

Table 1 Suppl. Primers used for RT-qPCR.

Gene ID	F/R	Primer sequence
<i>Actin</i>	F	5' GTTGCTATCCAGGCTGTTCT 3'
	R	5' ACTGCTCTTAGCCGTCTCC 3'
29794.t000071	F	5' GGTCAATCCCATCTGGAGCGT 3'
	R	5' AGAACAATGGAGGCGAGTGC 3'
30147.t000162	F	5' GCAGCAAGGGCATGATAAGA 3'
	R	5' AAAGCACCCGAGACCGAAAA 3'
30008.t000036	F	5' CATAAGAATCACGGGCTGAG 3'
	R	5' AATGTAAATGGGGAAAAGGG 3'
29844.t000211	F	5' TACAGGTCTGCCCCGTTCTCC 3'
	R	5' CCTTCGGTATTCCATGATGC 3'
30142.t000005	F	5' GTGTGATATGCATTTCAGACAAGGA 3'
	R	5' AAGGTACAAAAGAAAGGAGGGACC 3'
29673.t000033	F	5' CATAACAAGCGACAAGCAACAG 3'
	R	5' ACAAGAGGATACCGCACCCAAT 3'
29756.t000030	F	5' ACAATTAGAGAGGCGAAAAAGCA 3'
	R	5' TTGAGCAAAGGGTCGAGAGACC 3'
30174.t000396	F	5' TTGATGGATCTGGAGAAGAGAAT 3'
	R	5' GTTAGGCGTTGAATGGGTGT 3'
29801.t000101	F	5' AGTACCATAATCCATTGTGTGC 3'
	R	5' CGTCATCTATCTCTGTGCTGTC 3'
29637.t000044	F	5' TTGTCCTTTCTCTCCTCTCGA 3'
	R	5' CCACTTAACCCAATCTTTCCA 3'

Table 2 Suppl. List of 49 key enzymes associated with lipid biosynthesis measured at different developmental stages S1 - S3.

Symbol	Gene ID	Enzymes	FPKM S1	S2	S3
OLE	29794.t000071	oleosin	300.13167	1184.99	4728.43
OLE	30147.t000162	oleosin	209.81667	1114.6433	2037.9733
PXG	30008.t000036	peroxygenase	181.31967	1240.0167	1505.6067
LACS7	29844.t000211	Long chain acyl-CoA synthetase	7.6448519	20.128587	522.61953
PLA2	30142.t000005	Phospholipase A2	7.7352281	30.860313	224.60337
PXG4	29673.t000033	peroxygenase	11.297743	34.004144	54.65325
PLC	29756.t000030	phospholipase C	0.1422333	9.26752	28.639033
ACCCase- α	30174.t000396	Acetyl-coenzyme A carboxylase carboxyl transferase	1.4735763	6.5043693	18.375142
DGAT	29801.t000101	diacylglycerol o-acyltransferase	1.177666	4.3720267	9.7639633
