

**Additional file 1 related to: Wang, M.-Y., Ding, Y., Zhang, Y., Sun, L., Song, X.-Q., Hao, D.-C., Li, W.-S., Tang, M.-Q., Ling, P., Xie, S.-Q. (2023). Transcriptome analysis of genes involved in flower and leaf color of *Oncidium* by RNA-seq. *Acta Sci. Pol. Hortorum Cultus*, 22(5), 3–17. <https://doi.org/10.24326/asphc.2023.4831>**

Table S1. Annotation of unigenes

| Database   | Flower  | Percentage (%) | Leaf    | Percentage |
|------------|---------|----------------|---------|------------|
| COG        | 38,090  | 9.99           | 54,202  | 11.95      |
| GO         | 19,250  | 5.05           | 30,840  | 6.80       |
| KEGG       | 15,030  | 3.94           | 26,358  | 5.81       |
| Swiss-prot | 54,291  | 14.24          | 72,148  | 15.91      |
| NR         | 116,179 | 30.48          | 151,643 | 33.43      |
| Total      | 381,136 | \              | 453,566 | \          |

Table S4. Statistical of functional annotation in DEGs

| Database   | No. of DEGs in flower | No. of DEGs in leaf |
|------------|-----------------------|---------------------|
| Swiss-prot | 385 (58.16%)          | 719 (54.31%)        |
| GO         | 252 (38.07%)          | 430 (32.48%)        |
| KEGG       | 178 (26.89%)          | 291 (21.98%)        |
| COG        | 445 (67.22%)          | 779 (58.84%)        |
| Nr         | 274 (41.39%)          | 649 (49.02%)        |
| Total      | 662                   | 1,324               |

Table S9. The results of Differential expression analysis of identified DEGs

| Unigene_id        | sampleA | sampleB | log2FoldChange | p-value  | p-adj    |
|-------------------|---------|---------|----------------|----------|----------|
| DN30777_c0_g1_i2  | NF      | WF      | -1.459876695   | 7.00E-07 | 2.63E-04 |
| DN6864_c0_g2_i6   | NF      | WF      | 3.120591873    | 2.79E-10 | 3.08E-07 |
| DN351_c0_g1_i2    | NF      | WF      | 1.561711197    | 1.60E-04 | 1.57E-02 |
| DN44326_c0_g1_i6  | NF      | WF      | 3.391735706    | 5.85E-09 | 4.06E-06 |
| DN6254_c0_g1_i3   | NF      | WF      | 2.089353897    | 1.54E-04 | 1.52E-02 |
| DN10386_c0_g1_i1  | NF      | WF      | 1.110071042    | 5.78E-06 | 1.35E-03 |
| DN12198_c0_g1_i16 | NL      | SL      | -6.418609464   | 7.04E-07 | 1.14E-04 |
| DN42588_c0_g2_i4  | NL      | SL      | -6.715950473   | 1.92E-05 | 1.49E-03 |
| DN45643_c0_g1_i4  | NL      | SL      | -6.200608881   | 2.72E-04 | 1.06E-02 |
| DN4894_c1_g2_i1   | NL      | SL      | -1.439762479   | 7.93E-06 | 7.78E-04 |
| DN47031_c0_g1_i1  | NL      | SL      | -2.742320022   | 4.96E-04 | 1.64E-02 |
| DN10768_c0_g1_i10 | NL      | SL      | -1.831003218   | 3.98E-05 | 2.57E-03 |
| DN30120_c0_g1_i2  | NL      | SL      | -2.717920128   | 2.88E-14 | 5.00E-11 |
| DN79020_c0_g1_i2  | NL      | SL      | -3.955369775   | 6.55E-06 | 6.75E-04 |

