

## Supplementary material for:

# An extensive endoplasmic reticulum-localised glycoprotein family in trypanosomatids

Harriet Allison<sup>1</sup>, Amanda J. O'Reilly<sup>1</sup>, Jeremy Sternberg<sup>2</sup> and Mark C. Field<sup>1\*</sup>

<sup>1</sup>Division of Biological Chemistry and Drug Discovery, University of Dundee, Dundee, Scotland, DD1 5EH and <sup>2</sup>School of Biological Sciences, University of Aberdeen, Aberdeen, AB24 2TZ, UK.

**Corresponding author:** Telephone: +44 (0)751-550-7880, email: mfield@mac.com

## Supplementary 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.hsls.pitt.edu/obrc/index.php?page=URL\\_1043959648](http://www.hsls.pitt.edu/obrc/index.php?page=URL_1043959648)) 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](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](http://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.**  $1 \times 10^7$  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

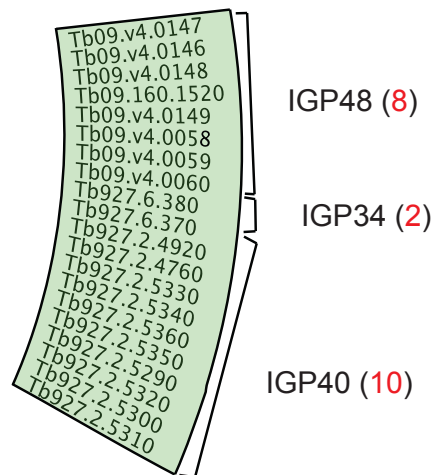
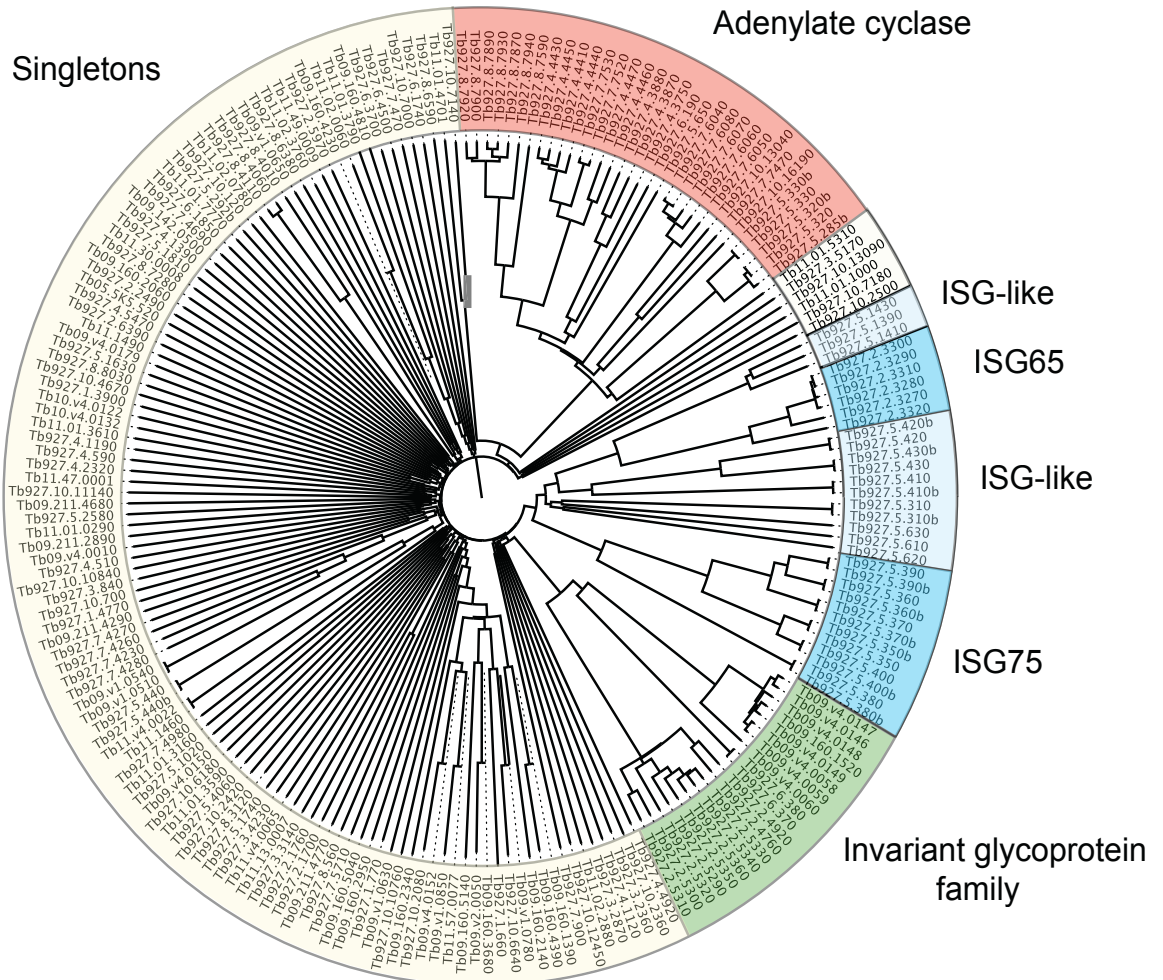


