNANETASEELNGTD

Tbg97291330 -----NISFTNTRARSTRFFMVLCE
Tbg97291280 -----NISFTNTRARSTRFFMVLCE
Tbg97291270 -----NISFTNTRARSTRFFMVLCE
Tbg97291300 -----NISFTNTRARSTRFFMVLCE
Tb09v40146 -----NISFTNTRARSTRFFMVLCE
Tb09v40147 -----NISFTNTRARSTRFFMVLCE
Tb091601520 -----ISMFTNTRGRSTRFFMVLCE
Tb09v40149 -----ISMFTNTRGRSTRFFMVLCE
Tb09v40059 -----ISMFTNTRGRSTRFFMVLCE
Tb09v40058 -----ISMFTNTRGRSTRFFMVLCE
Tb09v40148 -----ISMFTNTRGRSTRFFMVLCE
Tbg97291380 -----ISPFTNVRGRSIYYFKVLCE
Tb09v40060 -----NINLMNVRSAVSRDIYILCE
Tbg97291360 -----NINLMNVRSAVGRGICILCE
Tc00104705351105310 -----QLFLMFRMDTNQ
Tc00104705350763120 -----QLFLMFRMDTNQ
Tc00104705350401180 -----QLFLMFRMDTNQ
Tc001047053511859200 -----QLFLMLRMDTSQ
Tc00104705350601110 -----QLFLMLRMDTSQ
Tc00104705351104770 -----QLFLMFRMDTSQ
Tc00104705350453350 -----KTFMLRLKKE
Tc001047053508735100 -----KTFMLRLKKTRE
Tc0010475350894510 -----KTFMLRLKMTD
Tc00104705350863740 -----KTFMLRLKNTTD
Tc00104705351112960 -----KTFMLRLKTTD
Tc00104705351191190 -----KTFMLRLKTTD
Tc00104705351024930 -----KTFMLRLKTTD
Tc00104705350735910 -----KTFMLRLKTTD
TvY486_0201870 -----SSAKVPIEKTLLSNYIACVE
TvY486_0600050 -----SSAKVPIEKTLLSNYIACVE
TvY486_0028480 -----YFAPTPILYTYVTNYIACVE
TvY486_0201850 -----HYAQAPIQGTYYVTSYIACVE
Tbg97223580 -----IKWASDNPDTKTENYVILCE
Tbg97223450 -----IKWASDNPDTKTENYVILCE
Tbg97223390 -----IKWASDNPDTKTENYVILCE
Tbg97223430 -----IKWASDNPDTKTENYVILCE
Tbg97223760 -----IKWASDNPDTKTENYVILCE
Tbg97223550 -----IKWASDNPDTKTENYVILCE
Tbg97223410 -----IKWASDNPDTKTENYVILCE
Tbg97223680 -----IKWASDNPDTKTENYVILCE
Tbg97223740 -----IKWASDNPDTKTENYVILCE
Tbg97223540 -----IKWASDNPDTKTENYVILCE
Tb92725360 -----IKWASDNPDTKTENYVILCE
Tb92725340 -----IKGTSKNPATKTENYVILCE
Tb92725330 -----IKWTSKNPATKTENYVILCE
Tbg97223600 -----IKGTSKNPATKTENYVILCE
Tbg97223520 -----IKGTSKNPATKTENYVILCE
Tbg97223370 -----IKGTSKNPATKTENYVILCE
Tbg97223470 -----IKGTSKNPATKTENYVILCE
Tbg97223700 -----IKGTSKNPATKTENYVILCE
Tbg97223620 -----IKWTSKNPATKTENYVILCE

Tbg97223490 -----IKGTSKNPATKTENYVILCE
Tbg97223660 -----IKGTSKNPATKTENYVILCE
Tbg97223640 -----IKGTSKNPATKTENYVILCE
Tb92725350 -----IKGTSKNPATKTENYVILCE
Tbg97223330 -----IKWASDNPDTKTENYVILCE
Tb92725290 -----IKWASDNPDTKTENYVILCE
Tbg97223720 -----LVAASNNPETTNKNYVILCE
Tb92725320 -----LVAASNNPETTNKNYVILCE
Tbg97223350 -----IRWTSRNFDTKSQDYVIVCE
Tbg97223500 -----IRWTSRNFDTKSQDYVIVCE
Tb92725300 -----IRWTSRNFDTKSQDYVIVCE
Tb92725310 -----IRWTSRNFDTKSQDYVIVTCE
Tbg97222800 -----IRWTSQNFETKSQDYVVVCE
Tb92724760 -----IRWTSQNFETKSQDYVVVCE
Tbg97222940 -----IRWTSQNFETKSQDYVVVCE
Tb92724920 -----IRWTSQNFETKSQDYVVVCE
TcIL30002110 -----NRRSSRNPGTKSEEYRILCE
TcIL3000013740 -----DRRSSRNPGTKSEEYRILCE
TcIL3000027940 -----DRKSSRNPGTKSEEYHILCE
TcIL3000001110 -----DRKTSRNPGTKSGEYHILCE
TcIL3000033420 -----DRKTSRNPGTKSDEYRMLCE
Tb9276380 -----GGEVSGNKPGGKAPGY
Tbg972630 -----GGEVSGNKPGGKAPGY
Tb9276370 -----GGEVSGNKPGGKAPGY
TcIL3000050510 ASETAGEELNGTNTNETASEELNGTNTNETASEGLNGTNANETASEELNGTNTNETASEE
TcIL3000050500 ASETAGEELNGTSANETASEELNGTNANETASEELNGTNANETASEELNGTNANETASEE
TcIL3000016620 -----D-----ENASEELNGTNANETESEELNGTNTNETESEED
TcIL3000016630 -----VTLETAGSSTEGSVLDE
TcIL3000047260 ANETASEELNGTDANETASEELNGTNANETASEELNGTDANETASEELNGTDTNETASEE

Tbg97291330 ASAVPTPLPP-----ASPHSENT
Tbg97291280 ASAVPTPLPP-----ASPHSENT
Tbg97291270 ASAVPTPLPP-----ASPHSENT
Tbg97291300 ASAVPTPLPP-----ASPHSENT
Tb09v40146 ASAVPTPLPP-----ASPHSENT
Tb09v40147 ASAVPTPLPP-----ASPHSENT
Tb091601520 ASAVPTPLPP-----ASPHSENT
Tb09v40149 ASAVPTPLPP-----ASPHSENT
Tb09v40059 ASAVPTPLPP-----ASPHSENT
Tb09v40058 ASAVPTPLPP-----ASPHSENT
Tb09v40148 ASAVPTPLPP-----ASPHSENT
Tbg97291380 ASAVPTPLPP-----ASPHSENT
Tb09v40060 ASAVPTPLPP-----ASPHSENT
Tbg97291360 TSLIVAVAAENLIDADTFVNERKQSVNDKQSSGNTSAVGNITVREGKRPDGNSEDKNT
Tc00104705351105310 TSLTVALAAENLFATDTFAVNERKQSVNDKQCSGNTSAVGNISVREGKKGENTSDDKNT
Tc00104705350763120 NDEKATWYDG-----Q
Tc00104705350401180 NDEKATWYDG-----Q
Tc001047053511859200 SDEKATWYDG-----Q
Tc00104705350601110 SDKKATWYDG-----Q
Tc00104705351104770 SDKNATWYDG-----Q
Tc00104705350453350 SYEKATWYDG-----Q
Tc001047053508735100 NSGNATWYDW-----Y
Tc0010475350894510 NSEQATWYDW-----Y
Tc00104705350863740 NSEKATWYDW-----Y
Tc0010470535112960 NSEKATWYDW-----Y
Tc00104705351191190 NNGNATWYDW-----Y
Tc00104705351024930 NNEQATWYDW-----Y
Tc00104705350735910 NNGNATWYDW-----Y
TvY486_0201870 NSGNATWYDW-----Y
TvY486_0600050 VQDSISTSTT-----T
TvY486_0028480 VQDSISTSTT-----T
TvY486_0201850 VQDSVSTTGT-----G
Tbg97223580 SQDSISSSTT-----T
Tbg97223450 VHDSIS---T-----T
Tbg97223390 VHDSIS---T-----T
Tbg97223430 VHDSIS---T-----T
Tbg97223760 VHDSIS---T-----T
Tbg97223550 VHDSIS---T-----T
Tbg97223410 VHDSIS---T-----T
Tbg97223680 VHDSIS---T-----T
Tbg97223740 VHDSIS---T-----T
Tbg97223540 VHDSIS---T-----T
Tb92725360 VHDSISTT-T-----T
Tb92725340 VHDSISTT-T-----T
Tb92725330 VHDSISTT-T-----T
Tbg97223600 VHDSIS-----
Tbg97223520 VHDSIS-----
Tbg97223370 VHDSIS-----

Tbg97223470	VHDSIS-----
Tbg97223700	VHDSIS-----
Tbg97223620	VHDSIS-----
Tbg97223490	VHDSIS-----
Tbg97223660	VHDSIS-----
Tbg97223640	VHDSIS-----
Tb92725350	VHDSISTT-T-----T
Tbg97223330	VHDSISTT-T-----T
Tb92725290	VHDSISTT-T-----T
Tbg97223720	VHDSIST-----
Tb92725320	VHDSIS-----
Tbg97223350	VQRYVTVA-A-----D
Tbg97223500	VQRYVTVA-A-----D
Tb92725300	VQRYVTVA-A-----D
Tb92725310	VQTDIITT-T-----T
Tbg97222800	VHDSIS-----
Tb92724760	VHDSIST-----
Tbg97222940	VHDSIST-----
Tb92724920	VHDSIS-----
TcIL30002110	VHOSIAKPTT-----T
TcIL3000013740	VHOSIAKPTT-----T
TcIL3000027940	VHOSIAKPTT-----T
TcIL3000001110	VHOSIAKS-----
TcIL3000033420	VHRSIAKP-----
Tb9276380	KSLTYFAALC-----E
Tbg972630	KSLTYFAALC-----E
Tb9276370	KSLTYFAALC-----E
TcIL3000050510	LNGTNTNETA-----S
TcIL3000050500	LNGTANETA-----S
TcIL3000016620	LNGTNTNETA-----S
TcIL3000016630	RNSTLT-----
TcIL3000047260	LNGDTNETA-----S

