

Supplementary information for

Berriman *et al.*, The genome of the African trypanosome, *Trypanosoma brucei*

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Additional Material:

HGTTrees.pdf is a searchable PDF of all phylogenetic trees described in Table S11

Materials and Methods

Sequencing

The methodology for preparation of *Trypanosoma brucei* strain TREU (Trypanosomiasis Research Edinburgh University) 927/4 (GPAL/KE/70/EATRO 1534) single VAT derivative GUTat 10.1 stocks, DNA library construction and sequencing have been described elsewhere (1, 2). The two sequencing centres employed different sequencing strategies. Chromosome 1 and 9-11 were sequenced at the WTSI, using a whole chromosome shotgun approach (1). For the latter, chromosomal homologues were assembled into haploid consensus sequences annotated with polymorphisms where found. However, in Tb, homologous chromosome pairs are known to vary in size (3) and individual homologues of chromosome 1 and 9 could be partially separated and isolated from pulsed-field gels, increasing the proportion of DNA of that homologue in the shotgun-sequencing library. Chromosomes 2-8 were sequenced at TIGR using a BAC walking approach (2), whereby overlapping 85-170 kb BAC clones were mapped to individual chromosomes and ‘shotgun’ sequenced. Consequently, the sequences of chromosomes 2-8 also represent a ‘mosaic’ assembly of both chromosomal homologues. Due to under-representation in the BAC library, not all telomeres were sequenced. In one instance however (left hand end of chromosome 8), the sequence of two BACs representing the two homologues could be assembled separately. Optical (D Schwartz, unpublished) and genetic (4) maps were used to order and orientate contiguous sequences (contigs) during gap closure.

The sequence analysis published here constitutes release 4 of the *T. brucei* genome accessible via the curated genome database GeneDB (<http://www.genedb.org>) and the following FTP sites: ftp://ftp.tigr.org/pub/data/Eukaryotic_Projects/t_brucei and ftp://ftp.sanger.ac.uk/pub/databases/T.brucei_sequences. Chromosomes 1 – 10 were assembled into

single pseudomolecules while chromosome 11 is presented as 3 scaffolds of known order (Table S1). Where appropriate, the gaps between consecutive contigs within scaffolds are represented as strings of 100 letter Ns in the sequence. With some exceptions, the assembled pseudomolecules end in the subtelomeric region (Table S1). As the optical maps generated for each chromosome represent a mixture of both homologues, comparisons between the subtelomeric sequences with the respective optical maps provided little indication as to the distance from the telomeric hexamer repeat due to variations between homologues in this region.

Annotation

Putative protein coding regions (>30 codons) were predicted by combining the output of the gene finding algorithm Glimmer (5) with similarity data and manual annotation of open reading frames as described previously (1, 2). This annotation included the assignment of Gene Ontology (GO) terms (6). Further refinement of gene models (additions, deletions and alterations to boundary coordinates) were done manually based on detailed comparisons with the *T. cruzi* and *L. major* genomes (see Tritryp comparative paper). Genes on finished chromosomes were assigned systematic identifiers according to the scheme described previously (2). Genes on chr3-8 were also assigned a secondary systematic name based on the chromosome and the BAC from which they originated (e.g. Tb03.27F10.410). Genes on unfinished chromosomes were given temporary identifiers. The analysis presented here does not include short predicted coding sequences (less than 150 codons) with no additional evidence of coding potential, these ‘unlikely coding sequences’ are included in the available annotation with the following product line ‘hypothetical protein, unlikely’.

To limit annotation discrepancies between the two centres, common standards for the annotation were defined. Gene products were assigned a putative function when they shared significant similarity with experimentally characterised gene products or when they contained functionally known protein domains. Remaining gene products were labelled either “hypothetical protein”, or

“hypothetical protein, conserved” in the case of products showing significant similarity with proteins or domains of unknown function from other organisms. In addition, the same 100 kb contig from chromosome 10 was annotated at WTSI and TIGR to standardise annotation criteria.

To enable both centres to annotate as well as analyse the whole *T. brucei* genome, sequence data and annotation were regularly exchanged. Both in-house databases, TGAD (<http://www.tigr.org/tdb/e2k1/tba1/tba1.shtml>) at TIGR and GeneDB (<http://www.genedb.org>) at WTSI, were synchronised by transferring and comparing data in an XML format (<ftp://ftp.tigr.org/pub/data/DTDs/tigrxml.dtd>). Comparisons included changes to gene attributes, such as gene product names, as well as the addition and deletion of genes, and changes to coordinates. Annotation updates committed by one centre as well as conflicting annotations were identified using custom Perl scripts and a purpose-written MySQL relational database. Updates at both TIGR and WTSI were performed automatically with conflicts subsequently resolved manually, as a collaborative exercise between both centres.

Protein-coding genes were clustered into gene families using TRIBE-MCL (7) with an inflation value parameter of 4. An E-value of 1e-15 was used as a BLASTP cut-off to generate the families shown in Tables S2.

Analysis

VSG analysis

Putative *VSG*s were identified by similarity searches using the TBLASTX algorithm (8) against the UniProt protein database (9). Putative *VSG* genes were checked for presence of a predicted signal peptide using the SignalP2.0 prediction tool (10) and of a GPI anchor signal sequence by similarity with conserved *VSG* GPI signal sequences (11) as well as using two GPI signal prediction programs, big-PI predictor (12) and DGPI (http://129.194.185.165/dgpi/DGPI_demo_en.html). The domain composition of each putative *VSG* was established by the presence and spacing of cysteine residues

and according to the domain type to which it best aligned to, taking account of gaps where appropriate (11, 13). Where applicable, the boundary between the two N and C terminal domain was set at 50 amino acids upstream of the first conserved cysteine in the C terminal domain.

Putative *VSG* genes/proteins were classified into 4 categories: (1) Putative full-length coding sequences, with signal peptide and GPI signal both predicted to be functional and bearing an intact cysteine pattern. (2) Atypical *VSG* genes, full-length coding sequences that have diverged from the expressed *VSG* consensus sequence (with respect to signal peptide, GPI signal, or cysteine pattern). (3) Pseudogenes, defined as genes with frameshifts, stop codons or incomplete sequences. (4) *VSG*-related proteins were defined by their inclusion into a distinct cluster in a multiple alignment [using ClustalW (<http://www.ebi.ac.uk/clustalw>)] against characterised *VSG*s.

76-bp repeat sequences were manually annotated based on the published consensus sequence (14). The ~29-bp-long GC-rich subtelomeric element (15) was mapped similarly, using a consensus sequence generated from sequences available in public databases using the MEME software (16).

Trafficking & Cytoskeleton

To identify potential components of the cytoskeleton as well as the trafficking pathways, the annotation of the *Trityp* genomes was searched in GeneDB using keywords. In addition, the *Trityp* genomes were queried (using BLASTP, TBLASTN) (8) against a reference set of proteins from the yeasts (*S. cerevisiae*, *S. pombe*), humans, plants (*A. thaliana*) and other organisms for which a complete or near complete genome sequence (e.g. *P. falciparum*, *C. parvum*, *G. lamblia*, *E. cuniculi*) was available. This was complemented by Pfam searches for domains characteristic of cytoskeletal proteins (<http://www.sanger.ac.uk/Software/Pfam/>). From this starting set, unlikely members (including fragments and predicted proteins lacking essential domains) were removed. Multiple alignments of predicted protein sequence were created using the ClustalX software

(<http://www.ebi.ac.uk/clustalw>) followed by manual adjustment (see Table S6 for the reference set detailing cytoskeletal proteins).

To confirm or refute orthology of proteins involved in trafficking, the sequences of putative Tritryp homologues were in turn searched against the non-redundant database at NCBI (<http://www.ncbi.nlm.nih.gov/BLAST/>) or alternatively, the yeast, human or other selected completed genomes as appropriate. In addition to similarity searches, protein sequences were analysed for the presence of defining domains (presence of the WDTAQ box and a (mostly) C terminal prenylation motifs in the case of Rab proteins, and N-terminal acylation signals in the case of ARFs). Classification of Tritryp Rab proteins were made in comparison to a previously described reference set (17). Phylogenetic analyses of proteins involved in trafficking and the cytoskeleton were carried out using the maximum-parsimony schema PAUP 4.0 (<http://paup.csit.fsu.edu>) using a distance algorithm and Neighbour Joining method and, where appropriate, data were subjected to bootstrapping analyses.

Transporter

The entire Tritryp predicted gene complement (37,332 CDS) were assessed by similarity searches (BLASTP) (8) against transporter components lodged in the TCDB database (<http://tcdb.ucsd.edu/index.php>). All proteins in the TCDB database have been annotated with an International Union of Biochemistry and Molecular Biology number (IUBMB, <http://www.chem.qmul.ac.uk/iubmb/>) approved classification system for membrane transport proteins: the Transporter Classification (TC) system. Tritryp proteins were classified transitively from the respective TCDB protein, and hence TC, exhibiting the highest BLASTP similarity. A maximum E-value cut-off of 1e-05 was applied.

Metabolism

To reconstruct metabolic pathways, each predicted coding sequence was automatically associated with GO terms using the GOtcha program (18). Predicted GO annotations with a P-score in excess of 50% and GO annotations manually curated from the scientific literature were converted to the EC number classification of enzyme-catalysed reactions (International Union of Biochemistry and Molecular Biology, www.chem.qmul.ac.uk/iubmb/enzyme/), using EC number-GO term mapping provided by the Gene Ontology Consortium (www.geneontology.org). This analysis was performed for all three genomes and the EC numbers mapped to metabolic pathway diagrams from the Kyoto Encyclopaedia of Genes and Genomes (www.genome.jp/kegg/). The diagrams were coloured to indicate, for each enzyme, the predicted likelihood of it being present in each organism. This facilitated a rapid assessment of the metabolic pathways, the supporting evidence for each assignment being reached by clicking through the relevant metabolic map to obtain the candidate gene lists and provide hyperlinks to each gene's annotation in GeneDB. Ambiguous hits were reassessed manually by detailed examination of BLASTP similarity search results against the non-redundant protein database at NCBI.

Phylogenetic trees for detecting prokaryote to eukaryote HGT

The trees included as supplementary information are consensus Bayesian trees generated using the following approach.

A crude BLAST based screen was performed to prepare a list of candidates cases of horizontal transfer from prokaryotes. BLASTP 2.0 was used to search each gene against the non-redundant Uniprot database. Genes with a greater top BLAST score to a prokaryotic than to a eukaryote were subjected to a phylogenetic analysis.

For each candidate HGT identified we searched all available databases, including those based upon EST surveys, to maximize sampling - particularly for eukaryotic sequences. Sequences from Blast searches were included in alignments if they showed at least 40% similarity over >70 and <200% of

the length of the query sequence. The recovered sequences were aligned as proteins using ClustalW followed by manual inspection to remove positions of uncertain alignment and gap regions. Each edited alignment was analyzed by MrBayes (19) using the WAG matrix, a gamma correction for site rate variation and a proportion (pinvar) of invariant sites. The analyses were run for 600,000 generations and sampled every 100 generations, with the first 2000 samples (33%) discarded as a conservative burn-in. A consensus tree was made from the remaining samples. Because posterior probabilities, the support values used by Bayesian analysis to indicate confidence in groups, have been criticized (20), we also use bootstrapping to provide an additional indication of support for relationships. Each data set was bootstrapped (100 replicates) and used to make distance matrices under the same evolutionary model as in the Bayesian analysis, using custom (P4) software (p.foster@nhm.ac.uk). Trees were made from the distance matrices using FastME (21) and a bootstrap consensus tree made using P4.

Interpretation of trees and support values

Posterior probabilities and bootstrap support values (PP/BS) are given on the Bayesian consensus trees, an asterisk following a BS value is given when the relationship was not recovered in the distance bootstrap consensus tree but appeared in some bootstrap replicates, no BS value means that the relationship did not appear among the bootstrap replicates.

Figure legends of supplementary information

Fig. S1. Homology-based dendrogram of VSG proteins, colour-coded by the array in which they are localised. Colours are entirely randomly mixed, indicating a lack of conservation between VSGs of the same array

Fig. S2. Differences between the two chromosomal homologues at the left hand of chromosome 8.

The grey bars represent the forward and reverse strands of BAC 27P2 (top) and the left hand end of the assembled chromosome 8 (bottom). The coloured boxes denote annotated gene models. The red lines between the sequences represent 6 frame translated DNA versus 6 frame translated DNA similarities (TBLASTX matches, HSP overlap 150 nt, Score 150, Id 50%) between the two sequences.

Fig. S3. Phylogenetic reconstruction of the ARF subfamily of small GTPases in the Trityps.

Low sequence conservation between the trypanosome and higher eukaryote ARF family results in poor segregation by local alignment. Hence a large tree consisting of all ARF and ARL family sequences from Tb, Tc and Lm, together with sequences of ARF1-6 and ARL1-8 from mammals was used to identify the ARF and ARL families in the trypanosome genomes (data not shown). These sequences were then used to build a limited tree containing only the ARF family. Note that the mammalian and kinetoplastid sequences fully segregate, indicating that the last common ancestor has a single ARF. Note also the presence of several nodes that contain multiple copies of near or fully identical ORFs (highlighted in red). Phylogenetic reconstruction was performed by alignment of retrieved ARF sequences from GeneDB using ClustalX and default parameters, followed by trimming of sequences with abnormal N or C –terminal extensions. The tree was built with PAUP 4.0* using the distance algorithm and Neighbour Joining routine and was subjected to 1000 bootstraps. *; branches supported by bootstrap values <75%. Overall, the reconstruction is highly robust. Sequences in the phylogenetic analyses were: human ARF1 (P32889), human ARF3 (P16587), human ARF4 (P18085), human ARF5 (P26437), human AFR6 (P26438) and bovine ARF2 (P84081).

Fig. S4. Phylogenetic tree-based evidenced for horizontal transfer of genes for haem biosynthesis in *L. major*.

(a) coproporphyrinogen III oxidase, (b) protoporphyrinogen IX oxidase, (c) ferrochelatase.

Fig. S5. Phylogenetic evidence for horizontal transfer of 2-aminoethylphosphonate:pyruvate aminotransferase