**1** Tb09.v4.0204

**208**

Figure S1

# Figure S2A



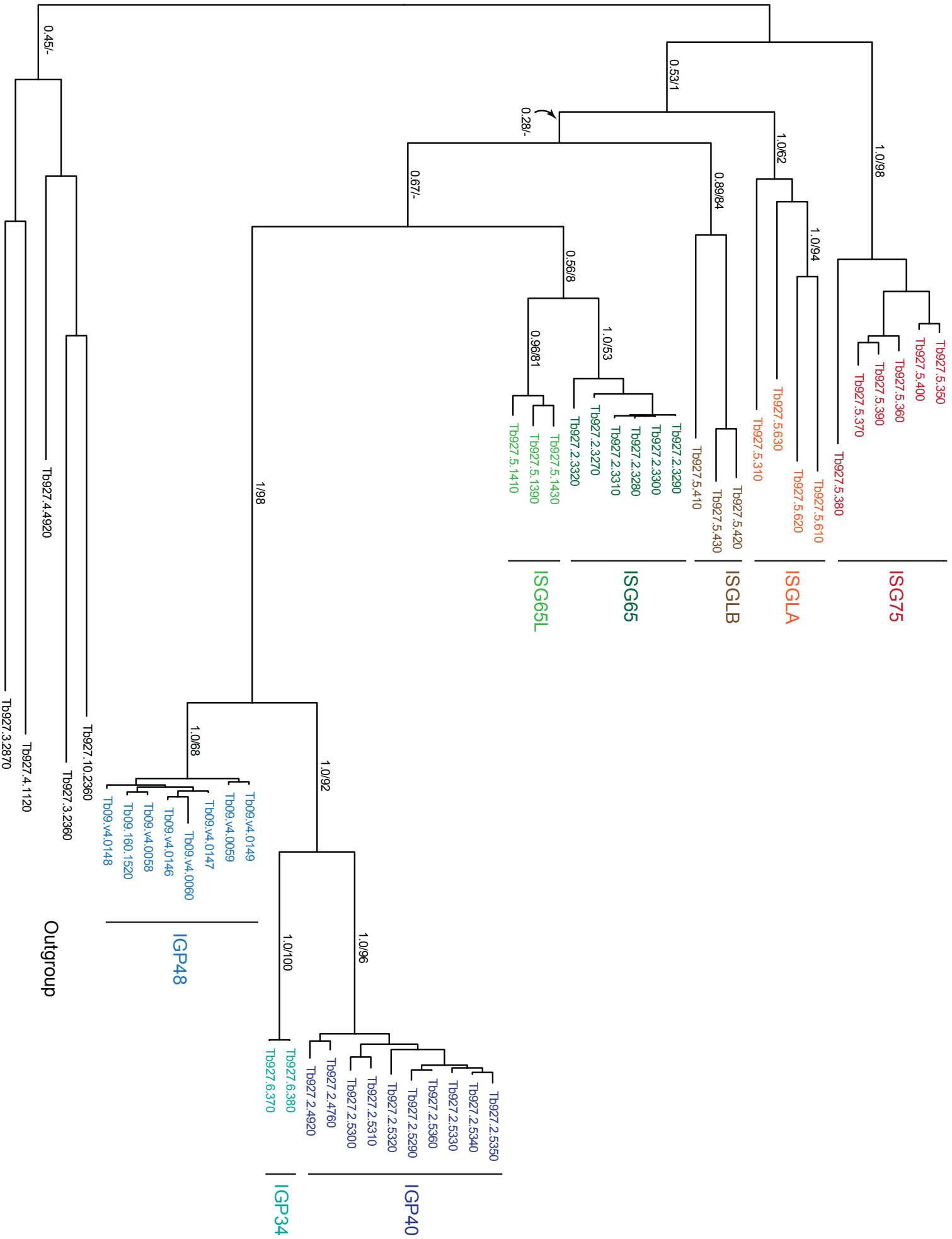


Figure S2B







# Figure S3B

## CLUSTAL W (1.8) multiple sequence alignment

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Tbg97291280 -----  
Tbg97291270 -----  
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Tb09v40147 -----  
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TcIL3000050510 YTVRAERPVGIFYVALCNIVVFTTSAPVPOPEST-----  
TcIL3000050500 YTVRAERPVGIFYVALCNIVVFTTSAPVPOPEST-----  
TcIL3000016620 HVVRKEKQVKNFVLLCNIVVPTTSAPVPOPESE-----  
TcIL3000016630 -----  
TcIL3000047260 YEVFRFRTHLILCQLQNKKPAPLPPSPGPATADNEELNGTDANETASEELNGTDANETA-----

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TvY486\_0028480 -----  
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TcIL3000027940 -----  
TcIL3000001110 -----  
TcIL3000033420 -----  
Tb9276380 -----  
Tbg972630 -----  
Tb9276370 -----  
TcIL3000050510 -----ETESEEHNGTNTNETESEELNGTNANETASEELNGTNVNETAGEELNGTN  
TcIL3000050500 -----ETESEEHNGTNTNETASEELNGTNANETASEELNGTNVNETAGEELNGTN  
TcIL3000016620 -----  
TcIL3000016630 -----  
TcIL3000047260 -----SEELNGTDANETASEELNGTNANETASEELNGTDANETASEELNGTNANETASEELNGTD

Tbg97291330 -----NISFTNTRARSTRFFMVLCE  
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Tbg97291270 -----NISFTNTRARSTRFFMVLCE  
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Tb09v40146 -----NISFTNTRARSTRFFMVLCE  
Tb09v40147 -----NISFTNTRARSTRFFMVLCE  
Tb091601520 -----ISMFTNTRGRSTRFFMVLCE  
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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 -----KTFMLRLKTTD  
Tc00104705350863740 -----KTFMLRLKTTD  
Tc00104705351112960 -----KTFMLRLKTTD  
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Tc00104705351024930 -----KTFMLRLKTTD  
Tc00104705350735910 -----KTFMLRLKTTD  
TvY486\_0201870 -----SSAKVPIEKTLLSNYIAVCE  
TvY486\_0600050 -----SSAKVPIEKTLLSNYIAVCE  
TvY486\_0028480 -----YFAPTPILYTYVTNYIAVCE  
TvY486\_0201850 -----HYAQAPIQGTYYVTSYIAVCE  
Tbg97223580 -----IKWASDNPDTKTENYVILCE  
Tbg97223450 -----IKWASDNPDTKTENYVILCE  
Tbg97223390 -----IKWASDNPDTKTENYVILCE  
Tbg97223430 -----IKWASDNPDTKTENYVILCE  
Tbg97223760 -----IKWASDNPDTKTENYVILCE  
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Tbg97223740 -----IKWASDNPDTKTENYVILCE  
Tbg97223540 -----IKWASDNPDTKTENYVILCE  
Tb92725360 -----IKWASDNPDTKTENYVILCE  
Tb92725340 -----IKGTSKNPATKTENYVILCE  
Tb92725330 -----IKWTSKNPATKTENYVILCE  
Tbg97223600 -----IKGTSKNPATKTENYVILCE  
Tbg97223520 -----IKGTSKNPATKTENYVILCE  
Tbg97223370 -----IKGTSKNPATKTENYVILCE  
Tbg97223470 -----IKGTSKNPATKTENYVILCE  
Tbg97223700 -----IKGTSKNPATKTENYVILCE  
Tbg97223620 -----IKWTSKNPATKTENYVILCE

