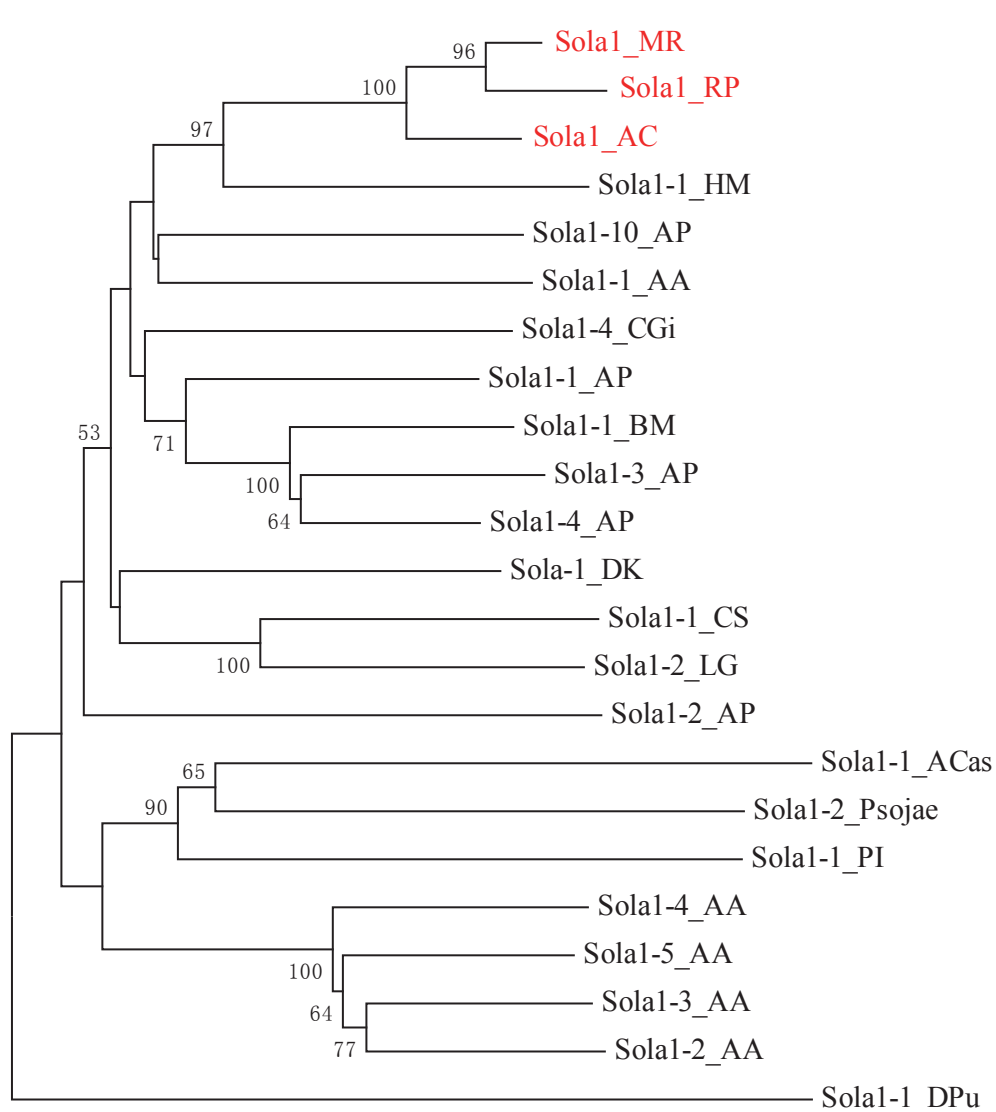
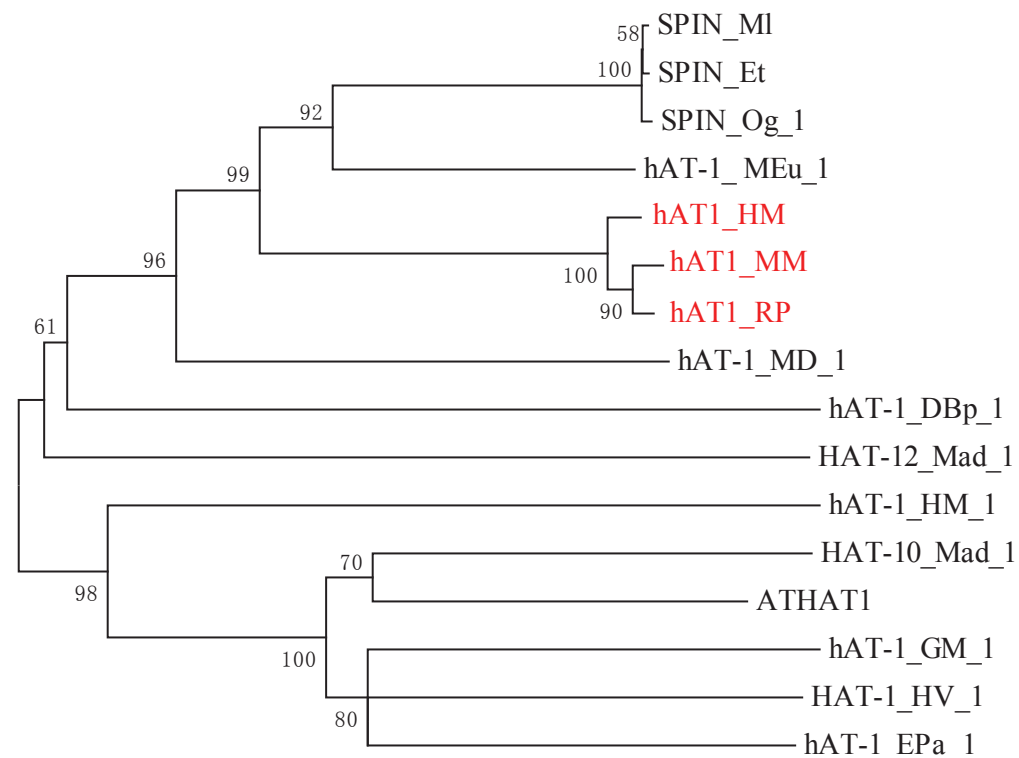


