Appendix A . Primers used in this study.

Gene ID[a]	Gene name	Forward primer (5'-3')	Reverse primer (5'-3')	Fragement length (bp)
101761265	Zeaxanthin epoxidase, chloroplastic-like	ATCCCGATTCCCAACGGCAG	TCTGTTGCCTGTCTCGTGCG	239
101770668	9-cis-epoxycarotenoid dioxygenase NCED5	GCGGACCAGGGAGAGGATGTAG	CAAGGTGTCCGGGTTCGCCA	157
101757363	putative aldehyde oxidase-like protein	CAGATTTGGATCTTCCAGTTCAGCA	CGACACAAGCCCCACAACCA	104
101770287	probable protein phosphatase 2C 59	GCCCACATCACAAAGCCACC	ACGGCATGTTTGCTGGTTAAGT	199
101763654	serine/threonine-protein kinase SAPK3	GGAGGGTCGTTTCATGGTGAGG	TAGGGTGTCGGAGCGACTGG	181
101776070	bZIP transcription factor 46	CTTCAGCAGGCTACCACGGG	TCTCCTCCGACAACGCTCCA	148
101763536	putative 12-oxophytodienoate reductase 11	ACCGCAGTGTTGCCTTCCTC	CGTTGCATGTCATCCGCAG	193
101786707	protein TIFY 11e	CCTCTGGGACGTCGTCAAGC	CTCAGCCAGTTCGTCAGGGC	196
101775420	delta-1-pyrroline-5-carboxylate synthase 2	TCCTGTTGCTTGCAGGTGGG	CCCTTGAAAGTTCAGTTGTTTCAC	198
101777261	glutathione transferase GST 23	CCCGCTTCTGGTGCCACTT	CCCGAGCTGCACAAACATCG	140

Note: a) Gene ID against the NCBI database

Appendix B. Time course of the changes in RWC, ABA and proline, MDA contents in leaves of two genotypes DM and HN.

	Indices[*]	**Time courses of drought-treatment**[§]			
		0 h	24 h	48 h	72h
	RWC in leaf (%)	$52.40^{a}\pm0.36$	$50.73^{b}\pm0.66$	$49.74^{b}\pm0.62$	$47.87^{c}\pm1.22$
	Soluble sugar in leaf (mg•g^{-1} FW)	$5.50^{c}\pm0.72$	$6.60^{b}\pm0.70$	$6.20^{a}\pm1.14$	$6.50^{a}\pm0.14$
	Proline content in leaf (mg•g^{-1} FW)	$0.10^{d}\pm0.004$	$0.14^{c}\pm0.001$	$0.18^{b}\pm0.0003$	$0.20^{a}\pm0.003$
	MDA in leaf	$0.019^{c}\pm0.002$	$0.026^{b}\pm0.002$	$0.031^{b}\pm0.002$	$0.040^{a}\pm0.002$

DM	**(μmol•g^{-1} FW)**				
	ABA content in leaf (μg.g^{-1} FW)	2.53^{d}±0.01	3.50^{c}±0.00	3.54^{b}±0.02	3.60^{a}±0.03
	Chlorophyll a (mg•g^{-1} FW)	0.93^{a}±0.01	0.75^{b}±0.02	0.60^{c}±0.02	0.61^{c}±0.02
	Chlorophyll b (mg•g^{-1} FW)	0.65^{a}±0.02	0.42^{b}±0.03	0.40^{c}±0.03	0.45^{b}±0.03
HN	**Indices**[*]	**Time courses of drought-treatment**[§]			
		0 h	24 h	48 h	72h
	RWC in leaf (%)	75.00^{a}±0.80	72.32^{b}±1.43	66.93^{c}±0.58	61.61^{d}±0.85
	Soluble sugar in leaf (mg•g^{-1} FW)	10.7^{c}±0.72	10.9^{b}±0.70	14.0^{a}±1.14	18.7a±0.14
	Proline content in leaf (mg•g^{-1} FW)	0.54^{d}±0.001	0.71^{c}±0.001	0.09^{b}±0.002	0.10^{a}±0.003
	MDA in leaf (μmol•g^{-1} FW)	0.013^{a}±0.001	0.013^{a}±0.000	0.014^{a}±0.001	0.140^{a}±0.000
	ABA content in leaf (μg.g^{-1} FW)	2.55^{d}±0.01	2.60^{c}±0.01	2.72^{b}±0.01	2.91^{a}±0.00
	Chlorophyll a (mg•g^{-1} FW)	0.77^{a}±0.01	0.67^{b}±0.02	0.51^{c}±0.02	0.55^{c}±0.02
	Chlorophyll b (mg•g^{-1} FW)	0.28^{a}±0.02	0.23^{b}±0.03	0.20^{c}±0.03	0.28^{a}±0.03

[*] RWC, Relative water content; FW, Fresh weight; MDA, Malondialdehyde; ABA, Abscisic acid.

[§] mean values with the same letters in the same indices indicate non-significant difference, and means with different letters show significant difference at *P*<0.05 level.

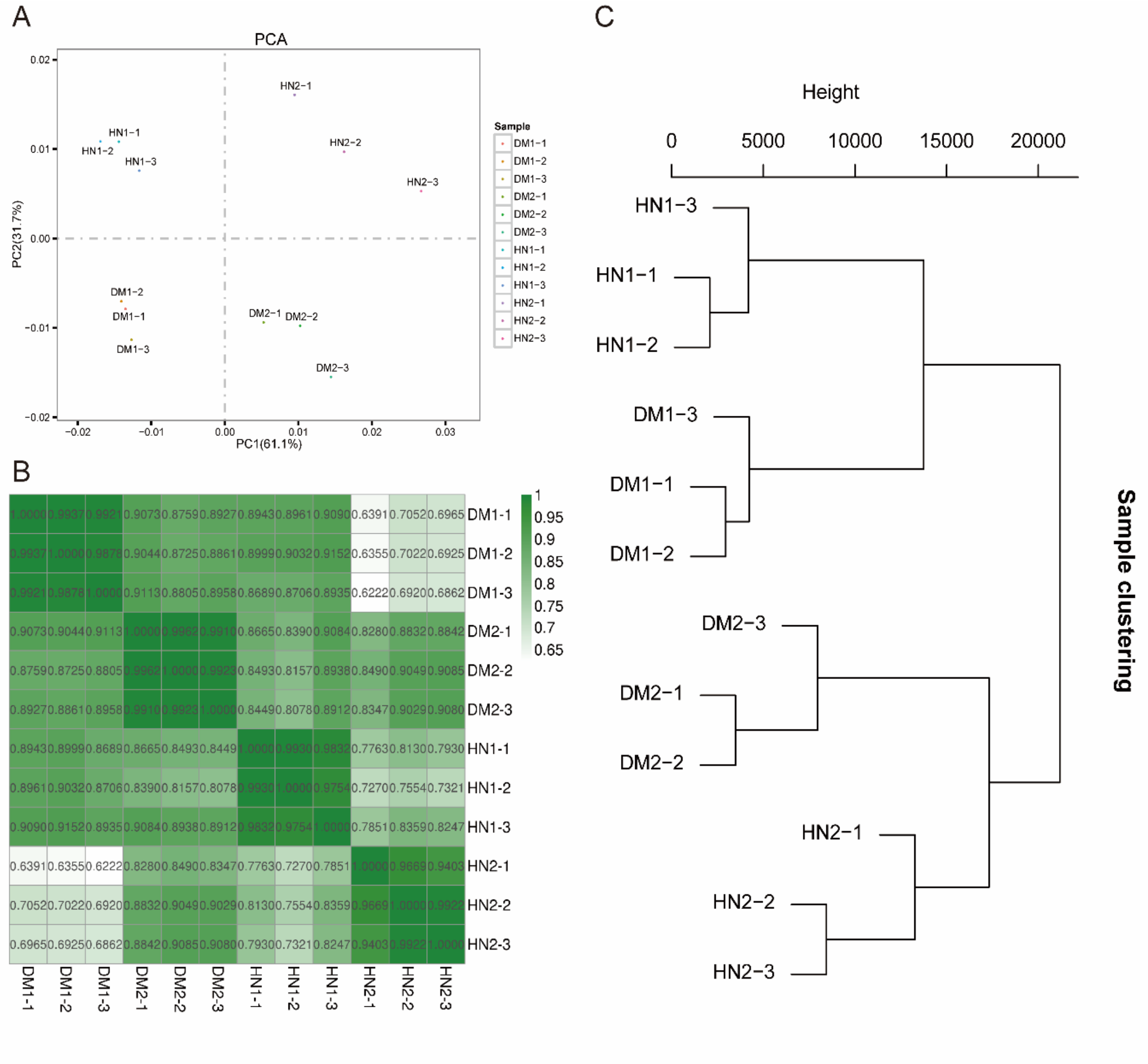
Appendix C. Number of known genes and new genes.

Group Name	Known Gene Num (%[a])	New Gene Num	All Gene Num
DM1	26134 (72.94%)	929	27063
DM2	26073 (72.77%)	923	26996
HN1	26684 (74.47%)	957	27641
HN2	26736 (74.62%)	965	27701
Mean	264067(73.70%)	944	27350

[a] %= Known Gene Num / All Reference Gene Num *100%

Length >= 200bp and exon number >=2 as the screening condition for new genes.

Appendix D. Data quality evaluation of mRNA-seq data and correlation analysis of samples. A: Principle Component Analysis (PCA) of all samples to assess data quality, PC1(61%) is on behalf of the contribution value of principal component 'PC1' in explaining the population variance;**B**: Heatmap visualization of Pearson's r, Color key indicates Pearson's r value between libraries. DM1 and DM2 stand for foxtail millet cultivar DM,short-term drought treatment 0h and 24h , respectively; HN1 and HN2 stand for foxtail millet cultivar DM, short-term drought treatment 0h and 24h, respectively. Numbers 1, 2 and 3 indicate the three biological replicates;**C:** Hierarchical clustering.



DM1-1	DM1-2	DM1-3	DM2-1	DM2-2	DM2-3	HN1-1	HN1-2	HN1-3	HN2-1	HN2-2	HN2-3	
1.0000	0.9937	0.9921	0.9073	0.8759	0.8927	0.8943	0.8961	0.9090	0.6391	0.7052	0.6965	DM1-1
0.9937	1.0000	0.9878	0.9044	0.8725	0.8861	0.8999	0.9032	0.9152	0.6355	0.7022	0.6925	DM1-2
0.9921	0.9878	1.0000	0.9113	0.8805	0.8958	0.8689	0.8706	0.8935	0.6222	0.6920	0.6862	DM1-3
0.9073	0.9044	0.9113	1.0000	0.9962	0.9910	0.8665	0.8390	0.9084	0.8280	0.8832	0.8842	DM2-1
0.8759	0.8725	0.8805	0.9962	1.0000	0.9923	0.8493	0.8157	0.8938	0.8490	0.9049	0.9085	DM2-2
0.8927	0.8861	0.8958	0.9910	0.9923	1.0000	0.8449	0.8078	0.8912	0.8347	0.9029	0.9080	DM2-3
0.8943	0.8999	0.8689	0.8665	0.8493	0.8449	1.0000	0.9930	0.9832	0.7763	0.8130	0.7930	HN1-1
0.8961	0.9032	0.8706	0.8390	0.8157	0.8078	0.9930	1.0000	0.9754	0.7270	0.7554	0.7321	HN1-2
0.9090	0.9152	0.8935	0.9084	0.8938	0.8912	0.9832	0.9754	1.0000	0.7851	0.8359	0.8247	HN1-3
0.6391	0.6355	0.6222	0.8280	0.8490	0.8347	0.7763	0.7270	0.7851	1.0000	0.9669	0.9403	HN2-1
0.7052	0.7022	0.6920	0.8832	0.9049	0.9029	0.8130	0.7554	0.8359	0.9669	1.0000	0.9922	HN2-2
0.6965	0.6925	0.6862	0.8842	0.9085	0.9080	0.7930	0.7321	0.8247	0.9403	0.9922	1.0000	HN2-3

S1 Fig. Data quality evaluation of mRNA-seq data and correlation analysis of samples. A: Principle Component Analysis (PCA) of all samples to assess data quality, PC1(61%) is on behalf of the contribution value of principal component 'PC1' in explaining the population variance; B: Heatmap visualization of Pearson's r, Color key indicates Pearson's r value between libraries. DM1 and DM2 stand for foxtail millet cultivar DM, short-term drought treatment 0h and 24h , respectively; HN1 and HN2 stand for foxtail millet cultivar DM, short-term drought treatment 0h and 24h, respectively. Numbers 1, 2 and 3 indicate the three biological replicates; C: Hierarchical clustering.

Appendix E. Gene Ontology (GO) terms of Biological Process of co-modulated DEGs in DM2-vs-DM1 and HN2-vs-HN1 using agriGO.

DM1-vs-DM2_HN1-vs-HN2 GO Enrichment (Biological Process)

#	GO ID	Description	GeneRatio (554)	BgRatio (15411)	pvalue	p.adjust
1	GO:0007017	microtubule-based process	18 (3.25%)	184 (1.19%)	0.000116	0.096675
2	GO:0009408	response to heat	6 (1.08%)	26 (0.17%)	0.000262	0.108795
3	GO:0050896	response to stimulus	135 (24.37%)	2913 (18.9%)	0.000688	0.173065
4	GO:0008643	carbohydrate transport	6 (1.08%)	34 (0.22%)	0.001197	0.173065
5	GO:1902410	mitotic cytokinetic process	10 (1.81%)	92 (0.6%)	0.001700	0.173065
6	GO:0000281	mitotic cytokinesis	10 (1.81%)	93 (0.6%)	0.001846	0.173065
7	GO:0061640	cytoskeleton-dependent cytokinesis	10 (1.81%)	94 (0.61%)	0.002000	0.173065
8	GO:0048444	floral organ morphogenesis	6 (1.08%)	38 (0.25%)	0.002176	0.173065
9	GO:0048563	post-embryonic organ morphogenesis	6 (1.08%)	38 (0.25%)	0.002176	0.173065
10	GO:0001101	response to acid chemical	21 (3.79%)	294 (1.91%)	0.002244	0.173065
11	GO:0006950	response to stress	76 (13.72%)	1532 (9.94%)	0.002288	0.173065
12	GO:0032506	cytokinetic process	10 (1.81%)	97 (0.63%)	0.002529	0.175359
13	GO:0000910	cytokinesis	10 (1.81%)	99 (0.64%)	0.002940	0.188160
14	GO:0048569	post-embryonic organ development	7 (1.26%)	56 (0.36%)	0.003764	0.223688
15	GO:0048449	floral organ formation	5 (0.9%)	31 (0.2%)	0.004617	0.255215
16	GO:0051726	regulation of cell cycle	12 (2.17%)	141 (0.91%)	0.004908	0.255215
17	GO:0031324	negative regulation of cellular metabolic process	12 (2.17%)	143 (0.93%)	0.005488	0.268595
18	GO:1903047	mitotic cell cycle process	10 (1.81%)	109 (0.71%)	0.005858	0.270767
19	GO:0006631	fatty acid metabolic process	22 (3.97%)	345 (2.24%)	0.006905	0.299121
20	GO:0009068	aspartate family amino acid catabolic process	2 (0.36%)	4 (0.03%)	0.007375	0.299121
21	GO:0030162	regulation of proteolysis	6 (1.08%)	49 (0.32%)	0.007909	0.299121
22	GO:0045861	negative regulation of proteolysis	6 (1.08%)	49 (0.32%)	0.007909	0.299121
23	GO:0034728	nucleosome organization	5 (0.9%)	36 (0.23%)	0.008845	0.311392
24	GO:0051301	cell division	10 (1.81%)	116 (0.75%)	0.008982	0.311392
25	GO:0048513	animal organ development	14 (2.53%)	193 (1.25%)	0.010053	0.334552
26	GO:0032787	monocarboxylic acid metabolic process	42 (7.58%)	815 (5.29%)	0.012008	0.381279
27	GO:0071824	protein-DNA complex subunit organization	5 (0.9%)	39 (0.25%)	0.012373	0.381279
28	GO:1901987	regulation of cell cycle phase transition	5 (0.9%)	41 (0.27%)	0.015192	0.435852
29	GO:1901990	regulation of mitotic cell cycle phase transition	5 (0.9%)	41 (0.27%)	0.015192	0.435852
30	GO:0048523	negative regulation of cellular process	12 (2.17%)	165 (1.07%)	0.016135	0.447481
31	GO:0000278	mitotic cell cycle	10 (1.81%)	130 (0.84%)	0.018880	0.506709
32	GO:0009887	organ morphogenesis	10 (1.81%)	132 (0.86%)	0.020771	0.524300
33	GO:0051259	protein oligomerization	3 (0.54%)	17 (0.11%)	0.021576	0.524300
34	GO:0032269	negative regulation of cellular protein	6 (1.08%)	62 (0.4%)	0.023578	0.524300

