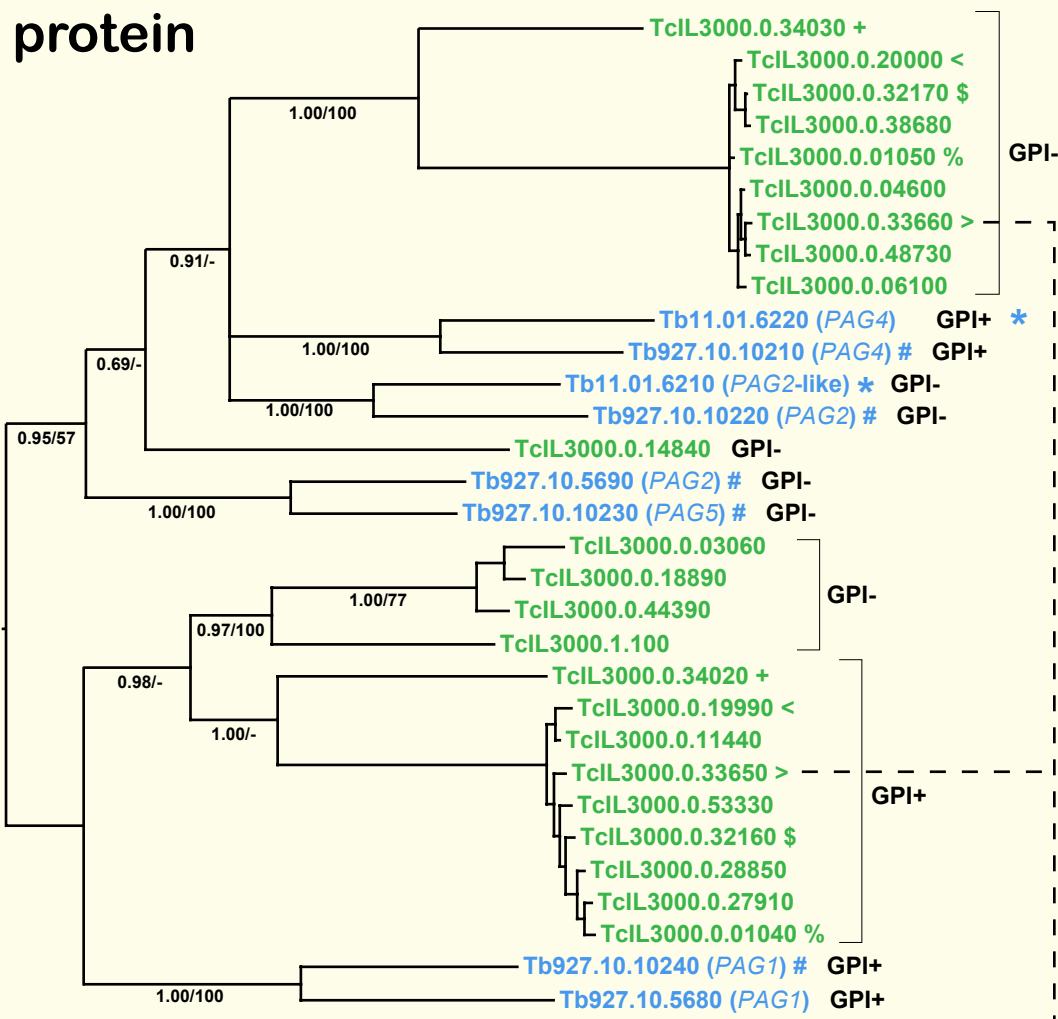
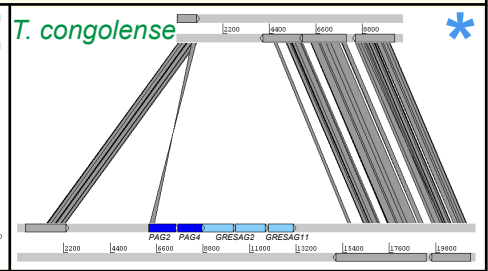
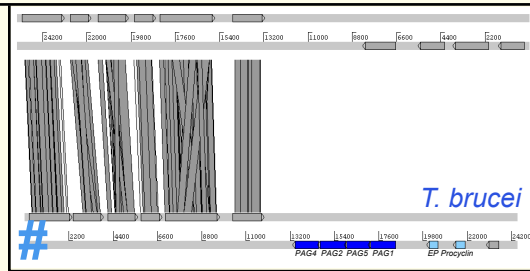


If you use these data, please cite:

Jackson, AP et al. 2012. A cell-surface phylome for African Trypanosomes. *manuscript submitted*.

Fam14: PAG-type transferrin receptor-like protein



The paraphyly of *T. brucei* and *T. congolense* PAG-like genes indicates that this family diversified prior to the separation of the two species, and suggests that genes switch to new genomic positions relatively easily.

0.25 rep/site

Key: *Tb927.*
T. brucei

TcIL3000.
T. congolense

GPI+/-
GPI anchor
present/
absent

! *T. brucei* procyclin-associated genes (PAG) are found at strand-switch regions that are not conserved in *T. congolense*, (insets showing ACT comparisons for PAG loci on chromosome 10 (#) and 11(*) in which vertical grey bars represent significant BLASTp matches and genes of interest are coloured).

T. congolense PAG-like genes form two clades, paraphyletic with *T. brucei* PAG, one of which displays a predicted GPI anchor (reminiscent of the bloodstream stage TFR heterodimer in *T. brucei* (ESAG6/7)). These are often arranged in tandem pairs. Each pair includes one gene from each clade, as indicated by shared symbols following gene IDs. These loci do not appear to be conserved in *T. brucei* and may occur in subtelomeric regions (inset showing Artemis view of a PAG-like locus in *T. congolense*).



NOTES: Fam14 consists of the procyclin-associated genes from *T. brucei* and their homologs in *T. congolense*, which encode transferrin receptor-like proteins. GPI anchors were predicted using *Fraganchor*.

The Bayesian phylogram was estimated from a multiple protein sequence alignment of 451 characters, using MrBayes under default settings. The tree is mid-point rooted. Selected nodes are supported by posterior probabilities and non-parametric bootstraps generated from a maximum likelihood analysis using an LG model with rate heterogeneity.