

If you use this data, please cite:

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

Fam4:  
Putative  
membrane  
protein

Tb927.4.3200

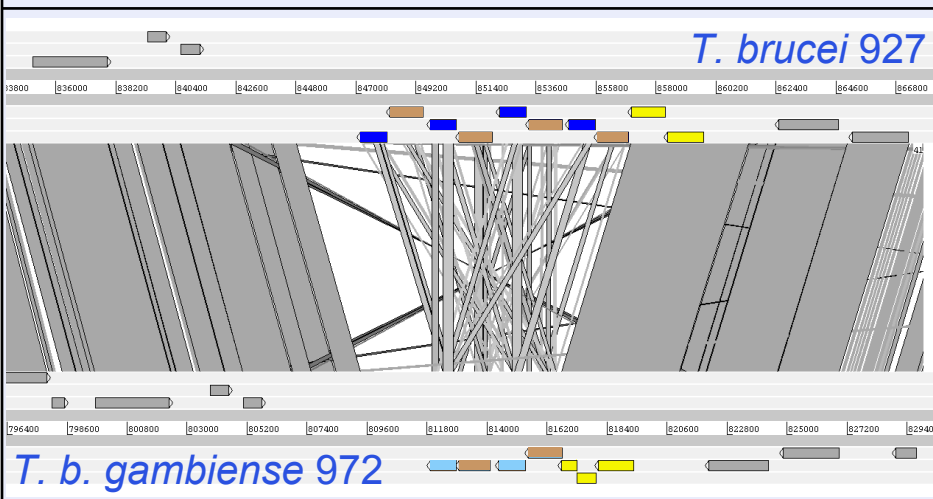
Tb927.4.3260

1.00

0.1 sub/site

Tb927.4.3220

Tb927.4.3240



**NOTES:** Fam4 consists of four tandem gene copies at a strand-switch region on chromosome 4. Each gene encodes a hypothetical protein with predicted signal peptide and ranging in length between 309 and 315 amino acids.

Fam4 is the second component of a bipartite tandem gene array; the first component is an ESAG11-like gene belonging to Fam3 (inset, showing an ACT comparison of a strand-switch region conserved in *T. brucei* and *T. b. gambiense* containing Fam4 (blue) alternating with Fam3 (brown) and followed downstream by two Fam13 gene copies (i.e. VSG/ESAG2-like).)

The Bayesian phylogram was estimated from a multiple nucleotide sequence alignment of 957 characters, using MrBayes under default settings. The tree is unrooted. Nodes are supported by posterior probability values.