

# Evolutionary diversification of cytokinin-specific glucosyltransferases in angiosperms and enigma of missing *cis*-zeatin O-glucosyltransferase gene in Brassicaceae

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**Figure S2. A.** Maximum parsimony phylogenetic tree of *cis*-zeatin O-glucosyltransferase based on combined data from Phytozome v12 and GenBank. Twenty-seven species were included in 376 sequences with 1719 positions in the final data set. Length 21265, CI=0.27, RI=0.75. The *cis*ZOG homologs of *Amborella trichopoda* were used for rooting. Numbers below branches indicate bootstrap support values and fifteen conserved motifs are shown for each sequence. **B.** Maximum likelihood (left) and maximum parsimony (right) simplified phylogenetic trees. Numbers below branches indicate bootstrap support values >50%. Trees are divided into fifteen main groups corresponding with maximum likelihood tree (Fig. 4): O1. Amborellaceae, O2. Areaceae-Musaceae-Orchidaceae, O3. Areaceae-Bromeliaceae-Musaceae-Poaceae, O4. Ranunculaceae, O5. Nelumbonaceae, O6. Myrtaceae, O7. Malvaceae-Phymaceae-Rutaceae-Solanaceae-Vitaceae, O8. Vitaceae, O9. Apiaceae-Araliaceae-Asteraceae-Convulvaceae-Phymaceae-Rubiaceae-Solanaceae, O10. Amaranthaceae-Bignoniaceae-Pedaliaceae-Phymaceae, O11. Fagaceae-Juglandaceae, O12. Moraceae-Rhamnaceae-Rosaceae, O13. Caricaceae-Euphorbiaceae-Malvaceae-Rutaceae-Salicaceae, O14. Cucurbitaceae, O15. Fabaceae. Numbers below branches indicate bootstrap support values and fifteen conserved motifs are shown for each sequence.

