

Table 1 Suppl. Primers used in this study.

Primer name	Primers for amplification (5'-3')
MYB1f	ATGGACAAGAAAATATGCAATAA
MYB1r	TCTCCATTAAGTAACTGGATGGA
dMYB1f	CTGCGGTGGCTCAACTACCTT
dMYB1r	CATGCAGCTCCACAATCAAAA
MYB1f1	CCCGAAGCTTGGGATGGACAAGAAAATATGCAATAAT
MYB1r1	ACGCGTCGACGTCGGTCACCATTAAGTAACTGGATGGA
MYB1-f	ATGGACAAGAAAATATGCAATAA
MYB1-r	TCTCCATTAAGTAACTGGATGGA
dMYB1-f	CTGCGGTGGCTCAACTACCTT
dMYB1-r	CATGCAGCTCCACAATCAAAA
dPAL-f	GGCTTGGCTTCAGTTGTTCTTT
dPAL-r	GATGGTGCTTTAGTTTGTGCGT
dPAL1-f	TGGTGCAACATCACATAGGAGAAC
dPAL1-r	GCAGAGTTTGGGATGATTCAGTTC
dCHS-f	GATATTGTGGTGGTGGAAAGTG
dCHS-r	TGCAGAAGATTAAATGGGTGA
CHI-f	CTCCTCCATTCTATTCACTCA
CHI-r	CAACGATTATTTGCTGCTAT
dCHI-f	ATTGGTGAGCACGGTGTTTCCC
dCHI-r	CGTTTGGCATGGTGGTCTTCTT
dF3H-f	ACGGAGGAGTATAGCGACAAG
dF3H-r	TTGGATAGAAATTCACGACCA
dFLS-f	ACCATTACCATTCTTGTCCTA
dFLS-r	CTTCCCATTGCTCAATATCTCA
dDFR-f	CATCACTCCAACCTTCCCACC
dDFR-r	ATGAGCGTCGCATAGATCGTC
dANS-f	CGGTAATGTTCAAGGGTATG
dANS-r	GGAACCTTAGGCCAAATGTC
ACTIN-f	CGTGGCACTTGACTATGAA
ACTIN-r	TCTGGGCAACGGAATCTCT
18s RNA-f	GGAGAGGGAGCCTGAGAAAC
18s RNA-r	GCCAACGTAATAGGACCGAA

Table 2 Suppl. Statistical results of sequencing data.

Samples	BMK-ID	Read number	Base number	GC content [%]	[%] $\geq$ Q30
DO	T01	27475198	6892989310	43.64	91.88
DJ	T02	24547401	6164011070	43.69	89.53
DS	T03	27514095	6905162540	43.54	91.40
DA	T04	26079942	6544132194	43.45	91.68
YO	T05	27722398	6957001914	43.50	91.36
YJ	T06	28420554	7130751008	43.43	91.89
YS	T07	31683095	7949812656	43.60	91.55
YA	T08	34016142	8538650782	43.44	91.72

Table 3 Suppl. Assembly results of unigenes.

	Group1 unigenes	Group2 unigenes	All unigenes
200-300	38522(37.96%)	39805(37.06%)	50013(35.21%)
300-500	27392(26.99%)	29568(27.53%)	36534(25.72%)
500-1000	18540(18.27%)	19990(18.61%)	27217(19.16%)
1000-2000	10285(10.13%)	10893(10.14%)	16345(11.51%)
2000+	6752(6.65%)	7143(6.65%)	11920(8.39%)
Total number	101491	107399	142029
Total length	67923578	72066383	105385618
N50 length	1083	1068	1300
Mean length	669.26	671.02	742.00

Table 4 Suppl. The number of differentially expressed genes (DEGs).

DEG set	All DEGs	Upregulated	Downregulated
D0-vs-DJ	1669	896	773
D0-vs-DS	2369	1478	891
D0-vs-DA	2532	1709	823
Y0-vs-D0	4394	2223	2171
Y0-vs-YJ	1957	976	981
Y0-vs-YS	2191	1535	656
Y0-vs-YA	1852	1214	638

Table 5 Suppl. Unigene annotations.

