



Figure S1. Comparison of the morphological characteristics of different parts of 'Alabama' and 'X'. (A) Flower plants of 'Alabama' (left) and 'X' (right). 'Alabama' is a red potted variety. 'X' is a white potted variety. (B) Flowers of 'Alabama' (left) and 'X' (right). The spathe and pedicel of 'Alabama' were both red and contained cyanidin. The spathe and pedicel of 'X' were white and green, respectively. (C) Roots of 'Alabama' (left) and 'X' (right). The roots of 'Alabama' were brownish red, and those of 'X' were green. (D) Young leaves of 'Alabama' (left) and 'X' (right). The leaf blade and petiole of 'Alabama' showed red staining, and those of 'X' were both green. All bars represent 1 cm.



Figure S2. The spathe and leaves of 'Alabama' and 'X' at five growth stages. Spathe growth stage 1 (S1): the initial appearance of the spathe (pedicel absent); growth stage 2 (S2): pedicels present; growth stage 3 (S3): the pedicel length approaches 2–3 cm; growth stage 4 (S4): pedicel elongation occurs, but the length does not exceed that of the leaf, and the spathe is not unfolded; growth stage 5 (S5): spathe is completely unfolded (the spadix does not turn white or green). Leaf growth stage 1 (S1): the initial appearance of leaves (petioles

absent); growth stage 2 (S2): appearance of petioles; growth stage 3 (S3): petiole elongation, and leaves begin to unfold; growth stage 4 (S4): leaves unfold and appear red. In growth stage 5 (S5), the leaf color changes from red to dark green, and the leaves are mature. Bar represents 1 cm.

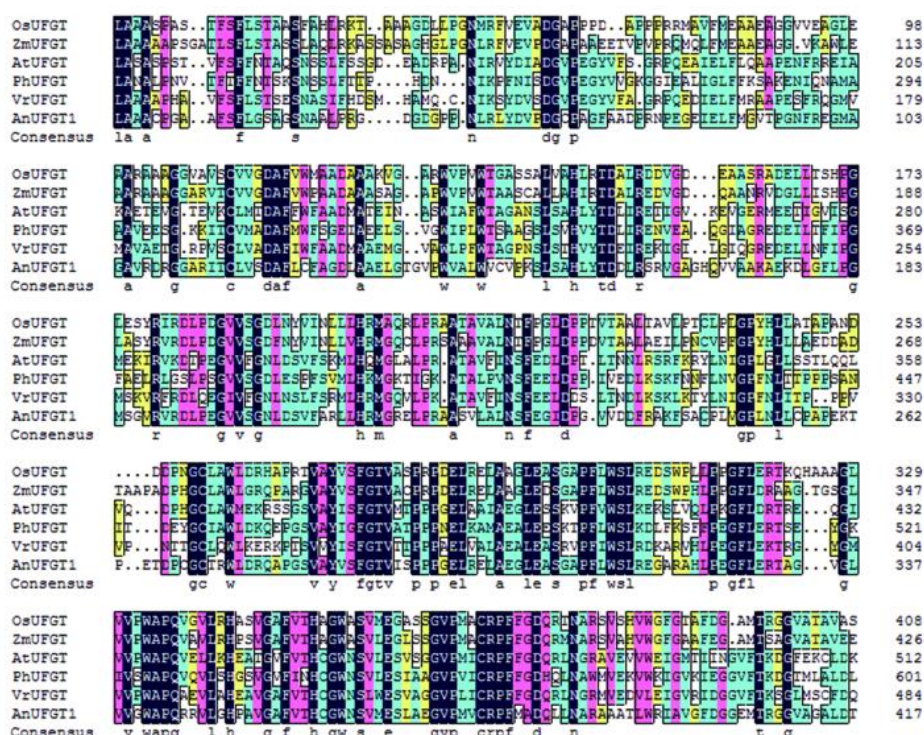


Figure S3. Sequence alignment of the amino acid sequences of UFGTs from *Anthurium andraeanum* and other plants. The UFGT amino acid sequences were downloaded from the NCBI database. OsUFGT (*Oryza sativa*, XP_015643442.1); ZmUFGT (*Zea mays*, ABF72120.1); AsUFGT (*Arabidopsis thaliana*, AAM91139.1); PhUFGT (*Petunia × hybrida*, AAD55985.1); VrUFGT (*Vitis rotundifolia*, AGS57502.1).



Figure S4. Comparison of the predicted domains of *AnUFGT1* and those of other plants. Functional domain prediction was conducted with the online software MEME. *AtUFGT*: *Arabidopsis thaliana*; *OsUFGT*: *Oryza sativa*; *PhUFGT*: *Petunia × hybrida*; *ZmUFGT*: *Zea mays*; *VrUFGT*: *Vitis rotundifolia*.

Table S1. Primers used for qRT-PCR analysis.

Gene	Forward Primer (5' to 3')	Reverse Primer (3' to 5')	Product (bp)
β-actin	GGTGGAGCCACGACCTTA	CTCTCATTGGGATGGAAGC	85
AnUFGT1	TATGCGTGCCAAAAGCCT	GGCGAAGACGGAGTCCA	189