Genome-wide identification and expression pattern analysis of *CrLBD* family genes reveal their involvement in floral morphology in *Chionanthus retusus*

Mengmeng Wang[1,2], Liyang Guo[1,2], Haiyan Wang[3], Yuzhu Wu[1,2], Shicong Zhao[1,2], Wenjing Song[1,2], Jihong Li[1,2], Jinnan Wang[1,2*]

[1]College of Forestry, Shandong Agricultural University, Tai'an, Shandong Province 271018, China.

[2]State Forestry and Grassland Administration Key Laboratory of Silviculture in Downstream Areas of the Yellow River, Tai'an, Shandong Province 271018, China.

[3]Heze Forestry Technology Service Center, Heze, Shandong Province 274000, China.

*Correspondence: Jinnan Wang (Wjn@sdau.edu.cn)

Supplemental Figures

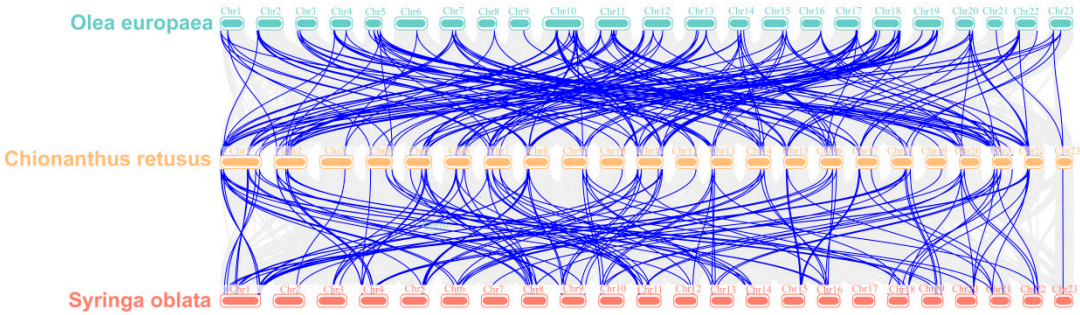

Figure S1. Collinearity analysis of LBD gene family in *C. retusus*, *Syringa oblata* and *Olea europaea*.'So' represents the chromosome of *Syringa oblata*, 'Cr'represents the chromosome of *C. retusus*, and 'Oe'represents the chromosome of *Olea europaea*. The blue line represents a collinear ARF gene pair, while the gray ribbon represents a collinear segment of the chromosome.The intersection point between each blue line and the chromosome represents the position of the corresponding LBD gene.