



Figure S4. Comparative analyses of 46 *T. castaneum* satDNAs identified in this work with respect to: **A)** the proportion of scattered repeats among annotated monomer copies, **B)** the number of chromosomes/unplaced sequences at which a satDNA is annotated, **C)** genome abundance, **D)** nucleotide divergence calculated for annotated monomers. The charts are based on the data presented in the Table S3.