References for supplementary material

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Figure S1

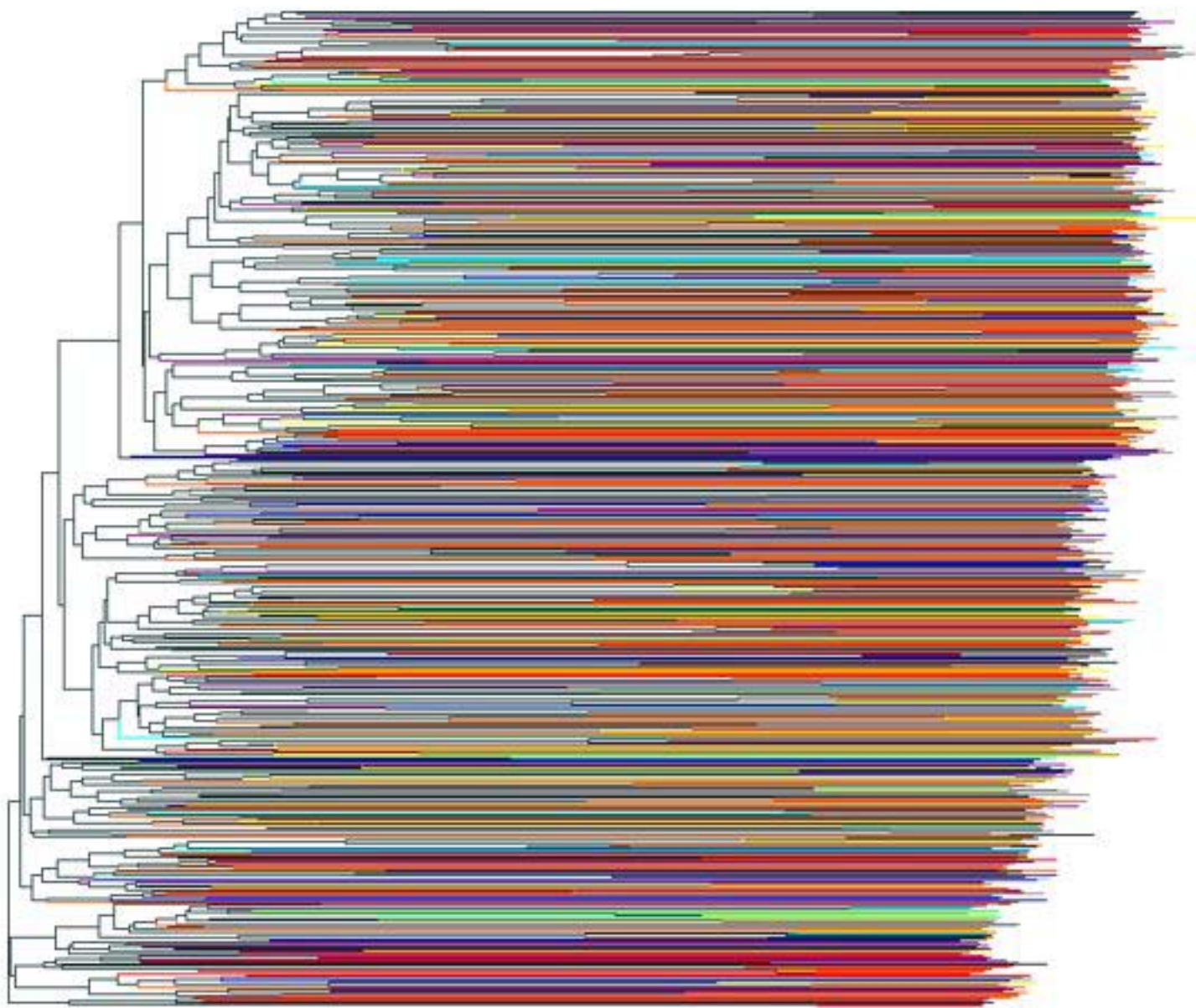


Figure S2

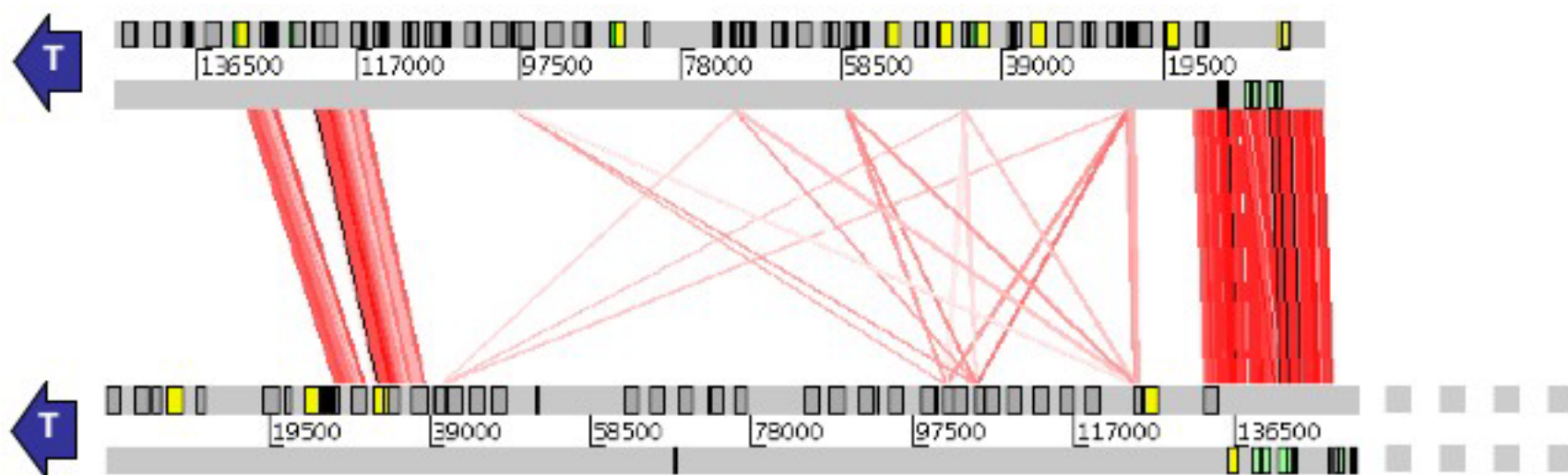


Figure S3

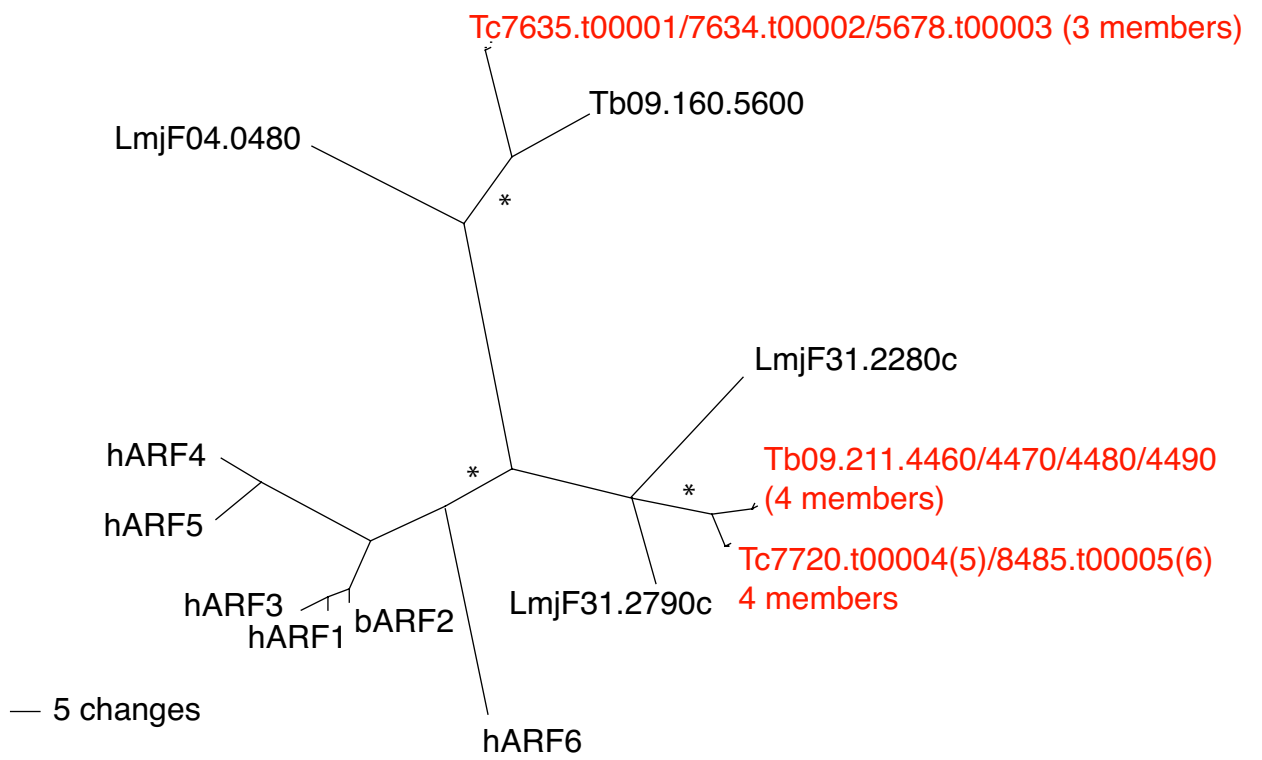


Figure S4B

LM0208

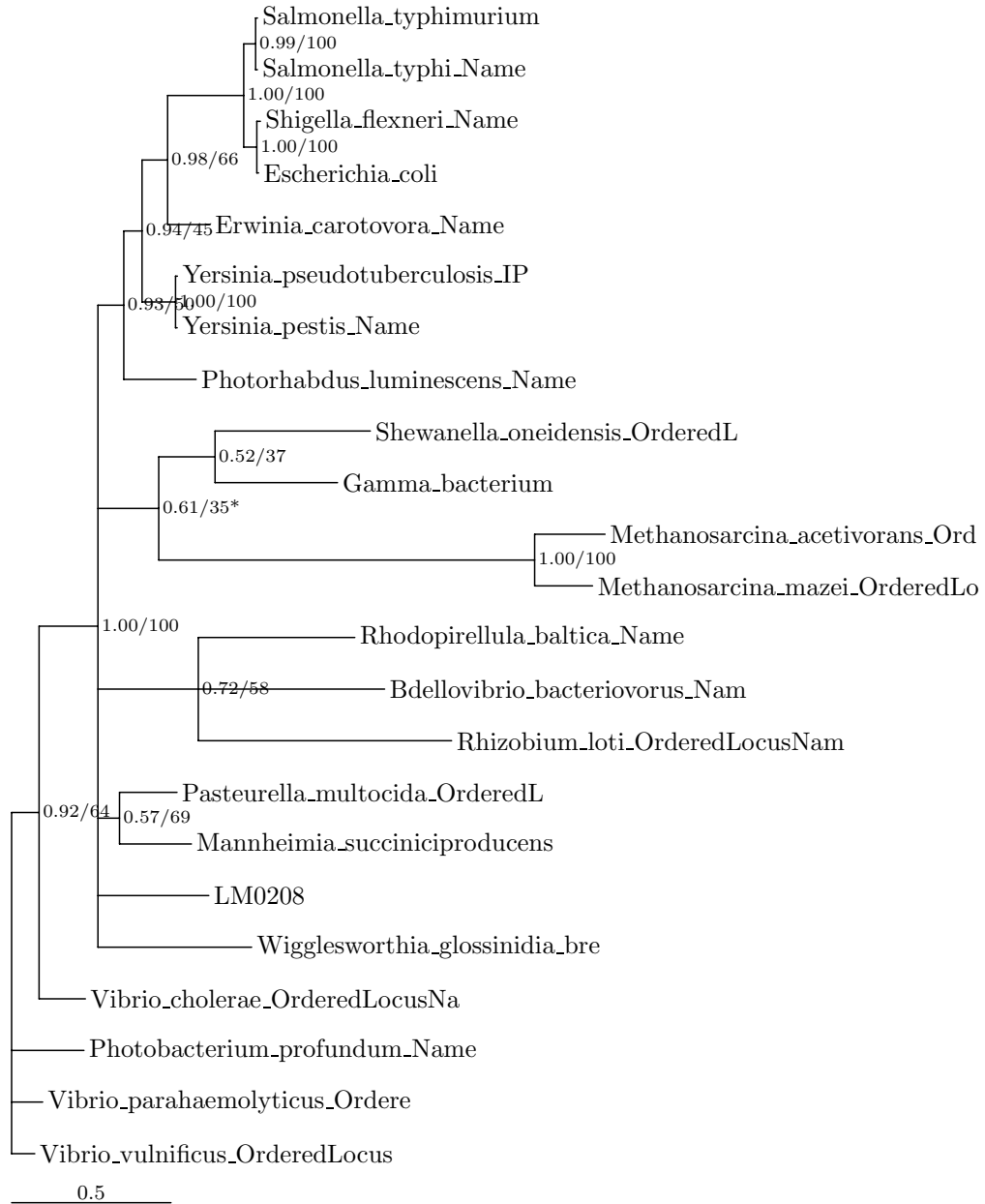


Figure S4C

LM0165

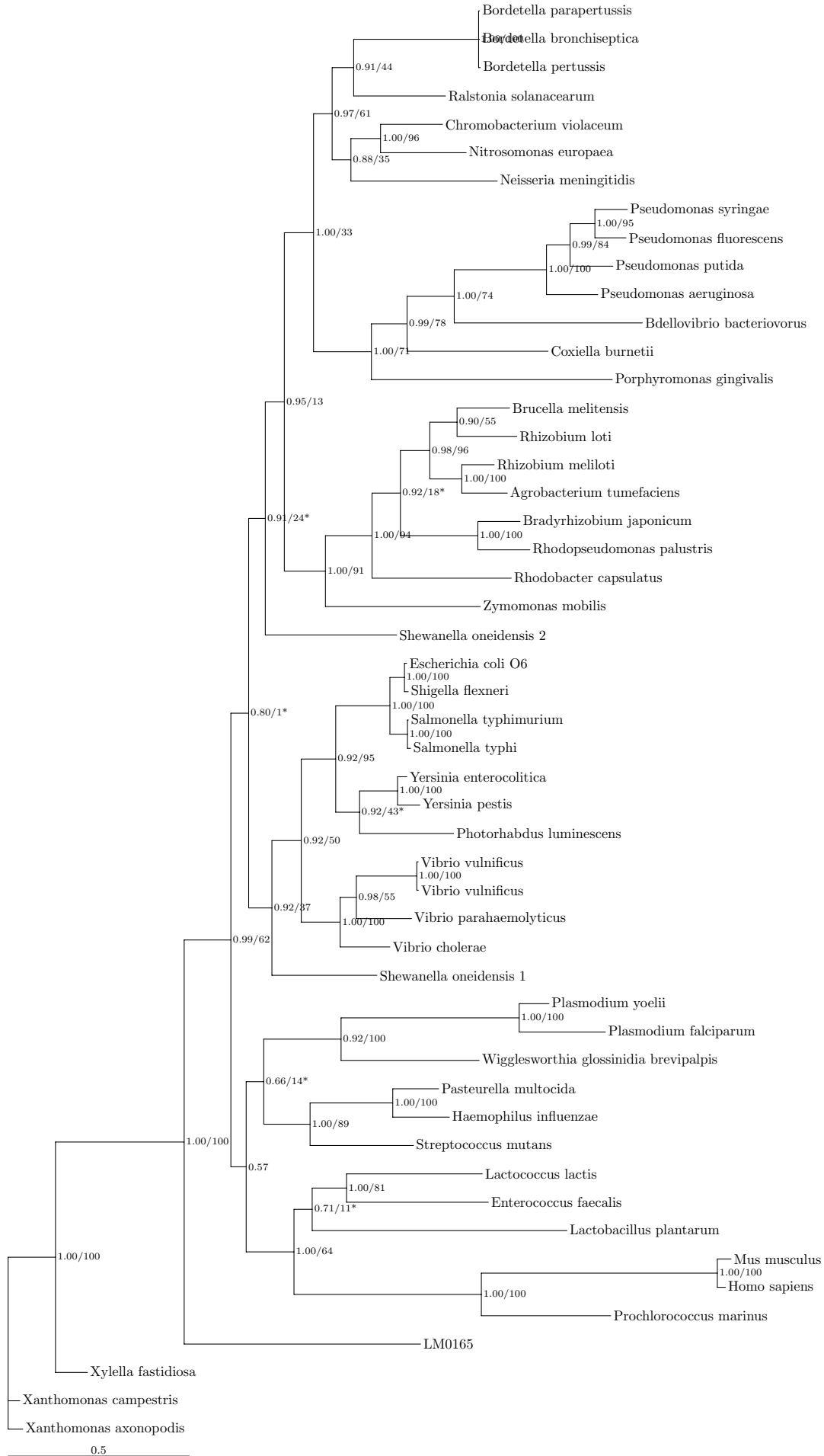
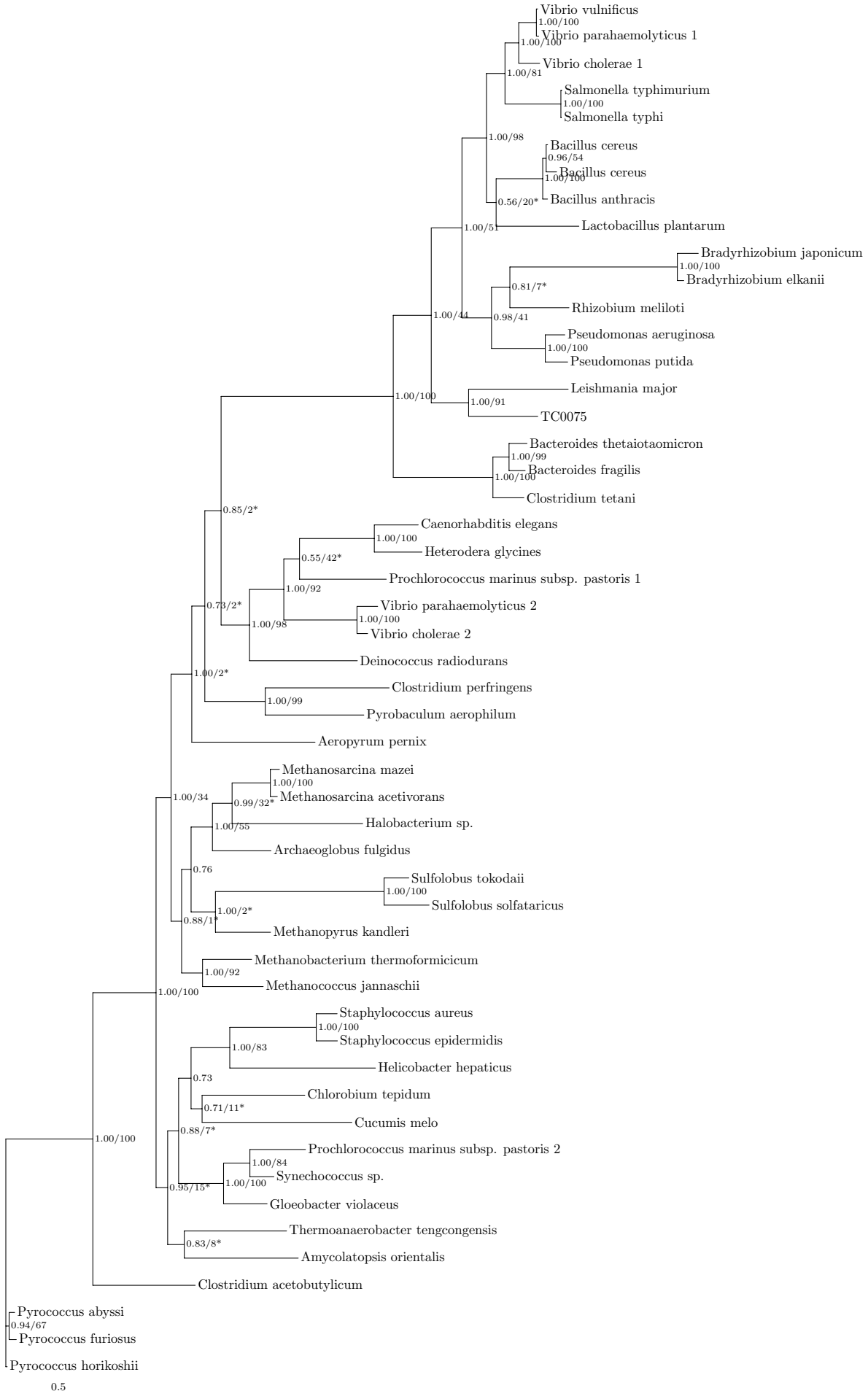


Figure S5

TC0075



Supplementary Table S1.

Sequence status of the *T. brucei* megabase chromosomes

Chromosome	Sequence gaps	Physical gaps	Sequence	at ends of pseudomolecules
1	2	0	left right	telomeric hexamer repeats ¹ telomeric hexamer repeats 29-bp repeats ²
2	0	2	left right	
3	0	2	left right	
4	0	2	left right	
5	0	2	left right	
6	0	2	left right	
7	0	2	left right	
8	0	2	left right	
9	2	2	left right	~70-bp repeat arrays ³
10	1	0	left right	telomeric hexamer repeats GUTat 10.1 VSG donor copy ⁴ telomeric hexamer repeats
11	24 ⁵	3	left right	telomeric hexamer repeats metacyclic expression site ⁶ 29-bp repeats

¹ TTAGGG

² previously described [R. F. Aline, Jr., K. Stuart, *Exp Parasitol* **68**, 57 (Jan, 1989)]

³ previously described [R. Aline, Jr. *et al.*, *Nucleic Acids Res* **13**, 3161 (May 10, 1985)]

⁴ previously described [D. J. LaCount *et al.*, *Nucleic Acids Res* **29**, 2012 (May 15, 2001)]

⁵ Chromosome assembled into 3 ordered scaffolds, where scaffold 1 is linked to scaffold 2 by genetic marker and scaffold 2 is in turn linked to scaffold 3 by genetic marker.

⁶ personal communication: Dave Barry, University of Glasgow, UK.