PDAT	29637.t000044	phospholipid:diacylglycerol acyltransferase	1.7130821	5.688424	7.8233972
PDCT1	29841.t000129	phosphatidylcholine:diacylglycerol cholinephosphotransferase	311.7588	789.182	23.409183
KASII	29739.t000147	ketoacyl-ACP synthase	313.5476	731.42053	227.24962
PDAT1	29912.t000012	phospholipid:diacylglycerol acyltransferase	60.709167	180.833	14.797667
ACBP3	30170.t000172	acyl CoA-binding protein	15.353417	92.041941	67.144712
DGAT	29742.t000056	diacylglycerol o-acyltransferase	14.2604	55.828033	49.293967
NPC1	29681.t000039	non-specific phospholipase C	21.838433	54.581733	47.316367
NPC1	30128.t000330	non-specific phospholipase C	10.312405	32.80059	2.0702596
LPAAT4	30170.t000402	acyl-CoA:lysophosphatidic acid acyltransferase	2.2660386	31.061332	27.199688
LACS1	30076.t000180	Long chain acyl-CoA synthetase	3.2211146	15.527644	16.708722
PLA2	30170.t000326	phospholipase A	1.0831813	11.330667	7.6624767
ACCCase- α	27798.t000006	Acetyl-coenzyme A carboxylase carboxyl transferase	402.48322	250.66139	23.730979
ACP1	29709.t000042	acyl carrier protein	118.93578	58.626163	38.37234
ACP1	30128.t000131	acyl carrier protein	4629.7453	2896.101	481.0746
ACP1	29726.t000092	acyl carrier protein	165.381	234.77833	26.823
ACP2	29929.t000054	acyl carrier protein	149.29667	67.0871	53.349567
ACP3	29826.t000005	acyl carrier protein	33.300933	26.094433	9.6033633
ACP4	PB.3905	acyl carrier protein	21.331167	29.630233	3.4419767
KASIII	28455.t000015	ketoacyl-ACP synthase	120.21223	85.262233	11.182363
KASIII	29693.t000072	ketoacyl-ACP synthase	573.41973	436.14067	54.465917
SAD	29929.t000018	stearoyl-ACP desaturase	5.5058737	0.8313366	0.2869924