		metabolic process				
35	GO:0051248	negative regulation of protein metabolic process	6 (1.08%)	62 (0.4%)	0.023578	0.524300
36	GO:0009266	response to temperature stimulus	10 (1.81%)	135 (0.88%)	0.023861	0.524300
37	GO:0033045	regulation of sister chromatid segregation	2 (0.36%)	7 (0.05%)	0.024024	0.524300
38	GO:0051983	regulation of chromosome segregation	2 (0.36%)	7 (0.05%)	0.024024	0.524300
39	GO:0015833	peptide transport	5 (0.9%)	47 (0.3%)	0.026122	0.524300
40	GO:0034968	histone lysine methylation	8 (1.44%)	100 (0.65%)	0.027529	0.524300
41	GO:0010466	negative regulation of peptidase activity	5 (0.9%)	48 (0.31%)	0.028328	0.524300
42	GO:0052547	regulation of peptidase activity	5 (0.9%)	48 (0.31%)	0.028328	0.524300
43	GO:0051346	negative regulation of hydrolase activity	5 (0.9%)	49 (0.32%)	0.030648	0.524300
44	GO:0046337	phosphatidylethanolamine metabolic process	2 (0.36%)	8 (0.05%)	0.031279	0.524300
45	GO:0051052	regulation of DNA metabolic process	7 (1.26%)	84 (0.55%)	0.031336	0.524300
46	GO:0018022	peptidyl-lysine methylation	8 (1.44%)	103 (0.67%)	0.032089	0.524300
47	GO:0006820	anion transport	17 (3.07%)	291 (1.89%)	0.034269	0.524300
48	GO:0060255	regulation of macromolecule metabolic process	86 (15.52%)	1981 (12.85%)	0.034792	0.524300
49	GO:0006004	fucose metabolic process	1 (0.18%)	1 (0.01%)	0.035948	0.524300
50	GO:0006915	apoptotic process	1 (0.18%)	1 (0.01%)	0.035948	0.524300
51	GO:0009087	methionine catabolic process	1 (0.18%)	1 (0.01%)	0.035948	0.524300
52	GO:0010322	regulation of isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway	1 (0.18%)	1 (0.01%)	0.035948	0.524300
53	GO:0015837	amine transport	1 (0.18%)	1 (0.01%)	0.035948	0.524300
54	GO:0015843	methylammonium transport	1 (0.18%)	1 (0.01%)	0.035948	0.524300
55	GO:0071071	regulation of phospholipid biosynthetic process	1 (0.18%)	1 (0.01%)	0.035948	0.524300
56	GO:1903725	regulation of phospholipid metabolic process	1 (0.18%)	1 (0.01%)	0.035948	0.524300
57	GO:0015849	organic acid transport	10 (1.81%)	145 (0.94%)	0.036550	0.524300
58	GO:0046942	carboxylic acid transport	10 (1.81%)	145 (0.94%)	0.036550	0.524300
59	GO:0042886	amide transport	5 (0.9%)	52 (0.34%)	0.038310	0.539896
60	GO:0009886	post-embryonic morphogenesis	8 (1.44%)	107 (0.69%)	0.038935	0.539896
61	GO:0007346	regulation of mitotic cell cycle	5 (0.9%)	54 (0.35%)	0.044011	0.562368
62	GO:0006560	proline metabolic process	2 (0.36%)	10 (0.06%)	0.047944	0.562368
63	GO:0016119	carotene metabolic process	2 (0.36%)	10 (0.06%)	0.047944	0.562368
64	GO:0015740	C4-dicarboxylate transport	3 (0.54%)	23 (0.15%)	0.047980	0.562368
65	GO:0015711	organic anion transport	11 (1.99%)	174 (1.13%)	0.049761	0.562368
66	GO:0010468	regulation of gene expression	79 (14.26%)	1836 (11.91%)	0.050079	0.562368
67	GO:0007568	aging	4 (0.72%)	39 (0.25%)	0.050405	0.562368
68	GO:0006772	thiamine metabolic process	2 (0.36%)	11 (0.07%)	0.057233	0.562368

69	GO:0006633	fatty acid biosynthetic process	7 (1.26%)	96 (0.62%)	0.057532	0.562368
70	GO:0006342	chromatin silencing	6 (1.08%)	77 (0.5%)	0.058415	0.562368
71	GO:0045814	negative regulation of gene expression, epigenetic	6 (1.08%)	77 (0.5%)	0.058415	0.562368
72	GO:0045892	negative regulation of transcription, DNA-templated	6 (1.08%)	77 (0.5%)	0.058415	0.562368
73	GO:1903507	negative regulation of nucleic acid-templated transcription	6 (1.08%)	77 (0.5%)	0.058415	0.562368
74	GO:0016052	carbohydrate catabolic process	4 (0.72%)	41 (0.27%)	0.058727	0.562368
75	GO:2000113	negative regulation of cellular macromolecule biosynthetic process	6 (1.08%)	78 (0.51%)	0.061458	0.562368
76	GO:0072330	monocarboxylic acid biosynthetic process	7 (1.26%)	98 (0.64%)	0.062910	0.562368
77	GO:0043086	negative regulation of catalytic activity	5 (0.9%)	60 (0.39%)	0.064014	0.562368
78	GO:0044092	negative regulation of molecular function	5 (0.9%)	60 (0.39%)	0.064014	0.562368
79	GO:0048437	floral organ development	6 (1.08%)	79 (0.51%)	0.064592	0.562368
80	GO:1902679	negative regulation of RNA biosynthetic process	6 (1.08%)	79 (0.51%)	0.064592	0.562368
81	GO:0019856	pyrimidine nucleobase biosynthetic process	2 (0.36%)	12 (0.08%)	0.067085	0.562368
82	GO:0033044	regulation of chromosome organization	2 (0.36%)	12 (0.08%)	0.067085	0.562368
83	GO:0010558	negative regulation of macromolecule biosynthetic process	6 (1.08%)	80 (0.52%)	0.067818	0.562368
84	GO:0048646	anatomical structure formation involved in morphogenesis	6 (1.08%)	80 (0.52%)	0.067818	0.562368
85	GO:0051253	negative regulation of RNA metabolic process	6 (1.08%)	80 (0.52%)	0.067818	0.562368
86	GO:0006354	DNA-templated transcription, elongation	1 (0.18%)	2 (0.01%)	0.070607	0.562368
87	GO:0006706	steroid catabolic process	1 (0.18%)	2 (0.01%)	0.070607	0.562368
88	GO:0008645	hexose transport	1 (0.18%)	2 (0.01%)	0.070607	0.562368
89	GO:0009250	glucan biosynthetic process	1 (0.18%)	2 (0.01%)	0.070607	0.562368
90	GO:0009313	oligosaccharide catabolic process	1 (0.18%)	2 (0.01%)	0.070607	0.562368
91	GO:0009733	response to auxin	1 (0.18%)	2 (0.01%)	0.070607	0.562368
92	GO:0009734	auxin-activated signaling pathway	1 (0.18%)	2 (0.01%)	0.070607	0.562368
93	GO:0015695	organic cation transport	1 (0.18%)	2 (0.01%)	0.070607	0.562368
94	GO:0015749	monosaccharide transport	1 (0.18%)	2 (0.01%)	0.070607	0.562368
95	GO:0015822	ornithine transport	1 (0.18%)	2 (0.01%)	0.070607	0.562368
96	GO:0018131	oxazole or thiazole biosynthetic process	1 (0.18%)	2 (0.01%)	0.070607	0.562368
97	GO:0019474	L-lysine catabolic process to acetyl-CoA	1 (0.18%)	2 (0.01%)	0.070607	0.562368
98	GO:0034308	primary alcohol metabolic process	1 (0.18%)	2 (0.01%)	0.070607	0.562368
99	GO:0034433	steroid esterification	1 (0.18%)	2 (0.01%)	0.070607	0.562368
100	GO:0043100	pyrimidine nucleobase salvage	1 (0.18%)	2 (0.01%)	0.070607	0.562368
101	GO:0044724	single-organism carbohydrate catabolic	1 (0.18%)	2 (0.01%)	0.070607	0.562368

		process				
102	GO:0046484	oxazole or thiazole metabolic process	1 (0.18%)	2 (0.01%)	0.070607	0.562368
103	GO:0071365	cellular response to auxin stimulus	1 (0.18%)	2 (0.01%)	0.070607	0.562368
104	GO:0045934	negative regulation of nucleobase-containing compound metabolic process	6 (1.08%)	81 (0.53%)	0.071137	0.562368
105	GO:0051172	negative regulation of nitrogen compound metabolic process	6 (1.08%)	81 (0.53%)	0.071137	0.562368
106	GO:0010564	regulation of cell cycle process	5 (0.9%)	62 (0.4%)	0.071648	0.562368
107	GO:0031327	negative regulation of cellular biosynthetic process	6 (1.08%)	82 (0.53%)	0.074547	0.579656
108	GO:0009890	negative regulation of biosynthetic process	6 (1.08%)	83 (0.54%)	0.078049	0.601120
109	GO:0006305	DNA alkylation	7 (1.26%)	104 (0.67%)	0.080820	0.601120
110	GO:0009642	response to light intensity	7 (1.26%)	104 (0.67%)	0.080820	0.601120
111	GO:0042221	response to chemical	53 (9.57%)	1215 (7.88%)	0.081043	0.601120
112	GO:0015893	drug transport	6 (1.08%)	84 (0.55%)	0.081642	0.601120
113	GO:0042493	response to drug	6 (1.08%)	84 (0.55%)	0.081642	0.601120
114	GO:0009908	flower development	6 (1.08%)	85 (0.55%)	0.085327	0.622734
115	GO:0015698	inorganic anion transport	7 (1.26%)	106 (0.69%)	0.087383	0.629425
116	GO:0006835	dicarboxylic acid transport	3 (0.54%)	30 (0.19%)	0.091708	0.629425
117	GO:0009696	salicylic acid metabolic process	4 (0.72%)	48 (0.31%)	0.093140	0.629425
118	GO:0042537	benzene-containing compound metabolic process	4 (0.72%)	48 (0.31%)	0.093140	0.629425
119	GO:0006304	DNA modification	7 (1.26%)	108 (0.7%)	0.094238	0.629425
120	GO:0043269	regulation of ion transport	6 (1.08%)	88 (0.57%)	0.096918	0.629425
121	GO:0042723	thiamine-containing compound metabolic process	2 (0.36%)	15 (0.1%)	0.099508	0.629425
122	GO:1901606	alpha-amino acid catabolic process	2 (0.36%)	15 (0.1%)	0.099508	0.629425
123	GO:0019752	carboxylic acid metabolic process	59 (10.65%)	1391 (9.03%)	0.101678	0.629425
124	GO:0006629	lipid metabolic process	45 (8.12%)	1032 (6.7%)	0.102313	0.629425
125	GO:0000098	sulfur amino acid catabolic process	1 (0.18%)	3 (0.02%)	0.104021	0.629425
126	GO:0006554	lysine catabolic process	1 (0.18%)	3 (0.02%)	0.104021	0.629425
127	GO:0006842	tricarboxylic acid transport	1 (0.18%)	3 (0.02%)	0.104021	0.629425
128	GO:0007063	regulation of sister chromatid cohesion	1 (0.18%)	3 (0.02%)	0.104021	0.629425
129	GO:0010675	regulation of cellular carbohydrate metabolic process	1 (0.18%)	3 (0.02%)	0.104021	0.629425
130	GO:0019477	L-lysine catabolic process	1 (0.18%)	3 (0.02%)	0.104021	0.629425
131	GO:0019627	urea metabolic process	1 (0.18%)	3 (0.02%)	0.104021	0.629425
132	GO:0019747	regulation of isoprenoid metabolic process	1 (0.18%)	3 (0.02%)	0.104021	0.629425
133	GO:0044273	sulfur compound catabolic process	1 (0.18%)	3 (0.02%)	0.104021	0.629425
134	GO:0045995	regulation of embryonic development	1 (0.18%)	3 (0.02%)	0.104021	0.629425
135	GO:0046440	L-lysine metabolic process	1 (0.18%)	3 (0.02%)	0.104021	0.629425

136	GO:0051304	chromosome separation	1 (0.18%)	3 (0.02%)	0.104021	0.629425
137	GO:0060771	phyllotactic patterning	1 (0.18%)	3 (0.02%)	0.104021	0.629425
138	GO:0018958	phenol-containing compound metabolic process	4 (0.72%)	50 (0.32%)	0.104400	0.629425
139	GO:0018205	peptidyl-lysine modification	9 (1.62%)	155 (1.01%)	0.106860	0.631206
140	GO:0018193	peptidyl-amino acid modification	11 (1.99%)	200 (1.3%)	0.107157	0.631206
141	GO:0044255	cellular lipid metabolic process	37 (6.68%)	833 (5.41%)	0.107168	0.631206
142	GO:0019222	regulation of metabolic process	92 (16.61%)	2262 (14.68%)	0.107730	0.631206
143	GO:0006457	protein folding	2 (0.36%)	16 (0.1%)	0.111117	0.637583
144	GO:0042214	terpene metabolic process	2 (0.36%)	16 (0.1%)	0.111117	0.637583
145	GO:0046112	nucleobase biosynthetic process	2 (0.36%)	16 (0.1%)	0.111117	0.637583
146	GO:0099402	plant organ development	11 (1.99%)	202 (1.31%)	0.112721	0.642354
147	GO:0005976	polysaccharide metabolic process	24 (4.33%)	515 (3.34%)	0.117261	0.663293
148	GO:1901565	organonitrogen compound catabolic process	6 (1.08%)	93 (0.6%)	0.117990	0.663293
149	GO:0048731	system development	21 (3.79%)	444 (2.88%)	0.122278	0.682786
150	GO:0009311	oligosaccharide metabolic process	9 (1.62%)	161 (1.04%)	0.126606	0.686962
151	GO:0043436	oxoacid metabolic process	60 (10.83%)	1441 (9.35%)	0.127281	0.686962
152	GO:0006082	organic acid metabolic process	60 (10.83%)	1442 (9.36%)	0.128425	0.686962
153	GO:0006637	acyl-CoA metabolic process	4 (0.72%)	54 (0.35%)	0.128651	0.686962
154	GO:0016128	phytosteroid metabolic process	4 (0.72%)	54 (0.35%)	0.128651	0.686962
155	GO:0035383	thioester metabolic process	4 (0.72%)	54 (0.35%)	0.128651	0.686962
156	GO:0065007	biological regulation	143 (25.81%)	3659 (23.74%)	0.132802	0.686962
157	GO:0006206	pyrimidine nucleobase metabolic process	2 (0.36%)	18 (0.12%)	0.135286	0.686962
158	GO:0006109	regulation of carbohydrate metabolic process	1 (0.18%)	4 (0.03%)	0.136236	0.686962
159	GO:0006140	regulation of nucleotide metabolic process	1 (0.18%)	4 (0.03%)	0.136236	0.686962
160	GO:0006561	proline biosynthetic process	1 (0.18%)	4 (0.03%)	0.136236	0.686962
161	GO:0006885	regulation of pH	1 (0.18%)	4 (0.03%)	0.136236	0.686962
162	GO:0009956	radial pattern formation	1 (0.18%)	4 (0.03%)	0.136236	0.686962
163	GO:0016117	carotenoid biosynthetic process	1 (0.18%)	4 (0.03%)	0.136236	0.686962
164	GO:0030004	cellular monovalent inorganic cation homeostasis	1 (0.18%)	4 (0.03%)	0.136236	0.686962
165	GO:0030641	regulation of cellular pH	1 (0.18%)	4 (0.03%)	0.136236	0.686962
166	GO:0019725	cellular homeostasis	10 (1.81%)	188 (1.22%)	0.140658	0.698732
167	GO:0009267	cellular response to starvation	4 (0.72%)	56 (0.36%)	0.141579	0.698732
168	GO:0042594	response to starvation	4 (0.72%)	56 (0.36%)	0.141579	0.698732
169	GO:0006090	pyruvate metabolic process	16 (2.89%)	331 (2.15%)	0.141930	0.698732
170	GO:0009657	plastid organization	12 (2.17%)	237 (1.54%)	0.147432	0.718981
171	GO:0006553	lysine metabolic process	2 (0.36%)	19 (0.12%)	0.147771	0.718981