Tbg97223490 -----IKGTSKNPATKTENYVILCE  
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 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 TSLIVAVAAENLIDADTFVNERKQSVNDKQSSGNTSAVGNITVREGKRPDGNKNT  
 Tc00104705351105310 TSLTVALAAENLFATDTFAVNERKQSVNDKQCSGNTSAVGNISVREGKKGENTSDDKNT  
 Tc00104705350763120 NDEKATWYDG-----Q  
 Tc00104705350401180 SDEKATWYDG-----Q  
 Tc001047053511859200 SDKKATWYDG-----Q  
 Tc00104705350601110 SDKNATWYDG-----Q  
 Tc00104705351104770 SYEKATWYDG-----Q  
 Tc00104705350453350 NSGNATWYDW-----Y  
 Tc001047053508735100 NSEQATWYDW-----Y  
 Tc0010475350894510 NSEKATWYDW-----Y  
 Tc00104705350863740 NSEKATWYDW-----Y  
 Tc0010470535112960 NNGNATWYDW-----Y  
 Tc00104705351191190 NNEQATWYDW-----Y  
 Tc00104705351024930 NNGNATWYDW-----Y  
 Tc00104705350735910 NSGNATWYDW-----Y  
 TvY486\_0201870 VQDSISTSTT-----T  
 TvY486\_0600050 VQDSISTSTT-----T  
 TvY486\_0028480 VQDSVSTTGT-----G  
 TvY486\_0201850 SQDSISSSTT-----T  
 Tbg97223580 VHDSIS---T-----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

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Tbg97291280	TADEN-----TTVDGNTNAD-----
Tbg97291270	TADEN-----TTADGNTNADE-----
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-SSVADGNTSDDSTTSHENRSYDDSSVADGNTSDDSTTSHENRSYDDS
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-----TTTTTTTTTTTTTTTTSTT-----
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-----  
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Tbg97223470 -----TTTTTTTTTT-----  
Tbg97223700 -----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-----YTTTTTT-----  
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

Tbg97291330 -----  
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Tbg97291270 -----  
Tbg97291300 -----  
Tb09v40146 -----  
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Tb091601520 -----  
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Tb09v40059 -----  
Tb09v40058 -----  
Tb09v40148 -----  
Tbg97291380 TTADG-----  
Tb09v40060 SVADG-----  
Tbg97291360 SVADGNSSDDESTSDDESTSDYESTAGENTNADGNTSNEKNTTTHEYRSYDDSSVADGNT  
Tc00104705351105310 -----  
Tc00104705350763120 -----  
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Tbg97223680 -----  
Tbg97223740 -----  
Tbg97223540 -----



Tbg97223680 -----  
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Tb92725340 -----  
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Tb92725300 -----  
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Tbg97222940 -----  
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TcIL30002110 -----  
TcIL3000013740 -----  
TcIL3000027940 -----  
TcIL3000001110 -----  
TcIL3000033420 -----  
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Tbg972630 -----  
Tb9276370 -----  
TcIL3000050510 -----  
TcIL3000050500 -----  
TcIL3000016620 -----  
TcIL3000016630 -----  
TcIL3000047260 -----

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Tb09v40146 -----  
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Tb091601520 -----  
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TvY486\_0600050 -----  
TvY486\_0028480 -----  
TvY486\_0201850 -----  
Tbg97223580 -----  
Tbg97223450 -----  
Tbg97223390 -----  
Tbg97223430 -----

SYDDSSVADGNTSDEESTTSHENRSYDDSSVAMGTQVTMKVLPMMRVLVTMSTAGENTKA

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Tb92725360 -----  
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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 -----

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  
Tc00104705351105310 -----  
Tc00104705350763120 -----  
Tc00104705350401180 -----  
Tc001047053511859200 -----  
Tc00104705350601110 -----  
Tc00104705351104770 -----  
Tc00104705350453350 -----  
Tc001047053508735100 -----  
Tc0010475350894510 -----  
Tc00104705350863740 -----  
Tc00104705351112960 -----  
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 -----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 EELNGTNANETASEELNGTNANETASEELNGTNANETASEELNGTSANETASEELN-----  
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 -----