Database	Annotated_number	300≤Length<1 000	Length≥1 000
<i>COG_</i>	12602	2871	8298
<i>GO_</i>	26941	9181	12712
<i>KEGG_</i>	16985	5727	8430
<i>KOG_</i>	27429	8972	13790
<i>Pfam_</i>	29812	8138	18364
<i>Swissprot_</i>	31380	10496	15877
<i>Nr</i>	50168	18128	22541
<i>All_</i>	50918	18408	22601

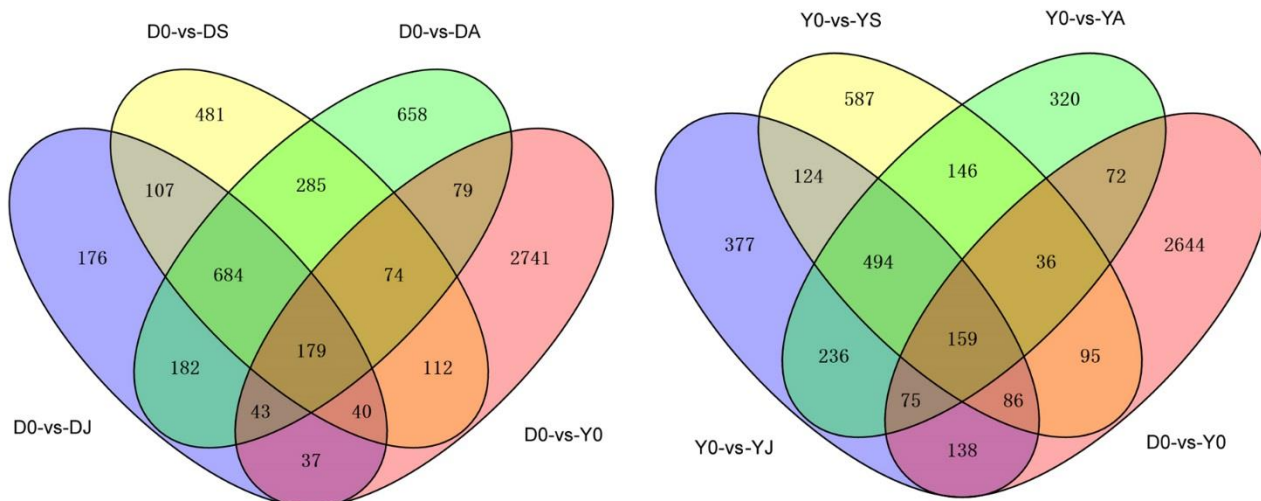


Fig. 1 Suppl. A Venn diagram presenting the number of genes classified in different combinations.

