

Expanded View Figures

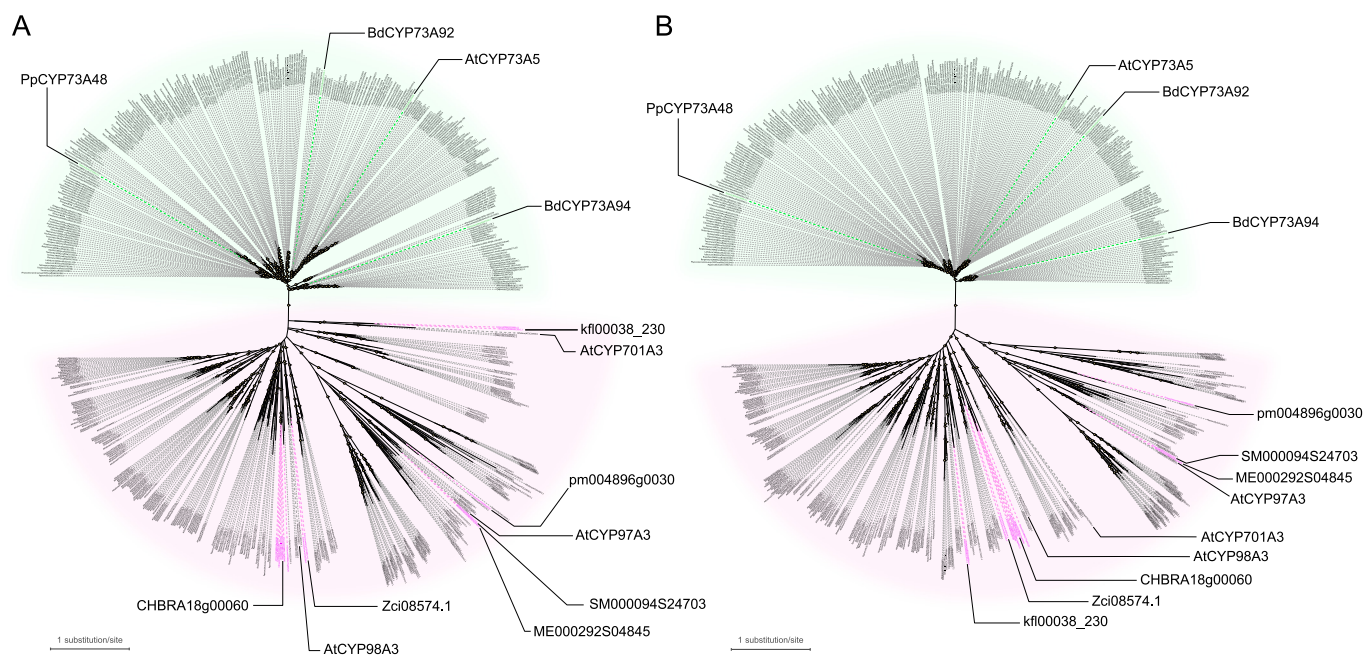


Figure EV1. Phylogenetic analysis of CYP73 and clan 71 CYP sequences.

Maximum-likelihood trees of 275 CYP73 sequences and 271 additional outgroup sequences derived from *A. thaliana*, *P. patens* and charophytes (AtCYP73A5 tBLASTn bit-score >100). (A) Unrooted ML nucleotide tree (IQ-TREE2, SYM + I + R10). (B) Unrooted ML amino acid tree (IQ-TREE2, Q.insect+I + R8). Relevant CYP73 homologs, *A. thaliana* clan 71 CYP members and charophyte sequences corresponding to BLASTp best hits (see Appendix Tab. S1) are shown. Ultrafast bootstrap support values equal or superior to 80 are annotated on branch as yellow dots. Trees are drawn to scale; scale bars represent the number of substitutions per site.