172	GO:0031668	cellular response to extracellular stimulus	4 (0.72%)	58 (0.38%)	0.154997	0.737365
173	GO:0031669	cellular response to nutrient levels	4 (0.72%)	58 (0.38%)	0.154997	0.737365
174	GO:0071496	cellular response to external stimulus	4 (0.72%)	58 (0.38%)	0.154997	0.737365
175	GO:0016571	histone methylation	9 (1.62%)	169 (1.1%)	0.155723	0.737365
176	GO:0032259	methylation	11 (1.99%)	216 (1.4%)	0.156137	0.737365
177	GO:0009690	cytokinin metabolic process	2 (0.36%)	20 (0.13%)	0.160477	0.737365
178	GO:1901700	response to oxygen-containing compound	17 (3.07%)	363 (2.36%)	0.161515	0.737365
179	GO:0000272	polysaccharide catabolic process	3 (0.54%)	39 (0.25%)	0.164079	0.737365
180	GO:0010965	regulation of mitotic sister chromatid separation	1 (0.18%)	5 (0.03%)	0.167295	0.737365
181	GO:0015743	malate transport	1 (0.18%)	5 (0.03%)	0.167295	0.737365
182	GO:0030071	regulation of mitotic metaphase/anaphase transition	1 (0.18%)	5 (0.03%)	0.167295	0.737365
183	GO:0032776	DNA methylation on cytosine	1 (0.18%)	5 (0.03%)	0.167295	0.737365
184	GO:0033047	regulation of mitotic sister chromatid segregation	1 (0.18%)	5 (0.03%)	0.167295	0.737365
185	GO:0043090	amino acid import	1 (0.18%)	5 (0.03%)	0.167295	0.737365
186	GO:0043092	L-amino acid import	1 (0.18%)	5 (0.03%)	0.167295	0.737365
187	GO:0046890	regulation of lipid biosynthetic process	1 (0.18%)	5 (0.03%)	0.167295	0.737365
188	GO:1902099	regulation of metaphase/anaphase transition of cell cycle	1 (0.18%)	5 (0.03%)	0.167295	0.737365
189	GO:0006325	chromatin organization	18 (3.25%)	390 (2.53%)	0.167502	0.737365
190	GO:0032879	regulation of localization	6 (1.08%)	104 (0.67%)	0.171442	0.739401
191	GO:0051049	regulation of transport	6 (1.08%)	104 (0.67%)	0.171442	0.739401
192	GO:0006026	aminoglycan catabolic process	2 (0.36%)	21 (0.14%)	0.173373	0.739401
193	GO:0009063	cellular amino acid catabolic process	2 (0.36%)	21 (0.14%)	0.173373	0.739401
194	GO:0006479	protein methylation	9 (1.62%)	174 (1.13%)	0.175442	0.739401
195	GO:0005975	carbohydrate metabolic process	38 (6.86%)	903 (5.86%)	0.175551	0.739401
196	GO:0009694	jasmonic acid metabolic process	4 (0.72%)	61 (0.4%)	0.175963	0.739401
197	GO:0009991	response to extracellular stimulus	4 (0.72%)	61 (0.4%)	0.175963	0.739401
198	GO:0031667	response to nutrient levels	4 (0.72%)	61 (0.4%)	0.175963	0.739401
199	GO:0071705	nitrogen compound transport	11 (1.99%)	224 (1.45%)	0.184261	0.770380
200	GO:0006397	mRNA processing	2 (0.36%)	22 (0.14%)	0.186427	0.770437
201	GO:1901136	carbohydrate derivative catabolic process	2 (0.36%)	22 (0.14%)	0.186427	0.770437
202	GO:0070838	divalent metal ion transport	6 (1.08%)	108 (0.7%)	0.193012	0.770437
203	GO:0072511	divalent inorganic cation transport	6 (1.08%)	108 (0.7%)	0.193012	0.770437
204	GO:0044042	glucan metabolic process	16 (2.89%)	350 (2.27%)	0.194641	0.770437
205	GO:0005984	disaccharide metabolic process	8 (1.44%)	155 (1.01%)	0.195220	0.770437
206	GO:0022402	cell cycle process	13 (2.35%)	276 (1.79%)	0.195703	0.770437
207	GO:0005996	monosaccharide metabolic process	10 (1.81%)	203 (1.32%)	0.196183	0.770437
208	GO:0006306	DNA methylation	1 (0.18%)	6 (0.04%)	0.197239	0.770437

209	GO:0006333	chromatin assembly or disassembly	1 (0.18%)	6 (0.04%)	0.197239	0.770437
210	GO:0008655	pyrimidine-containing compound salvage	1 (0.18%)	6 (0.04%)	0.197239	0.770437
211	GO:0019216	regulation of lipid metabolic process	1 (0.18%)	6 (0.04%)	0.197239	0.770437
212	GO:0031497	chromatin assembly	1 (0.18%)	6 (0.04%)	0.197239	0.770437
213	GO:0044728	DNA methylation or demethylation	1 (0.18%)	6 (0.04%)	0.197239	0.770437
214	GO:0051336	regulation of hydrolase activity	5 (0.9%)	87 (0.56%)	0.203306	0.790424
215	GO:0009892	negative regulation of metabolic process	17 (3.07%)	383 (2.49%)	0.218497	0.844285
216	GO:0034754	cellular hormone metabolic process	3 (0.54%)	45 (0.29%)	0.219189	0.844285
217	GO:0006066	alcohol metabolic process	9 (1.62%)	185 (1.2%)	0.222491	0.845137
218	GO:0006020	inositol metabolic process	1 (0.18%)	7 (0.05%)	0.226109	0.845137
219	GO:0055088	lipid homeostasis	1 (0.18%)	7 (0.05%)	0.226109	0.845137
220	GO:0097305	response to alcohol	1 (0.18%)	7 (0.05%)	0.226109	0.845137
221	GO:0006022	aminoglycan metabolic process	2 (0.36%)	25 (0.16%)	0.226273	0.845137
222	GO:0016265	death	4 (0.72%)	68 (0.44%)	0.228150	0.845137
223	GO:0042445	hormone metabolic process	4 (0.72%)	68 (0.44%)	0.228150	0.845137
224	GO:0009808	lignin metabolic process	3 (0.54%)	46 (0.3%)	0.228726	0.845137
225	GO:0043414	macromolecule methylation	10 (1.81%)	211 (1.37%)	0.229182	0.845137
226	GO:0050789	regulation of biological process	128 (23.1%)	3352 (21.75%)	0.230097	0.845137
227	GO:0010605	negative regulation of macromolecule metabolic process	14 (2.53%)	311 (2.02%)	0.230584	0.845137
228	GO:0040029	regulation of gene expression, epigenetic	7 (1.26%)	139 (0.9%)	0.233930	0.851932
229	GO:0044262	cellular carbohydrate metabolic process	18 (3.25%)	415 (2.69%)	0.238589	0.851932
230	GO:0009687	abscisic acid metabolic process	2 (0.36%)	26 (0.17%)	0.239701	0.851932
231	GO:0043288	apocarotenoid metabolic process	2 (0.36%)	26 (0.17%)	0.239701	0.851932
232	GO:1902644	tertiary alcohol metabolic process	2 (0.36%)	26 (0.17%)	0.239701	0.851932
233	GO:0008213	protein alkylation	9 (1.62%)	189 (1.23%)	0.240699	0.851932
234	GO:0006865	amino acid transport	4 (0.72%)	70 (0.45%)	0.243730	0.851932
235	GO:0009064	glutamine family amino acid metabolic process	4 (0.72%)	70 (0.45%)	0.243730	0.851932
236	GO:0009066	aspartate family amino acid metabolic process	3 (0.54%)	48 (0.31%)	0.248019	0.851932
237	GO:0016129	phytosteroid biosynthetic process	3 (0.54%)	48 (0.31%)	0.248019	0.851932
238	GO:0044036	cell wall macromolecule metabolic process	5 (0.9%)	94 (0.61%)	0.249425	0.851932
239	GO:0019318	hexose metabolic process	7 (1.26%)	142 (0.92%)	0.250139	0.851932
240	GO:0018904	ether metabolic process	2 (0.36%)	27 (0.18%)	0.253165	0.851932
241	GO:0042592	homeostatic process	13 (2.35%)	292 (1.89%)	0.253298	0.851932
242	GO:0003333	amino acid transmembrane transport	1 (0.18%)	8 (0.05%)	0.253941	0.851932
243	GO:0007349	cellularization	1 (0.18%)	8 (0.05%)	0.253941	0.851932
244	GO:0009625	response to insect	1 (0.18%)	8 (0.05%)	0.253941	0.851932

245	GO:0019755	one-carbon compound transport	1 (0.18%)	8 (0.05%)	0.253941	0.851932
246	GO:0031124	mRNA 3'-end processing	1 (0.18%)	8 (0.05%)	0.253941	0.851932
247	GO:0051260	protein homooligomerization	1 (0.18%)	8 (0.05%)	0.253941	0.851932
248	GO:0071941	nitrogen cycle metabolic process	1 (0.18%)	8 (0.05%)	0.253941	0.851932
249	GO:0044710	single-organism metabolic process	178 (32.13%)	4745 (30.79%)	0.257102	0.859071
250	GO:0016570	histone modification	11 (1.99%)	243 (1.58%)	0.259247	0.862775
251	GO:0006766	vitamin metabolic process	3 (0.54%)	50 (0.32%)	0.267546	0.880349
252	GO:0006767	water-soluble vitamin metabolic process	3 (0.54%)	50 (0.32%)	0.267546	0.880349
253	GO:0016569	covalent chromatin modification	11 (1.99%)	245 (1.59%)	0.267702	0.880349
254	GO:0022622	root system development	4 (0.72%)	74 (0.48%)	0.275541	0.895037
255	GO:0048364	root development	4 (0.72%)	74 (0.48%)	0.275541	0.895037
256	GO:0030003	cellular cation homeostasis	2 (0.36%)	29 (0.19%)	0.280124	0.895037
257	GO:0006573	valine metabolic process	1 (0.18%)	9 (0.06%)	0.280775	0.895037
258	GO:0007088	regulation of mitotic nuclear division	1 (0.18%)	9 (0.06%)	0.280775	0.895037
259	GO:0015807	L-amino acid transport	1 (0.18%)	9 (0.06%)	0.280775	0.895037
260	GO:0016116	carotenoid metabolic process	1 (0.18%)	9 (0.06%)	0.280775	0.895037
261	GO:1903825	organic acid transmembrane transport	1 (0.18%)	9 (0.06%)	0.280775	0.895037
262	GO:0006811	ion transport	33 (5.96%)	825 (5.35%)	0.286040	0.908341
263	GO:1901615	organic hydroxy compound metabolic process	13 (2.35%)	301 (1.95%)	0.288156	0.911581
264	GO:0010260	organ senescence	2 (0.36%)	30 (0.19%)	0.293582	0.925228
265	GO:0009791	post-embryonic development	16 (2.89%)	381 (2.47%)	0.296970	0.928950
266	GO:0006970	response to osmotic stress	10 (1.81%)	228 (1.48%)	0.305293	0.928950
267	GO:0015696	ammonium transport	1 (0.18%)	10 (0.06%)	0.306645	0.928950
268	GO:0019852	L-ascorbic acid metabolic process	1 (0.18%)	10 (0.06%)	0.306645	0.928950
269	GO:0033692	cellular polysaccharide biosynthetic process	1 (0.18%)	10 (0.06%)	0.306645	0.928950
270	GO:0034637	cellular carbohydrate biosynthetic process	1 (0.18%)	10 (0.06%)	0.306645	0.928950
271	GO:0051783	regulation of nuclear division	1 (0.18%)	10 (0.06%)	0.306645	0.928950
272	GO:0098656	anion transmembrane transport	1 (0.18%)	10 (0.06%)	0.306645	0.928950
273	GO:0009112	nucleobase metabolic process	2 (0.36%)	31 (0.2%)	0.307005	0.928950
274	GO:0009414	response to water deprivation	2 (0.36%)	31 (0.2%)	0.307005	0.928950
275	GO:0046471	phosphatidylglycerol metabolic process	3 (0.54%)	54 (0.35%)	0.307045	0.928950
276	GO:0006816	calcium ion transport	2 (0.36%)	32 (0.21%)	0.320377	0.965774
277	GO:0090567	reproductive shoot system development	7 (1.26%)	156 (1.01%)	0.329481	0.981778
278	GO:0006323	DNA packaging	1 (0.18%)	11 (0.07%)	0.331586	0.981778
279	GO:0006549	isoleucine metabolic process	1 (0.18%)	11 (0.07%)	0.331586	0.981778
280	GO:0006555	methionine metabolic process	1 (0.18%)	11 (0.07%)	0.331586	0.981778
281	GO:0009084	glutamine family amino acid biosynthetic process	1 (0.18%)	11 (0.07%)	0.331586	0.981778
282	GO:0048519	negative regulation of biological process	17 (3.07%)	418 (2.71%)	0.335303	0.989261
283	GO:0009607	response to biotic stimulus	13 (2.35%)	315 (2.04%)	0.344934	0.999990

284	GO:0043207	response to external biotic stimulus	13 (2.35%)	315 (2.04%)	0.344934	0.999990
285	GO:0009415	response to water	2 (0.36%)	34 (0.22%)	0.346917	0.999990
286	GO:0048367	shoot system development	9 (1.62%)	211 (1.37%)	0.348237	0.999990
287	GO:0016109	tetraterpenoid biosynthetic process	4 (0.72%)	83 (0.54%)	0.348994	0.999990
288	GO:0008610	lipid biosynthetic process	16 (2.89%)	397 (2.58%)	0.355336	0.999990
289	GO:0042742	defense response to bacterium	1 (0.18%)	12 (0.08%)	0.355632	0.999990
290	GO:0044743	intracellular protein transmembrane import	1 (0.18%)	12 (0.08%)	0.355632	0.999990
291	GO:0071554	cell wall organization or biogenesis	11 (1.99%)	266 (1.73%)	0.360832	0.999990
292	GO:0072527	pyrimidine-containing compound metabolic process	6 (1.08%)	136 (0.88%)	0.364069	0.999990
293	GO:0000302	response to reactive oxygen species	4 (0.72%)	85 (0.55%)	0.365442	0.999990
294	GO:0034285	response to disaccharide	4 (0.72%)	85 (0.55%)	0.365442	0.999990
295	GO:0002252	immune effector process	2 (0.36%)	36 (0.23%)	0.373104	0.999990
296	GO:0006714	sesquiterpenoid metabolic process	2 (0.36%)	36 (0.23%)	0.373104	0.999990
297	GO:0016108	tetraterpenoid metabolic process	4 (0.72%)	86 (0.56%)	0.373661	0.999990
298	GO:0071229	cellular response to acid chemical	4 (0.72%)	86 (0.56%)	0.373661	0.999990
299	GO:0007005	mitochondrion organization	1 (0.18%)	13 (0.08%)	0.378814	0.999990
300	GO:0008154	actin polymerization or depolymerization	1 (0.18%)	13 (0.08%)	0.378814	0.999990
301	GO:0010565	regulation of cellular ketone metabolic process	1 (0.18%)	13 (0.08%)	0.378814	0.999990
302	GO:0043241	protein complex disassembly	1 (0.18%)	13 (0.08%)	0.378814	0.999990
303	GO:0043624	cellular protein complex disassembly	1 (0.18%)	13 (0.08%)	0.378814	0.999990
304	GO:0046916	cellular transition metal ion homeostasis	1 (0.18%)	13 (0.08%)	0.378814	0.999990
305	GO:0009743	response to carbohydrate	7 (1.26%)	165 (1.07%)	0.382377	0.999990
306	GO:0018208	peptidyl-proline modification	2 (0.36%)	37 (0.24%)	0.386039	0.999990
307	GO:0034762	regulation of transmembrane transport	2 (0.36%)	37 (0.24%)	0.386039	0.999990
308	GO:0034765	regulation of ion transmembrane transport	2 (0.36%)	37 (0.24%)	0.386039	0.999990
309	GO:0006873	cellular ion homeostasis	3 (0.54%)	62 (0.4%)	0.386206	0.999990
310	GO:0055082	cellular chemical homeostasis	3 (0.54%)	62 (0.4%)	0.386206	0.999990
311	GO:0051186	cofactor metabolic process	18 (3.25%)	459 (2.98%)	0.386288	0.999990
312	GO:0016568	chromatin modification	11 (1.99%)	273 (1.77%)	0.392990	0.999990
313	GO:0006551	leucine metabolic process	1 (0.18%)	14 (0.09%)	0.401163	0.999990
314	GO:0022411	cellular component disassembly	1 (0.18%)	14 (0.09%)	0.401163	0.999990
315	GO:0032984	macromolecular complex disassembly	1 (0.18%)	14 (0.09%)	0.401163	0.999990
316	GO:0051302	regulation of cell division	1 (0.18%)	14 (0.09%)	0.401163	0.999990
317	GO:0055067	monovalent inorganic cation homeostasis	1 (0.18%)	14 (0.09%)	0.401163	0.999990
318	GO:0065002	intracellular protein transmembrane transport	1 (0.18%)	14 (0.09%)	0.401163	0.999990
319	GO:0009605	response to external stimulus	19 (3.43%)	491 (3.19%)	0.403875	0.999990
320	GO:0044699	single-organism process	292 (52.71%)	8039	0.414125	0.999990

