Supplementary information

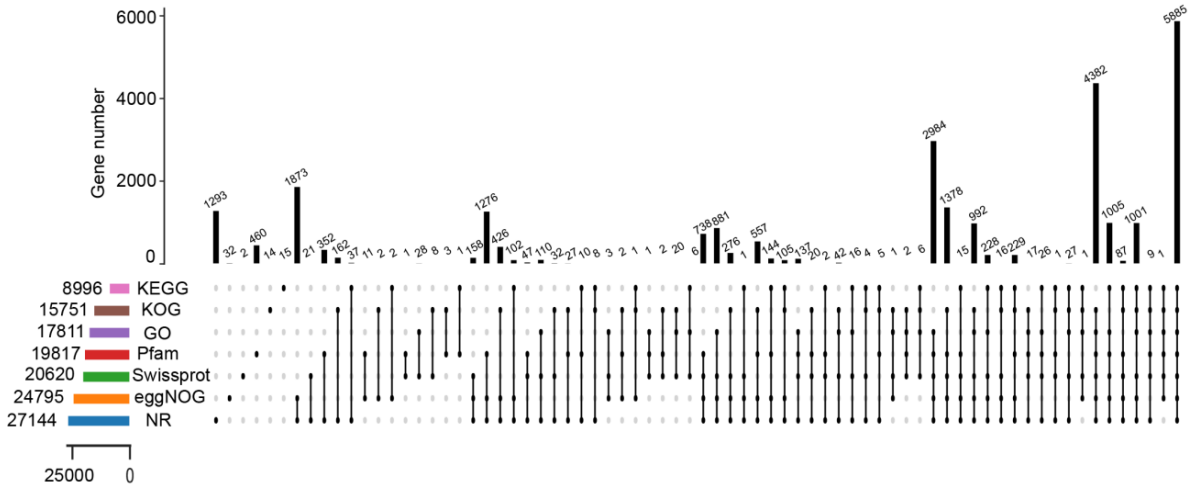


Figure S1. Annotation information obtained from seven different databases. The lower left columns represent the total number of unigenes in each database, the lower right lines represent combinations of databases, and the top bar chart represents the number of unigenes in each combination of databases.

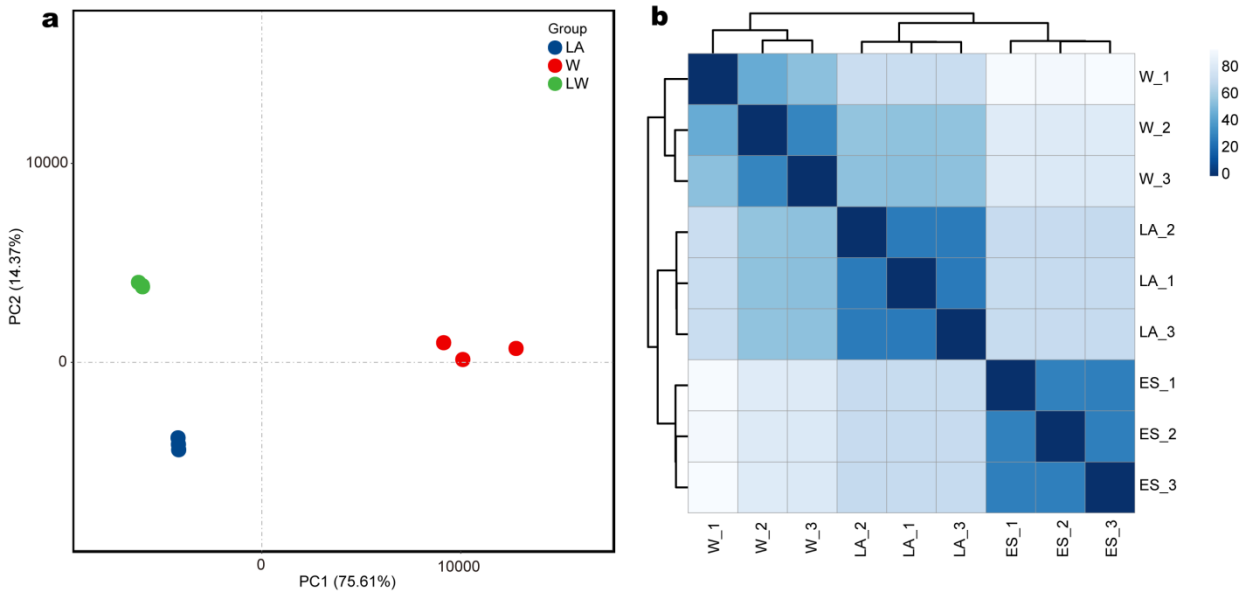


Figure S2. Chart showing the results of the quality assessment chart of transcriptome samples. (**a**) Principal component analysis (PCA). The *x*- and *y*-axes represent the first principal component (PC1) and the second principal component (PC2), respectively. The dots represent the samples. (**b**) Cluster analysis of samples based on transcriptome data. The *x*- and *y*-axes represent the corresponding sample names, and the color represents the size of the correlation coefficient. Sample abbreviations are as follows: ES, early spring; LA, late autumn; and W, winter. LA_1, LA_2, and LA_3 represent 3 biological replicates.

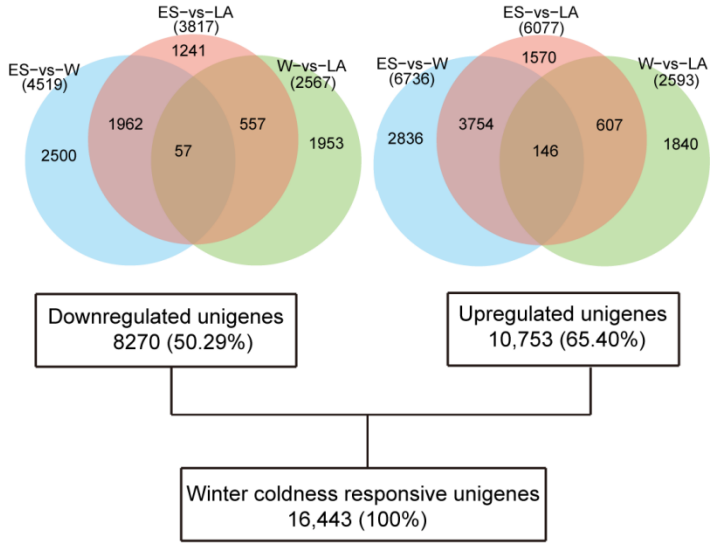


Figure S3. Venn diagram of differentially expressed unigenes (DEGs) in overwintering *C. fortunei*. Sample abbreviations are as follows: ES, early spring; LA, late autumn; and W, winter.

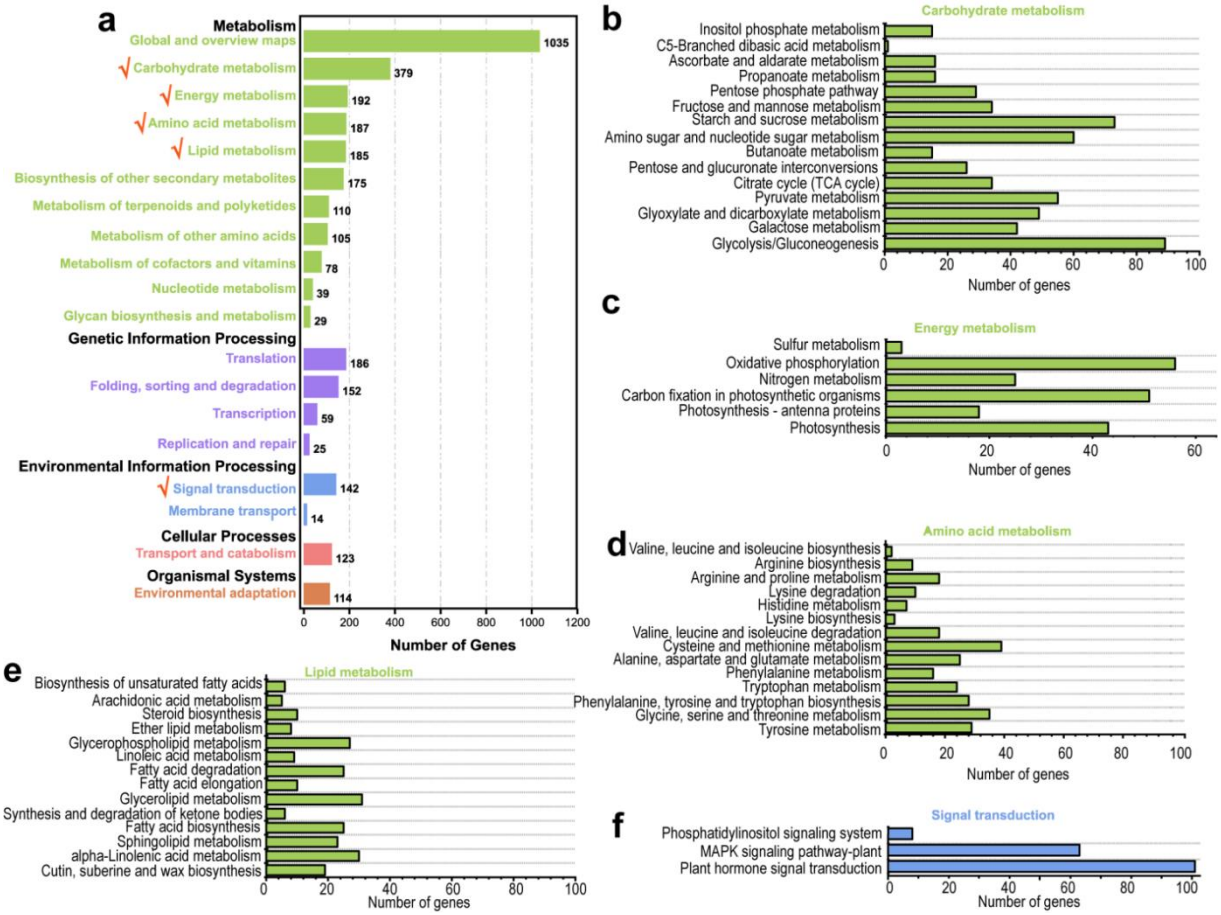


Figure S4. Kyoto Encyclopedia of Genes and Genomes (KEGG) functional annotations of DEGs in overwintering *C. fortunei*. (**a**) KEGG functional annotation of DEGs in overwintering *C. fortunei*. (**b**-**e**) DEGs were enriched in carbohydrate metabolism (**b**), energy metabolism (**c**), amino acid metabolism (**d**), lipid metabolism (**e**) and signal transduction pathways (**f**). The *x*-axis represents number of genes, and the *y*-axis represents pathways.

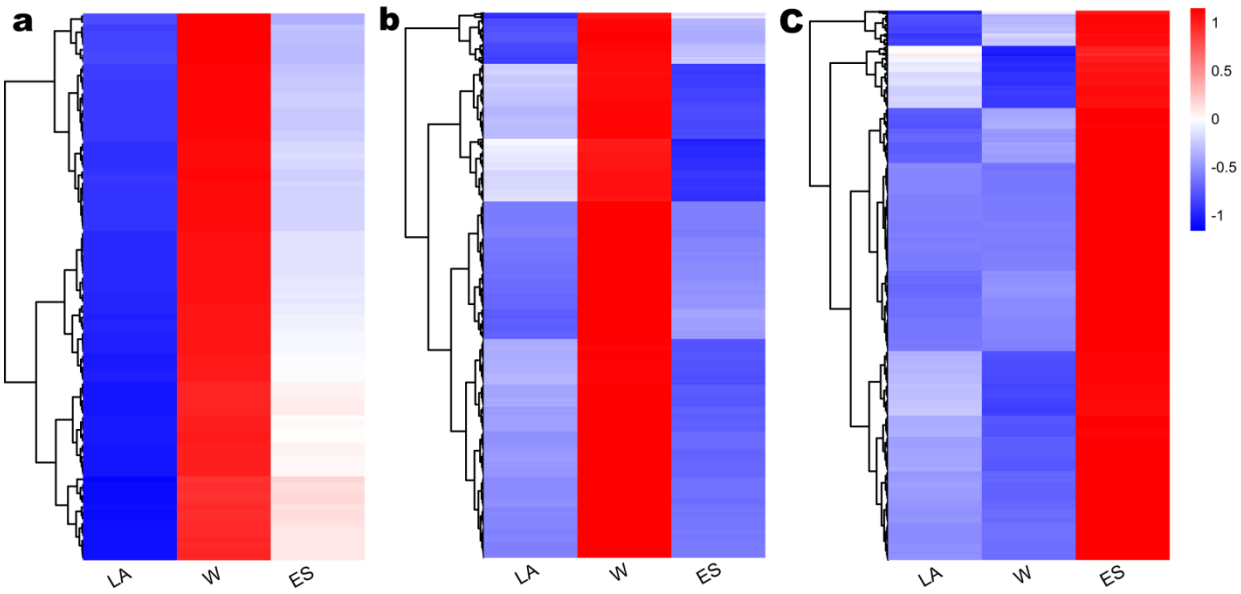


Figure S5. Hierarchical clustering heatmap of unigenes. (**a**) Unigenes in the magenta module, (**b**) unigenes in the brown module, and (**c**) unigenes in the turquoise module. Each column and row represent each sample and unigene, respectively. The color represents unigene expression levels after normalizing the row data. Sample abbreviations are as follows: ES, early spring; LA, late autumn; and W, winter

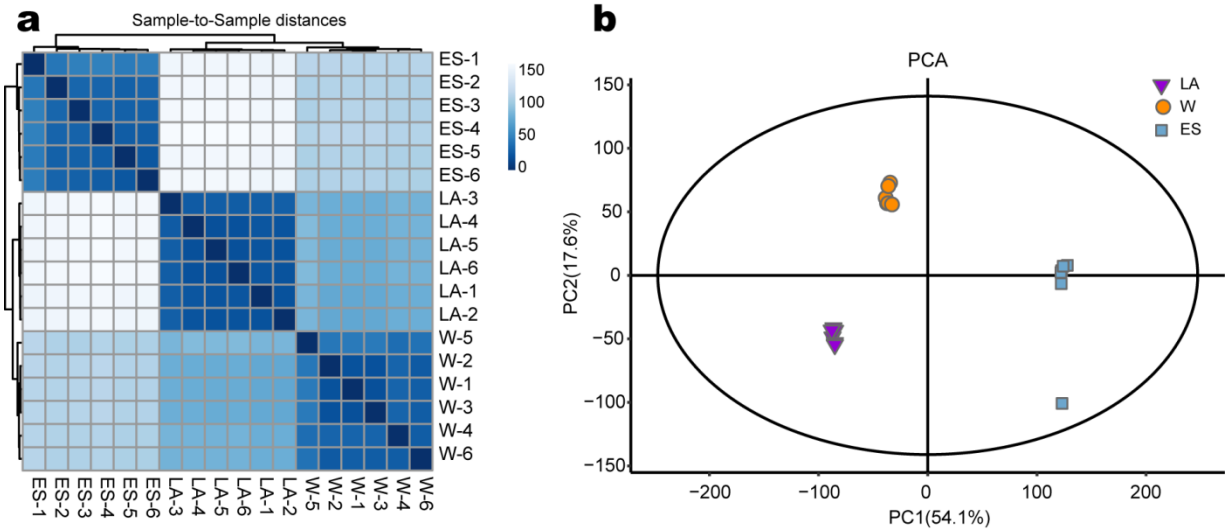


Figure S6. Quality control chart of metabolome samples. (**a**) Cluster analysis of samples. The *x*- and *y*-axes represent the corresponding sample names, and the color represents the size of the correlation coefficient. (**b**) PCA score plot of all samples. The *x*-axis represents the first principal component (PC1), and the *y*-axis represents the second principal component (PC2). Graphic marks in different colors indicate samples from different stages. Sample abbreviations are as follows: ES, early spring; LA, late autumn; and W, winter. LA_1, LA_2, LA_3, LA_4, LA_5, and LA_6 represent three biological samples in duplicate (6 samples for one sampling period).

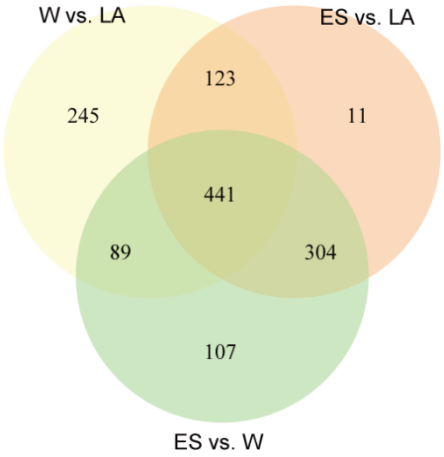


Figure S7. Venn diagrams of differentially synthesized metabolites (DSMs). Sample abbreviations are as follows: ES, early spring; LA, late autumn; and W, winter.

