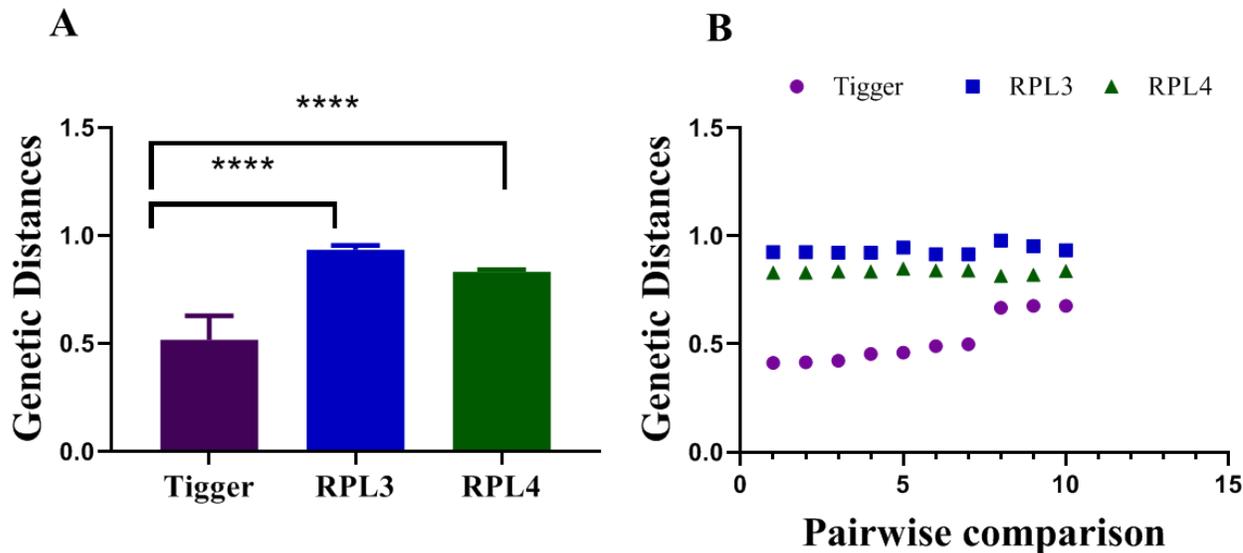
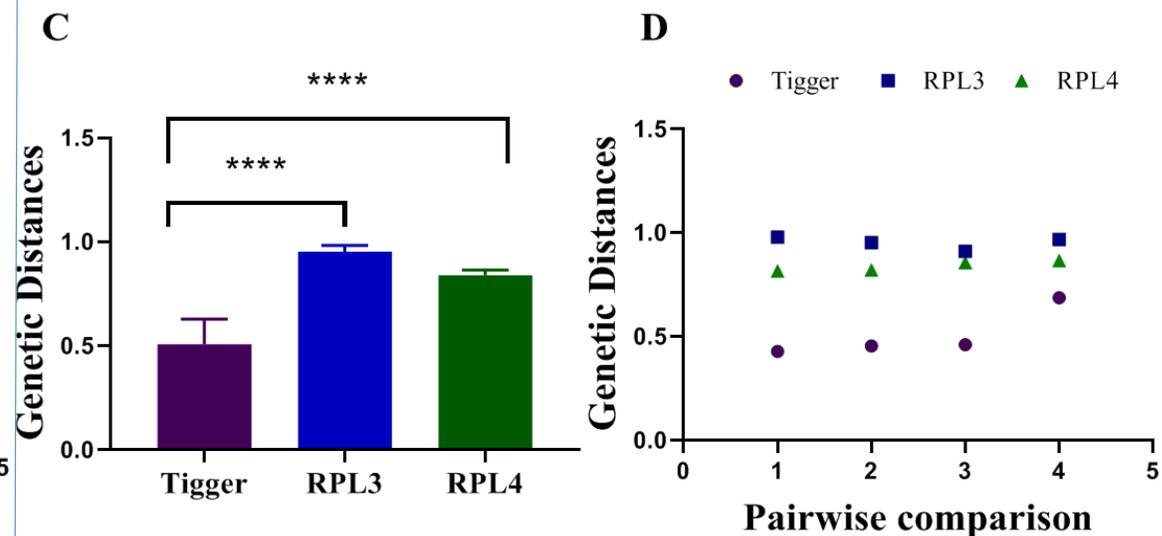