				(52.16%)		
321	GO:0008202	steroid metabolic process	6 (1.08%)	144 (0.93%)	0.415657	0.999990
322	GO:0051188	cofactor biosynthetic process	8 (1.44%)	198 (1.28%)	0.419215	0.999990
323	GO:0006952	defense response	9 (1.62%)	225 (1.46%)	0.420052	0.999990
324	GO:0005982	starch metabolic process	6 (1.08%)	145 (0.94%)	0.422088	0.999990
325	GO:0019566	arabinose metabolic process	1 (0.18%)	15 (0.1%)	0.422710	0.999990
326	GO:0030258	lipid modification	1 (0.18%)	15 (0.1%)	0.422710	0.999990
327	GO:0033554	cellular response to stress	15 (2.71%)	390 (2.53%)	0.431667	0.999990
328	GO:0019219	regulation of nucleobase-containing compound metabolic process	16 (2.89%)	418 (2.71%)	0.434634	0.999990
329	GO:0009668	plastid membrane organization	6 (1.08%)	147 (0.95%)	0.434920	0.999990
330	GO:1901701	cellular response to oxygen-containing compound	6 (1.08%)	148 (0.96%)	0.441318	0.999990
331	GO:0006084	acetyl-CoA metabolic process	1 (0.18%)	16 (0.1%)	0.443483	0.999990
332	GO:0007186	G-protein coupled receptor signaling pathway	1 (0.18%)	16 (0.1%)	0.443483	0.999990
333	GO:0009085	lysine biosynthetic process	1 (0.18%)	16 (0.1%)	0.443483	0.999990
334	GO:0009608	response to symbiont	1 (0.18%)	16 (0.1%)	0.443483	0.999990
335	GO:0051640	organelle localization	1 (0.18%)	16 (0.1%)	0.443483	0.999990
336	GO:0071806	protein transmembrane transport	1 (0.18%)	16 (0.1%)	0.443483	0.999990
337	GO:0010243	response to organonitrogen compound	3 (0.54%)	68 (0.44%)	0.444211	0.999990
338	GO:0080090	regulation of primary metabolic process	23 (4.15%)	615 (3.99%)	0.453072	0.999990
339	GO:0044802	single-organism membrane organization	7 (1.26%)	177 (1.15%)	0.453128	0.999990
340	GO:0002376	immune system process	7 (1.26%)	178 (1.16%)	0.458973	0.999990
341	GO:0006073	cellular glucan metabolic process	12 (2.17%)	315 (2.04%)	0.460374	0.999990
342	GO:0032446	protein modification by small protein conjugation	12 (2.17%)	315 (2.04%)	0.460374	0.999990
343	GO:0071396	cellular response to lipid	2 (0.36%)	43 (0.28%)	0.460907	0.999990
344	GO:0050790	regulation of catalytic activity	5 (0.9%)	124 (0.8%)	0.461752	0.999990
345	GO:0009308	amine metabolic process	4 (0.72%)	97 (0.63%)	0.462793	0.999990
346	GO:0006839	mitochondrial transport	1 (0.18%)	17 (0.11%)	0.463509	0.999990
347	GO:0044281	small molecule metabolic process	77 (13.9%)	2115 (13.72%)	0.470873	0.999990
348	GO:0009108	coenzyme biosynthetic process	3 (0.54%)	71 (0.46%)	0.472410	0.999990
349	GO:0009850	auxin metabolic process	2 (0.36%)	44 (0.29%)	0.472867	0.999990
350	GO:0006355	regulation of transcription, DNA-templated	13 (2.35%)	346 (2.25%)	0.475444	0.999990
351	GO:1903506	regulation of nucleic acid-templated transcription	13 (2.35%)	346 (2.25%)	0.475444	0.999990
352	GO:0009755	hormone-mediated signaling pathway	12 (2.17%)	319 (2.07%)	0.477916	0.999990
353	GO:0032870	cellular response to hormone stimulus	12 (2.17%)	319 (2.07%)	0.477916	0.999990
354	GO:0071495	cellular response to endogenous stimulus	12 (2.17%)	319 (2.07%)	0.477916	0.999990

355	GO:0046165	alcohol biosynthetic process	4 (0.72%)	99 (0.64%)	0.478572	0.999990
356	GO:0061024	membrane organization	8 (1.44%)	209 (1.36%)	0.479152	0.999990
357	GO:0006778	porphyrin-containing compound metabolic process	7 (1.26%)	182 (1.18%)	0.482211	0.999990
358	GO:0006779	porphyrin-containing compound biosynthetic process	5 (0.9%)	127 (0.82%)	0.482638	0.999990
359	GO:0006928	movement of cell or subcellular component	1 (0.18%)	18 (0.12%)	0.482817	0.999990
360	GO:0046148	pigment biosynthetic process	1 (0.18%)	18 (0.12%)	0.482817	0.999990
361	GO:0048528	post-embryonic root development	1 (0.18%)	18 (0.12%)	0.482817	0.999990
362	GO:0048608	reproductive structure development	8 (1.44%)	210 (1.36%)	0.484538	0.999990
363	GO:0061458	reproductive system development	8 (1.44%)	210 (1.36%)	0.484538	0.999990
364	GO:0019220	regulation of phosphate metabolic process	2 (0.36%)	45 (0.29%)	0.484666	0.999990
365	GO:0051174	regulation of phosphorus metabolic process	2 (0.36%)	45 (0.29%)	0.484666	0.999990
366	GO:0007275	multicellular organism development	30 (5.42%)	819 (5.31%)	0.484838	0.999990
367	GO:0009698	phenylpropanoid metabolic process	4 (0.72%)	100 (0.65%)	0.486394	0.999990
368	GO:0009628	response to abiotic stimulus	30 (5.42%)	820 (5.32%)	0.487608	0.999990
369	GO:0048878	chemical homeostasis	5 (0.9%)	128 (0.83%)	0.489540	0.999990
370	GO:0033013	tetrapyrrole metabolic process	7 (1.26%)	184 (1.19%)	0.493728	0.999990
371	GO:0044723	single-organism carbohydrate metabolic process	19 (3.43%)	517 (3.35%)	0.494244	0.999990
372	GO:0044264	cellular polysaccharide metabolic process	12 (2.17%)	323 (2.1%)	0.495353	0.999990
373	GO:0009812	flavonoid metabolic process	2 (0.36%)	46 (0.3%)	0.496300	0.999990
374	GO:0010053	root epidermal cell differentiation	2 (0.36%)	46 (0.3%)	0.496300	0.999990
375	GO:0019321	pentose metabolic process	2 (0.36%)	46 (0.3%)	0.496300	0.999990
376	GO:0033993	response to lipid	2 (0.36%)	46 (0.3%)	0.496300	0.999990
377	GO:0090627	plant epidermal cell differentiation	2 (0.36%)	46 (0.3%)	0.496300	0.999990
378	GO:2001141	regulation of RNA biosynthetic process	13 (2.35%)	351 (2.28%)	0.496378	0.999990
379	GO:0033014	tetrapyrrole biosynthetic process	5 (0.9%)	129 (0.84%)	0.496407	0.999990
380	GO:0090501	RNA phosphodiester bond hydrolysis	3 (0.54%)	74 (0.48%)	0.499940	0.999990
381	GO:0065008	regulation of biological quality	19 (3.43%)	519 (3.37%)	0.501141	0.999990
382	GO:0006222	UMP biosynthetic process	1 (0.18%)	19 (0.12%)	0.501430	0.999990
383	GO:0009739	response to gibberellin	1 (0.18%)	19 (0.12%)	0.501430	0.999990
384	GO:0010476	gibberellin mediated signaling pathway	1 (0.18%)	19 (0.12%)	0.501430	0.999990
385	GO:0046049	UMP metabolic process	1 (0.18%)	19 (0.12%)	0.501430	0.999990
386	GO:0071370	cellular response to gibberellin stimulus	1 (0.18%)	19 (0.12%)	0.501430	0.999990
387	GO:0007049	cell cycle	15 (2.71%)	408 (2.65%)	0.502061	0.999990
388	GO:0051276	chromosome organization	20 (3.61%)	548 (3.56%)	0.505138	0.999990
389	GO:0006586	indolalkylamine metabolic process	2 (0.36%)	47 (0.3%)	0.507764	0.999990
390	GO:0006787	porphyrin-containing compound catabolic process	2 (0.36%)	47 (0.3%)	0.507764	0.999990

391	GO:0033015	tetrapyrrole catabolic process	2 (0.36%)	47 (0.3%)	0.507764	0.999990
392	GO:0042546	cell wall biogenesis	2 (0.36%)	47 (0.3%)	0.507764	0.999990
393	GO:0051187	cofactor catabolic process	2 (0.36%)	47 (0.3%)	0.507764	0.999990
394	GO:0035194	posttranscriptional gene silencing by RNA	3 (0.54%)	75 (0.49%)	0.508954	0.999990
395	GO:0090305	nucleic acid phosphodiester bond hydrolysis	3 (0.54%)	75 (0.49%)	0.508954	0.999990
396	GO:1901617	organic hydroxy compound biosynthetic process	4 (0.72%)	103 (0.67%)	0.509566	0.999990
397	GO:0051252	regulation of RNA metabolic process	13 (2.35%)	356 (2.31%)	0.517124	0.999990
398	GO:0012501	programmed cell death	2 (0.36%)	48 (0.31%)	0.519058	0.999990
399	GO:0009173	pyrimidine ribonucleoside monophosphate metabolic process	1 (0.18%)	20 (0.13%)	0.519375	0.999990
400	GO:0009174	pyrimidine ribonucleoside monophosphate biosynthetic process	1 (0.18%)	20 (0.13%)	0.519375	0.999990
401	GO:0006955	immune response	5 (0.9%)	133 (0.86%)	0.523516	0.999990
402	GO:0009617	response to bacterium	5 (0.9%)	133 (0.86%)	0.523516	0.999990
403	GO:0045087	innate immune response	5 (0.9%)	133 (0.86%)	0.523516	0.999990
404	GO:0000041	transition metal ion transport	3 (0.54%)	77 (0.5%)	0.526723	0.999990
405	GO:0016143	S-glycoside metabolic process	3 (0.54%)	77 (0.5%)	0.526723	0.999990
406	GO:0019757	glycosinolate metabolic process	3 (0.54%)	77 (0.5%)	0.526723	0.999990
407	GO:0040007	growth	6 (1.08%)	162 (1.05%)	0.528784	0.999990
408	GO:0071702	organic substance transport	34 (6.14%)	947 (6.14%)	0.529284	0.999990
409	GO:1901607	alpha-amino acid biosynthetic process	2 (0.36%)	49 (0.32%)	0.530177	0.999990
410	GO:0006006	glucose metabolic process	4 (0.72%)	106 (0.69%)	0.532254	0.999990
411	GO:0006979	response to oxidative stress	4 (0.72%)	106 (0.69%)	0.532254	0.999990
412	GO:0006875	cellular metal ion homeostasis	1 (0.18%)	21 (0.14%)	0.536675	0.999990
413	GO:0009226	nucleotide-sugar biosynthetic process	1 (0.18%)	21 (0.14%)	0.536675	0.999990
414	GO:0042440	pigment metabolic process	1 (0.18%)	21 (0.14%)	0.536675	0.999990
415	GO:0006732	coenzyme metabolic process	12 (2.17%)	333 (2.16%)	0.538296	0.999990
416	GO:0010035	response to inorganic substance	5 (0.9%)	136 (0.88%)	0.543426	0.999990
417	GO:0016441	posttranscriptional gene silencing	3 (0.54%)	79 (0.51%)	0.544130	0.999990
418	GO:0044767	single-organism developmental process	39 (7.04%)	1094 (7.1%)	0.546701	0.999990
419	GO:0044765	single-organism transport	61 (11.01%)	1710 (11.1%)	0.546763	0.999990
420	GO:0044712	single-organism catabolic process	5 (0.9%)	137 (0.89%)	0.549976	0.999990
421	GO:0006525	arginine metabolic process	1 (0.18%)	22 (0.14%)	0.553354	0.999990
422	GO:0009409	response to cold	4 (0.72%)	109 (0.71%)	0.554412	0.999990
423	GO:0006721	terpenoid metabolic process	7 (1.26%)	195 (1.27%)	0.555465	0.999990
424	GO:0006220	pyrimidine nucleotide metabolic process	4 (0.72%)	110 (0.71%)	0.561673	0.999990
425	GO:0006694	steroid biosynthetic process	4 (0.72%)	110 (0.71%)	0.561673	0.999990
426	GO:0016114	terpenoid biosynthetic process	4 (0.72%)	110 (0.71%)	0.561673	0.999990
427	GO:0042044	fluid transport	2 (0.36%)	52 (0.34%)	0.562470	0.999990
428	GO:0034645	cellular macromolecule biosynthetic process	55 (9.93%)	1550 (10.06%)	0.562832	0.999990

429	GO:0065009	regulation of molecular function	5 (0.9%)	139 (0.9%)	0.562937	0.999990
430	GO:0031323	regulation of cellular metabolic process	23 (4.15%)	651 (4.22%)	0.565300	0.999990
431	GO:0009653	anatomical structure morphogenesis	18 (3.25%)	510 (3.31%)	0.566554	0.999990
432	GO:0000271	polysaccharide biosynthetic process	1 (0.18%)	23 (0.15%)	0.569433	0.999990
433	GO:0006612	protein targeting to membrane	1 (0.18%)	23 (0.15%)	0.569433	0.999990
434	GO:0009130	pyrimidine nucleoside monophosphate biosynthetic process	1 (0.18%)	23 (0.15%)	0.569433	0.999990
435	GO:0009218	pyrimidine ribonucleotide metabolic process	1 (0.18%)	23 (0.15%)	0.569433	0.999990
436	GO:0009220	pyrimidine ribonucleotide biosynthetic process	1 (0.18%)	23 (0.15%)	0.569433	0.999990
437	GO:0009813	flavonoid biosynthetic process	1 (0.18%)	23 (0.15%)	0.569433	0.999990
438	GO:0010087	phloem or xylem histogenesis	1 (0.18%)	23 (0.15%)	0.569433	0.999990
439	GO:0046132	pyrimidine ribonucleoside biosynthetic process	1 (0.18%)	23 (0.15%)	0.569433	0.999990
440	GO:0046134	pyrimidine nucleoside biosynthetic process	1 (0.18%)	23 (0.15%)	0.569433	0.999990
441	GO:0009072	aromatic amino acid family metabolic process	3 (0.54%)	82 (0.53%)	0.569529	0.999990
442	GO:0051707	response to other organism	11 (1.99%)	312 (2.02%)	0.569662	0.999990
443	GO:0010817	regulation of hormone levels	4 (0.72%)	112 (0.73%)	0.576000	0.999990
444	GO:0050801	ion homeostasis	4 (0.72%)	112 (0.73%)	0.576000	0.999990
445	GO:0072528	pyrimidine-containing compound biosynthetic process	4 (0.72%)	112 (0.73%)	0.576000	0.999990
446	GO:0071822	protein complex subunit organization	16 (2.89%)	457 (2.97%)	0.579700	0.999990
447	GO:1902578	single-organism localization	61 (11.01%)	1728 (11.21%)	0.581691	0.999990
448	GO:0006650	glycerophospholipid metabolic process	7 (1.26%)	200 (1.3%)	0.582421	0.999990
449	GO:0010015	root morphogenesis	2 (0.36%)	54 (0.35%)	0.583100	0.999990
450	GO:0044786	cell cycle DNA replication	2 (0.36%)	54 (0.35%)	0.583100	0.999990
451	GO:0005985	sucrose metabolic process	1 (0.18%)	24 (0.16%)	0.584934	0.999990
452	GO:0016051	carbohydrate biosynthetic process	1 (0.18%)	24 (0.16%)	0.584934	0.999990
453	GO:0006644	phospholipid metabolic process	8 (1.44%)	230 (1.49%)	0.588198	0.999990
454	GO:0044283	small molecule biosynthetic process	16 (2.89%)	461 (2.99%)	0.593849	0.999990
455	GO:0006091	generation of precursor metabolites and energy	12 (2.17%)	347 (2.25%)	0.596190	0.999990
456	GO:0005991	trehalose metabolic process	1 (0.18%)	25 (0.16%)	0.599878	0.999990
457	GO:0009129	pyrimidine nucleoside monophosphate metabolic process	1 (0.18%)	25 (0.16%)	0.599878	0.999990
458	GO:0009683	indoleacetic acid metabolic process	1 (0.18%)	25 (0.16%)	0.599878	0.999990
459	GO:0009692	ethylene metabolic process	1 (0.18%)	25 (0.16%)	0.599878	0.999990
460	GO:0019932	second-messenger-mediated signaling	1 (0.18%)	25 (0.16%)	0.599878	0.999990
461	GO:0031123	RNA 3'-end processing	1 (0.18%)	25 (0.16%)	0.599878	0.999990
462	GO:0043449	cellular alkene metabolic process	1 (0.18%)	25 (0.16%)	0.599878	0.999990