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 -----GHHPTGSAVTAVTATKPPPTAPDVSEWV-----  
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-----  
TcIL3000001110 -----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-----VKISWVHKRWYVILIAILVPVIVAVLITVCFRCRCRGGADDE  
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 SSATFVPPVPGAKQVGRDASSTWAERYWYVILLSLLVAIAAVLIVLCLCLRCCAG--D  
TvY486\_0201850 GNATSAPPVPGGAGHAGLGASSTWAERYWYVILLVFLSVIVAIVLIVLFLVFCRSRSR--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 VTTVLSLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V  
Tb92725340 VTTVLSLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V  
Tb92725330 VTTVLSLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V  
Tbg97223600 VTTVLSLEERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V  
Tbg97223520 VTTVLSLEERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V  
Tbg97223370 VTTVLSLEERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V  
Tbg97223470 VTTVLSLEERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V  
Tbg97223700 VTTVLSLEERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V  
Tbg97223620 VTTVLSLEERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V  
Tbg97223490 VTTVLSLEERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V  
Tbg97223660 VTTVLSLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V  
Tbg97223640 VTTVLSLEERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V  
Tb92725350 VTTVLSLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V  
Tbg97223330 VTTVLSLEERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V  
Tb92725290 VTTVLSLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V  
Tbg97223720 VTTVLSLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V  
Tb92725320 VTTVLSLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V  
Tbg97223350 VTTVLSLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V  
Tbg97223500 VTTVLSLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V  
Tb92725300 VTTVLSLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V  
Tb92725310 VTTVLSLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYD--V  
Tbg97222800 VTTASLEERI-----DLIILIALISVSVLIVLFLFLRWFCYDYN--V  
Tb92724760 VTTVLSLEERI-----DLIILIALISVSVLIVLFLFLRWFCYDYN--V  
Tbg97222940 VTTASLEERS-----NWHIILIALISVVALIVLFLFLRWFCYDYN--V  
Tb92724920 VTTASLEERS-----NWHIILIALISVSVLIVLFLFLRWFCYDYN--V  
TcIL30002110 TTTTAQPEASEGK-GSG-----YIILIVLFLLLAALIAALLLAYCCFSAG--G  
TcIL3000013740 TTTTAQPEASEGK-GSG-----YIILIVLFLLLAALIAALLLAYCCFSAG--G  
TcIL3000027940 TTTTAQPEASEGK-GSG-----YIILIVLFLLLAALIAALLLAYCCFSAG--G  
TcIL3000001110 TTTTAQPEASEGSDGSSG-ASTSWGTRNWIILIVLFLLLAALIAALLLAYCCFSAG--G  
TcIL3000033420 TTTTAQPEASEGSDGSSG-ASASWGTRNWIILIVFLLAALIAALLLAYCCFSAG--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-----VNGGVLALAILLPIIAIVLFLLLWYFCVWGK--N

: ; :

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

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-LMLDATLGDDEVLMTPPGYEFV
Tc00104705350863740	SKWVVHMLREMNDNP---LYAIDRNDRIHNN-NG-LMLDATLGDDEVLMNVPPGYEFV
Tc00104705351112960	SKWVVHMLREVKKREP---LYAIDGNDGIYNN-NQMLRSLTLGDDEVVMTVPSGYEFV
Tc00104705351191190	SKWVVHMLREVKKREP---LYAIDGNDGIYNNDSQMLRSLTLGDDEVMTVPSGYENFEV
Tc00104705351024930	SKWVVHMLREMNDSP---LYAIDGNDGIHNN-NSQMLRSLTLGDDEVLTTPVPSGYGNFEV
Tc00104705350735910	SKWVVHMLREVKKREP---LYAIDRNDGIHND-ASQMKEDSTLGDGMPMTVSSGHENAIEV
TvY486_0201870	GEKVTMVLRESAGAPLCVAVPVGDGDAYYAD-----VPPFVPSHADGAGY
TvY486_0600050	GEKVTMVLRESAGAPLCVAVPVGDGDAYYAD-----VPPFVPSHADGAGY
TvY486_0028480	GEKVTMVLRESAGAPLCVAVPVGDGDAYYAD-----VPPFVPSHADGMWL
TvY486_0201850	GEKVTMVLRESFHPV-YMVGTTANDTGAYYAD-----APPFVPPQNRGMER
Tbg97223580	KKEIIPMTVREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223450	-----
Tbg97223390	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223430	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223760	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
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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
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Tbg97223700	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223620	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
Tbg97223490	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFDAPPLALQYYD----
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Tbg97223640	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
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Tb92725290	KKEIIPMTLREVVGEP---LFVLESTPFVPPE-----GFAAPPLALQYYNQMR
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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----
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TcIL3000013740	GKELTPMTLREVTGLP---VRAVEPESYAAPD-----EAYDIPQPLGYHYAQGN
TcIL3000027940	GKELTPMTLREVTGLP---VRAVEPESYAAPD-----EAYDIPQPLGYHYAQGN
TcIL3000001110	GKELTPMTLREVCGLP---LCAADSESYAAPD-----EAYDIPQPLSYHNAQGH
TcIL3000033420	GKELTPMTLREVCGLP---LCAAGSESYAAPD-----EAYGIPPPQSYHNAQGH
Tb9276380	-----
Tbg972630	-----
Tb9276370	-----
TcIL3000050510	EKEDTPLSLREVYSPA---ECSPVEAPLTSE-----GGGAAEGGSPNASPAVA
TcIL3000050500	EKEDAPLSLREVYSPA---ECSPVEAPLTSE-----GGGAAEGGSPNASPAVA
TcIL3000016620	EKEDAPLSLREVYSPA---ECSPVEAPLTSE-----GGGAAEGGSPNASPVVA
TcIL3000016630	EKEDAPLSLREVYSPA---ECSPVEAPLTSE-----GGGAAEGGSPNASPAVA
TcIL3000047260	DKEITCMRLRETFLSP---ACLSPAEVPLTNG-----GGGVAKAGSPNASPMGA
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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-----
Tbg97223410	SE-----
Tbg97223680	SE-----
Tbg97223740	SE-----
Tbg97223540	-----
Tb92725360	SE-----
Tb92725340	SE-----
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-----