Tbg97291330	TADEN-----TTVDGNTNADG-----
Tbg97291280	TADEN-----TTVDGNTNAD-----
Tbg97291270	TADEN-----TTADGNTNAD-----
Tbg97291300	TADEN-----TTADENTTADG-----
Tb09v40146	TADEN-----TTADENTTVDE-----
Tb09v40147	TADEN-----TTVDENTTVDE-----
Tb091601520	TADEN-----TTVDENTTVDE-----
Tb09v40149	TADEN-----TTADENTTAD-----
Tb09v40059	TVDEN-----TTADENTTVDE-----
Tb09v40058	TVDEN-----TTADENTTVDE-----
Tb09v40148	TADEN-----TTADGNTTVDE-----
Tbg97291380	TADEN-----TTADGNTTADGNTTADGNTNADGNTTADGNTTADGNTNADGN
Tb09v40060	TSHENRSYDD-SSVADGNTSEDKNTTSHENSSHDDSSVADGNTSEDKNTTSHENSSHDDS
Tbg97291360	TSHENRSYND-SSVADGNTSDDESTTSHENRSYDSSVADGNTSDDESTTSHENRSYDSS
Tc00104705351105310	G-----VPKYDKE-----
Tc00104705350763120	G-----VPRGDGE-----
Tc00104705350401180	G-----VPKYDKE-----
Tc001047053511859200	G-----VPRYDGE-----
Tc00104705350601110	G-----VPRYDGE-----
Tc00104705351104770	G-----VPWYDGE-----
Tc00104705350453350	P-----APKDHD-----
Tc001047053508735100	P-----APKTHID-----
Tc0010475350894510	P-----APKTHID-----
Tc00104705350863740	P-----APKDHD-----
Tc00104705351112960	P-----APKDHTD-----
Tc00104705351191190	P-----APKDHTD-----
Tc00104705351024930	P-----APKDHTD-----
Tc00104705350735910	P-----APKDHTD-----
TvY486_0201870	T-----TTTTTTTTTTTTTTTTST-----
TvY486_0600050	T-----TTTTTTTTTTTTTTTT-----
TvY486_0028480	NGE---SASLASGAKLPFTSTNDAG-----
TvY486_0201850	TRAPTTTTTTTTTEAPRTTTTTST-----
Tbg97223580	T-----TTTTTTTTTTTT-----
Tbg97223450	T-----TTTTTTTTTTTT-----
Tbg97223390	T-----TTTTTTTTTTTT-----
Tbg97223430	T-----TTTTTTTTTTTT-----
Tbg97223760	T-----TTTTTTTTTTTT-----
Tbg97223550	T-----TTTTTTTTTTTT-----
Tbg97223410	T-----TTTTTTTTTTTT-----
Tbg97223680	T-----TTTTTTTTTTTT-----
Tbg97223740	T-----TTTTTTTTTTTT-----
Tbg97223540	T-----TTTTTTTTTTTT-----
Tb92725360	T-----TTTTTTTTTTTT-----
Tb92725340	T-----TTTTTTTTTTTT-----
Tb92725330	T-----TTTTTTTTTTTT-----

Tbg97223600 -----TTTTTTTTTT-----
Tbg97223520 -----TTTTTTTTTT-----
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Tbg97223470 -----TTTTTTTTTT-----
Tbg97223700 -----TTTTTTTTTT-----
Tbg97223620 -----TTTTTTTTTT-----
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Tbg97223640 -----TTTTTTTTTT-----
Tb92725350 T-----TTTTTTTTTT-----
Tbg97223330 T-----TTTTTTTTTT-----
Tb92725290 T-----TTTTTTTTTT-----
Tbg97223720 -----TTTTTTTTTT-----
Tb92725320 -----TTTTTTTTTT-----
Tbg97223350 N-----YTTTTTTTTTTTT-----
Tbg97223500 N-----YTTTTTTTTTTTT-----
Tb92725300 N-----YTTTTTTT-----
Tb92725310 -----TTTTTT-----
Tbg97222800 -----TTTTTTTTTT-----
Tb92724760 -----TTTTTTTTTT-----
Tbg97222940 -----TTTTTTTTTT-----
Tb92724920 -----TTTTTT-----
TcIL30002110 T-----TTTTTTTTTT-----
TcIL3000013740 T-----TTTTTTTTTT-----
TcIL3000027940 T-----TTTTTTTTTT-----
TcIL3000001110 -----TTTTTTTTTT-----
TcIL3000033420 -----TTTTTTTTTT-----
Tb9276380 VT-----VPQPSHPVPGNGNS-----
Tbg972630 VT-----VPQPSNPVPGNGNSP-----
Tb9276370 VT-----VPQPSHPVPGNGNS-----
TcIL3000050510 EE-----LNGTNANETASEELNGTNETASEGLNGTNANETASEELNGTNA-----
TcIL3000050500 EE-----LNGTNANETASEELNGTNANETASEELNGTNETASEELNGTNA-----
TcIL3000016620 EE-----LNGTNETASEELN-----GTNANETASEELNGTNA-----
TcIL3000016630 G-----IVGHIQHETPVAPPS-----P-----
TcIL3000047260 EE-----LNGTDTNETASEELNGTDTNETASEELNGTNANETASEELNGTDANETAS

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Tbg97291270 -----
Tbg97291300 -----
Tb09v40146 -----
Tb09v40147 -----
Tb091601520 -----
Tb09v40149 -----
Tb09v40059 -----
Tb09v40058 -----
Tb09v40148 -----
Tbg97291380 TTADG-----
Tb09v40060 SVADG-----
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Tc00104705350401180 -----
Tc001047053511859200 -----
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Tc0010475350894510 -----
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Tc00104705351024930 -----
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TvY486_0028480 -----
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Tb92724920
TcIL30002110
TcIL3000013740
TcIL3000027940
TcIL3000001110
TcIL3000033420
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Tbg972630
Tb9276370
TcIL3000050510
TcIL3000050500
TcIL3000016620
TcIL3000016630
TcIL3000047260

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Tbg97291270
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Tb09v40147
Tb091601520
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Tb09v40059
Tb09v40058
Tb09v40148
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Tb09v40060
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Tc00104705350763120
Tc00104705350401180
Tc001047053511859200
Tc00104705350601110
Tc00104705351104770
Tc00104705350453350
Tc001047053508735100
Tc0010475350894510
Tc00104705350863740
Tc00104705351112960
Tc00104705351191190
Tc00104705351024930
Tc00104705350735910
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TvY486_0600050
TvY486_0028480
TvY486_0201850
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Tbg97223390
Tbg97223430

SYDDSSVADGNTSDEESTTSHENRSYDDSSVAMGTQVTMKVLPMMRVLVTMSTAGENTKA

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Tb92725330 -----
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Tbg97223720 -----
Tb92725320 -----
Tbg97223350 -----
Tbg97223500 -----
Tb92725300 -----
Tb92725310 -----
Tbg97222800 -----
Tb92724760 -----
Tbg97222940 -----
Tb92724920 -----
TcIL30002110 -----
TcIL3000013740 -----
TcIL3000027940 -----
TcIL3000001110 -----
TcIL3000033420 -----
Tb9276380 -----
Tbg972630 -----
Tb9276370 -----
TcIL3000050510 -----
TcIL3000050500 -----
TcIL3000016620 -----
TcIL3000016630 -----
TcIL3000047260 -----

Tbg97291330 -----NTNADENTTA
Tbg97291280 -----
Tbg97291270 -----N-----TTA
Tbg97291300 -----N-----TNA
Tb09v40146 -----NTTADENTTA
Tb09v40147 -----NTTADENTTA
Tb091601520 -----NTTADENTTV
Tb09v40149 -----N-----
Tb09v40059 -----N-----
Tb09v40058 -----N-----
Tb09v40148 -----NTTADENTTV
Tbg97291380 N-----ITTDGNTNADGNTTA
Tb09v40060 --NTSEDKNTTSHENRSYDDSSVADGNTSEDKNTTSHENRSYDDSSVADGNTSDDKNTTS
Tbg97291360 DGNTSDESTTSHENRSYDDSSVADGNTSDDKSTTSHENRSYDDSSVADGNTSDDKNTTS
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Tc00104705350763120 -----
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Tc00104705350735910 -----
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TvY486_0600050 -----
TvY486_0028480 -----
TvY486_0201850 -----
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Tbg97223410 -----
Tbg97223680 -----
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Tbg97223540 -----
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Tb92725340 -----
Tb92725330 -----
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Tbg97223520 -----
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TcIL3000013740 -----
TcIL3000027940 -----
TcIL3000001110 -----
TcIL3000033420 -----
Tb9276380 -----
Tbg972630 -----AN
Tb9276370 -----
TcIL3000050510 -----NETAS
TcIL3000050500 -----NETAS
TcIL3000016620 -----NETES
TcIL3000016630 -----
TcIL3000047260 -----NGDTONETAS

Tbg97291330 DENTTADENTTADGNTNADENTTADEN-----
Tbg97291280 -EN-----TTADGNTNADEN-----
Tbg97291270 DENTTADENTTADGNTTADENTTVDEN-----
Tbg97291300 DENTTADGNTTADGNTNADENTTVDEN-----
Tb09v40146 DENTTADENTTADENTTADENTTVDEN-----
Tb09v40147 DENTTVDENTTADENTTADENTTADEN-----
Tb091601520 DENATVDENTTVDENTTADENTTADEN-----
Tb09v40149 -----TTVDGNTNADENTTADEN-----
Tb09v40059 -----TTVDENTNADENTTADEN-----
Tb09v40058 -----ATVDENTTADENTTVDEN-----
Tb09v40148 DENTTVDENTTADGNTNADENTTADEN-----
Tbg97291380 DGNTTADGNTTADGNTNADGNTTTDEN-----
Tb09v40060 HENRSYDDSSVADGNTSDDKNTTSHENRSYDDSSVADGNTSEDKNTTSHENRSYDDSSVA
Tbg97291360 HENRSCDDSSVADGNTSDDKNTTSHENRSYDDSSVADGNTSDDKNTTSHENRSYDDSSVA
Tc00104705351105310 -----TPEKTFG-----
Tc00104705350763120 -----TPENTFG-----
Tc00104705350401180 -----TPEKTFG-----
Tc001047053511859200 -----TPEDTFG-----
Tc00104705350601110 -----TPEDTFG-----
Tc00104705351104770 -----TPENTFG-----
Tc00104705350453350 -----TPYRSFG-----
Tc001047053508735100 -----TPYRSFG-----
Tc0010475350894510 -----TPYRSFG-----
Tc00104705350863740 -----TPYLSFG-----
Tc00104705351112960 -----TPYRSFG-----
Tc00104705351191190 -----TPYRSFG-----
Tc00104705351024930 -----TPYRSFG-----
Tc00104705350735910 -----TPYRSFG-----
TvY486_0201870 --TTTTKPTTPTPTTT--TTTTTKP-----
TvY486_0600050 -----TKPPTTPTPTTT--TTTTTKP-----