463	GO:1900673	olefin metabolic process	1 (0.18%)	25 (0.16%)	0.599878	0.999990
464	GO:0098542	defense response to other organism	3 (0.54%)	86 (0.56%)	0.602002	0.999990
465	GO:0008219	cell death	2 (0.36%)	56 (0.36%)	0.603004	0.999990
466	GO:0042430	indole-containing compound metabolic process	2 (0.36%)	56 (0.36%)	0.603004	0.999990
467	GO:0016310	phosphorylation	6 (1.08%)	176 (1.14%)	0.610120	0.999990
468	GO:1901605	alpha-amino acid metabolic process	10 (1.81%)	294 (1.91%)	0.616039	0.999990
469	GO:0016458	gene silencing	8 (1.44%)	236 (1.53%)	0.617316	0.999990
470	GO:0006261	DNA-dependent DNA replication	2 (0.36%)	58 (0.38%)	0.622181	0.999990
471	GO:0030001	metal ion transport	11 (1.99%)	325 (2.11%)	0.624082	0.999990
472	GO:0042743	hydrogen peroxide metabolic process	5 (0.9%)	149 (0.97%)	0.624739	0.999990
473	GO:0071555	cell wall organization	5 (0.9%)	149 (0.97%)	0.624739	0.999990
474	GO:0006720	isoprenoid metabolic process	8 (1.44%)	239 (1.55%)	0.631462	0.999990
475	GO:0009756	carbohydrate mediated signaling	2 (0.36%)	59 (0.38%)	0.631498	0.999990
476	GO:0071322	cellular response to carbohydrate stimulus	2 (0.36%)	59 (0.38%)	0.631498	0.999990
477	GO:0046486	glycerolipid metabolic process	7 (1.26%)	210 (1.36%)	0.633810	0.999990
478	GO:0019748	secondary metabolic process	8 (1.44%)	240 (1.56%)	0.636113	0.999990
479	GO:0009725	response to hormone	14 (2.53%)	416 (2.7%)	0.638447	0.999990
480	GO:0009081	branched-chain amino acid metabolic process	1 (0.18%)	28 (0.18%)	0.641565	0.999990
481	GO:0017038	protein import	1 (0.18%)	28 (0.18%)	0.641565	0.999990
482	GO:0006812	cation transport	19 (3.43%)	563 (3.65%)	0.645323	0.999990
483	GO:0009746	response to hexose	2 (0.36%)	61 (0.4%)	0.649593	0.999990
484	GO:0034284	response to monosaccharide	2 (0.36%)	61 (0.4%)	0.649593	0.999990
485	GO:0051235	maintenance of location	2 (0.36%)	61 (0.4%)	0.649593	0.999990
486	GO:0016053	organic acid biosynthetic process	12 (2.17%)	362 (2.35%)	0.654350	0.999990
487	GO:0046394	carboxylic acid biosynthetic process	12 (2.17%)	362 (2.35%)	0.654350	0.999990
488	GO:0006213	pyrimidine nucleoside metabolic process	1 (0.18%)	29 (0.19%)	0.654473	0.999990
489	GO:0046131	pyrimidine ribonucleoside metabolic process	1 (0.18%)	29 (0.19%)	0.654473	0.999990
490	GO:0009658	chloroplast organization	3 (0.54%)	93 (0.6%)	0.654823	0.999990
491	GO:0010038	response to metal ion	3 (0.54%)	93 (0.6%)	0.654823	0.999990
492	GO:0043933	macromolecular complex subunit organization	28 (5.05%)	828 (5.37%)	0.660142	0.999990
493	GO:0010629	negative regulation of gene expression	8 (1.44%)	246 (1.6%)	0.663321	0.999990
494	GO:0000160	phosphorelay signal transduction system	1 (0.18%)	30 (0.19%)	0.666918	0.999990
495	GO:0009067	aspartate family amino acid biosynthetic process	1 (0.18%)	30 (0.19%)	0.666918	0.999990
496	GO:0009225	nucleotide-sugar metabolic process	1 (0.18%)	30 (0.19%)	0.666918	0.999990
497	GO:0009814	defense response, incompatible interaction	2 (0.36%)	63 (0.41%)	0.666975	0.999990

498	GO:0032268	regulation of cellular protein metabolic process	7 (1.26%)	217 (1.41%)	0.667556	0.999990
499	GO:0051246	regulation of protein metabolic process	7 (1.26%)	217 (1.41%)	0.667556	0.999990
500	GO:0051171	regulation of nitrogen compound metabolic process	16 (2.89%)	483 (3.13%)	0.667739	0.999990
501	GO:0009719	response to endogenous stimulus	15 (2.71%)	454 (2.95%)	0.668570	0.999990
502	GO:0008299	isoprenoid biosynthetic process	4 (0.72%)	127 (0.82%)	0.674416	0.999990
503	GO:0006739	NADP metabolic process	5 (0.9%)	158 (1.03%)	0.675640	0.999990
504	GO:0001558	regulation of cell growth	1 (0.18%)	31 (0.2%)	0.678915	0.999990
505	GO:0042127	regulation of cell proliferation	1 (0.18%)	31 (0.2%)	0.678915	0.999990
506	GO:0070647	protein modification by small protein conjugation or removal	12 (2.17%)	369 (2.39%)	0.679872	0.999990
507	GO:0071103	DNA conformation change	3 (0.54%)	97 (0.63%)	0.682665	0.999990
508	GO:0072593	reactive oxygen species metabolic process	5 (0.9%)	160 (1.04%)	0.686306	0.999990
509	GO:0007154	cell communication	28 (5.05%)	839 (5.44%)	0.687073	0.999990
510	GO:0006996	organelle organization	43 (7.76%)	1272 (8.25%)	0.688648	0.999990
511	GO:0031326	regulation of cellular biosynthetic process	14 (2.53%)	431 (2.8%)	0.689582	0.999990
512	GO:0006869	lipid transport	1 (0.18%)	32 (0.21%)	0.690481	0.999990
513	GO:0009664	plant-type cell wall organization	1 (0.18%)	32 (0.21%)	0.690481	0.999990
514	GO:0009826	unidimensional cell growth	1 (0.18%)	32 (0.21%)	0.690481	0.999990
515	GO:0010876	lipid localization	1 (0.18%)	32 (0.21%)	0.690481	0.999990
516	GO:0031347	regulation of defense response	1 (0.18%)	32 (0.21%)	0.690481	0.999990
517	GO:0072657	protein localization to membrane	1 (0.18%)	32 (0.21%)	0.690481	0.999990
518	GO:0090150	establishment of protein localization to membrane	1 (0.18%)	32 (0.21%)	0.690481	0.999990
519	GO:0010383	cell wall polysaccharide metabolic process	2 (0.36%)	66 (0.43%)	0.691735	0.999990
520	GO:0009059	macromolecule biosynthetic process	56 (10.11%)	1646 (10.68%)	0.692023	0.999990
521	GO:0010033	response to organic substance	27 (4.87%)	816 (5.29%)	0.701444	0.999990
522	GO:0008037	cell recognition	2 (0.36%)	68 (0.44%)	0.707385	0.999990
523	GO:0090558	plant epidermis development	2 (0.36%)	68 (0.44%)	0.707385	0.999990
524	GO:0009620	response to fungus	3 (0.54%)	101 (0.66%)	0.708802	0.999990
525	GO:0010941	regulation of cell death	3 (0.54%)	101 (0.66%)	0.708802	0.999990
526	GO:0043067	regulation of programmed cell death	3 (0.54%)	101 (0.66%)	0.708802	0.999990
527	GO:0060560	developmental growth involved in morphogenesis	1 (0.18%)	34 (0.22%)	0.712379	0.999990
528	GO:0016144	S-glycoside biosynthetic process	2 (0.36%)	69 (0.45%)	0.714958	0.999990
529	GO:0019758	glycosinolate biosynthetic process	2 (0.36%)	69 (0.45%)	0.714958	0.999990
530	GO:0055080	cation homeostasis	2 (0.36%)	69 (0.45%)	0.714958	0.999990
531	GO:0046496	nicotinamide nucleotide metabolic process	5 (0.9%)	166 (1.08%)	0.716866	0.999990

532	GO:0006790	sulfur compound metabolic process	11 (1.99%)	350 (2.27%)	0.717938	0.999990
533	GO:0098771	inorganic ion homeostasis	2 (0.36%)	70 (0.45%)	0.722367	0.999990
534	GO:0000723	telomere maintenance	1 (0.18%)	35 (0.23%)	0.722742	0.999990
535	GO:0032200	telomere organization	1 (0.18%)	35 (0.23%)	0.722742	0.999990
536	GO:2000112	regulation of cellular macromolecule biosynthetic process	13 (2.35%)	413 (2.68%)	0.727250	0.999990
537	GO:0006221	pyrimidine nucleotide biosynthetic process	3 (0.54%)	104 (0.67%)	0.727298	0.999990
538	GO:1901361	organic cyclic compound catabolic process	4 (0.72%)	137 (0.89%)	0.730601	0.999990
539	GO:0019362	pyridine nucleotide metabolic process	5 (0.9%)	169 (1.1%)	0.731332	0.999990
540	GO:0006544	glycine metabolic process	1 (0.18%)	36 (0.23%)	0.732731	0.999990
541	GO:0032844	regulation of homeostatic process	1 (0.18%)	36 (0.23%)	0.732731	0.999990
542	GO:0060249	anatomical structure homeostasis	1 (0.18%)	36 (0.23%)	0.732731	0.999990
543	GO:0080134	regulation of response to stress	1 (0.18%)	36 (0.23%)	0.732731	0.999990
544	GO:0051704	multi-organism process	11 (1.99%)	355 (2.3%)	0.734787	0.999990
545	GO:0048285	organelle fission	4 (0.72%)	139 (0.9%)	0.740920	0.999990
546	GO:0006468	protein phosphorylation	3 (0.54%)	107 (0.69%)	0.744862	0.999990
547	GO:0048856	anatomical structure development	28 (5.05%)	865 (5.61%)	0.745934	0.999990
548	GO:0003006	developmental process involved in reproduction	20 (3.61%)	629 (4.08%)	0.746527	0.999990
549	GO:0006568	tryptophan metabolic process	1 (0.18%)	38 (0.25%)	0.751646	0.999990
550	GO:0043473	pigmentation	1 (0.18%)	38 (0.25%)	0.751646	0.999990
551	GO:0043476	pigment accumulation	1 (0.18%)	38 (0.25%)	0.751646	0.999990
552	GO:0043478	pigment accumulation in response to UV light	1 (0.18%)	38 (0.25%)	0.751646	0.999990
553	GO:0043479	pigment accumulation in tissues in response to UV light	1 (0.18%)	38 (0.25%)	0.751646	0.999990
554	GO:0043480	pigment accumulation in tissues	1 (0.18%)	38 (0.25%)	0.751646	0.999990
555	GO:0010556	regulation of macromolecule biosynthetic process	13 (2.35%)	422 (2.74%)	0.754418	0.999990
556	GO:0009889	regulation of biosynthetic process	14 (2.53%)	453 (2.94%)	0.756436	0.999990
557	GO:0072524	pyridine-containing compound metabolic process	5 (0.9%)	175 (1.14%)	0.758641	0.999990
558	GO:0031047	gene silencing by RNA	3 (0.54%)	110 (0.71%)	0.761513	0.999990
559	GO:0016072	rRNA metabolic process	7 (1.26%)	240 (1.56%)	0.764203	0.999990
560	GO:0051273	beta-glucan metabolic process	4 (0.72%)	144 (0.93%)	0.765403	0.999990
561	GO:0006576	cellular biogenic amine metabolic process	2 (0.36%)	77 (0.5%)	0.769781	0.999990
562	GO:0044106	cellular amine metabolic process	2 (0.36%)	77 (0.5%)	0.769781	0.999990
563	GO:0007165	signal transduction	24 (4.33%)	760 (4.93%)	0.773973	0.999990
564	GO:0016049	cell growth	2 (0.36%)	78 (0.51%)	0.775947	0.999990
565	GO:0023052	signaling	24 (4.33%)	761 (4.94%)	0.776079	0.999990
566	GO:0044700	single organism signaling	24 (4.33%)	761 (4.94%)	0.776079	0.999990

567	GO:0016054	organic acid catabolic process	3 (0.54%)	113 (0.73%)	0.777273	0.999990
568	GO:0046395	carboxylic acid catabolic process	3 (0.54%)	113 (0.73%)	0.777273	0.999990
569	GO:0016101	diterpenoid metabolic process	1 (0.18%)	41 (0.27%)	0.777541	0.999990
570	GO:0055076	transition metal ion homeostasis	1 (0.18%)	41 (0.27%)	0.777541	0.999990
571	GO:0035556	intracellular signal transduction	8 (1.44%)	276 (1.79%)	0.779994	0.999990
572	GO:0000226	microtubule cytoskeleton organization	1 (0.18%)	42 (0.27%)	0.785560	0.999990
573	GO:0006997	nucleus organization	1 (0.18%)	42 (0.27%)	0.785560	0.999990
574	GO:0006733	oxidoreduction coenzyme metabolic process	5 (0.9%)	185 (1.2%)	0.799439	0.999990
575	GO:0050794	regulation of cellular process	58 (10.47%)	1773 (11.5%)	0.799893	0.999990
576	GO:0009416	response to light stimulus	13 (2.35%)	439 (2.85%)	0.800639	0.999990
577	GO:0008033	tRNA processing	1 (0.18%)	44 (0.29%)	0.800741	0.999990
578	GO:0044282	small molecule catabolic process	3 (0.54%)	118 (0.77%)	0.801631	0.999990
579	GO:0044707	single-multicellular organism process	31 (5.6%)	983 (6.38%)	0.802466	0.999990
580	GO:0003002	regionalization	2 (0.36%)	83 (0.54%)	0.804654	0.999990
581	GO:0016071	mRNA metabolic process	2 (0.36%)	83 (0.54%)	0.804654	0.999990
582	GO:0071310	cellular response to organic substance	14 (2.53%)	472 (3.06%)	0.805874	0.999990
583	GO:0006664	glycolipid metabolic process	1 (0.18%)	45 (0.29%)	0.807925	0.999990
584	GO:0009767	photosynthetic electron transport chain	1 (0.18%)	45 (0.29%)	0.807925	0.999990
585	GO:0010212	response to ionizing radiation	1 (0.18%)	45 (0.29%)	0.807925	0.999990
586	GO:1903509	liposaccharide metabolic process	1 (0.18%)	45 (0.29%)	0.807925	0.999990
587	GO:0000280	nuclear division	3 (0.54%)	120 (0.78%)	0.810730	0.999990
588	GO:0070887	cellular response to chemical stimulus	14 (2.53%)	475 (3.08%)	0.812972	0.999990
589	GO:0032501	multicellular organismal process	31 (5.6%)	991 (6.43%)	0.815978	0.999990
590	GO:1901657	glycosyl compound metabolic process	4 (0.72%)	157 (1.02%)	0.820606	0.999990
591	GO:0051716	cellular response to stimulus	38 (6.86%)	1202 (7.8%)	0.820838	0.999990
592	GO:0006101	citrate metabolic process	1 (0.18%)	47 (0.3%)	0.821526	0.999990
593	GO:0009793	embryo development ending in seed dormancy	1 (0.18%)	47 (0.3%)	0.821526	0.999990
594	GO:0072350	tricarboxylic acid metabolic process	1 (0.18%)	47 (0.3%)	0.821526	0.999990
595	GO:0009799	specification of symmetry	1 (0.18%)	48 (0.31%)	0.827961	0.999990
596	GO:0009639	response to red or far red light	4 (0.72%)	159 (1.03%)	0.828072	0.999990
597	GO:0000003	reproduction	22 (3.97%)	729 (4.73%)	0.830964	0.999990
598	GO:0044702	single organism reproductive process	8 (1.44%)	294 (1.91%)	0.834163	0.999990
599	GO:0033043	regulation of organelle organization	2 (0.36%)	89 (0.58%)	0.834753	0.999990
600	GO:0000725	recombinational repair	1 (0.18%)	50 (0.32%)	0.840145	0.999990
601	GO:0006405	RNA export from nucleus	1 (0.18%)	50 (0.32%)	0.840145	0.999990
602	GO:0070192	chromosome organization involved in meiotic cell cycle	1 (0.18%)	50 (0.32%)	0.840145	0.999990
603	GO:0071669	plant-type cell wall organization or biogenesis	1 (0.18%)	50 (0.32%)	0.840145	0.999990
604	GO:0098655	cation transmembrane transport	1 (0.18%)	50 (0.32%)	0.840145	0.999990
605	GO:1901698	response to nitrogen compound	4 (0.72%)	164 (1.06%)	0.845612	0.999990
606	GO:0051168	nuclear export	1 (0.18%)	51 (0.33%)	0.845911	0.999990

