

Appendix A Summary of unigene annotation in major public databases

Databases	Unigenes with predicted coding regions	
	Gene number (percent)	Transcript number (percent)
GO	23970 (0.7090)	23970 (0.7090)
KEGG	12661 (0.3745)	12661 (0.3745)
KOG	29190 (0.8634)	29190 (0.8634)
NR	31010 (0.9172)	31010 (0.9172)
Swiss-Prot	23371 (0.6912)	23371 (0.6912)
Pfam	24456 (0.7233)	24456 (0.7233)
Total annotation	31631 (0.9356)	31631 (0.9356)
Total	33810 (1)	33810 (1)

Note: A total of 31631 unique sequences were annotated based on blastx alignment searches of six public databases including Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG), euKaryotic Ortholog Groups (KOG), non-redundant protein sequences (NR), Swiss-Prot, and Pfam databases.

Appendix B The list of 984 differentially expressed genes (DEGs, FDR<0.05) along with their fold changes and annotations

Number	Gene id	Gene description	Fold change	Regulation	Number	Gene id	Gene description	Fold change	Regulation
1	Solyc12g042980.1	-	8.775	up	493	Solyc01g107820.2	Glycosyltransferase	2.271	up
2	Solyc02g090450.2	Peroxidase	9.003	up	494	Solyc04g080840.1	Beta-galactosidase	2.102	up
3	Solyc01g015080.2	Peroxidase	7.166	up	495	Solyc02g068460.1	-	2.469	up
4	Solyc10g080460.1	-	4.995	up	496	Solyc10g076180.1	-	0.468	down
5	Solyc02g090470.2	Peroxidase	6.645	up	497	Solyc01g095980.2	-	0.478	down
6	Solyc03g034320.2	-	3.761	up	498	Solyc06g066590.2	-	2.264	up
7	Solyc09g011520.2	-	5.366	up	499	Solyc02g062500.2	-	0.489	down
8	Solyc01g104780.2	-	0.158	down	500	Solyc01g103660.2	-	2.291	up
9	Solyc06g071060.1	-	4.535	up	501	Solyc01g106630.2	-	0.453	down
10	Solyc05g047580.2	Lanosterol synthase	7.906	up	502	Solyc10g005500.2	-	2.933	up
11	Solyc08g006100.2	-	7.199	up	503	Solyc06g073590.2	Aquaporin NIP3-1	2.865	up
12	Solyc08g078080.2	Pentatricopeptide repeat-containing protein At4g16835, mitochondrial	3.802	up	504	Solyc09g074430.2	Flavin-containing monooxygenase	2.629	up
13	Solyc06g007180.2	Asparagine synthetase	8.567	up	505	Solyc08g082790.2	-	0.326	down
14	Solyc02g071560.2	-	5.189	up	506	Solyc09g011590.2	-	2.594	up
15	Solyc05g007770.2	-	2.926	up	507	Solyc07g054870.2	-	2.461	up
16	Solyc02g077000.2	-	4.402	up	508	Solyc04g080330.2	Peroxidase	2.544	up
17	Solyc06g060760.2	Tonoplast intrinsic protein 23	4.267	up	509	Solyc05g007610.2	-	2.891	up
18	Solyc03g025350.2	-	6.499	up	510	Solyc04g011740.2	-	3.167	up
19	Solyc12g100270.1	-	5.264	up	511	Solyc06g083850.2	-	0.383	down