TvY486_0028480 --GNILIPNSSPSSSTNNAPVSSLTAMPTVDEASLAASGGGNSGTNGA-----
TvY486_0201850 --TSTTTTTTKAPTSTTT---STTATVAPTNTTSSSSTTESPSSPTTMADG-----
Tbg97223580 -----TTAAPASGVVPEP-----
Tbg97223450 -----TTAAPASGVVPEP-----
Tbg97223390 -----TTAAPASGVVPEP-----
Tbg97223430 -----TTAAPASGVVPEP-----
Tbg97223760 -----TTAAPASGVVPEP-----
Tbg97223550 -----TTAAPASGVVPEP-----
Tbg97223410 -----TTAAPASGVVPEP-----
Tbg97223680 -----TTAAPASGVVPEP-----
Tbg97223740 -----TTAAPASGVVPEP-----
Tbg97223540 -----TTAAPASGVVPEP-----
Tb92725360 -----TTAAPASGEVPEP-----
Tb92725340 -----TTAAPASGEVPEP-----
Tb92725330 -----TTAAPASGEVPEP-----
Tbg97223600 -----TTAAPASGEVPEP-----
Tbg97223520 -----TTAAPASGEVPEP-----
Tbg97223370 -----TTAAPASGEVPEP-----
Tbg97223470 -----TTAAPASGEVPEP-----
Tbg97223700 -----TTAAPASGEVPEP-----
Tbg97223620 -----TTAAPASGEVPEP-----
Tbg97223490 -----TTAAPASGEVPEP-----
Tbg97223660 -----TTAAPASGEVPEP-----
Tbg97223640 -----TTAAPASGEVPEP-----
Tb92725350 -----TTAAPASGEVPEP-----
Tbg97223330 -----TTAAPASGVVPEP-----
Tb92725290 -----TTAAPASGEVPEP-----
Tbg97223720 -----TTAAPASGEVPEP-----
Tb92725320 -----TTAAPASGEVPEP-----
Tbg97223350 -----TTAAPASGEVPEP-----
Tbg97223500 -----TTAAPASGEVPEP-----
Tb92725300 -----TTAAPASGEVPEP-----
Tb92725310 -----TTAAPASGEVPEP-----
Tbg97222800 -----AAPASGEVPEP-----
Tb92724760 -----TAPASGEVPEP-----
Tbg97222940 -----AAPASGEVPEP-----
Tb92724920 -----AAPASGEVPEP-----
TcIL30002110 -----TTTTTTTTKKPENTTTSTTT-----
TcIL3000013740 -----TTTTTTTTKKPENTTTSTTT-----
TcIL3000027940 -----TTTTTTTTKKPENTTTSTTT-----
TcIL3000001110 -----TPTTTTTTKQPEN-----
TcIL3000033420 -----TTTTTTTTKQPEN-----
Tb9276380 -----TANEELAVINESLHSDEE-----
Tbg972630 EDEVSGNGNSTANEELAVINESLHSDEE-----
Tb9276370 -----TANEELAVINESLHSDEE-----
TcIL3000050510 EELNGTNTNETASEELNGTNANETG-----
TcIL3000050500 EELNGTNANETASEELNGTNANETASEELNGTNANETESEELNGTSANETESEELN-----
TcIL3000016620 EELNGTSANETASEELNGTNVNETE-----
TcIL3000016630 --LSGPEGSETASEELNGTNVNETE-----
TcIL3000047260 EELNGTDANETASEELNGTNANETASEELNGTDANETASEELNGTDANETASEELNGTDA

Tbg97291330 -----TTADENTTVDGD-----TNAD-----
Tbg97291280 -----
Tbg97291270 -----
Tbg97291300 -----TTVDEN-----
Tb09v40146 -----TTVDENTTVDENTTADGNTNADENTTAD-----
Tb09v40147 -----TTVDENTTADEN-----TTVD-----
Tb091601520 -----TTADEN-----
Tb09v40149 -----TTADEN-----
Tb09v40059 -----TTVDENTNADEN-----TTAD-----
Tb09v40058 -----TTVDEN-----
Tb09v40148 -----TTVDEN-----TTVD-----
Tbg97291380 -----TTADENTNADGNTTDTGNTNADGNTTADGNI TDTGNTNADGNTTADGNTTA
Tb09v40060 DGNTSDDKNTTSHENSSHDDSSVADGNTSEDKNTTSHENRSHDDSSVADGNTSEDKNTTS
Tbg97291360 DGNSSDDKNTTSHENRSYDDSSVADGNSDDKNTTSHENRSYDDSSVADGNTSDDKNTTT
Tc00104705351105310 -----
Tc00104705350763120 -----
Tc00104705350401180 -----
Tc001047053511859200 -----
Tc00104705350601110 -----
Tc00104705351104770 -----
Tc00104705350453350 -----
Tc001047053508735100 -----
Tc0010475350894510 -----
Tc00104705350863740 -----
Tc00104705351112960 -----
Tc00104705351191190 -----
Tc00104705351024930 -----

Tc0010470535112960 -----
Tc00104705351191190 -----
Tc00104705351024930 -----
Tc00104705350735910 -----
TvY486_0201870 -----
TvY486_0600050 -----
TvY486_0028480 -----
TvY486_0201850 -----
Tbg97223580 -----
Tbg97223450 -----
Tbg97223390 -----
Tbg97223430 -----
Tbg97223760 -----
Tbg97223550 -----
Tbg97223410 -----
Tbg97223680 -----
Tbg97223740 -----
Tbg97223540 -----
Tb92725360 -----
Tb92725340 -----
Tb92725330 -----
Tbg97223600 -----
Tbg97223520 -----
Tbg97223370 -----
Tbg97223470 -----
Tbg97223700 -----
Tbg97223620 -----
Tbg97223490 -----
Tbg97223660 -----
Tbg97223640 -----
Tb92725350 -----
Tbg97223330 -----
Tb92725290 -----
Tbg97223720 -----
Tb92725320 -----
Tbg97223350 -----
Tbg97223500 -----
Tb92725300 -----
Tb92725310 -----
Tbg97222800 -----
Tb92724760 -----
Tbg97222940 -----
Tb92724920 -----
TcIL30002110 -----
TcIL3000013740 -----
TcIL3000027940 -----
TcIL3000001110 -----
TcIL3000033420 -----
Tb9276380 -----
Tbg972630 -----
Tb9276370 -----
TcIL3000050510 -----
TcIL3000050500 -----
TcIL3000016620 -----
TcIL3000016630 -----
TcIL3000047260 ----- NGTDANETASEELNGTDANETASEELNGTDANETASEELNGTDANETASEELNGTDANET

Tbg97291330 -----
Tbg97291280 -----
Tbg97291270 -----
Tbg97291300 -----
Tb09v40146 -----
Tb09v40147 -----
Tb091601520 -----
Tb09v40149 -----
Tb09v40059 -----
Tb09v40058 -----
Tb09v40148 -----
Tbg97291380 -----
Tb09v40060 ----- DGNTSEDKNTTSHENRSYDDSSVADGNTSEDKNTTSHENRSYGDTSVADLSSSDDESTSD
Tbg97291360 ----- DGNTSDDKNTTSHENRSYDDSSVADGNTSDDKNTTSHENRSCDDSSVADGNTSDDDESTSD
Tc00104705351105310 -----
Tc00104705350763120 -----
Tc00104705350401180 -----
Tc001047053511859200 -----
Tc00104705350601110 -----
Tc00104705351104770 -----
Tc00104705350453350 -----

Tc001047053508735100	-----
Tc0010475350894510	-----
Tc00104705350863740	-----
Tc00104705351112960	-----
Tc00104705351191190	-----
Tc00104705351024930	-----
Tc00104705350735910	-----
TvY486_0201870	-----
TvY486_0600050	-----
TvY486_0028480	-----
TvY486_0201850	-----
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Tbg97223450	-----
Tbg97223390	-----
Tbg97223430	-----
Tbg97223760	-----
Tbg97223550	-----
Tbg97223410	-----
Tbg97223680	-----
Tbg97223740	-----
Tbg97223540	-----
Tb92725360	-----
Tb92725340	-----
Tb92725330	-----
Tbg97223600	-----
Tbg97223520	-----
Tbg97223370	-----
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Tbg97223700	-----
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Tbg97223490	-----
Tbg97223660	-----
Tbg97223640	-----
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Tbg97223500	-----
Tb92725300	-----
Tb92725310	-----
Tbg97222800	-----
Tb92724760	-----
Tbg97222940	-----
Tb92724920	-----
TcIL30002110	-----
TcIL3000013740	-----
TcIL3000027940	-----
TcIL3000001110	-----
TcIL3000033420	-----
Tb9276380	-----
Tbg972630	-----
Tb9276370	-----
TcIL3000050510	-----
TcIL3000050500	-----
TcIL3000016620	-----
TcIL3000016630	-----
TcIL3000047260	-----
ASEELNGTDANETASEELNGTDANETASEELNGTDTNETASEELNGTDANETASEELNGT	

Tbg97291330	-----ENTTVDENTTVDEN-----
Tbg97291280	-----TTVDEN-----
Tbg97291270	-----TTVDENTTVDEN-----
Tbg97291300	-----TTVDENTTVDEN-----
Tb09v40146	-----ENTTVDENTTVDEN-----
Tb09v40147	-----ENTTVDENTTVDEN-----
Tb091601520	-----TTADENATADEN-----
Tb09v40149	-----TTADENTTADEN-----
Tb09v40059	-----ENTNVDETTADEN-----
Tb09v40058	-----TNVDENTTADEN-----
Tb09v40148	-----ENTTVDENTTVDEN-----
Tbg97291380	-----ENTTADENTNADGNTTVDETTADGN-----
Tb09v40060	DESTSDYESTADEEYSLYNN---GIWKENTTADENTTADENTTVDETTADEN-----
Tbg97291360	DESTSDYESTADEEYSLYNN---GIWKENTTADENTTVDETTADENTTVDEN-----
Tc00104705351105310	-----VVCETOEGYV-----
Tc00104705350763120	-----VVCETOEGYV-----
Tc00104705350401180	-----VVCETOEGYV-----
Tc001047053511859200	-----VVCETOEGYV-----