Sequence gaps are defined as gaps spanned by paired reads from either a sequencing clone, originating from a small (2-4kb) insert library, or a BAC clone (insert size 20-25kb or 50-120kb). The gap between consecutive contigs has been arbitrarily set to 100 bases (represented as "n"s in the sequence). In instances where scaffolds are linked by genetic markers (McLeod *et al.* unpublished), this has been defined as physical gaps. Physical gaps have also been included where pseudomolecule sequence assembly does not extend to recognisable telomeric sequences.

The sequence at the ends of the pseudomolecules was analysed for repeats as described in the Materials and Methods. 'Left' refers to the left hand end of the respective chromosome, whilst 'right' refers to the right hand end. Where left blank, pseudomolecule assemblies end in the subtelomeric region but not in recognisable repeats.

1. R. F. Aline, Jr., K. Stuart, *Exp Parasitol* **68**, 57 (Jan, 1989).
2. R. Aline, Jr. *et al.*, *Nucleic Acids Res* **13**, 3161 (May 10, 1985).
3. D. J. LaCount *et al.*, *Nucleic Acids Res* **29**, 2012 (May 15, 2001).

Supplementary Table S5 Complete list of proteins discussed in the trafficking section

Adaptin complexes

Gene product	<i>T.brucei</i>	<i>L.major</i>	<i>T.cruzi</i>
AP-1			
Beta AP1/2 ^a	Tb10.6k15.2500	LmjF36.6770	Tc00.1047053506247.200
Gamma	Tb04.5E12.910	LmjF34.3970	Tc00.1047053508257.260
Mu1	Tb07.13M20.120	LmjF22.1140	Tc00.1047053511821.30
Sigma1	Tb03.28C22.160	LmjF29.1440	Tc00.1047053509623.19
AP-2			
Beta 1/2 ^a	-	LmjF11.0990	Tc00.1047053506297.180
Alpha	-	LmjF07.0050	Tc00.1047053511391.140
Mu2	-	LmjF36.3030	Tc00.1047053509715.20
Sigma2	-	LmjF34.2330	Tc00.1047053506559.330
AP-3			
Beta3	Tb11.01.2420	LmjF36.5260	Tc00.1047053506673.60
Delta	Tb05.6E7.370	LmjF08.0090	Tc00.1047053507811.20
Mu3	Tb04.29M18.670	LmjF34.2590	Tc00.1047053510877.50
Sigma3	Tb08.30K1.560	LmjF24.1540	Tc00.1047053509243.50
AP-4			
Beta4	Tb10.6k15.1180	-	Tc00.1047053504137.60
Epsilon	Tb06.5F5.640	-	Tc00.1047053511751.200
Mu4	Tb08.10K10.770	pseudogene	Tc00.1047053505073.30
Sigma4	Tb10.61.2530	pseudogene	Tc00.1047053511283.109

Rab GTPases

Gene product	<i>T.brucei</i>	<i>L.major</i>	<i>T.cruzi</i>
Rab1a	Tb08.12O16.530	LmjF27.0760	Tc00.1047053503715.30
Rab1b	Tb09.244.2070		
Rab2	Tb11.01.6890	LmjF32.2030	Tc00.1047053506425.169 Tc00.1047053503897.4 Tc00.1047053511711.80
Rab4	Tb11.01.5320	LmjF32.0490	Tc00.1047053510911.30
Rab5a	Tb10.389.0550	LmjF18.1130	Tc00.1047053509805.60 Tc00.1047053511269.4
Rab5b	Tb11.02.2160	LmjF13.0220	Tc00.1047053506227.180
Rab6	Tb927.2.2130	LmjF02.0260	Tc00.1047053510077.40 Tc00.1047053505037.50
Rab7	Tb09.211.2330	LmjF18.0890	Tc00.1047053508461.270
Rab11a	Tb08.29H22.590	LmjF10.0910	Tc00.1047053506151.30 Tc00.1047053511407.60
Rab14	-	LmjF07.0560	Tc00.1047053504741.240 Tc00.1047053511621.120
Rab18	Tb08.4A8.450	LmjF33.1840	Tc00.1047053508837.74 Tc00.1047053508963.20
Rab21	Tb10.70.6420	LmjF21.0790	Tc00.1047053506977.130 Tc00.1047053509247.20
Rab23	Tb10.6k15.1990	LmjF36.6250	Tc00.1047053506355.60 Tc00.1047053511043.20

Rab28	Tb06.5F5.770	LmjF30.1710	Tc00.1047053507023.110 Tc00.1047053511751.130
Rab32	-	-	Tc00.1047053506289.80
X1	Tb08.4A8.220	LmjF10.1160	Tc00.1047053503689.4
X2	Tb08.4A8.230	LmjF10.1170	Tc00.1047053503689.10 Tc00.1047053509573.10
X3	Tb11.01.6670	LmjF32.1840	Tc00.1047053508445.10

Cytosolic coat proteins (COPs)

Gene product	<i>T.brucei</i>	<i>L.major</i>	<i>T.cruzi</i>
emp47	-	-	-
emp24	Tb09.244.2760 Tb11.01.6880 Tb04.1D20.110	LmjF35.1850 LmjF32.2020 LmjF36.2150	Tc00.1047053510765.30 Tc00.1047053509671.90 Tc00.1047053511711.90 Tc00.1047053503987.10

COPII

Sec13	Tb10.61.2630	LmjF32.0050	Tc00.1047053506525.20
Sec23	Tb10.6k15.2840	LmjF36.6430	Tc00.1.47053506249.20
Sec24	Tb03.1J15.730 Tb03.5L5.630	LmjF25.1340 LmjF29.0220	Tc00.1047053509453.70 Tc00.1047053508409.130
Sec31	Tb11.02.4040	LmjF11.1160	Tc00.1047053506297.290

COPI

alpha	Tb04.5D20.570	LmjF34.4310	Tc00.1047053510689.10
beta	Tb927.1.2570	LmjF20.1350	Tc00.1047053506563.30
beta'	Tb927.2.6050	LmjF33.3210	Tc00.1047053506815.30
delta	Tb08.5H5.420	LmjF16.1180	Tc00.1047053511217.140
epsilon	Tb11.01.6530	LmjF32.1730	Tc00.1047053504217.10
gamma	Tb11.01.3740	LmjF28.2620	Tc00.1047053511211.20
zeta	Tb10.70.2980	LmjF35.0110	Tc00.1047053506295.90

ADP ribosylation factors (Arfs)

Gene product	<i>T.brucei</i>	<i>L.major</i>	<i>T.cruzi</i>
	Tb09.160.5600	LmjF04.0480	Tc00.1047053508199.10 Tc00.1047053434945.4 Tc00.1047053509297.30 Tc00.1047053508197.20
	Tb09.211.4460 Tb09.211.4470 Tb09.211.4480 Tb09.211.4490	LmjF31.2790	Tc00.1047053508415.40 Tc00.1047053508415.40 Tc00.1047053510755.50 Tc00.1047053510755.60
	-	LmjF31.2280	-
	Tb10.70.1880	LmjF36.0820	Tc00.1047053506009.100 Tc00.1047053510297.100

Arf-like proteins (Arls)

Gene product	<i>T.brucei</i>	<i>L.major</i>	<i>T.cruzi</i>
ARL1	Tb07.2F2.550	LmjF17.0070	Tc00.1047053508919.60 Tc00.1047053506513.60
ARL1B	Tb09.160.5300	LmjF04.0340	Tc00.1047053506627.60

ARL2 ^c			
ARL3	Tb10.6k15.1960	LmjF29.0880 LmjF36.6230	Tc00.1047053504433.10 Tc00.1047053507951.170
ARL3B	Tb06.4F7.880	LmjF30.2370	Tc00.1047053511511.170 Tc00.1047053506941.170
ARL4 ^c			
ARL5 ^c			
ARL6	Tb10.70.3000 Tb08.5H5.790	LmjF16.1380 LmjF35.0130	Tc00.1047053508961.4 Tc00.1047053508839.60 Tc00.1047053506295.80 Tc00.1047053511469.24
ARL7 ^c			
	Tb05.26C7.80	LmjF05.0030	Tc00.1047053509539.50 Tc00.1047053419417.4

^a AP1 and AP2 beta chains are indistinguishable using phylogenetics

^b Tb06.5F5.640 has a probable N-terminal extension:

MQGLIVVTTV SHLFIAISHE REISFSNFFF FIEITGGHLC VTA

^c forms too divergent in Tritryps to be assigned

Colour scheme:

	absent in the Tritryps
	present in Lm, Tb, Tc
	only present in Lm
	only present in Tb
	only present in Tc
	only present in Lm, Tb
	only present in Lm, Tc
	only present in Tb, Tc

Table S6. Coatomer and adaptin family representation in the Kinetoplastida, metazoans and fungi.

Functional assignments based on work in metazoan and yeast systems. Not all of these functions are likely to be represented in the Kinetoplastida.

Note that the adaptins, coatomers and other classes described here, with the exception of COP II, are all considered to have a common evolutionary origin (Boehm and Bonifacino 2001). ‘+’ indicates the presence of at least one copy of a given orthologue in the species, while ‘-’ indicates its absence.

S.c., *Saccharomyces cerevisiae*; *H.s.*, *Homo sapiens*

Complex	Known or proposed function(s)	<i>T.b</i>	<i>T.c</i>	<i>L.m</i>	<i>S.c</i>	<i>H.s</i>
AP-1	Sorting at the <i>trans</i> -Golgi network (TGN)	+	+	+	+	+
AP-2	Endocytic vesicle assembly at the plasma membrane	-	+	+	+	+
AP-3	Sorting from early endosomes to later organelles in secretory pathway	+	+	+	+	+
AP-4	Targeting proteins from the TGN to basolateral plasma membrane	+	+	-	-	+
COP I	Intra-Golgi and post-Golgi transport. Retrograde transport.	+	+	+	+	+
GGA	Targeting proteins from the TGN to the lysosome and other destinations	-	-	-	+	+
Stonin	Endocytosis; interaction with AP-complexes	-	-	-	-	+
COP II	Exit from the ER, ER to Golgi transport.	+	+	+	+	+

Table S7. Rab family GTPase representation in Kinetoplastida, Apicomplexa, fungi and metazoans.

The Rab nomenclature is based on previous reports {Ackers, in press #418}, {Pereira-Leal, 2000 #421}. The functional assignments are based on work in metazoan and yeast systems, as well as direct analysis of members of the *T. brucei* and *L. major* Rab families. ‘+’ indicates the presence of at least one copy of a given orthologue in the species, while ‘-’ indicates its absence. For the Kinetoplastida, the number in parenthesis specifies the number of isoforms. (*P.f.*, *Plasmodium falciparum*; *S.c.*, *Saccharomyces cerevisiae*; *H.s.*, *Homo sapiens*).

Rab	Known or proposed function(s) ¹	<i>T.b</i>	<i>T.c</i>	<i>L.m</i>	<i>P.f</i>	<i>S.c</i>	<i>H.s</i>
1	ER to Golgi transport, intra-Golgi transport	+(2)	+	+	+	+	+
2	ER to Golgi transport, intra-Golgi transport	+	+	+	+	-	+
4	Rapid recycling and lysosomal targeting	+	+	+	-	-	+
5	Endocytosis	+(2)	+(2)	+(2)	+	+	+
6	Retrograde transport through the Golgi stack	+	+	+	+	-	+
7	Late endosome and lysosomal delivery	+	+	+	+	+	+
11	Recycling of plasma membrane components	+	+	+	+	+	+
18	Golgi localized, probable role in exocytosis	+	+	+	+	-	+
14	Transport from the Golgi to endosomes	-	+	+	-	-	+
21	Not known	+	+	+	-	-	+
23	Endosomal function (metazoans); nuclear function (tryps)	+	+	+	-	-	+
28	Not known – possibly similar to Rab23	+	+	+	-	-	+
32	mitochondrial anchoring of PKA and mitochondrial dynamics, possible role in melanocyte biogenesis.	-	+	-	-	-	+
X1	Not known – ER localised	+	+	+	-	-	-
X2	Not known – Golgi localised	+	+	+	-	-	-
X3	Not known	+	+	+	-	-	-

Supplementary Table S8.
Complete list of proteins discussed in the cytoskeleton section.

Actin-based cytoskeleton

Gene product	<i>T.brucei</i>	<i>L.major</i>	<i>T.cruzi</i>
Actin	Tb09.211.0620	LmjF04.1230	Tc00.1047053510571.30

G-actin binding

ADF/cofilin	Tb03.5L5.210	LmjF29.0510	Tc00.1047053508411.10
profilin	Tb11.01.5350	LmjF32.0520	Tc00.1047053458759.10
twinfilin	Tb04.1H19.700	LmjF34.2290	Tc00.1047053506559.300
CAP/Srv2p	Tb10.6k15.1160	LmjF36.5590	Tc00.1047053504137.80 Tc00.1047053509799.30
thymosin	-	-	-

ARP2/3 complex

ARP2	Tb10.61.0500	LmjF19.1200	Tc00.1047053511361.40 Tc00.1047053508899.110
ARP3	Tb09.160.3850	LmjF15.1360	Tc00.1047053508277.260 Tc00.1047053503913.20
ARPC1	Tb10.389.0270	LmjF18.0920	Tc00.1047053511275.30 Tc00.1047053504215.40
ARPC2	Tb08.29h22.800	LmjF10.1000	Tc00.1047053509569.90 Tc00.1047053506865.10
ARPC3	Tb10.70.2680	-	Tc00.1047053508625.30 Tc00.1047053510963.70
ARPC4	Tb927.2.2900	LmjF02.0600	Tc00.1047053508737.194 Tc00.1047053509127.104
ARPC5	Tb10.406.0320	-	Tc00.1047053511635.30

Other nucleators of F-actin

Formins	Tb05.3C6.300	LmjF17.0930	Tc00.1047053511313.30 Tc00.1047053511755.80
	Tb11.02.3470	LmjF24.1110	Tc00.1047053508641.320 Tc00.1047053506203.80

Activators of ARP2/3 complex

WASP/Scar	-	-	-
verprolin/Vrp1p	-	-	-
Las17p/Bee1p	-	-	-
EPS15/Pan1p	-	-	-
End3p	-	-	-
Sla1p	-	-	-
ABP1	-	-	-
ActA	-	-	-

Dynactin complex

ARP1	-	-	-
dynactin1/p150(glued)	-	-	-
dynactin2	-	-	-
dynactin3	-	-	-
dynactin4	-	-	-
dynactin6	-	-	-

F-actin capping

CapZ-alpha	-	-	Tc00.1047053506181.90 Tc00.1047053506177.120
CapZ-beta	-	-	Tc00.1047053506363.60

F-actin bundling/cross-linking/severing

gelsolin	-	-	-
fimbrin	-	-	-
villin	-	-	-
alpha-actinin	-	-	-
plastin	-	-	-
spectrin	-	-	-
filamin	-	-	-

Intermediate filament-based cytoskeleton

Gene product	<i>T.brucei</i>	<i>L.major</i>	<i>T.cruzi</i>
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Lamins

laminA/C	-	-	-
laminB1	-	-	-
keratin, typeI	-	-	-
keratin, typeII	-	-	-
vimentin	-	-	-
nestin	-	-	-

Septins

Spn1-7	-	-	-
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Classical cadherins

catenin	-	-	-
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Desmosomal

desmocollin1	-	-	-
demoglein1	-	-	-
desmoplakin	-	-	-
plakoglobin	-	-	-
plakophilin1	-	-	-

Hemidesmosomal

integrin-alpha	-	-	-
integrin-beta	-	-	-
collagen	-	-	-
BPA1 precursor	-	-	-
plectin1	-	-	-

Tubulin-based cytoskeleton

Gene product	<i>T.brucei</i>	<i>L.major</i>	<i>T.cruzi</i>
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Tubulin

alpha tubulin (* = array not fully resolved)	Tb927.1.2340/360/ 380/400*	LmjF13.0280/9 0/300/310/320/ 330/340/350/3 60/370/380/39 0	Tc00.1047053411235.9*
beta tubulin (* = array not fully resolved)	Tb927.1.2330/50/7 0/90*	LmjF33.0804 LmjF08.1230 LmjF21.1860	Tc00.1047053506563.40* Tc00.1047053509003.70*

		LmjF33.0792/9 4/96/98/800/80 2/806/808/810/ 812/814/816/8 18/819/820	
delta tubulin	Tb11.01.2695	LmjF36.4990	Tc00.1047053503969.10 Tc00.1047053506807.10
epsilon tubulin	Tb10.70.6950	LmjF21.1010	Tc00.1047053509967.160 Tc00.1047053509695.120
zeta tubulin	Tb927.1.1150	LmjF20.0470	Tc00.1047053511423.90 Tc00.1047053507949.110

Tubulin sequestering

stathmin	-	-	-
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Microtubule nucleation

gamma-tubulin	Tb03.27F10.510	LmjF25.0960	Tc00.1047053511867.190
GCP2/Spc97p	Tb10.6k15.0540	LmjF36.4390	Tc00.1047053504147.170
GCP3/Spc98p	Tb11.01.3150	LmjF28.2760	Tc00.1047053511211.150
GCP4	-	-	-
GCP5	-	-	-
GCP6	-	-	-

Microtubule minus-end organisation

centrins	Tb04.1H19.410	LmjF34.2390	Tc00.1047053506559.380
	Tb11.01.5470	LmjF32.0660	Tc00.1047053509161.40
	Tb10.6k15.1830	LmjF36.6110	Tc00.1047053503797.20
	Tb08.29O4.130	LmjF07.0710	Tc00.1047053503727.10 Tc00.1047053506401.90
	Tb07.28B13.660	LmjF22.1410	Tc00.1047053511825.40/50 Tc00.1047053508323.60/70
pericentrin	-	-	-
LIP1	-	-	-
LIP8	-	-	-
Spc72p	-	-	-
Spc42p	-	-	-
Spc29p	-	-	-
Kar1p	-	-	-

Microtubule capping

EB1/Bim1p	Tb09.160.1440	-	Tc00.1047053508347.30 Tc00.1047053506145.20
CLIP170/Tip1p	-	-	-
APC	-	-	-
Tea1p	-	-	-