20	Solyc04g006950.2	-	0.149	down	512	Solyc04g082220.1	-	2.617	up
21	Solyc06g053610.2	THM18 protein	0.397	down	513	Solyc11g071210.1	-	0.496	down
22	Solyc10g083340.1	-	0.246	down	514	Solyc01g057910.2	-	2.415	up
23	Solyc01g081600.2	Non-specific lipid-transfer protein 8	3.456	up	515	Solyc11g069560.1	-	2.541	up
24	Solyc01g068410.2	Auxin efflux carrier component	0.141	down	516	Solyc04g074220.2	-	0.459	down
25	Solyc04g064880.2	-	3.364	up	517	Solyc05g005090.2	-	0.444	down
26	Solyc09g097960.2	-	4.061	up	518	Solyc01g010080.2	-	2.121	up
27	Solyc04g008250.1	-	0.214	down	519	Solyc04g080650.2	-	0.363	down
28	Solyc01g108100.2	-	2.23	up	520	Solyc01g091250.2	-	2.656	up
29	Solyc12g005920.1	-	3.722	up	521	Solyc12g036120.1	-	2.499	up
30	Solyc10g078550.1	Glutamate dehydrogenase	2.087	up	522	Solyc07g062810.2	-	2.422	up
31	Solyc02g080830.1	-	4.135	up	523	Solyc10g085620.1	-	0.46	down
32	Solyc05g013530.2	-	0.189	down	524	Solyc10g047040.1	-	0.453	down
33	Solyc07g006500.2	Probable alpha, alpha-trehalose-phosph ate synthase	2.356	up	525	Solyc02g072480.2	-	2.973	up
34	Solyc03g093140.2	-	0.3	down	526	Solyc08g079060.2	Trehalose 6-phosphate phosphatase	2.118	up
35	Solyc02g087070.2	-	3.528	up	527	Solyc02g084980.2	Hexosyltransferase	2.148	up
36	Solyc04g025040.1	-	0.241	down	528	Solyc11g011080.1	-	2.258	up
37	Solyc10g080130.1	-	3.982	up	529	Solyc12g006800.1	-	0.44	down
38	Solyc03g113970.2	-	4.813	up	530	Solyc07g032490.2	-	3.246	up
39	Solyc06g007580.1	-	0.299	down	531	Solyc04g011600.2	-	2.622	up

40	Solyc10g054910.1	Peptidyl-prolylcis-trans isomerase	0.225	down	532	Solyc05g012370.2	-	0.488	down
41	Solyc04g007730.2	-	0.287	down	533	Solyc06g070990.2	-	2.846	up
42	Solyc06g082420.2	Peroxidase	0.254	down	534	Solyc01g094260.2	-	2.025	up
43	Solyc04g074700.2	-	0.47	down	535	Solyc01g090610.2	-	2.571	up
44	Solyc02g083250.2	-	0.317	down	536	Solyc07g063370.2	-	2.922	up
45	Solyc05g052410.1	-	3.494	up	537	Solyc05g051880.2	Trehalose 6-phosphate phosphatase	0.343	down
46	Solyc06g067860.2	-	3.594	up	538	Solyc01g112070.2	-	2.45	up
47	Solyc11g017470.1	NAC4 domain protein	2.526	up	539	Solyc05g009210.1	-	0.441	down
48	Solyc12g005940.1	-	3.93	up	540	Solyc09g009520.2	-	2.656	up
49	Solyc03g020060.2	-	3.437	up	541	Solyc06g074140.1	RING-type E3 ubiquitin transferase	0.494	down
50	Solyc01g091470.2	-	3.11	up	542	Solyc01g008420.2	Protein detoxification	3.06	up
51	Solyc02g086970.2	-	2.738	up	543	Solyc06g083160.1	-	0.402	down
52	Solyc08g014490.1	-	0.325	down	544	Solyc10g080540.1	-	0.458	down
53	Solyc04g078930.2	Alpha-amylase	2.93	up	545	Solyc12g062940.1	-	2.634	up
54	Solyc04g007780.2	-	0.203	down	546	Solyc03g006490.2	-	2.06	up
55	Solyc06g061200.1	-	2.541	up	547	Solyc11g064840.1	-	0.457	down
56	Solyc04g081560.2	-	2.817	up	548	Solyc09g083030.1	-	0.398	down
57	Solyc01g108350.2	-	0.285	down	549	Solyc02g081120.2	Homeobox protein shoot meristemless	0.472	down
58	Solyc07g006230.1	-	2.659	up	550	Solyc03g093410.2	-	2.01	up
59	Solyc10g080610.1	-	0.416	down	551	Solyc10g008490.2	-	2.288	up
60	Solyc04g040120.1	-	3.723	up	552	Solyc01g102910.2	-	2.235	up
61	Solyc12g056460.1	-	3.982	up	553	Solyc03g096420.1	-	3.167	up