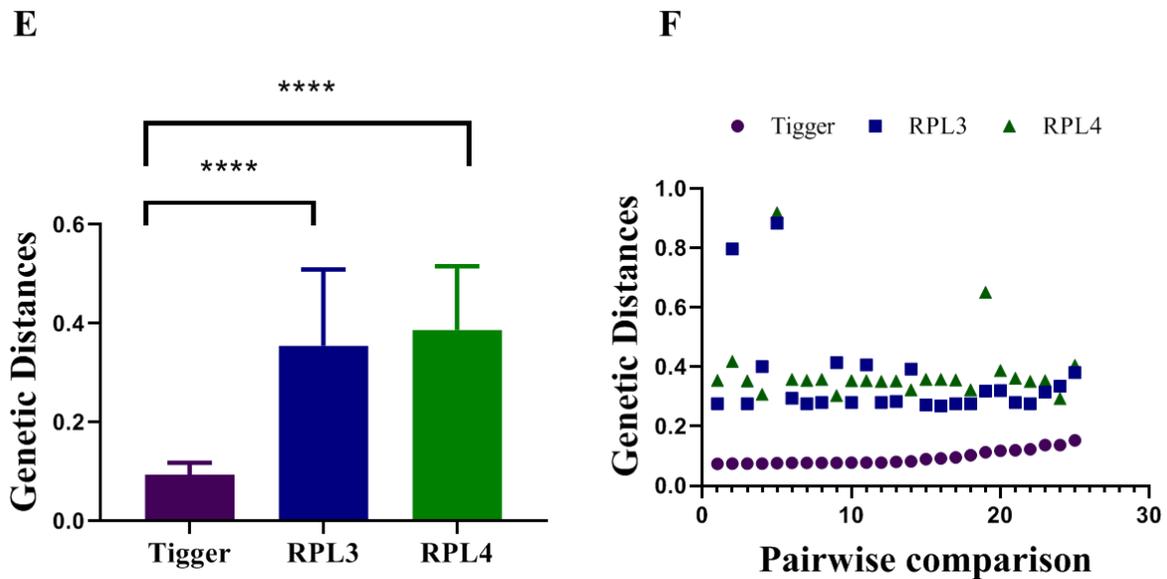
HT1



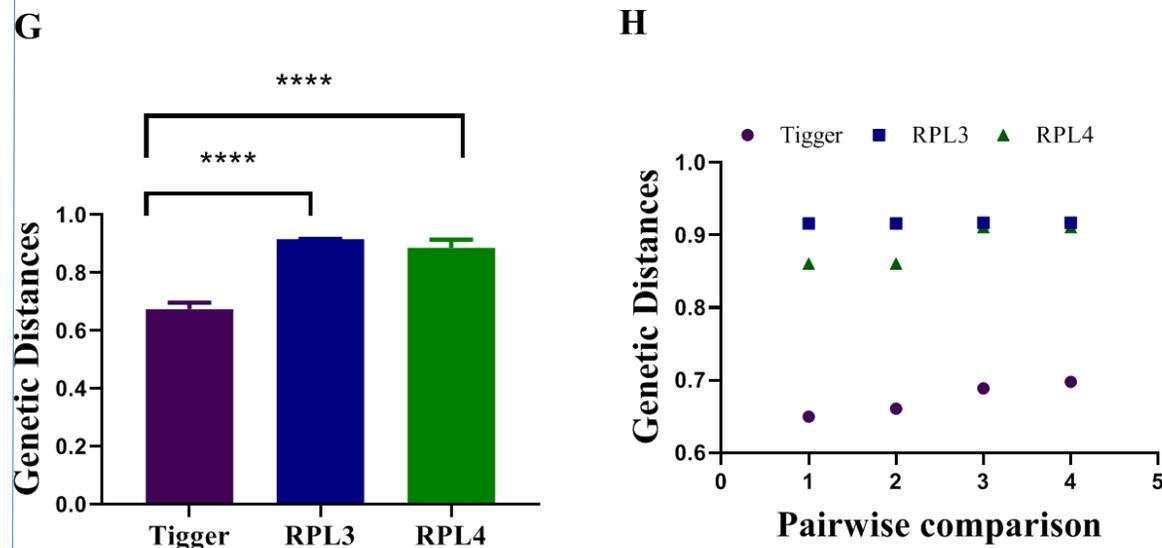
HT2

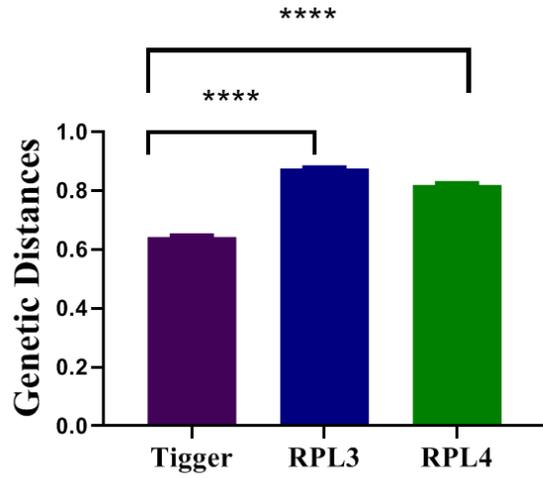
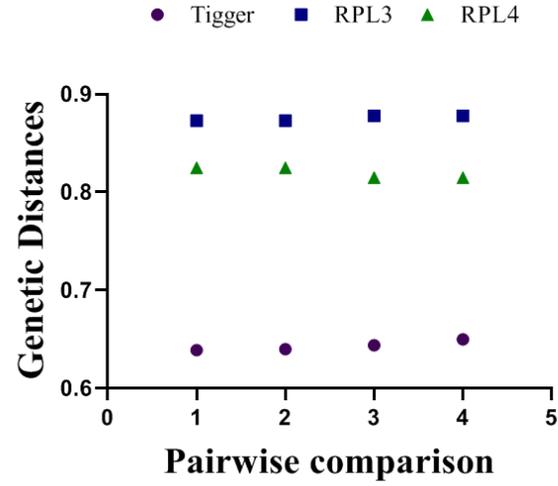
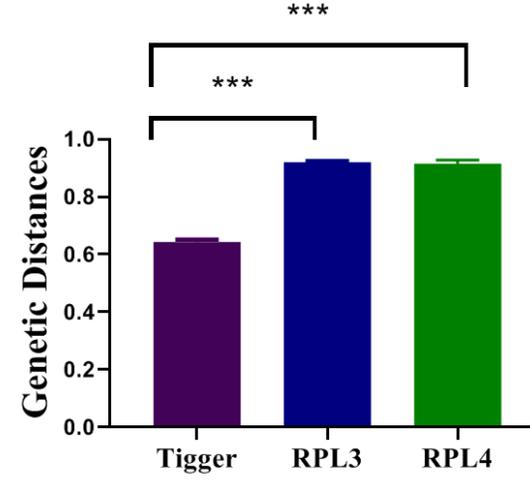
