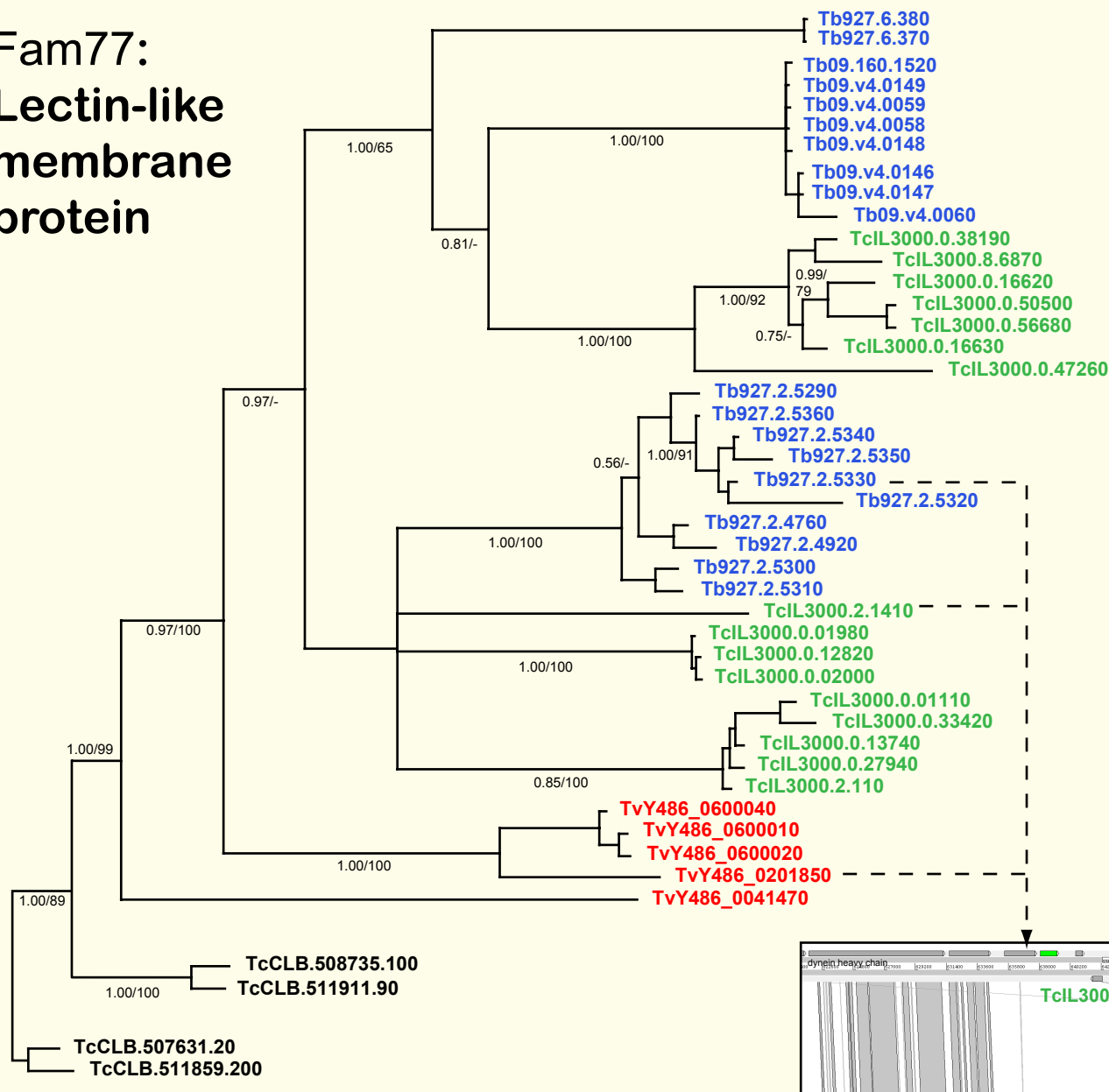


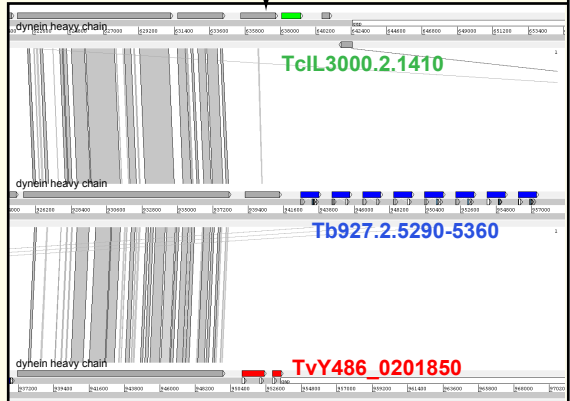
If you use these data, please cite:

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

Fam77: Lectin-like membrane protein



Key: **Tb927.** **TcIL3000.**
T. brucei *T. congolense*
TvY486. **TcCLB.**
T. vivax *T. cruzi*



NOTES: Fam77 comprises predicted membrane proteins from all species. All members have have predicted signal peptides and a transmembrane domain towards the 3' end. They range in length from 316 to 561 amino acids, largely due to a highly repetitive domain. The conserved part of the protein is similar to a C-lectin, or carbohydrate-binding, domain and these proteins have occasionally been referred to as 'mucin-like'. The C-lectin domain is evident in particular family members only, i.e. Tb09.v4.0149, although a homologous region is well conserved in all other genes. There is a single locus conserved across *Trypanosoma* (inset showing an ACT comparison in which vertical grey bars represent significant BLASTp matches and Fam77 members are coloured), which corresponds to the tandem gene array on chromosome 2 in *T. brucei*. Additionally, there are multiple species-specific loci in subtelomeric regions. It is likely that further gene copies reside within subtelomeric regions of *T. congolense* and *T. vivax*, which have not been resolved here.

The Bayesian phylogram was estimated from a multiple protein sequence alignment of 247 characters, using MrBayes under default settings. The tree is mid-point rooted with *T. cruzi* sequences. Selected nodes are supported by posterior probabilities and non-parametric bootstraps generated from a maximum likelihood analysis under a GTR+Γ model.