62	Solyc11g010400.1	-	5.3	up	554	Solyc03g097580.2	Bidirectional sugar transporter SWEET	0.323	down
63	Solyc06g082780.2	-	2.561	up	555	Solyc01g103060.2	Lipid transfer-like protein VAS	2.495	up
64	Solyc01g102900.2	-	4.557	up	556	Solyc08g067510.1	-	0.392	down
65	Solyc09g092470.2	TPS14	3.963	up	557	Solyc08g080290.2	-	2.216	up
66	Solyc02g064830.2	-	2.802	up	558	Solyc01g110500.2	-	2.062	up
67	Solyc02g036350.2	1-aminocyclopropane-1-carboxylate oxidase	0.301	down	559	Solyc10g085100.1	-	0.439	down
68	Solyc07g055970.1	-	0.204	down	560	Solyc09g075140.2	-	2.01	up
69	Solyc03g070380.2	-	3.517	up	561	Solyc01g080230.2	-	2.615	up
70	Solyc10g076220.1	Peroxidase	3.238	up	562	Solyc02g062690.2	-	0.418	down
71	Solyc07g006020.2	-	0.324	down	563	Solyc06g084330.2	-	2.217	up
72	Solyc06g076220.2	-	0.445	down	564	Solyc04g078270.2	-	2.492	up
73	Solyc04g009900.2	Phosphoenolpyruvate carboxylase kinase	0.232	down	565	Solyc10g085380.1	-	2.417	up
74	Solyc06g009150.1	-	0.235	down	566	Solyc06g083910.2	-	2.245	up
75	Solyc01g105370.2	-	3.342	up	567	Solyc06g069150.1	-	2.192	up
76	Solyc08g078460.2	-	2.371	up	568	Solyc01g096730.2	-	2.204	up
77	Solyc01g097880.2	-	2.182	up	569	Solyc02g067430.2	-	2.482	up
78	Solyc02g082450.2	-	4.812	up	570	Solyc08g074260.2	-	3.068	up
79	Solyc01g108860.2	-	3.357	up	571	Solyc01g006060.2	Dirigent protein	0.492	down
80	Solyc05g008370.1	-	0.401	down	572	Solyc08g081710.2	-	0.444	down
81	Solyc07g042190.2	-	0.333	down	573	Solyc01g095750.2	-	2.121	up
82	Solyc02g064970.2	Peroxidase	4.653	up	574	Solyc02g081690.1	-	2.527	up
83	Solyc01g103390.2	-	2.669	up	575	Solyc11g012500.1	-	0.368	down

84	Solyc03g093550.1	-	0.345	down	576	Solyc03g113210.2	-	0.435	down
85	Solyc05g054470.2	-	3.408	up	577	Solyc02g076630.1	-	2.574	up
86	Solyc01g108360.2	-	0.302	down	578	Solyc09g005690.2	Type I inositol polyphosphate 5-phosphatase 8	2.342	up
87	Solyc02g092460.2	-	3.285	up	579	Solyc05g007950.2	Ribonuclease T2	0.418	down
88	Solyc03g119340.2	-	2.53	up	580	Solyc09g014900.2	-	2.346	up
89	Solyc02g073580.1	-	2.909	up	581	Solyc01g111350.2	-	0.472	down
90	Solyc06g009130.2	Magnesium/proton exchanger family member	0.435	down	582	Solyc03g097610.2	Bidirectional sugar transporter SWEET	0.386	down
91	Solyc03g093560.1	-	0.384	down	583	Solyc12g045020.1	-	2.626	up
92	Solyc02g078570.2	-	2.145	up	584	Solyc07g006800.1	Glycosyltransferase	2.89	up
93	Solyc04g025750.2	WAT1-related protein	5.403	up	585	Solyc11g010760.1	-	0.467	down
94	Solyc08g082130.2	-	0.306	down	586	Solyc02g068140.2	-	0.45	down
95	Solyc10g085830.1	-	0.267	down	587	Solyc01g106920.2	-	2.615	up
96	Solyc07g056470.2	-	3.215	up	588	Solyc04g077240.2	-	2.144	up
97	Solyc05g006750.2	-	3.102	up	589	Solyc03g006650.1	-	3.031	up
98	Solyc06g062560.1	Putative phosphatase	0.182	down	590	Solyc09g005040.1	-	2.615	up
99	Solyc03g112200.1	-	0.243	down	591	Solyc10g007600.2	Peroxisomal (S)-2-hydroxy-acid oxidase GLO5	0.483	down
100	Solyc07g056480.2	-	2.453	up	592	Solyc01g105210.2	-	2.309	up
101	Solyc11g071940.1	-	0.183	down	593	Solyc07g052480.2	Isocitrate lyase	0.499	down
102	Solyc02g065000.1	-	0.349	down	594	Solyc07g043710.2	-	2.231	up
103	Solyc04g080660.2	Jasmonate	0.198	down	595	Solyc09g075540.1	-	2.795	up

