

Figure S1: Sample cluster analysis. IFB_1, IFB_2, IFB_3: buds in once flowering rose; CFB_1, CFB_2, CFB_3: buds in continuous flowering rose; IFL_1, IFL_2, IFL_3: leaves in once flowering rose; CFL_1, CFL_2, CFL_3: leaves in continuous flowering rose.

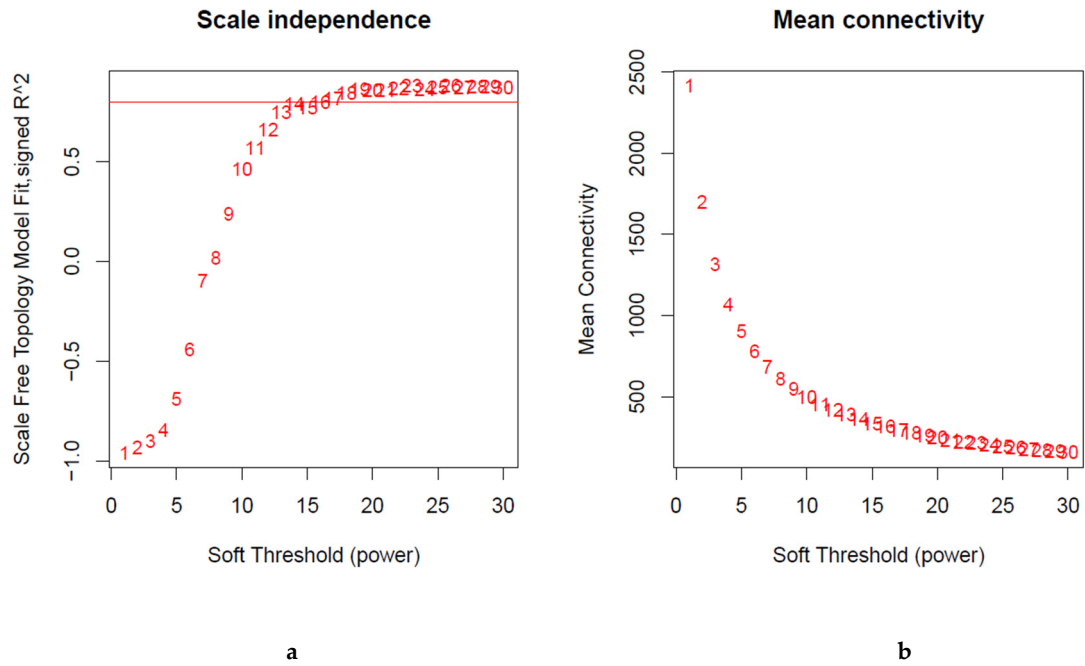


Figure S2. Analysis of network topology for various soft-thresholding powers. (a) the curve of Power; (b) the curve of mean connectivity.