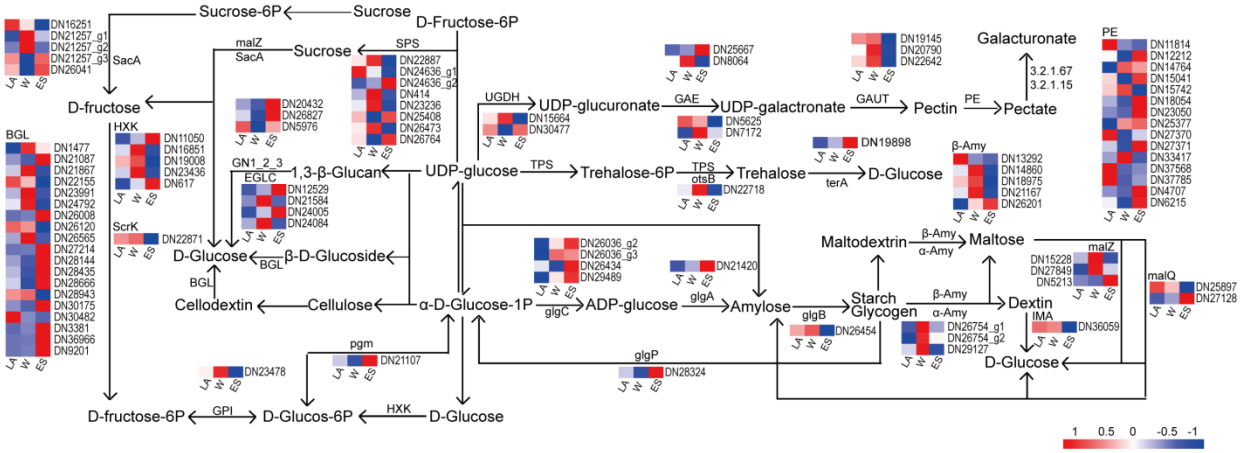


Figure S8. Unigenes in the starch and sucrose metabolism pathways that were differentially expressed in overwintering *C. fortunei*. The heatmap represents unigene expression levels after normalizing the row data, and red and blue represent high and low expression, respectively. Each column and each row represent sample and unigene, respectively. Sample abbreviations are as follows: ES, early spring; LA, late autumn; and W, winter. Gene abbreviations are as follows: *α-Amy, alpha-amylase; β-Amy, beta-amylase; BGL, beta-glucosidase; EGLC, glucan endo-1,3-beta-D-glucosidase; GAE, UDP-glucuronate 4-epimerase; GAUT, alpha-1,4-galacturonosyltransferase; glgA, starch synthase; glgB, 1,4-alpha-glucan branching enzyme; glgC, glucose-1-phosphate adenylyltransferase; glgP, glycogen phosphorylase; GN1_2_3, glucan endo-1,3-beta-glucosidase 1/2/3; GPI, glucose-6-phosphate isomerase; HXK, hexokinase; IMA, oligo-1,6-glucosidase; malQ, 4-alpha-glucanotransferase; malZ, alpha-glucosidase; otsB, trehalose 6-phosphate phosphatase; PE, pectinesterase; pgm, phosphoglucomutase; sacA, beta-fructofuranosidase; scrK, fructokinase; SPS, sucrose-phosphate synthase; SUS, sucrose synthase; TPS, trehalose 6-phosphate synthase/phosphatase; treA, alpha, alpha-trehalase; XYL4, xylan 1,4-beta-xylosidase; UGD, UDP-glucuronate decarboxylase;* and *UGDH, UDPglucose 6-dehydrogenase.*

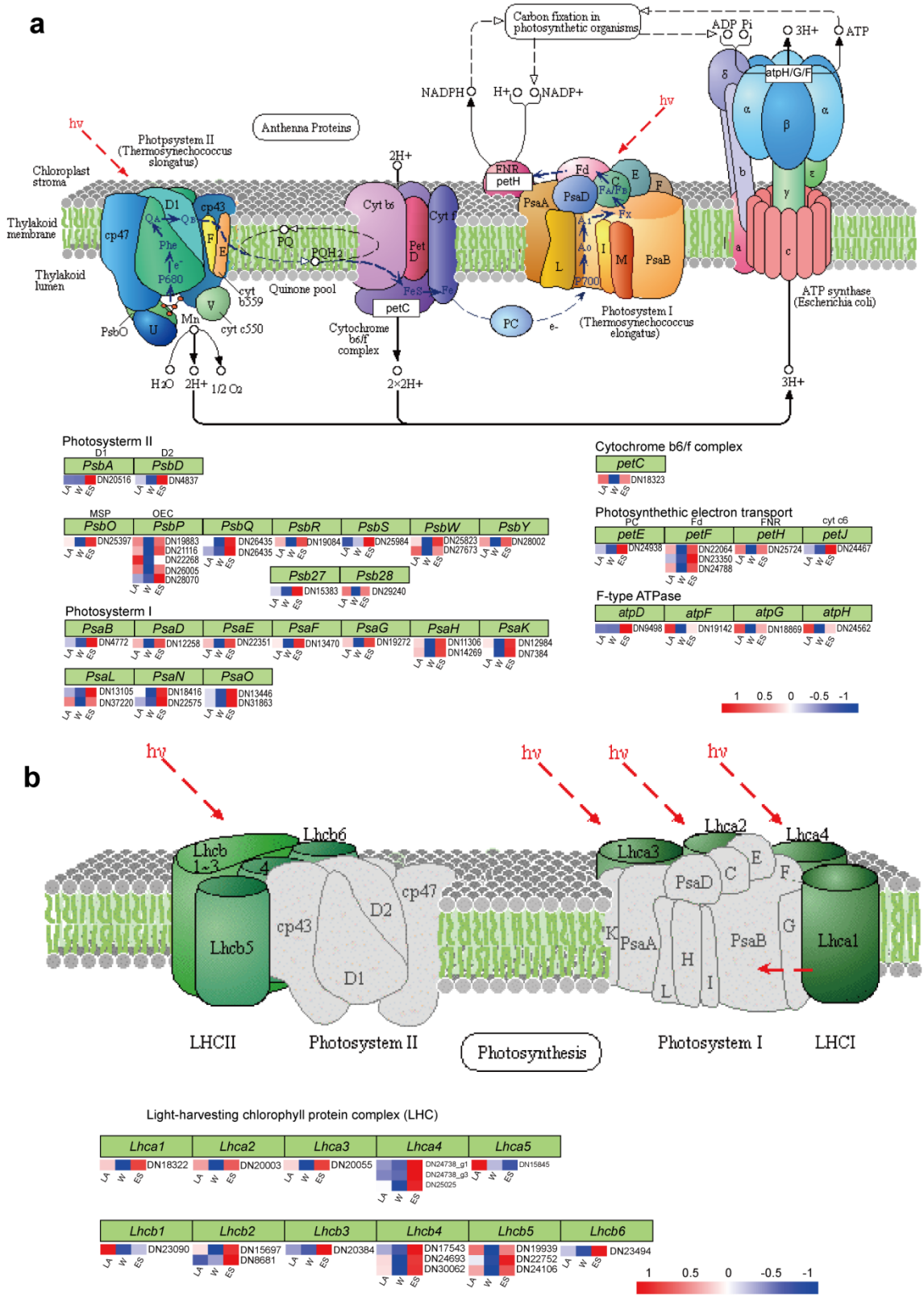


Figure S9. Unigenes in photosynthesis-related metabolism pathways that were differentially expressed in overwintering *C. fortunei*. (**a**) Photosynthesis biosynthesis (ko00195), and (**b**) photosynthesis-antenna protein biosynthesis (ko00196). Colors represent unigene expression levels after normalizing the row data, red represents unigenes with high expression, and blue represents unigenes with low expression.

Table S1. All primers for unigenes used in this study.

Unigenes	Gene	Gene name	Forward primer sequence (5' to 3')	Reverse primer sequence (5' to 3')
TRINITY_DN26201_c9_g1_i5_1	*β-Amy*	*beta-amylase*	TGCCCAGTGCTCACCAGA	GCCTTTCCTTCACCCATTTT
TRINITY_DN28063_c0_g1_i6_2	*ARR-B*	*two-component response regulator ARR-B family*	GCGGTGAATAAAGTGGGAATC	ACGAAGCAACTGGGCAAGA
TRINITY_DN25209_c0_g1_i1_1	*AUX1*	*auxin influx carrier*	CTGTCCATGCCTTATTCCTATTCA	ACTTCAGCCAGGGTCCAACTA
TRINITY_DN17061_c0_g1_i2_1	*CYP73A*	*trans-cinnamate 4-monooxygenase*	ATGGCGGACGTACAGCAAG	CCAAAGGACCAGGTGGAAGC
TRINITY_DN20534_c0_g1_i2_3	*ETR*	*ethylene receptor*	TCGCCAAGAGGCTGAAACA	CAAGATTATGAACCTCACGGAAC
TRINITY_DN16859_c0_g1_i3_3	*F3H*	*naringenin 3-dioxygenase*	ATTTCTTCGCCCTCCCTTTG	CGCATGGTGGGTGGCTTAT
TRINITY_DN19878_c0_g1_i2_1	*HCT*	*shikimate O-hydroxycinnamoyltransferase*	CGCAGACGACAGCGAACA	AGGCAGGTGGAGACAAGAATG
TRINITY_DN18322_c0_g2_i1_3	*LHCA1*	*light-harvesting complex I chlorophyll a/b binding protein 1*	TCTCAGGAAGCAGCAGCACA	TGGAACGGCACCTAAACCC
TRINITY_DN13470_c0_g1_i1_3	*psaF*	*photosystem I subunit III*	GGCTCGGAATCGAACAAGG	GGTCGCCATCAACAATCAGG
TRINITY_DN15502_c0_g1_i1_3	*SAUR*	*small-auxin-up-RNA*	AGGGTGAACAACACCAGCGATTC*GT*	AGGTCCTGCACATACTGGAAAA

Table S4. Annotation statistics of *C. fortunei* unigenes.

Database	Number of unigenes
eggNOG	24,795
GO	17,811
KEGG	8996
KOG	15,751
NR	27,144
Pfam	19,817
SwissProt	20,620
Total	27,769

Table S13. Transcription factors (TFs) in the magenta module.

Gene family	Number	Unigene
AP2/ERF	2	*TRINITY_DN18448_c0_g1_i1_1* *TRINITY_DN33957_c0_g1_i1_3*
MYB	1	*TRINITY_DN6474_c0_g1_i1_3*
MYB-related	1	*TRINITY_DN25111_c0_g1_i1_2*
Trihelix	1	*TRINITY_DN20177_c0_g1_i1_2*

Table S14. TFs in the brown module.

Gene family	Number	Unigene	Gene family	Number	Unigene
AP2/ERF	5	*TRINITY_DN17018_c0_g1_i1_3*	*MYB*	5	*TRINITY_DN12223_c0_g1_i1_1*
		TRINITY_DN31462_c0_g1_i1_1			*TRINITY_DN17020_c0_g1_i2_3*
		TRINITY_DN33154_c0_g1_i1_1			*TRINITY_DN19328_c0_g1_i4_2*
		TRINITY_DN8750_c0_g1_i1_3			*TRINITY_DN20151_c0_g1_i4_3*
		TRINITY_DN9682_c0_g1_i3_3			*TRINITY_DN21921_c0_g1_i2_1*
B3	2	*TRINITY_DN16484_c0_g2_i1_3*	*MYB-related*	2	*TRINITY_DN17163_c0_g1_i1_3*
		TRINITY_DN23621_c0_g1_i1_3			*TRINITY_DN23365_c0_g1_i3_3*
bHLH	1	*TRINITY_DN35242_c0_g1_i1_1*			*TRINITY_DN14991_c0_g1_i1_1*
bZIP	1	*TRINITY_DN27789_c0_g1_i2_2*			*TRINITY_DN23685_c0_g2_i3_1*
C2C2-Dof	1	*TRINITY_DN8073_c0_g1_i1_1*	*NAC*	5	*TRINITY_DN23774_c0_g1_i4_2*
GARP-G2-like	2	*TRINITY_DN22061_c0_g1_i3_1*			*TRINITY_DN23774_c0_g1_i4_2*
		TRINITY_DN5249_c0_g1_i2_3			*TRINITY_DN27138_c0_g1_i1_2*
HSF	1	*TRINITY_DN27820_c0_g1_i6_2*	*TCP*	1	*TRINITY_DN10295_c0_g1_i1_3*
LOB	5	*TRINITY_DN22289_c4_g1_i4_1*	*Tify*	1	*TRINITY_DN21802_c0_g1_i6_3*
		TRINITY_DN25172_c5_g1_i2_3			*TRINITY_DN20632_c0_g1_i2_1*
		TRINITY_DN25172_c5_g2_i1_3			*TRINITY_DN20769_c0_g1_i2_1*
		TRINITY_DN25172_c5_g2_i1_3			*TRINITY_DN20976_c0_g1_i2_1*
MADS-MIKC	1	*TRINITY_DN4572_c0_g1_i2_1*	*WRKY*	8	*TRINITY_DN20976_c1_g4_i2_1*
		TRINITY_DN22525_c0_g1_i2_3			*TRINITY_DN21551_c0_g1_i1_3*
					TRINITY_DN23796_c0_g1_i3_3
					TRINITY_DN25249_c0_g1_i1_2
					TRINITY_DN4959_c0_g1_i1_1

Table S15. TFs in the turquoise module.

Gene family	Number	Unigene	Gene family	Number	Unigene
Alfin-like	1	*TRINITY_DN20893_c0_g1_i4_3*	*GeBP*	1	*TRINITY_DN22656_c0_g2_i1_3*
		TRINITY_DN11958_c0_g1_i1_2	*GRAS*	1	*TRINITY_DN26552_c0_g1_i1_2*
		TRINITY_DN13326_c0_g1_i1_2	*GRF*	1	*TRINITY_DN21094_c0_g1_i1_3*
		TRINITY_DN13829_c0_g1_i1_3	*HB-BELL*	1	*TRINITY_DN18102_c0_g1_i1_3*
		TRINITY_DN13829_c0_g2_i1_3			*TRINITY_DN16049_c0_g1_i1_2*
		TRINITY_DN14736_c0_g1_i2_2	*HB-HD-ZIP*	4	*TRINITY_DN21096_c0_g1_i4_1*
		TRINITY_DN16656_c0_g1_i1_2			*TRINITY_DN23046_c0_g1_i2_2*
		TRINITY_DN16754_c0_g1_i2_3			*TRINITY_DN8930_c0_g1_i1_3*
		TRINITY_DN17431_c0_g1_i1_3	*HB-other*	1	*TRINITY_DN26007_c0_g1_i2_1*
		TRINITY_DN17846_c0_g1_i1_2	*HB-WOX*	1	*TRINITY_DN27179_c0_g1_i4_2*
		TRINITY_DN26276_c1_g1_i3_3			*TRINITY_DN17175_c0_g1_i3_3*
		TRINITY_DN26276_c1_g5_i1_3	*LOB*	3	*TRINITY_DN27719_c0_g2_i1_2*
AP2/ERF	25	*TRINITY_DN26276_c1_g7_i1_3*			*TRINITY_DN6135_c0_g1_i2_1*
		TRINITY_DN26276_c1_g8_i2_3			*TRINITY_DN19203_c0_g1_i1_3*
		TRINITY_DN27499_c0_g1_i2_3			*TRINITY_DN21175_c0_g1_i1_3*
		TRINITY_DN27592_c0_g2_i1_3			*TRINITY_DN23808_c0_g1_i2_1*
		TRINITY_DN27592_c0_g3_i1_3			*TRINITY_DN24409_c1_g1_i1_3*
		TRINITY_DN28223_c1_g2_i1_2	*MADS-MIKC*	9	*TRINITY_DN25331_c3_g1_i2_1*
		TRINITY_DN28223_c1_g6_i1_2			*TRINITY_DN25359_c0_g1_i6_3*
		TRINITY_DN31663_c0_g1_i1_2			*TRINITY_DN26591_c1_g1_i1_1*
		TRINITY_DN33823_c0_g1_i1_3			*TRINITY_DN27298_c1_g1_i3_3*
		TRINITY_DN3484_c0_g1_i1_2			*TRINITY_DN28465_c1_g3_i2_2*
		TRINITY_DN4719_c0_g1_i2_2	*MADS-M-type*	1	*TRINITY_DN28465_c1_g5_i1_2*
		TRINITY_DN4757_c0_g1_i1_2			*TRINITY_DN14412_c0_g3_i1_1*
		TRINITY_DN7224_c0_g1_i1_2			*TRINITY_DN17554_c0_g1_i1_1*
		TRINITY_DN7931_c0_g2_i1_2			*TRINITY_DN25087_c0_g2_i2_3*
B3-ARF	2	*TRINITY_DN23265_c0_g2_i1_2*			*TRINITY_DN25987_c0_g2_i1_1*
		TRINITY_DN30190_c0_g1_i15_2	*MYB*	9	*TRINITY_DN27253_c0_g1_i1_3*
		TRINITY_DN12526_c0_g1_i1_2			*TRINITY_DN28210_c0_g1_i13_2*
		TRINITY_DN15713_c0_g1_i2_2			*TRINITY_DN4695_c0_g1_i1_3*
		TRINITY_DN15895_c0_g1_i1_2			*TRINITY_DN8659_c0_g1_i1_2*
bHLH	14	*TRINITY_DN16477_c0_g1_i2_2*			*TRINITY_DN8974_c0_g1_i1_2*
		TRINITY_DN16881_c0_g1_i1_2			*TRINITY_DN14814_c0_g1_i1_3*
		TRINITY_DN18998_c0_g1_i1_3	*MYB-related*	7	*TRINITY_DN16313_c0_g1_i2_2*
		TRINITY_DN19293_c0_g1_i1_2			*TRINITY_DN17283_c0_g1_i3_3*
		TRINITY_DN19977_c0_g1_i7_3			*TRINITY_DN19654_c0_g1_i1_2*

