

Table 1 Suppl. Primers used in real time quantitative PCR.

Gene name	Accession number (RNA-seq)	Forward primer	Reverse primer
<i>PSY</i>	c58514_g2	TTGTCATCGGCCATAGCAGG	TGAATCACCAATTCGAGGTTG
<i>PDS</i>	c49360_g1	TTGGGTTGGTTTCCGCTGTC	TTCGGGTTGGCCTCATCCTT
<i>ZISO</i>	c59461_g2	ATAGGCGAGAAATTCGTTGG	AAAAGGTTGAAGGTGGAGGG
<i>ZDS</i>	c56346_g1	CCTCCAGAACCTGAGCACTA	TGTCCACAAAGGAACCAACT
<i>BCH</i>	c55986_g1	CTGCTTGCCTTCGGCTTCTT	CCTCCTGCTCACCTCCTTCT
<i>CRTISO</i>	c62785_g1	TTCTCCCCTTCCAAAACCCC	CTGCTCTTTCCACGCTGACG
<i>β-LYC</i>	c48928_g1	GGAGTTCGATCAGAGGTCA	GATATGGCTCGTTGTCTAAGTG
<i>CCD2</i>	c40525_g1	CCTAACCCCAAGTTTGCTCC	GCTGTATTACCCGTCCTCT
<i>CCD4b</i>	C40281_g1	AACGGTCCCAACCCAAACCA	AACCCGCACAACCCCGAGAA
<i>CAP</i>	c55919_g1	CCCACAAGCCCATCTTCGTT	AGTCCCCTATCGGTGCCGTA
<i>β-GSGV1</i>	c56534_g1	ACTATGGGCTGCTGGGAAAC	GCCACGACGTAACGGAACCT
<i>β-GS7</i>	c61813_g1	TCGCCGTACTGGTCGTAGAT	TGGGTGGAGGAAGAATAAAGA
<i>UGT85U1</i>	c59086_g2	ATCAACCCGACCACCAACA	GGGGATGCCGAACCTCCTTAG
<i>UGT85U2</i>	c52564_g1	AGTTCCTGTCTCCGTTCCGTG	GGATGCCGAACCTCCTTAGCG
<i>18S</i>		AGTTTGAGGCAATAACAGGTCT	GATGAAATTTCCCAAGATTACC

Table 2 Suppl. The number and distribution rate of unigenes in the *NR-NCBI*, *NTNCBI*, *KEGG*, *KO*, *SwissProt*, *PFAM*, *GO*, and *KOG* databases. The *NR-NCBI* was used for non-redundant protein sequences, *NT-NCBI* for nucleotide sequences, *KO* and *KEGG* for orthologs, *PFAM* for protein family, and *KOG* for eukaryotic ortholog groups.

Database	Number of unigenes	Percentage
<i>NR</i>	36805	33.72
<i>NT</i>	21138	19.36
<i>KO</i>	13481	12.35
<i>SwissProt</i>	28616	26.22
<i>PFAM</i>	25324	23.20
<i>GO</i>	25606	23.46
<i>KOG</i>	13104	12.00
All databases	4892	4.48
Annotated in at least one database	4 6793	42.87
Total unigenes	109136	100.00

Table 3 Suppl. The relationships of the expressions of unigenes among three different *Crocus* flower tissues.

Correlation coefficient (R ²)	Stigma	Petal	Stamen
Stamen	0.178	0.215	1.000
Petal	0.157	1.000	0.215
Stigma	1.000	0.157	0.178