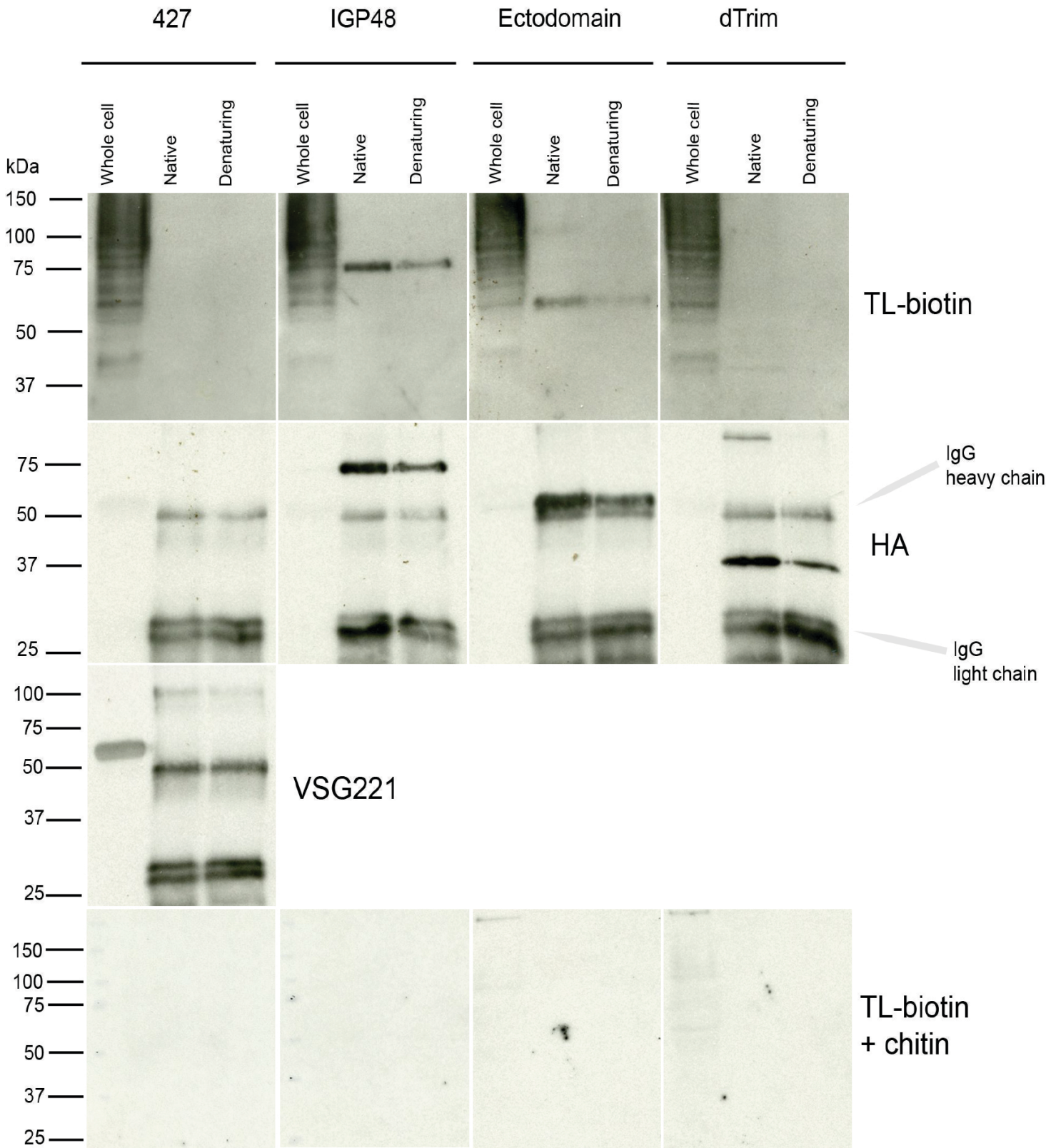


Figure S4

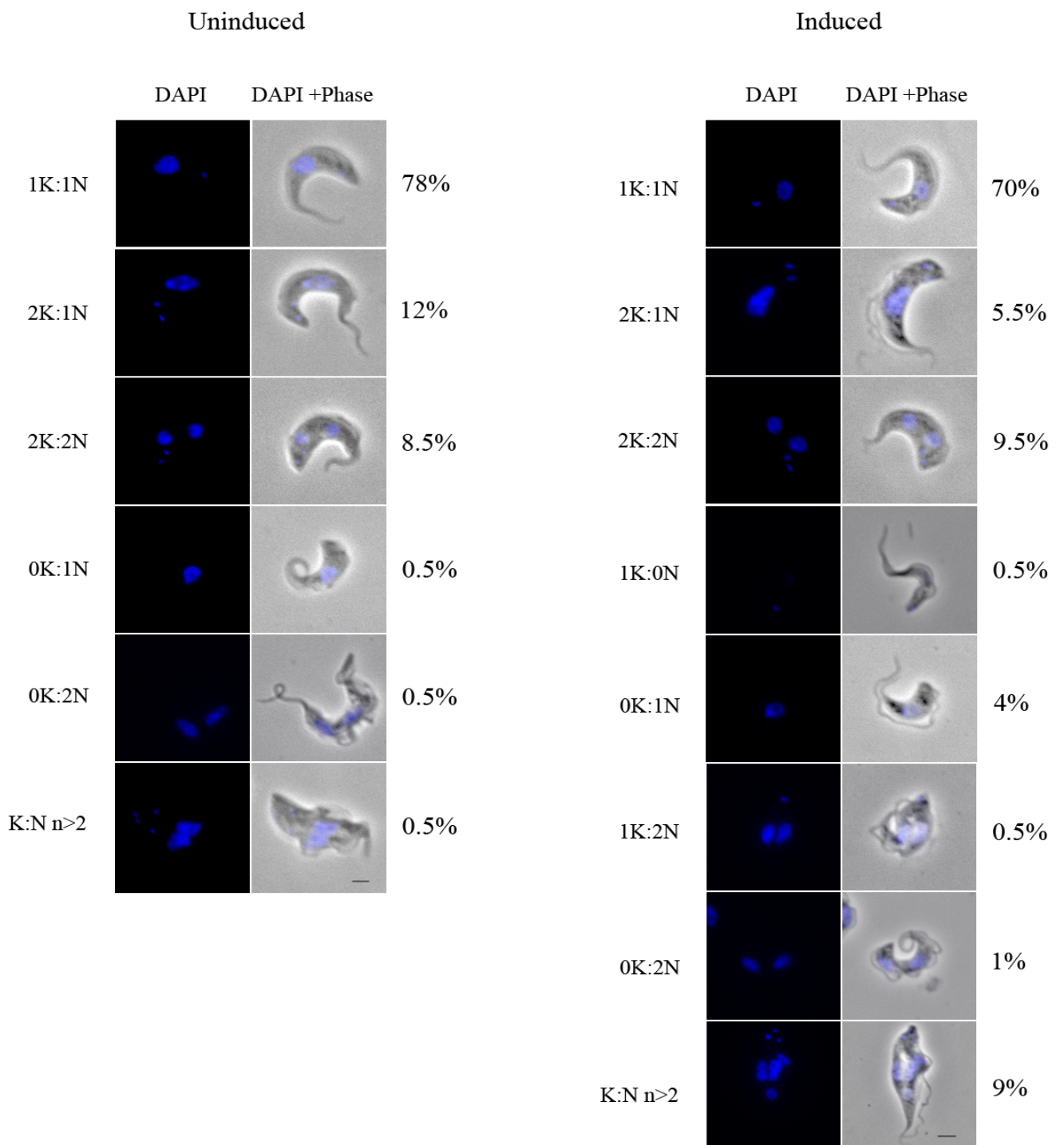


Figure S5

Figure S6

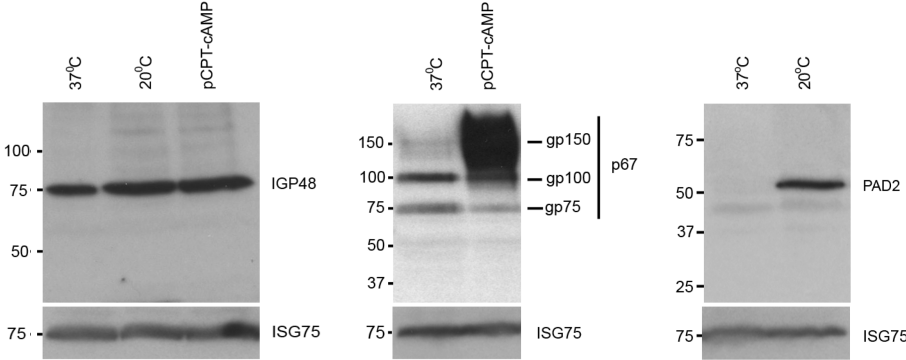