		TRINITY_DN21716_c0_g1_i22_2			*TRINITY_DN20349_c0_g1_i9_1*
		TRINITY_DN26187_c0_g2_i2_2			*TRINITY_DN25976_c0_g2_i1_1*
		TRINITY_DN26450_c0_g3_i1_1			*TRINITY_DN31632_c0_g1_i1_3*
		TRINITY_DN28833_c0_g1_i6_3	*NAC*	1	*TRINITY_DN21760_c0_g1_i1_2*
		TRINITY_DN29898_c2_g2_i1_2	*NF-YB*	2	*TRINITY_DN18816_c0_g1_i1_3*
		TRINITY_DN32367_c0_g1_i1_2			*TRINITY_DN25509_c0_g1_i5_2*
		TRINITY_DN20029_c0_g1_i3_2	*NF-YC*	1	*TRINITY_DN19004_c0_g1_i4_2*
bZIP	4	*TRINITY_DN21070_c0_g1_i5_3*	*OFP*	1	*TRINITY_DN33991_c0_g1_i1_2*
		TRINITY_DN27671_c0_g1_i7_2			*TRINITY_DN19028_c0_g1_i2_3*
		TRINITY_DN7644_c0_g1_i1_3			*TRINITY_DN22534_c0_g1_i2_2*
C2C2-CO-like	2	*TRINITY_DN20010_c0_g1_i6_2*	*SBP*	4	*TRINITY_DN27399_c0_g1_i1_2*
		TRINITY_DN21288_c0_g1_i3_3			*TRINITY_DN29358_c0_g1_i22_2*
C2C2-GATA	2	*TRINITY_DN19847_c0_g1_i6_3*			*TRINITY_DN19747_c0_g1_i4_3*
		TRINITY_DN26094_c0_g1_i2_2	*TCP*	4	*TRINITY_DN22670_c1_g1_i1_2*
C2C2-YABBY	3	*TRINITY_DN14678_c0_g1_i1_1*			*TRINITY_DN23383_c1_g1_i1_3*
		TRINITY_DN17469_c0_g1_i4_3			*TRINITY_DN24067_c0_g1_i4_3*
		TRINITY_DN20806_c0_g1_i2_2			*TRINITY_DN19523_c0_g1_i2_2*
C2H2	2	*TRINITY_DN17416_c0_g1_i1_3*	*Trihelix*	3	*TRINITY_DN22814_c0_g1_i1_2*
		TRINITY_DN26274_c0_g1_i3_2			*TRINITY_DN26604_c1_g1_i10_1*
		TRINITY_DN21956_c0_g1_i2_2	*TUB*	2	*TRINITY_DN21298_c0_g1_i3_2*
C3H	4	*TRINITY_DN24389_c0_g1_i8_1*			*TRINITY_DN23906_c0_g1_i2_2*
		TRINITY_DN24389_c0_g1_i8_1			*TRINITY_DN1159_c0_g1_i1_3*
		TRINITY_DN29888_c0_g1_i10_2			*TRINITY_DN14332_c0_g1_i2_1*
		TRINITY_DN12763_c0_g1_i3_3	*WRKY*	6	*TRINITY_DN15928_c0_g1_i2_2*
		TRINITY_DN14030_c0_g1_i3_3			*TRINITY_DN15928_c0_g1_i2_2*
GARP-G2-like	6	*TRINITY_DN19992_c0_g1_i1_3*			*TRINITY_DN18257_c0_g1_i2_1*
		TRINITY_DN20182_c0_g2_i1_1			*TRINITY_DN5054_c0_g1_i1_1*
		TRINITY_DN29261_c0_g1_i1_2			
		TRINITY_DN33553_c0_g1_i1_1			

Table S16. TFs in the black, tan and green–yellow modules.

Gene family	Number	Unigene
AP2/ERF	3	*TRINITY_DN18334_c0_g1_i1_1*
		TRINITY_DN33149_c0_g1_i1_1
		TRINITY_DN23572_c0_g1_i3_1
CSD	1	*TRINITY_DN9813_c0_g1_i1_2*
GARP-G2-like	1	*TRINITY_DN23160_c0_g1_i10_1*
MYB	2	*TRINITY_DN14412_c0_g2_i1_1*
		TRINITY_DN18260_c0_g1_i2_1
MYB-related	5	*TRINITY_DN17547_c0_g1_i1_1*
		TRINITY_DN24199_c4_g1_i1_3
		TRINITY_DN24199_c4_g1_i1_3
		TRINITY_DN29821_c0_g2_i1_2
		TRINITY_DN29821_c0_g2_i1_2
NAC	1	*TRINITY_DN17812_c0_g1_i1_2*

Table S19. KEGG analysis of DSMs in W vs. LA.

Metabolic pathway	Pathway ID annotation	Pathway annotation	Number	*p* value	Matching metabolite IDs
Carbohydrate metabolism (38)	ath00010	Glycolysis/Gluconeogenesis	1	0.4976	C05378 (beta-D-Fructose 1,6-bisphosphate)
	ath00052	Galactose metabolism	7	0	C00029 (UDP-glucose), C00137 (myo-Inositol), C00243 (Alpha-Lactose), C03785 (D-Tagatose 1,6-bisphosphate), C05399 (Melibiitol), C05401 (Galactosylglycerol), C05404 (D-Gal alpha 1->6D-Gal alpha 1->6D-Glucose)
	ath00630	Glyoxylate and dicarboxylate metabolism	2	0.3953	C00025 (L-Glutamate), C00058 (Calcium formate)
	ath00620	Pyruvate metabolism	3	0.0292	C00058 (Calcium formate), C00546 (APC), C02504 (2-Isopropylmalic acid)
	ath00040	Pentose and glucuronate interconversions	2	0.3478	C00029 (UDP-glucose), C03033 (15-hydroxynorandrostene-3,17-dione glucuronide)
	ath00650	Butanoate metabolism	3	0.0629	C00025 (L-Glutamate), C00356 ((3S)-3-hydroxy-3-methylglutaryl-CoA), C06010 ((S)-2-Acetolactate)
	ath00520	Amino sugar and nucleotide sugar metabolism	2	0.6911	C00029 (UDP-glucose), C01019 (L-Fucose)
	ath00500	Starch and sucrose metabolism	2	0.1934	C00029 (UDP-glucose), C00721 (Dextrin)
	ath00051	Fructose and mannose metabolism	4	0.0294	C01019 (L-Fucose), C01355 (Levan), C01768 (Alginic acid), C05378 (beta-D-Fructose 1,6-bisphosphate)
	ath00030	Pentose phosphate pathway	2	0.1775	C00257 (Gluconic acid), C05378 (beta-D-Fructose 1,6-bisphosphate)
	ath00640	Propanoate metabolism	1	0.6565	C00546 (APC)
	ath00053	Ascorbate and aldarate metabolism	5	0.0040	C00029 (UDP-glucose), C00137 (myo-Inositol), C01041 (Ascorbic acid), C01620 (Threonic acid), C01825 (L-Galactose)
	ath00660	C5-Branched dibasic acid metabolism	2	0.1696	C00025 (L-Glutamate), C06010 ((S)-2-Acetolactate)
	ath00562	Inositol phosphate metabolism	2	0.2747	C00137 (myo-Inositol), C03659 ((-)-Bornesitol)
Biosynthesis of other	ath00940	Phenylpropanoid biosynthesis	2	0.4412	C00852 (Chlorogenic acid), C10434 (Dattelic acid)

secondary metabolites (31)	ath00941	Flavonoid biosynthesis	12	0	C00389 (Quercetin), C00509 ((-)-Naringenin), C00774 (Phloretin), C00852 (Chlorogenic acid), C00974 (Aromadendrin), C01477 (Apigenin), C05631 (Eriodictyol), C05903 (Kaempferol), C09727 (Epigallocatechin), C09789(Naringin), C10044 (Galangin), C10434 (Dattelic acid)
	ath00945	Stilbenoid, diarylheptanoid and gingerol biosynthesis	2	0.1026	C00852 (Chlorogenic acid), C10434 (Dattelic acid)
	ath00300	Lysine biosynthesis	1	0.5405	C05560 (L-2-Aminoadipate adenylate)
	ath00944	Flavone and flavonol biosynthesis	6	0	C00389 (Quercetin), C01477 (Apigenin), C01750 (Quercitrin), C05625 (Rutin), C05903 (Kaempferol), C12249 (Astragalin)
	ath00998	Biosynthesis of various secondary metabolites - part 2	1	0.8366	C00078 (L-Tryptophan)
	ath00960	Tropane, piperidine and pyridine alkaloid biosynthesis	1	0.7808	C00166 (Phenylpyruvic acid)
	ath00942	Anthocyanin biosynthesis	4	0.0551	C08604 (Chrysanthemin), C08725 (Pelargonin), C12139 (Petunidin 3-glucoside), C12140 (Oenin)
	ath00966	Glucosinolate biosynthesis	1	0.8211	C00078 (L-Tryptophan)
	ath00965	Betalain biosynthesis	1	0.4129	C00822 (Dopaquinone)
	ath00350	Tyrosine metabolism	1	0.8251	C00822 (Dopaquinone)
	ath00260	Glycine, serine and threonine metabolism	2	0.2992	C00078 (L-Tryptophan), C00546 (APC)
	ath00400	Phenylalanine, tyrosine and tryptophan biosynthesis	3	0.0371	C00078 (L-Tryptophan), C00166 (Phenylpyruvic acid), C00296 (Quinic acid)
Amino acid metabolism (23)	ath00360	Phenylalanine metabolism	4	0.0411	C00166 (Phenylpyruvic acid), C02763 (Enol-phenylpyruvate), C05332 (Phenylethylamine), C12621 (m-Coumaric acid)
	ath00250	Alanine, aspartate and glutamate metabolism	1	0.4629	C00025 (L-Glutamate)
	ath00380	Tryptophan metabolism	1	0.8438	C00078 (L-Tryptophan)
	ath00280	Valine, leucine and isoleucine degradation	1	0.5982	C00356 ((3S)-3-hydroxy-3-methylglutaryl-CoA)

	ath00340	Histidine metabolism	1	0.6487	C00025 (L-Glutamate)
	ath00310	Lysine degradation	1	0.6715	C03273 (5-oxo-pentanoic acid)
	ath00330	Arginine and proline metabolism	3	0.2426	C00025 (L-Glutamate), C00148 (L-Proline), C05938 (L-4-Hydroxyglutamate semialdehyde)
	ath00220	Arginine biosynthesis	2	0.0890	C00025 (L-Glutamate), C00327 (Citrulline)
	ath00290	Valine, leucine and isoleucine biosynthesis	3	0.0130	C02504 (2-Isopropylmalic acid), C04272 ((R)-2,3-Dihydroxy-isovalerate), C06010 ((S)-2-Acetolactate)
	ath00904	Diterpenoid biosynthesis	2	0.7541	C11867 (Gibberellin A7), C11871 (Gibberellin A5)
	ath00908	Zeatin biosynthesis	1	0.5798	C00029 (UDP-glucose)
Metabolism of terpenoids and polyketides (12)	ath00900	Terpenoid backbone biosynthesis	1	0.6326	C00356 ((3S)-3-hydroxy-3-methylglutaryl-CoA)
	ath00906	Carotenoid biosynthesis	3	0.4579	C08614 (Violaxanthin), C09190 (Strigol), C15981 (alpha-Cryptoxanthin)
	ath00902	Monoterpenoid biosynthesis	2	0.3717	C09893 ((+)-Pulegone), C11673 (Geniposidic acid)
	ath00903	Limonene and pinene degradation	2	0.4108	C11412 ((1R,4S)-Iso-dihydrocarvone), C11415 ((1S,4S)-Dihydrocarvone)
	ath00901	Indole alkaloid biosynthesis	1	0.7905	C00078 (L-Tryptophan)
	ath00072	Synthesis and degradation of ketone bodies	1	0.1244	C00356 ((3S)-3-hydroxy-3-methylglutaryl-CoA)
	ath00561	Glycerolipid metabolism	2	0.2014	C00029 (UDP-glucose), C05401 (Galactosylglycerol)
	ath00062	Fatty acid elongation	2	0.2014	C05269 (3-Ketohexanoyl-CoA), C05270 (Hexanoyl-CoA)
Lipid metabolism (18)	ath00071	Fatty acid degradation	2	0.2992	C05269 (3-Ketohexanoyl-CoA), C05270 (Hexanoyl-CoA)
	ath00564	Glycerophospholipid metabolism	1	0.6859	C00307 (Citicoline)
	ath00100	Steroid biosynthesis	2	0.3638	C02530 (22:2 Cholesterol ester), C11455 (4-Hydroxyandrostenedione glucuronide)
	ath00590	Arachidonic acid metabolism	6	0.0055	C00427 (PGH2), C05949 (12-oxo-LTB4), C05951 (Leukotriene D4), C05957 (PGJ2), C14780 (11R-hydroxy-5E,8Z,12Z,14Z-eicosatetraenoic acid), C14807 (12-oxo-ETE)
	ath00600	Sphingolipid metabolism	2	0.1026	C00195 (Ceramide (d18:1/25:0)), C06124 (Sphingosine-1-phosphate)
Metabolism of cofactors and vitamins (5)	ath00860	Porphyrin and chlorophyll metabolism	1	0.9554	C00025 (L-Glutamate)
	ath00130	Ubiquinone and other terpenoid-quinone	1	0.7952	C00156 (4-Hydroxybenzoic acid)

		biosynthesis			
	ath00790	Folate biosynthesis	1	0.7255	C00156 (4-Hydroxybenzoic acid)
	ath00770	Pantothenate and, CoA biosynthesis	2	0.1389	C04272 ((R)-2,3-Dihydroxy-isovalerate), C06010 ((S)-2-Acetolactate)
Metabolism of other amino acids (4)	ath00440	Phosphonate and phosphinate metabolism	1	0.6929	C00058 (Calcium formate)
	ath00480	Glutathione metabolism	2	0.2014	C00025 (L-Glutamate), C00127 (Oxidized glutathione)
	ath00430	Taurine and hypotaurine metabolism	1	0.3861	C00025 (L-Glutamate)
Membrane transport (3)	ath02010	ABC transporters	3	0.3327	C00025 (L-Glutamate), C00137 (myo-Inositol), C00243 (Alpha-Lactose)
Energy metabolism (3)	ath00710	Carbon fixation in photosynthetic organisms	1	0.3996	C00447 (Sedoheptulose 1,7-bisphosphate)
	ath00910	Nitrogen metabolism	2	0.0636	C00025 (L-Glutamate), C00058 (Calcium formate)
Nucleotide metabolism (1)	ath00240	Pyrimidine metabolism	1	0.7655	C00029 (UDP-glucose)
Translation (3)	ath00970	Aminoacyl-tRNA biosynthesis	3	0.1039	C00025 (L-Glutamate), C00078 (L-Tryptophan), C00148 (L-Proline)
Signal transduction (1)	ath04070	Phosphatidylinositol signaling system	1	0.4747	C00137 (myo-Inositol)

Table S20. KEGG analysis of DSMs in ES vs. W.