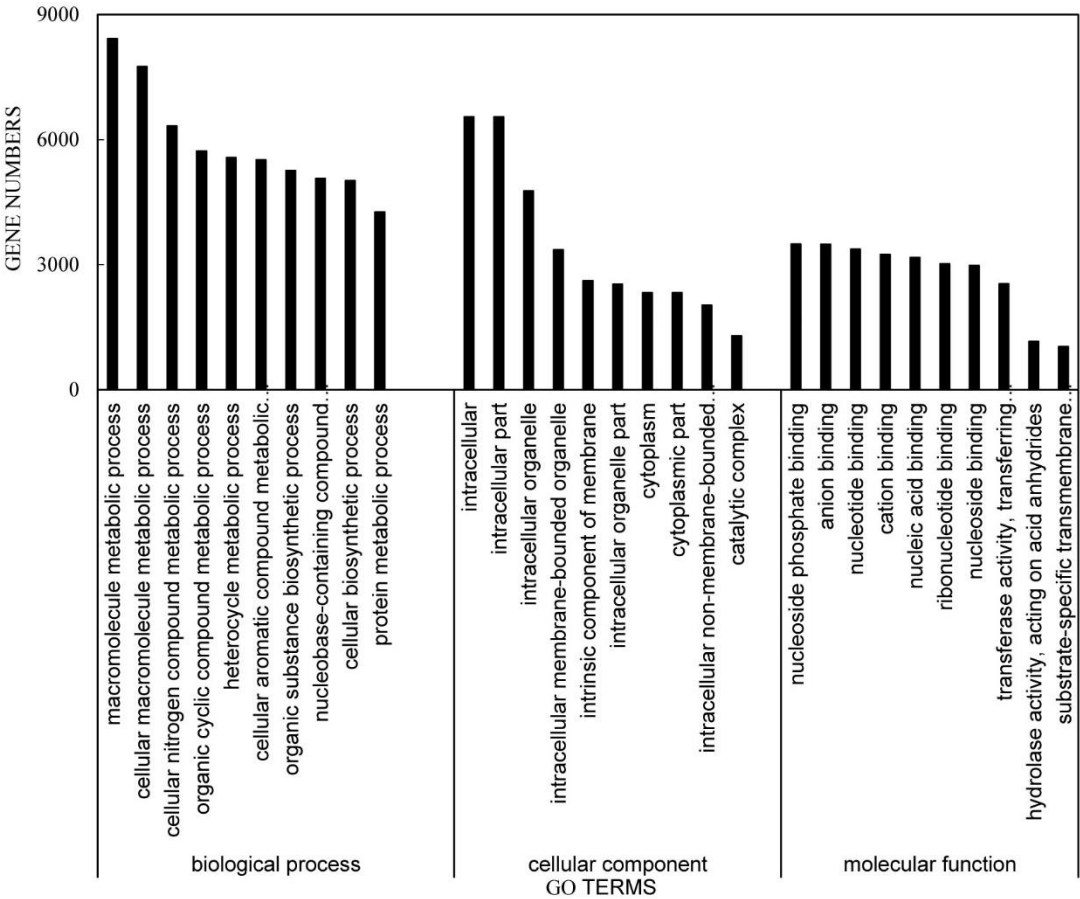


Fig. 1 Suppl. The *Gene Ontology* (GO) annotation of non-redundant consensus sequences.

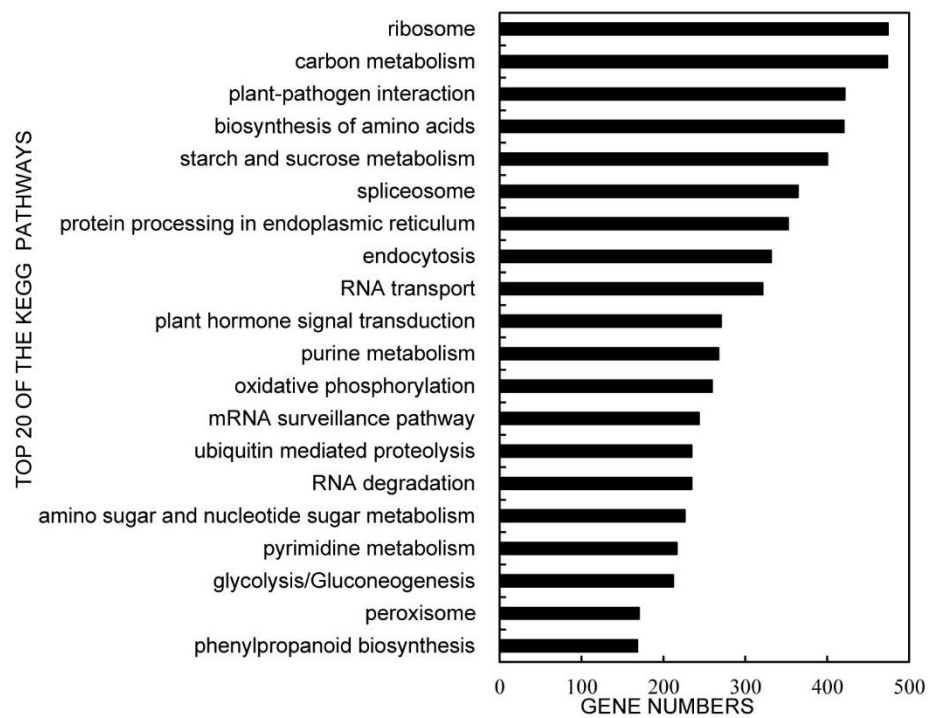


Fig. 2 Suppl. The *Kyoto Encyclopedia of Genes and Genomes (KEGG)* classification of unigenes.

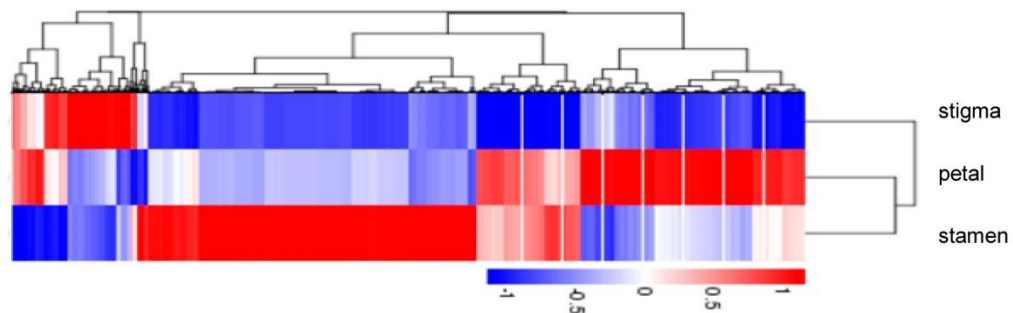


Fig. 3 Suppl. Hierarchical cluster analysis of differentially expressed genes (DEGs) in different tissues. Results are displayed as $\log_{10}(\text{FOKM}+1)$ values on a colour scale from red (high) to blue (low) expression of each DEG.