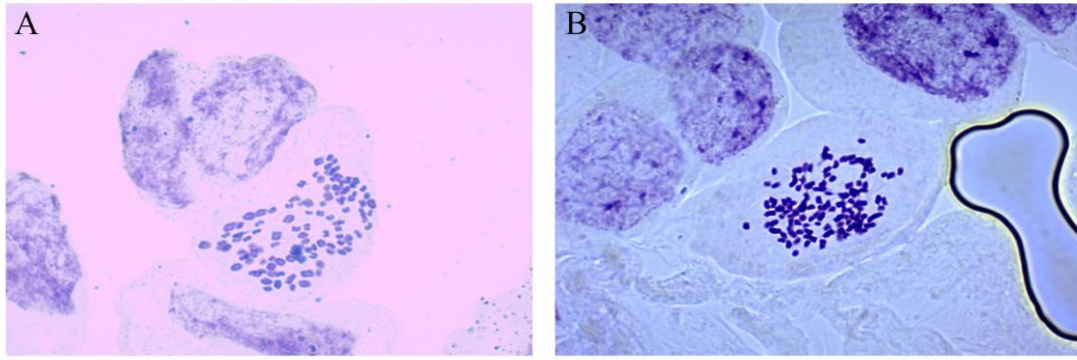


Figure S1. A: Chromosome morphology of Ningmenghuang cultivar somatic cells;

