

Supplementary Figures

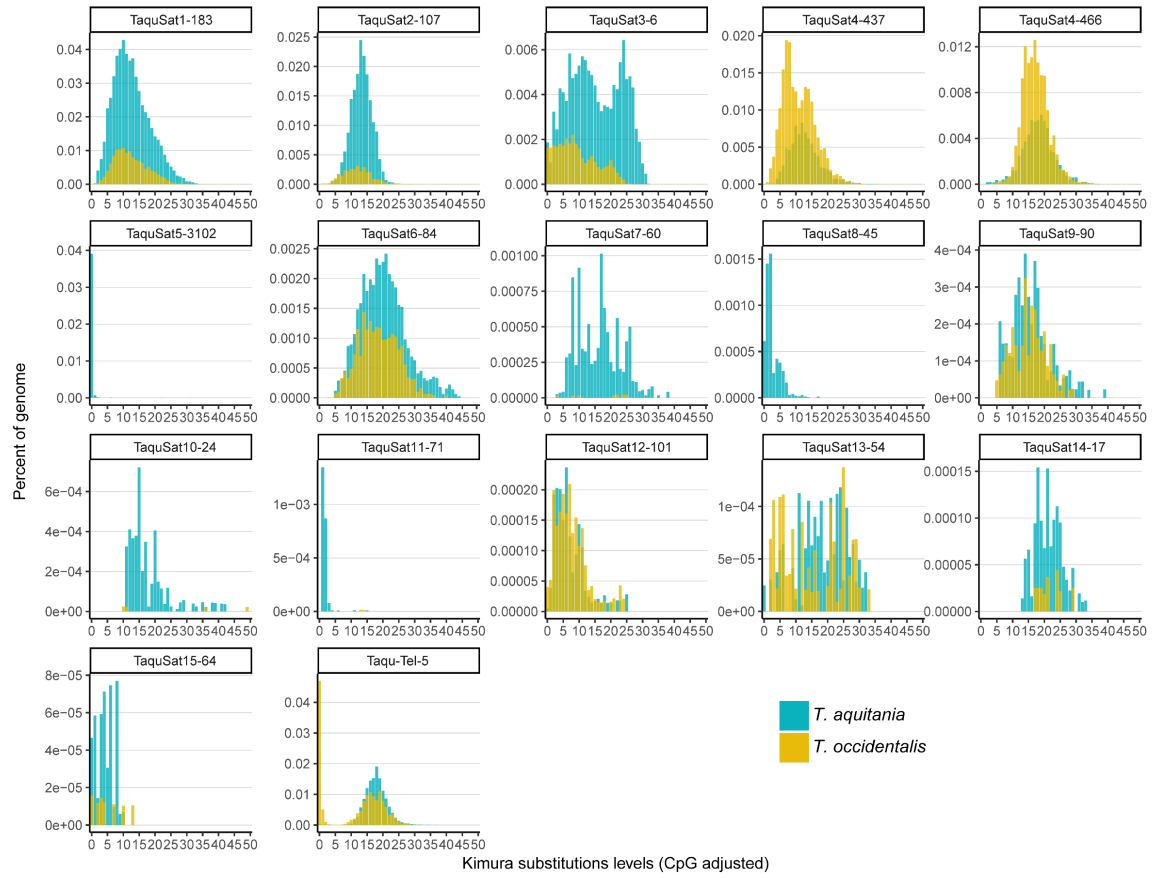


Figure S1. Satellitome landscapes (abundance versus divergence) of *Talpa aquitania* satDNA families on *Talpa aquitania* and *Talpa occidentalis* genomes.