Figure S7

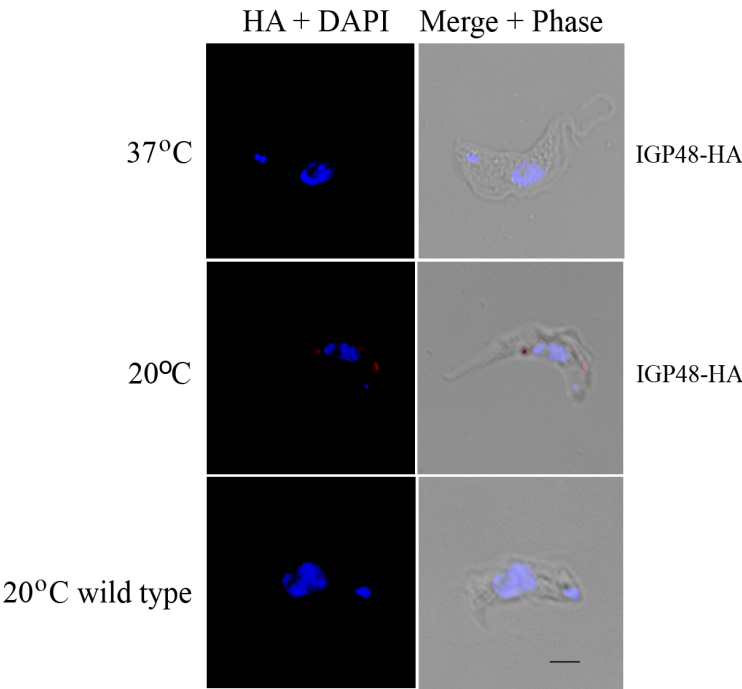
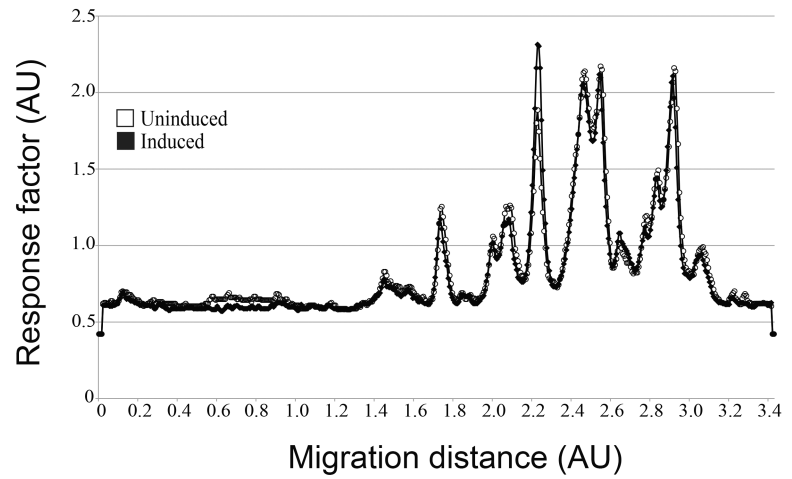
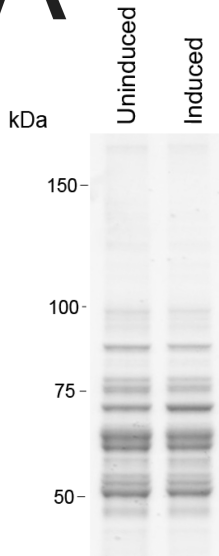