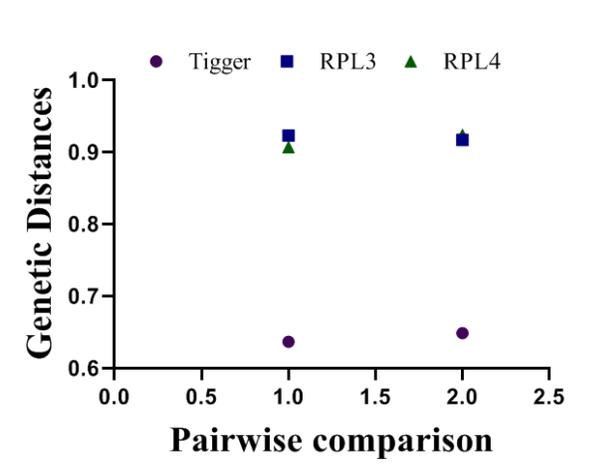
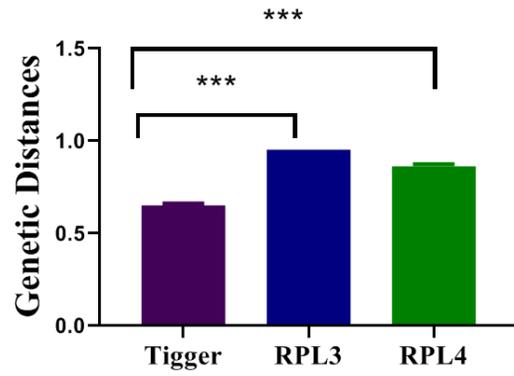
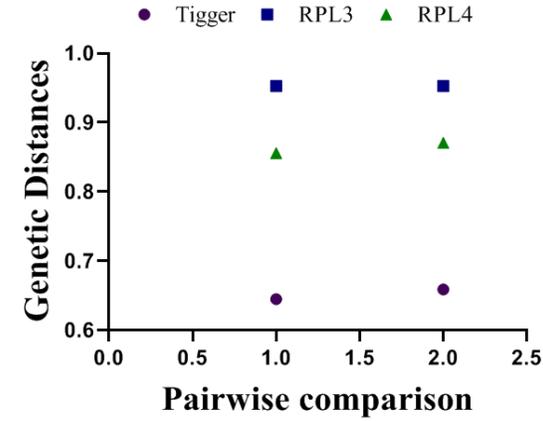
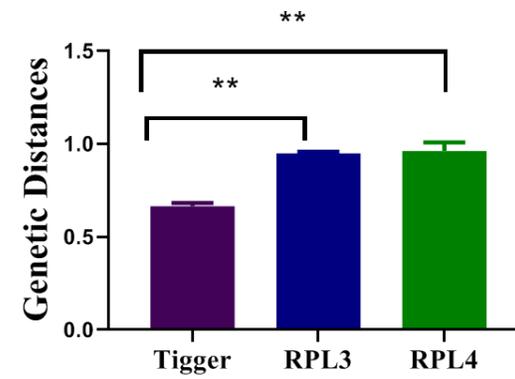
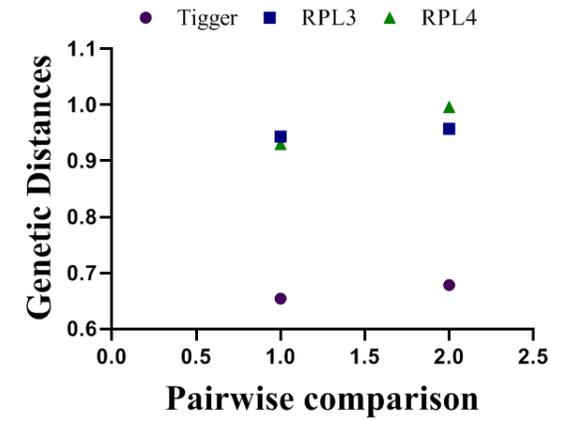