Tc00104705350601110 -----VVCETQEGYV-----
Tc00104705351104770 -----VVCETQEGYV-----
Tc00104705350453350 -----VVCETQKGYV-----
Tc001047053508735100 -----VVCETQKGYV-----
Tc0010475350894510 -----VVCEAQKGYV-----
Tc00104705350863740 -----VVCEAQKGYV-----
Tc00104705351112960 -----VVCEAQKGYV-----
Tc00104705351191190 -----VVCEAQKGYV-----
Tc00104705351024930 -----VVCEAQKGYV-----
Tc00104705350735910 -----VVCEAQKGYV-----
TvY486_0201870 -----PT-----KTTTTT-----TSAPDVSEWV-----
TvY486_0600050 -----PT-----TTTTTT-----TSAPDVSEWV-----
TvY486_0028480 -----GHHPTGSAVTAVTATKPPPTSAVDSEWV-----
TvY486_0201850 -----SSGPGGGAAGTPSSS--SG-TASATSPGPV-----
Tbg97223580 -----TVTKDEEVT-----
Tbg97223450 -----TVTKDEEVT-----
Tbg97223390 -----TVTKDEEVT-----
Tbg97223430 -----TVTKDEEVT-----
Tbg97223760 -----TVTKDEEVT-----
Tbg97223550 -----TVTKDEEVT-----
Tbg97223410 -----TVTKDEEVT-----
Tbg97223680 -----TVTKDEEVT-----
Tbg97223740 -----TVTKDEEVT-----
Tbg97223540 -----TVTKDEEVT-----
Tb92725360 -----TVTKDEEVT-----
Tb92725340 -----TVTKDEEVT-----
Tb92725330 -----TVTKDEEVT-----
Tbg97223600 -----TVTKDEEVT-----
Tbg97223520 -----TVTKDEEVT-----
Tbg97223370 -----TVTKDEEVT-----
Tbg97223470 -----TVTKDEEVT-----
Tbg97223700 -----TVTKDEEVT-----
Tbg97223620 -----TVTKDEEVT-----
Tbg97223490 -----TVTKDEEVT-----
Tbg97223660 -----TVTKDEEVT-----
Tbg97223640 -----TVTKDEEVT-----
Tb92725350 -----TVTKDEEVT-----
Tbg97223330 -----TVTKDEEVT-----
Tb92725290 -----TVTKDEEVT-----
Tbg97223720 -----TVTKDEEVT-----
Tb92725320 -----TVTKDEEVT-----
Tbg97223350 -----TVTKDEEVT-----
Tbg97223500 -----TVTKDEEVT-----
Tb92725300 -----TVTKDEEVT-----
Tb92725310 -----TVTKDEEVT-----
Tbg97222800 -----TVTKDEEVT-----
Tb92724760 -----TVTKDEEVT-----
Tbg97222940 -----TVTKDEEVT-----
Tb92724920 -----TVTKDEEVT-----
TcIL30002110 -----TTTTTAEPENT-T-----
TcIL3000013740 -----TTTTTAEPENT-T-----
TcIL3000027940 -----TTTTTAEPENT-T-----
TcIL300001110 -----TTTTTKEPENN-T-----
TcIL3000033420 -----TTTTTKEPENTTT-----
Tb9276380 -----STNSQDQ-----
Tbg972630 -----STNSQDQ-----
Tb9276370 -----STNSQDQ-----
TcIL3000050510 -----SEDSSSG-----
TcIL3000050500 -----GTNANETASEELNGTNANETESDDSSSG-----
TcIL3000016620 -----SDDSSSG-----
TcIL3000016630 -----SDDSSSG-----
TcIL3000047260 NANETASEELNGTDTNETASEELNGTNANETASEELNGTDANETASEDPSG-----

Tbg97291330 TNTDEISNGSNEASDKTVPSTASDGE GSGGAGAAVVIIFILLVLLVLLYFCCFAG--H
Tbg97291280 TNTDEISNGSNEASDKTVPSTSSDGE GSGGAGAAVVIIFILLVLLVLLYFCCFAG--H
Tbg97291270 TNTDEISNGSNEASDKTVPSTASDGE GSGGAGAAVVIIFILLVLLVLLYFCCFAG--H
Tbg97291300 TNTDEISNGSNEASDKTVPSTASDGE GSGGAGAAVVIIFILLVLLVLLYFCCFAG--H
Tb09v40146 TNADEISNGSNEASDKTVPSTASDGE GSGGAGAAVVIIFILLAVLLLILLYFCCFAG--H
Tb09v40147 TNADEISNGSNEASDKTVPSTASDGE GSGGAGAAVVIIFILLAVLLLILLYFCCFAG--H
Tb091601520 TIADEISNGSNEASDKTVPSTASDGE GSGGAGAAVVIIFILLAVLLLILLYFCCFAG--H
Tb09v40149 TNADEISNGSNEASDKTVPSTASDGE GSGGAGAAVVIIFILLAVLLLILLYFCCFAG--H
Tb09v40059 TIADEISNGSNEASDKTVPSTASDGE GSGGAGAAVVIIFILLAVLLLILLYFCCFAG--H
Tb09v40058 TIADEISNGSNEASDKTVPSTASDGE GSGGAGAAVVIIFILLAVLLLILLYFCCFAG--H
Tb09v40148 TNADEISNGSNEASDKTVPSTASDGE GSGGAGAAVVIIFILLAVLLLILLYFCCFAG--H
Tbg97291380 TTADEISNGSNEASDKTVPSTASDGE GSGGAGAAVVIIFILLVLLVLLYFCCFAG--H
Tb09v40060 TNADEISNGSNEASDKTVPSTASDGE GSGGAGAAVVIIFILLAVLLLILLYFCCFAG--H
Tbg97291360 TNTDEISNGSNEASDKTVPSTSSDGE GSGGAGAAVVIIFILLVLLVLLYFCCFAG--H
Tc00104705351105310 VSTTTLPPT-----VEISVWHKRWYVILIAILVPIVAVAIITVCFRSCGHDH

Tc00104705350763120 VSTTTLPPPT-----VEIPWVHKRWYVILIAILVPVIVAVAIITVYFCRSCGGHDE
Tc00104705350401180 VSTTTLPPPT-----VEIPWVHKRWYVILIAILVPVIVAVAIITACFCRCRGADDE
Tc001047053511859200 VSTTTLPPPT-----VEISWVRKNWYFVLIILVPVIVAVAILITVCFRCRCRGGADDE
Tc00104705350601110 VSTTTLPPPT-----VKISWVHKRWYVILIAILVPVIVAVTLITVCFRCRCRGGADDE
Tc00104705351104770 VSTTTLPPA-----VEISWVQKNWYFVLAAILVPVIVAVVLLITACFCRCRCRGGADDE
Tc00104705350453350 VSTTTLPPA-----IVVPWLQKNWYVVLIVVLLPVVVAVALITVCFYRCRGGVDE
Tc001047053508735100 VSTTTLPPA-----VVVPWLQKNWYVVLIVVLLPVVVAVALITVCFYRCRGGVDE
Tc0010475350894510 VSTTTLPPA-----VVVPWLQKNWYVVLAVLLPVIAAALITVCFYRCRGGV-DE
Tc00104705350863740 VSTTTLPPA-----VVVPWLQKNWYFVLLAVLLPVIAAALITVCFYRCRGGVYDE
Tc00104705351112960 VSTTTLPPA-----VVVPWLQKNWYVVLMAVLLPVIAAVALITVCFYRCRGGVEDE
Tc00104705351191190 VSTTTLPPA-----VVVPWLQKNWYVVLIAVLLPVIAAVALITVCFYRCRGGVDE
Tc00104705351024930 VSTTTLPPA-----VVVPWLQKNWYVVLIAVLLPVIAAVALITVCFYRCRGGVDE
Tc00104705350735910 VSTTTLPPA-----VVVPWLQKNWYFVLAAILPVIAAVALITVCFRCRCRGGVDE
TvY486_0201870 SSATFVPPVPGAKQVGRDASSTWAERYWYVILLGLLVAIAAVLIVLCLCLRCCAG--D
TvY486_0600050 SSATFVPPVPGAKQVGRDASSTWAERYWYVILLGLLVAIAAVLIVLCLCLRCCAG--D
TvY486_0028480 SSATFVPPVPGAKQVGRDASSTWAERYWYVILLGLLVAIAAVLIVLCLCLRCCAG--D
TvY486_0201850 GNATSAPPVPGGAGHAGLGASSTWAERYWYVILLVFLSVIVAIVLIVLFLVFCRSR--D
Tbg97223580 VTTASLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V
Tbg97223450 VTTASLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V
Tbg97223390 VTTASLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V
Tbg97223430 VTTASLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V
Tbg97223760 VTTASLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V
Tbg97223550 VTTASLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V
Tbg97223410 VTTASLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V
Tbg97223680 VTTASLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V
Tbg97223740 VTTASLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V
Tbg97223540 VTTASLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V
Tb92725360 VTTVSLERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V
Tb92725340 VTTVSLERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V
Tb92725330 VTTVSLERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V
Tbg97223600 VTTVSLERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V
Tbg97223520 VTTVSLERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V
Tbg97223370 VTTVSLERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V
Tbg97223470 VTTVSLERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V
Tbg97223700 VTTVSLERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V
Tbg97223620 VTTVSLERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V
Tbg97223490 VTTVSLERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V
Tbg97223660 VTTVSLERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V
Tbg97223640 VTTVSLERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V
Tb92725350 VTTVSLERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V
Tbg97223330 VTTVSLERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V
Tb92725290 VTTVSLERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V
Tbg97223720 VTTVSLERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V
Tb92725320 VTTVSLERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V
Tbg97223350 VTTVSLERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V
Tbg97223500 VTTVSLERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V
Tb92725300 VTTVSLERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V
Tb92725310 VTTVSLERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V
Tbg97222800 VTTASLEERI-----DLIILIALISVSVLIVLFLFLRWFCYDYN--V
Tb92724760 VTTVSLERI-----DLIILIALISVSVLIVLFLFLRWFCYDYN--V
Tbg97222940 VTTASLEERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V
Tb92724920 VTTASLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V
TcIL30002110 TTTTAQPEASEGK-GSG-----YIILIVLFLLAALIALLLAYCCFSAG--G
TcIL3000013740 TTTTAQPEASEGK-GSG-----YIILIVLFLLAALIALLLAYCCFSAG--G
TcIL3000027940 TTTTAQPEASEGK-GSG-----YIILIVLFLLAALIALLLAYCCFSAG--G
TcIL3000001110 TTTTAQPEASEGSDGSSG-ASTSWGTRNWIILIVLFLLAALIALLLAYCCFSAG--G
TcIL3000033420 TTTTAQPEASEGSDGSSG-ASASWGTRNWIILIVLFLLAALIALLLAYCCFSAG--G
Tb9276380 PSATPKPKGE-----AETTLTSLSHITICVGGELCLLIVFFSLAIV--C
Tbg972630 PSATPKPKGE-----AETTLTSLSHITICVGGELCLLIVFFSLAIV--C
Tb9276370 PSATPKPKGE-----AETTLTSLSHITICVGGELCLLIVFFSLAIV--C
TcIL3000050510 VSSTEAPAGK-----VNGGVLAVAILLPIIAIALLLLWYFCFRRR--D
TcIL3000050500 VSSTEAPAGK-----VNGGVLAVAILLPIIAIALLLLWYFCFRRR--D
TcIL3000016620 VSSTEAPAGK-----VNGGVLALAILLPIIAIALLLLWYFCFRRR--D
TcIL3000016630 VSSTEAPAGK-----VNGGVLAVAILLPIIAIALLLLWYFCFRRR--D
TcIL3000047260 VSSTAAPAGK-----VNGGVLALAILLPIIAIVLFLWYFCVWGK--N

: ; :