Microtubule severing

katanin p60	Tb11.01.0200	LmjF28.0400	Tc00.1047053508821.10 Tc00.1047053506163.80
	Tb10.70.6880	LmjF13.096	Tc00.1047053509695.50 Tc00.1047053509967.70
katanin p80	Tb09.211.1500	LmjF35.4670	Tc00.1047053510731.40 Tc00.1047053506887.50

Microtubule decoration

TOG/MOR1/MAP215/Dis1p	Tb06.5F5.840	LmjF30.1760	Tc00.1047053511751.70 Tc00.1047053507023.160
Asp	Tb10.70.7180	LmjF21.1110	Tc00.1047053511131.30 Tc00.1047053506855.360
MAST/CLASPs	-	-	-
MAP1-6	-	-	-
tau	-	-	-

Flagellar

PF16/SPAG6	Tb927.1.2670	LmjF20.1400	Tc00.1047053509005.10 Tc00.1047053510955.40
PF20	Tb10.61.2920	LmjF18.0470	Tc00.1047053511277.340
DIP13	Tb10.61.2720	LmjF34.4540	Tc00.1047053511281.56 Tc00.1047053507993.369
LF4	Tb09.211.0960	LmjF35.5010	Tc00.1047053506885.120
RIB43	Tb08.4A8.250	LmjF10.1190	Tc00.1047053509573.30 Tc00.1047053503689.30
RIB72	Tb10.6k15.2920	LmjF36.6380	Tc00.1047053508231.180 Tc00.1047053506251.10
RSP4	Tb11.02.2060	LmjF13.0430	Tc00.1047053504001.3 Tc00.1047053504089.50
ODA1	Tb11.01.7750	LmjF32.2900	Tc00.1047053508707.170 Tc00.1047053509073.40
MBO2	Tb11.01.2670	LmjF36.5020	Tc00.1047053509825.20 Tc00.1047053510425.10 Tc00.1047053510423.70
tektin	-	-	-

Inner kinetochore

CENP-A	-	-	-
CENP-B	-	-	-
CENP-C	-	-	-
CENP-G	-	-	-
Mis12	-	-	-
Cbf1p	-	-	-
cyclinA/Skp1p	Tb11.02.3990	LmjF11.1210	Tc00.1047053508041.10 Tc00.1047053506297.350
Cep3p	-	-	-
Ndc10	-	-	-
Ctf13p	-	-	-

Outer kinetochore

CENP-E	-	-	-
CENP-F	-	-	-
HEC1/Ndc80	-	-	-
Nuf2	-	-	-
Spc25	-	-	-
Spc24	-	-	-
TOG/MOR1/MAP215/Dis1p	Tb06.5F5.840	LmjF30.1760	Tc00.1047053511751.70 Tc00.1047053507023.160
Mif2p	-	-	-
Ctf19p	-	-	-
Mcm21p	-	-	-
Okp1p	-	-	-
Slk19p	-	-	-
Mtw1p	-	-	-
Tid3p	-	-	-
Dam1p	-	-	-
Stu2p	-	-	-
Bik1p	-	-	-

Spindle checkpoint

BUB1	-	-	-
BUB3	-	-	-
Mad1p	-	-	-
Mad2p	Tb03.30P12.370	LmjF25.1670	Tc00.1047053510421.290

			Tc00.1047053510091.40
Mad3p	-	-	-
ZW10	-	-	-

Motor families

Family/clade	<i>T.brucei</i>	<i>L.major</i>	<i>T.cruzi</i>
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Myosins

MyoI	Tb04.26G5.60	LmjF34.1000	Tc00.1047053507739.110
Kinetoplastid-specific Myo2	Tb11.01.7990	LmjF32.3870	Tc00.1047053511527.70
	-	-	Tc00.1047053511649.80
	-	-	Tc00.1047053507811.120
	-	-	Tc00.1047053506779.190
	-	-	Tc00.1047053511151.100
	-	-	Tc00.1047053504867.120
	-	-	Tc00.1047053503847.20
	-	-	Tc00.1047053504103.30
	-	-	Tc00.1047053510943.190
	-	-	Tc00.1047053509663.10
	-	-	Tc00.1047053507093.210

Dyneins

Cytoplasmic dynein HC	Tb07.13M20.140	LmjF22.1110	Tc00.1047053510533.10 Tc00.1047053511821.10
CHE3 dynein	Tb11.02.0030	LmjF27.1750	Tc00.1047053504153.90
	Tb04.5D20.720	LmjF34.4160	-
ODA4 dynein	Tb11.02.0760	LmjF13.1650	Tc00.1047053509585.10
ODA2 dynein	Tb03.27F10.490	LmjF25.0980	-
IDA1alpha dynein	Tb04.5E12.710	LmjF34.3880	Tc00.1047053508257.170
IDA1beta dynein	Tb08.28L1.260	LmjF23.1310	-
other axonemal dynein	Tb11.01.3010	LmjF28.2880	Tc00.1047053506937.40 Tc00.1047053510437.10
	Tb07.29K4.310	LmjF26.1020	Tc00.1047053508879.30
	Tb11.01.0390	LmjF28.0610	-
	Tb10.70.1720	LmjF36.0950	Tc00.1047053506679.110
	Tb927.2.5270	LmjF27.2590	Tc00.1047053506347.10 Tc00.1047053505231.10
	-	LmjF14.1060	-

Kinesins

Kinesin-1/conventional KHC	Tb927.1.1350	LmjF20.0640	Tc00.1047053506479.60
Kinesin-2/KRP85/95	Tb05.1P6.90	LmjF17.0800	-
	Tb11.01.5490	LmjF32.0680	Tc00.1047053509161.30
Kinesin-3/Unc104/Kif1	Tb11.02.0090	LmjF33.2560	Tc00.1047053504153.150
	-	LmjF34.4260	-
Kinesin-4/Chromokinesin/Kif4	-	-	-
Kinesin-5/BimC/Eg5	-	-	-
Kinesin-6/MKLP1	-	-	-
Kinesin-7/CENP-E	-	-	-
Kinesin-8/Kip3	-	-	-
Kinesin-9/Kif9	Tb03.30P12.1000	LmjF25.1970	Tc00.1047053504047.40
	Tb07.21H15.40	LmjF05.0630	Tc00.1047053500611.30
	Tb07.2F2.620	LmjF17.0160	Tc00.1047053508917.30
Kinesin-10/Kid	-	-	-
Kinesin-11/Smy1p/Vab8	-	-	-

Kinesin-12/Kif15	-	-	-
Kinesin-13/MCAK/Kif2	Tb09.211.1400	LmjF35.4700	Tc00.1047053506885.450
	Tb11.02.2260	LmjF13.0130	-
	Tb04.1D20.830	LmjF31.0290	Tc00.1047053508921.30
	Tb11.02.2970	LmjF24.0640	Tc00.1047053504125.60
	Tb09.160.2260	LmjF01.0030	Tc00.1047053508501.290
	Tb11.02.0790	LmjF13.1610	Tc00.1047053509589.30
Kinesin-14/C-terminal	Tb10.61.1750	LmjF19.0260	Tc00.1047053508899.140
	Tb11.01.0850	LmjF28.1850	Tc00.1047053500901.50
Kinetoplastid-specific K39 clade	Tb08.26A17.630	LmjF23.0560	Tc00.1047053504427.260
	Tb07.13M20.410	LmjF22.0960	Tc00.1047053501817.220
	Tb08.4A8.660	LmjF16.1470	Tc00.1047053501215.70
	Tb03.48K5.730	LmjF29.0970	Tc00.1047053506485.40
	Tb07.6C8.180	LmjF14.1100/10/20	Tc00.1047053501253.20
	Tb07.5F10.480	LmjF14.0810	-
	Tb03.3K10.480/90	LmjF29.2380/90	Tc00.1047053500323.120
Other/ungrouped	Tb05.3C6.520	LmjF17.1110	Tc00.1047053501307.10
	Tb04.2H8.1400	LmjF34.1540	Tc00.1047053506635.120
	Tb07.26A24.300	LmjF06.0180	Tc00.1047053508579.30
	Tb11.01.3990	LmjF09.0120	Tc00.1047053501127.60
	Tb07.10C21.350	LmjF06.1030	Tc00.1047053507559.50
	Tb11.02.4260	LmjF33.2140	-
	Tb11.02.0400	LmjF11.0870	Tc00.1047053500101.280
	Tb06.26G9.930	LmjF30.3060	Tc00.1047053509167.180
	Tb06.28P18.680	LmjF30.0350	Tc00.1047053501491.60
	Tb08.30K1.750	LmjF24.1430	Tc00.1047053507991.50
	Tb06.5F5.490	LmjF30.1450	Tc00.1047053507021.50
	Tb09.244.2560	LmjF35.2090	Tc00.1047053500769.130
	Tb08.4A8.540	LmjF16.1580	Tc00.1047053501383.20
	Tb10.389.1270	LmjF18.1600	Tc00.1047053507625.180
	-	LmjF09.0290	Tc00.1047053501127.200
	Tb10.389.1210	LmjF18.1530	-
	Tb03.30P12.970	LmjF25.1950	Tc00.1047053504047.30
	Tb10.70.6990	LmjF21.1040	Tc00.1047053509695.150
	Tb07.21H15.240	LmjF05.0760	Tc00.1047053500613.20
	Tb10.61.1020	LmjF19.0680/90	Tc00.1047053506503.90
	Tb10.61.0990	LmjF19.0700	Tc00.1047053506503.80
	-	LmjF13.0700	-
	Tb10.70.7260	-	-
	-	-	Tc00.1047053501385.80
	-	LmjF22.0560	Tc00.1047053509207.150

Colour scheme:

	absent in the Tritryps
	present in Lm, Tb, Tc
	only present in Lm
	only present in Tb
	only present in Tc
	only present in Lm, Tb
	only present in Lm, Tc

Bill Wickstead (bill.wickstead@pathology.oxford.ac.uk), University of Oxford
Keith Gull (keith.gull@pathology.oxford.ac.uk), University of Oxford
Christiane Hertz-Fowler (chf@sanger.ac.uk), Wellcome Trust Sanger Institute

	only present in Tb, Tc
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Supplementary Table S9.
Tritryp transporters.

The entire Tritryp predicted gene complement (37,332 CDS) were assessed by similarity searches (BLASTP) against transporter components lodged in the TCDB database (<http://tcdb.ucsd.edu/index.php>). All proteins in the TCDB database have been annotated with an IUBMB approved classification system for membrane transport proteins: the Transporter Classification (TC) system.

Tritryp proteins were classified transitively from the TCDB protein, and hence TC, exhibiting the highest BLASTP similarity. A maximum E-value cut-off of 1e-05 was applied.

TCDB class	Lm	Tb	Tc
<u>1.A.1.10.1</u>			
	-	-	Tc00.1047053504105.130
<u>1.A.1.11.3</u>			
	LmjF17.1440 LmjF34.0480	Tb10.70.4750	-
<u>1.A.1.15.2</u>			
	LmjF14.0530	-	Tc00.1047053506661.140 Tc00.1047053511245.24
<u>1.A.1.15.3</u>			
	LmjF14.0530	-	Tc00.1047053506661.140 Tc00.1047053511245.24
<u>1.A.1.15.4</u>			
	LmjF14.0530 LmjF14.0540	-	Tc00.1047053506661.140 Tc00.1047053511245.24
<u>1.A.1.16.2</u>			
	LmjF14.0530 LmjF14.0540	-	Tc00.1047053506661.130 Tc00.1047053506661.140 Tc00.1047053511245.24 Tc00.1047053511245.30
<u>1.A.1.2.3</u>			
	-	Tb10.61.0090	Tc00.1047053507213.30 Tc00.1047053511301.140
<u>1.A.1.4.1</u>			
	LmjF26.0310	-	Tc00.1047053508207.230 Tc00.1047053509509.30
<u>1.A.1.4.2</u>			
	-	-	Tc00.1047053504013.60 Tc00.1047053510879.50
<u>1.A.1.5.1</u>			

	<u>LmjF32.3970</u>	-	-
<u>1.A.1.5.3</u>			
	-	<u>Tb10.61.0620</u>	<u>Tc00.1047053508903.110</u>
<u>1.A.1.6.1</u>			
	-	<u>Tb09.160.3380</u>	<u>Tc00.1047053510155.210</u> <u>Tc00.1047053511585.220</u>
<u>1.A.11.2.2</u>			
	<u>LmjF01.0180</u>	-	<u>Tc00.1047053504797.140</u> <u>Tc00.1047053511577.4</u>
<u>1.A.11.3.1</u>			
	-	-	<u>Tc00.1047053509647.90</u>
<u>1.A.11.3.2</u>			
	<u>LmjF04.1000</u> <u>LmjF32.3370</u> <u>LmjF33.1060</u>	<u>Tb09.211.0430</u> <u>Tb10.26.0220</u> <u>Tb11.01.8420</u>	<u>Tc00.1047053507089.200</u> <u>Tc00.1047053510243.100</u> <u>Tc00.1047053510575.130</u> <u>Tc00.1047053511027.10</u>
<u>1.A.20.1.2</u>			
	<u>LmjF30.1610</u>	<u>Tb11.02.1990</u>	-
<u>1.A.20.1.3</u>			
	-	-	<u>Tc00.1047053506179.10</u> <u>Tc00.1047053507665.30</u>
<u>1.A.20.2.1</u>			
	<u>LmjF09.0910</u> <u>LmjF09.0920</u> <u>LmjF09.0930</u> <u>LmjF21.1630</u>	<u>Tb10.70.7970</u> <u>Tb11.01.4621</u> <u>Tb11.01.4622</u> <u>Tb11.01.4623</u> <u>Tb11.01.4624</u>	<u>Tc00.1047053504035.130</u> <u>Tc00.1047053506391.10</u> <u>Tc00.1047053506391.20</u> <u>Tc00.1047053506869.50</u> <u>Tc00.1047053506963.90</u> <u>Tc00.1047053507483.39</u> <u>Tc00.1047053507483.50</u> <u>Tc00.1047053507991.70</u> <u>Tc00.1047053510519.60</u>
<u>1.A.20.4.1</u>			
	<u>LmjF30.1610</u>	<u>Tb11.02.1990</u>	-
<u>1.A.23.1.1</u>			
	<u>LmjF31.0230</u>	<u>Tb09.160.0520</u> <u>Tb11.01.2670</u>	<u>Tc00.1047053506147.100</u>
<u>1.A.23.1.2</u>			
	<u>LmjF22.1370</u> <u>LmjF35.0180</u>	<u>Tb04.1D20.400</u> <u>Tb05.6E7.590</u> <u>Tb08.4A8.660</u> <u>Tb11.01.1300</u>	<u>Tc00.1047053503479.40</u> <u>Tc00.1047053503925.70</u> <u>Tc00.1047053506355.80</u> <u>Tc00.1047053506559.559</u> <u>Tc00.1047053506775.60</u>

			<u>Tc00.1047053510349.40</u> <u>Tc00.1047053511167.110</u>
<u>1.A.23.2.1</u>			
	-	<u>Tb10.6k15.1400</u>	-
<u>1.A.3.1.1</u>			
	<u>LmjF16.0280</u> <u>LmjF36.6340</u>	<u>Tb10.6k15.2090</u> <u>Tb11.02.0880</u>	<u>Tc00.1047053507099.40</u> <u>Tc00.1047053508231.60</u>
<u>1.A.3.2.1</u>			
	-	<u>Tb08.26A17.880</u>	<u>Tc00.1047053509461.90</u> <u>Tc00.1047053510507.60</u>
<u>1.A.33.1.1</u>			
	<u>LmjF28.1200</u> <u>LmjF28.2820</u> <u>LmjF29.1240</u>	<u>Tb10.61.2390</u> <u>Tb11.02.5450</u> <u>Tb11.02.5500</u>	<u>Tc00.1047053506585.40</u> <u>Tc00.1047053508813.15</u> <u>Tc00.1047053509543.50</u> <u>Tc00.1047053510437.79</u> <u>Tc00.1047053511211.220</u>
<u>1.A.33.1.2</u>			
	<u>LmjF30.2460</u> <u>LmjF30.2470</u> <u>LmjF30.2480</u> <u>LmjF30.2490</u> <u>LmjF30.2550</u>	<u>Tb06.4F7.670</u> <u>Tb06.4F7.740</u> <u>Tb06.4F7.750</u> <u>Tb07.29K4.60</u>	<u>Tc00.1047053432677.20</u> <u>Tc00.1047053503899.10</u> <u>Tc00.1047053506729.9</u> <u>Tc00.1047053506941.280</u> <u>Tc00.1047053507029.30</u> <u>Tc00.1047053507513.50</u> <u>Tc00.1047053511517.5</u> <u>Tc00.1047053511745.10</u>
<u>1.A.33.1.3</u>			
	<u>LmjF18.1370</u> <u>LmjF26.1240</u> <u>LmjF28.2770</u> <u>LmjF28.2780</u> <u>LmjF35.4710</u>	<u>Tb07.29K4.620</u> <u>Tb09.160.3090</u> <u>Tb09.211.1390</u> <u>Tb10.389.0880</u> <u>Tb11.01.3080</u> <u>Tb11.01.3110</u>	<u>Tc00.1047053418069.10</u> <u>Tc00.1047053503721.39</u> <u>Tc00.1047053506135.9</u> <u>Tc00.1047053506885.440</u> <u>Tc00.1047053507831.60</u> <u>Tc00.1047053508457.20</u> <u>Tc00.1047053510155.70</u> <u>Tc00.1047053510439.10</u> <u>Tc00.1047053510439.61</u> <u>Tc00.1047053511211.160</u> <u>Tc00.1047053511211.170</u> <u>Tc00.1047053511257.10</u> <u>Tc00.1047053511263.9</u> <u>Tc00.1047053511585.70</u>
<u>1.A.35.3.1</u>			
	<u>LmjF15.1310</u>	<u>Tb09.160.3990</u>	<u>Tc00.1047053506445.30</u> <u>Tc00.1047053508277.350</u>
<u>1.A.4.1.1</u>			