607	GO:1902589	single-organism organelle organization	14 (2.53%)	492 (3.19%)	0.849643	0.999990
608	GO:0044550	secondary metabolite biosynthetic process	3 (0.54%)	130 (0.84%)	0.851087	0.999990
609	GO:0048588	developmental cell growth	1 (0.18%)	52 (0.34%)	0.851468	0.999990
610	GO:0032502	developmental process	44 (7.94%)	1403 (9.1%)	0.852129	0.999990
611	GO:0043648	dicarboxylic acid metabolic process	1 (0.18%)	53 (0.34%)	0.856826	0.999990
612	GO:0019439	aromatic compound catabolic process	3 (0.54%)	132 (0.86%)	0.858196	0.999990
613	GO:0006310	DNA recombination	2 (0.36%)	95 (0.62%)	0.860602	0.999990
614	GO:0051128	regulation of cellular component organization	3 (0.54%)	133 (0.86%)	0.861638	0.999990
615	GO:0009699	phenylpropanoid biosynthetic process	1 (0.18%)	54 (0.35%)	0.861990	0.999990
616	GO:0009790	embryo development	1 (0.18%)	54 (0.35%)	0.861990	0.999990
617	GO:0009863	salicylic acid mediated signaling pathway	1 (0.18%)	54 (0.35%)	0.861990	0.999990
618	GO:0010154	fruit development	1 (0.18%)	54 (0.35%)	0.861990	0.999990
619	GO:0040008	regulation of growth	1 (0.18%)	54 (0.35%)	0.861990	0.999990
620	GO:0048316	seed development	1 (0.18%)	54 (0.35%)	0.861990	0.999990
621	GO:0071446	cellular response to salicylic acid stimulus	1 (0.18%)	54 (0.35%)	0.861990	0.999990
622	GO:0007059	chromosome segregation	2 (0.36%)	96 (0.62%)	0.864532	0.999990
623	GO:0009751	response to salicylic acid	1 (0.18%)	55 (0.36%)	0.866969	0.999990
624	GO:0016246	RNA interference	1 (0.18%)	55 (0.36%)	0.866969	0.999990
625	GO:0030422	production of siRNA involved in RNA interference	1 (0.18%)	55 (0.36%)	0.866969	0.999990
626	GO:0015672	monovalent inorganic cation transport	3 (0.54%)	135 (0.88%)	0.868302	0.999990
627	GO:0044270	cellular nitrogen compound catabolic process	3 (0.54%)	135 (0.88%)	0.868302	0.999990
628	GO:0046700	heterocycle catabolic process	3 (0.54%)	135 (0.88%)	0.868302	0.999990
629	GO:1901659	glycosyl compound biosynthetic process	3 (0.54%)	135 (0.88%)	0.868302	0.999990
630	GO:0006461	protein complex assembly	9 (1.62%)	342 (2.22%)	0.870766	0.999990
631	GO:0009404	toxin metabolic process	1 (0.18%)	56 (0.36%)	0.871769	0.999990
632	GO:0044711	single-organism biosynthetic process	33 (5.96%)	1091 (7.08%)	0.873160	0.999990
633	GO:0070271	protein complex biogenesis	9 (1.62%)	344 (2.23%)	0.874922	0.999990
634	GO:0022414	reproductive process	20 (3.61%)	695 (4.51%)	0.875963	0.999990
635	GO:0006401	RNA catabolic process	1 (0.18%)	57 (0.37%)	0.876395	0.999990
636	GO:0055065	metal ion homeostasis	1 (0.18%)	57 (0.37%)	0.876395	0.999990
637	GO:0009058	biosynthetic process	95 (17.15%)	2921 (18.95%)	0.877754	0.999990
638	GO:0055085	transmembrane transport	3 (0.54%)	139 (0.9%)	0.880787	0.999990
639	GO:0006403	RNA localization	1 (0.18%)	58 (0.38%)	0.880855	0.999990
640	GO:0006625	protein targeting to peroxisome	1 (0.18%)	58 (0.38%)	0.880855	0.999990
641	GO:0019684	photosynthesis, light reaction	1 (0.18%)	58 (0.38%)	0.880855	0.999990
642	GO:0043574	peroxisomal transport	1 (0.18%)	58 (0.38%)	0.880855	0.999990

643	GO:0050657	nucleic acid transport	1 (0.18%)	58 (0.38%)	0.880855	0.999990
644	GO:0050658	RNA transport	1 (0.18%)	58 (0.38%)	0.880855	0.999990
645	GO:0051236	establishment of RNA localization	1 (0.18%)	58 (0.38%)	0.880855	0.999990
646	GO:0072662	protein localization to peroxisome	1 (0.18%)	58 (0.38%)	0.880855	0.999990
647	GO:0072663	establishment of protein localization to peroxisome	1 (0.18%)	58 (0.38%)	0.880855	0.999990
648	GO:0016042	lipid catabolic process	2 (0.36%)	101 (0.66%)	0.882702	0.999990
649	GO:1901576	organic substance biosynthetic process	88 (15.88%)	2733 (17.73%)	0.889423	0.999990
650	GO:0009163	nucleoside biosynthetic process	1 (0.18%)	61 (0.4%)	0.893294	0.999990
651	GO:0042455	ribonucleoside biosynthetic process	1 (0.18%)	61 (0.4%)	0.893294	0.999990
652	GO:0006520	cellular amino acid metabolic process	16 (2.89%)	582 (3.78%)	0.894653	0.999990
653	GO:0065003	macromolecular complex assembly	10 (1.81%)	389 (2.52%)	0.897109	0.999990
654	GO:0006511	ubiquitin-dependent protein catabolic process	1 (0.18%)	62 (0.4%)	0.897145	0.999990
655	GO:0048827	phyllome development	1 (0.18%)	62 (0.4%)	0.897145	0.999990
656	GO:0006464	cellular protein modification process	76 (13.72%)	2393 (15.53%)	0.897168	0.999990
657	GO:0015992	proton transport	2 (0.36%)	106 (0.69%)	0.898597	0.999990
658	GO:0010410	hemicellulose metabolic process	1 (0.18%)	63 (0.41%)	0.900857	0.999990
659	GO:0045491	xylan metabolic process	1 (0.18%)	63 (0.41%)	0.900857	0.999990
660	GO:0048589	developmental growth	1 (0.18%)	63 (0.41%)	0.900857	0.999990
661	GO:0009260	ribonucleotide biosynthetic process	2 (0.36%)	107 (0.69%)	0.901525	0.999990
662	GO:0046390	ribose phosphate biosynthetic process	2 (0.36%)	107 (0.69%)	0.901525	0.999990
663	GO:1902580	single-organism cellular localization	2 (0.36%)	108 (0.7%)	0.904374	0.999990
664	GO:0006605	protein targeting	9 (1.62%)	362 (2.35%)	0.907625	0.999990
665	GO:0006913	nucleocytoplasmic transport	1 (0.18%)	65 (0.42%)	0.907886	0.999990
666	GO:0007031	peroxisome organization	1 (0.18%)	65 (0.42%)	0.907886	0.999990
667	GO:0051169	nuclear transport	1 (0.18%)	65 (0.42%)	0.907886	0.999990
668	GO:0014070	response to organic cyclic compound	4 (0.72%)	187 (1.21%)	0.908017	0.999990
669	GO:0036211	protein modification process	76 (13.72%)	2408 (15.63%)	0.908035	0.999990
670	GO:1901575	organic substance catabolic process	15 (2.71%)	563 (3.65%)	0.912201	0.999990
671	GO:0010608	posttranscriptional regulation of gene expression	4 (0.72%)	190 (1.23%)	0.914243	0.999990
672	GO:0046488	phosphatidylinositol metabolic process	1 (0.18%)	67 (0.43%)	0.914416	0.999990
673	GO:0048509	regulation of meristem development	1 (0.18%)	67 (0.43%)	0.914416	0.999990
674	GO:0015979	photosynthesis	1 (0.18%)	68 (0.44%)	0.917507	0.999990
675	GO:0045229	external encapsulating structure organization	10 (1.81%)	403 (2.62%)	0.918458	0.999990
676	GO:0007015	actin filament organization	1 (0.18%)	69 (0.45%)	0.920485	0.999990
677	GO:0006399	tRNA metabolic process	3 (0.54%)	156 (1.01%)	0.922856	0.999990
678	GO:0048580	regulation of post-embryonic development	4 (0.72%)	196 (1.27%)	0.925579	0.999990

679	GO:0009069	serine family amino acid metabolic process	1 (0.18%)	71 (0.46%)	0.926124	0.999990
680	GO:0006259	DNA metabolic process	19 (3.43%)	706 (4.58%)	0.927819	0.999990
681	GO:0009156	ribonucleoside monophosphate biosynthetic process	1 (0.18%)	72 (0.47%)	0.928792	0.999990
682	GO:1903046	meiotic cell cycle process	1 (0.18%)	72 (0.47%)	0.928792	0.999990
683	GO:0009165	nucleotide biosynthetic process	4 (0.72%)	198 (1.28%)	0.929047	0.999990
684	GO:0009314	response to radiation	13 (2.35%)	513 (3.33%)	0.930425	0.999990
685	GO:0000902	cell morphogenesis	3 (0.54%)	160 (1.04%)	0.930544	0.999990
686	GO:1901362	organic cyclic compound biosynthetic process	19 (3.43%)	709 (4.6%)	0.930694	0.999990
687	GO:0009161	ribonucleoside monophosphate metabolic process	1 (0.18%)	73 (0.47%)	0.931364	0.999990
688	GO:0009888	tissue development	5 (0.9%)	238 (1.54%)	0.933069	0.999990
689	GO:0006643	membrane lipid metabolic process	1 (0.18%)	74 (0.48%)	0.933843	0.999990
690	GO:0072594	establishment of protein localization to organelle	1 (0.18%)	74 (0.48%)	0.933843	0.999990
691	GO:0006281	DNA repair	3 (0.54%)	162 (1.05%)	0.934118	0.999990
692	GO:0007389	pattern specification process	2 (0.36%)	121 (0.79%)	0.935038	0.999990
693	GO:0009259	ribonucleotide metabolic process	2 (0.36%)	121 (0.79%)	0.935038	0.999990
694	GO:0019693	ribose phosphate metabolic process	2 (0.36%)	121 (0.79%)	0.935038	0.999990
695	GO:0009451	RNA modification	5 (0.9%)	240 (1.56%)	0.935996	0.999990
696	GO:0019751	polyol metabolic process	1 (0.18%)	75 (0.49%)	0.936233	0.999990
697	GO:0008652	cellular amino acid biosynthetic process	6 (1.08%)	277 (1.8%)	0.936428	0.999990
698	GO:0009116	nucleoside metabolic process	1 (0.18%)	76 (0.49%)	0.938536	0.999990
699	GO:0009119	ribonucleoside metabolic process	1 (0.18%)	76 (0.49%)	0.938536	0.999990
700	GO:0043038	amino acid activation	1 (0.18%)	77 (0.5%)	0.940757	0.999990
701	GO:0043039	tRNA aminoacylation	1 (0.18%)	77 (0.5%)	0.940757	0.999990
702	GO:0051321	meiotic cell cycle	1 (0.18%)	77 (0.5%)	0.940757	0.999990
703	GO:1902582	single-organism intracellular transport	11 (1.99%)	456 (2.96%)	0.941124	0.999990
704	GO:0009057	macromolecule catabolic process	10 (1.81%)	424 (2.75%)	0.943382	0.999990
705	GO:0009893	positive regulation of metabolic process	2 (0.36%)	126 (0.82%)	0.944141	0.999990
706	GO:0009411	response to UV	1 (0.18%)	79 (0.51%)	0.944960	0.999990
707	GO:0016043	cellular component organization	61 (11.01%)	2026 (13.15%)	0.945561	0.999990
708	GO:0034470	ncRNA processing	1 (0.18%)	80 (0.52%)	0.946949	0.999990
709	GO:0018130	heterocycle biosynthetic process	14 (2.53%)	565 (3.67%)	0.948215	0.999990
710	GO:1901293	nucleoside phosphate biosynthetic process	4 (0.72%)	211 (1.37%)	0.948250	0.999990
711	GO:0030029	actin filament-based process	1 (0.18%)	81 (0.53%)	0.948866	0.999990
712	GO:0030036	actin cytoskeleton organization	1 (0.18%)	81 (0.53%)	0.948866	0.999990
713	GO:0044249	cellular biosynthetic process	84 (15.16%)	2721 (17.66%)	0.950004	0.999990
714	GO:0051179	localization	86 (15.52%)	2781	0.950370	0.999990

				(18.05%)		
715	GO:0006753	nucleoside phosphate metabolic process	11 (1.99%)	466 (3.02%)	0.950481	0.999990
716	GO:0009124	nucleoside monophosphate biosynthetic process	1 (0.18%)	82 (0.53%)	0.950714	0.999990
717	GO:0033365	protein localization to organelle	1 (0.18%)	82 (0.53%)	0.950714	0.999990
718	GO:0034655	nucleobase-containing compound catabolic process	1 (0.18%)	82 (0.53%)	0.950714	0.999990
719	GO:0034660	ncRNA metabolic process	9 (1.62%)	398 (2.58%)	0.951827	0.999990
720	GO:0006164	purine nucleotide biosynthetic process	1 (0.18%)	83 (0.54%)	0.952495	0.999990
721	GO:0009152	purine ribonucleotide biosynthetic process	1 (0.18%)	83 (0.54%)	0.952495	0.999990
722	GO:0009056	catabolic process	15 (2.71%)	604 (3.92%)	0.952579	0.999990
723	GO:0032392	DNA geometric change	1 (0.18%)	84 (0.55%)	0.954212	0.999990
724	GO:0000096	sulfur amino acid metabolic process	3 (0.54%)	176 (1.14%)	0.954756	0.999990
725	GO:1901135	carbohydrate derivative metabolic process	9 (1.62%)	402 (2.61%)	0.955342	0.999990
726	GO:0009123	nucleoside monophosphate metabolic process	1 (0.18%)	85 (0.55%)	0.955867	0.999990
727	GO:0019637	organophosphate metabolic process	19 (3.43%)	742 (4.81%)	0.956459	0.999990
728	GO:0043412	macromolecule modification	81 (14.62%)	2649 (17.19%)	0.956615	0.999990
729	GO:0006351	transcription, DNA-templated	1 (0.18%)	86 (0.56%)	0.957463	0.999990
730	GO:0007010	cytoskeleton organization	2 (0.36%)	135 (0.88%)	0.957551	0.999990
731	GO:0006810	transport	67 (12.09%)	2235 (14.5%)	0.958144	0.999990
732	GO:0000375	RNA splicing, via transesterification reactions	1 (0.18%)	87 (0.56%)	0.959000	0.999990
733	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	1 (0.18%)	87 (0.56%)	0.959000	0.999990
734	GO:0015931	nucleobase-containing compound transport	1 (0.18%)	87 (0.56%)	0.959000	0.999990
735	GO:0006974	cellular response to DNA damage stimulus	3 (0.54%)	180 (1.17%)	0.959436	0.999990
736	GO:0009117	nucleotide metabolic process	10 (1.81%)	445 (2.89%)	0.961390	0.999990
737	GO:0070918	production of small RNA involved in gene silencing by RNA	1 (0.18%)	89 (0.58%)	0.961911	0.999990
738	GO:0022607	cellular component assembly	10 (1.81%)	446 (2.89%)	0.962103	0.999990
739	GO:0051239	regulation of multicellular organismal process	5 (0.9%)	264 (1.71%)	0.963158	0.999990
740	GO:2000026	regulation of multicellular organismal development	5 (0.9%)	264 (1.71%)	0.963158	0.999990
741	GO:0031050	dsRNA fragmentation	1 (0.18%)	90 (0.58%)	0.963289	0.999990
742	GO:0043331	response to dsRNA	1 (0.18%)	90 (0.58%)	0.963289	0.999990