Figure S8

A



B

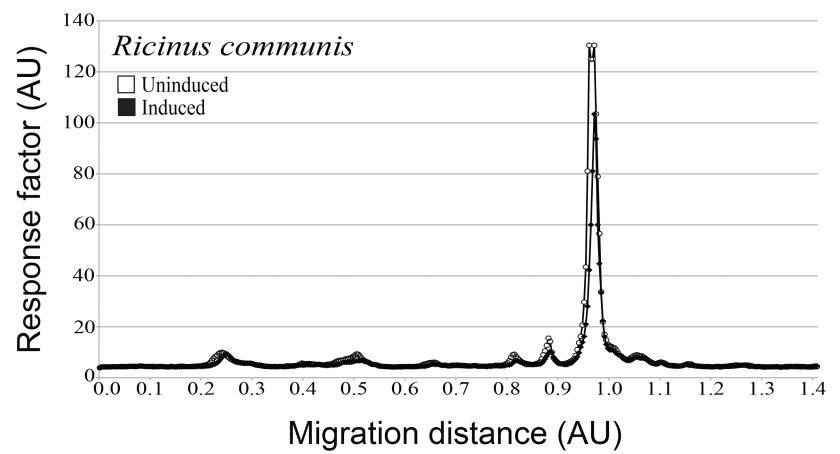
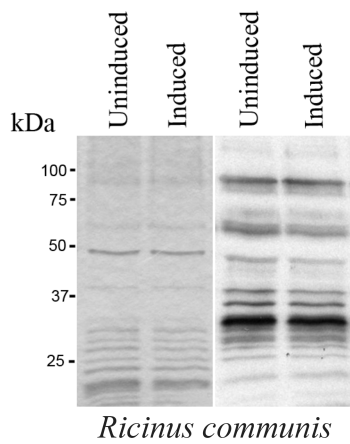
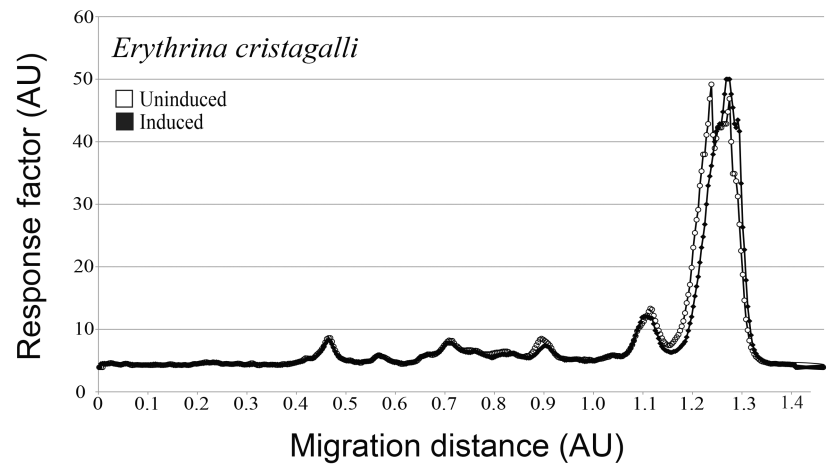
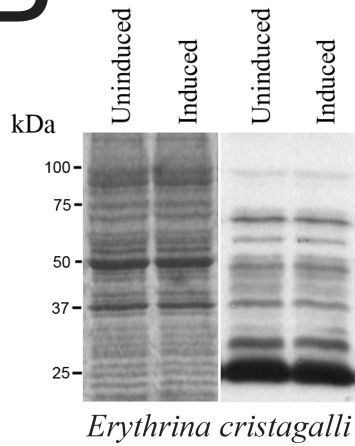


