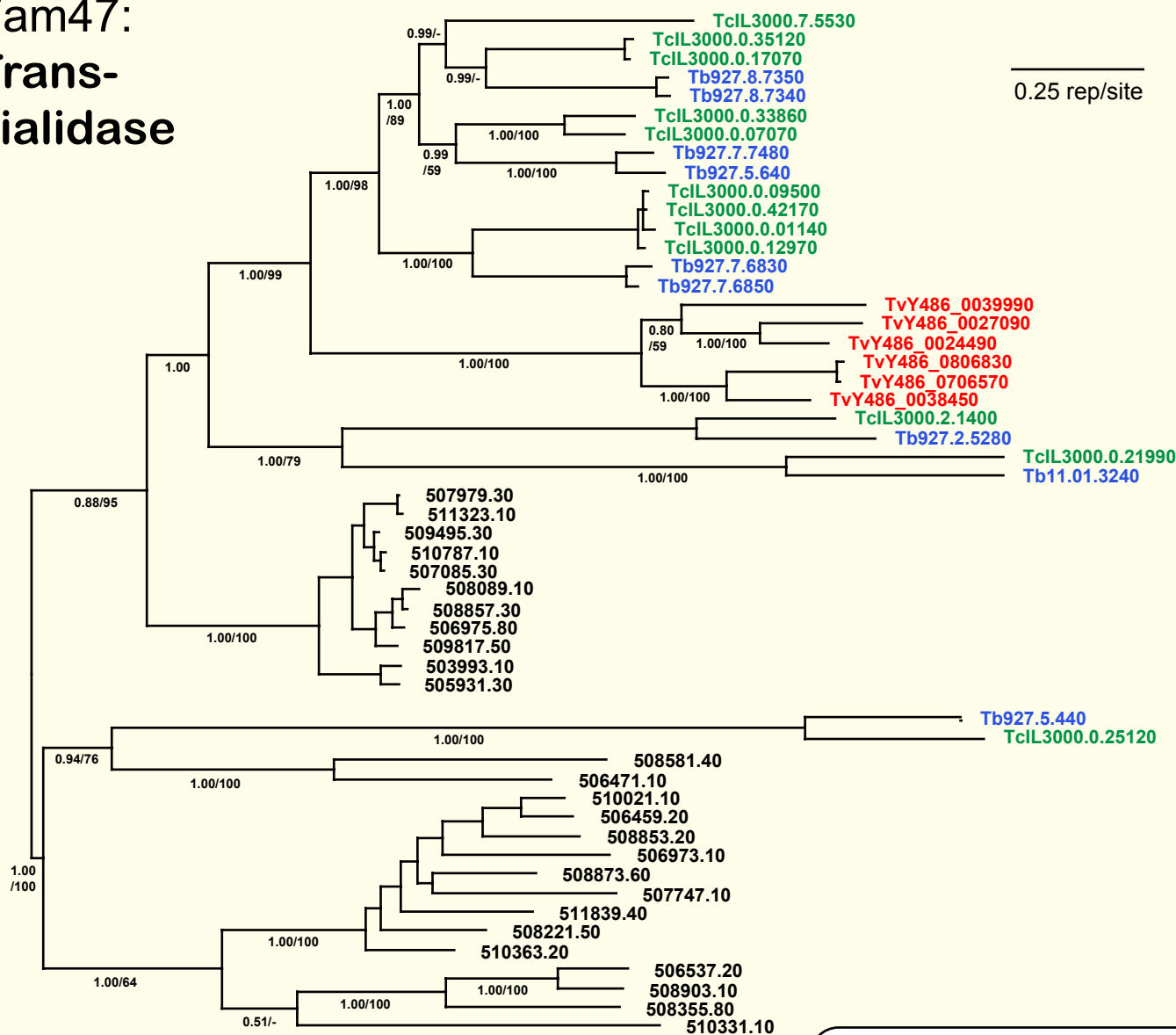


If you use these data, please cite:

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

Fam47: Trans- sialidase

0.25 rep/site



T. vivax has no orthologs to single-copy loci conserved in *T. brucei* and *T. congolense*: Tb927.5.440, Tb927.2.5280 and Tb11.01.3240.

This was confirmed after searching unassembled *T. vivax* reads for reciprocal matches.

The basal position of these lineages, with *T. cruzi* providing out-groups, indicates that these represent gene losses in *T. vivax*.

NOTES: Fam47 comprises predicted trans-sialidases from various loci throughout genomes from all species. All members have predicted signal peptides. The Bayesian phylogram was estimated from a multiple protein sequence alignment of 805 characters, using MrBayes under default settings. The tree is mid-point rooted. Nodes are supported by posterior probability values and non-parametric bootstraps generated from a maximum likelihood analysis using an LG model with rate heterogeneity.

There are >1000 trans-sialidase genes in the *T. cruzi* genome; a selection was made for rooting this tree that nevertheless represents the phylogenetic diversity of the family in *T. cruzi*.