

If you use this data, please cite:

Jackson, AP et al. 2011. Divergent evolution of antigenic variation in African Trypanosomes. *manuscript submitted.*

# Fam0b: b-type VSG

! Telomeric VSG from bloodstream expression sites are shown here in yellow boxes. These are largely taken from *T. brucei* 427, and the expression site number is given\*. Three VSG from *T. brucei* 927 expression sites are also included (marked with a hash #).

It is clear from their distribution that telomeric VSG are not a distinct subset of all VSG, but are instead a random sample of total diversity.

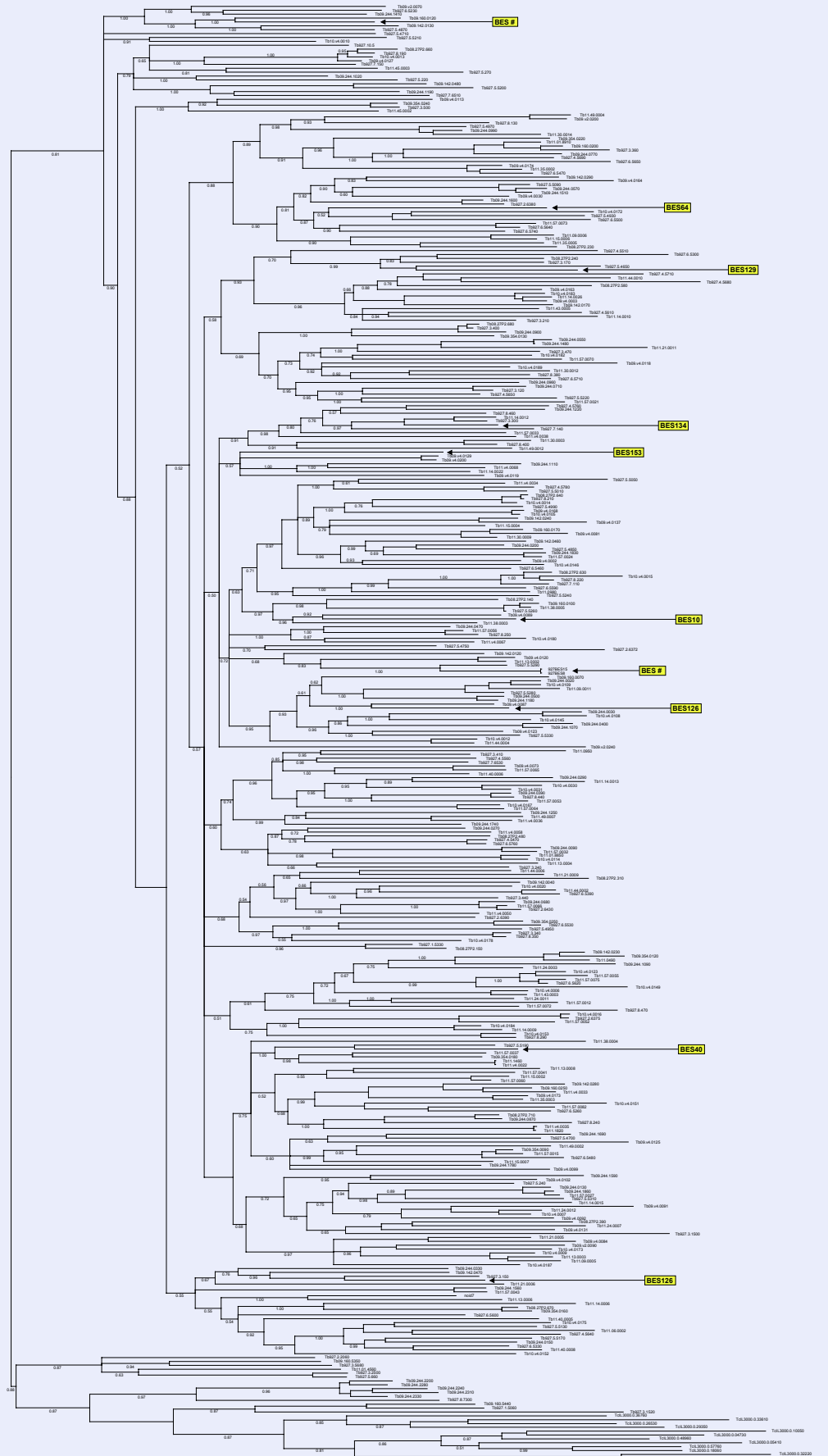
0.1 sub/site

## NOTES:

**Fam0b** includes the b-type variant surface glycoprotein genes from *T. brucei*. All full-length genes and pseudogenes (n=352) were selected from vsgDB ([www.vsgdb.net](http://www.vsgdb.net)).

The Bayesian phylogram was estimated from a multiple nucleotide sequence alignment of 2026 characters, using MrBayes with a GTR+I<sup>†</sup> model and default settings. This included the C-terminal domain. The tree is rooted using VSG from *T. congolense* and VSG-related genes (VR) from *T. brucei*. Selected nodes are supported by posterior probability values.

\* Hertz-Fowler et al. (2008). *PLoS One*, 3(10): e3527.



Outgroup:  
b-VSG from  
*T. congolense*  
and *T. brucei*