		<u>Tb07.5F10.460</u>	Tc00.1047053506269.99 Tc00.1047053506291.10 Tc00.1047053507905.39 Tc00.1047053507959.110 Tc00.1047053508433.180 Tc00.1047053508831.150 Tc00.1047053510013.310 Tc00.1047053510989.60 Tc00.1047053511183.280 Tc00.1047053511245.210 Tc00.1047053511603.380 Tc00.1047053511605.80 Tc00.1047053511613.110 Tc00.1047053511671.50
<u>1.A.4.5.6</u>			
	<u>LmjF36.4550</u>	-	-
<u>1.A.4.5.8</u>			
	LmjF25.0680 LmjF36.4540 LmjF36.4700	Tb04.3M17.320 Tb08.10K10.110	Tc00.1047053509011.100 Tc00.1047053510681.20
<u>1.A.4.6.1</u>			
	-	<u>Tb09.244.2600</u>	-
<u>1.A.4.6.2</u>			
	LmjF04.0520 LmjF28.0680	-	-
<u>1.A.4.7.1</u>			
	LmjF05.0640 LmjF11.0690 LmjF25.0930 LmjF28.2050 LmjF29.1100 LmjF34.3560	Tb03.48O8.70 Tb07.21H15.60 Tb07.27M11.980 Tb08.26E13.490 Tb09.160.5650 Tb10.61.0580 Tb11.01.0440 Tb11.01.6010	Tc00.1047053476733.10 Tc00.1047053503865.50 Tc00.1047053504033.220 Tc00.1047053506241.124 Tc00.1047053506825.90 Tc00.1047053506833.9 Tc00.1047053507763.10 Tc00.1047053508153.950 Tc00.1047053508199.50 Tc00.1047053508693.180 Tc00.1047053508815.120 Tc00.1047053508899.20 Tc00.1047053509805.30 Tc00.1047053510103.17 Tc00.1047053510769.80 Tc00.1047053511269.30 Tc00.1047053511867.160
<u>1.A.4.7.2</u>			
	LmjF03.0480 LmjF03.0800	Tb03.48K5.840 Tb04.5E12.250	Tc00.1047053503453.90 Tc00.1047053503557.20

	LmjF19.1130 LmjF24.0140 LmjF29.0570 LmjF30.3260 LmjF33.0140 LmjF34.4280 LmjF35.2040 LmjF35.2670	Tb06.26G9.420 Tb09.211.3970 Tb10.61.0950 Tb10.70.2480 Tb10.70.3990 Tb11.02.2520	Tc00.1047053503891.80 Tc00.1047053506649.10 Tc00.1047053506793.20 Tc00.1047053506959.74 Tc00.1047053507001.30 Tc00.1047053507669.160 Tc00.1047053508181.20 Tc00.1047053509489.10 Tc00.1047053509877.40 Tc00.1047053509995.20 Tc00.1047053510287.50 Tc00.1047053510575.10 Tc00.1047053510611.40 Tc00.1047053511725.40 Tc00.1047053511731.40
1.A.44.1.1			
	LmjF36.5340	Tb04.29M18.750 Tb10.70.5385 Tb11.01.2530	Tc00.1047053508323.20 Tc00.1047053511557.50
1.A.6.2.2			
	LmjF05.1040 LmjF35.0070	Tb05.29K2.700	Tc00.1047053506591.30 Tc00.1047053506989.220 Tc00.1047053508397.30 Tc00.1047053509885.30
1.A.8.12.1			
	LmjF22.1420 LmjF32.2370 LmjF32.2380	-	Tc00.1047053504159.40 Tc00.1047053504159.50 Tc00.1047053506821.170 Tc00.1047053506821.180 Tc00.1047053508323.80 Tc00.1047053511825.60
1.A.8.13.2			
	LmjF34.3850	-	Tc00.1047053508257.140
1.A.8.9.1			
	-	Tb06.28P18.240 Tb10.61.2650	-
1.A.8.9.2			
	LmjF31.0020	Tb10.61.2640	-
1.B.12.2.2			
	-	Tb06.28P18.620 Tb07.15M23.170 Tb07.15M23.180 Tb11.01.2885	Tc00.1047053507429.70 Tc00.1047053509481.10 Tc00.1047053511671.60
1.C.1.2.1			

	<u>LmjF17.0800</u>	<u>Tb05.1P6.90</u>	<u>Tc00.1047053503939.130</u> <u>Tc00.1047053504835.29</u> <u>Tc00.1047053507933.10</u> <u>Tc00.1047053510351.110</u> <u>Tc00.1047053511743.20</u>
<u>1.C.1.2.2</u>			
	<u>LmjF23.0080</u> <u>LmjF35.1240</u> <u>LmjF36.5020</u>	<u>Tb07.6C8.180</u> <u>Tb08.11J15.740</u> <u>Tb08.29O4.360</u> <u>Tb10.70.4130</u>	<u>Tc00.1047053507949.150</u> <u>Tc00.1047053509805.70</u> <u>Tc00.1047053511423.50</u>
<u>1.C.1.2.3</u>			
	<u>LmjF16.1460</u>	<u>Tb05.26C7.90</u> <u>Tb05.5K5.160</u> <u>Tb11.01.5490</u> <u>Tb927.2.4810</u>	<u>Tc00.1047053506885.330</u> <u>Tc00.1047053507103.29</u> <u>Tc00.1047053507649.50</u> <u>Tc00.1047053508179.30</u> <u>Tc00.1047053508965.90</u>
<u>1.C.12.1.3</u>			
	-	-	<u>Tc00.1047053401569.10</u> <u>Tc00.1047053508343.10</u> <u>Tc00.1047053508831.140</u> <u>Tc00.1047053509495.30</u> <u>Tc00.1047053510787.10</u>
<u>1.C.36.3.1</u>			
	<u>LmjF14.1110</u>	-	-
<u>1.C.63.1.1</u>			
	<u>LmjF18.1100</u>	<u>Tb10.389.0520</u>	<u>Tc00.1047053510265.90</u> <u>Tc00.1047053510311.20</u>
<u>2.A.1.1.16</u>			
	<u>LmjF33.0290</u>	-	-
<u>2.A.1.1.17</u>			
	<u>LmjF36.6280</u> <u>LmjF36.6290</u> <u>LmjF36.6300</u>	<u>Tb04.1H19.570</u> <u>Tb10.6k15.2020</u> <u>Tb10.6k15.2030</u> <u>Tb10.6k15.2040</u>	<u>Tc00.1047053424937.10</u> <u>Tc00.1047053506355.10</u> <u>Tc00.1047053506355.5</u> <u>Tc00.1047053508231.9</u> <u>Tc00.1047053508551.30</u> <u>Tc00.1047053508551.39</u> <u>Tc00.1047053511041.40</u>
<u>2.A.1.1.20</u>			
	<u>LmjF24.0680</u>	<u>Tb11.02.3020</u>	<u>Tc00.1047053505183.130</u>
<u>2.A.1.1.30</u>			
	<u>LmjF22.1050</u>	-	-
<u>2.A.1.13.3</u>			
	-	<u>Tb927.1.750</u>	<u>Tc00.1047053508397.70</u>

			Tc00.1047053509885.70
2.A.1.15.1			
	-	-	Tc00.1047053510531.50
2.A.1.15.2			
	-	Tb11.02.5200	-
2.A.1.15.5			
	-	Tb07.13M20.210	Tc00.1047053511819.10
2.A.1.2.20			
	-	-	Tc00.1047053508465.40 Tc00.1047053510659.20
2.A.1.2.4			
	LmjF35.2780 LmjF35.2810 LmjF35.2820	Tb09.211.3870	Tc00.1047053507001.100 Tc00.1047053508465.100 Tc00.1047053508465.30 Tc00.1047053510659.28
2.A.1.2.8			
	LmjF09.0270	-	-
2.A.1.27.1			
	-	Tb10.389.1870	Tc00.1047053506567.34 Tc00.1047053507049.30
2.A.1.28.1			
	LmjF03.0410 LmjF17.1430 LmjF20.0350 LmjF21.0080	Tb10.70.4090	Tc00.1047053503505.20 Tc00.1047053506669.4 Tc00.1047053508059.10 Tc00.1047053508953.10 Tc00.1047053510309.20 Tc00.1047053511421.210
2.A.1.3.16			
	-	-	Tc00.1047053506369.20 Tc00.1047053510225.59
2.A.1.3.4			
	-	-	Tc00.1047053506947.50 Tc00.1047053507057.60
2.A.1.4.6			
	-	-	Tc00.1047053510661.100 Tc00.1047053510741.170
2.A.1.42.2			
	-	-	Tc00.1047053504177.10
2.A.1.8.11			
	-	-	Tc00.1047053506779.90 Tc00.1047053511153.110

<u>2.A.17.2.1</u>			
	<u>LmjF33.0710</u>	-	-
<u>2.A.17.3.2</u>			
	-	-	<u>Tc00.1047053506577.60</u>
<u>2.A.17.4.1</u>			
	-	-	<u>Tc00.1047053507709.60</u>
<u>2.A.18.6.1</u>			
	<u>LmjF07.1160</u> <u>LmjF27.0670</u> <u>LmjF27.0680</u> <u>LmjF27.1580</u> <u>LmjF31.0320</u> <u>LmjF31.0330</u> <u>LmjF31.0340</u> <u>LmjF31.0350</u> <u>LmjF31.0570</u> <u>LmjF31.0870</u> <u>LmjF31.0880</u> <u>LmjF31.1790</u> <u>LmjF31.1800</u> <u>LmjF31.1820</u> <u>LmjF35.5360</u> <u>LmjF36.6830</u>	<u>Tb04.1D20.560</u> <u>Tb04.1D20.590</u> <u>Tb04.1D20.620</u> <u>Tb04.1D20.650</u> <u>Tb04.3I12.20</u> <u>Tb04.3I12.30</u> <u>Tb04.3M17.30</u> <u>Tb04.3M17.40</u> <u>Tb04.3M17.50</u> <u>Tb04.3M17.60</u> <u>Tb08.30P3.120</u> <u>Tb08.30P3.130</u> <u>Tb08.30P3.140</u> <u>Tb08.30P3.150</u> <u>Tb08.30P3.160</u> <u>Tb08.30P3.170</u> <u>Tb08.30P3.190</u> <u>Tb08.30P3.200</u> <u>Tb08.30P3.210</u> <u>Tb08.30P3.230</u> <u>Tb08.4A8.350</u> <u>Tb08.4A8.356</u> <u>Tb08.4A8.362</u> <u>Tb08.4A8.368</u> <u>Tb08.4A8.374</u> <u>Tb11.01.7590</u> <u>Tb11.01.7600</u>	<u>Tc00.1047053503393.10</u> <u>Tc00.1047053504223.10</u> <u>Tc00.1047053504223.20</u> <u>Tc00.1047053506053.10</u> <u>Tc00.1047053506153.10</u> <u>Tc00.1047053507101.10</u> <u>Tc00.1047053507585.10</u> <u>Tc00.1047053507659.20</u> <u>Tc00.1047053507659.30</u> <u>Tc00.1047053507811.100</u> <u>Tc00.1047053508017.30</u> <u>Tc00.1047053508557.20</u> <u>Tc00.1047053508707.10</u> <u>Tc00.1047053508923.10</u> <u>Tc00.1047053510187.540</u> <u>Tc00.1047053510245.10</u> <u>Tc00.1047053510251.10</u> <u>Tc00.1047053511325.25</u> <u>Tc00.1047053511325.40</u> <u>Tc00.1047053511411.30</u> <u>Tc00.1047053511543.30</u> <u>Tc00.1047053511649.100</u> <u>Tc00.1047053511837.100</u>
<u>2.A.18.6.2</u>			
	<u>LmjF35.5350</u>	<u>Tb10.70.0300</u>	<u>Tc00.1047053503837.20</u> <u>Tc00.1047053506227.10</u>
<u>2.A.18.6.3</u>			
	<u>LmjF22.0230</u>	<u>Tb04.1D20.780</u>	<u>Tc00.1047053510431.30</u>
<u>2.A.18.6.5</u>			
	<u>LmjF36.0420</u>	<u>Tb11.01.7500</u> <u>Tb11.01.7520</u>	<u>Tc00.1047053509463.10</u> <u>Tc00.1047053510507.40</u> <u>Tc00.1047053511325.50</u>
<u>2.A.18.6.6</u>			
	<u>LmjF31.0580</u>	<u>Tb04.3I12.190</u>	<u>Tc00.1047053506153.20</u>

Scott Landfear (landfear@ohsu.edu), University of Oregon
 Al Ivens (alicat@sanger.ac.uk), Wellcome Trust Sanger Institute

	<u>LmjF32.2660</u> <u>LmjF33.1420</u>	<u>Tb08.30P3.270</u> <u>Tb10.6k15.0450</u>	<u>Tc00.1047053511545.80</u>
<u>2.A.18.7.1</u>			
	-	<u>Tb10.70.1170</u>	<u>Tc00.1047053509733.160</u>
<u>2.A.18.8.1</u>			
	<u>LmjF10.0710</u> <u>LmjF10.0715</u> <u>LmjF10.0720</u>	-	<u>Tc00.1047053504069.120</u> <u>Tc00.1047053504229.110</u>
<u>2.A.18.8.2</u>			
	-	<u>Tb08.5H5.40</u>	-
<u>2.A.19.4.1</u>			
	<u>LmjF20.0260</u> <u>LmjF26.2170</u>	<u>Tb04.5E12.260</u> <u>Tb11.01.4400</u>	<u>Tc00.1047053509925.10</u> <u>Tc00.1047053510979.50</u>
<u>2.A.20.2.1</u>			
	<u>LmjF03.0500</u>	-	<u>Tc00.1047053511417.80</u> <u>Tc00.1047053511417.90</u>
<u>2.A.20.2.2</u>			
	-	-	<u>Tc00.1047053506989.60</u>
<u>2.A.20.2.3</u>			
	<u>LmjF29.0650</u>	-	<u>Tc00.1047053505999.10</u> <u>Tc00.1047053505999.20</u> <u>Tc00.1047053510149.110</u>
<u>2.A.20.2.4</u>			
	<u>LmjF10.0030</u> <u>LmjF10.1300</u>	<u>Tb927.1.580</u> <u>Tb927.1.600</u>	-
<u>2.A.29.1.1</u>			
	<u>LmjF07.0530</u> <u>LmjF14.0990</u> <u>LmjF19.0200</u> <u>LmjF19.0210</u> <u>LmjF30.0230</u>	<u>Tb07.5F10.810</u> <u>Tb08.29O4.550</u> <u>Tb10.61.1810</u> <u>Tb10.61.1820</u> <u>Tb10.61.1830</u>	<u>Tc00.1047053506211.160</u> <u>Tc00.1047053506401.304</u> <u>Tc00.1047053510835.24</u> <u>Tc00.1047053511289.70</u>
<u>2.A.29.10.1</u>			
	<u>LmjF15.0120</u> <u>LmjF32.1110</u>	<u>Tb05.30H13.730</u>	<u>Tc00.1047053506247.360</u> <u>Tc00.1047053506739.80</u> <u>Tc00.1047053510819.100</u> <u>Tc00.1047053511725.140</u>
<u>2.A.29.10.2</u>			
	<u>LmjF32.1120</u> <u>LmjF35.3330</u>	<u>Tb09.211.3200</u> <u>Tb11.01.5950</u> <u>Tb11.01.5960</u>	<u>Tc00.1047053508989.20</u> <u>Tc00.1047053509569.110</u> <u>Tc00.1047053510663.64</u> <u>Tc00.1047053510737.30</u> <u>Tc00.1047053511725.134</u>

Scott Landfear (landfear@ohsu.edu), University of Oregon
 Al Ivens (alicat@sanger.ac.uk), Wellcome Trust Sanger Institute

<u>2.A.29.11.1</u>			
	-	<u>Tb04.2L9.1150</u>	<u>Tc00.1047053504057.140</u>
<u>2.A.29.12.1</u>			
	<u>LmjF19.1110</u> <u>LmjF36.0510</u>	<u>Tb10.61.0610</u> <u>Tb10.70.2290</u>	<u>Tc00.1047053508659.18</u> <u>Tc00.1047053510291.14</u> <u>Tc00.1047053511365.80</u>
<u>2.A.29.13.1</u>			
	<u>LmjF36.6610</u>	<u>Tb09.211.2370</u> <u>Tb10.389.0340</u> <u>Tb927.2.2970</u>	<u>Tc00.1047053506979.20</u> <u>Tc00.1047053508461.284</u> <u>Tc00.1047053508737.150</u> <u>Tc00.1047053509127.50</u>
<u>2.A.29.14.1</u>			
	-	-	<u>Tc00.1047053511249.10</u>
<u>2.A.29.14.2</u>			
	<u>LmjF07.0110</u>	<u>Tb11.01.5040</u>	<u>Tc00.1047053506755.74</u> <u>Tc00.1047053510359.69</u>
<u>2.A.29.15.1</u>			
	<u>LmjF30.1050</u>	-	-
<u>2.A.29.16.1</u>			
	<u>LmjF34.3060</u>	-	-
<u>2.A.29.17.1</u>			
	-	-	<u>Tc00.1047053503521.39</u>
<u>2.A.29.18.1</u>			
	<u>LmjF23.1370</u> <u>LmjF32.0110</u>	<u>Tb10.61.2510</u>	<u>Tc00.1047053506525.130</u> <u>Tc00.1047053511283.124</u>
<u>2.A.29.2.1</u>			
	<u>LmjF18.1260</u> <u>LmjF18.1265</u> <u>LmjF18.1270</u> <u>LmjF18.1275</u> <u>LmjF18.1280</u> <u>LmjF18.1285</u> <u>LmjF18.1290</u> <u>LmjF18.1300</u>	<u>Tb10.389.0690</u>	<u>Tc00.1047053503939.20</u> <u>Tc00.1047053509805.190</u>
<u>2.A.29.2.5</u>			
	<u>LmjF02.0670</u>	-	-
<u>2.A.29.3.1</u>			
	<u>LmjF09.1270</u>	-	-
<u>2.A.29.4.1</u>			
	<u>LmjF05.0290</u> <u>LmjF35.4420</u>	<u>Tb09.211.1750</u> <u>Tb10.406.0470</u>	<u>Tc00.1047053503425.5</u> <u>Tc00.1047053509551.30</u>