Tbg97291330 EKYITVMSLREKVTSP---VSNVEAAEVAAP-----SNGEEHLSITSHOQETP
Tbg97291280 EKYITVMSLREKVTSP---VSNVEAAEVAAP-----SNGEEHLSITSHOQETP
Tbg97291270 EKYITVMSLREKVTSP---VSNVEAAEVAAP-----SNGEEHLSITSHOQETP
Tbg97291300 EKYITVMSLREKVTSP---VSNVEAAEVAAP-----SNGEEHLSITSHOQETP
Tb09v40146 EKYITVMSLREKVTSP---VSNVEAAEVAAP-----SNGEEHLSITSHOQETP
Tb09v40147 EKYITVMSLREKVTSP---VSNVEAAEVAAP-----SNGEEHLSITSHOQETP
Tb091601520 EKYITVMSLREKVTSP---VSNVEAAEVAAP-----SNGEEHLSITSHOQETP
Tb09v40149 EKYITVMSLREKVTSP---VSNVEAAEVAAP-----SNGEEHLSITSHOQETP
Tb09v40059 EKYITVMSLREKVTSP---VSNVEAAEVAAP-----SNGEEHLSITSHOQETP
Tb09v40058 EKYITVMSLREKVTSP---VSNVEAAEVAAP-----SNGEEHLSITSHOQETP
Tb09v40148 EKYITVMSLREKVTSP---VSNVEAAEVAAP-----SNGEEHLSITSHOQETP
Tbg97291380 EKYITVMSLREKVTSP---VSNVEAAEVAAP-----SNGEEHLSITSHOQETP

Tb09v40060	EKYITVMSLREKVTSP---VSNVEAAEVAAPV-----SNGEEHLSITNHQOETP
Tbg97291360	EKYITVMSLREKVTSP---VSNVEAAEVAAPV-----SNGEEHLSITSHQOETP
Tc00104705351105310	SKWVVHMLREVNGEP---LHPIDGDDGIYND-DSPMMRYSTLGDGVPMTAPSGYENVEV
Tc00104705350763120	SKWVVHMLREVNGEP---LHPIDGDDGIYND-DSPMMRYSTLGDGVPMTAPSGYENVEV
Tc00104705350401180	SKWVVHMLREVNSEP---LHPIDGDDGIYND-DSQMMRYSTLGDGVPMTAPSGYENVEV
Tc001047053511859200	SKWVVHMLREVNGKP---LHPIDGDDGIYND-NSPMMRYSTLGDGVPMTTPFAYENVEV
Tc00104705350601110	SKWVVHMLREVNSEP---LHPIDGDDGIYND-NSPMMRYSTLGDGVPMTTPFAYENVEV
Tc00104705351104770	SKWVVHMLREVNGKP---FHVTDNRNGGIYND-DSPMMRYSTLGDGVPMTAPFAYENVEV
Tc00104705350453350	SKWVVHMLREINDNP---LYAIDRNDGIYNN-DGQMKQDSTLGDGMP'TTPSWHENAIEV
Tc001047053508735100	SKWVAHMLREINDNP---LYAIDRNDGIHNN-DSQMKQDSTLGDGMP'TTPVSEHENAIEV
Tc0010475350894510	SKWVVHMLREMNDNP---LYAIDRNDRIHNN-NG-LMLDATLGDDEVLMTPVPGYEFV
Tc00104705350863740	SKWVVHMLREMNDNP---LYAIDRNDRIHNN-NG-LMLDATLGDDEVLMNVVPGYEFV
Tc00104705351112960	SKWVVHMLREVKREP---LYAIDGNDGIYNN-NGQMLRSLTLGDDEVVMTVPSGYEFV
Tc00104705351191190	SKWVVHMLREVKREP---LYAIDGNDGIYNN-NSQMLRSLTLGDDEVLMTPVSGYENFEV
Tc00104705351024930	SKWVVHMLREMNDSP---LYAIDGNDGIHNN-NSQMLRSLTLGDDEVLTTPVSGYGNFEV
Tc00104705350735910	SKWVVHMLREVKREP---LYAIDRNDGIHND-ASQMKEDSTLGDGMPMTVSSGHENAIEV
TvY486_0201870	GEKVTMVLRESAGAPLCVAVPVGDGDYAD-----VPPFVPSHADGAGY
TvY486_0600050	GEKVTMVLRESAGAPLCVAVPVGDGDYAD-----VPPFVPSHADGAGY
TvY486_0028480	GEKVTMVLRESAGAPLCVAVPVGDGDYAD-----VPPFVPSHADGMWL
TvY486_0201850	GEKVTMVLRESFHPV-YMVGTTANDTGAYAD-----APPFVPPQNRGMER
Tbg97223580	KKEIIPMTVREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223450	-----
Tbg97223390	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223430	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223760	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223550	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223410	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223680	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223740	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223540	KKEIIPMTLREVVG-----
Tb92725360	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tb92725340	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tb92725330	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223600	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223520	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223370	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223470	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223700	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223620	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223490	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFDAPPLALQYYD----
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Tbg97223640	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tb92725350	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
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Tb92725290	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223720	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tb92725320	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFDAPPLALQYYNQMR
Tbg97223350	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223500	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tb92725300	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tb92725310	KKEIIPMTLREVVGEP---LFVLESTPFAPPE-----GFAAPPLALQYYNQMR
Tbg97222800	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMMT
Tb92724760	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMMT
Tbg97222940	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFDAPPLALQYYD----
Tb92724920	KKEIIPMTLREVVGEP---LFVLESTPFAPPE-----GFDAPPLALQYYG----
TcIL30002110	GKELTPMTLREVTGLP---VRAVEPESYAAPD-----EAYDIPQPLGYHYAQGN
TcIL3000013740	GKELTPMTLREVTGLP---VRAVEPESYAAPD-----EAYDIPQPLGYHYAQGN
TcIL3000027940	GKELTPMTLREVTGLP---VRAVEPESYAAPD-----EAYDIPQPLGYHYAQGN
TcIL3000001110	GKELTPMTLREVCGLP---LCAADSESYAAPD-----EAYDIPQPLSYHNAQGH
TcIL3000033420	GKELTPMTLREVCGLP---LCAAGSESYAAPD-----EAYGIPPPQSYHNAQGH
Tb9276380	-----
Tbg972630	-----
Tb9276370	-----
TcIL3000050510	EKEDTPLSLREVYSPA---ECPSPEAPLTSE-----GGGAAEGGSPNASPAVA
TcIL3000050500	EKEDAPLSLREVYSPA---ECPSPEAPLTSE-----GGGAAEGGSPNASPAVA
TcIL3000016620	EKEDAPLSLREVYSPA---ECPSPEAPLTSE-----GGGAAEGGSPNASPVVA
TcIL3000016630	EKEDAPLSLREVYSPA---ECPSPEAPLTSE-----GGGAAEGGSPNASPAVA
TcIL3000047260	DKEITCMRLRETFLSP---ACLSPAEVPLTNG-----GGGVAKAGSPNASPMGA
Tbg97291330	AADE-----
Tbg97291280	AADE-----
Tbg97291270	AGDE-----
Tbg97291300	AGDE-----
Tb09v40146	AVDE-----
Tb09v40147	AADE-----
Tb091601520	AADE-----
Tb09v40149	AADE-----
Tb09v40059	AADE-----

Tb09v40058	AADE-----
Tb09v40148	AVDE-----
Tbg97291380	AGDE-----
Tb09v40060	AADE-----
Tbg97291360	AADE-----
Tc00104705351105310	PRVIKNQETTVYDDGDVL
Tc00104705350763120	PRVIKNQETTVYDDGDVL
Tc00104705350401180	PRVIKNQETTVYDDGDVF
Tc001047053511859200	PRVIKNQENTVYDDGDVF
Tc00104705350601110	PRVIKNQENTVYDDGDVF
Tc00104705351104770	PKVIKNE-----
Tc00104705350453350	PTVIASQESTVYDLGDVF
Tc001047053508735100	PTVIASQESTVYDLGDIL
Tc0010475350894510	PTVIKNQGSTVYDDGDVA
Tc00104705350863740	PTVIKNQGSTVYDDGDVF
Tc00104705351112960	PTVIKNQGSTVYDDGDVV
Tc00104705351191190	PKVVKNQGSTVYDDGDVA
Tc00104705351024930	PKVIKNQGSTVYDDGDVA
Tc00104705350735910	PKVTASQESTVYDFGDIL
TvY486_0201870	DGAW-----
TvY486_0600050	DGAW-----
TvY486_0028480	PQC-----
TvY486_0201850	VHAW-----
Tbg97223580	SE-----
Tbg97223450	-----
Tbg97223390	SE-----
Tbg97223430	SE-----
Tbg97223760	SE-----
Tbg97223550	SE-----
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Tb92725330	SE-----
Tbg97223600	SE-----
Tbg97223520	SE-----
Tbg97223370	SE-----
Tbg97223470	SE-----
Tbg97223700	SE-----
Tbg97223620	SE-----
Tbg97223490	-----
Tbg97223660	SE-----
Tbg97223640	SE-----
Tb92725350	SE-----
Tbg97223330	SE-----
Tb92725290	SE-----
Tbg97223720	SE-----
Tb92725320	SE-----
Tbg97223350	SE-----
Tbg97223500	SE-----
Tb92725300	SE-----
Tb92725310	SE-----
Tbg97222800	GQSY-----
Tb92724760	GQSY-----
Tbg97222940	-----
Tb92724920	-----
TcIL30002110	GDEW-----
TcIL3000013740	GDEW-----
TcIL3000027940	GDEW-----
TcIL3000001110	EGQW-----
TcIL3000033420	EGQW-----
Tb9276380	-----
Tbg972630	-----
Tb9276370	-----
TcIL3000050510	Q-----
TcIL3000050500	Q-----
TcIL3000016620	Q-----
TcIL3000016630	Q-----
TcIL3000047260	R-----