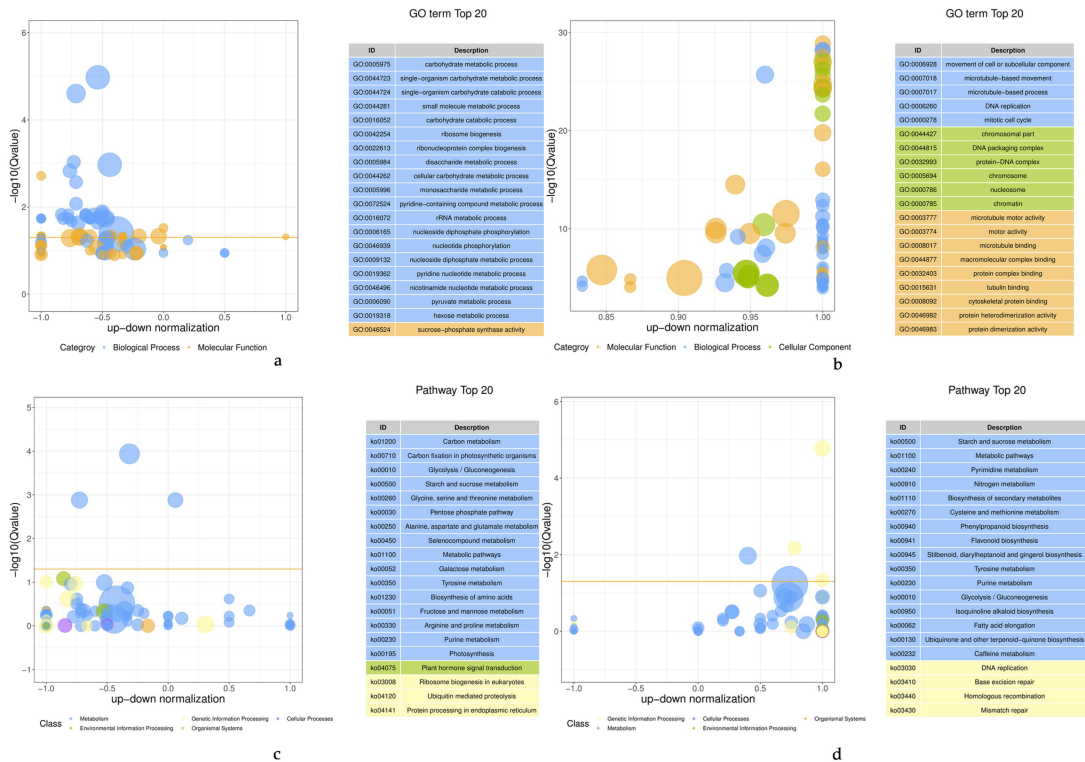


Figure S3. Z-score bubble plot of enrichment analysis. Up-down normalization represents the proportion of the difference between the number of up-regulated genes and the number of down-regulated genes in the total differential genes; The bubble size represents gene count, different colors represent different GO or KEGG categories, and the orange line represents the threshold value of Q-value=0.05; On the right side of every figure is the GO term / Pathway list

[illegible]

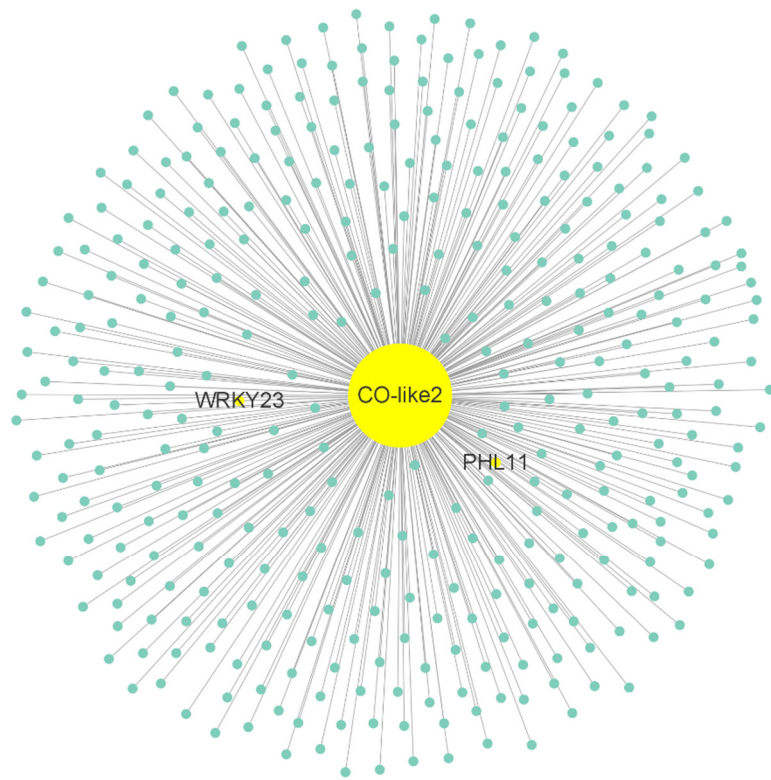


Figure S5. Regulatory network of *CO-like 2* gene in blue module