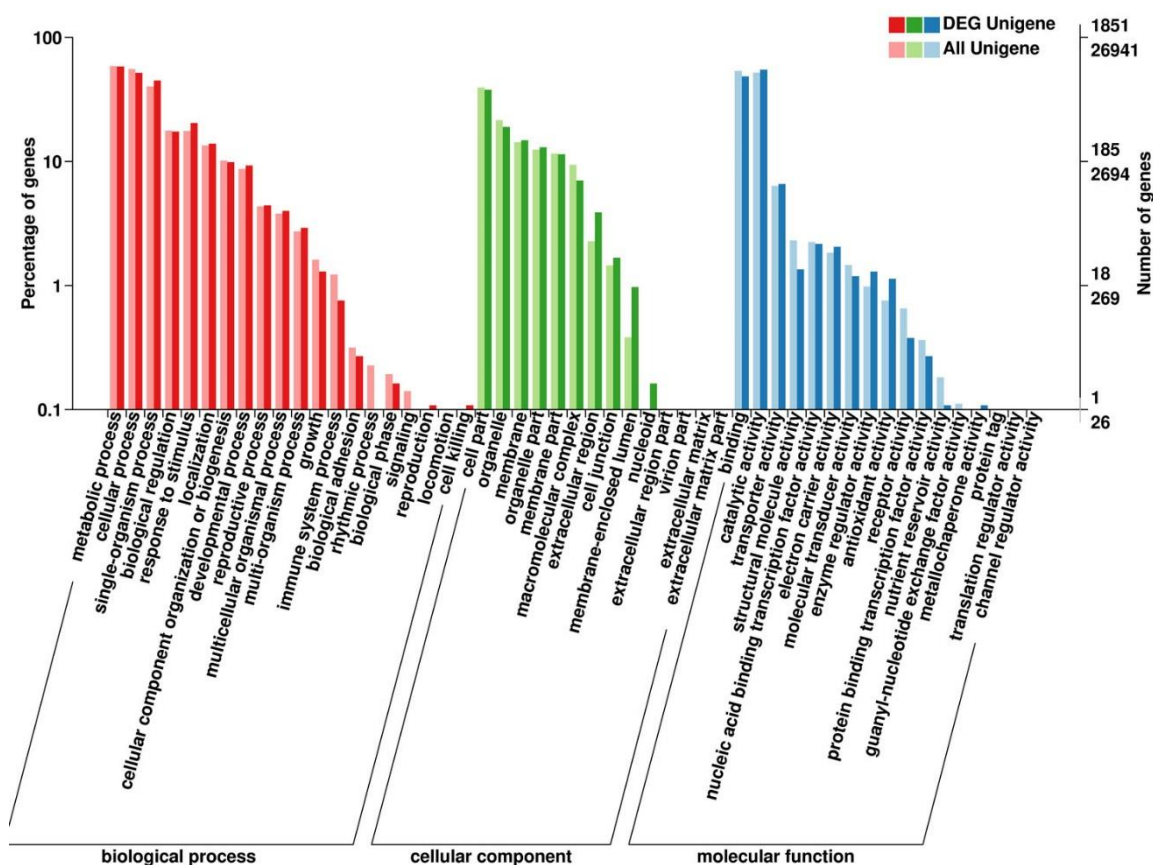


Fig. 2 Suppl. The GO annotation of differentially expressed genes for Y0-vs-D0.

COG Function Classification of Consensus Sequence

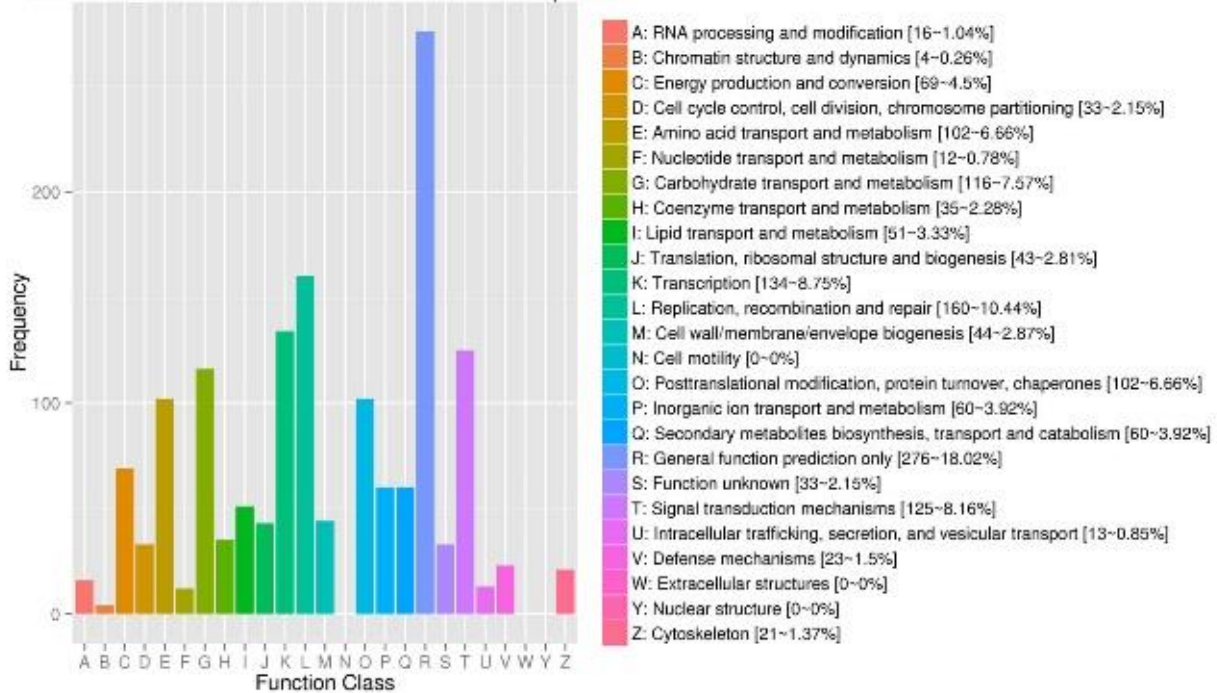


Fig. 3 Suppl. The COG function classification of consensus sequences for Y0-vs-D0.

