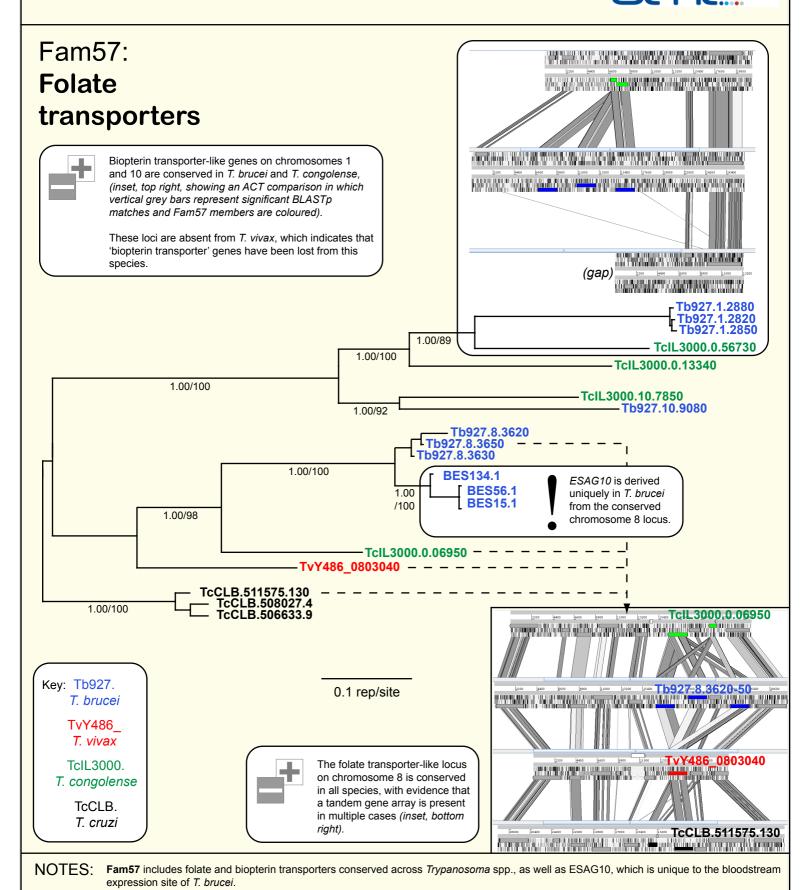
If you use these data, please cite:

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





The Bayesian phylogram was estimated from a multiple protein sequence alignment of 604 characters, using MrBayes under default settings. The tree is rooted with *T. cruzi* sequences. Selected nodes are supported by posterior probabilities and non-parametric bootstraps generated from a maximum likelihood analysis using an LG model with rate heterogeneity.