Metabolic pathway	Pathway ID annotation	Pathway annotation	Number	*p* value	Matching metabolite IDs
Carbohydrate metabolism (37)	ath00010	Glycolysis/Gluconeogenesis	1	0.4845	C00022 (Pyruvic acid)
	ath00052	Galactose metabolism	4	0.0152	C00029 (UDP-glucose), C00085 (D-Fructose 6-phosphate), C00243 (Alpha-Lactose), C05399 (Melibiitol)
	ath00630	Glyoxylate and dicarboxylate metabolism	3	0.1411	C00022 (Pyruvic acid), C00025 (L-Glutamate), C00158 (Citric acid)
	ath00620	Pyruvate metabolism	3	0.0265	C00022 (Pyruvic acid), C00546 (APC), C02504 (2-Isopropylmalic acid)
	ath00020	Citrate cycle (TCA cycle)	2	0.0652	C00022 (Pyruvic acid), C00158 (Citric acid)
	ath00040	Pentose and glucuronate interconversions	2	0.3311	C00022 (Pyruvic acid), C00029 (UDP-glucose)
	ath00650	Butanoate metabolism	4	0.0111	C00022 (Pyruvic acid), C00025 (L-Glutamate), C00356 ((3S)-3-hydroxy-3-methylglutaryl-CoA), C06010 ((S)-2-Acetolactate)
	ath00520	Amino sugar and nucleotide sugar metabolism	1	0.9030	C00029 (UDP-glucose)
	ath00500	Starch and sucrose metabolism	3	0.0418	C00029 (UDP-glucose), C00085 (D-Fructose 6-phosphate), C00721 (Dextrin)
	ath00051	Fructose and mannose metabolism	1	0.6859	C01355 (Levan)
	ath00030	Pentose phosphate pathway	2	0.1674	C00022 (Pyruvic acid), C00257 (Gluconic acid)
	ath00640	Propanoate metabolism	1	0.6425	C00546 (APC)
	ath00053	Ascorbate and aldarate metabolism	5	0.0034	C00022 (Pyruvic acid), C00029 (UDP-glucose), C01041 (Ascorbic acid), C01620 (Threonic acid), C01825 (L-Galactose)
	ath00660	C5-Branched dibasic acid metabolism	4	0.0052	C00022 (Pyruvic acid), C00025 (L-Glutamate), C00490 (Itaconic acid), C06010 ((S)-2-Acetolactate)
	ath00562	Inositol phosphate metabolism	1	0.6347	C03659 ((-)-Bornesitol)
Biosynthesis of other secondary metabolites (31)	ath00940	Phenylpropanoid biosynthesis	3	0.1715	C00852 (Chlorogenic acid), C09315 (Umbelliferone), C10434 (Dattelic acid)
	ath00941	Flavonoid biosynthesis	12	0	C00389 (Quercetin), C00509 ((-)-Naringenin), C00774 (Phloretin), C00852 (Chlorogenic

					acid), C00974 (Aromadendrin), C01477 (Apigenin), C05631 (Eriodictyol), C05903 (Kaempferol), C09727 (Epigallocatechin), C09789 (Naringin), C10044 (Galangin), C10434 (Dattelic acid)
	ath00945	Stilbenoid, diarylheptanoid and gingerol biosynthesis	2	0.0963	C00852 (Chlorogenic acid), C10434 (Dattelic acid)
	ath00950	Isoquinoline alkaloid biosynthesis	1	0.9287	C08526 (GALANTHAMINE)
	ath00944	Flavone and flavonol biosynthesis	6	0.0006	C00389 (Quercetin), C01477 (Apigenin), C01750 (Quercitrin), C05625 (Rutin), C05903 (Kaempferol), C12249 (Astragalin)
	ath00261	Monobactam biosynthesis	1	0.5660	C00022 (Pyruvic acid)
	ath00960	Tropane, piperidine and pyridine alkaloid biosynthesis	1	0.7680	C00166 (Phenylpyruvic acid)
	ath00942	Anthocyanin biosynthesis	5	0.0120	C08604 (Chrysanthemin), C08725 (Pelargonin), C12139 (Petunidin 3-glucoside), C12140 (Oenin), C12141 (Peonidin 3-O-glucoside)
	ath00350	Tyrosine metabolism	1	0.8133	C00022 (Pyruvic acid)
	ath00260	Glycine, serine and threonine metabolism	2	0.2841	C00022 (Pyruvic acid), C00546 (APC)
	ath00400	Phenylalanine, tyrosine and tryptophan biosynthesis	2	0.1599	C00166 (Phenylpyruvic acid), C00296 (Quinic acid)
	ath00360	Phenylalanine metabolism	5	0.0081	C00022 (Pyruvic acid), C00166 (Phenylpyruvic acid), C02763 (Enol-phenylpyruvate), C05332 (Phenylethylamine), C14145 ((3S)-3-Hydroxyadipyl-CoA)
Amino acid metabolism (25)	ath00250	Alanine, aspartate and glutamate metabolism	3	0.0202	C00022 (Pyruvic acid), C00025 (L-Glutamate), C00158 (Citric acid)
	ath00270	Cysteine and methionine metabolism	1	0.7415	C00022 (Pyruvic acid)
	ath00280	Valine, leucine and isoleucine degradation	1	0.5842	C00356 ((3S)-3-hydroxy-3-methylglutaryl-CoA)
	ath00340	Histidine metabolism	1	0.6347	C00025 (L-Glutamate)
	ath00310	Lysine degradation	1	0.6576	C03273 (5-oxo-pentanoic acid)
	ath00330	Arginine and proline metabolism	3	0.2257	C00022 (Pyruvic acid), C00025 (L-Glutamate), C00148

					(L-Proline)
	ath00220	Arginine biosynthesis	1	0.3881	C00025 (L-Glutamate)
	ath00290	Valine, leucine and isoleucine biosynthesis	4	0.0012	C00022 (Pyruvic acid), C02504 (2-Isopropylmalic acid), C04272 ((R)-2,3-Dihydroxy-isovalerate), C06010 ((S)-2-Acetolactate)
	ath00904	Diterpenoid biosynthesis	2	0.7351	C11854 (Gibberellin A51-catabolite), C11867 (Gibberellin A7)
	ath00908	Zeatin biosynthesis	2	0.1979	C00029 (UDP-glucose), C00235 (DMPP)
	ath00900	Terpenoid backbone biosynthesis	3	0.0679	C00022 (Pyruvic acid), C00235 (DMPP), C00356 ((3S)-3-hydroxy-3-methylglutaryl-CoA)
	ath00906	Carotenoid biosynthesis	3	0.4333	C06082 ((S)-(+)-Abscisic acid), C08614 (Violaxanthin), C15981 (alpha-Cryptoxanthin)
Metabolism of terpenoids and polyketides (18)	ath00902	Monoterpenoid biosynthesis	2	0.3543	C01767 ((-)-Carvone), C11673 (Geniposidic acid)
	ath00903	Limonene and pinene degradation	4	0.0447	C01767 ((-)-Carvone), C11398 ((1R,4R)-Dihydrocarvone), C11401 ((1S,4R)-Iso-dihydrocarvone), C11412 ((1R,4S)-Iso-dihydrocarvone)
	ath00909	Sesquiterpenoid and triterpenoid biosynthesis	1	0.8465	C09627 (capsidiol)
	ath00901	Indole alkaloid biosynthesis	1	0.7779	C07204 (Vincristine)
	ath00072	Synthesis and degradation of ketone bodies	1	0.1200	C00356 ((3S)-3-hydroxy-3-methylglutaryl-CoA)
	ath00561	Glycerolipid metabolism	1	0.5565	C00029 (UDP-glucose)
	ath00062	Fatty acid elongation	1	0.5565	C05270 (Hexanoyl-CoA)
	ath00071	Fatty acid degradation	1	0.6576	C05270 (Hexanoyl-CoA)
Lipid metabolism (14)	ath00564	Glycerophospholipid metabolism	2	0.2998	C00307 (Citicoline), C04230 (PC(16:0/0:0))
	ath00100	Steroid biosynthesis	1	0.7119	C11455 (4-Hydroxyandrostenedione glucuronide)
	ath00590	Arachidonic acid metabolism	7	0.0009	C05951 (Leukotriene D4), C06462 (LTF4), C14732 (5-Oxo-ETE), C14748 (20-HETE), C14749 (19S-HETE), C14780 (11R-hydroxy-5E,8Z,12Z,14Z-eicosatetraenoic acid), C14807 (12-oxo-ETE)
Metabolism of cofactors and	ath00860	Porphyrin and, Chlorophyll metabolism	2	0.7954	C00025 (L-Glutamate), C02191 (Protoporphyrin IX)

vitamins (10)	ath00130	Ubiquinone and other terpenoid-quinone biosynthesis	1	0.7826	C00156 (4-Hydroxybenzoic acid)
	ath00730	Thiamine metabolism	1	0.4845	C00022 (Pyruvic acid)
	ath00760	Nicotinate and nicotinamide metabolism	2	0.3233	C00022 (Pyruvic acid), C01004 (Trigonelline)
	ath00790	Folate biosynthesis	1	0.7119	C00156 (4-Hydroxybenzoic acid)
	ath00770	Pantothenate and CoA biosynthesis	3	0.0243	C00022 (Pyruvic acid), C04272 ((R)-2,3-Dihydroxy-isovalerate), C06010 ((S)-2-Acetolactate)
Metabolism of other amino acids (4)	ath00440	Phosphonate and phosphinate metabolism	1	0.6790	C00022 (Pyruvic acid)
	ath00480	Glutathione metabolism	1	0.5565	C00025 (L-Glutamate)
	ath00430	Taurine and hypotaurine metabolism	2	0.0771	C00022 (Pyruvic acid), C00025 (L-Glutamate)
Membrane transport (3)	ath02010	ABC transporters	3	0.3119	C00025 (L-Glutamate), C00243 (Alpha-Lactose), C01630 (Xylobiose)
Energy metabolism (3)	ath00710	Carbon fixation in photosynthetic organisms	2	0.0834	C00022 (Pyruvic acid), C00085 (D-Fructose 6-phosphate)
	ath00910	Nitrogen metabolism	1	0.3333	C00025 (L-Glutamate)
Nucleotide metabolism (2)	ath00240	Pyrimidine metabolism	2	0.3999	C00029 (UDP-glucose), C00239 (dCMP)
Translation (2)	ath00970	Aminoacyl-tRNA biosynthesis	2	0.2998	C00025 (L-Glutamate), C00148 (L-Proline)
Signal transduction (1)	ath04075	Plant hormone signal transduction	1	0.1745	C06082 ((S)-(+)-Abscisic acid)

Table S21. KEGG analysis of DSMs in ES vs. LA.

Metabolic pathway	Pathway ID annotation	Pathway annotation	Number	*p* value	Matching metabolite IDs
Carbohydrate metabolism (40)	ath00010	Glycolysis/Gluconeogenesis	1	0.4801	C00022 (Pyruvic acid)
	ath00052	Galactose metabolism	4	0.0146	C00029 (UDP-glucose), C00243 (Alpha-Lactose), C03785 (D-Tagatose 1,6-bisphosphate), C05399 (Melibiitol)
	ath00630	Glyoxylate and dicarboxylate metabolism	4	0.0389	C00022 (Pyruvic acid), C00025 (L-Glutamate), C00058 (Calcium formate), C00158 (Citric acid)
	ath00620	Pyruvate metabolism	4	0.0036	C00022 (Pyruvic acid), C00058 (Calcium formate), C00546 (APC), C02504 (2-Isopropylmalic acid)
	ath00040	Pentose and glucuronate interconversions	3	0.1096	C00022 (Pyruvic acid), C00029 (UDP-glucose), C03033 (15-hydroxynorandrostene-3,17-dione glucuronide)
	ath00650	Butanoate metabolism	4	0.0106	C00022 (Pyruvic acid), C00025 (L-Glutamate), C00356 ((3S)-3-hydroxy-3-methylglutaryl-CoA), C06010 ((S)-2-Acetolactate)
	ath00520	Amino sugar and nucleotide sugar metabolism	2	0.6639	C00029 (UDP-glucose), C01019 (L-Fucose)
	ath00500	Starch and sucrose metabolism	2	0.1789	C00029 (UDP-glucose), C00721 (Dextrin)
	ath00051	Fructose and mannose metabolism	3	0.1010	C01019 (L-Fucose), C01355 (Levan), C01768 (Alginic acid)
	ath00030	Pentose phosphate pathway	2	0.1640	C00022 (Pyruvic acid), C00257 (Gluconic acid)
	ath00640	Propanoate metabolism	1	0.6377	C00546 (APC)
	ath00053	Ascorbate and aldarate metabolism	4	0.0181	C00022 (Pyruvic acid), C00029 (UDP-glucose), C01620 (Threonic acid), C01825 (L-Galactose)
	ath00660	C5-Branched dibasic acid metabolism	4	0.0050	C00022 (Pyruvic acid), C00025 (L-Glutamate), C00490 (Itaconic acid), C06010 ((S)-2-Acetolactate)
	ath00020	Citrate cycle (TCA cycle)	2	0.0637	C00022 (Pyruvic acid), C00158 (Citric acid)
Biosynthesis of other secondary metabolites (29)	ath00940	Phenylpropanoid biosynthesis	3	0.1670	C00852 (Chlorogenic acid), C09315 (Umbelliferone), C10434 (Dattelic acid)
	ath00941	Flavonoid biosynthesis	12	0	C00389 (Quercetin), C00509 ((-)-Naringenin), C00774 (Phloretin), C00852 (Chlorogenic acid), C00974 (Aromadendrin), C01477 (Apigenin), C05631 (Eriodictyol), C05903 (Kaempferol), C09727

					(Epigallocatechin), C09789 (Naringin), C10044 (Galangin), C10434 (Dattelic acid)
	ath00945	Stilbenoid, diarylheptanoid and gingerol biosynthesis	2	0.0942	C00852 (Chlorogenic acid), C10434 (Dattelic acid)
	ath00944	Flavone and flavonol biosynthesis	5	0.0038	C00389 (Quercetin), C01477 (Apigenin), C01750 (Quercitrin), C05903 (Kaempferol), C12249 (Astragalin)
	ath00960	Tropane, piperidine and pyridine alkaloid biosynthesis	1	0.7636	C00166 (Phenylpyruvic acid)
	ath00942	Anthocyanin biosynthesis	4	0.0472	C08604 (Chrysanthemin), C08725 (Pelargonin), C12139 (Petunidin 3-glucoside), C12141 (Peonidin 3-O-glucoside)
	ath00261	Monobactam biosynthesis	1	0.5612	C00022 (Pyruvic acid)
	ath00950	Isoquinoline alkaloid biosynthesis	1	0.9262	C08526 (GALANTHAMINE)
	ath00350	Tyrosine metabolism	1	0.8092	C00022 (Pyruvic acid)
	ath00260	Glycine, serine and threonine metabolism	2	0.2790	C00022 (Pyruvic acid), C00546 (APC)
	ath00400	Phenylalanine, tyrosine and tryptophan biosynthesis	1	0.5121	C00166 (Phenylpyruvic acid)
	ath00360	Phenylalanine metabolism	5	0.0076	C00022 (Pyruvic acid), C00166 (Phenylpyruvic acid), C02763 (Enol-phenylpyruvate), C12621 (m-Coumaric acid), C14145 ((3S)-3-Hydroxyadipyl-CoA)
Amino acid metabolism (25)	ath00250	Alanine, aspartate and glutamate metabolism	3	0.0195	C00022 (Pyruvic acid), C00025 (L-Glutamate), C00158 (Citric acid)
	ath00270	Cysteine and methionine metabolism	1	0.7369	C00022 (Pyruvic acid)
	ath00280	Valine, leucine and isoleucine degradation	1	0.5795	C00356 ((3S)-3-hydroxy-3-methylglutaryl-CoA)
	ath00340	Histidine metabolism	1	0.6299	C00025 (L-Glutamate)
	ath00310	Lysine degradation	1	0.6528	C03273 (5-oxo-pentanoic acid)
	ath00330	Arginine and proline metabolism	4	0.0777	C00022 (Pyruvic acid), C00025 (L-Glutamate), C00148 (L-Proline), C05938 (L-4-Hydroxyglutamate semialdehyde)
	ath00220	Arginine biosynthesis	1	0.3842	C00025 (L-Glutamate)

