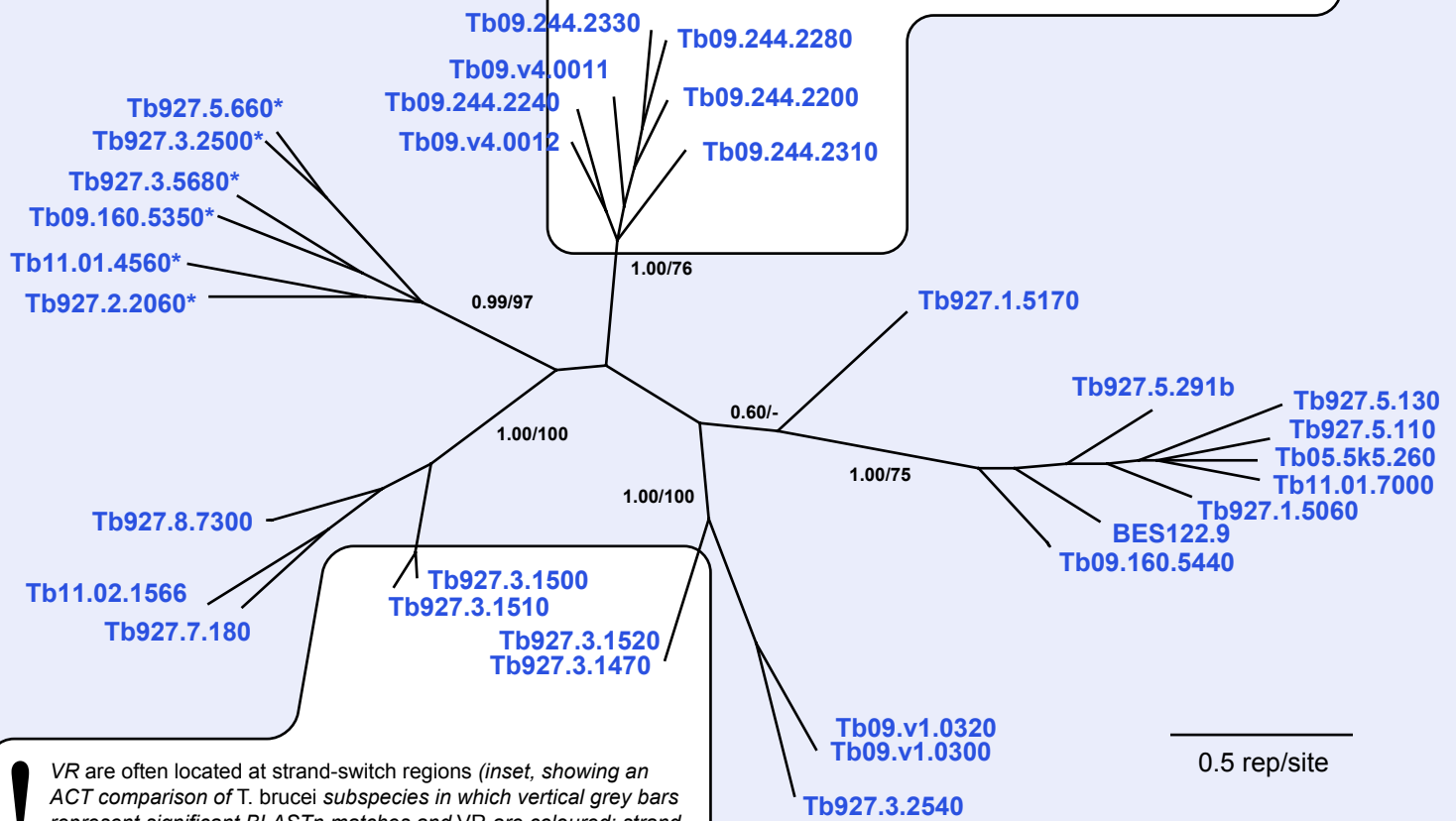
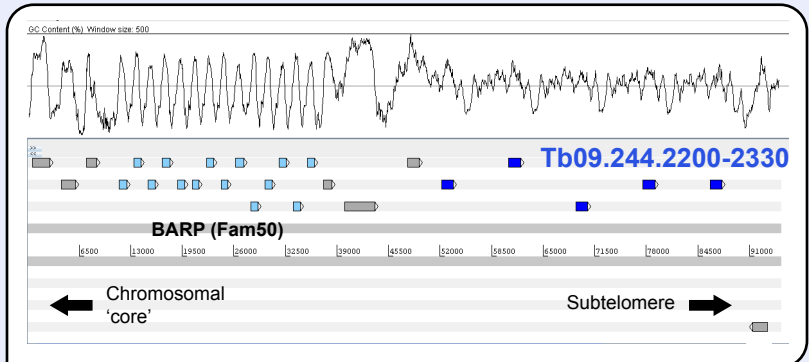


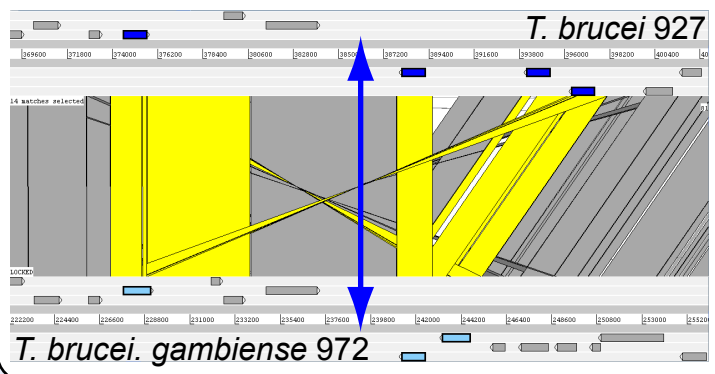
If you use this data, please cite:

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

Fam9: VSG-related (VR) genes



! VR are often located at strand-switch regions (*inset, showing an ACT comparison of T. brucei subspecies in which vertical grey bars represent significant BLASTn matches and VR are coloured; strand-switch denoted by blue arrow*). Unlike canonical VSG, VR are usually conserved in position and sequence between *T. brucei* subspecies, suggesting that they do not recombine.



NOTES: Fam9 comprises all VR genes, which are unique to *T. brucei*. These include two genes with products currently annotated as 'hypothetical' (Tb927.3.3200 and Tb927.5.660). Also included are six genes initially annotated as 'atypical' VSG (*denoted with an asterisk**), these genes possess partial N- and C-terminal domains that are diagnostic of canonical b-VSG but cluster with VR based on the sequences of their conserved cores, (i.e. they have the appearance of intermediates between VR and b-VSG). All members have predicted signal peptides.

The Bayesian phylogram was estimated from a multiple protein sequence alignment of 213aa, representing the conserved core with variable N- and C-terminal domains removed, using MrBayes under default settings. The tree is unrooted. Nodes are supported by posterior probability values and non-parametric bootstraps generated from a maximum likelihood analysis using an LG model with rate heterogeneity.