Figure S9

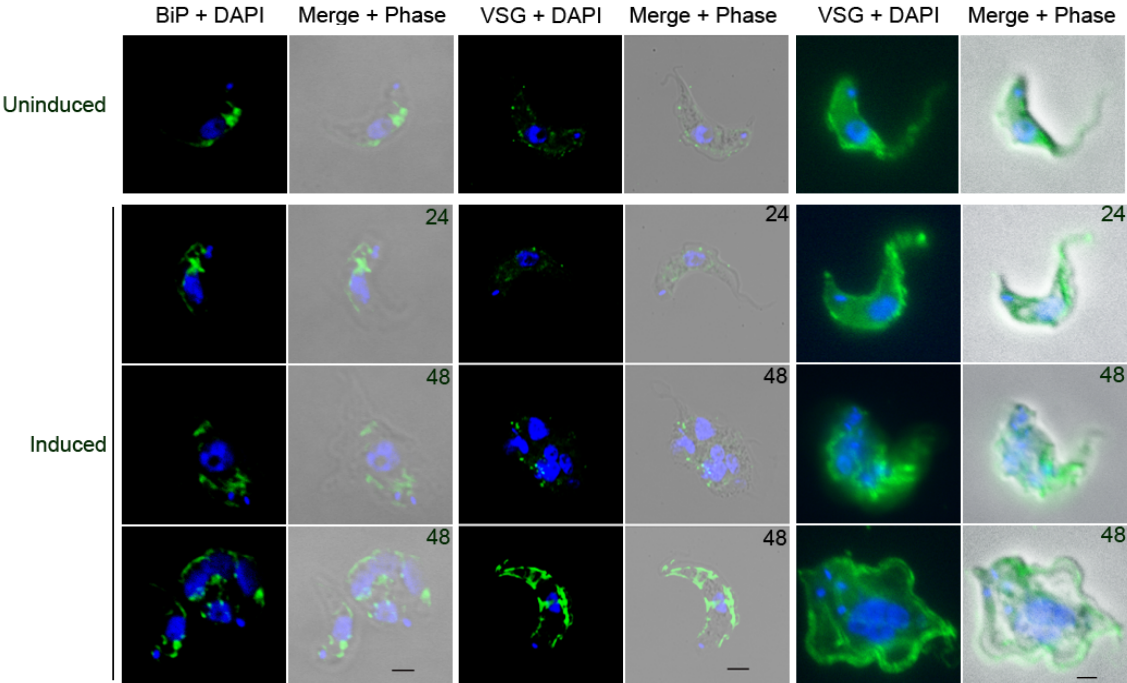


Figure S10

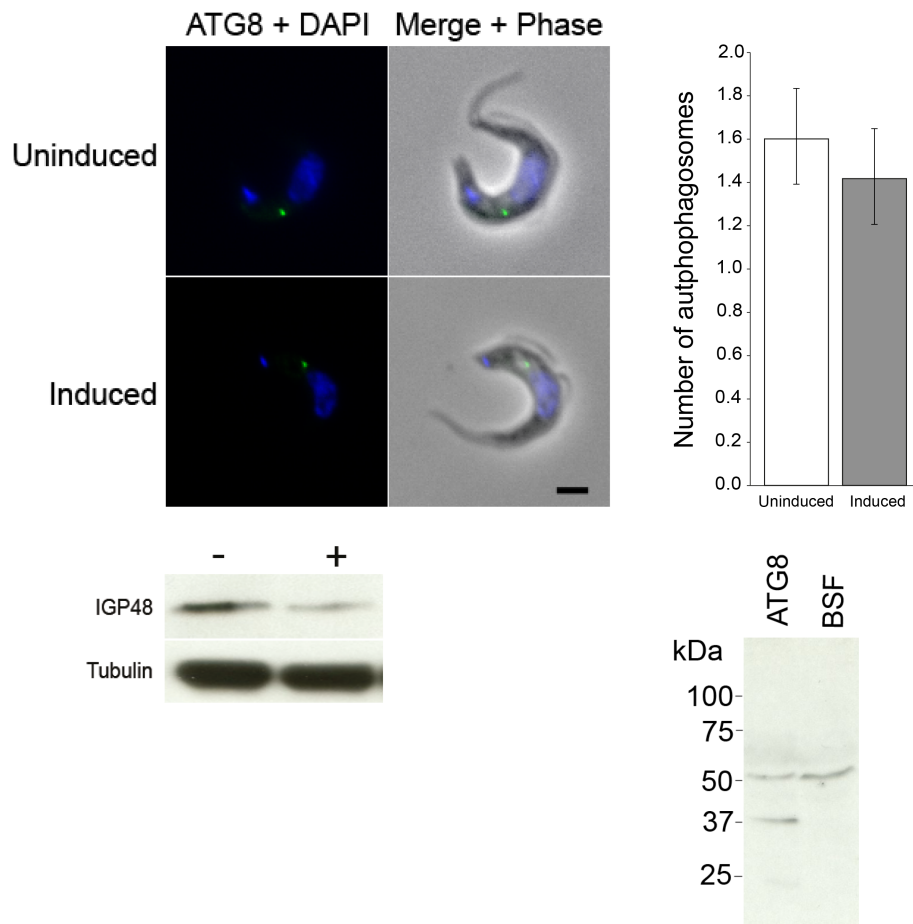




Table S1

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 <sub>2</sub> H:FP	CTCGAAA <b>AAGCTT</b> ATGGAAATCCGCATGGTGCCA	HindIII	-
IGP48-CO <sub>2</sub> H:RP (HA)	TGCTAT <b>CCCGGG</b> TCAGCGTAATCTGGAACATCGTATGGGTACTCATCAGCTGCTGGAGT	SmaI	HA
IGP48-CO <sub>2</sub> H:RP (FLAG)	AGCCAT <b>GGATCCT</b> CACTTGTTCGTCATCGTCTTTGTAGTCTCATCAGCTGCTGGAGTTTC	BamHI	FLAG
IGP48-65:RP	ACTATCAAAGTCGGCACCACCGCCACTTCCCTC	-	-
48-ISG65:FP	GGCGGTGGTGCCGACTTTGATAGTCTCCTAGAT	-	-
ISG65:RP	GCCAC <b>CCCGGG</b> TCAGCGTAATCTGGAACATCGTATGGGTACTACTTTTACGCTAGA	SmaI	HA
BiP-IGP48:FP	GCGGCC <b>GCTAGC</b> AGTAATGAAGCATCAGATAAG	NheI	-
BiP-IGP48:RP	TGCCTT <b>GAATTC</b> CACTCATCAGCTGCTGG	EcoRI	-
IGP40-CO <sub>2</sub> H:FP	GCTAT <b>GAAGCTT</b> ATGAGCATGGACACCCGT	HindIII	-
IGP40-CO <sub>2</sub> H:RP	ACTGCAC <b>CCCGGG</b> TTAAGCGTAATCTGGAACATCGTATGGGTATTCACTGGTTCTCATTG	SmaI	HA
IGP40-65: RP	ACTATCAAAGTCGTGCCAATTACTTCTCTTTC	-	-
40-ISG65:FP	AGTAATTGGCACGACTTTGATAGTCTCCTAGAT	-	-
BiP-IGP40:FP	GCAGAT <b>GCTAGC</b> GAAGTACCGGAACCAACTGTG	NheI	-
BiP-IGP40:RP	GACCTA <b>GAATTC</b> TATTCACTGGTTCTCATTG	EcoRI	-
dCLECT:FP	TCTATT <b>GCTAGC</b> CCAACCTCCGCTTCCACCTGCT	NheI	-
dCLECT:RP	TGCCTT <b>GAATTC</b> CACTCATCAGCTGCTGG	EcoRI	-
dTRIM:FP	ATCGTC <b>GAATTC</b> GTGCCATCTACAGCTTCCGAT	EcoRI	-
dTRIM:RP	GTACAT <b>GAATTC</b> AGCAGGTGGAAGCGGAGTTGG	EcoRI	-
Supplementary Table S1			

Table S2

<b>Accession Number</b>	<b>Description</b>	<b>Accession Number</b>
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
<b>Accession Number</b>	<b>Description</b>	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	<b>Accession Number</b>
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	
Tb11.02.0780	Singleton	
Tb09.211.4770	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	
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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	

<b>Description</b>	<b>Accession Number</b>	<b>Description</b>
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		
	<b>Accession Number</b>	<b>Description</b>
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
<b>Description</b>	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.