

Figure S2: Phylogenetic tree of *GATL* genes constructed by MEGA software version 7.0 using minimum evolution (ME) method. The prefixes Gh, Ga, Gr, At, Os, Sobic, Zm, Thecc, VIT, Prupe, Potri, MD, Glyma, Pp3c and Sphfalx represent *G. hirsutum*, *G. arboreum*, *G. raimondii*, *Arabidopsis thaliana*, *Oryza sativa*, *Sorghum bicolor*, *Zea mays*, *Theobroma cacao*, *Vitis vinifera* Genoscope, *Prunus persica*, *Populus trichocarpa*, *Malus domestica*, *Glycine max*, *Physcomitrella patens* and *Sphagnum fallax*, respectively. “At” and “Dt” indicate the A- and D- subgenomes in *G. hirsutum* respectively. Bootstrapping was used to provide reliability for nodes.