	ath00290	Valine, leucine and isoleucine biosynthesis	4	0.0011	C00022 (Pyruvic acid), C02504 (2-Isopropylmalic acid), C04272 ((R)-2,3-Dihydroxy-isovalerate), C06010 ((S)-2-Acetolactate)
	ath00904	Diterpenoid biosynthesis	2	0.7285	C11854 (Gibberellin A51-catabolite), C11867 (Gibberellin A7)
	ath00908	Zeatin biosynthesis	2	0.1940	C00029 (UDP-glucose), C00235 (DMPP)
	ath00900	Terpenoid backbone biosynthesis	3	0.0658	C00022 (Pyruvic acid), C00235 (DMPP), C00356 ((3S)-3-hydroxy-3-methylglutaryl-CoA)
Metabolism of terpenoids and polyketides (15)	ath00906	Carotenoid biosynthesis	3	0.4250	C06082 ((S)-(+)-Abscisic acid), C08614 (Violaxanthin), C09190 (Strigol)
	ath00902	Monoterpenoid biosynthesis	1	0.7134	C09893 ((+)-Pulegone)
	ath00903	Limonene and pinene degradation	2	0.3862	C11401 ((1S,4R)-Iso-dihydrocarvone), C11412 ((1R,4S)-Iso-dihydrocarvone)
	ath00901	Indole alkaloid biosynthesis	1	0.7735	C07204 (Vincristine)
	ath00909	Sesquiterpenoid and triterpenoid biosynthesis	1	0.8428	C09627 (capsidiol)
	ath00072	Synthesis and degradation of ketone bodies	1	0.1185	C00356 ((3S)-3-hydroxy-3-methylglutaryl-CoA)
	ath00561	Glycerolipid metabolism	1	0.5518	C00029 (UDP-glucose)
	ath00062	Fatty acid elongation	1	0.5518	C05270 (Hexanoyl-CoA)
	ath00071	Fatty acid degradation	1	0.6528	C05270 (Hexanoyl-CoA)
Lipid metabolism (15)	ath00564	Glycerophospholipid metabolism	2	0.2946	C00307 (Citicoline), C04230 (PC(16:0/0:0))
	ath00100	Steroid biosynthesis	1	0.7072	C02530 (22:2 Cholesterol ester)
	ath00590	Arachidonic acid metabolism	7	0.0008	C05951 (Leukotriene D4), C06462 (LTF4), C14732 (5-Oxo-ETE), C14748 (20-HETE), C14749 (19S-HETE), C14780 (11R-hydroxy-5E,8Z,12Z,14Z-eicosatetraenoic acid), C14807 (12-oxo-ETE)
	ath00600	Sphingolipid metabolism	1	0.4097	C06124 (Sphingosine-1-phosphate)
	ath00860	Porphyrin and Chlorophyll metabolism	2	0.7894	C00025 (L-Glutamate), C02191 (Protoporphyrin IX)
Metabolism of cofactors and vitamins (10)	ath00130	Ubiquinone and other terpenoid-quinone biosynthesis	1	0.7783	C00156 (4-Hydroxybenzoic acid)
	ath00790	Folate biosynthesis	1	0.7072	C00156 (4-Hydroxybenzoic acid)
	ath00770	Pantothenate and CoA biosynthesis	3	0.0235	C00022 (Pyruvic acid), C04272 ((R)-2,3-Dihydroxy-isovalerate), C06010 ((S)-2-Acetolactate)
	ath00760	Nicotinate and	2	0.3178	C00022 (Pyruvic acid), C01004

		nicotinamide metabolism			(Trigonelline)
	ath00730	Thiamine metabolism	1	0.4801	C00022 (Pyruvic acid)
Metabolism of other amino acids (5)	ath00440	Phosphonate and phosphinate metabolism	2	0.3023	C00022 (Pyruvic acid), C00058 (Calcium formate)
	ath00480	Glutathione metabolism	1	0.5518	C00025 (L-Glutamate)
	ath00430	Taurine and hypotaurine metabolism	2	0.0754	C00022 (Pyruvic acid), C00025 (L-Glutamate)
Membrane transport (3)	ath02010	ABC transporters	3	0.3049	C00025 (L-Glutamate), C00243 (Alpha-Lactose), C01630 (Xylobiose)
Energy metabolism (5)	ath00710	Carbon fixation in photosynthetic organisms	2	0.0815	C00022 (Pyruvic acid), C00447 (Sedoheptulose 1,7-bisphosphate)
	ath00910	Nitrogen metabolism	2	0.0581	C00025 (L-Glutamate), C00058 (Calcium formate)
Nucleotide metabolism (1)	ath00240	Pyrimidine metabolism	1	0.7479	C00029 (UDP-glucose)
Translation (2)	ath00970	Aminoacyl-tRNA biosynthesis	2	0.2946	C00025 (L-Glutamate), C00148 (L-Proline)
Signal transduction (1)	ath04075	Plant hormone signal transduction	1	0.1725	C06082 ((S)-(+)-Abscisic acid)

Table S22. DEGs in the phenylpropanoid biosynthesis pathway.

KEGG gene name	Unigene	LA [1]	W	ES	KEGG gene description
4CL	*TRINITY_DN11731_c0_g1_i2_2*	0	0	0.75	*4-coumarate--CoA ligase*
	TRINITY_DN20133_c0_g1_i5_2	321.53	286.28	39.13	
	TRINITY_DN22667_c0_g1_i1_1	0	0.03	0.90	
	TRINITY_DN22967_c0_g1_i1_3	11.08	24.04	5.02	
ALDH2	*TRINITY_DN23767_c0_g2_i1_3*	14.39	32.17	9.18	*coniferyl-aldehyde dehydrogenase*
	TRINITY_DN25009_c0_g1_i5_1	0.03	0.34	4.57	
BGL	*TRINITY_DN1477_c0_g1_i1_3*	0.95	3.71	2.53	*beta-glucosidase*
	TRINITY_DN21087_c0_g1_i10_1	0.70	0.16	3.91	
	TRINITY_DN21867_c0_g1_i11_3	9.41	14.58	6.82	
	TRINITY_DN22155_c0_g1_i2_3	6.77	5.78	3.21	
	TRINITY_DN23991_c0_g2_i1_3	5.31	9.27	3.94	
	TRINITY_DN24792_c0_g1_i2_2	8.86	13.20	5.63	
	TRINITY_DN26008_c0_g3_i4_1	0.27	0.61	7.57	
	TRINITY_DN26120_c0_g1_i7_1	35.26	33.13	15.55	
	TRINITY_DN26565_c2_g2_i1_3	18.05	28.54	15.51	
	TRINITY_DN27214_c0_g1_i24_3	0.57	0.57	4.70	
	TRINITY_DN28144_c0_g1_i22_2	0.53	0.15	2.25	
	TRINITY_DN28435_c2_g2_i4_2	0.55	0.29	1.26	
	TRINITY_DN28666_c0_g1_i1_2	4.52	2.26	8.72	
	TRINITY_DN28943_c0_g3_i1_3	18.19	19.40	7.58	
	TRINITY_DN30175_c0_g2_i2_2	3.56	2.95	8.39	
	TRINITY_DN30482_c0_g1_i2_2	32.45	15.35	13.63	
	TRINITY_DN3381_c0_g1_i2_2	0.06	0.10	0.57	
	TRINITY_DN36966_c0_g1_i1_1	0.05	0.06	0.42	
	TRINITY_DN9201_c0_g1_i2_2	0.08	0.09	0.47	
C3'H	*TRINITY_DN28619_c0_g1_i6_3*	92.52	85.43	49.16	*coumaroylquinate(coumaroylshikimate) 3'-monooxygenase*
CAD	*TRINITY_DN21891_c0_g1_i1_3*	2.29	1.48	17.68	*cinnamyl-alcohol dehydrogenase*
	TRINITY_DN22571_c0_g1_i2_1	13.10	5.34	11.48	
	TRINITY_DN27331_c0_g1_i17_1	31.38	69.01	29.54	
	TRINITY_DN27854_c0_g1_i7_3	35.12	120.04	34.70	
	TRINITY_DN28156_c1_g3_i1_2	1.06	0.10	0.05	
	TRINITY_DN29329_c0_g1_i20_2	83.69	158.81	72.55	
CCoAOMT	*TRINITY_DN31293_c0_g1_i1_1*	0.11	0.13	1.14	*caffeoyl-CoA O-methyltransferase*
	TRINITY_DN8262_c0_g1_i1_3	0.17	1.53	0.56	
	TRINITY_DN24176_c0_g1_i2_3	545.17	452.12	182.29	
	TRINITY_DN28677_c0_g1_i2_2	57.79	140.91	14.03	
CCR	*TRINITY_DN12638_c0_g1_i1_3*	0.17	0.52	1.40	*cinnamoyl-CoA reductase*
	TRINITY_DN19233_c0_g1_i1_3	0	0	1.94	
	TRINITY_DN22090_c0_g1_i2_3	1.75	23.54	1.09	

	TRINITY_DN26159_c0_g1_i2_2	14.45	31.30	14.60	
	TRINITY_DN13667_c0_g1_i1_2	0.82	0.47	3.55	
	TRINITY_DN14701_c0_g1_i1_3	0.19	0.50	1.10	*caffeic acid 3-O-methyltransferase*
COMT	*TRINITY_DN21303_c0_g1_i2_3*	2.80	2.09	5.11	
	TRINITY_DN27012_c0_g2_i1_3	1.07	1.43	2.78	
	TRINITY_DN27662_c0_g1_i3_3	22.23	117.93	12.41	
	TRINITY_DN17061_c0_g1_i2_1	277.17	243.02	14.53	
	TRINITY_DN21549_c0_g1_i2_1	5.91	5.60	1.25	
	TRINITY_DN22223_c0_g1_i1_3	2.96	1.76	0.35	
CYP73A	*TRINITY_DN22223_c0_g2_i1_3*	38.84	29.43	7.84	*trans-cinnamate 4-monooxygenase*
	TRINITY_DN23436_c0_g1_i3_2	117.96	84.27	18.39	
	TRINITY_DN24904_c0_g1_i2_3	0.10	0.68	0.70	
	TRINITY_DN24904_c0_g2_i1_3	0.07	0.43	1.43	
F5H	*TRINITY_DN25901_c0_g1_i1_1*	31.23	12.84	25.07	*ferulate-5-hydroxylas*
	TRINITY_DN10681_c0_g1_i1_2	1.06	0.93	2.24	
	TRINITY_DN12233_c0_g1_i1_3	1.15	0.49	1.57	
HCT	*TRINITY_DN19878_c0_g1_i2_1*	8.68	6.10	14.52	*shikimate O-hydroxycinnamoyl transferase*
	TRINITY_DN22850_c0_g2_i1_2	1.01	0.34	1.72	
	TRINITY_DN28047_c0_g1_i4_3	19.28	23.65	56.22	
	TRINITY_DN6140_c0_g1_i1_3	3.40	7.66	2.74	
	TRINITY_DN10748_c0_g1_i1_3	0.08	0.66	0.01	
katG	*TRINITY_DN11417_c0_g1_i1_1*	0.15	0.56	0.03	*catalase-peroxidase*
	TRINITY_DN24451_c0_g1_i1_1	0.07	0.43	0.01	
	TRINITY_DN17599_c0_g1_i1_1	6.75	7.29	17.44	
	TRINITY_DN19173_c0_g1_i2_1	172.53	160.15	19.39	
PAL	*TRINITY_DN26444_c0_g1_i2_1*	1.57	0.82	4.98	*phenylalanine ammonia-lyase*
	TRINITY_DN26969_c0_g1_i3_1	1.62	9.47	0.59	
	TRINITY_DN5067_c0_g1_i1_1	187.22	197.77	24.79	
	TRINITY_DN9612_c0_g1_i1_2	3.53	5.34	1.87	
	TRINITY_DN10910_c0_g1_i1_1	1.18	11.46	0.57	
	TRINITY_DN13922_c0_g1_i3_3	5.82	36.81	2.26	
	TRINITY_DN14199_c0_g1_i2_2	0.88	0.23	0.35	
	TRINITY_DN15434_c0_g1_i3_1	24.26	28.72	6.77	
	TRINITY_DN15888_c0_g1_i1_1	13.31	8.72	3.12	
	TRINITY_DN16192_c0_g1_i1_1	0.30	0.36	1.20	
	TRINITY_DN19013_c0_g2_i2_1	47.88	21.80	23.28	
POD	*TRINITY_DN19387_c0_g1_i2_3*	8.88	3.99	7.52	*peroxidase*
	TRINITY_DN19814_c0_g1_i1_2	0.89	0.57	0.34	
	TRINITY_DN19884_c0_g1_i2_1	2.91	1.62	4.39	
	TRINITY_DN21692_c0_g1_i12_1	25.16	14.59	5.00	
	TRINITY_DN21921_c0_g1_i4_2	2.14	2.26	6.37	
	TRINITY_DN22146_c0_g1_i1_2	1.34	1.75	5.15	
	TRINITY_DN22350_c0_g1_i1_2	0.75	0.14	0.61	
	TRINITY_DN22923_c0_g1_i2_3	5.24	9.82	4.59	
	TRINITY_DN22981_c0_g3_i1_1	16.78	5.33	0.84	

	TRINITY_DN23495_c0_g1_i1_3	2.46	3.30	6.97	
	TRINITY_DN24593_c0_g1_i1_3	2.99	18.21	2.79	
	TRINITY_DN24813_c0_g1_i4_2	4.60	1.34	2.04	
	TRINITY_DN24924_c0_g2_i1_3	0.95	1.20	23.75	
	TRINITY_DN24924_c0_g3_i3_3	4.47	19.18	10.45	
	TRINITY_DN25151_c0_g1_i3_3	1.71	0.47	3.68	
	TRINITY_DN25637_c0_g1_i6_2	13.02	49.95	48.84	
	TRINITY_DN25637_c0_g2_i2_2	0.13	0.02	0.86	
	TRINITY_DN26105_c0_g1_i4_3	88.37	59.11	13.24	
	TRINITY_DN26888_c0_g1_i2_1	2.39	18.02	0.86	
	TRINITY_DN26897_c0_g3_i1_1	25.82	42.19	13.37	
	TRINITY_DN26901_c0_g1_i1_2	12.21	5.97	11.24	
	TRINITY_DN27327_c0_g1_i21_3	189.30	349.75	77.59	
	TRINITY_DN28931_c0_g1_i5_2	105.24	132.23	27.45	
	TRINITY_DN3394_c0_g1_i1_1	1.74	3.50	1.65	
	TRINITY_DN3972_c0_g1_i2_1	4.10	2.04	1.93	
	TRINITY_DN6860_c0_g1_i2_1	9.34	1.79	9.54	
	TRINITY_DN22475_c0_g1_i5_2	41.64	45.44	9.13	
	TRINITY_DN22671_c0_g1_i4_3	100.01	191.63	8.87	
PRDX6	*TRINITY_DN22825_c0_g1_i6_1*	130.98	255.32	19.99	*peroxiredoxin 6,1-Cys peroxiredoxin*
	TRINITY_DN26558_c1_g1_i13_1	5.86	4.53	12.95	
	TRINITY_DN28810_c0_g1_i24_3	8.97	17.15	4.37	
	TRINITY_DN30589_c2_g1_i17_2	9.24	5.47	19.05	
UGT72E	*TRINITY_DN25533_c0_g1_i1_1*	0.71	2.01	0.63	*coniferyl-alcohol glucosyltransferase*

[1] The value of each gene expression level in the graph is the average of 3 replicates (n = 3).

Table S23. DEGs in the flavonoid biosynthesis pathway.