	<u>LmjF35.4430</u>		
<u>2.A.29.5.1</u>			
	<u>LmjF10.1020</u> <u>LmjF29.2780</u>	<u>Tb03.27C5.440</u> <u>Tb08.29H22.850</u>	<u>Tc00.1047053508153.630</u> <u>Tc00.1047053509769.90</u> <u>Tc00.1047053510315.20</u>
<u>2.A.29.5.2</u>			
	-	<u>Tb08.28L1.350</u>	-
<u>2.A.29.6.1</u>			
	-	-	<u>Tc00.1047053506771.18</u>
<u>2.A.29.7.1</u>			
	-	-	<u>Tc00.1047053503897.170</u> <u>Tc00.1047053504033.90</u> <u>Tc00.1047053509561.30</u> <u>Tc00.1047053510339.74</u>
<u>2.A.29.8.1</u>			
	<u>LmjF16.0200</u> <u>LmjF25.0210</u>	<u>Tb08.11J15.1150</u> <u>Tb11.03.0870</u>	<u>Tc00.1047053504109.70</u> <u>Tc00.1047053504217.19</u> <u>Tc00.1047053506221.40</u> <u>Tc00.1047053506247.260</u> <u>Tc00.1047053509109.114</u> <u>Tc00.1047053510603.90</u>
<u>2.A.29.8.2</u>			
	<u>LmjF35.3990</u>	<u>Tb11.02.2960</u>	<u>Tc00.1047053504125.50</u> <u>Tc00.1047053504131.190</u>
<u>2.A.29.9.1</u>			
	<u>LmjF16.0210</u> <u>LmjF36.6720</u>	-	-
<u>2.A.3.1.10</u>			
	<u>LmjF18.0450</u>	<u>Tb10.70.7080</u> <u>Tb10.70.7090</u> <u>Tb10.70.7100</u>	<u>Tc00.1047053508671.20</u> <u>Tc00.1047053509695.210</u> <u>Tc00.1047053509695.220</u> <u>Tc00.1047053509695.230</u>
<u>2.A.3.11.1</u>			
	-	-	<u>Tc00.1047053504213.110</u>
<u>2.A.3.3.1</u>			
	-	<u>Tb06.26G9.340</u>	<u>Tc00.1047053506833.70</u> <u>Tc00.1047053511729.70</u>
<u>2.A.3.6.1</u>			
	<u>LmjF14.0320</u> <u>LmjF35.4410</u>	<u>Tb09.211.1760</u> <u>Tb11.02.4520</u>	<u>Tc00.1047053506773.90</u> <u>Tc00.1047053508799.120</u>
<u>2.A.3.8.1</u>			
	-	-	<u>Tc00.1047053506985.40</u>

<u>2.A.36.7.1</u>			
	<u>LmjF23.0830</u>	-	<u>Tc00.1047053509459.60</u> <u>Tc00.1047053510511.9</u>
<u>2.A.38.2.1</u>			
	<u>LmjF35.0080</u>	-	-
<u>2.A.38.2.3</u>			
	-	<u>Tb10.70.2940</u>	<u>Tc00.1047053506295.120</u> <u>Tc00.1047053511469.60</u>
<u>2.A.4.2.1</u>			
	-	<u>Tb04.3M17.290</u>	-
<u>2.A.4.2.2</u>			
	<u>LmjF19.1380</u>	-	<u>Tc00.1047053506009.60</u> <u>Tc00.1047053510297.60</u> <u>Tc00.1047053510679.30</u> <u>Tc00.1047053511439.50</u>
<u>2.A.4.3.1</u>			
	<u>LmjF31.2390</u>	<u>Tb08.10K10.70</u>	-
<u>2.A.4.4.3</u>			
	<u>LmjF27.1265</u>	<u>Tb11.42.0002</u>	<u>Tc00.1047053508355.420</u> <u>Tc00.1047053508357.80</u>
<u>2.A.43.1.1</u>			
	-	-	<u>Tc00.1047053503559.70</u> <u>Tc00.1047053511693.130</u>
<u>2.A.43.3.1</u>			
	<u>LmjF14.1090</u>	<u>Tb07.6C8.150</u>	<u>Tc00.1047053511249.90</u>
<u>2.A.47.2.1</u>			
	<u>LmjF28.2930</u>	<u>Tb11.01.2950</u>	<u>Tc00.1047053508831.60</u>
<u>2.A.49.1.1</u>			
	-	-	<u>Tc00.1047053508317.50</u> <u>Tc00.1047053509849.10</u>
<u>2.A.5.1.1</u>			
	<u>LmjF28.1930</u>	-	-
<u>2.A.5.1.2</u>			
	<u>LmjF31.3060</u> <u>LmjF31.3070</u> <u>LmjF33.3200</u>	<u>Tb11.01.0720</u> <u>Tb11.01.0725</u> <u>Tb11.01.0730</u> <u>Tb11.01.0760</u> <u>Tb11.01.0770</u>	<u>Tc00.1047053450161.10</u> <u>Tc00.1047053507527.40</u> <u>Tc00.1047053507527.50</u> <u>Tc00.1047053508699.130</u> <u>Tc00.1047053508701.10</u> <u>Tc00.1047053508701.20</u> <u>Tc00.1047053509197.10</u> <u>Tc00.1047053509197.20</u>

			<u>Tc00.1047053509197.30</u> <u>Tc00.1047053509197.39</u>
<u>2.A.50.1.1</u>			
	<u>LmjF19.1000</u> <u>LmjF19.1320</u> <u>LmjF19.1330</u> <u>LmjF19.1340</u> <u>LmjF19.1345</u> <u>LmjF19.1347</u>	<u>Tb10.61.0380</u>	<u>Tc00.1047053503809.100</u> <u>Tc00.1047053503809.90</u> <u>Tc00.1047053508943.4</u> <u>Tc00.1047053511355.40</u> <u>Tc00.1047053511355.50</u>
<u>2.A.53.2.7</u>			
	<u>LmjF28.1690</u>	-	-
<u>2.A.53.3.1</u>			
	-	<u>Tb05.30H13.230</u>	<u>Tc00.1047053509601.110</u> <u>Tc00.1047053509767.110</u>
<u>2.A.54.1.1</u>			
	<u>LmjF01.0570</u> <u>LmjF05.0680</u>	<u>Tb09.160.2910</u>	<u>Tc00.1047053510153.19</u> <u>Tc00.1047053511583.40</u>
<u>2.A.57.2.1</u>			
	<u>LmjF15.1230</u> <u>LmjF15.1240</u>	-	<u>Tc00.1047053506445.110</u>
<u>2.A.57.2.2</u>			
	-	<u>Tb03.6N20.700</u> <u>Tb09.218.0180</u> <u>Tb09.244.2020</u>	-
<u>2.A.57.2.3</u>			
	<u>LmjF11.0550</u> <u>LmjF36.1940</u>	-	<u>Tc00.1047053508645.70</u>
<u>2.A.57.2.4</u>			
	-	<u>Tb06.28F21.780</u> <u>Tb09.160.5480</u> <u>Tb927.2.6150</u> <u>Tb927.2.6200</u> <u>Tb927.2.6220</u> <u>Tb927.2.6240</u> <u>Tb927.2.6280</u> <u>Tb927.2.6320</u>	<u>Tc00.1047053506203.10</u> <u>Tc00.1047053506773.50</u> <u>Tc00.1047053508645.40</u> <u>Tc00.1047053508799.150</u>
<u>2.A.57.2.5</u>			
	<u>LmjF13.1210</u>	<u>Tb11.02.1100</u> <u>Tb11.02.1105</u> <u>Tb11.02.1106</u>	<u>Tc00.1047053509683.110</u> <u>Tc00.1047053511051.30</u>
<u>2.A.6.5.3</u>			
	-	-	<u>Tc00.1047053508723.10</u> <u>Tc00.1047053509791.80</u>

<u>2.A.6.6.4</u>			
	<u>LmjF13.0010</u> <u>LmjF30.1400</u> <u>LmjF33.1230</u> <u>LmjF33.1240</u> <u>LmjF34.0470</u> <u>LmjF36.4820</u>	<u>Tb06.5F5.460</u> <u>Tb10.26.0030</u> <u>Tb10.6k15.0110</u> <u>Tb10.70.7300</u> <u>Tb11.01.2940</u>	<u>Tc00.1047053504009.4</u> <u>Tc00.1047053504105.110</u> <u>Tc00.1047053506567.134</u> <u>Tc00.1047053507021.30</u> <u>Tc00.1047053507049.119</u> <u>Tc00.1047053508173.54</u> <u>Tc00.1047053511753.50</u>
<u>2.A.6.6.5</u>			
	<u>LmjF30.3190</u>	<u>Tb06.26G9.610</u>	<u>Tc00.1047053506831.40</u> <u>Tc00.1047053509167.20</u>
<u>2.A.66.1.5</u>			
	<u>LmjF27.0790</u>	-	<u>Tc00.1047053507011.20</u> <u>Tc00.1047053510667.14</u>
<u>2.A.66.1.6</u>			
	<u>LmjF35.3630</u>	<u>Tb10.389.1330</u>	<u>Tc00.1047053507011.10</u> <u>Tc00.1047053510667.20</u>
<u>2.A.66.1.8</u>			
	<u>LmjF35.3580</u>	<u>Tb05.3C6.550</u> <u>Tb09.211.2900</u> <u>Tb09.211.2910</u> <u>Tb09.211.2920</u>	<u>Tc00.1047053503893.130</u> <u>Tc00.1047053507087.60</u> <u>Tc00.1047053507625.140</u> <u>Tc00.1047053508507.24</u> <u>Tc00.1047053511305.40</u> <u>Tc00.1047053511307.3</u>
<u>2.A.66.3.1</u>			
	<u>LmjF28.2410</u>	<u>Tb11.01.3540</u>	<u>Tc00.1047053503935.10</u> <u>Tc00.1047053506025.70</u>
<u>2.A.7.10.1</u>			
	<u>LmjF18.1540</u>	<u>Tb10.389.1220</u>	<u>Tc00.1047053507625.200</u> <u>Tc00.1047053509741.20</u>
<u>2.A.7.11.1</u>			
	<u>LmjF22.1010</u>	-	<u>Tc00.1047053510531.10</u> <u>Tc00.1047053511817.280</u>
<u>2.A.7.11.2</u>			
	-	<u>Tb07.13M20.270</u>	<u>Tc00.1047053508737.180</u> <u>Tc00.1047053509127.90</u>
<u>2.A.7.12.1</u>			
	<u>LmjF24.0360</u>	<u>Tb10.1730</u> <u>Tb10.61.3010</u> <u>Tb11.01.8280</u>	<u>Tc00.1047053506579.80</u>
<u>2.A.7.13.1</u>			
	-	-	<u>Tc00.1047053506753.60</u>

<u>2.A.7.13.2</u>			
	<u>LmjF34.3120</u>	<u>Tb04.2L9.1060</u>	<u>Tc00.1047053504057.120</u> <u>Tc00.1047053510355.220</u>
<u>2.A.7.15.1</u>			
	<u>LmjF18.0400</u>	-	<u>Tc00.1047053504085.60</u> <u>Tc00.1047053507089.40</u> <u>Tc00.1047053511277.400</u>
<u>2.A.7.15.2</u>			
	-	-	<u>Tc00.1047053506793.40</u> <u>Tc00.1047053510611.20</u>
<u>2.A.7.16.1</u>			
	<u>LmjF19.1490</u> <u>LmjF19.1510</u>	<u>Tb06.4F7.380</u>	<u>Tc00.1047053511301.50</u> <u>Tc00.1047053511517.150</u> <u>Tc00.1047053511737.70</u>
<u>2.A.7.9.1</u>			
	<u>LmjF30.2680</u>	-	-
<u>2.A.7.9.2</u>			
	-	-	<u>Tc00.1047053511353.30</u>
<u>2.A.71.1.1</u>			
	<u>LmjF06.1260</u> <u>LmjF35.5150</u>	-	-
<u>2.A.71.1.2</u>			
	<u>LmjF04.0020</u>	-	-
<u>2.A.71.1.3</u>			
	<u>LmjF06.0310</u> <u>LmjF10.0020</u> <u>LmjF10.0360</u> <u>LmjF10.0370</u> <u>LmjF10.0380</u> <u>LmjF10.0385</u> <u>LmjF10.0390</u> <u>LmjF10.0400</u> <u>LmjF10.1310</u> <u>LmjF19.0920</u>	-	-
<u>2.A.71.1.4</u>			
	-	<u>Tb08.10J17.790</u> <u>Tb08.10J17.810</u> <u>Tb08.10J17.820</u> <u>Tb10.6k15.1350</u> <u>Tb927.1.2820</u> <u>Tb927.1.2850</u> <u>Tb927.1.2880</u>	<u>Tc00.1047053505945.90</u> <u>Tc00.1047053506149.10</u> <u>Tc00.1047053506633.90</u> <u>Tc00.1047053508027.40</u> <u>Tc00.1047053511575.130</u>
<u>2.A.71.2.1</u>			

	<u>LmjF32.3720</u>	-	-
<u>2.A.82.1.1</u>			
	<u>LmjF11.1200</u>	-	-
<u>2.A.9.1.1</u>			
	-	-	<u>Tc00.1047053506297.310</u>
<u>2.C.1.2.1</u>			
	<u>LmjF14.1120</u> <u>LmjF15.0440</u> <u>LmjF16.0980</u> <u>LmjF22.1320</u> <u>LmjF24.2180</u> <u>LmjF26.2660</u> <u>LmjF28.0530</u> <u>LmjF28.1520</u> <u>LmjF30.3170</u> <u>LmjF30.3210</u> <u>LmjF32.2220</u> <u>LmjF35.4280</u> <u>LmjF36.5930</u>	<u>Tb03.48K5.730</u> <u>Tb06.3A7.740</u> <u>Tb08.10J17.380</u> <u>Tb09.211.1230</u> <u>Tb10.6k15.0240</u> <u>Tb11.01.1170</u> <u>Tb11.01.3520</u>	<u>Tc00.1047053443971.10</u> <u>Tc00.1047053503905.30</u> <u>Tc00.1047053503975.40</u> <u>Tc00.1047053504019.3</u> <u>Tc00.1047053504625.70</u> <u>Tc00.1047053506155.30</u> <u>Tc00.1047053506491.20</u> <u>Tc00.1047053506601.40</u> <u>Tc00.1047053507527.20</u> <u>Tc00.1047053508067.10</u> <u>Tc00.1047053508321.40</u> <u>Tc00.1047053508851.200</u> <u>Tc00.1047053509569.170</u> <u>Tc00.1047053509631.140</u> <u>Tc00.1047053510247.10</u> <u>Tc00.1047053510859.30</u> <u>Tc00.1047053510961.10</u> <u>Tc00.1047053510961.30</u> <u>Tc00.1047053511071.130</u> <u>Tc00.1047053511131.80</u> <u>Tc00.1047053511215.70</u>
<u>3.A.1.1.12</u>			
	-	-	<u>Tc00.1047053511501.30</u>
<u>3.A.1.1.16</u>			
	-	-	<u>Tc00.1047053464879.9</u> <u>Tc00.1047053508637.150</u>
<u>3.A.1.1.17</u>			
	<u>LmjF27.1700</u>	-	-
<u>3.A.1.108.1</u>			
	-	<u>Tb927.2.5410</u> <u>Tb927.2.6130</u>	<u>Tc00.1047053506817.20</u> <u>Tc00.1047053507105.70</u>
<u>3.A.1.120.1</u>			
	<u>LmjF33.0310</u>	-	-
<u>3.A.1.120.2</u>			
	<u>LmjF03.0160</u>	<u>Tb10.329.0040</u>	<u>Tc00.1047053509105.130</u>
<u>3.A.1.120.4</u>			
	<u>LmjF19.0800</u>	<u>Tb10.61.0840</u>	<u>Tc00.1047053508897.30</u>

3.A.1.121.2			
	-	<u>Tb10.70.4330</u>	<u>Tc00.1047053504867.20</u> <u>Tc00.1047053510943.80</u>
3.A.1.122.1			
	<u>LmjF12.1190</u> <u>LmjF34.2070</u>	-	<u>Tc00.1047053509617.80</u> <u>Tc00.1047053509669.30</u>
3.A.1.123.4			
	<u>LmjF29.1640</u>	-	-
3.A.1.125.1			
	<u>LmjF11.0040</u>	-	<u>Tc00.1047053506905.40</u> <u>Tc00.1047053510381.20</u>
3.A.1.126.1			
	<u>LmjF30.1330</u>	<u>Tb06.5F5.330</u>	-
3.A.1.16.1			
	-	-	<u>Tc00.1047053511753.100</u>
3.A.1.2.6			
	<u>LmjF29.0930</u>	-	-
3.A.1.201.1			
	<u>LmjF26.2670</u> <u>LmjF34.0990</u>	<u>Tb927.1.4420</u>	-
3.A.1.201.4			
	-	-	<u>Tc00.1047053506619.90</u> <u>Tc00.1047053508809.30</u>
3.A.1.203.1			
	<u>LmjF27.0470</u> <u>LmjF31.0540</u> <u>LmjF33.1860</u>	<u>Tb04.1D20.510</u> <u>Tb11.03.0030</u>	<u>Tc00.1047053506925.530</u> <u>Tc00.1047053508927.20</u> <u>Tc00.1047053509237.30</u>
3.A.1.203.3			
	-	<u>Tb11.02.0630</u>	<u>Tc00.1047053510431.150</u>
3.A.1.204.1			
	<u>LmjF06.0080</u> <u>LmjF06.0090</u> <u>LmjF06.0100</u> <u>LmjF15.0890</u>	<u>Tb09.160.4600</u> <u>Tb10.6k15.2900</u>	<u>Tc00.1047053506249.70</u> <u>Tc00.1047053506579.10</u> <u>Tc00.1047053507241.39</u> <u>Tc00.1047053508231.190</u>
3.A.1.204.2			
	<u>LmjF21.0880</u> <u>LmjF23.0380</u> <u>LmjF36.2890</u>	<u>Tb08.26A17.190</u> <u>Tb10.6k15.3320</u>	<u>Tc00.1047053503593.60</u> <u>Tc00.1047053504425.70</u> <u>Tc00.1047053506127.120</u> <u>Tc00.1047053507681.100</u> <u>Tc00.1047053507951.280</u> <u>Tc00.1047053509331.200</u>

