If you use these data, please cite:

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



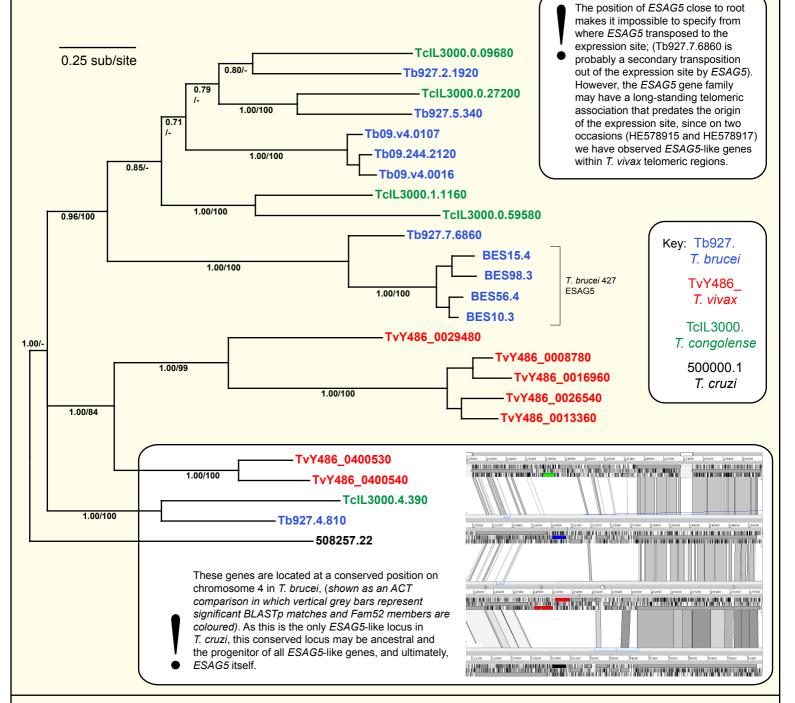


Fam52:

Expression siteassociated gene 5-like genes



Fam52 has evolved through a series of duplicative transpositions in Salivarian trypanosomes, relative to the single-copy state in *T. cruzi* and *L. major*, suggesting that their functions have been selected. Most core chromosomal loci (n=4) have orthologs in *T. congolense* and so were transposed from the ancestral locus prior to the *T. brucei/T. congolense* split. Conversely, all *T. vivax ESAG5*-like genes (n=7) are monophyletic. We can view the unique derivation of *ESAG5* in *T. brucei* as part of this process, and functional differentiation is supported by a significant acceleration of substitution rate along the *ESAG5* lineage, when compared with *T. brucei* core chromosomal loci.



NOTES: Fam52 includes ESAG5 sequences from *T. brucei* 427 telomeric contigs (Hertz-Fowler *et al.* 2008, PLoS One, **3**,10:e3527) and all homologs. The Bayesian phylogram was estimated from a multiple protein sequence alignment of 593 characters, using MrBayes under default settings. The tree is rooted with a *T. cruzi* outgroup. Selected nodes are supported by posterior probabiliies and non-parametric bootstraps generated from a maximum likelihood analysis using an LG model with rate heterogeneity.