KEGG gene name	Unigene	LA [1]	W	ES	KEGG gene description
ANR	*TRINITY_DN19656_c0_g1_i7_3*	871.72	558.88	79.28	*anthocyanidin reductase*
	TRINITY_DN22180_c0_g1_i3_2	65.16	43.33	4.67	
	TRINITY_DN23909_c0_g1_i8_1	151.54	94.69	17.98	
C3'H	*TRINITY_DN28619_c0_g1_i6_3*	92.52	85.43	49.16	*coumaroylquinate(coumaroylshikimate) 3'-monooxygenase*
CCoAOMT	*TRINITY_DN24176_c0_g1_i2_3*	545.17	452.12	182.29	*caffeoyl-CoA O-methyltransferase*
	TRINITY_DN28677_c0_g1_i2_2	57.79	140.91	14.03	
CHI	*TRINITY_DN22891_c0_g1_i1_3*	22.35	10.65	5.96	*chalcone isomerase*
CHS	*TRINITY_DN26891_c0_g2_i2_3*	318.55	294.45	87.18	*chalcone synthase*
	TRINITY_DN27120_c0_g1_i2_3	141.40	380.76	29.07	
	TRINITY_DN27527_c1_g1_i12_1	1186.80	1383.67	254.63	
	TRINITY_DN28258_c0_g1_i5_2	511.56	651.06	141.89	
	TRINITY_DN28885_c0_g1_i27_3	1481.76	1296.61	383.42	
	TRINITY_DN30758_c0_g1_i20_2	525.21	600.46	148.99	
CYP73A, C4H	*TRINITY_DN17061_c0_g1_i2_1*	277.17	243.02	14.53	*trans-cinnamate 4-monooxygenase*
	TRINITY_DN21549_c0_g1_i2_1	5.91	5.60	1.25	
	TRINITY_DN22223_c0_g1_i1_3	2.96	1.76	0.35	
	TRINITY_DN22223_c0_g2_i1_3	38.84	29.43	7.84	
	TRINITY_DN23436_c0_g1_i3_2	117.96	84.27	18.39	
DFR	*TRINITY_DN24904_c0_g1_i2_3*	0.10	0.68	0.70	*bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase*
	TRINITY_DN24904_c0_g2_i1_3	0.07	0.43	1.43	
	TRINITY_DN13277_c0_g1_i1_3	1.97	1.05	2.80	
	TRINITY_DN23801_c0_g1_i2_3	305.48	233.10	55.95	
	TRINITY_DN25831_c0_g3_i1_1	3.22	2.37	11.26	
	TRINITY_DN25921_c0_g1_i5_2	381.08	293.11	66.57	
	TRINITY_DN26304_c0_g5_i4_3	0.33	3.47	2.17	
	TRINITY_DN26740_c0_g2_i2_1	0.32	0.44	2.80	
	TRINITY_DN29942_c0_g1_i12_2	83.92	32.82	218.44	
	TRINITY_DN29942_c0_g3_i4_2	1.80	0.83	4.82	
	TRINITY_DN9954_c0_g1_i1_2	1.12	0.34	0.42	
F3'5'H	*TRINITY_DN6995_c0_g1_i1_1*	2.69	17.05	0.58	*flavonoid 3',5'-hydroxylase*
F3H	*TRINITY_DN12332_c0_g1_i1_2*	0.47	0.23	18.11	*naringenin 3-dioxygenase*
	TRINITY_DN16859_c0_g1_i3_3	7.56	10.25	23.59	
	TRINITY_DN19610_c1_g1_i2_1	345.89	282.46	15.45	
	TRINITY_DN20671_c0_g1_i3_1	16.95	22.11	53.93	
F3'H	*TRINITY_DN23607_c0_g1_i6_3*	1076.26	1182.34	182.87	*flavonoid 3'-monooxygenase*
	TRINITY_DN16507_c0_g1_i2_3	12.04	14.12	0.71	
	TRINITY_DN20065_c0_g1_i4_2	313.67	301.96	25.02	

FLS	*TRINITY_DN22787_c0_g1_i1_3*	10.41	8.13	4.33	*flavonol synthase*
	TRINITY_DN22787_c0_g2_i1_3	0.23	2.25	0.64	
	TRINITY_DN15993_c0_g1_i2_1	1.77	2.70	8.77	
	TRINITY_DN20278_c0_g1_i4_3	30.18	11.86	8.51	
	TRINITY_DN20278_c0_g2_i2_3	12.83	31.23	1.90	
HCT	*TRINITY_DN10681_c0_g1_i1_2*	1.06	0.93	2.24	*shikimate O-hydroxycinnamoyltransferase*
	TRINITY_DN12233_c0_g1_i1_3	1.15	0.49	1.57	
	TRINITY_DN19878_c0_g1_i2_1	8.68	6.10	14.52	
	TRINITY_DN22850_c0_g2_i1_2	1.01	0.34	1.72	
	TRINITY_DN28047_c0_g1_i4_3	19.28	23.65	56.22	
LAR	*TRINITY_DN6140_c0_g1_i1_3*	3.40	7.66	2.74	*leucoanthocyanidin reductase*
	TRINITY_DN17978_c0_g1_i2_2	12.60	17.81	31.56	
	TRINITY_DN18073_c0_g1_i2_1	0.13	0.01	1.94	
	TRINITY_DN21566_c0_g1_i2_2	0.19	0.03	2.19	
	TRINITY_DN23847_c0_g1_i4_1	7.03	10.60	1.38	
	TRINITY_DN25041_c0_g2_i3_3	141.62	169.77	14.25	
	TRINITY_DN26822_c0_g1_i7_2	3.28	5.11	0.44	
LDOX	*TRINITY_DN27808_c0_g1_i2_3*	1534.17	885.86	121.42	*leucoanthocyanidin dioxygenase*

[1] The value of each gene expression level in the graph is the average of 3 replicates (n = 3).

Table S24. DEGs associated with plant hormone signal transduction.

Unigene	LA [1]	W	ES	KEGG gene	KEGG gene description
ABA					
TRINITY_DN21648_c0_g2_i2_3	18.15	29.75	11.10		
TRINITY_DN25973_c0_g1_i8_1	0.19	1.14	0.11	*ABF*	*ABA responsive element binding factor*
TRINITY_DN27789_c0_g1_i2_2	17.82	29.2	7.16		
TRINITY_DN6126_c0_g1_i1_3	39.02	46.28	15.02		
TRINITY_DN24587_c0_g1_i2_1	3.25	0.98	0.89	*PYL*	*abscisic acid receptor PYR/PYL family*
TRINITY_DN5207_c0_g1_i1_3	4.56	7.38	32.71		
TRINITY_DN13139_c0_g1_i1_3	3.27	12.73	2.83		
TRINITY_DN19641_c0_g1_i4_3	0.98	4.67	3.66		
TRINITY_DN22882_c0_g1_i1_1	0.27	2.40	0.62		
TRINITY_DN24041_c0_g1_i4_1	2.68	6.14	2.29		
TRINITY_DN25465_c0_g1_i2_1	7.80	13.43	3.04	*PP2C*	*protein phosphatase 2C*
TRINITY_DN25465_c0_g2_i2_1	5.72	22.18	5.97		
TRINITY_DN28271_c0_g2_i1_2	44.25	77.85	33.53		
TRINITY_DN29527_c0_g2_i3_2	1.59	0.87	0.83		
TRINITY_DN9119_c0_g1_i1_1	1.09	2.88	0.51		
*TRINITY_DN21966_c0_g1_i10_*	20.28	55.25	13.87		
TRINITY_DN23923_c0_g1_i3_2	4.47	3.52	15.68	*SNRK2*	*serine/threonine-protein kinase SRK2*
*TRINITY_DN23929_c0_g1_i11_*	10.49	9.77	3.34		
IAA					
TRINITY_DN25209_c0_g1_i1_1	26.73	63.52	18.09	*AUX1, LAX*	*auxin influx carrier (AUX1, LAX family)*
TRINITY_DN1868_c0_g1_i1_2	0.74	1.43	2.54	*GH3*	*auxin responsive GH3 gene family*
TRINITY_DN20686_c0_g1_i3_3	21.88	18.35	45.59		
TRINITY_DN21667_c0_g1_i4_2	15.46	11.52	28.32		
TRINITY_DN23574_c0_g2_i1_1	30.35	28.31	67.04	*IAA*	*auxin-responsive protein IAA*
TRINITY_DN23947_c0_g1_i2_2	5.93	16.36	6.94		
TRINITY_DN8115_c0_g1_i1_1	3.32	2.10	1.09		
TRINITY_DN9275_c0_g1_i1_2	2.48	4.91	1.75		
TRINITY_DN12525_c0_g1_i1_2	4.53	0.49	22.23		
TRINITY_DN13176_c0_g1_i1_3	12.46	13.31	6.57		
TRINITY_DN14475_c0_g1_i1_3	0.17	1.00	2.26		
TRINITY_DN15502_c0_g1_i1_3	12.11	17.52	41.65		
TRINITY_DN15939_c0_g1_i1_3	0.63	0.71	3.43		
TRINITY_DN16938_c0_g1_i2_2	0.82	0.09	0.43		
TRINITY_DN17567_c0_g1_i1_2	1.74	1.90	7.33	*SAUR*	*SAUR family protein*
TRINITY_DN19237_c0_g1_i1_3	0	0.38	0.76		
TRINITY_DN20488_c0_g1_i2_2	4.72	4.20	16.2		
TRINITY_DN20850_c0_g1_i1_2	1.09	0.30	6.08		
TRINITY_DN20926_c0_g1_i1_3	1.67	3.90	11.30		
TRINITY_DN22278_c0_g1_i1_3	8.64	12.11	20.15		
TRINITY_DN25684_c0_g1_i2_3	1.83	4.46	2.23		

TRINITY_DN32211_c0_g1_i1_3	0	0.05	0.76		
TRINITY_DN38677_c0_g1_i1_2	0.12	0	0.48		
CTK					
TRINITY_DN23913_c1_g1_i1_1	2.00	1.15	5.14	*AHK2_3_4*	*Arabidopsis histidine kinase 2/3/4 (cytokinin receptor)*
TRINITY_DN28113_c0_g1_i1_2	2.75	1.68	11.69		
TRINITY_DN22881_c0_g1_i2_3	21.91	10.94	24.05	*AHP*	*histidine-containing phosphotransfer protein*
TRINITY_DN25187_c0_g1_i3_1	12.85	6.18	19.82		
TRINITY_DN19356_c0_g2_i4_1	0.14	1.58	0.46		
TRINITY_DN19880_c0_g1_i4_2	9.24	3.30	6.67		
TRINITY_DN23894_c0_g1_i1_2	1.45	3.00	1.73	*ARR-A*	*two-component response regulator ARR-A family*
TRINITY_DN26962_c0_g1_i6_2	8.59	2.77	4.81		
TRINITY_DN32526_c0_g1_i1_2	0.37	1.6	0.31		
TRINITY_DN34205_c0_g1_i1_3	0.68	1.24	3.30		
TRINITY_DN22061_c0_g1_i3_1	4.37	13.41	1.85		
TRINITY_DN22299_c0_g1_i2_3	4.37	6.45	2.78		
TRINITY_DN23806_c0_g1_i2_3	1.32	2.70	3.32	*ARR-B*	*two-component response regulator ARR-B family*
TRINITY_DN23806_c0_g2_i1_3	5.77	8.03	14.00		
TRINITY_DN28063_c0_g1_i6_2	14.95	10.96	28.75		
TRINITY_DN29376_c0_g1_i3_2	13.45	18.56	8.23		
GA					
TRINITY_DN26493_c1_g1_i6_3	1.89	1.41	3.57	*DELLA*	*DELLA protein*
TRINITY_DN16332_c0_g1_i1_1	0.68	0.96	0.32		
TRINITY_DN18047_c0_g1_i1_3	5.75	4.15	10.25		
TRINITY_DN19146_c0_g1_i1_2	19.26	8.71	50.61	*GID2*	*F-box protein GID2*
TRINITY_DN19209_c0_g1_i1_3	0.99	16.03	1.00		
TRINITY_DN34160_c0_g1_i1_2	0.17	0.11	0.88		
TRINITY_DN22857_c0_g1_i2_2	4.34	3.52	8.01		
TRINITY_DN23487_c0_g2_i2_2	2.58	1.69	6.51	*GID1*	*gibberellin receptor GID1*
TRINITY_DN31445_c0_g1_i1_2	1.02	0.19	0.10		
TRINITY_DN28833_c0_g1_i6_3	3.82	3.68	14.16	*PIF3*	*phytochrome-interacting factor 3*
Ethylene					
TRINITY_DN594_c0_g1_i1_1	13.96	20.85	8.59	*EBF1_2*	*EIN3-binding F-box protein*
TRINITY_DN18641_c0_g1_i1_1	7.76	5.57	3.74		
TRINITY_DN20534_c0_g1_i2_3	12.91	11.89	37.35	*ETR*	*ethylene receptor*
TRINITY_DN22076_c0_g1_i6_1	7.48	6.04	15.31		
TRINITY_DN22571_c0_g1_i5_3	4.46	4.76	2.33		
TRINITY_DN8750_c0_g1_i1_3	2.14	10.94	0.26	*ERF1*	*ethylene-responsive transcription factor 1*
TRINITY_DN28076_c0_g1_i5_3	21.88	20.6	11.24	*CTR1*	*serine/threonine-protein kinase CTR1*
TRINITY_DN18259_c0_g1_i1_3	64.98	112.35	43.77	*MPK6*	*mitogen-activated protein kinase 6*
BR					
TRINITY_DN17484_c0_g1_i1_1	30.83	34.02	17.44	*BSK*	*BR-signaling kinase*
TRINITY_DN22711_c0_g3_i1_1	1.27	1.57	0.29		
TRINITY_DN9292_c0_g1_i1_2	0.86	0.12	0.74	*CYCD3*	*cyclin D3, plant*

TRINITY_DN26772_c0_g1_i7_1	3.02	84.62	5.33		
TRINITY_DN26772_c0_g2_i4_1	12.53	89.89	88.69		
TRINITY_DN26772_c0_g3_i1_1	1.93	3.33	6.64		
*TRINITY_DN26835_c0_g1_i20_*	2.84	17.63	4.64	*TCH4*	*xyloglucan:xyloglucosyl transferase TCH4*
TRINITY_DN27591_c0_g1_i1_1	1.70	2.39	3.64		
TRINITY_DN29023_c1_g1_i4_2	2.18	9.83	12.04		
TRINITY_DN30853_c1_g1_i5_2	16.11	100.83	82.28		
TRINITY_DN10250_c0_g1_i1_2	0.57	0.04	1.98	*BRI1*	*protein brassinosteroid insensitive*
SA					
TRINITY_DN19725_c1_g1_i2_3	1.43	0.42	107.11	*PR1*	*pathogenesis-related protein 1*
TRINITY_DN20718_c0_g1_i1_1	1.56	0.90	5.08		
TRINITY_DN25438_c0_g2_i1_1	0.96	0.95	2.46	*TGA*	*transcription factor TGA*
TRINITY_DN27671_c0_g1_i7_2	0.99	0.79	2.15		
TRINITY_DN21498_c0_g1_i1_3	20.32	13.77	8.69	*NPR1*	*regulatory protein NPR1*
TRINITY_DN28300_c1_g3_i1_2	1.32	1.26	0.59		
JA					
TRINITY_DN20650_c0_g1_i3_1	0.41	2.09	0.45		
TRINITY_DN21802_c0_g1_i6_3	2.27	23.49	2.68	*JAZ*	*jasmonate ZIM domain-containing protein*
TRINITY_DN27009_c0_g2_i6_2	0.19	1.00	0.96		
TRINITY_DN14725_c0_g1_i3_1	1.74	6.16	2.59	*JAR1*	*jasmonic acid-amino synthetase*
TRINITY_DN1816_c0_g1_i1_1	7.43	16.81	9.72	*MYC2*	*transcription factor MYC2*
TRINITY_DN23951_c0_g1_i3_1	8.55	18.88	7.18		
TRINITY_DN15954_c0_g1_i2_1	41.38	25.56	81.59		
TRINITY_DN17994_c0_g1_i1_2	36.00	41.78	20.16	*COI-1*	*coronatine-insensitive protein 1*
TRINITY_DN23266_c0_g1_i4_1	0.97	1.16	2.76		

[1] The value of each gene expression level in the graph is the average of 3 replicates (n = 3).

Table S25. DEGs involved in starch and sucrose metabolism.