SAD	27985.t000040	stearoyl-ACP desaturase	532.974	891.11933	227.31033
KAR	29929.t000235	ketoacyl-ACP reductase	360.139	214.905	24.7012
FATA	30217.t000013	fatty acyl-ACP thioesterase	107.3094	171.24225	14.70705
EAR1	27843.t000004	enoyl-ACP reductase	497.13361	312.34155	14.901687
LACS2	29851.t000115	long chain acyl-CoA synthetase	1.7063892	2.1170474	0.711608
LACS9	29908.t000237	long chain acyl-CoA synthetase	244.30152	260.10791	32.762251
LPCAT 1	30190.t000362	lysophosphatidylcholine acyltransferase	360.71367	317.40633	86.9816
ACBP4	30138.t000128	acyl CoA-binding protein	17.323998	9.1199355	8.4925802
ACBP4	29726.t000117	acyl CoA-binding protein	31.70465	11.19502	5.5423537
ACBP4	28872.t000006	acyl CoA-binding protein	19.816859	39.068963	16.625685
LPAAT2	27810.t000017	acyl-CoA:lysophosphatidic acid acyltransferase	136.46533	136.29333	61.753733
LPAAT3	30169.t000210	acyl-CoA:lysophosphatidic acid acyltransferase	15.052767	6.2975267	2.36856
PLC4	30147.t000759	phospholipase C	8.5622567	16.011213	6.5455859
PLC	29801.t000111	phospholipase C	15.802909	14.31254	5.2682363
PDAT2	29991.t000008	phospholipid:diacylglycerol acyltransferase	72.884833	43.192567	4.8444833
DGAT	29983.t000068	diacylglycerol o-acyltransferase	3.8607433	0.807289	0.521294
PLD	30170.t000702	phospholipase D	16.61993	7.56022	6.1703167
PLD	28725.t000003	phospholipase D	0.5641618	0.1856258	0.0883132
PLA2	29840.t000027	phospholipase A	128.59689	15.811307	2.7830464

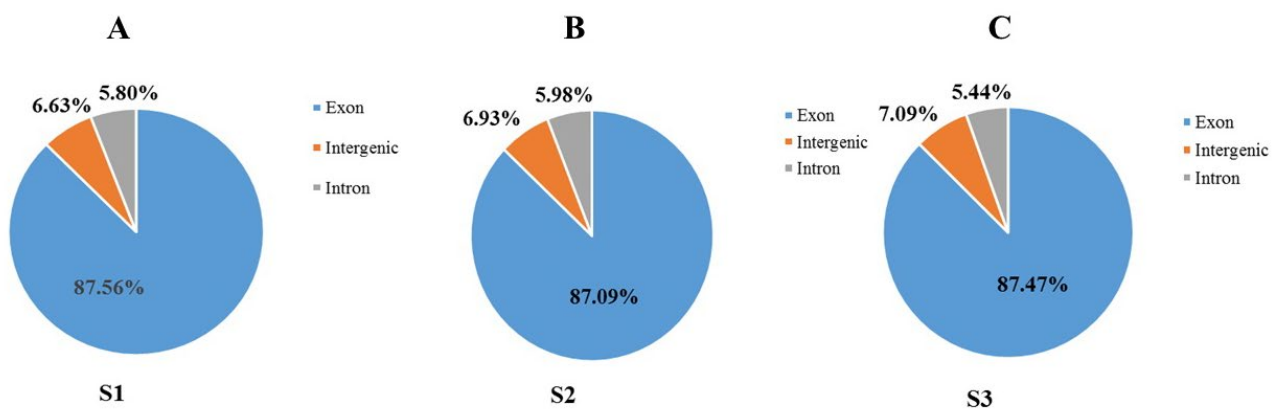
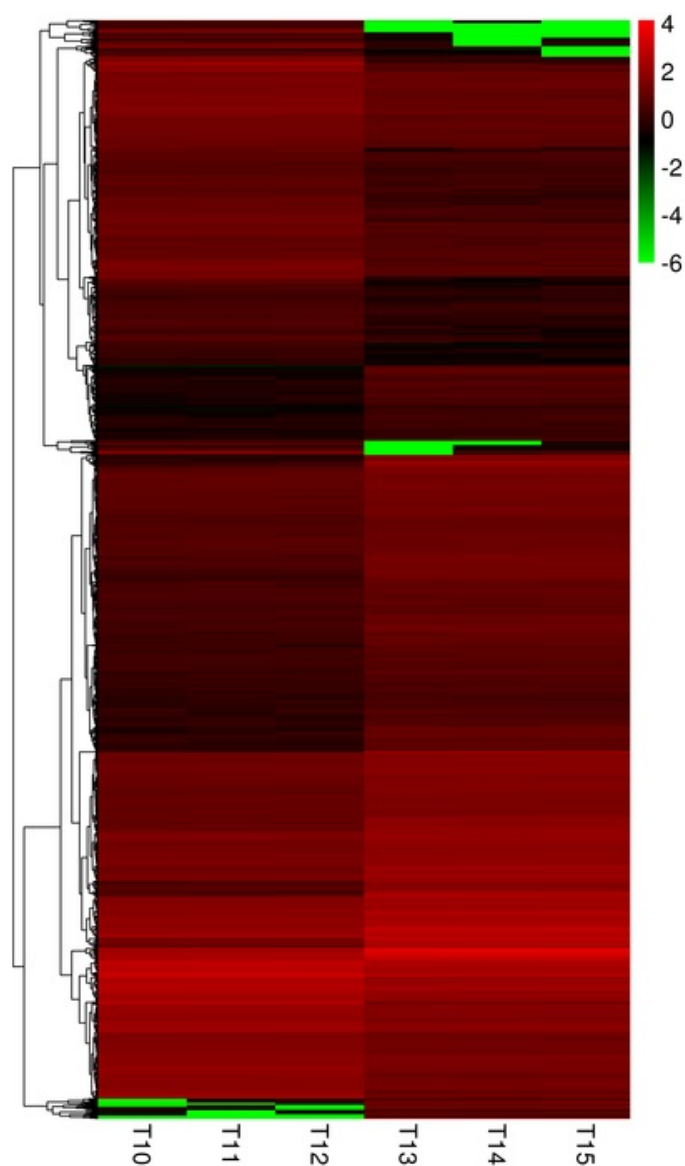
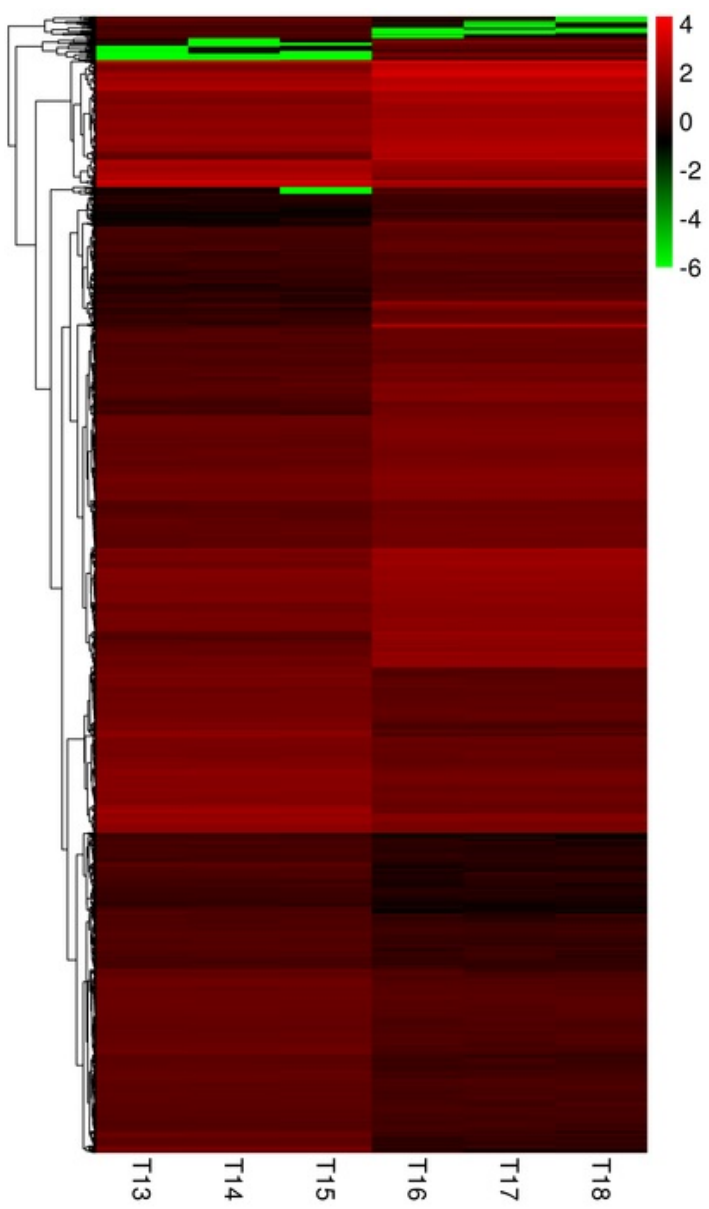


Fig. 1 Suppl. Statistics of mapped reads in different regions of the genome for three libraries S1 (A), S2 (B), and S3 (C).





