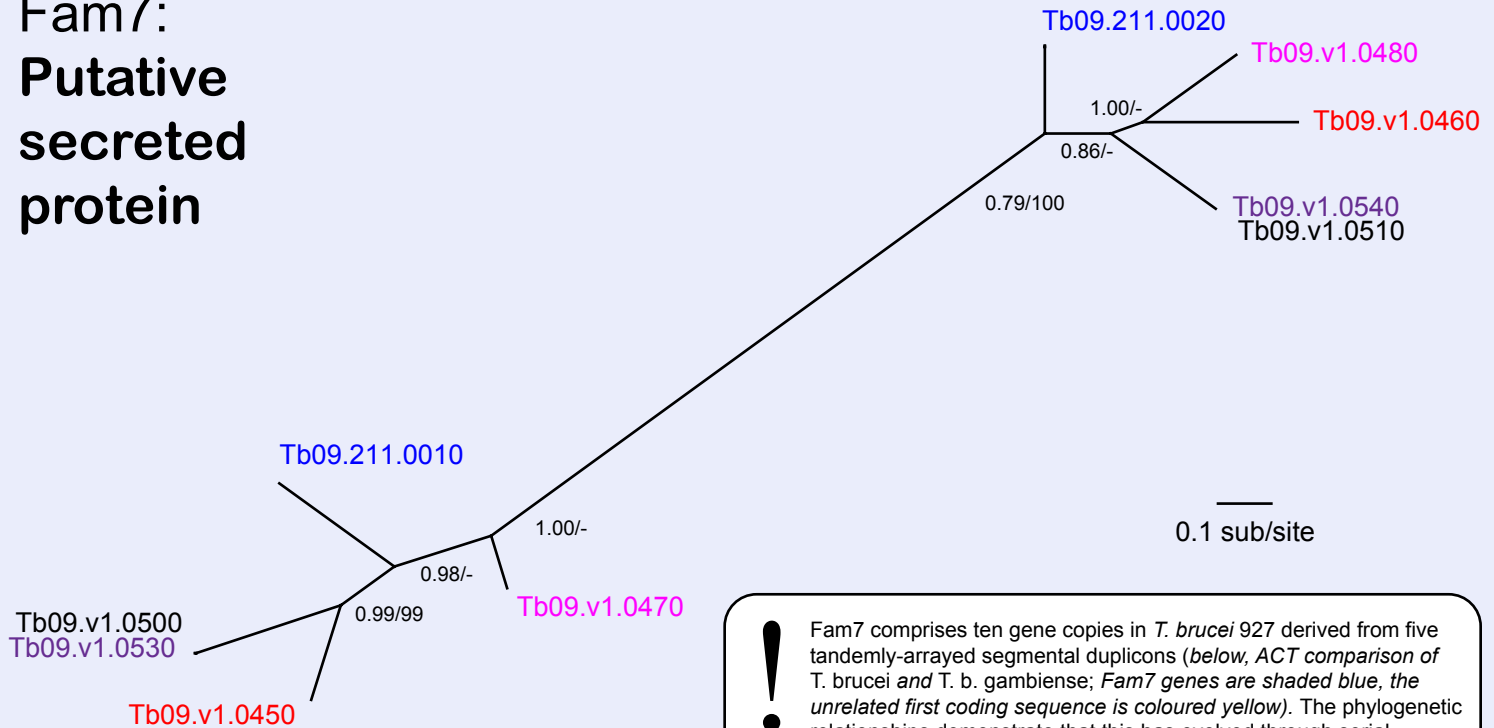


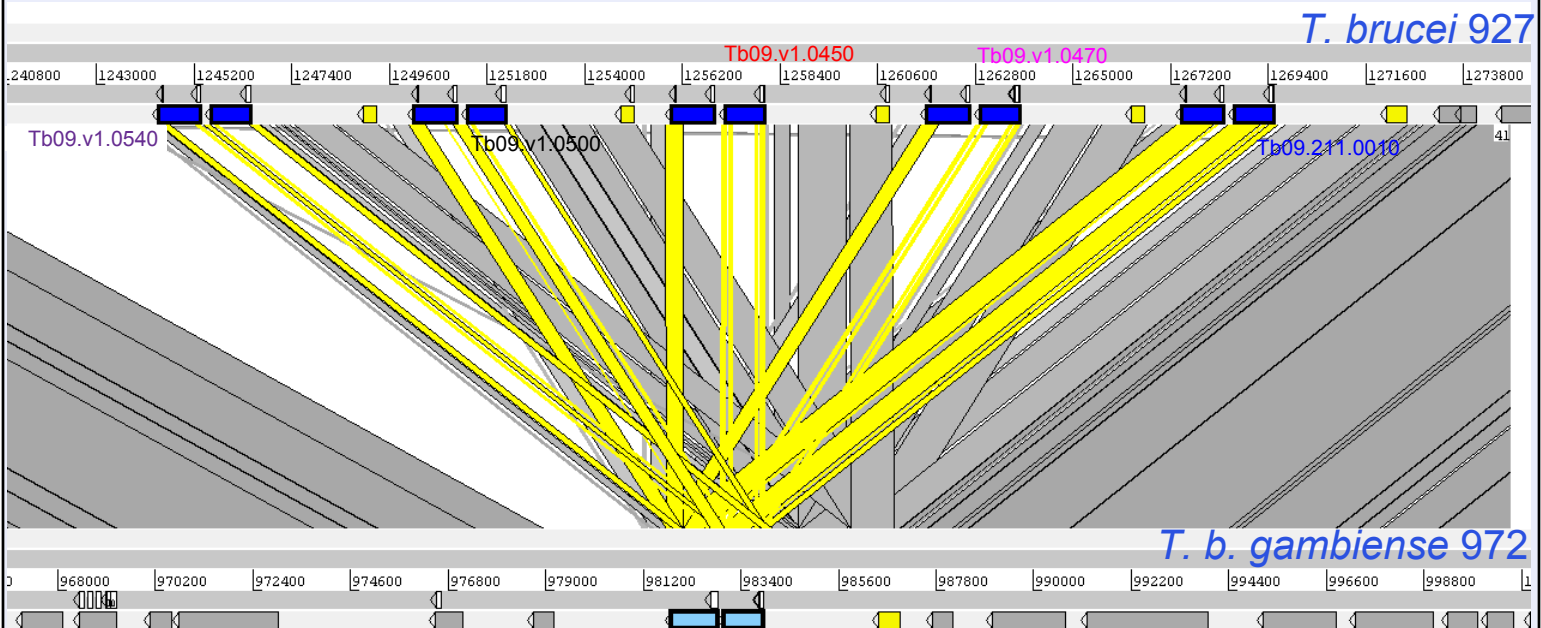
If you use this data, please cite:

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

Fam7: Putative secreted protein



Fam7 comprises ten gene copies in *T. brucei* 927 derived from five tandemly-arrayed segmental duplicons (below, ACT comparison of *T. brucei* and *T. b. gambiense*; Fam7 genes are shaded blue, the unrelated first coding sequence is coloured yellow). The phylogenetic relationships demonstrate that this has evolved through serial duplication of an initial pair of tandem duplicates, resulting in two clades corresponding to the second and third coding sequences in the duplcon (gene labels are shaded to indicate the partners in each of five tandem repeats). Two genes corresponding to a single repeat are conserved in *T. b. gambiense* DAL972.



NOTES: Fam7 genes are arranged in a tandemly-arrayed segmental duplication on chromosome 9. The duplication includes three coding sequences; the second and third coding sequences, which comprise Fam6, encode homologous hypothetical proteins with predicted signal peptides. The third coding sequence has a predicted GPI anchor.

The Bayesian phylogram was estimated from a multiple nucleotide sequence alignment of 792bp, using MrBayes with a GTR+ Γ model and default settings. The tree is unrooted. Selected nodes are supported by posterior probabilities and non-parametric bootstraps generated from a maximum likelihood analysis under a GTR+ Γ model.