



Supplemental Figure S14. Relationships between the *T. freemani* satDNAs and their *T. castaneum* orthologs associated with DNA transposons from the Rehavkus superfamily. **A)** Phylogenetic relationships between the *TfSat15* and *TCsat23* repeats present in the inverted termini of the Rehavkus-1_TC DNA transposon. The schematic of the Rehavkus-1_TC is shown in the center, while the relationships between the *T. freemani*/*T. castaneum* satDNA repeats from the inverted termini and the relationships between the central part of the transposon sequence are shown in the upper and lower panels, respectively. The sequences of *T. freemani* are represented by blue dots, while red dots indicate *T. castaneum* sequences. The maximum likelihood trees were inferred in iTOL with nodal supports based on 100 bootstrap replicates. **B)** Phylogenetic relationships between the *TfSat23* and its orthologous *T. castaneum* copies present in the inverted termini of the Rehavkus-3_TC DNA transposon. The same description of the tree applies as for the previous one. **C)** The principal component analysis (PCA) of the *TfSat25* repeats present in the Rehavkus-like element in *T. freemani* and the orthologous repeats of the *T. castaneum* satDNA *TCsat12* present in the 80.5 kb long array on *T. castaneum* Chromosome LG4. In the PCA plot, the *T. freemani* repeats are indicated by blue dots, while the *T. castaneum* repeats are indicated by red dots. Schematic on the right illustrates the different organization of the orthologous repeats in the two sibling species.