KEGG gene name	Unigene	LA [1]	W	ES	KEGG description
glgB	*TRINITY_DN26454_c0_g1_i3_2*	157.93	175.03	87.06	*1,4-alpha-glucan branching enzyme*
malQ	*TRINITY_DN25897_c0_g1_i3_2*	22.67	18.90	9.69	*4-alpha-glucanotransferase*
	TRINITY_DN27128_c0_g1_i1_1	0.68	0.95	2.23	
treA	*TRINITY_DN19898_c0_g1_i1_2*	4.60	6.27	11.19	*alpha, alpha-trehalase*
GAUT	*TRINITY_DN19145_c0_g3_i1_1*	13.29	14.01	4.84	*alpha-1,4-galacturonosyltransferase*
	TRINITY_DN20790_c0_g1_i1_2	1.67	2.66	0.71	
	TRINITY_DN22642_c0_g1_i1_2	6.32	7.59	4.07	
α-Amy	*TRINITY_DN26754_c0_g1_i15_1*	1.67	9.12	3.18	*alpha-amylase*
	TRINITY_DN26754_c0_g2_i1_1	8.24	23.49	16.30	
	TRINITY_DN29127_c0_g1_i10_2	67.75	146.77	23.22	
malZ	*TRINITY_DN15228_c0_g1_i1_2*	0.70	1.33	0.47	*alpha-glucosidase*
	TRINITY_DN27849_c0_g2_i2_3	6.60	13.76	9.10	
	TRINITY_DN5213_c0_g1_i1_3	0.58	0.49	2.01	
β-Amy	*TRINITY_DN13292_c0_g1_i1_1*	6.18	2.96	2.66	*beta-amylase*
	TRINITY_DN14860_c0_g1_i2_1	7.78	11.59	4.95	
	TRINITY_DN18975_c0_g1_i1_3	138.35	189.09	31.61	
	TRINITY_DN21167_c0_g1_i4_1	1.81	2.54	1.29	
	TRINITY_DN26201_c9_g1_i5_1	67.10	122.83	155.54	
sacA	*TRINITY_DN16251_c0_g1_i1_1*	0.86	0.53	0.04	*beta-fructofuranosidase*
	TRINITY_DN21257_c0_g1_i1_3	0.09	1.17	0.40	
	TRINITY_DN21257_c0_g2_i1_3	0.45	3.12	0.38	
	TRINITY_DN21257_c0_g3_i1_3	0.84	0.35	0.91	
BGL	*TRINITY_DN26041_c0_g1_i5_2*	0.91	0.45	1.08	*beta-glucosidase*
	TRINITY_DN1477_c0_g1_i1_3	0.95	3.71	2.53	
	TRINITY_DN21087_c0_g1_i10_1	0.70	0.16	3.91	
	TRINITY_DN21867_c0_g1_i11_3	9.41	14.58	6.82	
	TRINITY_DN22155_c0_g1_i2_3	6.77	5.78	3.21	
	TRINITY_DN23991_c0_g2_i1_3	5.31	9.27	3.94	
	TRINITY_DN24792_c0_g1_i2_2	8.86	13.20	5.63	
	TRINITY_DN26008_c0_g3_i4_1	0.27	0.61	7.57	
	TRINITY_DN26120_c0_g1_i7_1	35.26	33.13	15.55	
	TRINITY_DN26565_c2_g2_i1_3	18.05	28.54	15.51	
	TRINITY_DN27214_c0_g1_i24_3	0.57	0.57	4.70	
	TRINITY_DN28144_c0_g1_i22_2	0.53	0.15	2.25	
	TRINITY_DN28435_c2_g2_i4_2	0.55	0.29	1.26	
	TRINITY_DN28666_c0_g1_i1_2	4.52	2.26	8.72	
	TRINITY_DN28943_c0_g3_i1_3	18.19	19.40	7.58	
	TRINITY_DN30175_c0_g2_i2_2	3.56	2.95	8.39	
	TRINITY_DN30482_c0_g1_i2_2	32.45	15.35	13.63	
	TRINITY_DN3381_c0_g1_i2_2	0.06	0.10	0.57	

	TRINITY_DN36966_c0_g1_i1_1	0.05	0.06	0.42	
	TRINITY_DN9201_c0_g1_i2_2	0.08	0.09	0.47	
scrK	*TRINITY_DN22871_c0_g1_i3_1*	74.31	78.07	41.92	*fructokinase*
	TRINITY_DN12529_c0_g1_i1_1	0.00	0.16	0.75	
EGLC	*TRINITY_DN21584_c0_g1_i2_1*	0.17	0.76	0.11	*glucan endo-1,3-beta-D-glucosidase*
	TRINITY_DN24005_c0_g1_i1_2	0.00	0.27	0.85	
	TRINITY_DN24084_c0_g1_i1_1	0.26	0.91	0.07	
GN1_2_3	*TRINITY_DN20432_c0_g1_i1_2*	5.19	1.94	21.33	*glucan endo-1,3-beta-glucosidase 1/2/3*
	TRINITY_DN26827_c0_g1_i3_2	13.20	7.83	22.14	
	TRINITY_DN5976_c0_g1_i1_2	2.41	1.10	2.17	
	TRINITY_DN26036_c0_g2_i7_1	64.96	127.25	168.42	
glgC	*TRINITY_DN26036_c0_g3_i2_1*	1.08	2.27	2.16	*glucose-1-phosphate adenylyltransferase*
	TRINITY_DN26434_c0_g6_i1_3	6.28	3.03	10.67	
	TRINITY_DN29489_c0_g1_i18_2	70.71	137.65	186.21	
GPI	*TRINITY_DN23478_c0_g1_i1_1*	0.16	0.29	0.00	*glucose-6-phosphate*
glgP	*TRINITY_DN28324_c0_g1_i2_3*	3.39	1.87	6.34	*glycogen phosphorylase*
	TRINITY_DN11050_c0_g2_i1_3	0.00	0.13	0.47	
	TRINITY_DN16851_c0_g1_i1_1	0.20	0.50	0.01	
HXK	*TRINITY_DN19008_c0_g1_i5_3*	9.58	11.21	4.77	*hexokinase*
	TRINITY_DN23436_c0_g1_i4_1	2.39	4.92	1.00	
	TRINITY_DN617_c0_g1_i1_2	0.00	0.09	0.24	
IMA	*TRINITY_DN36059_c0_g1_i1_1*	0.28	0.26	0.00	*oligo-1,6-glucosidase*
	TRINITY_DN11814_c0_g1_i2_3	3.14	1.71	1.57	
	TRINITY_DN12212_c0_g1_i1_2	1.53	0.52	2.57	
	TRINITY_DN14764_c0_g1_i1_1	46.97	113.38	102.48	
	TRINITY_DN15041_c0_g1_i1_2	0.92	0.31	1.29	
	TRINITY_DN15742_c0_g1_i1_1	0.46	0.58	0.23	
	TRINITY_DN18054_c0_g1_i1_2	0.41	0.02	1.71	
	TRINITY_DN23050_c0_g1_i2_3	2.49	1.45	12.61	
PE	*TRINITY_DN25377_c0_g2_i1_1*	1.26	3.04	3.24	*pectinesterase*
	TRINITY_DN27370_c0_g4_i2_2	0.91	0.16	0.43	
	TRINITY_DN27371_c0_g1_i2_3	1.81	1.16	3.09	
	TRINITY_DN33417_c0_g1_i1_3	0.33	1.34	0.10	
	TRINITY_DN37568_c0_g1_i1_2	0.86	0.05	0.12	
	TRINITY_DN37785_c0_g1_i1_2	0.70	0.00	0.11	
	TRINITY_DN4707_c0_g1_i2_3	0.25	0.19	0.78	
	TRINITY_DN6215_c0_g1_i1_3	1.17	0.22	2.33	
pgm	*TRINITY_DN21107_c0_g1_i3_1*	4.94	3.51	7.75	*phosphoglucomutase*
glgA	*TRINITY_DN21420_c0_g1_i1_3*	24.25	32.01	55.95	*starch synthase*
	TRINITY_DN22887_c0_g1_i3_2	72.63	101.33	34.57	
SUS	*TRINITY_DN24636_c0_g1_i1_1*	2.28	1.19	0.36	*sucrose synthase*
	TRINITY_DN24636_c0_g2_i1_1	0.00	0.11	0.67	
	TRINITY_DN414_c0_g1_i2_3	9.39	19.03	6.00	
SPS	*TRINITY_DN23236_c0_g1_i16_1*	13.22	20.94	7.03	*sucrose-phosphate synthase*
	TRINITY_DN25408_c0_g1_i24_3	125.92	56.97	151.03	

	TRINITY_DN26473_c0_g1_i9_3	60.64	92.65	20.63	
	TRINITY_DN26764_c0_g1_i12_2	53.63	26.08	71.83	
otsB	*TRINITY_DN22718_c0_g1_i6_2*	2.66	3.68	1.88	*trehalose 6-phosphate phosphatase*
TPS	*TRINITY_DN5625_c0_g1_i1_3*	11.86	10.48	4.92	*trehalose 6-phosphate synthase/phosphatase*
	TRINITY_DN7172_c0_g1_i2_1	1.64	3.70	2.40	
UGDH	*TRINITY_DN15664_c0_g1_i5_1*	175.65	223.72	107.32	*UDPglucose 6-dehydrogenase*
	TRINITY_DN30477_c0_g1_i1_1	2.21	0.26	2.42	
GAE	*TRINITY_DN25667_c0_g1_i1_3*	0.36	1.46	11.47	*UDP-glucuronate 4-epimerase*
	TRINITY_DN8064_c0_g1_i2_1	27.31	37.74	16.51	
UGD	*TRINITY_DN21668_c0_g1_i2_2*	139.00	178.04	71.83	*UDP-glucuronate decarboxylase*
	TRINITY_DN22754_c0_g1_i4_3	9.24	17.18	7.30	
XYL4	*TRINITY_DN15185_c0_g1_i1_1*	13.29	5.07	36.48	*xylan 1,4-beta-xylosidase*
	TRINITY_DN18625_c0_g1_i4_2	5.81	2.07	14.65	
	TRINITY_DN30301_c0_g3_i1_2	0.47	0.24	1.49	
	TRINITY_DN35376_c0_g1_i1_2	2.53	0.46	0.25	

[1] The value of each gene expression level in the graph is the average of 3 replicates (n = 3).

Table S26. DSMs associated with starch and sucrose metabolism.

Metabolites	LA [1]	W	ES	Pathway
D-Fructose 6-phosphate	1773.69	1658.06	2192.82	sucrose metabolism
Dextrin	1764.09	2228.20	3009.27	starch metabolism
UDP-glucose	1155.87	1694.92	2206.61	sucrose metabolism

[1] The value of metabolite content in the graph is the average of 6 replicates (n = 6).

Table S27. DEGs involved in photosynthesis.

KEGG gene name	Unigene	LA [1]	W	ES	KEGG description
Photosystem II					
psbA	*TRINITY_DN20516_c1_g1_i1_3*	0.83	0.81	1.90	*photosystem II protein D1*
psbD	*TRINITY_DN4837_c0_g1_i1_2*	0.65	0.31	1.36	*photosystem II D2 protein*
psbO	*TRINITY_DN25397_c0_g1_i2_2*	1234.42	546.60	1781.48	*oxygen-evolving enhancer*
psbP	*TRINITY_DN19883_c0_g1_i2_2*	1659.43	452.05	1735.14	*oxygen-evolving enhancer protein 2*
	TRINITY_DN21116_c0_g1_i3_3	91.38	43.30	106.42	
	TRINITY_DN22268_c0_g1_i3_1	52.79	22.27	37.92	
	TRINITY_DN26005_c0_g1_i8_2	7.55	2.06	7.68	
	TRINITY_DN28070_c0_g3_i2_3	1.55	0.49	5.76	
psbQ	*TRINITY_DN26435_c0_g1_i4_2*	537.04	220.04	861.84	*oxygen-evolving enhancer protein 3*
	TRINITY_DN26435_c0_g2_i1_2	7.03	2.43	22.96	
psbR	*TRINITY_DN19084_c0_g1_i3_3*	2491.33	1154.10	2975.99	*photosystem II 10k Da*
psbS	*TRINITY_DN25984_c0_g2_i1_1*	10.26	14.02	23.23	*photosystem II 22k Da*
psbW	*TRINITY_DN25823_c0_g1_i1_2*	586.05	236.01	806.35	*photosystem II PsbW protein*
	TRINITY_DN27673_c0_g1_i2_2	986.30	423.82	919.86	
psbY	*TRINITY_DN28002_c0_g1_i5_3*	400.18	148.66	452.13	*photosystem II PsbY protein*
psb27	*TRINITY_DN15383_c0_g1_i2_3*	38.24	3.45	96.58	*photosystem II Psb27 protein*
psb28	*TRINITY_DN29240_c0_g1_i3_2*	87.08	40.62	86.92	*photosystem II 13k Da*
Photosystem I					
psaB	*TRINITY_DN4772_c0_g1_i1_3*	0.93	0.46	2.00	*photosystem I P700 chlorophyll a apoprotein A2*
psaD	*TRINITY_DN12258_c0_g1_i1_2*	490.54	153.10	602.68	*photosystem I subunit II*
psaE	*TRINITY_DN22351_c0_g1_i3_3*	1014.93	361.90	1280.77	*photosystem I subunit IV*
psaF	*TRINITY_DN13470_c0_g1_i1_3*	703.66	224.97	1066.56	*photosystem I subunit III*
psaG	*TRINITY_DN19272_c0_g1_i1_2*	685.34	168.47	942.87	*photosystem I subunit V*
psaH	*TRINITY_DN11306_c0_g1_i2_1*	1205.43	411.81	1658.90	*photosystem I subunit VI*
	TRINITY_DN14269_c0_g1_i3_2	52.06	14.91	69.43	
psaK	*TRINITY_DN12984_c0_g1_i2_2*	419.08	77.00	664.04	*photosystem I subunit X*
	TRINITY_DN7384_c0_g1_i2_3	42.77	8.02	75.74	
psaL	*TRINITY_DN13105_c0_g1_i1_3*	6.44	2.11	20.41	*photosystem I subunit XI*
	TRINITY_DN37220_c0_g1_i1_1	1715.24	660.58	1756.34	
psaN	*TRINITY_DN18416_c0_g1_i2_1*	624.01	140.80	1086.85	*photosystem I subunit PsaN*
	TRINITY_DN22575_c0_g1_i2_2	2.25	0.84	6.84	
psaO	*TRINITY_DN13446_c0_g1_i5_3*	5.29	0.10	13.76	*photosystem I subunit PsaO*
	TRINITY_DN31863_c0_g1_i1_1	236.42	21.22	571.38	
Cytochrome b6/f complex					
petC	*TRINITY_DN18323_c0_g1_i7_1*	389.75	182.45	377.11	*cytochrome b6-f complex iron-sulfur subunit*

Photosynthethic electron transport					
petE	*TRINITY_DN24938_c0_g3_i2_2*	590.68	197.31	1515.57	*plastocyanin*
	TRINITY_DN22064_c0_g1_i2_2	232.46	113.02	269.83	
petF	*TRINITY_DN23350_c0_g1_i1_3*	26.47	13.21	61.12	*ferredoxin*
	TRINITY_DN24788_c0_g1_i2_2	1582.57	671.54	1845.08	
petH	*TRINITY_DN25724_c0_g1_i4_2*	597.28	196.37	598.53	*ferredoxin-NADP reductase*
petJ	*TRINITY_DN24467_c0_g1_i4_2*	1.26	0.78	2.52	*cytochrome c6*
F-type ATPase					
atpD	*TRINITY_DN9498_c0_g1_i1_2*	1.77	1.76	4.87	*F-type H^+ transporting ATPase subunit beta*
atpF	*TRINITY_DN19142_c0_g1_i1_3*	1142.98	437.73	849.07	*F-type H^+ transporting ATPase subunit b*
atpG	*TRINITY_DN18869_c0_g1_i1_1*	421.65	191.72	366.90	*F-type H^+ transporting ATPase subunit gamma*
atpH	*TRINITY_DN24562_c0_g2_i1_1*	351.15	147.91	278.61	*F-type H^+ transporting ATPase subunit delta*

[1] The value of each gene expression level in the graph is the average of 3 replicates (n = 3).

Table S28. DEGs in photosynthesis-antenna proteins.

KEGG gene name	Unigene	LA [1]	W	ES	KEGG description
LHCA1	*TRINITY_DN18322_c0_g2_i1_3*	640.70	157.41	875.07	*light-harvesting complex I chlorophyll a/b binding*
LHCA2	*TRINITY_DN20003_c0_g1_i3_3*	514.78	113.18	600.99	*light-harvesting complex I chlorophyll a/b binding*
LHCA3	*TRINITY_DN20055_c0_g1_i1_3*	329.30	81.85	470.88	*light-harvesting complex I chlorophyll a/b binding*
LHCA4	*TRINITY_DN24738_c0_g1_i1_3*	1.26	0.17	8.85	*light-harvesting complex I chlorophyll a/b binding*
LHCA4	*TRINITY_DN24738_c0_g3_i1_3*	20.76	4.04	272.36	*light-harvesting complex I chlorophyll a/b binding*
LHCA4	*TRINITY_DN25025_c0_g1_i1_2*	359.45	50.96	672.28	*light-harvesting complex I chlorophyll a/b binding*
LHCA5	*TRINITY_DN15845_c0_g1_i1_3*	112.22	61.80	42.09	*light-harvesting complex I chlorophyll a/b binding*
LHCB1	*TRINITY_DN23090_c0_g1_i1_2*	2498.74	1041.83	1485.08	*light-harvesting complex II chlorophyll a/b binding*
LHCB2	*TRINITY_DN15697_c0_g1_i1_2*	199.93	17.03	323.02	*light-harvesting complex II chlorophyll a/b binding*
LHCB2	*TRINITY_DN8681_c0_g1_i1_3*	0	0.09	0.52	*light-harvesting complex II chlorophyll a/b binding*
LHCB3	*TRINITY_DN20384_c0_g1_i3_2*	57.33	5.75	337.11	*light-harvesting complex II chlorophyll a/b binding*
LHCB4	*TRINITY_DN17543_c0_g1_i3_2*	1.00	0.30	3.51	*light-harvesting complex II chlorophyll a/b binding*
LHCB4	*TRINITY_DN24693_c0_g1_i2_3*	644.76	237.25	896.15	*light-harvesting complex II chlorophyll a/b binding*
LHCB4	*TRINITY_DN30062_c0_g1_i1_1*	181.38	28.11	286.21	*light-harvesting complex II chlorophyll a/b binding*
LHCB5	*TRINITY_DN19939_c0_g1_i3_1*	725.56	230.96	702.98	*light-harvesting complex II chlorophyll a/b binding*
LHCB5	*TRINITY_DN22752_c2_g1_i4_3*	258.11	81.41	487.01	*light-harvesting complex II chlorophyll a/b binding*
LHCB5	*TRINITY_DN24106_c1_g1_i1_2*	356.44	102.51	420.25	*light-harvesting complex II chlorophyll a/b binding*
LHCB6	*TRINITY_DN23494_c0_g1_i2_2*	124.06	28.85	330.74	*light-harvesting complex II chlorophyll a/b binding*

[1] The value of each gene expression level in the graph is the average of 3 replicates (n = 3).