743	GO:0071359	cellular response to dsRNA	1 (0.18%)	90 (0.58%)	0.963289	0.999990
744	GO:1901699	cellular response to nitrogen compound	1 (0.18%)	90 (0.58%)	0.963289	0.999990
745	GO:1901564	organonitrogen compound metabolic process	37 (6.68%)	1332 (8.64%)	0.964047	0.999990
746	GO:0035966	response to topologically incorrect protein	1 (0.18%)	91 (0.59%)	0.964616	0.999990
747	GO:0006886	intracellular protein transport	10 (1.81%)	450 (2.92%)	0.964842	0.999990
748	GO:0048507	meristem development	2 (0.36%)	142 (0.92%)	0.965791	0.999990
749	GO:0009062	fatty acid catabolic process	1 (0.18%)	92 (0.6%)	0.965896	0.999990
750	GO:0048583	regulation of response to stimulus	1 (0.18%)	92 (0.6%)	0.965896	0.999990
751	GO:0072329	monocarboxylic acid catabolic process	1 (0.18%)	92 (0.6%)	0.965896	0.999990
752	GO:0072522	purine-containing compound biosynthetic process	1 (0.18%)	92 (0.6%)	0.965896	0.999990
753	GO:0097659	nucleic acid-templated transcription	1 (0.18%)	92 (0.6%)	0.965896	0.999990
754	GO:0051234	establishment of localization	81 (14.62%)	2682 (17.4%)	0.967502	0.999990
755	GO:0044763	single-organism cellular process	178 (32.13%)	5508 (35.74%)	0.968688	0.999990
756	GO:0048869	cellular developmental process	8 (1.44%)	384 (2.49%)	0.968689	0.999990
757	GO:0006818	hydrogen transport	2 (0.36%)	148 (0.96%)	0.971610	0.999990
758	GO:0009150	purine ribonucleotide metabolic process	1 (0.18%)	97 (0.63%)	0.971633	0.999990
759	GO:0022900	electron transport chain	1 (0.18%)	97 (0.63%)	0.971633	0.999990
760	GO:0044242	cellular lipid catabolic process	1 (0.18%)	97 (0.63%)	0.971633	0.999990
761	GO:0055086	nucleobase-containing small molecule metabolic process	11 (1.99%)	499 (3.24%)	0.972761	0.999990
762	GO:0044272	sulfur compound biosynthetic process	4 (0.72%)	238 (1.54%)	0.973843	0.999990
763	GO:0034613	cellular protein localization	10 (1.81%)	469 (3.04%)	0.975577	0.999990
764	GO:0070727	cellular macromolecule localization	10 (1.81%)	469 (3.04%)	0.975577	0.999990
765	GO:0006260	DNA replication	2 (0.36%)	153 (0.99%)	0.975719	0.999990
766	GO:0000904	cell morphogenesis involved in differentiation	1 (0.18%)	103 (0.67%)	0.977260	0.999990
767	GO:0030154	cell differentiation	3 (0.54%)	201 (1.3%)	0.977401	0.999990
768	GO:0048468	cell development	2 (0.36%)	157 (1.02%)	0.978587	0.999990
769	GO:0032989	cellular component morphogenesis	3 (0.54%)	204 (1.32%)	0.979244	0.999990
770	GO:0050793	regulation of developmental process	5 (0.9%)	288 (1.87%)	0.979346	0.999990
771	GO:0044267	cellular protein metabolic process	87 (15.7%)	2913 (18.9%)	0.979778	0.999990
772	GO:0031399	regulation of protein modification process	1 (0.18%)	108 (0.7%)	0.981088	0.999990
773	GO:0071407	cellular response to organic cyclic compound	2 (0.36%)	162 (1.05%)	0.981713	0.999990
774	GO:0071840	cellular component organization or biogenesis	61 (11.01%)	2145 (13.92%)	0.983343	0.999990
775	GO:0006396	RNA processing	8 (1.44%)	416 (2.7%)	0.984087	0.999990
776	GO:0030243	cellulose metabolic process	1 (0.18%)	113 (0.73%)	0.984273	0.999990
777	GO:1901137	carbohydrate derivative biosynthetic	5 (0.9%)	300 (1.95%)	0.984671	0.999990

		process				
778	GO:0000097	sulfur amino acid biosynthetic process	2 (0.36%)	168 (1.09%)	0.984884	0.999990
779	GO:0034220	ion transmembrane transport	1 (0.18%)	117 (0.76%)	0.986430	0.999990
780	GO:0006163	purine nucleotide metabolic process	1 (0.18%)	122 (0.79%)	0.988717	0.999990
781	GO:0019538	protein metabolic process	105 (18.95%)	3514 (22.8%)	0.988979	0.999990
782	GO:0048518	positive regulation of biological process	2 (0.36%)	184 (1.19%)	0.990947	0.999990
783	GO:0019438	aromatic compound biosynthetic process	12 (2.17%)	601 (3.9%)	0.992445	0.999990
784	GO:0043094	cellular metabolic compound salvage	1 (0.18%)	134 (0.87%)	0.992755	0.999990
785	GO:0044085	cellular component biogenesis	12 (2.17%)	609 (3.95%)	0.993578	0.999990
786	GO:0051641	cellular localization	13 (2.35%)	653 (4.24%)	0.994430	0.999990
787	GO:0072521	purine-containing compound metabolic process	1 (0.18%)	143 (0.93%)	0.994805	0.999990
788	GO:0046907	intracellular transport	12 (2.17%)	620 (4.02%)	0.994879	0.999990
789	GO:0055114	oxidation-reduction process	1 (0.18%)	145 (0.94%)	0.995175	0.999990
790	GO:0051649	establishment of localization in cell	12 (2.17%)	624 (4.05%)	0.995287	0.999990
791	GO:0048229	gametophyte development	1 (0.18%)	147 (0.95%)	0.995519	0.999990
792	GO:0006793	phosphorus metabolic process	70 (12.64%)	2541 (16.49%)	0.995639	0.999990
793	GO:0008152	metabolic process	389 (70.22%)	11555 (74.98%)	0.995884	0.999990
794	GO:0030163	protein catabolic process	3 (0.54%)	261 (1.69%)	0.996110	0.999990
795	GO:0044257	cellular protein catabolic process	3 (0.54%)	261 (1.69%)	0.996110	0.999990
796	GO:0071704	organic substance metabolic process	288 (51.99%)	8850 (57.43%)	0.996226	0.999990
797	GO:1901360	organic cyclic compound metabolic process	76 (13.72%)	2749 (17.84%)	0.996657	0.999990
798	GO:0044260	cellular macromolecule metabolic process	170 (30.69%)	5551 (36.02%)	0.996896	0.999990
799	GO:0016482	cytoplasmic transport	2 (0.36%)	218 (1.41%)	0.997015	0.999990
800	GO:0008380	RNA splicing	1 (0.18%)	159 (1.03%)	0.997125	0.999990
801	GO:0034654	nucleobase-containing compound biosynthetic process	6 (1.08%)	410 (2.66%)	0.997310	0.999990
802	GO:0090407	organophosphate biosynthetic process	4 (0.72%)	323 (2.1%)	0.997455	0.999990
803	GO:0043170	macromolecule metabolic process	209 (37.73%)	6700 (43.48%)	0.997740	0.999990
804	GO:0044238	primary metabolic process	238 (42.96%)	7527 (48.84%)	0.997941	0.999990
805	GO:0032774	RNA biosynthetic process	1 (0.18%)	169 (1.1%)	0.998014	0.999990
806	GO:0016192	vesicle-mediated transport	2 (0.36%)	231 (1.5%)	0.998059	0.999990
807	GO:0015031	protein transport	11 (1.99%)	630 (4.09%)	0.998195	0.999990
808	GO:0044265	cellular macromolecule catabolic process	4 (0.72%)	339 (2.2%)	0.998398	0.999990
809	GO:0045184	establishment of protein localization	11 (1.99%)	639 (4.15%)	0.998527	0.999990

810	GO:0006725	cellular aromatic compound metabolic process	70 (12.64%)	2633 (17.09%)	0.998610	0.999990
811	GO:0006796	phosphate-containing compound metabolic process	65 (11.73%)	2490 (16.16%)	0.998855	0.999990
812	GO:0051603	proteolysis involved in cellular protein catabolic process	2 (0.36%)	248 (1.61%)	0.998900	0.999990
813	GO:1901566	organonitrogen compound biosynthetic process	15 (2.71%)	808 (5.24%)	0.998939	0.999990
814	GO:0090304	nucleic acid metabolic process	45 (8.12%)	1862 (12.08%)	0.999111	0.999990
815	GO:0046483	heterocycle metabolic process	64 (11.55%)	2491 (16.16%)	0.999269	0.999990
816	GO:0044271	cellular nitrogen compound biosynthetic process	12 (2.17%)	711 (4.61%)	0.999300	0.999990
817	GO:0016070	RNA metabolic process	23 (4.15%)	1132 (7.35%)	0.999411	0.999990
818	GO:0044248	cellular catabolic process	7 (1.26%)	518 (3.36%)	0.999508	0.999990
819	GO:0008104	protein localization	14 (2.53%)	806 (5.23%)	0.999518	0.999990
820	GO:0044237	cellular metabolic process	264 (47.65%)	8422 (54.65%)	0.999668	0.999990
821	GO:0019941	modification-dependent protein catabolic process	1 (0.18%)	223 (1.45%)	0.999732	0.999990
822	GO:0043632	modification-dependent macromolecule catabolic process	1 (0.18%)	223 (1.45%)	0.999732	0.999990
823	GO:0006807	nitrogen compound metabolic process	76 (13.72%)	2949 (19.14%)	0.999752	0.999990
824	GO:0006139	nucleobase-containing compound metabolic process	54 (9.75%)	2249 (14.59%)	0.999781	0.999990
825	GO:0043623	cellular protein complex assembly	2 (0.36%)	296 (1.92%)	0.999783	0.999990
826	GO:0043603	cellular amide metabolic process	1 (0.18%)	232 (1.51%)	0.999808	0.999990
827	GO:0033036	macromolecule localization	14 (2.53%)	862 (5.59%)	0.999866	0.999990
828	GO:0034641	cellular nitrogen compound metabolic process	62 (11.19%)	2578 (16.73%)	0.999924	0.999990
829	GO:0034622	cellular macromolecular complex assembly	2 (0.36%)	335 (2.17%)	0.999943	0.999990
830	GO:0009987	cellular process	340 (61.37%)	10638 (69.03%)	0.999960	0.999990
831	GO:0006508	proteolysis	2 (0.36%)	356 (2.31%)	0.999973	0.999990
832	GO:0010467	gene expression	21 (3.79%)	1251 (8.12%)	0.999990	0.999990

Appendix F. The co-modulated DEGs in DM1-vs-DM2 and HN1-vs-HN2 were categorized into 91 pathways

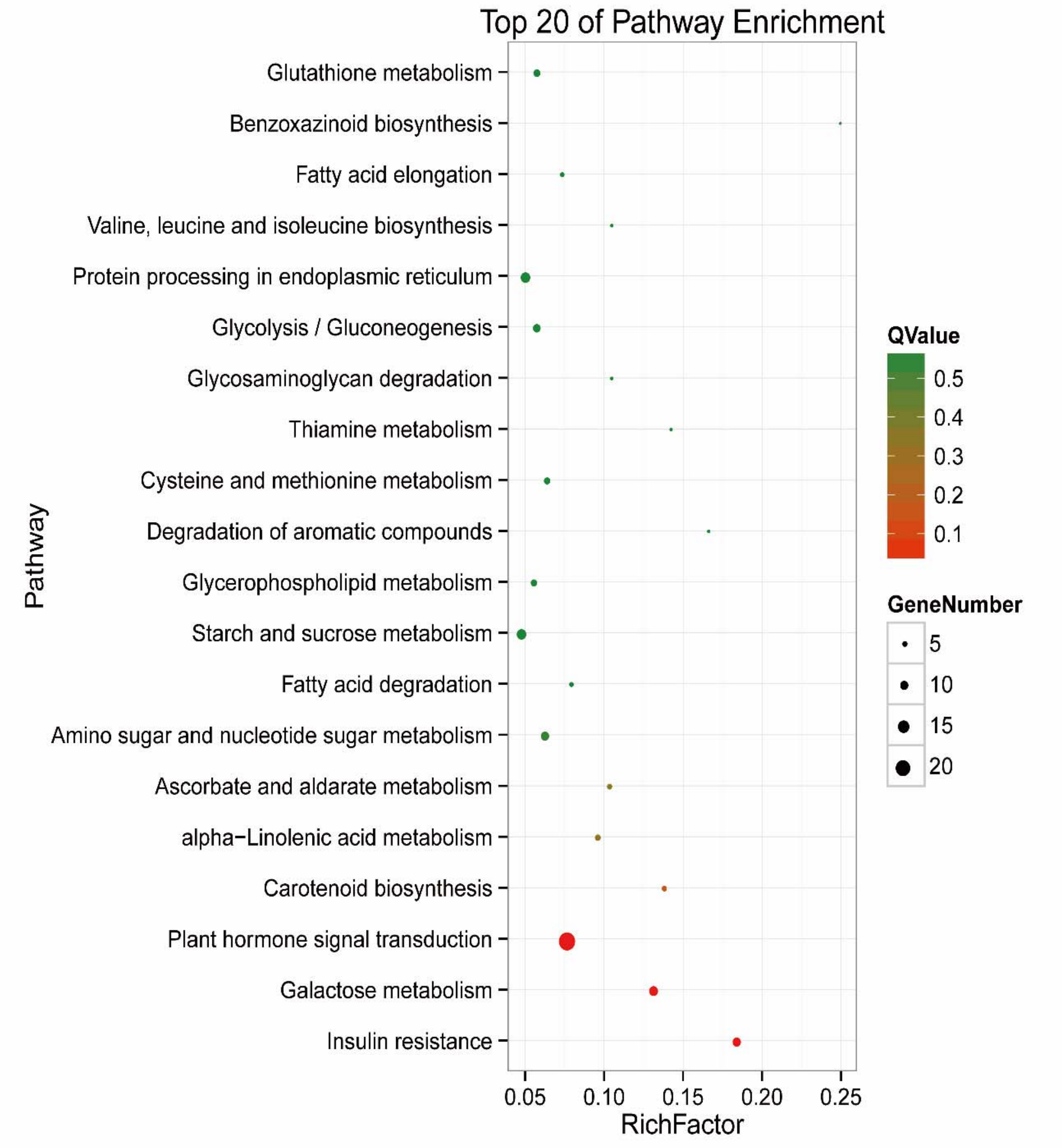
DM1-vs-DM2_HN1-vs-HN2 Pathway Enrichment

