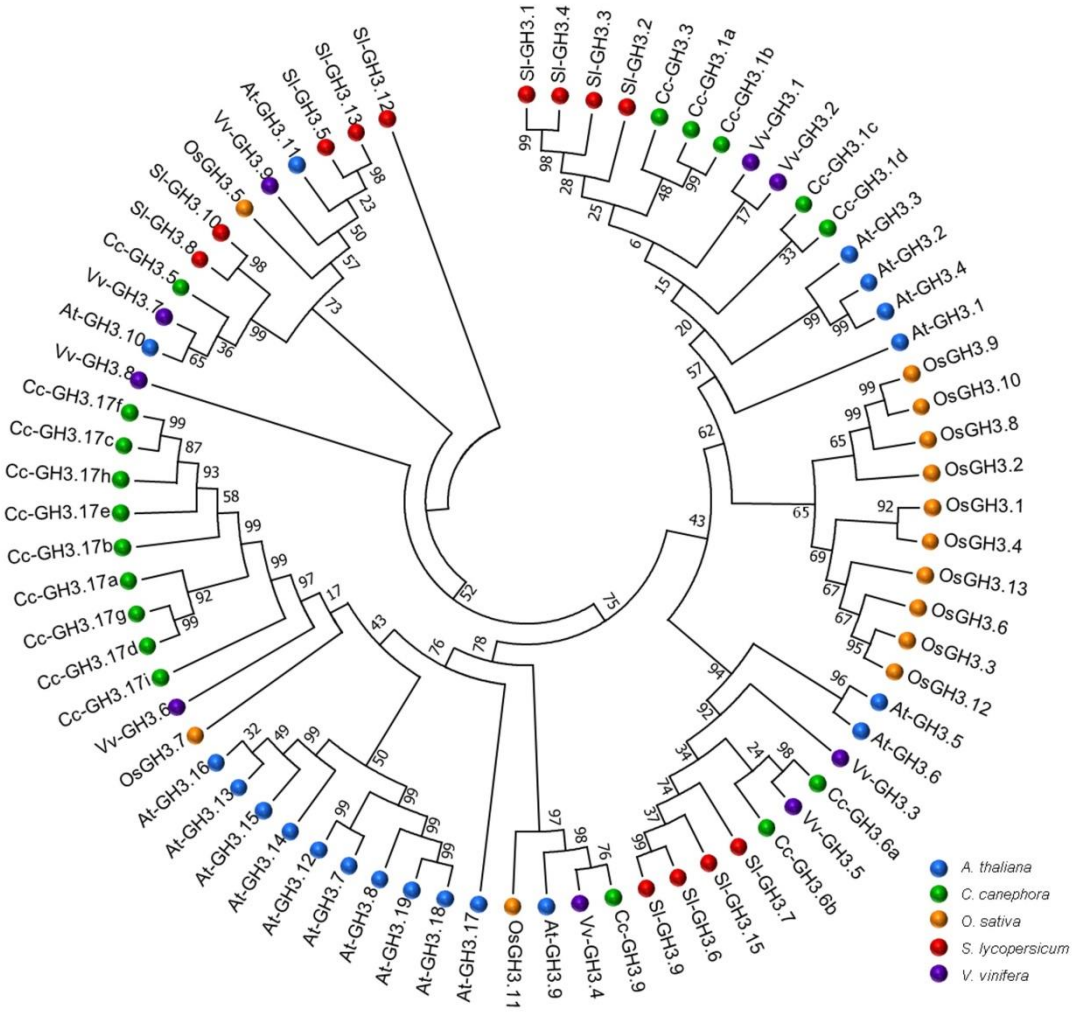

Figure S1. Analysis of the phylogenetic relationships of GH3 members in several species. A total of 19 sequences from *A. thaliana,* 18 from *C. canephora,* 15 from *S. lycopersicum,* 13 from *O. sativa*, and 8 from *V. vinifera* were used to construct a phylogenetic tree. GH3s belonging to one plant species are marked with the indicated leaf labels. The sequences were aligned in ClustalW, and analysis was conducted in MEGA7 using the Neighbor-Joining method. Bootstrap values (1000) are presented for all branches. All the GH3 members were clustered into different classes.