B: Chromosome morphology of Xuelian cultivar somatic cells

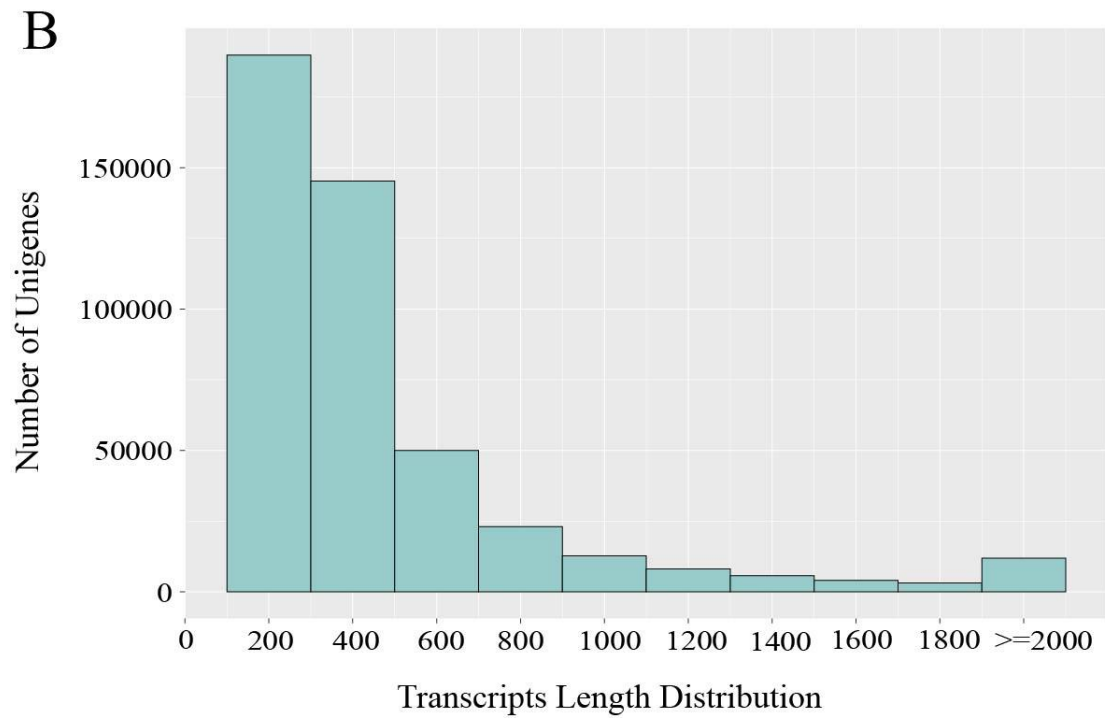
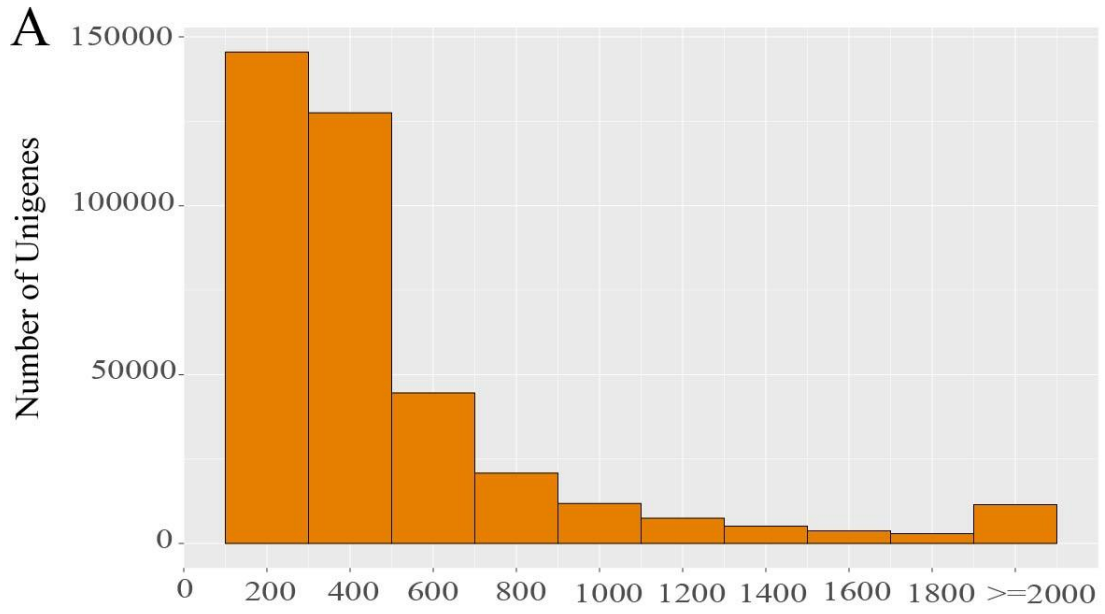