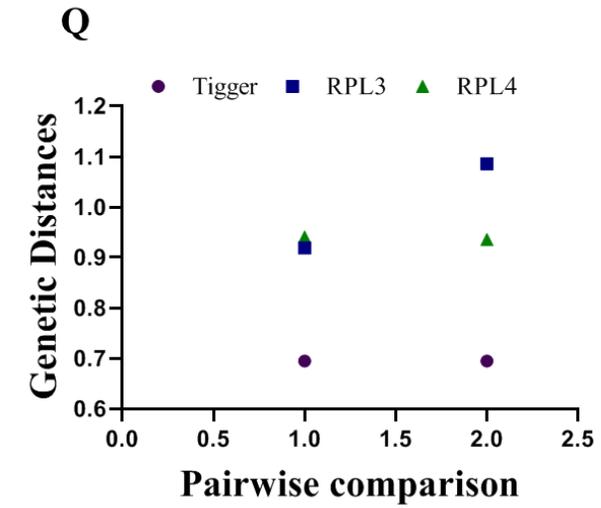
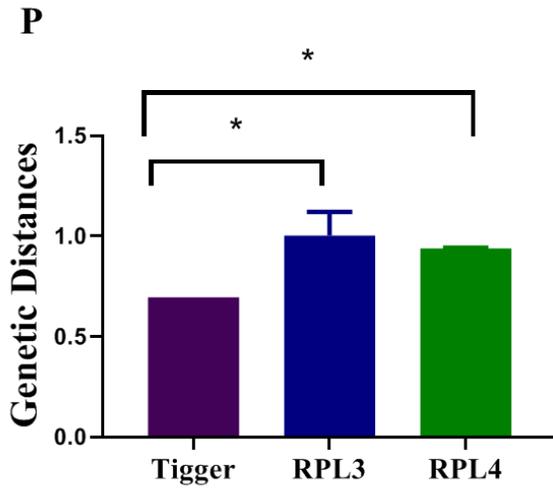
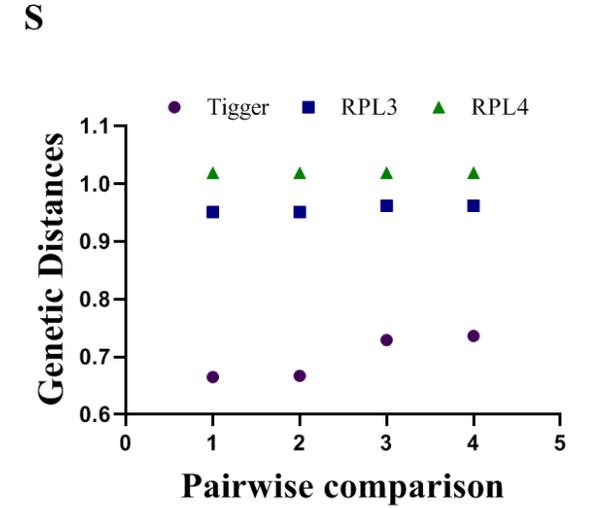
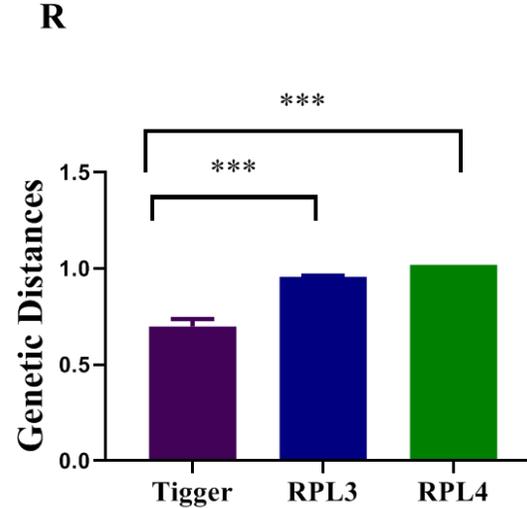