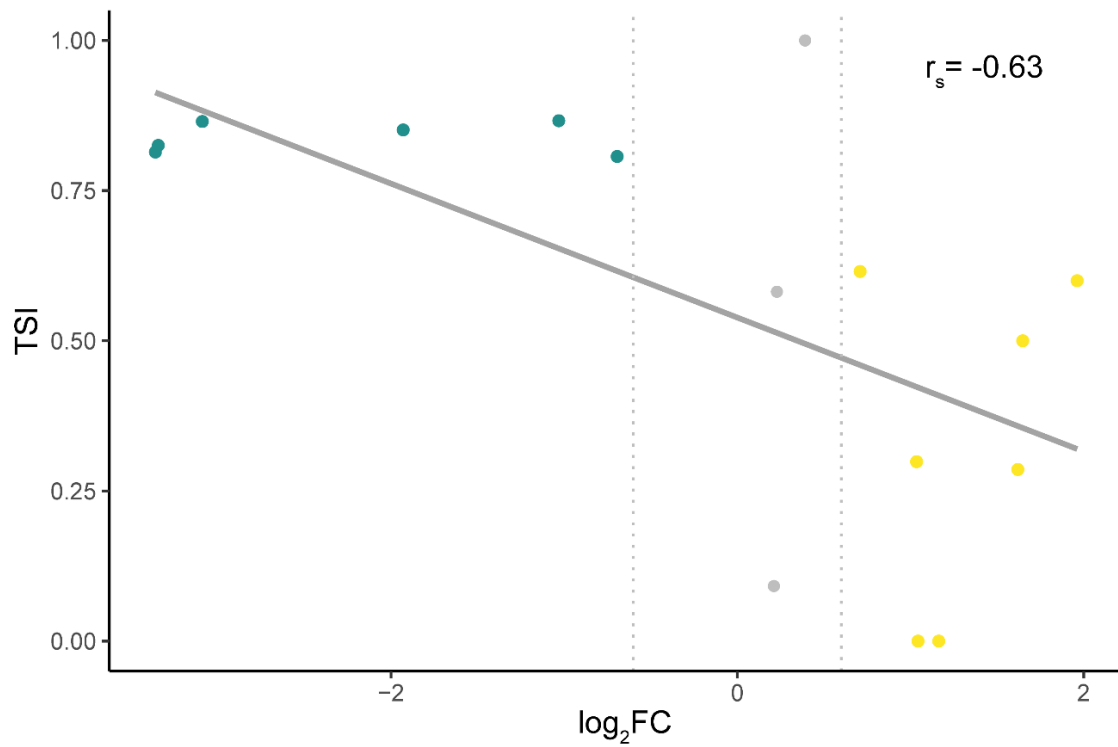


Figure S2. Correlation between the tandem structure index and the fold-change of satDNA family abundance among *Talpa occidentalis* assembled genome and *T. occidentalis* genome. The fold-change is expressed as log₂ of genome percentage among samples. SatDNA families with less of 1.5 fold-change between samples ($-0.6 < \log_2 \text{ratio} < 0.6$) are in grey, most abundant satDNA families on *T. occidentalis* assembly in yellow and most abundant on *T. occidentalis* unassembled reads in blue. Regression line is depicted in dark grey.

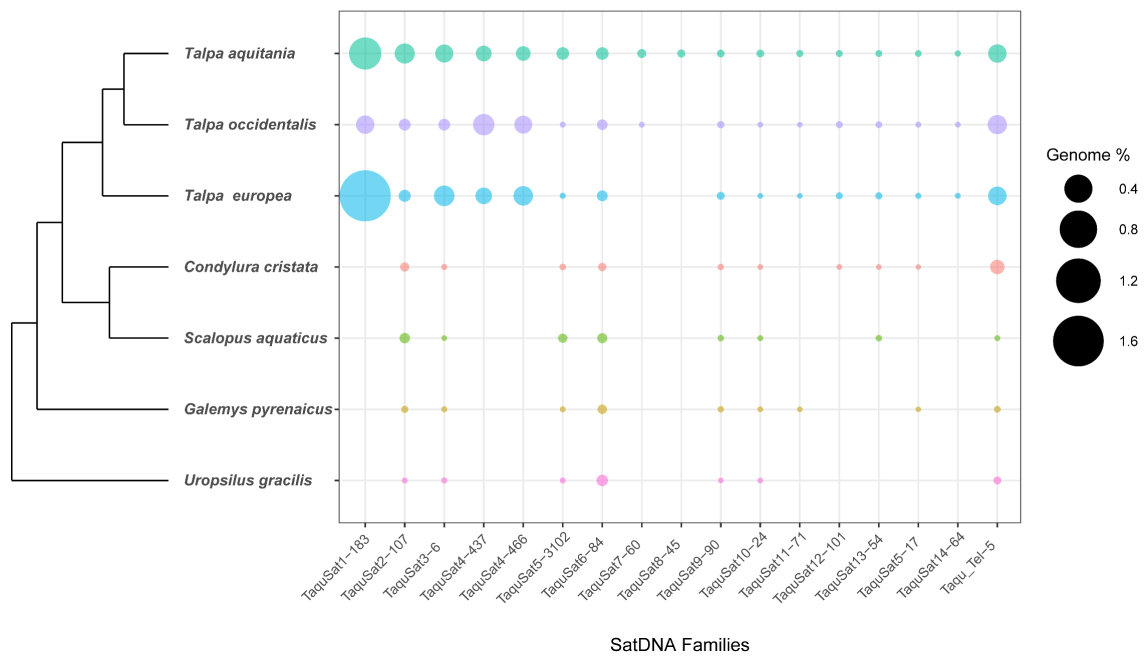


Figure S3: Presence and abundance of *Talpa aquitania* satDNA families across species of the family Talpaidea. The bubble size indicates the abundance of satDNA family.