		O-methyltransferase							
104	Solyc02g085400.2	-	0.332	down	596	Solyc07g065570.1	-	0.327	down
105	Solyc08g083190.2	-	0.308	down	597	Solyc12g006130.1	-	0.361	down
106	Solyc03g025330.2	-	3.166	up	598	Solyc03g111140.2	Malate synthase	2.708	up
107	Solyc08g067610.2	-	4.112	up	599	Solyc10g081840.1	-	2.331	up
108	Solyc01g108680.2	-	3.998	up	600	Solyc03g078620.1	-	2.537	up
		Ferric reduction							
109	Solyc03g112320.2	oxidase 8, mitochondrial	0.369	down	601	Solyc03g043880.2	Branched-chain-amino- acid aminotransferase	2.429	up
110	Solyc11g010990.1	-	4.315	up	602	Solyc02g077520.2	-	2.221	up
111	Solyc03g121420.2	-	0.297	down	603	Solyc01g096140.2	-	2.848	up
112	Solyc01g111080.2	Gibberellin-regulated protein 1	2.849	up	604	Solyc01g044420.2	-	2.308	up
113	Solyc04g007800.2	-	0.261	down	605	Solyc08g005790.2	Pectin acetylerase	2.634	up
114	Solyc04g015110.2	-	0.267	down	606	Solyc07g009100.2	-	2.723	up
115	Solyc06g062540.2	Putative acid phosphatase	0.212	down	607	Solyc06g010250.2	-	0.38	down
116	Solyc10g076610.1	Lysine--tRNA ligase	3.919	up	608	Solyc11g071720.1	-	2.929	up
117	Solyc06g075650.2	Tonoplast intrinsic protein 12	3.329	up	609	Solyc11g068440.1	-	2.02	up
		Methylcrotonoyl-CoA							
118	Solyc01g108030.2	carboxylase beta chain, mitochondrial	3.027	up	610	Solyc09g090990.2	PR10 protein	2.827	up
119	Solyc05g005170.2	-	0.273	down	611	Solyc08g068520.2	-	0.358	down
120	Solyc11g011180.1	-	0.394	down	612	Solyc01g109810.2	-	0.458	down
121	Solyc02g076670.2	-	3.654	up	613	Solyc03g031870.1	-	0.336	down

