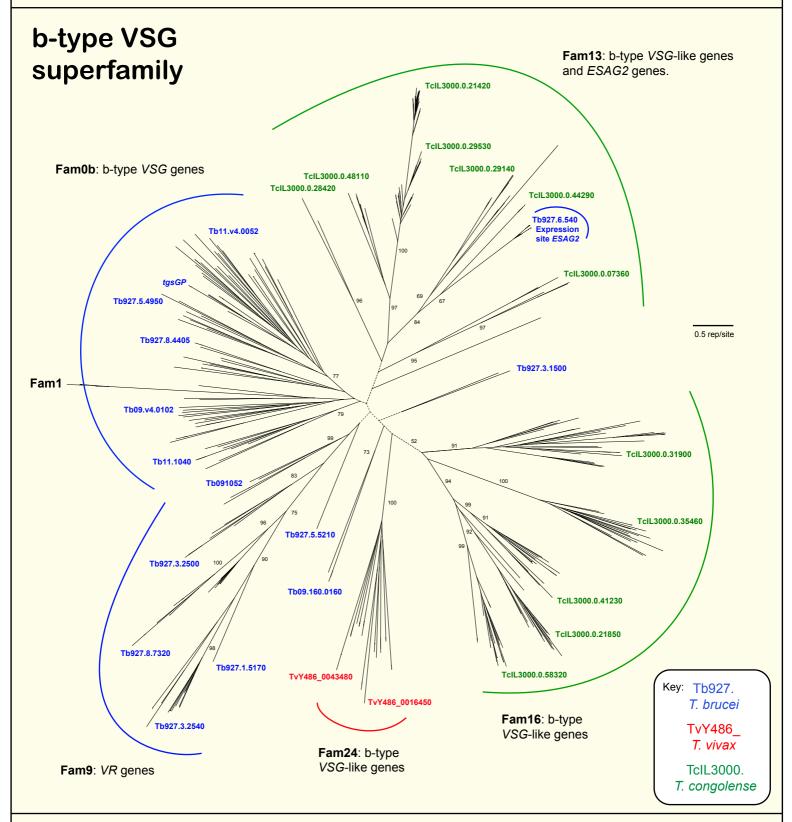
If you use these data, please cite:

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





NOTES: The maximum likelihood phylogram was estimated from a multiple protein sequence alignment of 660 characters, using RAxML with an LG model and corrections for rate heterogeneity. The tree is unrooted. Basal nodes are particularly unstable and have very little or no support, these regions are indicated by dashed branches. Selected nodes are supported by non-parametric bootstraps and posterior probability values generated from a Bayesian analysis of the same data set in MrBayes.

The tree contains major clades that correspond with BLAST-defined surface phylome families. In this tree, canonical *T. brucei VSG* include the atypical *VSG*-related Fam1 and *tgsGP* genes. All *VR* genes are positioned outside of canonical *T. brucei* VSG but are not monophyletic.