

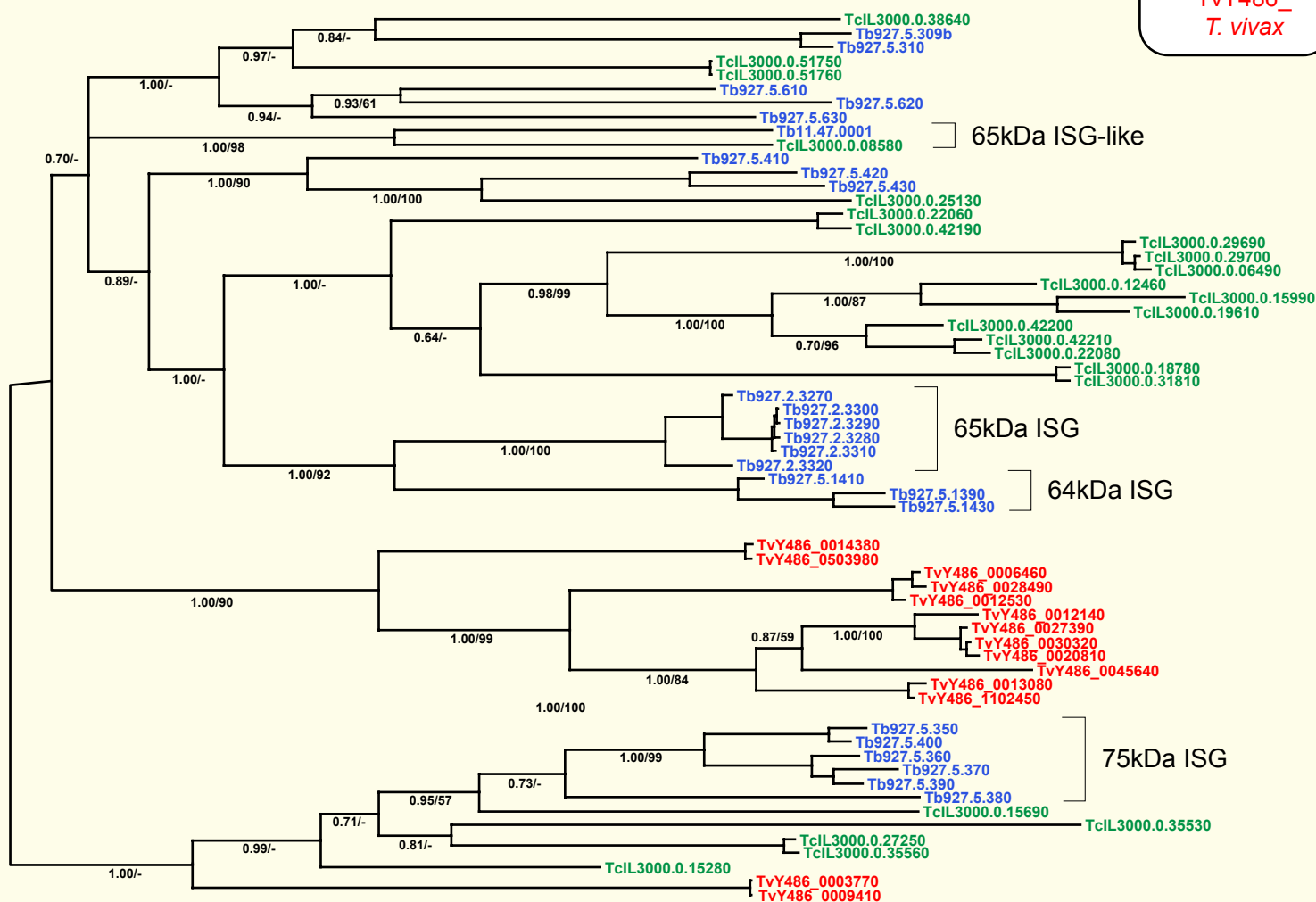
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Jackson, AP et al. 2012. A cell-surface phylome for African Trypanosomes. *manuscript submitted*.

## Fam49: Invariant surface glycoprotein

0.25 rep/site

Key: Tb927.  
*T. brucei*  
TcIL3000.  
*T. congolense*  
TvY486\_  
*T. vivax*



ISG are unique to the African trypanosomes, absent in *T. cruzi* or *Leishmania*. They split into two clades in this Bayesian phylogeny, roughly corresponding to 65kDa-like and 75kDa-like genes.

*T. brucei* lineages have orthologous lineages in *T. congolense*, indicating that the ISG repertoire is conserved between these species, although genomic locations may not be. Within the 65kDa-like clade, there is no orthology between individual loci in *T. brucei*/*T. congolense* and *T. vivax* (the sequences of which are monophyletic). This indicates that either ISG diversified independently in these two lineages, or, more likely, gene duplication proceeds quickly enough for ancestral sequence types to be replaced by derived, species-specific sequences.

ISG loci are typically arranged in tandem arrays and found at strand-switch regions or core/sub-telomeric boundaries in *T. brucei*. The draft data indicate that this is also true in *T. congolense* and *T. vivax*.

**NOTES:** Fam49 comprises the 64, 65, and 75kDa invariant surface glycoproteins as well as related sequences not previously annotated as ISG. While conserved across all African trypanosomes, ISG tend to be found at several species-specific loci throughout the core chromosomes and subtelomeric regions. All members encode proteins with a predicted signal peptide and a transmembrane helix towards the C-terminus.

The Bayesian phylogram was estimated from a multiple protein sequence alignment of 508 characters, using MrBayes under default settings. The tree is mid-point rooted as no homolog exists in *T. cruzi*. Selected nodes are supported by posterior probabilities and non-parametric bootstraps generated from a maximum likelihood analysis under a GTR+ $\Gamma$  model.