122	Solyc12g006110.1	-	4.274	up	614	Solyc02g065150.1	-	2.865	up
123	Solyc08g082190.2	-	0.311	down	615	Solyc02g081500.2	-	0.472	down
124	Solyc07g065910.1	-	0.267	down	616	Solyc08g081350.2	-	0.43	down
125	Solyc05g052830.2	-	3.287	up	617	Solyc12g005880.1	Hexosyltransferase	0.463	down
126	Solyc03g031940.2	-	0.472	down	618	Solyc10g005220.2	-	0.342	down
127	Solyc04g011770.2	-	2.728	up	619	Solyc03g082510.1	-	0.418	down
128	Solyc01g102890.2	-	3.138	up	620	Solyc06g008620.1	-	2.012	up
129	Solyc10g086680.1	-	0.291	down	621	Solyc03g078650.2	-	0.499	down
130	Solyc02g078500.2	-	3.548	up	622	Solyc03g063730.2	-	0.423	down
131	Solyc03g025870.2	-	3.889	up	623	Solyc07g008230.1	Glycosyltransferase	2.345	up
132	Solyc02g088200.2	-	0.363	down	624	Solyc01g080910.2	-	0.478	down
133	Solyc01g101050.2	Peroxidase	4.048	up	625	Solyc02g069600.2	-	0.447	down
134	Solyc05g046000.2	Peroxidase	3.596	up	626	Solyc10g076190.1	Peroxidase	2.305	up
135	Solyc05g012330.2	-	0.301	down	627	Solyc05g007790.2	CASP-like protein	2.406	up
136	Solyc03g031590.2	-	5.073	up	628	Solyc06g052020.2	-	0.424	down
137	Solyc06g053520.2	-	4.153	up	629	Solyc08g074970.1	-	0.432	down
138	Solyc08g060920.2	-	0.353	down	630	Solyc03g082550.2	-	0.358	down
139	Solyc01g108700.2	-	3.141	up	631	Solyc11g045110.1	-	0.467	down
140	Solyc07g049240.2	Peroxidase	4.383	up	632	Solyc12g087870.1	-	0.477	down
141	Solyc09g072700.2	Peroxidase	3.309	up	633	Solyc10g081970.1	-	2.341	up
142	Solyc07g063410.2	-	2.631	up	634	Solyc08g014240.2	-	2.952	up
143	Solyc07g008240.2	Non-symbiotic hemoglobin 1	2.238	up	635	Solyc04g014520.1	-	2.906	up
144	Solyc08g081620.2	Endoglucanase	0.262	down	636	Solyc03g006730.1	-	2.593	up
145	Solyc09g061410.1	-	0.387	down	637	Solyc01g105650.2	-	2.722	up
146	Solyc07g017570.2	-	3.306	up	638	Solyc08g007210.2	-	0.418	down

147	Solyc09g011710.2	-	0.35	down	639	Solyc02g067190.2	CASP-like protein	0.417	down
148	Solyc08g005580.2	-	0.387	down	640	Solyc02g090170.2	-	0.415	down
149	Solyc02g084410.2	-	0.279	down	641	Solyc11g005070.1	Amino acid transporter	0.487	down
150	Solyc08g082120.2	-	0.321	down	642	Solyc12g100250.1	-	2.437	up
151	Solyc07g049460.2	Laccase	4.253	up	643	Solyc07g055330.2	-	0.456	down
152	Solyc02g070080.2	-	4.646	up	644	Solyc01g108630.2	-	2.071	up
153	Solyc10g047810.1	Clade XVII lectin receptor kinase	4.346	up	645	Solyc08g080310.1	Protein Detoxification	2.947	up
154	Solyc09g011510.2	-	3.21	up	646	Solyc07g052460.2	-	2.163	up
155	Solyc12g005300.1	-	0.32	down	647	Solyc01g091160.2	Arginase 1	2.061	up
156	Solyc09g007830.2	Cytokinin riboside 5'-monophosphate phosphoribohydrolase	0.347	down	648	Solyc12g013620.1	Jasmonic acid 2	2.501	up
157	Solyc05g013630.1	-	0.384	down	649	Solyc11g005320.1	-	0.362	down
158	Solyc02g081390.2	-	2.349	up	650	Solyc08g007430.1	-	2.878	up
159	Solyc07g048060.1	-	2.77	up	651	Solyc02g093890.1	-	2.327	up
160	Solyc05g054050.2	Glutamate decarboxylase	3.944	up	652	Solyc01g103720.2	-	0.407	down
161	Solyc01g006310.2	Peroxidase	4.492	up	653	Solyc05g041920.2	-	2.366	up
162	Solyc03g006240.2	-	2.781	up	654	Solyc07g032390.1	-	0.492	down
163	Solyc03g026160.2	-	0.419	down	655	Solyc01g111250.2	-	2.122	up
164	Solyc11g013810.1	Nitrate reductase	2.943	up	656	Solyc01g087280.1	Polygalacturonase QRT2	0.343	down
165	Solyc12g005400.1	-	0.415	down	657	Solyc03g078470.2	-	2.834	up
166	Solyc04g082050.2	-	0.382	down	658	Solyc11g056360.1	-	2.836	up
167	Solyc02g091990.2	1-aminocyclopropane-	2.439	up	659	Solyc04g080920.1	Fe(3+)-Zn(2+) purple	0.381	down