Table S29. DEGs involved in fatty acid biosynthesis.

Unigene	LA [1]	W	ES	KEGG gene name	KEGG description
TRINITY_DN24918_c0_g1_i11_1	107.517	89.382	18.456	*ACACA*	*acetyl-CoA carboxylase / biotin carboxylase 1*
TRINITY_DN24918_c0_g2_i1_1	0.956	1.020	0.033		
TRINITY_DN25486_c0_g1_i4_1	2.299	2.445	6.665	*accB, bccP*	*acetyl-CoA carboxylase biotin carboxyl carrier protein*
TRINITY_DN25677_c0_g1_i2_3	1.805	2.108	3.876		
TRINITY_DN24308_c0_g2_i1_1	0.000	0.027	0.889	*ACSF3*	*malonyl-CoA/methyl malonyl-CoA synthetase*
TRINITY_DN13607_c0_g1_i1_2	0.116	0.044	0.903	*ACSL, fadD*	*long-chain acyl-CoA synthetase*
TRINITY_DN13607_c0_g2_i1_2	0.446	0.055	1.831		
TRINITY_DN17545_c0_g1_i1_3	9.068	9.730	26.123		
TRINITY_DN19161_c0_g1_i1_2	2.098	0.967	1.996		
TRINITY_DN23421_c0_g2_i1_1	0.084	0.095	0.823		
TRINITY_DN27538_c0_g2_i1_3	0	3.904	2.535		
TRINITY_DN564_c0_g1_i1_3	0.262	0.000	0.864		
TRINITY_DN16386_c0_g1_i1_3	2.464	2.708	0.606	*FAB2, SSI2, desA1*	*acyl-[acyl-carrier-protein] desaturase*
TRINITY_DN14165_c0_g1_i1_1	4.636	5.209	19.255	*fabF*	*3-oxoacyl-[acyl-carrier-protein] synthase II*
TRINITY_DN15997_c0_g1_i1_1	9.974	25.460	8.915	*fabG*	*3-oxoacyl-[acyl-carrier protein] reductase*
TRINITY_DN19085_c0_g1_i1_2	3.311	1.874	1.472		
TRINITY_DN21931_c0_g1_i1_1	8.783	17.661	14.037		
TRINITY_DN24788_c0_g1_i6_1	20.560	25.332	10.819	*FATA*	*fatty acyl-ACP thioesterase A*
TRINITY_DN16420_c0_g1_i5_1	32.716	23.146	53.184	*FATB*	*fatty acyl-ACP thioesterase B*
TRINITY_DN26022_c0_g1_i4_3	5.373	4.079	92.211		
TRINITY_DN26022_c0_g2_i1_3	3.248	2.585	5.931		
TRINITY_DN27224_c3_g3_i1_3	1.725	1.652	4.490		
TRINITY_DN27267_c0_g1_i4_2	0.910	1.398	16.706		
TRINITY_DN27267_c0_g3_i1_2	2.141	0.445	0.650		
TRINITY_DN7647_c0_g1_i1_3	0.488	2.810	0.154		

[1] The value of each gene expression level in the graph is the average of 3 replicates (n = 3).

Table S30. DEGs involved in the biosynthesis of unsaturated fatty acids.

Unigene	LA [1]	W	ES	KEGG gene name	Description
TRINITY_DN16386_c0_g1_i1_3	2.464	2.708	0.606	*FAB2, SSI2, desA1*	*acyl-[acyl-carrier-protein] desaturase*
TRINITY_DN25815_c0_g1_i3_1	80.911	191.235	80.667	*FAD2*	*omega-6 fatty acid desaturase/acyl-lipid omega-6 desaturase (Delta-12 desaturase)*
TRINITY_DN27187_c0_g1_i1_2	0.005	0.549	1.757	*SCD, desC*	*stearoyl-CoA desaturase (Delta-9 desaturase)*
TRINITY_DN27226_c0_g2_i1_2	1.062	0.538	2.181	*ACOX1, ACOX3*	*acyl-CoA oxidase*
TRINITY_DN20400_c0_g2_i3_3	46.927	51.707	3.920	*ELOVL4*	*elongation of very long chain fatty acids protein 4*
TRINITY_DN26514_c0_g1_i7_1	3.160	3.541	0.666		

[1] The value of each gene expression level in the graph is the average of 3 replicates (n = 3).

Table S31. DSMs in fatty acid biosynthesis.

Metabolites	LA [1]	W	ES
3-Ketohexanoyl-CoA	0.525	210.807	185.106
Hexanoyl-CoA	8912.063	36,297.157	72,788.576

[1] The value of metabolite content in the graph is the average of 6 replicates (n = 6).

Table S32. Low temperature related DEGs.

Unigene	LA [1]	W	ES	Gene	Description
TRINITY_DN15245_c0_g1_i1_3	270.494	306.997	64.610		
TRINITY_DN21903_c0_g1_i6_1	0.526	1.043	0.063	*COR*	*cold response gene*
TRINITY_DN24859_c0_g1_i1_1	570.116	422.755	112.791		
TRINITY_DN12120_c0_g1_i1_3	33.325	24.024	9.480	*ICE1*	*inducer of CBF expression 1*
TRINITY_DN15512_c0_g1_i2_2	0.362	0.773	1.597		
TRINITY_DN2558_c0_g1_i1_3	0	0	1.058	*DREB*	*dehydration-responsive element-binding*
TRINITY_DN272_c0_g1_i1_2	0.361	0.039	1.029		
TRINITY_DN22074_c0_g1_i1_2	3.677	21.812	13.641		
TRINITY_DN10721_c0_g1_i1_2	1.311	0.392	0.116		
TRINITY_DN12278_c0_g1_i1_2	1.146	0.931	2.240		
TRINITY_DN12644_c0_g1_i1_1	24.843	21.768	8.944		
TRINITY_DN12908_c0_g1_i1_3	0.406	1.458	5.367		
TRINITY_DN22542_c0_g1_i1_3	0.573	0.976	2.207		
TRINITY_DN22912_c0_g2_i1_3	0.600	3.262	10.894		
TRINITY_DN23396_c0_g1_i1_3	21.701	31.077	61.142	LEA	late embryogenesis abundant protein
TRINITY_DN23957_c0_g1_i1_3	44.595	25.104	23.747		
TRINITY_DN23973_c0_g1_i1_1	113.061	163.663	58.772		
TRINITY_DN26377_c0_g2_i3_1	10.260	34.886	177.307		
TRINITY_DN26434_c0_g3_i1_3	15.675	35.701	10.574		
TRINITY_DN27606_c0_g1_i4_3	0.954	2.191	6.717		
TRINITY_DN29190_c0_g1_i1_3	0.448	0.386	1.869		
TRINITY_DN35293_c0_g1_i1_1	3.893	1.534	0.659		
TRINITY_DN35506_c0_g1_i1_3	4.446	3.587	18.594		
TRINITY_DN10011_c0_g1_i1_3	133.258	121.587	65.736		
TRINITY_DN13241_c0_g1_i1_3	1.071	0.033	10.808		
TRINITY_DN14034_c0_g1_i2_2	35.628	197.037	23.189		
TRINITY_DN14779_c0_g1_i1_2	1.907	0.412	0.208	LTP	lipid transfer protein
TRINITY_DN16201_c0_g2_i1_2	0.724	2.084	2.173		
TRINITY_DN17221_c0_g2_i1_3	9.255	15.936	6.928		
TRINITY_DN17857_c0_g1_i3_3	1.396	1.178	4.247		

TRINITY_DN18471_c0_g2_i1_2	15.984	14.764	37.773		
TRINITY_DN19052_c0_g1_i3_1	1.035	7.830	0.503		
TRINITY_DN20507_c0_g1_i1_1	3.608	0.548	0.722		
TRINITY_DN21676_c0_g1_i1_2	5.755	1.778	0.461		
TRINITY_DN22193_c0_g1_i1_3	9.490	12.777	29.613		
TRINITY_DN23171_c0_g1_i2_2	7.542	5.408	26.104		
TRINITY_DN23351_c0_g1_i3_2	1.789	2.479	4.977		
TRINITY_DN27382_c0_g1_i2_2	34.306	38.579	9.591		
TRINITY_DN28035_c0_g1_i1_2	1.484	0.092	0.103		
TRINITY_DN28035_c1_g3_i1_2	1.799	0.052	0.096		
TRINITY_DN34618_c0_g1_i1_1	0.522	0.586	2.104		
TRINITY_DN36999_c0_g1_i1_2	0.079	0.030	1.792		
TRINITY_DN19526_c0_g1_i3_3	26.986	21.916	75.925	*GPAT6*	*glycerol-3-phosphate acyltransferase*
TRINITY_DN24790_c0_g1_i2_2	4.247	2.982	7.370		

[1] The value of each gene expression level in the graph is the average of 3 replicates (n = 3).

Table S33. Climate data in Nanjing from November 2019 to February 2020.

Date	Average temperature (°C)	Average humidity (%)	Precipitation (mm)
2019-11-01	17.878	56.309	0
2019-11-02	18.078	64.253	0
2019-11-03	18.393	66.790	0.001
2019-11-04	16.228	74.461	0.002
2019-11-05	14.955	67.640	0
2019-11-06	14.818	69.389	0
2019-11-07	16.056	67.036	0.001
2019-11-08	13.754	72.348	0
2019-11-09	13.174	68.054	0
2019-11-10	15.716	55.009	0
2019-11-11	15.436	51.291	0
2019-11-12	16.620	54.381	0.022
2019-11-13	16.372	60.814	0.368
2019-11-14	12.507	47.392	0
2019-11-15	14.515	49.284	0
2019-11-16	17.301	53.221	0
2019-11-17	16.931	75.589	2.322
2019-11-18	9.037	72.085	7.552
2019-11-19	6.836	53.388	0
2019-11-20	10.089	59.758	0
2019-11-21	13.182	67.504	0.004
2019-11-22	14.627	79.444	0
2019-11-23	18.246	83.342	0
2019-11-24	14.720	89.042	0.438
2019-11-25	5.554	83.062	3.369
2019-11-26	6.580	77.504	0.892
2019-11-27	5.614	95.437	25.342
2019-11-28	5.720	69.351	0.248
2019-11-29	6.185	72.329	0
2019-11-30	7.904	90.294	1.949
2019-12-01	6.319	92.948	6.429
2019-12-02	4.885	80.690	0.015
2019-12-03	4.359	71.724	0.003
2019-12-04	6.165	66.675	0.002
2019-12-05	6.489	65.989	0
2019-12-06	5.827	69.535	0
2019-12-07	4.837	68.037	0

2019-12-08	6.229	62.847	0
2019-12-09	9.243	59.781	0
2019-12-10	10.819	63.065	0
2019-12-11	9.731	56.517	0
2019-12-12	7.875	62.915	0
2019-12-13	9.731	68.198	0
2019-12-14	9.467	74.224	0
2019-12-15	11.601	78.472	0
2019-12-16	14.113	82.077	0.007
2019-12-17	8.503	95.478	6.762
2019-12-18	4.767	86.472	5.693
2019-12-19	3.497	86.559	2.818
2019-12-20	4.259	80.769	0.105
2019-12-21	6.944	94.631	5.830
2019-12-22	7.787	94.240	10.291
2019-12-23	6.901	93.151	0.234
2019-12-24	7.490	96.787	3.568
2019-12-25	9.318	97.549	8.231
2019-12-26	5.979	93.636	2.210
2019-12-27	2.977	78.806	0
2019-12-28	4.953	74.916	0.001
2019-12-29	7.954	89.122	4.312
2019-12-30	6.588	82.442	0.021
2019-12-31	0.448	58.815	0
2020-01-01	2.823	73.367	0.046
2020-01-02	6.671	87.987	0.656
2020-01-03	7.361	96.194	0.781
2020-01-04	7.838	87.801	1.342
2020-01-05	9.483	88.959	1.326
2020-01-06	10.733	96.262	3.549
2020-01-07	5.788	96.565	7.067
2020-01-08	3.558	78.377	0.077
2020-01-09	2.419	94.963	5.244
2020-01-10	5.060	98.020	8.893
2020-01-11	4.089	96.466	4.084
2020-01-12	2.969	89.053	0.041
2020-01-13	2.668	86.189	0
2020-01-14	2.968	78.761	0
2020-01-15	1.572	84.059	6.145
2020-01-16	2.359	98.848	11.793
2020-01-17	2.634	91.503	0.541
2020-01-18	3.410	81.880	0.007
2020-01-19	4.669	76.258	0.001
2020-01-20	4.824	71.837	0.002
2020-01-21	4.635	86.589	1.302

2020-01-22	6.506	98.902	8.634
2020-01-23	7.721	93.772	1.177
2020-01-24	7.117	85.478	1.603
2020-01-25	5.410	87.738	1.376
2020-01-26	4.361	98.245	23.083
2020-01-27	2.842	97.815	6.072
2020-01-28	3.724	84.428	0
2020-01-29	5.325	70.216	0
2020-01-30	4.414	64.034	0.027
2020-01-31	3.568	71.077	0.004
2020-02-01	5.786	58.124	0
2020-02-02	8.240	55.518	0.001
2020-02-03	6.842	73.677	0.001
2020-02-04	7.287	76.705	0
2020-02-05	6.269	77.640	0
2020-02-06	4.083	84.319	4.386
2020-02-07	4.704	95.590	3.390
2020-02-08	6.267	87.575	0.106
2020-02-09	6.707	78.014	0
2020-02-10	8.245	71.680	0.012
2020-02-11	9.257	93.950	3.459
2020-02-12	10.256	88.579	0.107
2020-02-13	10.354	97.121	0.350
2020-02-14	12.998	98.587	5.339
2020-02-15	4.869	98.409	10.396
2020-02-16	1.293	71.233	2.105
2020-02-17	3.760	52.659	0
2020-02-18	4.727	56.056	0.002
2020-02-19	7.228	57.005	0
2020-02-20	9.234	63.241	0
2020-02-21	8.919	79.408	0.010
2020-02-22	9.678	64.011	0
2020-02-23	10.818	58.149	0
2020-02-24	16.086	67.620	0
2020-02-25	14.959	85.406	1.168
2020-02-26	10.325	77.598	1.028
2020-02-27	8.842	71.828	0.033
2020-02-28	8.352	94.338	7.754
2020-02-29	8.600	93.979	5.303

Table S34. Climate data in Nanjing from 2000 to 2020.

Year	Average humidity (%)	Cumulative precipitation (mm)	Average temperature (°C)
2000	75.474	1019.429	16.461
2001	74.231	802.537	16.586
2002	76.459	1112.568	16.875
2003	76.531	1489.234	16.229
2004	71.232	952.370	17.021
2005	69.532	1073.622	16.498
2006	73.130	1123.703	17.098
2007	72.579	1083.955	17.341
2008	72.017	1033.750	16.360
2009	72.306	1286.804	16.583
2010	70.414	1220.696	16.353
2011	68.135	1076.466	16.007
2012	69.150	1032.910	15.990
2013	68.072	936.236	16.827
2014	75.536	1232.923	16.420
2015	76.114	1514.152	16.323
2016	76.367	1809.833	16.707
2017	73.608	1185.818	16.942
2018	75.322	1267.529	16.921
2019	74.245	789.792	16.936
2020	77.232	1428.114	16.967

Table S35. *Trehalose 6-phosphate synthase/phosphatase* (*TPS*) expression.

Gene id	LA [1]	W	ES	Gene name	Description
TRINITY_DN15927_c0_g1_i1_3	6.851	7.077	14.208		
TRINITY_DN19271_c0_g1_i2_1	12.214	9.519	19.522		*trehalose*
TRINITY_DN5625_c0_g1_i1_3	11.862	10.484	4.918	*TPS*	*6-phosphate*
TRINITY_DN7172_c0_g1_i2_1	1.635	3.699	2.397		*synthase/phos*
TRINITY_DN17825_c0_g1_i3_3	26.930	20.055	29.021		*phatase*
TRINITY_DN636_c0_g1_i1_1	4.276	5.018	3.819		
TRINITY_DN35813_c0_g1_i1_2	0.621	0.189	0.124		*trehalose*
TRINITY_DN29093_c0_g1_i2_2	5.066	4.502	5.044	*otsB*	*6-phosphate*
TRINITY_DN22718_c0_g1_i6_2	2.661	3.685	1.878		*phosphatase*

[1] The value of each gene expression level in the graph is the average of 3 replicates (n = 3).