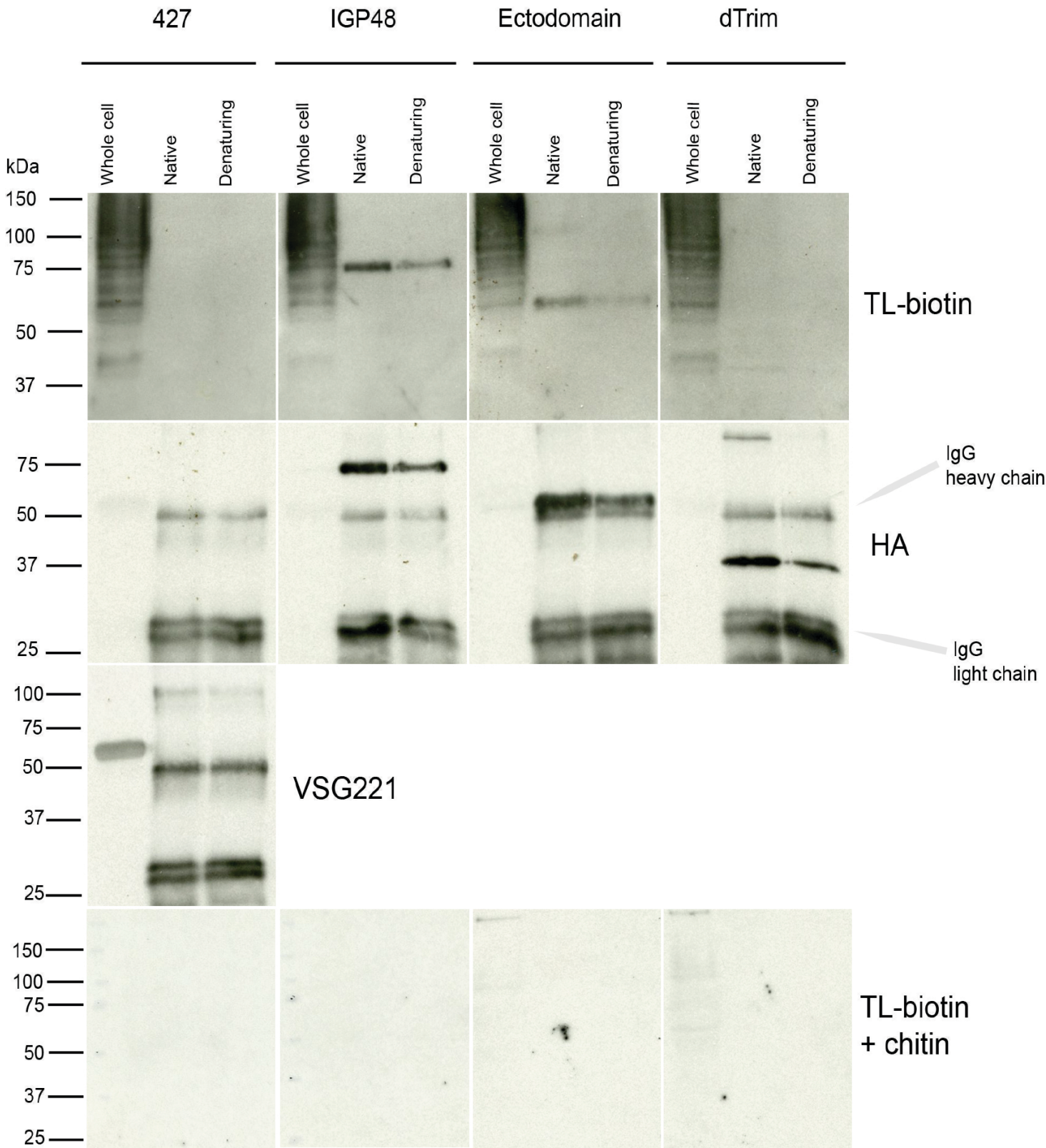


Figure S4

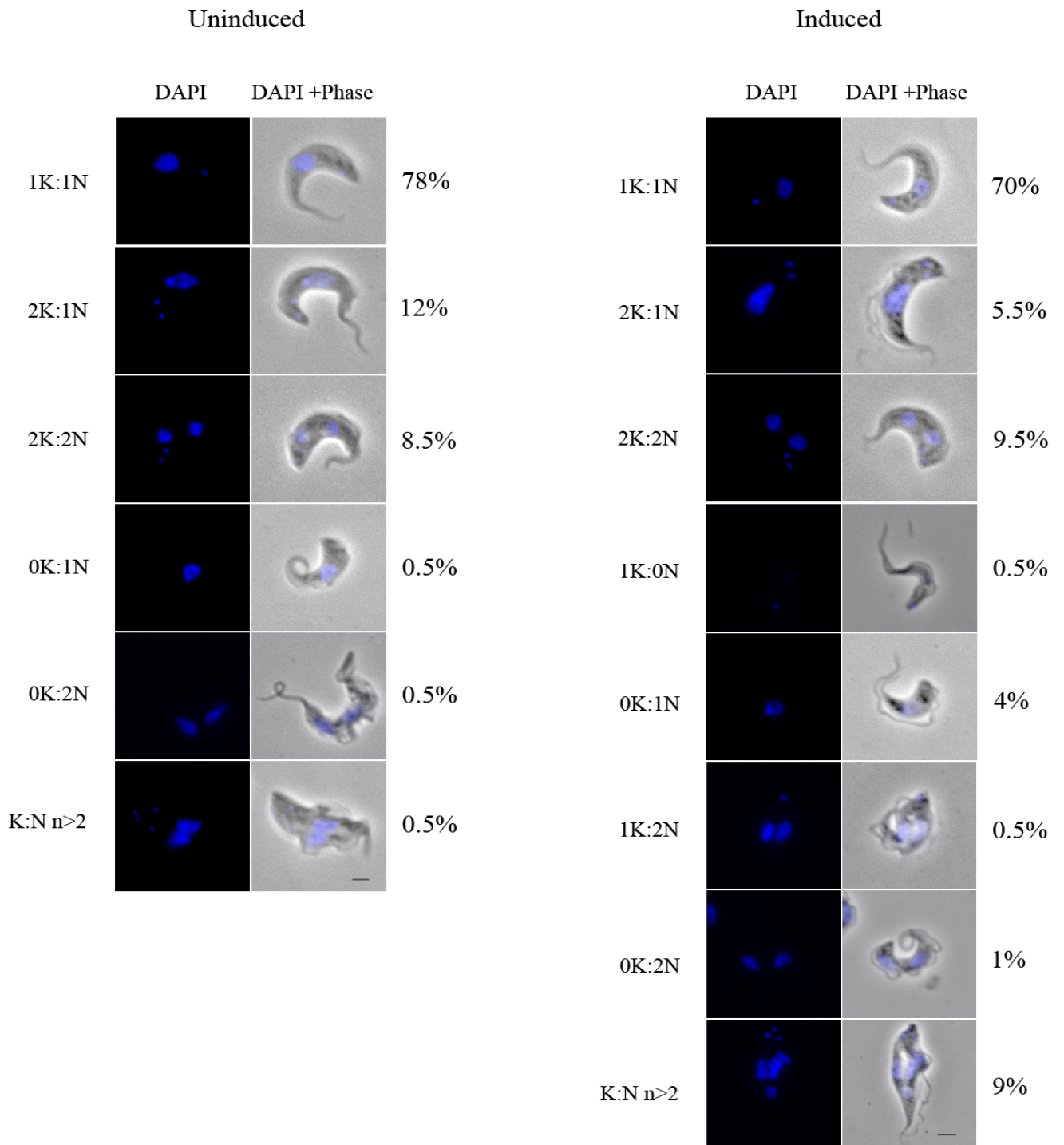


Figure S5

Figure S6

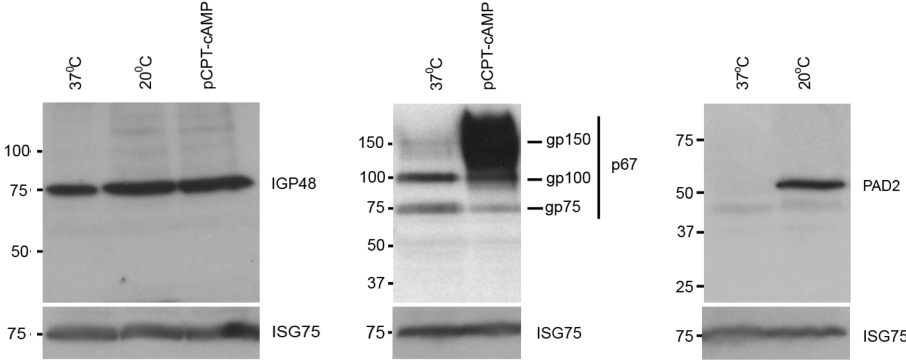


Figure S7

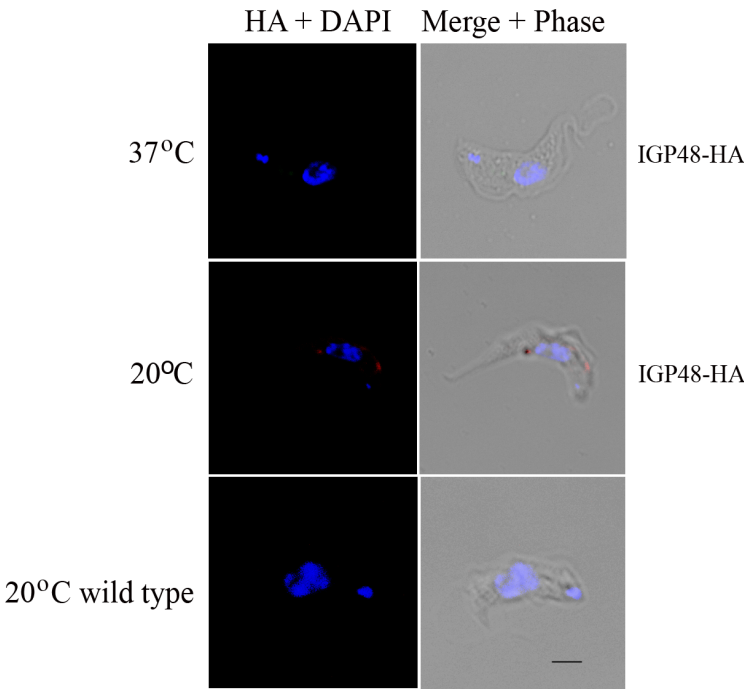


Figure S8

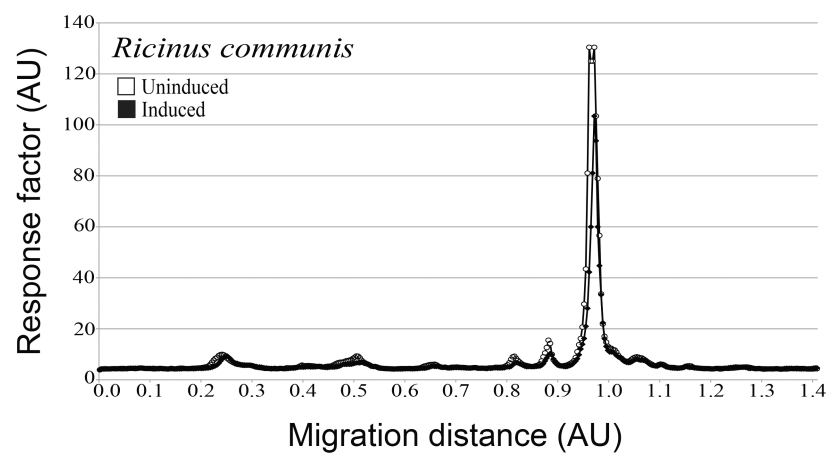
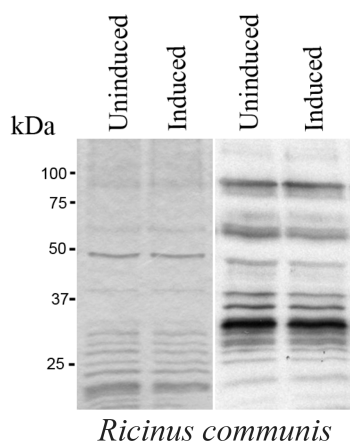
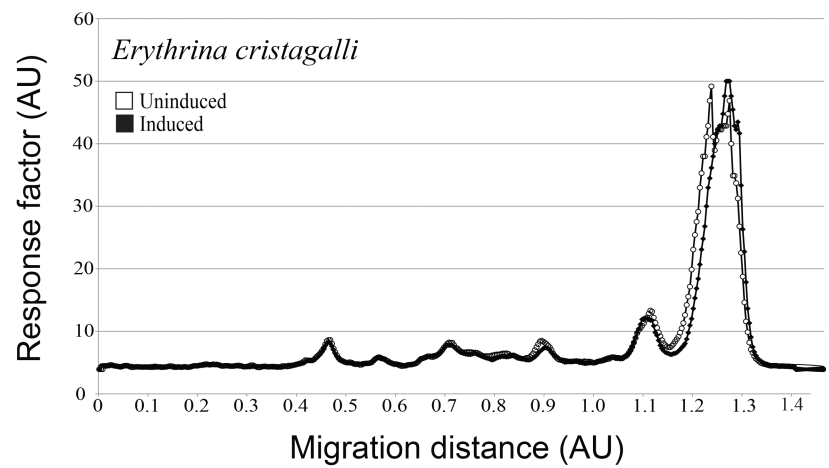
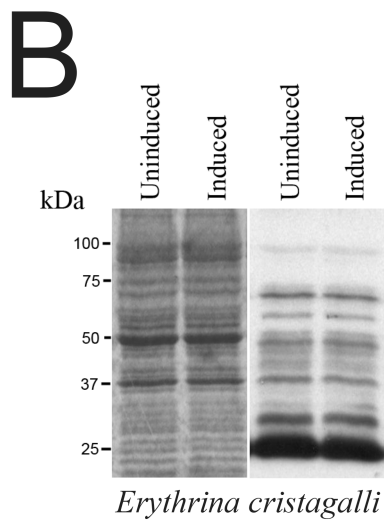
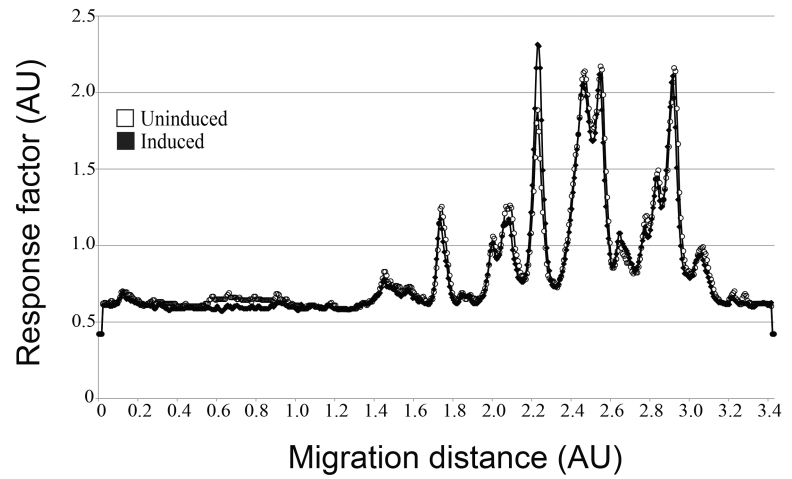
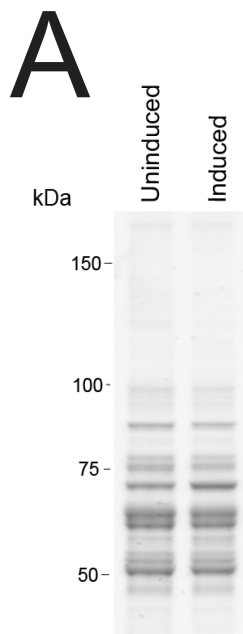


Figure S9

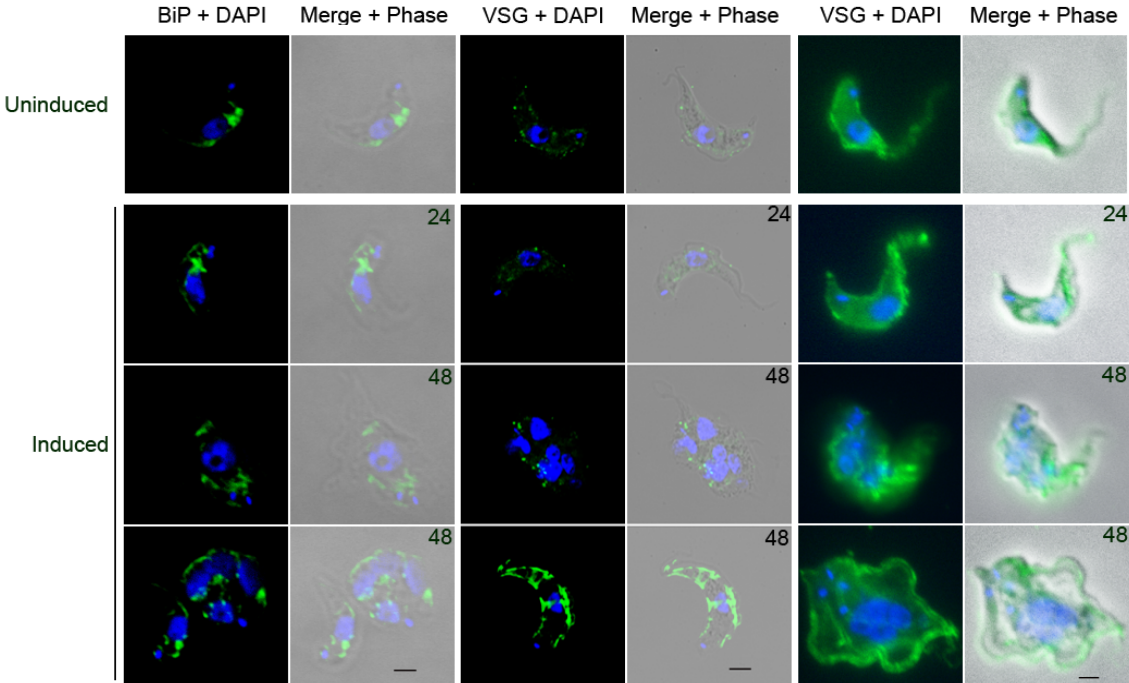


Figure S10

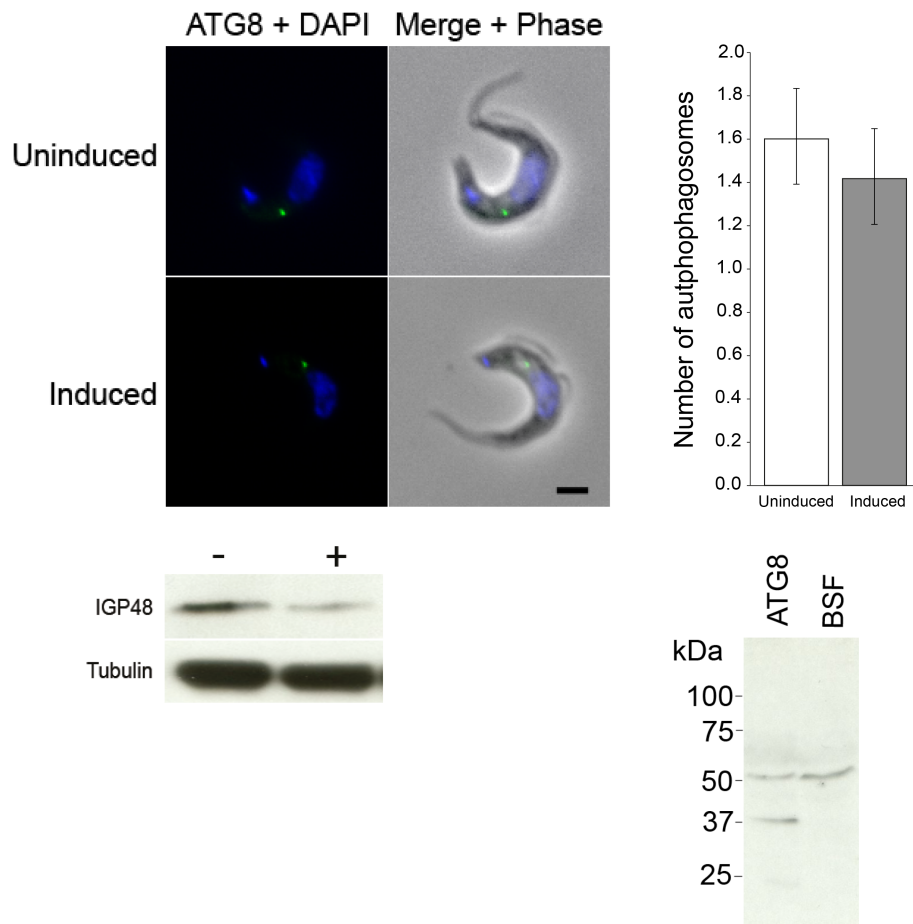


Table S1

Oligomers	Sequence	Restriction site	Epitope tag
<i>RNAi knock-down confirmation</i>			
IGP48:FP	GCCGGTGCTGCTGTTGTTA	-	-
IGP48:RP	ATACGGGTGAGGTAACCTTTT	-	-
IGP40:FP	TTGTGTGTATCGTTGGAATAAG	-	-
IGP40:RP	AGGATGGGTAACCATTTCATTG	-	-
IGP34:FP	CTCAAGATCAACCTTCGGCAA	-	-
IGP34:RP	GCACACAATTGCGAGGGAAA	-	-
<i>Localisation</i>			
IGP48-CO ₂ H:FP	CTCGAAA AAGCTT ATGGAAATCCGCATGGTGCCA	HindIII	-
