

Supplementary Table S1. DEG-enriched pathways under heat condition.

Pathway	Pathway ID	DEGs	Gene mapped to KEGG database	Percentage of DEGs in this pathway
Circadian rhythm - plant	ko04712	10	111	9.01
Isoflavonoid biosynthesis	ko00943	2	23	8.70
Arachidonic acid metabolism	ko00590	3	36	8.33
Sesquiterpenoid and triterpenoid biosynthesis	ko00909	2	28	7.14
Flavone and flavonol biosynthesis	ko00944	1	15	6.67
Ribosome biogenesis in eukaryotes	ko03008	13	199	6.53
Taurine and hypotaurine metabolism	ko00430	2	34	5.88
Thiamine metabolism	ko00730	2	35	5.71
C5-Branched dibasic acid metabolism	ko00660	1	20	5.00
Nicotinate and nicotinamide metabolism	ko00760	2	45	4.44
Sulfur metabolism	ko00920	3	70	4.29
Inositol phosphate metabolism	ko00562	5	125	4.00
Ubiquinone and other terpenoid-quinone biosynthesis	ko00130	3	85	3.53
Glycolysis / Gluconeogenesis	ko00010	10	288	3.47
Tyrosine metabolism	ko00350	3	90	3.33
Degradation of aromatic compounds	ko01220	1	31	3.23
Steroid biosynthesis	ko00100	3	97	3.09
Glutathione metabolism	ko00480	6	199	3.02
Galactose metabolism	ko00052	4	138	2.90
Glycosaminoglycan degradation	ko00531	1	35	2.86
Carotenoid biosynthesis	ko00906	2	71	2.82
Carbon fixation in photosynthetic organisms	ko00710	4	156	2.56
Folate biosynthesis	ko00790	1	40	2.50
2-Oxocarboxylic acid metabolism	ko01210	3	121	2.48
Isoquinoline alkaloid biosynthesis	ko00950	1	42	2.38
Phosphatidylinositol signaling system	ko04070	3	130	2.31
Biosynthesis of amino acids	ko01230	12	529	2.27
N-Glycan biosynthesis	ko00510	2	89	2.25
Zeatin biosynthesis	ko00908	1	45	2.22
Photosynthesis	ko00195	3	140	2.14

Carbon metabolism	ko01200	11	526	2.09
Cysteine and methionine metabolism	ko00270	4	199	2.01
Valine, leucine and isoleucine biosynthesis	ko00290	1	50	2.00
Cutin, suberine and wax biosynthesis	ko00073	1	51	1.96
Diterpenoid biosynthesis	ko00904	1	52	1.92
Pyruvate metabolism	ko00620	4	212	1.89
Protein processing in endoplasmic reticulum	ko04141	8	456	1.75
Purine metabolism	ko00230	6	347	1.73
RNA degradation	ko03018	4	232	1.72
Linoleic acid metabolism	ko00591	1	59	1.69
Tropane, piperidine and pyridine alkaloid biosynthesis	ko00960	1	59	1.69
Cyanoamino acid metabolism	ko00460	2	118	1.69
Alanine, aspartate and glutamate metabolism	ko00250	2	121	1.65
alpha-Linolenic acid metabolism	ko00592	2	121	1.65
Phagosome	ko04145	3	185	1.62
Fructose and mannose metabolism	ko00051	2	126	1.59
Ubiquitin mediated proteolysis	ko04120	4	256	1.56
Biosynthesis of unsaturated fatty acids	ko01040	1	65	1.54
Plant-pathogen interaction	ko04626	6	414	1.45
Phenylalanine metabolism	ko00360	4	276	1.45
Glycine, serine and threonine metabolism	ko00260	2	141	1.42
Regulation of autophagy	ko04140	1	75	1.33
Endocytosis	ko04144	4	311	1.29
RNA transport	ko03013	4	326	1.23
Ascorbate and aldarate metabolism	ko00053	1	87	1.15
Porphyrin and chlorophyll metabolism	ko00860	1	89	1.12
Amino sugar and nucleotide sugar metabolism	ko00520	3	276	1.09
SNARE interactions in vesicular transport	ko04130	1	97	1.03
Basal transcription factors	ko03022	1	103	0.97
beta-Alanine metabolism	ko00410	1	104	0.96
Terpenoid backbone biosynthesis	ko00900	1	108	0.93
Citrate cycle (TCA cycle)	ko00020	1	109	0.92
Plant hormone signal transduction	ko04075	7	769	0.91

Fatty acid degradation	ko00071	1	113	0.88
Pentose phosphate pathway	ko00030	1	118	0.85
Spliceosome	ko03040	3	356	0.84
Starch and sucrose metabolism	ko00500	4	475	0.84
mRNA surveillance pathway	ko03015	2	245	0.82
Glyoxylate and dicarboxylate metabolism	ko00630	1	124	0.81
Pyrimidine metabolism	ko00240	2	270	0.74
Oxidative phosphorylation	ko00190	2	275	0.73
Homologous recombination	ko03440	1	140	0.71
Fatty acid metabolism	ko01212	1	159	0.63
Ribosome	ko03010	4	652	0.61
Peroxisome	ko04146	1	176	0.57
Arginine and proline metabolism	ko00330	1	191	0.52
Glycerophospholipid metabolism	ko00564	1	197	0.51
Phenylpropanoid biosynthesis	ko00940	2	406	0.49