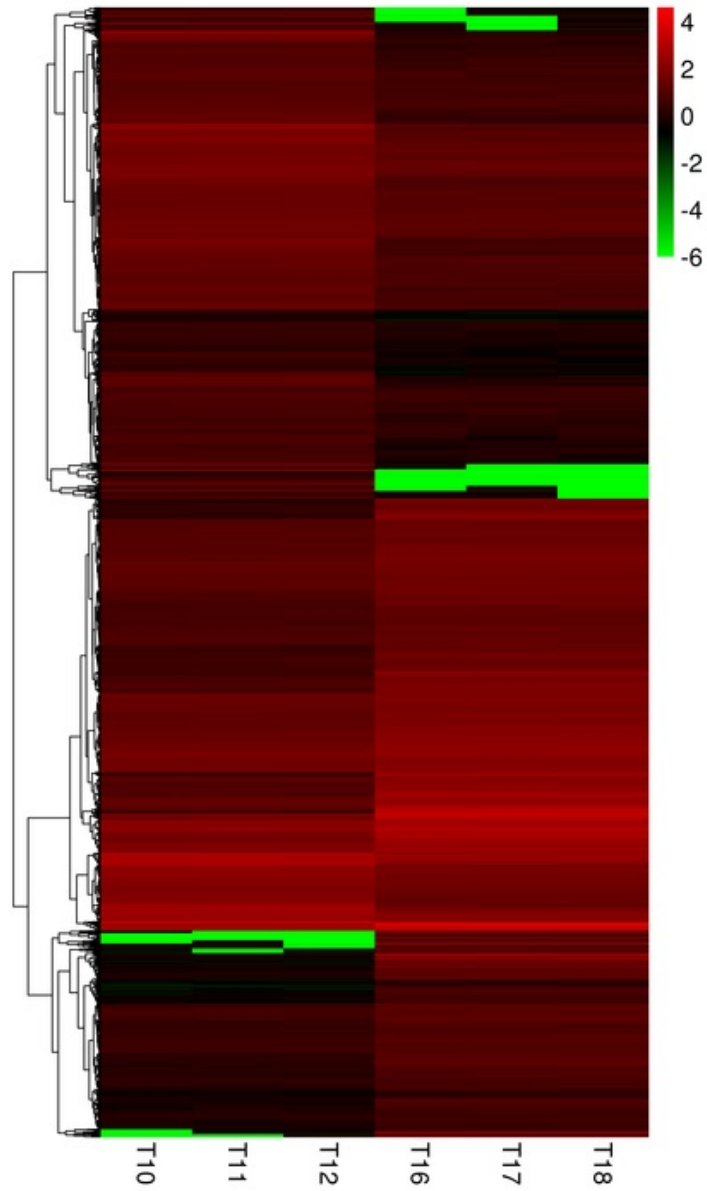
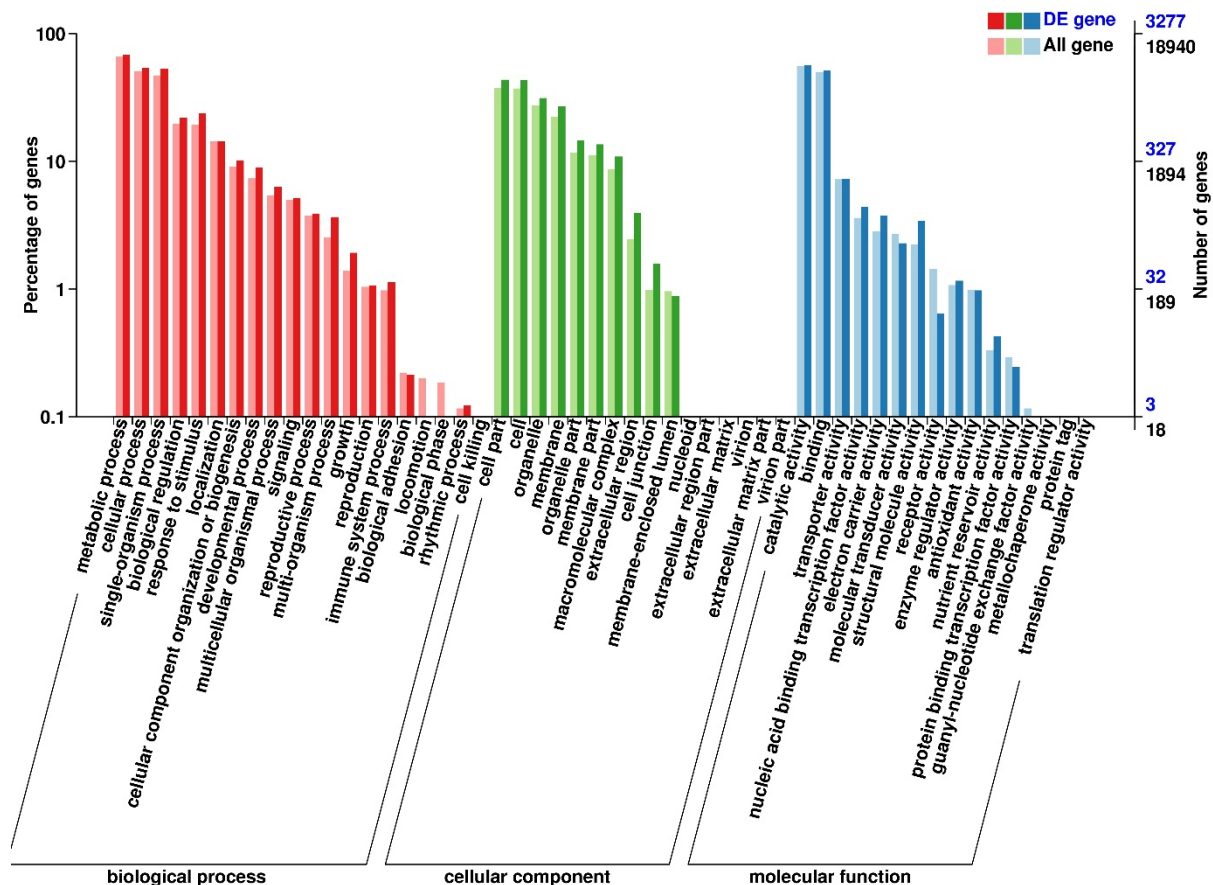
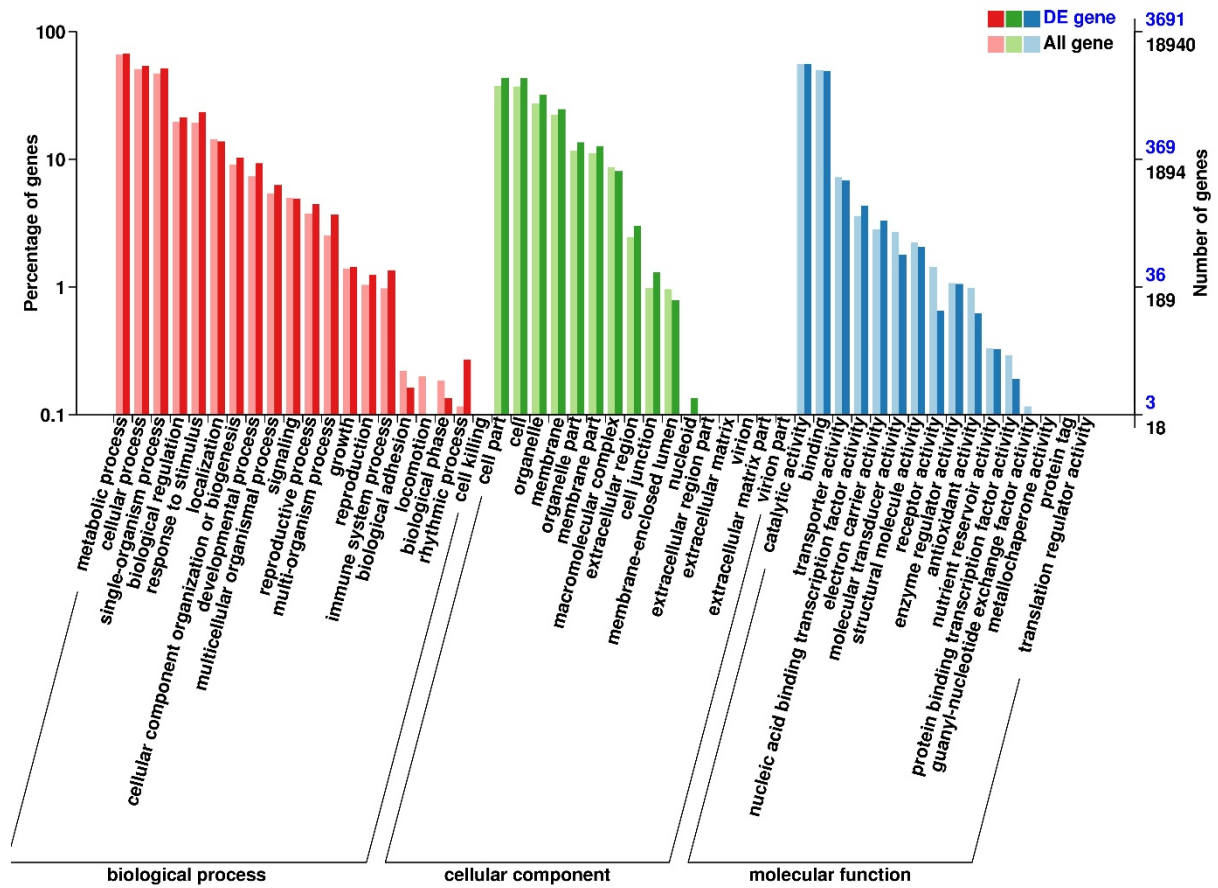


Fig. 2 Suppl. Hierarchical clustering analysis of intersectional DEGs in the three paired groups [S1 vs. S2 (*A*), S2 vs. S3 (*B*), and S1 vs. S3 (*C*)] based on data of log₂Ratio from one gene. The color bar ranging from *green* to *red* indicates low to high transcriptional expression level.