3.A.1.205.2			
	-	-	Tc00.1047053506457.149 Tc00.1047053509693.190
3.A.1.208.12			
	LmjF34.0670	-	-
3.A.1.208.2			
	-	-	Tc00.1047053510231.29
3.A.1.208.6			
	LmjF23.0210 LmjF23.0220 LmjF23.0250 LmjF31.1270 LmjF31.1280 LmjF31.1290 LmjF31.1430	Tb04.3I12.980 Tb08.26N11.730	Tc00.1047053457101.30 Tc00.1047053507079.30 Tc00.1047053508965.14 Tc00.1047053510785.10
3.A.1.208.8			
	-	-	Tc00.1047053447255.29 Tc00.1047053506559.100
3.A.1.208.9			
	-	Tb04.1H19.1030	-
3.A.1.21.1			
	-	-	Tc00.1047053506529.160 Tc00.1047053510885.70
3.A.1.210.1			
	-	-	Tc00.1047053511537.8
3.A.1.210.3			
	LmjF33.3260	-	-
3.A.1.210.4			
	LmjF32.3080	Tb11.01.8700	Tc00.1047053503749.60 Tc00.1047053511021.70
3.A.1.211.1			
	LmjF02.0300 LmjF11.1220 LmjF11.1240 LmjF11.1250 LmjF11.1270 LmjF11.1290 LmjF27.0970 LmjF27.0980 LmjF29.0620	-	Tc00.1047053503573.9 Tc00.1047053504149.20 Tc00.1047053504881.50 Tc00.1047053506989.30 Tc00.1047053507099.80 Tc00.1047053510045.20
3.A.1.211.2			
	-	Tb11.02.3950	Tc00.1047053511725.80

Scott Landfear (landfear@ohsu.edu), University of Oregon
 Al Ivens (alicat@sanger.ac.uk), Wellcome Trust Sanger Institute

<u>3.A.1.211.3</u>			
	<u>LmjF15.0760</u>	<u>Tb03.28C22.830</u>	<u>Tc00.1047053510149.80</u>
<u>3.A.1.212.1</u>			
	<u>LmjF25.0530</u>	<u>Tb11.03.0540</u>	<u>Tc00.1047053507093.260</u>
<u>3.A.1.3.2</u>			
	-	-	<u>Tc00.1047053507813.10</u>
<u>3.A.1.6.2</u>			
	<u>LmjF21.0710</u>	<u>Tb10.70.6290</u>	-
<u>3.A.1.6.3</u>			
	<u>LmjF32.2060</u>	-	-
<u>3.A.10.1.1</u>			
	<u>LmjF31.1220</u>	<u>Tb04.1D20.30</u> <u>Tb08.6H23.250</u>	<u>Tc00.1047053510773.20</u> <u>Tc00.1047053511385.30</u>
<u>3.A.11.1.1</u>			
	-	-	<u>Tc00.1047053509161.130</u>
<u>3.A.15.2.1</u>			
	-	<u>Tb11.02.4210</u>	-
<u>3.A.2.1.1</u>			
	-	<u>Tb10.100.0070</u>	<u>Tc00.1047053510395.10</u> <u>Tc00.1047053467287.30</u>
<u>3.A.2.1.2</u>			
	-	<u>Tb07.30D13.350</u> <u>Tb07.30D13.360</u>	<u>Tc00.1047053503617.40</u>
<u>3.A.2.1.3</u>			
	<u>LmjF05.0500</u> <u>LmjF05.0510</u> <u>LmjF25.1170</u> <u>LmjF25.1180</u> <u>LmjF30.3600</u> <u>LmjF21.1770</u>	<u>Tb03.1J15.500</u>	<u>Tc00.1047053509233.180</u> <u>Tc00.1047053506945.240</u> <u>Tc00.1047053504069.80</u> <u>Tc00.1047053511145.60</u>
<u>3.A.2.2.3</u>			
	<u>LmjF05.1140</u> <u>LmjF28.2430</u> <u>LmjF18.0560</u> <u>LmjF35.0700</u> <u>LmjF36.3100</u> <u>LmjF12.0520</u> <u>LmjF23.0340</u> <u>LmjF21.1340</u> <u>LmjF23.0130</u> <u>LmjF30.3660</u> <u>LmjF21.1790</u>	<u>Tb05.29K2.750</u> <u>Tb11.01.3560</u> <u>Tb10.1610</u> <u>Tb10.61.2840</u> <u>Tb10.70.3600</u> <u>Tb11.01.1190</u> <u>Tb927.1.3820</u> <u>Tb10.70.7480</u> <u>Tb10.100.0090</u> <u>Tb06.30P15.380</u> <u>Tb08.26N11.630</u>	<u>Tc00.1047053508397.10</u> <u>Tc00.1047053509885.10</u> <u>Tc00.1047053506025.50</u> <u>Tc00.1047053511209.10</u> <u>Tc00.1047053511277.240</u> <u>Tc00.1047053509017.30</u> <u>Tc00.1047053511001.190</u> <u>Tc00.1047053508851.59</u> <u>Tc00.1047053511589.10</u> <u>Tc00.1047053506529.516</u> <u>Tc00.1047053510889.231</u>

	LmjF21.1800 LmjF28.1160 LmjF23.1510 LmjF32.0920	Tb11.02.5470 Tb05.30H13.310	Tc00.1047053506855.80 Tc00.1047053508781.20 Tc00.1047053506945.300 Tc00.1047053504069.70 Tc00.1047053506163.40 Tc00.1047053506867.20 Tc00.1047053507623.129 Tc00.1047053508821.50 Tc00.1047053511145.50 Tc00.1047053509601.70 Tc00.1047053509767.70 Tc00.1047053511727.90
3.A.2.3.1			
	LmjF34.3670	Tb04.5E12.370	Tc00.1047053503929.10 Tc00.1047053506405.120
3.A.3.2.1			
	LmjF07.0630 LmjF07.0650 LmjF17.0600 LmjF33.1010	Tb08.29O4.320 Tb08.29O4.350 Tb10.26.0290	Tc00.1047053506401.170 Tc00.1047053508543.90 Tc00.1047053509647.150
3.A.3.2.2			
	-	Tb08.29O4.290	-
3.A.3.2.7			
	LmjF04.0010	Tb05.27M3.570 Tb08.12O16.210	Tc00.1047053503563.10 Tc00.1047053504141.9 Tc00.1047053509777.70
3.A.3.3.2			
	LmjF04.1110 LmjF18.1510 LmjF18.1520	Tb10.389.1170 Tb10.389.1180	Tc00.1047053505763.10 Tc00.1047053505763.19 Tc00.1047053506333.10 Tc00.1047053506649.20 Tc00.1047053507627.20 Tc00.1047053509809.39 Tc00.1047053510575.5 Tc00.1047053511261.4
3.A.3.3.4			
	LmjF07.1050	-	-
3.A.3.5.3			
	-	-	Tc00.1047053503703.50 Tc00.1047053503893.10 Tc00.1047053511445.160
3.A.3.5.6			
	LmjF33.2090	Tb11.47.0023	Tc00.1047053509015.10
3.A.3.8.1			

	<u>LmjF34.3220</u>	<u>Tb04.2L9.780</u> <u>Tb06.2N9.170</u>	<u>Tc00.1047053504057.11</u> <u>Tc00.1047053506941.60</u> <u>Tc00.1047053510877.80</u> <u>Tc00.1047053511003.10</u> <u>Tc00.1047053511511.60</u>
<u>3.A.3.8.2</u>			
	<u>LmjF34.2630</u>	-	-
<u>3.A.3.8.3</u>			
	<u>LmjF09.0890</u> <u>LmjF13.1530</u> <u>LmjF30.2260</u>	<u>Tb11.02.0850</u> <u>Tb11.52.0018</u>	<u>Tc00.1047053503999.100</u> <u>Tc00.1047053505171.10</u> <u>Tc00.1047053506655.7</u> <u>Tc00.1047053509591.60</u> <u>Tc00.1047053511559.70</u>
<u>3.A.3.9.2</u>			
	-	<u>Tb09.244.2570</u>	<u>Tc00.1047053506241.70</u> <u>Tc00.1047053509611.80</u> <u>Tc00.1047053510769.120</u>
<u>3.A.3.9.3</u>			
	<u>LmjF35.2080</u>	-	-
<u>3.A.4.1.1</u>			
	<u>LmjF11.0700</u>	-	<u>Tc00.1047053507763.30</u> <u>Tc00.1047053510101.490</u>
<u>3.A.5.1.1</u>			
	<u>LmjF24.0730</u>	<u>Tb11.02.3070</u>	<u>Tc00.1047053505183.80</u>
<u>3.A.5.8.1</u>			
	<u>LmjF14.1330</u> <u>LmjF18.1430</u> <u>LmjF21.0490</u> <u>LmjF25.1100</u> <u>LmjF26.1270</u> <u>LmjF27.2400</u> <u>LmjF30.1030</u> <u>LmjF31.3100</u> <u>LmjF33.0900</u> <u>LmjF34.3870</u> <u>LmjF35.4630</u> <u>LmjF36.0610</u> <u>LmjF36.6270</u> <u>LmjF36.3570</u>	<u>Tb03.27F10.420</u> <u>Tb03.1J15.410</u> <u>Tb07.28B13.340</u> <u>Tb07.8P12.820</u> <u>Tb08.10K10.810</u> <u>Tb09.211.1550</u> <u>Tb09.211.3680</u> <u>Tb10.389.1150</u> <u>Tb10.6k15.0460</u> <u>Tb10.6k15.2000</u> <u>Tb10.70.2160</u> <u>Tb10.70.5440</u> <u>Tb11.01.0135</u> <u>Tb11.01.8480</u> <u>Tb11.01.8750</u> <u>Tb11.03.0110</u> <u>Tb927.2.5160</u> <u>Tb10.70.3000</u> <u>Tb11.01.1650</u>	<u>Tc00.1047053511865.54</u> <u>Tc00.1047053511871.34</u> <u>Tc00.1047053503791.10</u> <u>Tc00.1047053504131.100</u> <u>Tc00.1047053506287.90</u> <u>Tc00.1047053506355.50</u> <u>Tc00.1047053506445.121</u> <u>Tc00.1047053506887.90</u> <u>Tc00.1047053506991.10</u> <u>Tc00.1047053507389.60</u> <u>Tc00.1047053508461.240</u> <u>Tc00.1047053508661.30</u> <u>Tc00.1047053509233.80</u> <u>Tc00.1047053509437.40</u> <u>Tc00.1047053509809.20</u> <u>Tc00.1047053509911.100</u> <u>Tc00.1047053509937.160</u> <u>Tc00.1047053510243.30</u> <u>Tc00.1047053510293.50</u> <u>Tc00.1047053510407.80</u>

			Tc00.1047053510575.200 Tc00.1047053510659.210 Tc00.1047053510731.80 Tc00.1047053510743.100 Tc00.1047053511025.100 Tc00.1047053511043.30 Tc00.1047053511261.20 Tc00.1047053511367.138 Tc00.1047053511531.9 Tc00.1047053511627.110 Tc00.1047053504433.10 Tc00.1047053507951.170 Tc00.1047053506337.210
3.A.5.9.1			
	LmjF11.1050	Tb11.02.4100	Tc00.1047053506297.240 Tc00.1047053510101.70
3.A.7.4.1			
	LmjF28.3010 LmjF31.2220	-	Tc00.1047053507357.140 Tc00.1047053507357.50 Tc00.1047053507953.170 Tc00.1047053511099.119
3.A.7.7.1			
	LmjF28.1780 LmjF36.3200	Tb10.70.5940 Tb11.01.0910 Tb11.01.1280	Tc00.1047053506493.80 Tc00.1047053508851.170 Tc00.1047053510121.160 Tc00.1047053510901.100 Tc00.1047053511589.120
3.A.8.1.1			
	LmjF30.0730 LmjF30.0735 LmjF22.0270 LmjF27.1130 LmjF24.1910	Tb06.4M18.480 Tb07.27M11.910 Tb11.55.0006 Tb08.11J15.400	Tc00.1047053507929.20 Tc00.1047053509045.20 Tc00.1047053506755.250 Tc00.1047053510359.260 Tc00.1047053511867.120 Tc00.1047053503885.70 Tc00.1047053511903.270
3.A.9.1.1			
	LmjF26.0900 LmjF02.0590 LmjF08.1110 LmjF18.0150 LmjF27.2390 LmjF29.0320 LmjF30.2740 LmjF32.2850 LmjF34.2430 LmjF35.4000	Tb03.5L5.520 Tb04.1H19.310 Tb05.26K5.210 Tb06.4F7.320 Tb08.5H5.750 Tb09.211.1220 Tb09.211.1350 Tb10.05.0110 Tb10.6k15.3490 Tb10.70.1950	Tc00.1047053511515.40 Tc00.1047053503687.40 Tc00.1047053504203.60 Tc00.1047053506009.30 Tc00.1047053506321.290 Tc00.1047053506435.400 Tc00.1047053506559.430 Tc00.1047053506577.70 Tc00.1047053506885.400 Tc00.1047053506943.100

	<u>LmjF35.4770</u> <u>LmjF35.4880</u> <u>LmjF36.0070</u> <u>LmjF36.0500</u>	<u>Tb10.70.2300</u> <u>Tb10.70.2770</u> <u>Tb11.01.7710</u> <u>Tb927.2.5150</u>	<u>Tc00.1047053507709.70</u> <u>Tc00.1047053507801.140</u> <u>Tc00.1047053507993.190</u> <u>Tc00.1047053508409.210</u> <u>Tc00.1047053508625.130</u> <u>Tc00.1047053508659.9</u> <u>Tc00.1047053508707.120</u> <u>Tc00.1047053508737.200</u> <u>Tc00.1047053508817.110</u> <u>Tc00.1047053508839.80</u> <u>Tc00.1047053509065.110</u> <u>Tc00.1047053509073.90</u> <u>Tc00.1047053509127.110</u> <u>Tc00.1047053509381.10</u> <u>Tc00.1047053509537.80</u> <u>Tc00.1047053509757.30</u> <u>Tc00.1047053510143.24</u> <u>Tc00.1047053510291.7</u> <u>Tc00.1047053510297.30</u> <u>Tc00.1047053511277.630</u> <u>Tc00.1047053511381.50</u> <u>Tc00.1047053511519.9</u> <u>Tc00.1047053511627.100</u> <u>Tc00.1047053511737.10</u>
<u>3.B.1.1.1</u>			
	-	-	<u>Tc00.1047053506635.80</u>
<u>3.B.1.1.2</u>			
	<u>LmjF11.0590</u> <u>LmjF28.0490</u>	-	-
<u>3.B.1.1.3</u>			
	<u>LmjF01.0050</u>	-	-
<u>3.B.1.1.5</u>			
	<u>LmjF31.3130</u>	<u>Tb11.02.4480</u> <u>Tb08.10K10.840</u>	<u>Tc00.1047053506773.40</u> <u>Tc00.1047053508369.50</u> <u>Tc00.1047053508799.170</u> <u>Tc00.1047053504835.20</u> <u>Tc00.1047053509913.10</u>
<u>3.D.1.2.1</u>			
	<u>LmjF05.0980</u> <u>LmjF17.0270</u> <u>LmjF18.1480</u> <u>LmjF27.0740</u>	<u>Tb05.29K2.470</u> <u>Tb07.33N13.230</u> <u>Tb10.389.1140</u> <u>Tb11.47.0017</u>	<u>Tc00.1047053507869.10</u> <u>Tc00.1047053508399.10</u> <u>Tc00.1047053506513.190</u> <u>Tc00.1047053511323.50</u> <u>Tc00.1047053509809.10</u> <u>Tc00.1047053511261.30</u> <u>Tc00.1047053503893.80</u> <u>Tc00.1047053508507.59</u>

<u>3.D.3.1.1</u>			
	<u>LmjF20.1180</u> <u>LmjF22.1690</u> <u>LmjF23.1640</u> <u>LmjF36.3090</u>	<u>Tb03.5L5.480</u> <u>Tb11.01.6740</u>	<u>Tc00.1047053427789.20</u> <u>Tc00.1047053506501.110</u> <u>Tc00.1047053506765.74</u> <u>Tc00.1047053508151.20</u> <u>Tc00.1047053508443.60</u> <u>Tc00.1047053509157.120</u> <u>Tc00.1047053511635.80</u>
<u>3.D.3.2.1</u>			
	-	<u>Tb09.211.4700</u>	<u>Tc00.1047053506999.90</u> <u>Tc00.1047053510759.120</u>
<u>3.D.3.3.1</u>			
	<u>LmjF07.0060</u> <u>LmjF35.1540</u>	<u>Tb08.26N11.340</u>	<u>Tc00.1047053511391.160</u>
<u>3.D.4.4.1</u>			
	<u>LmjF23.1520</u>	-	<u>Tc00.1047053505965.30</u> <u>Tc00.1047053509601.59</u> <u>Tc00.1047053509767.59</u> <u>Tc00.1047053510903.60</u>
<u>3.D.4.5.1</u>			
	<u>LmjF28.1320</u>	<u>Tb05.30H13.320</u>	-
<u>3.D.4.6.1</u>			
	<u>LmjF16.1310</u> <u>LmjF16.1320</u>	<u>Tb08.5H5.620</u>	<u>Tc00.1047053506949.50</u> <u>Tc00.1047053508959.4</u>
<u>3.D.5.1.1</u>			
	<u>LmjF13.1060</u> <u>LmjF15.0050</u> <u>LmjF22.0770</u> <u>LmjF35.1180</u>	<u>Tb07.13M20.760</u>	<u>Tc00.1047053503849.80</u> <u>Tc00.1047053510215.10</u> <u>Tc00.1047053511047.40</u> <u>Tc00.1047053511817.40</u> <u>Tc00.1047053511859.170</u>
<u>5.A.1.1.1</u>			
	-	-	<u>Tc00.1047053508209.140</u>
<u>5.B.2.1.2</u>			
	-	-	<u>Tc00.1047053503909.76</u> <u>Tc00.1047053511507.80</u>
<u>8.A.13.1.1</u>			
	-	-	<u>Tc00.1047053506855.250</u> <u>Tc00.1047053508837.170</u> <u>Tc00.1047053511133.30</u>
<u>8.A.15.1.1</u>			
	<u>LmjF30.3490</u> <u>LmjF30.3510</u> <u>LmjF32.3070</u>	<u>Tb09.211.2400</u> <u>Tb927.2.4420</u>	<u>Tc00.1047053508461.300</u> <u>Tc00.1047053509099.100</u> <u>Tc00.1047053509319.30</u>

