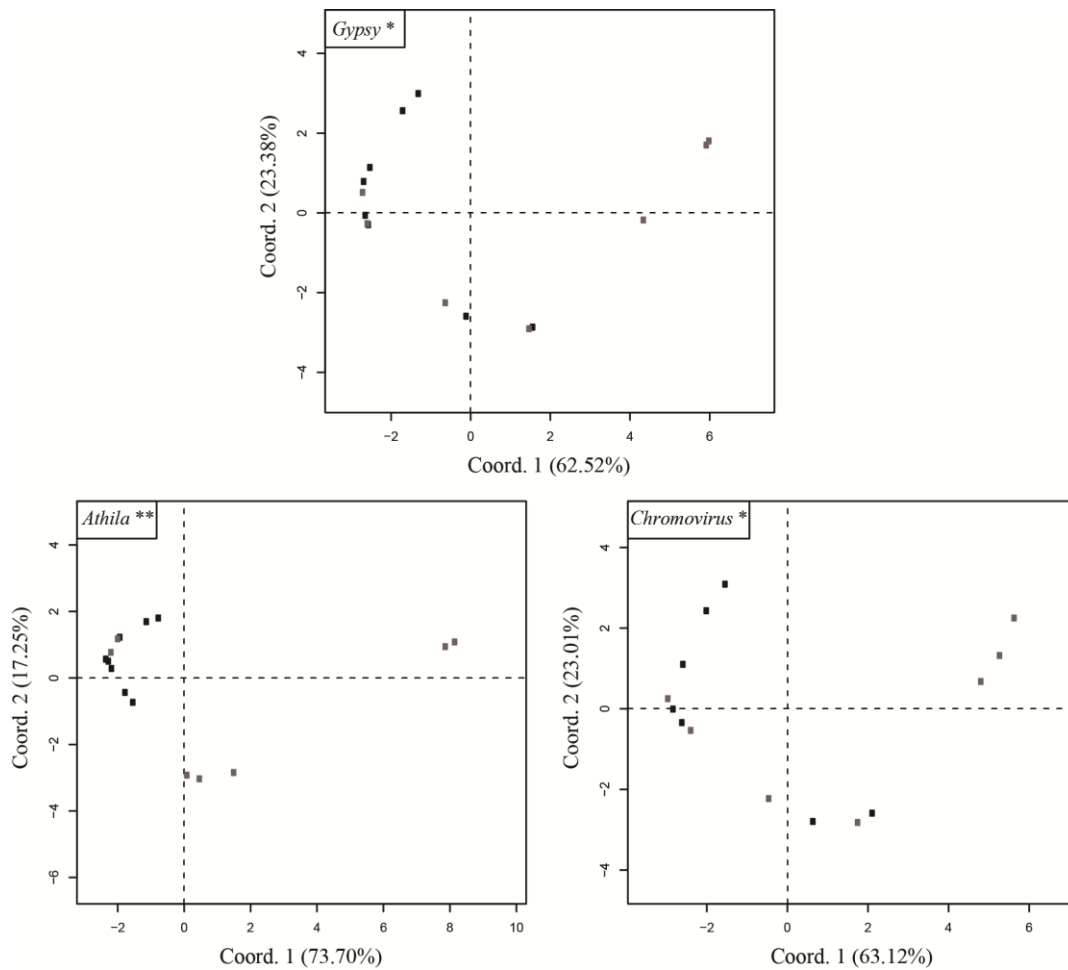


## Supplementary material 5



PCA plots of data on LTR-RTs proximity to genes of *Helianthus* genotypes for *Gypsy* superfamily, and for *Athila* and *Chromovirus* LTR-RT families in cultivars (dark dots) and wild accessions (light dots). The percentage of variation accounted by each axis is reported. Asterisks mark permutational MANOVA significance with the following significance codes: 0.01 ‘\*\*\*’ 0.05 ‘\*’.