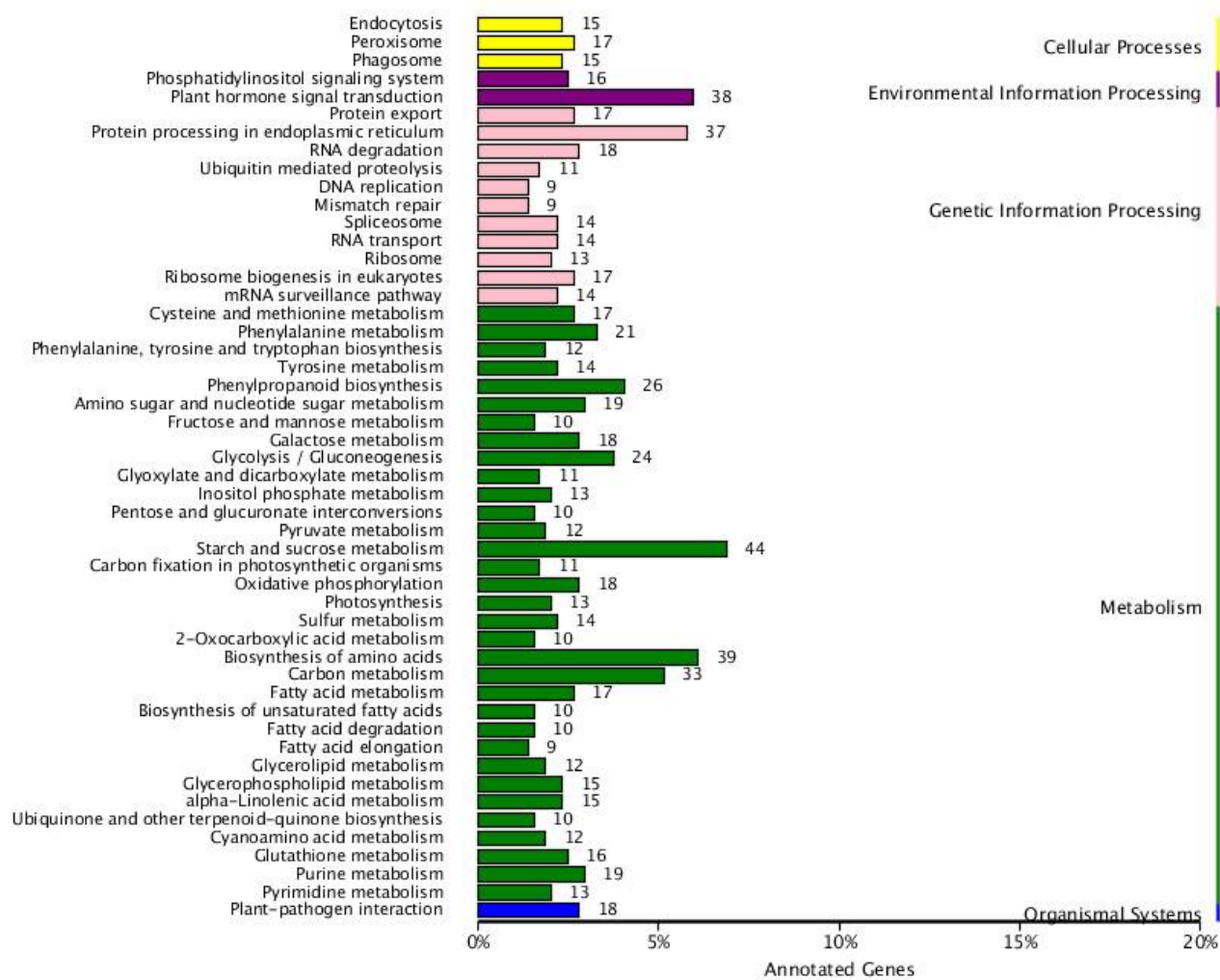


Fig. 4 Suppl. The KEGG pathway classification of differentially expressed genes for Y0-vs-D0.