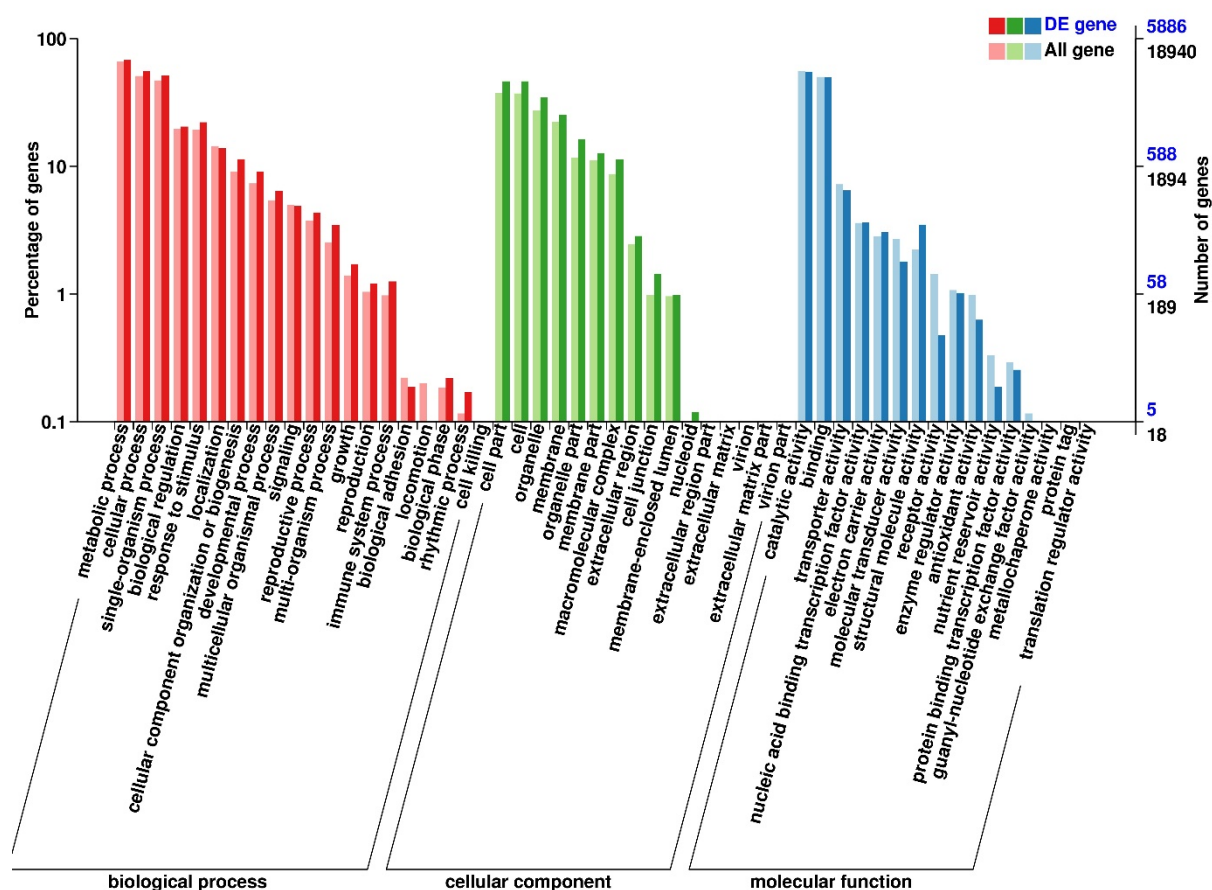
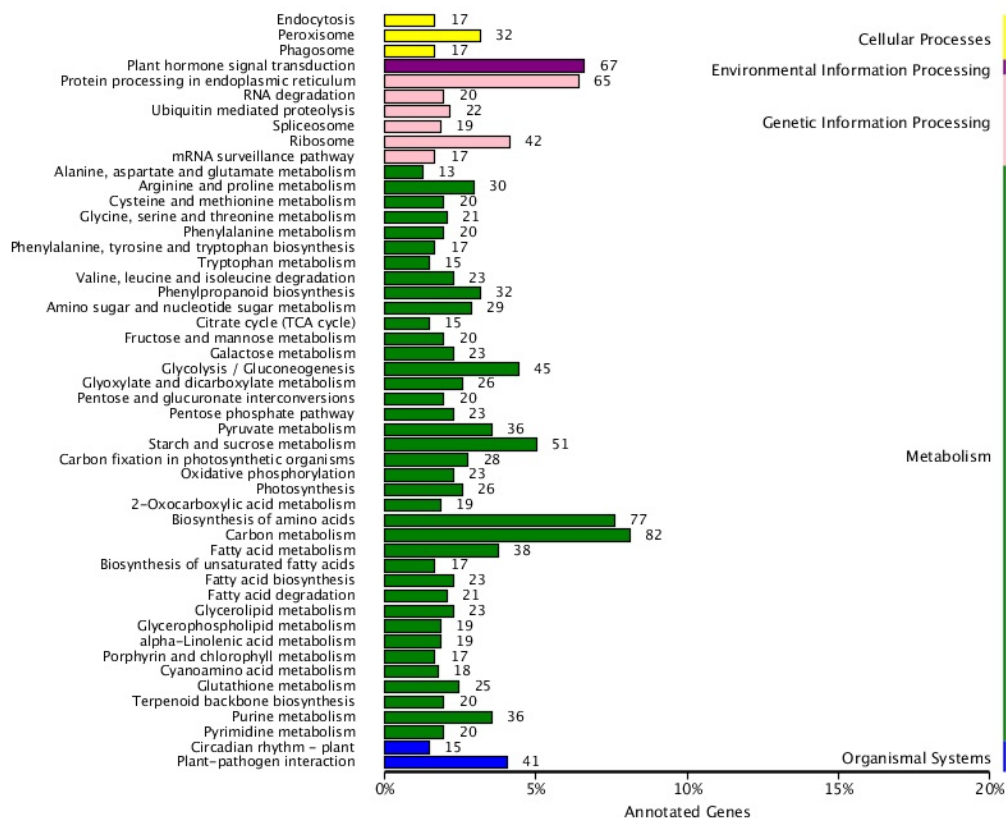
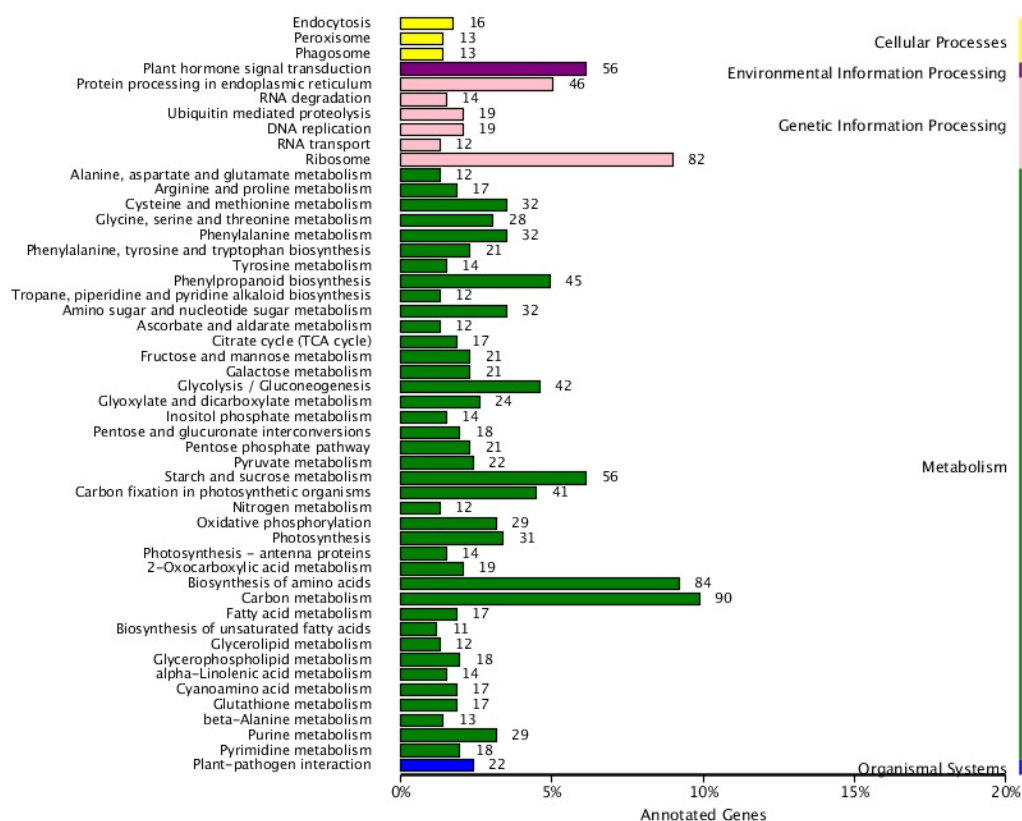


Fig. 3 Suppl. GO classifications of differentially expressed genes (DEGs) in the three paired groups [S1 vs. S2 (A), S2 vs. S3 (B), and S1 vs. S3 (C)]. DEGs are divided into three main categories: biological process, molecular function, and cellular component by GO analysis.