IGP48-CO ₂ H:RP (HA)	TGCTAT CCCGGG TCAAGCGTAATCTGGAACATCGTATGGGTACTCATCAGCTGCTGGAGT	SmaI	HA
IGP48-CO ₂ H:RP (FLAG)	AGCCAT GGATCCT CACTTGTTCGTCATCGTCTTTGTAGTCTCATCAGCTGCTGGAGTTTC	BamHI	FLAG
IGP48-65:RP	ACTATCAAAGTCGGCACCACCGCCACTTCCCTC	-	-
48-ISG65:FP	GGCGGTGGTGCCGACTTTGATAGTCTCCTAGAT	-	-
ISG65:RP	GCCAC CCCGGG TCAAGCGTAATCTGGAACATCGTATGGGTACTACTTTTACGCTAGA	SmaI	HA
BiP-IGP48:FP	GCGGCC GCTAGC AGTAATGAAGCATCAGATAAG	NheI	-
BiP-IGP48:RP	TGCCTT GAATTC CACTCATCAGCTGCTGG	EcoRI	-
IGP40-CO ₂ H:FP	GCTAT GAAGCTT ATGAGCATGGACACCCGT	HindIII	-
IGP40-CO ₂ H:RP	ACTGCAC CCCGGG TTAAGCGTAATCTGGAACATCGTATGGGTATTCACTGGTTCTCATTG	SmaI	HA
IGP40-65: RP	ACTATCAAAGTCGTGCCAATTACTTCTCTTTC	-	-
40-ISG65:FP	AGTAATTGGCACGACTTTGATAGTCTCCTAGAT	-	-
BiP-IGP40:FP	GCAGAT GCTAGC GAAGTACCGGAACCAACTGTG	NheI	-
BiP-IGP40:RP	GACCTA GAATTC TATTCACTGGTTCTCATTG	EcoRI	-
dCLECT:FP	TCTATT GCTAGC CCAACCTCCGCTTCCACCTGCT	NheI	-
dCLECT:RP	TGCCTT GAATTC CACTCATCAGCTGCTGG	EcoRI	-
dTRIM:FP	ATCGT GAATTC GTGCCATCTACAGCTTCCGAT	EcoRI	-
dTRIM:RP	GTACAT GAATTC AGCAGGTGGAAGCGGAGTTGG	EcoRI	-
Supplementary Table S1			

