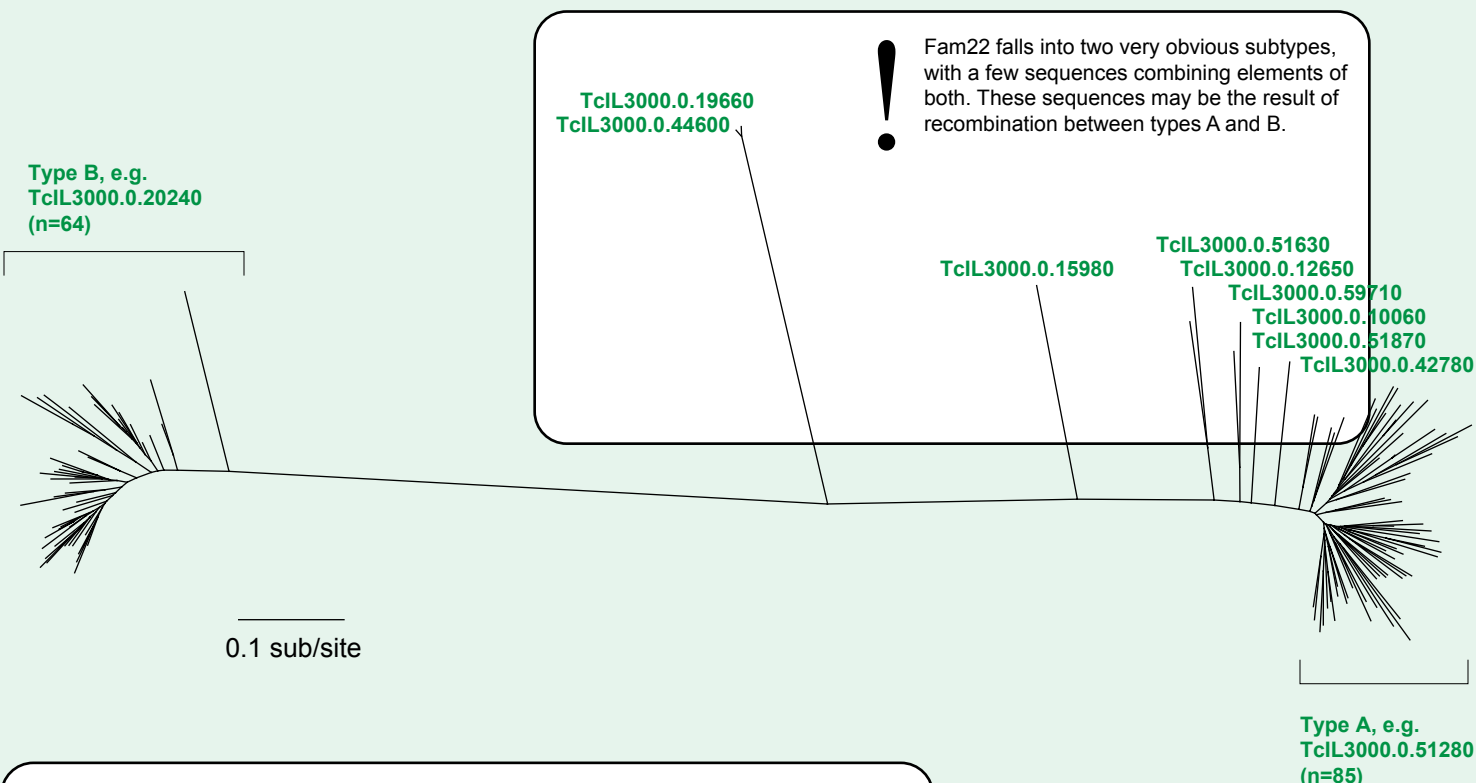
If you use this data, please cite:

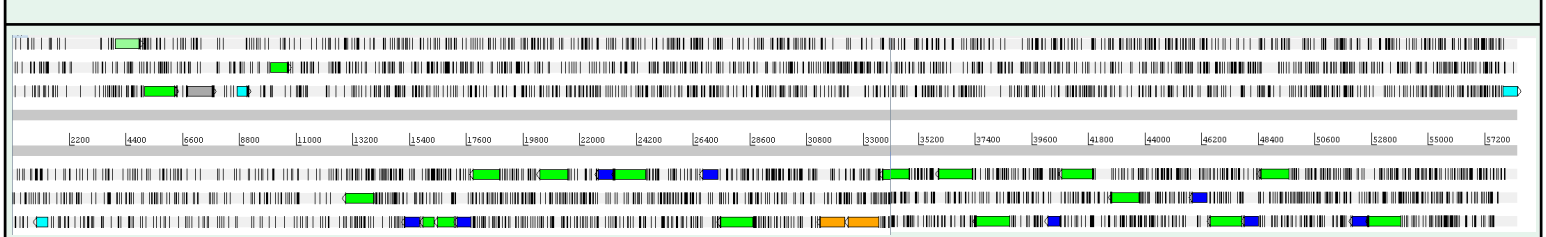
Jackson, AP et al. 2012. A cell-surface phylome for African Trypanosomes. *manuscript submitted.*

Fam22:
VSG-associated hypothetical protein



Fam22 is distributed throughout the *T. congolense* subtelomeric regions (*inset, showing a subtelomeric contig in Artemis; genes are shaded green (*VSG*), orange (*TFR-*like) and blue (Fam22)*). Fam22 genes are always positioned immediately downstream of *VSG* copies, (of various lineages). This might suggest that Fam22 is simply an open reading frame within the 3'UTR's of *VSG*. But it is known that these 3'UTR's are extremely short, perhaps only 15-30bp*.

Coupled with the observation that Fam22 transcripts are observed in all life stages except for bloodstream forms, (J. Donelson, unpublished data), this suggests that Fam22 is cotranscribed with *VSG*. However, it is not known if this mRNA is translated.



NOTES: **Fam22** comprises 157 putative coding regions from *T. congolense* subtelomeric regions. These open reading frames encode a predicted protein of 175-186 amino acids and have no matches to known protein sequences or domains. ~9% of sequences are predicted to have signal peptides (e.g. TcIL3000.0.13450), although this depends on where the start codon is placed, which is ambiguous.

* Rausch *et al.* (1994) *Eur. J. Biochem*. **223**: 813-821; Helm *et al.* (2008) *Mol. Biochem. Parasitol.* **168**: 34–42.

The maximum likelihood phylogram was estimated from a multiple nucleotide sequence alignment of 564 characters, using PHYML and a GTR+Γ model. The tree is unrooted.