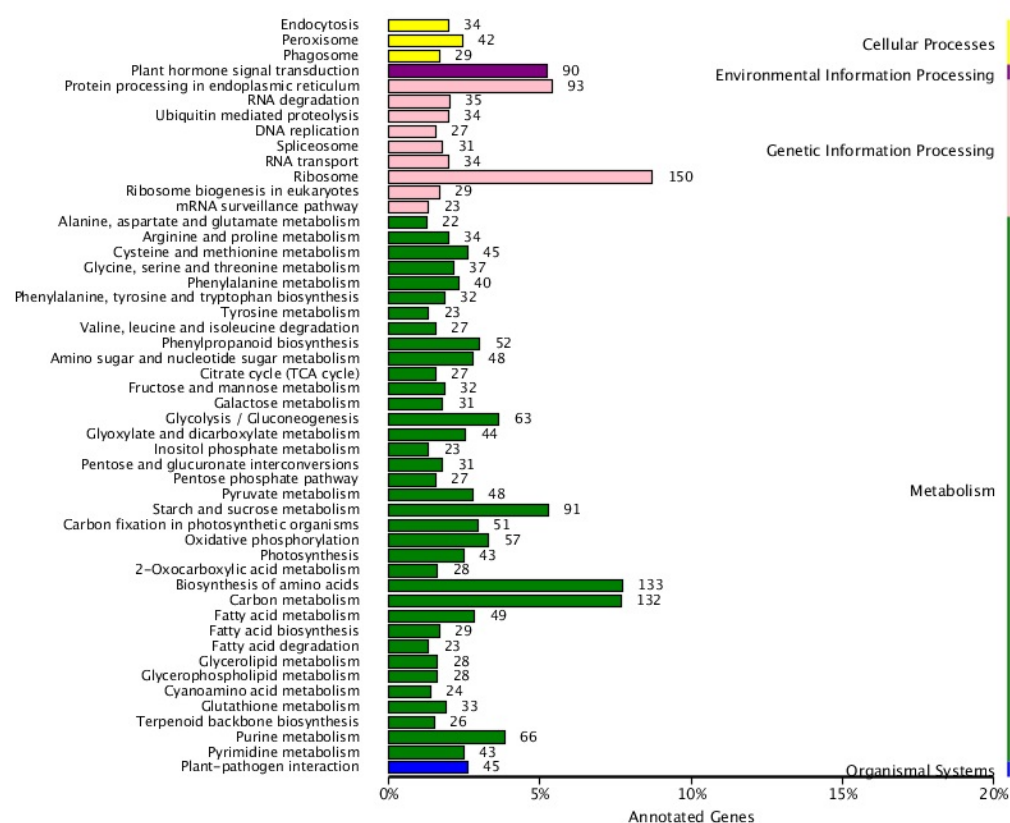


Fig. 4 Suppl. KEGG pathway categories of differentially expressed genes (DEGs) in the three paired groups [S1 vs. S2 (A), S2 vs. S3 (B), and S1 vs. S3 (C)].

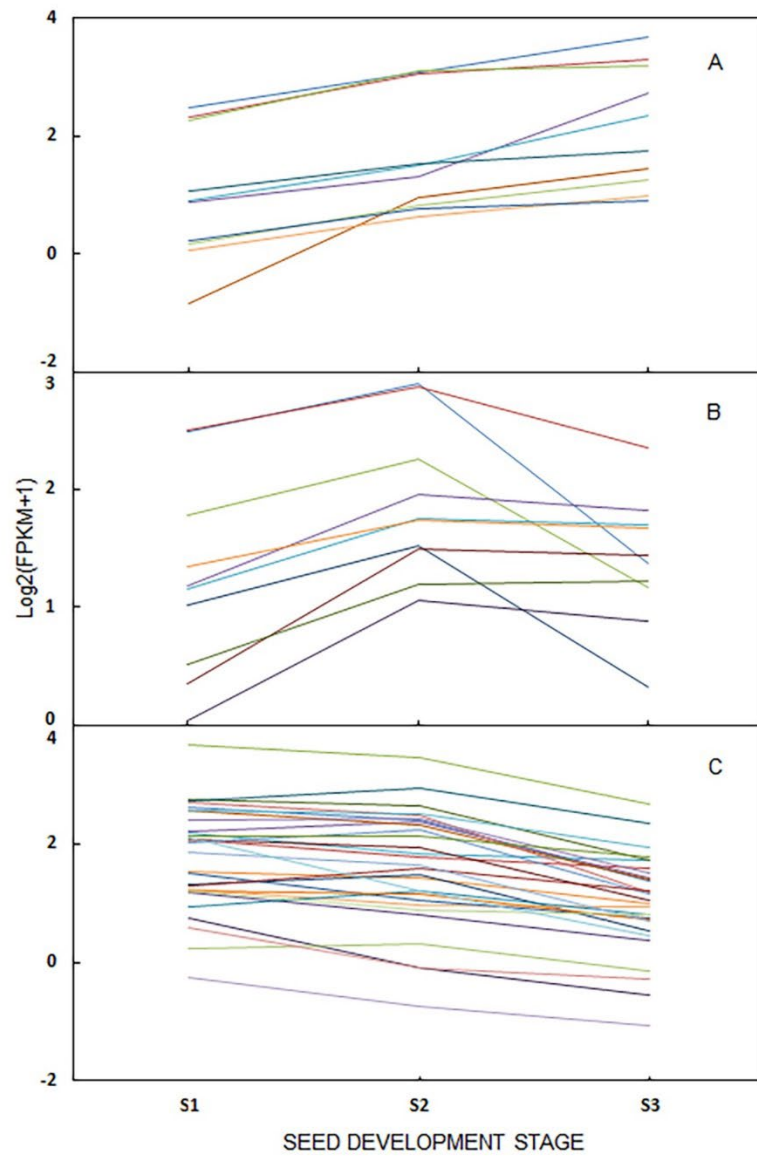


Fig. 5 Suppl. Three clusters with different gene expression patterns for all key enzyme genes. *A* - Cluster I: rising pattern; *B* - Cluster II: bell-shaped pattern; *C* - Cluster III: decreasing pattern.