



Figure S1. The number of high-putative (black) and low-putative (gray) satellite DNAs identified in the seven TAREAN clustering analyses (T1-T7). Genome coverage, corresponding to the total length of reads used in each TAREAN analysis, is indicated in parentheses. An asterisk marks an analysis in which reads belonging to the major satDNA TCAST were excluded from the initial subset of 1,500,000 reads.