



Supplemental Figure S5. Comparison of the consensus sequences *TfSat01* (defined in this work) and GenBank entry X58539 (Juan et al. 1993). **A)** The alignment of the consensus sequences. The nucleotide differences between the compared consensus are colored, and dashes indicate alignment gaps. **B)** Distribution of nucleotide sequence similarities between 228,060 monomers annotated in the *T. freemani* genome assembly Tfree1.0 and the consensus sequence *TfSat01* (left panel) and the consensus X58539 (right panel). The BLAST search was done by using the criteria of >70% sequence similarity and >70% query coverage. The black arrow points to the monomer group that has 82% similarity to the *TfSat01* consensus.