	<u>LmjF35.3970</u>		<u>Tc00.1047053511021.60</u> <u>Tc00.1047053511537.16</u>
<u>8.A.3.2.2</u>			
	<u>LmjF28.2470</u>	<u>Tb11.01.3600</u>	-
<u>8.A.3.3.2</u>			
	<u>LmjF33.0590</u>	-	-
<u>8.A.5.1.2</u>			
	-	<u>Tb11.02.2310</u>	<u>Tc00.1047053505183.120</u> <u>Tc00.1047053511287.49</u>
<u>8.A.5.1.3</u>			
	<u>LmjF31.2150</u> <u>LmjF31.2880</u> <u>LmjF32.0460</u>	-	-
<u>8.A.7.1.1</u>			
	<u>LmjF11.1000</u>	<u>Tb11.02.4150</u>	<u>Tc00.1047053506297.190</u> <u>Tc00.1047053510101.140</u>
<u>9.A.1.1.1</u>			
	<u>LmjF09.1020</u> <u>LmjF32.0510</u> <u>LmjF35.3400</u>	<u>Tb09.211.3110</u> <u>Tb11.01.4760</u> <u>Tb11.01.5340</u>	<u>Tc00.1047053458759.14</u> <u>Tc00.1047053506757.30</u> <u>Tc00.1047053507011.180</u> <u>Tc00.1047053510359.360</u> <u>Tc00.1047053510665.4</u> <u>Tc00.1047053510911.14</u>
<u>9.A.10.1.1</u>			
	<u>LmjF03.0950</u>	-	-
<u>9.A.11.1.1</u>			
	-	-	<u>Tc00.1047053507979.30</u>
<u>9.A.19.1.1</u>			
	-	<u>Tb05.1P6.110</u>	-
<u>9.A.19.2.1</u>			
	-	-	<u>Tc00.1047053509161.70</u>
<u>9.A.5.1.1</u>			
	<u>LmjF30.3010</u> <u>LmjF35.1420</u> <u>LmjF36.2280</u> <u>LmjF06.0030</u> <u>LmjF08.0410</u> <u>LmjF10.0110</u> <u>LmjF10.0780</u> <u>LmjF11.1160</u> <u>LmjF17.0170</u> <u>LmjF18.0470</u>	<u>Tb03.28C22.1010</u> <u>Tb04.30O21.70</u> <u>Tb04.5D20.570</u> <u>Tb05.27M3.360</u> <u>Tb06.28P18.830</u> <u>Tb07.26A24.470</u> <u>Tb07.28B13.840</u> <u>Tb07.2F2.630</u> <u>Tb07.8P12.840</u> <u>Tb08.11J15.360</u>	<u>Tc00.1047053508299.70</u> <u>Tc00.1047053511181.90</u> <u>Tc00.1047053503811.40</u> <u>Tc00.1047053503885.90</u> <u>Tc00.1047053503897.40</u> <u>Tc00.1047053506207.40</u> <u>Tc00.1047053506287.100</u> <u>Tc00.1047053506297.290</u> <u>Tc00.1047053506513.150</u> <u>Tc00.1047053506815.30</u>

<u>LmjF21.0060</u>	<u>Tb08.11J15.880</u>	<u>Tc00.1047053506887.50</u>
<u>LmjF21.1569</u>	<u>Tb08.26N11.450</u>	<u>Tc00.1047053506989.160</u>
<u>LmjF23.1165</u>	<u>Tb08.28F14.610</u>	<u>Tc00.1047053507105.10</u>
<u>LmjF24.1490</u>	<u>Tb08.29H22.320</u>	<u>Tc00.1047053507521.140</u>
<u>LmjF24.1720</u>	<u>Tb08.30K1.260</u>	<u>Tc00.1047053507583.40</u>
<u>LmjF24.1900</u>	<u>Tb08.30K1.680</u>	<u>Tc00.1047053507809.110</u>
<u>LmjF24.2260</u>	<u>Tb09.211.2550</u>	<u>Tc00.1047053508059.24</u>
<u>LmjF26.1400</u>	<u>Tb10.1690</u>	<u>Tc00.1047053508307.44</u>
<u>LmjF28.2740</u>	<u>Tb10.61.2920</u>	<u>Tc00.1047053508461.390</u>
<u>LmjF28.2750</u>	<u>Tb10.70.4780</u>	<u>Tc00.1047053508577.60</u>
<u>LmjF29.0740</u>	<u>Tb10.70.5990</u>	<u>Tc00.1047053508649.10</u>
<u>LmjF30.0410</u>	<u>Tb11.01.3170</u>	<u>Tc00.1047053508881.150</u>
<u>LmjF30.0950</u>	<u>Tb11.01.3180</u>	<u>Tc00.1047053508917.20</u>
<u>LmjF33.1910</u>	<u>Tb11.02.0570</u>	<u>Tc00.1047053508953.28</u>
<u>LmjF34.4310</u>	<u>Tb11.42.0004</u>	<u>Tc00.1047053509563.30</u>
<u>LmjF35.3880</u>	<u>Tb927.2.6050</u>	<u>Tc00.1047053509859.80</u>
<u>LmjF07.0370</u>	<u>Tb03.48O8.510</u>	<u>Tc00.1047053510065.40</u>
<u>LmjF25.2290</u>	<u>Tb10.70.0450</u>	<u>Tc00.1047053510431.220</u>
<u>LmjF28.1830</u>	<u>Tb10.61.0440</u>	<u>Tc00.1047053510515.100</u>
<u>LmjF36.1930</u>	<u>Tb10.100.0130</u>	<u>Tc00.1047053510533.130</u>
<u>LmjF19.1250</u>	<u>Tb04.1H19.1460</u>	<u>Tc00.1047053510687.149</u>
<u>LmjF02.0390</u>	<u>Tb04.26G5.210</u>	<u>Tc00.1047053510731.40</u>
<u>LmjF04.0680</u>	<u>Tb07.22O10.640</u>	<u>Tc00.1047053511075.20</u>
<u>LmjF07.0850</u>	<u>Tb08.11J15.680</u>	<u>Tc00.1047053511211.120</u>
<u>LmjF22.0610</u>	<u>Tb08.12O16.620</u>	<u>Tc00.1047053511211.130</u>
<u>LmjF24.2130</u>	<u>Tb11.01.5510</u>	<u>Tc00.1047053511277.340</u>
<u>LmjF32.0700</u>	<u>Tb11.01.5790</u>	<u>Tc00.1047053511491.140</u>
<u>LmjF32.0960</u>	<u>Tb927.2.2460</u>	<u>Tc00.1047053511659.9</u>
<u>LmjF33.2770</u>	<u>Tb927.2.3720</u>	<u>Tc00.1047053511821.120</u>
<u>LmjF34.0900</u>		<u>Tc00.1047053511903.290</u>
<u>LmjF35.1300</u>		<u>Tc00.1047053511907.260</u>
		<u>Tc00.1047053507641.236</u>
		<u>Tc00.1047053508479.190</u>
		<u>Tc00.1047053503809.20</u>
		<u>Tc00.1047053504069.50</u>
		<u>Tc00.1047053511145.40</u>
		<u>Tc00.1047053453445.20</u>
		<u>Tc00.1047053503515.14</u>
		<u>Tc00.1047053504055.81</u>
		<u>Tc00.1047053504643.30</u>
		<u>Tc00.1047053506435.300</u>
		<u>Tc00.1047053506789.200</u>
		<u>Tc00.1047053506859.10</u>
		<u>Tc00.1047053507715.80</u>
		<u>Tc00.1047053508137.30</u>
		<u>Tc00.1047053508303.4</u>
		<u>Tc00.1047053508387.100</u>
		<u>Tc00.1047053508569.20</u>
		<u>Tc00.1047053508741.280</u>
		<u>Tc00.1047053509161.10</u>

			<u>Tc00.1047053509607.10</u> <u>Tc00.1047053511071.70</u> <u>Tc00.1047053511111.50</u> <u>Tc00.1047053511179.160</u> <u>Tc00.1047053511813.20</u> <u>Tc00.1047053511903.30</u>
<u>9.A.8.1.1</u>			
	<u>LmjF26.0270</u>	<u>Tb07.29D18.100</u>	-
<u>9.A.8.1.2</u>			
	<u>LmjF33.2400</u>	<u>Tb11.02.0240</u>	<u>Tc00.1047053504153.300</u>
<u>9.A.8.1.3</u>			
	<u>LmjF36.2250</u>	<u>Tb09.211.0720</u>	<u>Tc00.1047053506883.30</u>
<u>9.B.17.1.1</u>			
	<u>LmjF24.1780</u>	-	<u>Tc00.1047053506799.10</u> <u>Tc00.1047053511907.110</u>
<u>9.B.17.1.4</u>			
	<u>LmjF01.0470</u> <u>LmjF01.0490</u> <u>LmjF01.0500</u> <u>LmjF01.0520</u> <u>LmjF01.0530</u> <u>LmjF03.0230</u> <u>LmjF13.0420</u> <u>LmjF19.0985</u> <u>LmjF19.0995</u> <u>LmjF19.1005</u> <u>LmjF23.0540</u> <u>LmjF23.0710</u>	<u>Tb08.26A17.430</u> <u>Tb09.160.2770</u> <u>Tb09.160.2780</u> <u>Tb09.160.2810</u> <u>Tb09.160.2840</u> <u>Tb10.70.4200</u> <u>Tb11.02.2070</u> <u>Tb11.02.5520</u>	<u>Tc00.1047053494675.10</u> <u>Tc00.1047053503575.50</u> <u>Tc00.1047053504089.40</u> <u>Tc00.1047053504177.20</u> <u>Tc00.1047053504427.110</u> <u>Tc00.1047053506261.10</u> <u>Tc00.1047053506829.100</u> <u>Tc00.1047053506829.110</u> <u>Tc00.1047053509331.30</u> <u>Tc00.1047053510151.10</u> <u>Tc00.1047053510943.33</u> <u>Tc00.1047053511581.10</u> <u>Tc00.1047053511581.20</u>
<u>9.B.17.1.6</u>			
	<u>LmjF28.1150</u>	-	<u>Tc00.1047053503559.100</u> <u>Tc00.1047053510151.19</u> <u>Tc00.1047053511693.100</u>
<u>9.B.24.1.1</u>			
	<u>LmjF24.1190</u>	<u>Tb11.02.3570</u>	<u>Tc00.1047053503487.70</u> <u>Tc00.1047053508641.200</u>
<u>9.B.26.2.1</u>			
	<u>LmjF19.0310</u>	-	<u>Tc00.1047053506211.50</u> <u>Tc00.1047053508895.70</u>
<u>9.B.30.1.1</u>			
	<u>LmjF36.5500</u>	-	-
<u>9.B.33.1.1</u>			
	<u>LmjF03.0370</u>	-	<u>Tc00.1047053430895.10</u>

Scott Landfear (landfear@ohsu.edu), University of Oregon
 Al Ivens (alicat@sanger.ac.uk), Wellcome Trust Sanger Institute

	<u>LmjF03.0380</u> <u>LmjF03.0390</u> <u>LmjF03.0400</u>		<u>Tc00.1047053479253.9</u> <u>Tc00.1047053504269.20</u> <u>Tc00.1047053505757.10</u> <u>Tc00.1047053505757.20</u> <u>Tc00.1047053506669.10</u> <u>Tc00.1047053508179.70</u>
<u>9.B.37.1.2</u>			
	<u>LmjF18.0140</u> <u>LmjF30.3030</u> <u>LmjF34.2650</u>	<u>Tb04.29M18.600</u> <u>Tb10.05.0100</u>	<u>Tc00.1047053507993.200</u> <u>Tc00.1047053509065.150</u> <u>Tc00.1047053510877.90</u>
<u>9.B.4.4.1</u>			
	-	-	<u>Tc00.1047053506459.270</u> <u>Tc00.1047053510161.20</u>

Dr Cecilia Alsmark (Cecilia.Alsmark@Newcastle.ac.uk)

Dr T. Martin Embley (Martin.Embley@ncl.ac.uk)

Table S11. List of strongest phylogenetic tree-based cases for prokaryote to eukaryote horizontal gene transfer in the Trityps.

For the analysis, shorter names were assigned due to software restrictions. Each tree is after one of the Trityp orthologues within it. The presence of orthologues in the other Trityp genomes is indicated. Phylogenetic trees for cases of HGT not mentioned in the text can be found in additional supplementary materials as a searchable PDF document (HGTTrees.pdf).

Identifier	Gene name	Product	Tree name	orthologs		
				Lm	Tb	Tc
LM0001	LmjF13.0090	carboxypeptidase, putative	LM0001tctb	x	x	x
LM0003	LmjF27.2660	peptidyl dipeptidase, putative	LM0003e	x		
LM0013	LmjF29.1570	glutamamyl carboxypeptidase, putative	LM13_89tbt2	x	x	X
LM0021	LmjF28.1350	haloacid dehalogenase-like hydrolase, putative	LM0021tctb2	x	x	X
LM0023	LmjF28.1370	haloacid dehalogenase-like hydrolase, putative	LM0023tbt2	x	x	X
LM0025	LmjF31.2880	aldehyde reductase, putative	LM0025tbt2	x		
LM0029	LmjF17.1050	hydrolase-like protein	LM0029tctb2	x	x	x
LM0031	LmjF29.2800	inosine-adenosine-guanosine-nucleoside hydrolase, putative	LM0031tbt2	x	x	x
LM0033	LmjF27.2340	sucrose hydrolase-like protein	LM33_43_79	x		
LM0045	LmjF06.0930	2,4-dienoyl-coa reductase-like protein	LM45_93tbt2	x	x	x
LM0047	LmjF36.0060	L-ribulokinase, putative	LM0047tc	x		x
LM0051	LmjF26.2710	glutamate 5-kinase, putative	LM0051	x		
LM0053	LmjF36.5960	glycerophosphoryl diester phosphodiesterase, putative	LM0053tc	x		
LM0063	LmjF28.2910	glutamate dehydrogenase, putative	LM0063tc	x		x
LM0065	LmjF36.5240	glycosyl hydrolase, putative	LM0065tctb2	x	x	x
LM0071	LmjF28.2510	acyl-CoA dehydrogenase, putative	LM0071tctb	x	x	x
LM0075	LmjF30.2090	alcohol dehydrogenase, putative	LM0075	x		
LM0077	LmjF33.2300	UDP-glucose 4'-epimerase, putative	LM0077tctb	x	x	x
LM0081	LmjF36.0260	xylulokinase, putative	LM0081	x		
LM0083	LmjF06.1270	coproporphyrinogen iii oxidase, putative	LM0083 (Fig. S4a)	x		
LM0085	LmjF04.0460	adenylosuccinate lyase, putative	LM0085tctb	x	x	x
LM0087	LmjF33.2550	isocitrate dehydrogenase, putative	LM0087	x		
LM0101	LmjF18.1580	NH, nonspecific nucleoside hydrolase	LM0101tbt2	x		
LM0103	LmjF31.0010	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase, putative	LM0103tb	x	x	
LM0111	LmjF33.0520	d-xylulose reductase, putative	LM0111	x		

Dr Cecilia Alsmark (Cecilia.Alsmark@Newcastle.ac.uk)

Dr T. Martin Embley (Martin.Embley@ncl.ac.uk)

LM0117	LmjF33.0560	hypothetical protein, conserved	LM0117tbtc	x	x	x
LM0135	LmjF14.1190	hypothetical protein, conserved	LM0135tbtc	x	x	x
LM0165	LmjF17.1460	ferrochelatase-like protein	LM0165 (Fig S4c)	x		
LM00175	LmjF23.0260	argininosuccinate synthase, putative	LM00175	x		
LM0208	LmjF06.1280	protoporphyrinogen oxidase-like protein	LM0208 (Fig S4b)	x		
LM0253	LmjF23.0690	3-ketoacyl-coa thiolase-like protein	LM0253	x	x	x
LM0262	LmjF26.2710	glutamate 5-kinase, putative	LM0262	x		
LM0285	LmjF29.2800	inosine-adenosine-guanosine-nucleoside hydrolase, putative	LM0285	x	x	x
LM0311	LmjF34.0610	Enoyl-[acyl-carrier-protein] reductase	LM0311	x		
TB0033	Tb05.1P6.110	inosine-5'-monophosphate dehydrogenase, putative	TB0033		x	
TB0055	Tb09.211.0700	isopentenyl-diphosphate delta-isomerase, putative	TB0055		x	
TB0142	Tb08.26N11.790	pteridine reductase, putative	TB0142	x	x	x
TC0035	Tc00.1047053408799.19	isopentenyl-diphosphate delta-isomerase, putative	TC0035tb	x	x	x
TC0037	Tc00.1047053506513.110	peptidase T, putative	TC0037lmtb2	x	x	x
TC0075	Tc00.1047053506457.60	2-aminoethylphosphonate:pyruvateaminotransferase	TC0075 (Fig S5)	x		x
TC0085	Tc00.1047053509935.29	proline racemase	TC0085			x
TC0199	Tc00.1047053505647.40	endoribonuclease L-PSP (pb5), putative	TC0199	x		x
TC0214	Tc00.1047053509717.80	glyceraldehyde 3-phosphate dehydrogenase, cytosolic	TC0214	x	x	x
TC0215	Tc00.1047053509937.20	hypothetical protein, conserved	TC0215	x		x
TC0218	Tc00.1047053511153.50	haloacid dehalogenase hydrolase	TC0218			x
TC0219	Tc00.1047053511309.20	hydrolase, putative	TC0219			x
TC0236	Tc00.1047053506559.80	NAD-dependent deacetylase; transcriptional regulator, Sir2 family protein; nicotinic acid mononucleotide 5,6-dimethylbenzimidazole (cobb) protein	TC0236	x	x	x

Colour scheme:

	absent in the Tritryps
	present in Lm, Tb, Tc
	only present in Lm
	only present in Tb
	only present in Tc
	only present in Lm, Tb
	only present in Lm, Tc
	only present in Tb, Tc