Figure S2. Distribution of unigenes length

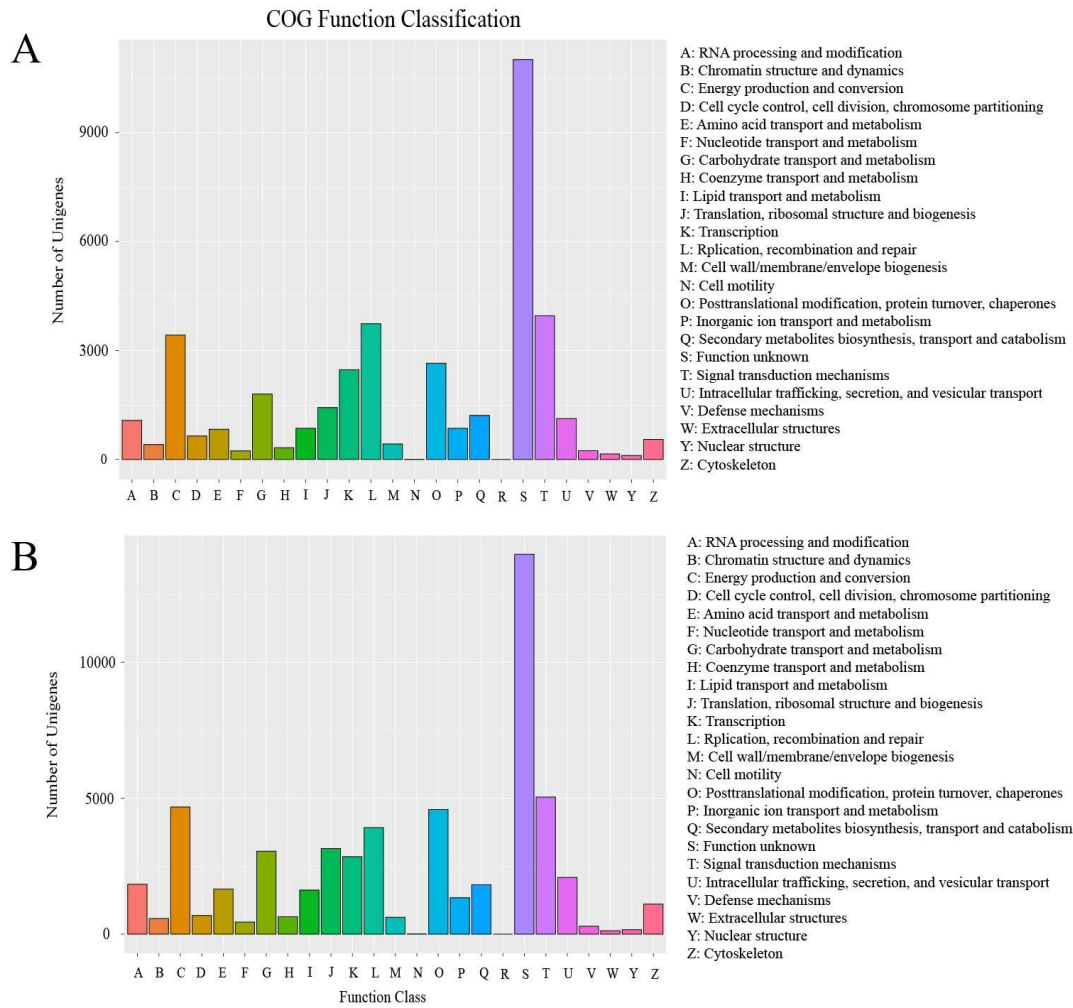


Figure S3. The COG annotation of unigenes

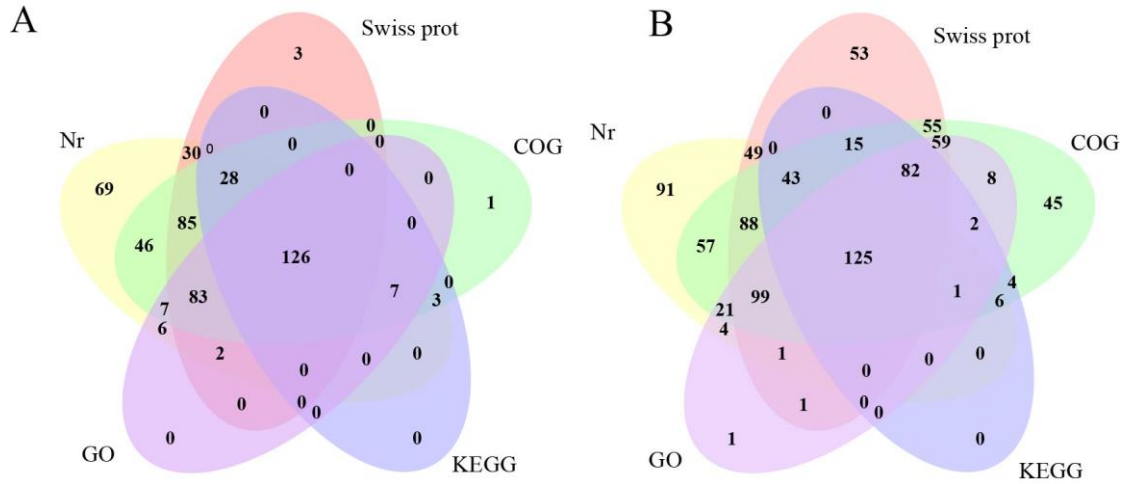


Figure S4. Venn graph of the five database annotation results (A: Statistics of DEGs annotation results of flower samples; B: Statistics of DEGs annotation results of leaf samples)