Table S2

Accession Number	Description	Accession Number
Tb927.5.390	ISG75	Tb09.v4.0147
Tb927.5.390b	ISG75	Tb09.v4.0146
Tb927.5.360	ISG75	Tb09.v4.0148
Tb927.5.360b	ISG75	Tb09.160.1520
Tb927.5.370	ISG75	Tb09.v4.0149
Tb927.5.370b	ISG75	Tb09.v4.0058
Tb927.5.350b	ISG75	Tb09.v4.0059
Tb927.5.350	ISG75	Tb09.v4.0060
Tb927.5.400	ISG75	
Tb927.5.400b	ISG75	Tb927.2.4920
Tb927.5.380	ISG75	Tb927.2.4760
Tb927.5.380b	ISG75	Tb927.2.5330
		Tb927.2.5340
		Tb927.2.5360
Accession Number	Description	Tb927.2.5350
Tb927.6.1850	Singleton	Tb927.2.5290
Tb09.160.4230	Singleton	Tb927.2.5300
Tb11.01.4701	Singleton	Tb927.2.5310
Tb927.10.7140	Singleton	Tb927.2.5320
Tb11.01.5310	Singleton	
Tb09.160.1390	Singleton	Tb927.6.380
Tb09.v1.0780	Singleton	Tb927.6.370
Tb927.8.4110	Singleton	
Tb927.8.4060	Singleton	
Tb927.8.4010	Singleton	Accession Number
Tb11.01.3590	Singleton	Tb927.5.1430
Tb09.160.3680	Singleton	Tb927.5.1390
Tb927.2.1700	Singleton	Tb927.5.1410
Tb927.2.1760	Singleton	Tb927.5.420b
Tb11.57.0077	Singleton	Tb927.5.420
Tb09.v4.0152	Singleton	Tb927.5.430b
Tb11.1460	Singleton	Tb927.5.430
Tb11.v4.0022	Singleton	Tb927.5.410
Tb927.7.4280	Singleton	Tb927.5.410b
Tb927.7.4230	Singleton	Tb927.5.310

Tb927.7.4260	Singleton	Tb927.5.310b
Tb927.5.440b	Singleton	
Tb927.5.440	Singleton	
Tb09.v1.0510	Singleton	
Tb09.v1.0540	Singleton	
Tb927.7.4270	Singleton	
Tb927.10.6180	Singleton	
Tb11.01.3610	Singleton	
Tb927.5.610	ISG-like	
Tb927.5.620	ISG-like	
Tb927.5.630	ISG-like	
Tb927.10.2360	Singleton	
Tb11.1490	Singleton	
Tb927.10.120	Singleton	
Tb927.3.2870	Singleton	
Tb927.10.11140	Singleton	
Tb09.160.2060	Singleton	
Tb927.1.3900	Singleton	
Tb11.47.0001	Singleton	
Tb927.1.660	Singleton	
Tb927.3.5170	Singleton	
Tb927.1.770	Singleton	
Tb09.v4.0010	Singleton	
Tb927.8.8030	Singleton	
Tb927.8.7280	Singleton	
Tb09.160.4390	Singleton	
Tb927.6.1740	Singleton	
Tb927.1.4770	Singleton	
Tb927.3.4230	Singleton	
Tb09.160.4810	Singleton	
Tb09.v1.0630	Singleton	
Tb927.4.590	Singleton	
Tb927.10.2080	Singleton	
Tb927.8.3120	Singleton	
Tb927.5.1810	Singleton	
Tb11.01.0290	Singleton	

Tb927.8.6380	Singleton	
Tb927.5.4060	Singleton	
Tb927.4.2320	Singleton	
Tb09.160.5140	Singleton	
Tb927.5.2580	Singleton	
Tb11.13.0007	Singleton	
Tb927.10.2420	Singleton	
Tb09.160.2950	Singleton	
Tb09.v1.0650	Singleton	
Tb09.160.2340	Singleton	
Tb927.10.10840	Singleton	
Tb09.211.4290	Singleton	
Tb09.160.2140	Singleton	
Tb927.4.1120	Singleton	
Tb927.10.12450	Singleton	
Tb927.3.840	Singleton	
Tb927.7.5710	Singleton	
Tb11.02.2880	Singleton	
Tb09.160.5040	Singleton	
Tb927.4.1390	Singleton	
Tb11.02.3760	Singleton	
Tb09.211.2890	Singleton	
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Tb927.10.10760	Singleton	
Tb927.3.2360	Singleton	
Tb927.7.900	Singleton	
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Tb09.v2.0050	Singleton	
Tb927.5.1020	Singleton	
Tb927.3.3140	Singleton	
Tb927.8.560	Singleton	
Tb927.2.6390	Singleton	
Tb927.4.5470	Singleton	
Tb927.10.13090	Singleton	
Tb927.2.5970	Singleton	
Tb927.5.1740	Singleton	

Tb927.7.470	Singleton	
Tb11.01.1000	Singleton	
Tb09.v1.0850	Singleton	
Tb09.211.4680	Singleton	
Tb927.10.700	Singleton	
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Tb11.01.7770	Singleton	
Tb927.4.4920	Singleton	
Tb11.01.3160	Singleton	
Tb927.8.6590	Singleton	
Tb927.4.510	Singleton	
Tb11.01.3790	Singleton	
Tb11.49.0009	Singleton	
Tb11.30.0008	Singleton	
Tb09.v4.0179	Singleton	
Tb10.v4.0122	Singleton	
Tb09.142.0500	Singleton	
Tb11.02.0060	Singleton	
Tb927.10.2500	Singleton	
Tb05.5K5.520	Singleton	
Tb927.10.4670	Singleton	
Tb927.5.292b	Singleton	
Tb927.2.2490	Singleton	
Tb927.7.4690	Singleton	
Tb11.v4.0065	Singleton	
Tb927.4.1190	Singleton	
Tb927.6.3700	Singleton	
Tb927.7.4980	Singleton	
Tb927.10.6640	Singleton	
Tb927.5.1630	Singleton	
Tb927.10.7000	Singleton	
Tb927.10.7180	Singleton	

Description	Accession Number	Description
IGP48	Tb927.2.3300	ISG65
IGP48	Tb927.2.3290	ISG65
IGP48	Tb927.2.3310	ISG65
IGP48	Tb927.2.3280	ISG65
IGP48	Tb927.2.3270	ISG65
IGP48	Tb927.2.3320	ISG65
IGP48		
IGP48		
	Accession Number	Description
IGP40	Tb927.8.7920	Adenylate Cyclase
IGP40	Tb927.8.7900	Adenylate Cyclase
IGP40	Tb927.8.7890	Adenylate Cyclase
IGP40	Tb927.8.7930	Adenylate Cyclase
IGP40	Tb927.8.7870	Adenylate Cyclase
IGP40	Tb927.8.7940	Adenylate Cyclase
IGP40	Tb927.8.7590	Adenylate Cyclase
IGP40	Tb927.4.4430	Adenylate Cyclase
IGP40	Tb927.4.4450	Adenylate Cyclase
IGP40	Tb927.4.4410	Adenylate Cyclase
	Tb927.4.4440	Adenylate Cyclase
IGP34	Tb927.7.7530	Adenylate Cyclase
IGP34	Tb927.7.7520	Adenylate Cyclase
	Tb927.4.4470	Adenylate Cyclase
	Tb927.4.4460	Adenylate Cyclase
Description	Tb927.4.3880	Adenylate Cyclase
ISG-like	Tb927.4.3870	Adenylate Cyclase
ISG-like	Tb927.4.3750	Adenylate Cyclase
ISG-like	Tb927.6.190	Adenylate Cyclase
ISG-like	Tb927.5.650	Adenylate Cyclase
ISG-like	Tb927.7.6040	Adenylate Cyclase
ISG-like	Tb927.7.6080	Adenylate Cyclase
ISG-like	Tb927.7.6070	Adenylate Cyclase
ISG-like	Tb927.7.6060	Adenylate Cyclase
ISG-like	Tb927.7.6050	Adenylate Cyclase
ISG-like	Tb927.10.13040	Adenylate Cyclase

Table S3: Serum immunoglobulin responses to IGP48 in *T. b. rhodesiense* patients.

	Patient ID	IgG response to rIGP48 (+/-)	IgM response to rIGP48 (+/-)	Disease stage	Age (years)	Parasitaemia	Serum IgG (g/l)	Serum IgM (g/l)
INFECTED								
	L2	-	-	Late	12	0.25	20.5	9.4
	L3	+	-	Late	15	1	30.1	10.2
	L16	+	+	Early	40	20	25.2	21.7
	L30	+	-	Late	18	3	45.3	7.6
	S3	-	-	Late	12	0	17.3	5.7
	S13	+	-	Early	16	50	16.6	1.3
	S48	+	+	Late	40	100	3.1	18.8
	S69	+	+	Early	15	20	51.3	2.7
	S79	+	-	Late	50	2	17.8	51.6
UNINFECTED								
	LC1	-	-	N/A				
	LC15	-	-					
	EUM1	-	-					
	EUF1	-	-					

a: Disease stage: Later stage (meningoencephalitic) criteria either CSF white cells $>5/\text{mm}^3$ or parasites observed in the CSF.

b: Parasitaemia: Number of Giemsa stained parasites observed per 10 fields, at 400x magnification.