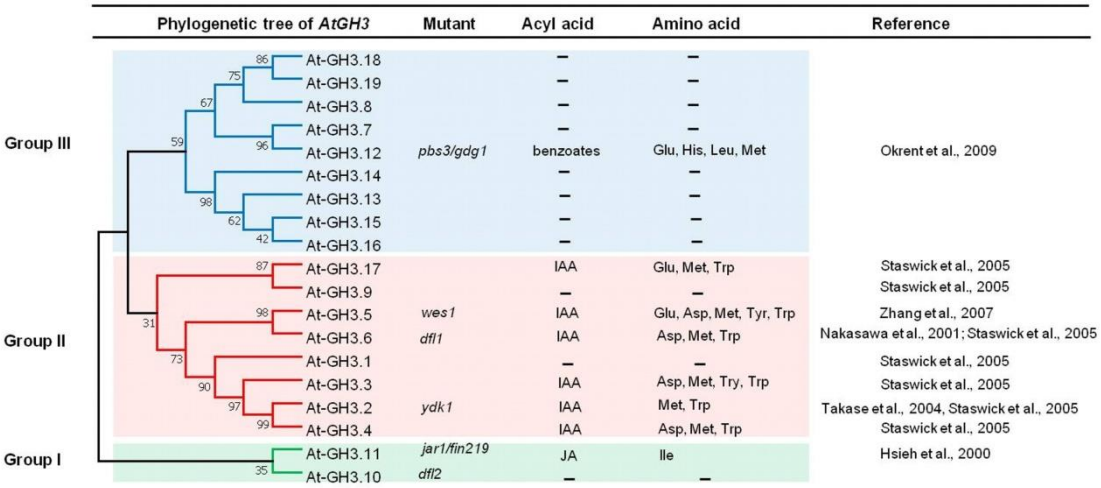

Figure S2. Phylogenetic relationship of the 19 GH3 genes reported in *A. thaliana*. Classification of groups I, II, and III, mutants associated with *AtGH3* and major acyl acid and amino acid substrates of the GH3 protein identified by substrate screening assays. The dashes in the table indicate unknown enzyme activity and substrate specificity.

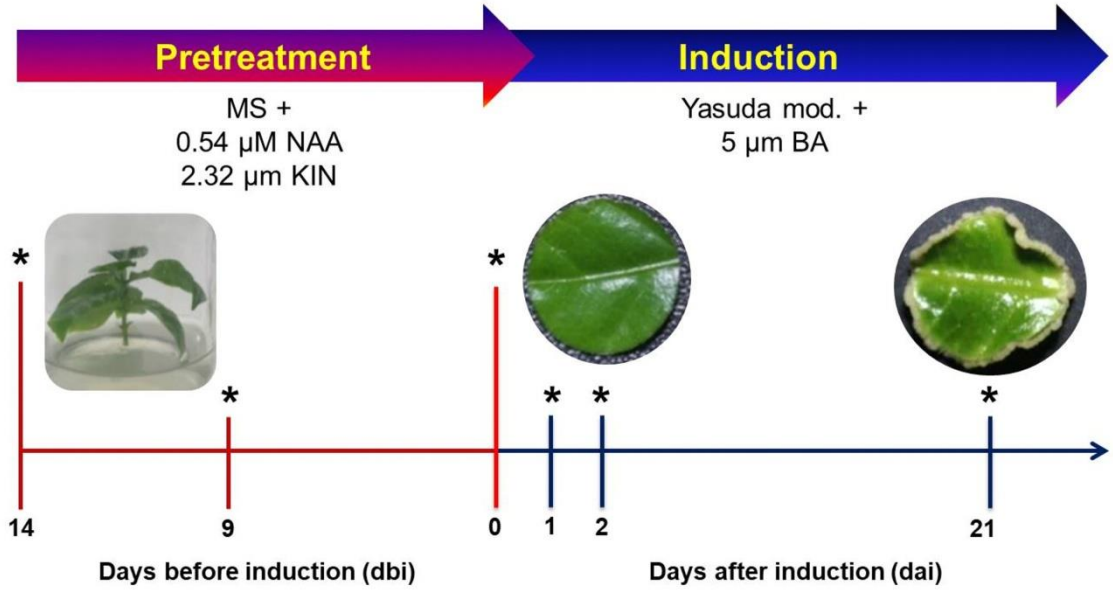

Figure S3. The SE induction process in *Coffea canephora* encompasses two stages: pretreatment and induction. First, the seedlings were preconditioned for 14 days in a semi-solid MS [63] medium supplemented with 0.54 µM NAA and 2.32 µM KIN under photoperiod conditions of 16 h light/8 h dark (150 µmol $m^{-2}s^{-1}$) at 25 ± 2 ºC. At the end of the pretreatment, the second and third pair of leaves were selected and cut into segments of 0.8 cm in diameter with the help of a sterile punch. Five explants were placed per 250 mL flask, with 50 mL of Yasuda liquid medium with the nitrogen source modified [42] and supplemented with 5 µM of BA, adjusted to pH 5.8 [37]. The flasks were incubated in the dark and shaking (55 rpm) at 25 ± 2 ºC for 56 days.