#	Pathway	Candidate genes with pathway annotation(194)	All genes with pathway annotation	Pvalue	Qvalue	Pathway ID
1	Insulin resistance	10(5.15%)	54 (0.95%)	0.000011	0.001008	ko04931
2	Galactose metabolism	11 (5.67%)	83 (1.46%)	0.000104	0.004023	ko00052
3	Plant hormone signal transduction	23 (11.86%)	292 (5.14%)	0.000133	0.004023	ko04075
4	Carotenoid biosynthesis	5 (2.58%)	36 (0.63%)	0.007036	0.160069	ko00906
5	alpha-Linolenic acid metabolism	6 (3.09%)	62 (1.09%)	0.018476	0.336269	ko00592
6	Ascorbate and aldarate metabolism	5 (2.58%)	48 (0.85%)	0.023016	0.349069	ko00053
7	Amino sugar and nucleotide sugar metabolism	10 (5.15%)	157 (2.76%)	0.041692	0.542001	ko00520
8	Degradation of aromatic compounds	2 (1.03%)	12 (0.21%)	0.061186	0.562318	ko01220
9	Cysteine and methionine metabolism	7 (3.61%)	108 (1.9%)	0.075424	0.562318	ko00270
10	Glycolysis / Gluconeogenesis	9 (4.64%)	154 (2.71%)	0.080025	0.562318	ko00010
11	Thiamine metabolism	2 (1.03%)	14 (0.25%)	0.080711	0.562318	ko00730
12	Fatty acid biosynthesis	4 (2.06%)	49 (0.86%)	0.085060	0.562318	ko00061
13	Fatty acid degradation	4 (2.06%)	50 (0.88%)	0.090111	0.562318	ko00071
14	Glutathione metabolism	8 (4.12%)	137 (2.41%)	0.095914	0.562318	ko00480
15	Protein processing in endoplasmic reticulum	12 (6.19%)	233 (4.1%)	0.100718	0.562318	ko04141
16	Fatty acid elongation	4 (2.06%)	54 (0.95%)	0.111697	0.562318	ko00062
17	Benzoxazinoid biosynthesis	1 (0.52%)	4 (0.07%)	0.129833	0.562318	ko00402
18	Glycerophospholipid metabolism	7 (3.61%)	124 (2.18%)	0.130784	0.562318	ko00564
19	Starch and sucrose metabolism	12 (6.19%)	245 (4.31%)	0.131819	0.562318	ko00500
20	Valine, leucine and isoleucine biosynthesis	2 (1.03%)	19 (0.33%)	0.135945	0.562318	ko00290
21	Glycosaminoglycan degradation	2 (1.03%)	19 (0.33%)	0.135945	0.562318	ko00531
22	Linoleic acid metabolism	2 (1.03%)	19 (0.33%)	0.135945	0.562318	ko00591
23	Phenylpropanoid biosynthesis	13 (6.7%)	284 (5%)	0.172085	0.645758	ko00940
24	Fructose and mannose metabolism	4 (2.06%)	65 (1.14%)	0.181017	0.645758	ko00051
25	Glycosphingolipid biosynthesis - globo series	2 (1.03%)	23 (0.41%)	0.184502	0.645758	ko00603
26	Biotin metabolism	2 (1.03%)	23 (0.41%)	0.184502	0.645758	ko00780
27	Brassinosteroid biosynthesis	2 (1.03%)	25 (0.44%)	0.209624	0.706510	ko00905
28	Glycosphingolipid biosynthesis - ganglio series	1 (0.52%)	8 (0.14%)	0.242884	0.756276	ko00604
29	Diterpenoid biosynthesis	2 (1.03%)	29 (0.51%)	0.260668	0.756276	ko00904
30	Stilbenoid, diarylheptanoid and gingerol biosynthesis	2 (1.03%)	29 (0.51%)	0.260668	0.756276	ko00945
31	RNA degradation	6 (3.09%)	129 (2.27%)	0.278206	0.756276	ko03018

32	Ether lipid metabolism	2 (1.03%)	31 (0.55%)	0.286299	0.756276	ko00565
33	Pantothenate and CoA biosynthesis	2 (1.03%)	31 (0.55%)	0.286299	0.756276	ko00770
34	Zeatin biosynthesis	2 (1.03%)	31 (0.55%)	0.286299	0.756276	ko00908
35	Valine, leucine and isoleucine degradation	3 (1.55%)	56 (0.99%)	0.299186	0.756276	ko00280
36	Arginine and proline metabolism	3 (1.55%)	56 (0.99%)	0.299186	0.756276	ko00330
37	Tyrosine metabolism	3 (1.55%)	58 (1.02%)	0.318078	0.782301	ko00350
38	Cutin, suberine and wax biosynthesis	2 (1.03%)	35 (0.62%)	0.337186	0.796400	ko00073
39	Vitamin B6 metabolism	1 (0.52%)	12 (0.21%)	0.341314	0.796400	ko00750
40	Inositol phosphate metabolism	3 (1.55%)	62 (1.09%)	0.355877	0.809621	ko00562
41	Fatty acid metabolism	4 (2.06%)	95 (1.67%)	0.408880	0.907514	ko01212
42	Spliceosome	8 (4.12%)	212 (3.73%)	0.438515	0.931538	ko03040
43	beta-Alanine metabolism	2 (1.03%)	44 (0.77%)	0.446747	0.931538	ko00410
44	Histidine metabolism	1 (0.52%)	18 (0.32%)	0.465594	0.931538	ko00340
45	Selenocompound metabolism	1 (0.52%)	19 (0.33%)	0.483908	0.931538	ko00450
46	Phosphatidylinositol signaling system	3 (1.55%)	76 (1.34%)	0.484195	0.931538	ko04070
47	Endocytosis	7 (3.61%)	192 (3.38%)	0.485689	0.931538	ko04144
48	Plant-pathogen interaction	9 (4.64%)	252 (4.44%)	0.495026	0.931538	ko04626
49	Taurine and hypotaurine metabolism	1 (0.52%)	20 (0.35%)	0.501598	0.931538	ko00430
50	Porphyrin and chlorophyll metabolism	2 (1.03%)	50 (0.88%)	0.514000	0.935479	ko00860
51	Biosynthesis of amino acids	9 (4.64%)	270 (4.75%)	0.579929	0.993446	ko01230
52	Other glycan degradation	1 (0.52%)	25 (0.44%)	0.581394	0.993446	ko00511
53	Butanoate metabolism	1 (0.52%)	26 (0.46%)	0.595757	0.993446	ko00650
54	2-Oxocarboxylic acid metabolism	2 (1.03%)	59 (1.04%)	0.604312	0.993446	ko01210
55	Propanoate metabolism	1 (0.52%)	29 (0.51%)	0.635971	0.993446	ko00640
56	Arginine biosynthesis	1 (0.52%)	36 (0.63%)	0.714990	0.993446	ko00220
57	Isoquinoline alkaloid biosynthesis	1 (0.52%)	37 (0.65%)	0.724788	0.993446	ko00950
58	SNARE interactions in vesicular transport	1 (0.52%)	38 (0.67%)	0.734251	0.993446	ko04130
59	Glycerolipid metabolism	2 (1.03%)	80 (1.41%)	0.764733	0.993446	ko00561
60	Sphingolipid metabolism	1 (0.52%)	43 (0.76%)	0.776926	0.993446	ko00600
61	Flavonoid biosynthesis	1 (0.52%)	43 (0.76%)	0.776926	0.993446	ko00941
62	Carbon fixation in photosynthetic organisms	2 (1.03%)	84 (1.48%)	0.787997	0.993446	ko00710
63	Steroid biosynthesis	1 (0.52%)	45 (0.79%)	0.792020	0.993446	ko00100
64	Pentose and glucuronate interconversions	2 (1.03%)	86 (1.51%)	0.798857	0.993446	ko00040
65	Regulation of autophagy	1 (0.52%)	47 (0.83%)	0.806097	0.993446	ko04140
66	Pyrimidine metabolism	4 (2.06%)	162 (2.85%)	0.811069	0.993446	ko00240
67	Ubiquitin mediated proteolysis	4 (2.06%)	162 (2.85%)	0.811069	0.993446	ko04120
68	mRNA surveillance pathway	3 (1.55%)	126 (2.22%)	0.811363	0.993446	ko03015
69	Ubiquinone and other terpenoid-quinone biosynthesis	1 (0.52%)	48 (0.85%)	0.812777	0.993446	ko00130

70	Lysine degradation	1 (0.52%)	49 (0.86%)	0.819227	0.993446	ko00310
71	Phenylalanine metabolism	1 (0.52%)	53 (0.93%)	0.842891	0.993446	ko00360
72	Phenylalanine, tyrosine and tryptophan biosynthesis	1 (0.52%)	53 (0.93%)	0.842891	0.993446	ko00400
73	Pentose phosphate pathway	1 (0.52%)	54 (0.95%)	0.848308	0.993446	ko00030
74	Alanine, aspartate and glutamate metabolism	1 (0.52%)	54 (0.95%)	0.848308	0.993446	ko00250
75	Circadian rhythm - plant	1 (0.52%)	57 (1%)	0.863471	0.993446	ko04712
76	Peroxisome	2 (1.03%)	108 (1.9%)	0.889411	0.993446	ko04146
77	Protein export	1 (0.52%)	66 (1.16%)	0.900490	0.993446	ko03060
78	Terpenoid backbone biosynthesis	1 (0.52%)	72 (1.27%)	0.919431	0.993446	ko00900
79	Cyanoamino acid metabolism	1 (0.52%)	76 (1.34%)	0.930018	0.993446	ko00460
80	DNA replication	1 (0.52%)	76 (1.34%)	0.930018	0.993446	ko03030
81	Glyoxylate and dicarboxylate metabolism	1 (0.52%)	80 (1.41%)	0.939221	0.993446	ko00630
82	Homologous recombination	1 (0.52%)	81 (1.43%)	0.941327	0.993446	ko03440
83	Phagosome	1 (0.52%)	82 (1.44%)	0.943361	0.993446	ko04145
84	Carbon metabolism	6 (3.09%)	302 (5.32%)	0.951333	0.993446	ko01200
85	Glycine, serine and threonine metabolism	1 (0.52%)	93 (1.64%)	0.961590	0.993446	ko00260
86	Pyruvate metabolism	1 (0.52%)	101 (1.78%)	0.971056	0.993446	ko00620
87	Ribosome biogenesis in eukaryotes	1 (0.52%)	108 (1.9%)	0.977412	0.993446	ko03008
88	Oxidative phosphorylation	2 (1.03%)	176 (3.1%)	0.985151	0.993446	ko00190
89	RNA transport	2 (1.03%)	200 (3.52%)	0.992970	0.993446	ko03013
90	Purine metabolism	2 (1.03%)	202 (3.56%)	0.993399	0.993446	ko00230
91	Ribosome	5 (2.58%)	346 (6.09%)	0.993446	0.993446	ko03010

Appendix G. Scatter plot of the top 20 KEGG enrichment results of co-modulated DEGs in two pairwise comparison. RichFactor is the ratio of DEG numbers annoted in this pathway term to all gene numbers annotated in this pathway term. A large RichFator represents greater intensiveness. The Q-value is the corrected P value ranging from 0 to 1, and a lower Q-value represents greater intensity.



Appendix H. TF families identified in DEGs of DM2-vs-DM1 and HN2-vs-HN1 and related genes.

Family	Count	Genes
bHLH	**39**	gene282;gene2003;gene2130;gene2371;gene2938;gene3188;gene3439;gene3700;gene4698;gene6375;gene6499;gene6716;gene6789; gene12953;gene13833;gene14569;gene15081;gene15294;gene17046;gene17310;gene17451;gene20165;gene22463;gene22673;gene23898;gene23901; gene23902;gene23903;gene24969;gene26081;gene28256;gene28719;gene30414;gene30527;gene30911;gene32846;gene34785;gene34900;gene35317
WRKY	**30**	gene381;gene659;gene1653;gene5854;gene6140;gene6141;gene8477;gene9152;gene9907;gene9910;gene10052;gene10284;gene10704;gene16236; gene17250;gene17251;gene18336;gene18564;gene19064;gene19083;gene19644;gene19678;gene19809;gene24797;gene26526;gene26989;gene28127; gene30288;gene33760;gene33843
NAC	**24**	gene1319;gene1331;gene2218;gene8498;gene8624;gene11018;gene12592;gene15829;gene18691;gene19954;gene20103;gene20830;gene24489;gene24707; gene25430;gene26567;gene26568;gene26944;gene26945;gene27215;gene29815;gene31162;gene33805;gene35192
ERF	**23**	gene284;gene1867;gene2622;gene2712;gene3480;gene5936;gene8914;gene9992;gene10933;gene13015;gene13783;gene14716;gene16060;gene17342; gene19991;gene21032;gene22224;gene23088;gene24436;gene25374;gene25814;gene27325;gene34764
MYB	**20**	gene2647;gene3245;gene3412;gene5406;gene6074;gene7642;gene8521;gene9120;gene12048;gene14972;gene19955;gene21347;gene22345;gene22407; gene24709;gene25092;gene25153;gene29287;gene33530;gene35118
bZIP	**19**	gene209;gene457;gene579;gene3489;gene4238;gene5741;gene6384;gene8252;gene10009;gene13677;gene17418;gene17876;gene18514;gene19242; gene19932;gene19985;gene22613;gene23233;gene27217
HD-ZIP	**18**	gene919;gene2139;gene2674;gene3540;gene6935;gene7811;gene12700;gene13135;gene13137;gene13707;gene15403;gene19462;gene25335;gene25962; gene31090;gene32683;gene32799;gene34704
C2H2	**13**	gene6221;gene8633;gene10897;gene12412;gene19410;gene19774;gene19778;gene22834;gene29774;gene29775;gene30235;gene34402;gene34710
GRAS	**12**	gene7558;gene7820;gene7850;gene7868;gene10525;gene13024;gene20573;gene24573;gene29413;gene29750;gene33163;gene35473
MYB_related	**10**	gene2899;gene9712;gene9937;gene10906;gene15848;gene15989;gene16803;gene17285;gene18382;gene34319
AP2	**8**	gene4247;gene8930;gene14959;gene22448;gene24238;gene30182;gene34484;gene34833
HSF	**8**	gene6374;gene6386;gene8221;gene10325;gene19080;gene29985;gene32018;gene34508
TCP	**6**	gene3359;gene4325;gene17427;gene25217;gene27398;gene30077
GRF	**5**	gene2861;gene3010;gene3568;gene30520;gene30887
B3	**4**	gene7660;gene12446;gene21042;gene31167
C3H	**4**	gene9710;gene10355;gene12223;gene16533
SBP	**4**	gene704;gene11099;gene14815;gene20386
TALE	**4**	gene322;gene15339;gene30543;gene30865
DBB	**3**	gene2667;gene9578;gene25326
GATA	**3**	gene19166;gene20782;gene32839
LBD	**3**	gene5925;gene27047;gene34064
Dof	**3**	gene8506;gene16432;gene32132
CO-like	**3**	gene693;gene8378;gene21753
WOX	**2**	gene8505;gene9030
ARF	**2**	gene8880;gene18654
Trihelix	**2**	gene24234;gene27295
ZF-HD	**2**	gene6122;gene22664
GeBP	**2**	gene3510;gene3527
G2-like	**2**	gene15615;gene25716
YABBY	**2**	gene25300;gene31033
EIL	**2**	gene8512;gene24672
CPP	**2**	gene12543;gene31116

FAR1	**2**	gene10241;gene30895
NF-YA	**1**	gene7969
E2F/DP	**1**	gene3307
SRS	**1**	gene11246
Nin-like	**1**	gene992
NF-YC	**1**	gene34327
MIKC	**1**	gene20930
NF-YB	**1**	gene5359
RAV	**1**	gene10208
Whirly	**1**	gene13185

S7 Table. The DEGs selected for qRT-PCR and the data of DEGs expression in RNA-seq and qRT-PCR

Groups	id in RNA-seq	Gene ID [a] in NCBI	Locus tag	log2(FC)from RNA-seq	qRT-PCR
DM2/DM1	gene12652	101770668	SETIT_024703mg	4.277984747	11.54
HN2/HN1	gene12652	101770668	SETIT_024703mg	4.149197835	10.145
DM2/DM1	gene13677	101776070	SETIT_006889mg	1.309929094	2.34
HN2/HN1	gene13677	101776070	SETIT_006889mg	2.595463099	6.35
DM2/DM1	gene15404	101770287	SETIT_007044mg	3.171933627	3.32
HN2/HN1	gene15404	101770287	SETIT_007044mg	5.238427433	21.54
DM2/DM1	gene17634	101763536	SETIT_001933mg	2.882202964	4.34
HN2/HN1	gene17634	101763536	SETIT_001933mg	4.851054937	24.33
DM2/DM1	gene19845	101775420	SETIT_000348mg	3.279423366	10.33
HN2/HN1	gene19845	101775420	SETIT_000348mg	4.043981095	10.145
DM2/DM1	gene2087	101761265	SETIT_018207mg	-2.950611973	0.071
HN2/HN1	gene2087	101761265	SETIT_018207mg	-1.303624655	0.145
DM2/DM1	gene24408	101777261	SETIT_022956mg	-2.39330052	0.032
HN2/HN1	gene24408	101777261	SETIT_022956mg	-6.996332249	0.275
DM2/DM1	gene32054	101786707	SETIT_038745mg	2.204514931	4.834
HN2/HN1	gene32054	101786707	SETIT_038745mg	2.861566605	4.275
DM2/DM1	gene32767	101763654	SETIT_036531mg	2.620444327	3.28
HN2/HN1	gene32767	101763654	SETIT_036531mg	2.404782972	4.76
DM2/DM1	gene5040	101757363	SETIT_028698mg	1.330645312	2.25
HN2/HN1	gene5040	101757363	SETIT_028698mg	2.463845783	3.28

Note: a) Gene ID against the NCBI database