A



B



C

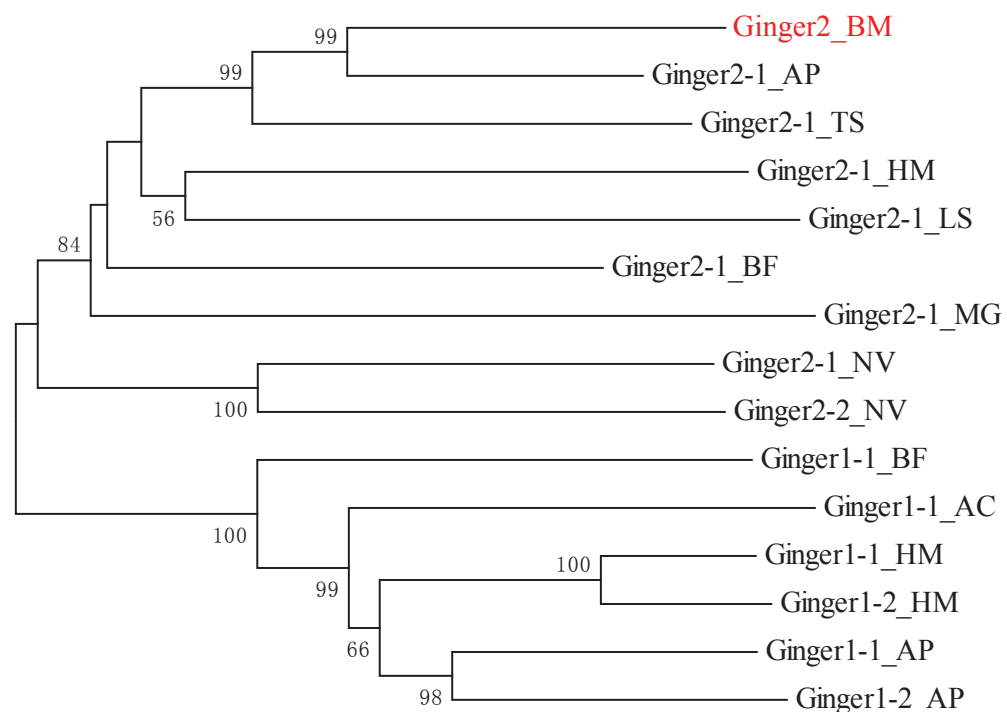


Fig.S5 Phylogenies of *Sola1* (A), *hAT1* (B) and *Ginger2* (C). Those transposons identified in this study are shown in red color. Phylogenetic trees were reconstructed using MEGA4. Bootstrap values higher than 50% are reported at the corresponding nodes. Species abbreviations are as follows: BM, *Bombyx mori*; AC, *Atta cephalotes*; MR, *Megachile rotundata*; CS, *Ciona savignyi*; DPu, *Daphnia pulex*; HM, *Hydra magnipapillata*; PI, *Phytophthora infestans*; AA, *Aedes aegypti*; AP, *Acyrtosiphon pisum*; LG, *Lottia gigantea*; Psojae, *Phytophthora sojae*; CGi, *Crassostrea gigas*; DK, *Drosophila kikkawai*; ACas, *Acanthamoeba castellanii*; AT, *Arabidopsis thaliana*; ET, *Echinops telfairi*; MI, *Myotis lucifugus*; Og, *Otolemur garnettii*; Mad, *Malus x domestica*; DBp, *Drosophila bipectinata*; HV, *Hordeum vulgare*; EPa, *Eutrema parvulum*; GM, *Glycine max*; MD, *Monodelphis domestica*; MEu, *Macropus eugenii*; RP, *Rhodnius prolixus*; BF, *Branchiostoma floridae*; LS, *Littorina saxatilis*; MG, *Malassezia globosa*; NV, *Nematostella vectensis*; TS, *Trichinella spiralis*; MM, *Mengenilla moldrzyki*. *Ginger2_RP* was not included in the phylogenetic analysis since we could not determine its coding sequences.