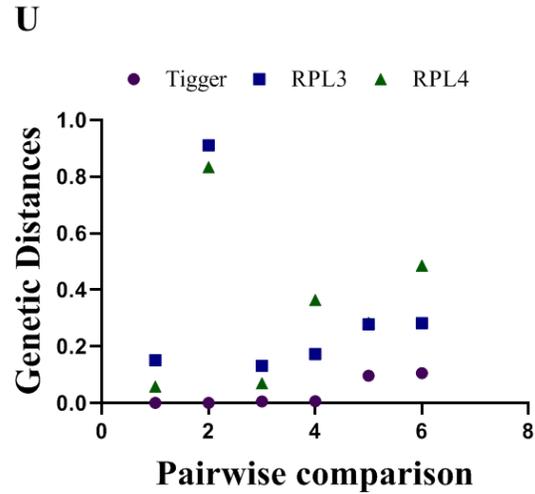
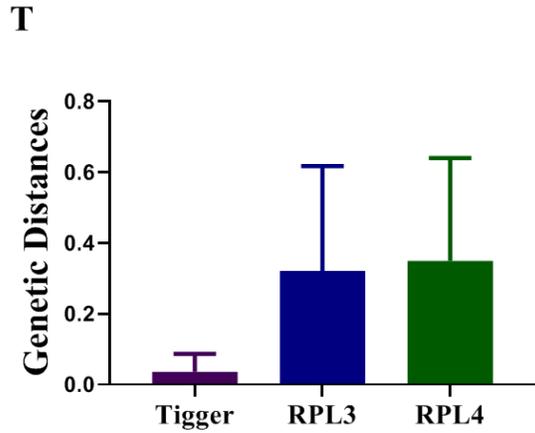
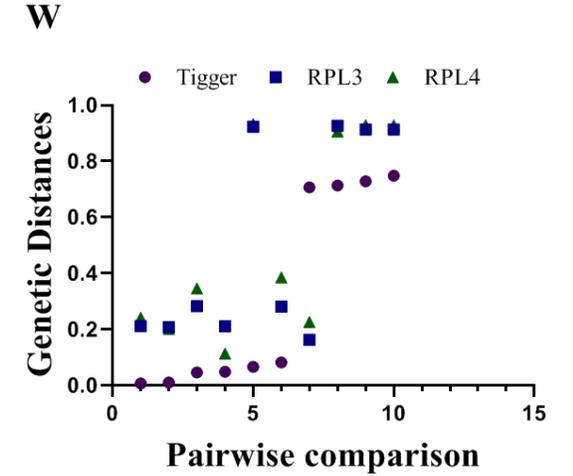
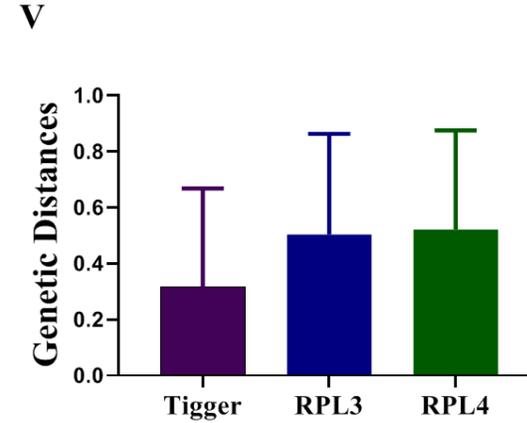
HT3