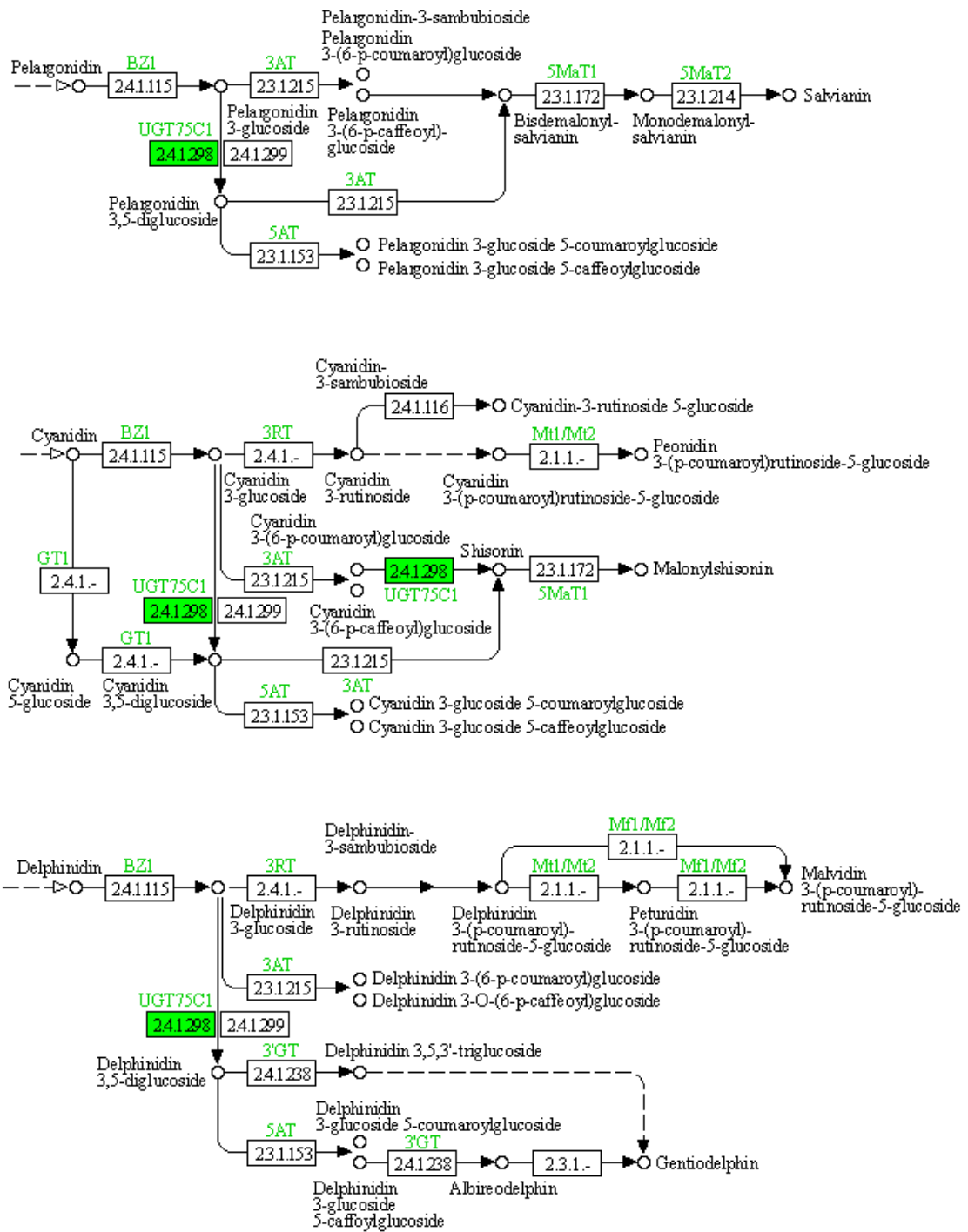


Figure S5. The identified DEG UGT75C1 enriched in Anthocyanin biosynthesis pathway of KEGG