



Supplementary Figure S2. Phylogenetic analysis of *Mangifera indica* L. and *Arabidopsis thaliana* polygalacturonases. The evolutionary history was inferred using the Neighbor-Joining method, while distances were computed using the Poisson correction method. The analysis involved 117 amino acid sequences, of which 48 sequences belong to mango (*MiPGs*). Taxa clustered together in the bootstrap test (2000 replicates). Evolutionary analyses were conducted in MEGA X.