HT4

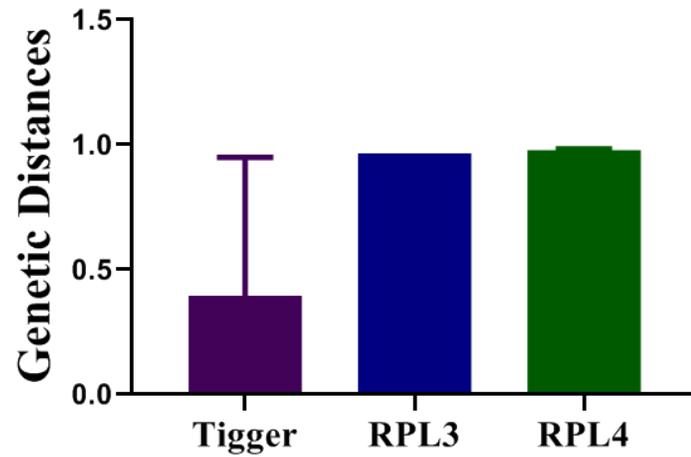


H**HT5****I****J****HT6****K****L****HT7****M****N****HT8****O**

HT9**HT10****HT11****HT12**

HT13

X



Y

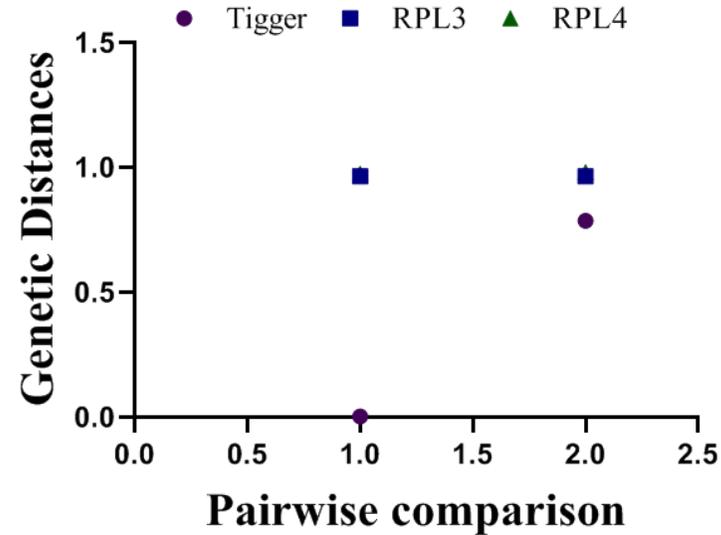


Figure S2: Genetic distances analysis for *Tigger* transposons and host genes. The graph illustrates the pairwise distances of *Tigger* and two host genes between the species involved in HT1, HT2, HT3, HT4, HT5, HT6, HT7, HT8, HT9, HT10, HT11, HT12, and HT13 events respectively. The distances were obtained from different phyla or classes pairwise comparisons between the species in which *Tigger* was identified.