1-carboxylate synthase					acid phosphatase 12				
		3							
168	Solyc07g048070.2	-	3.21	up	660	Solyc01g107080.2	-	2.014	up
169	Solyc09g082980.2	-	0.318	down	661	Solyc09g009810.1	-	0.356	down
170	Solyc07g007620.2	-	0.287	down	662	Solyc02g032800.1	-	0.408	down
171	Solyc03g116010.1	-	0.201	down	663	Solyc11g067330.1	-	2.361	up
172	Solyc02g087990.2	-	3.996	up	664	Solyc06g053830.2	Auxin-responsive protein	2.119	up
173	Solyc06g083900.2	-	0.442	down	665	Solyc07g006140.2	-	2.477	up
174	Solyc01g090890.2	-	0.264	down	666	Solyc02g079280.2	-	2.188	up
175	Solyc01g096400.2	-	0.372	down	667	Solyc10g050690.1	-	0.373	down
176	Solyc11g066140.1	-	4.368	up	668	Solyc04g081460.2	-	0.42	down
177	Solyc01g096740.2	-	2.65	up	669	Solyc01g107710.2	-	2.778	up
178	Solyc04g072890.2	-	2.19	up	670	Solyc06g061030.2	-	0.489	down
179	Solyc01g107790.2	-	0.376	down	671	Solyc09g092410.2	-	2.666	up
180	Solyc09g064170.1	-	2.554	up	672	Solyc07g066360.1	-	2.349	up
181	Solyc06g072350.2	CASP-like protein	0.297	down	673	Solyc03g097600.2	Bidirectional sugar transporter SWEET	0.391	down
182	Solyc03g096550.2	-	2.711	up	674	Solyc01g011430.2	-	2.281	up
183	Solyc08g079980.1	-	2.783	up	675	Solyc10g047170.1	-	2.823	up
184	Solyc04g015220.2	-	3.884	up	676	Solyc02g085290.2	-	0.438	down
185	Solyc10g084240.1	Peroxidase	0.345	down	677	Solyc04g064870.2	-	2.051	up
186	Solyc08g079860.1	-	0.26	down	678	Solyc09g098770.1	-	2.667	up
187	Solyc09g091060.2	-	0.314	down	679	Solyc01g100440.1	-	2.478	up
188	Solyc11g005350.1	WAT1-related protein	0.402	down	680	Solyc02g085870.2	3-ketoacyl-CoA synthase	0.474	down

189	Solyc01g067440.2	Monothiol glutaredoxin-S10	0.324	down	681	Solyc09g007190.2	-	0.478	down
190	Solyc07g053010.1	-	0.329	down	682	Solyc03g116910.2	Cinnamoyl-CoA reductase	2.223	up
191	Solyc03g098010.2	Purple acid phosphatase	0.292	down	683	Solyc03g031880.2	-	2.455	up
192	Solyc06g084380.2	-	3.267	up	684	Solyc04g017720.2	-	0.425	down
193	Solyc03g044300.2	APETALA2-like protein	2.689	up	685	Solyc03g120250.2	-	0.397	down
194	Solyc04g015210.2	-	2.974	up	686	Solyc08g074980.2	-	2.305	up
195	Solyc03g113120.2	-	2.91	up	687	Solyc07g006700.1	-	0.428	down
196	Solyc04g074470.1	-	2.685	up	688	Solyc02g062330.1	-	0.392	down
197	Solyc03g082530.1	-	2.528	up	689	Solyc12g006260.1	-	0.386	down
198	Solyc01g105310.2	Metacaspase 2	0.385	down	690	Solyc02g067310.2	-	0.452	down
199	Solyc03g117250.2	-	0.324	down	691	Solyc06g069130.2	Kinesin-like protein	2.456	up
200	Solyc11g008250.1	-	0.382	down	692	Solyc06g072400.1	-	2.43	up
201	Solyc10g084120.1	Plasmamembrane intrinsic protein 25 LOB	3.34	up	693	Solyc03g005980.2	-	0.449	down
202	Solyc05g009320.2	domain-containing protein 42	3.586	up	694	Solyc04g056380.2	Seipin-1	0.449	down
203	Solyc07g005920.1	-	3.912	up	695	Solyc11g005700.1	RING-type E3 ubiquitin transferase	0.458	down
204	Solyc12g088840.1	-	0.271	down	696	Solyc02g082170.1	-	2.643	up
205	Solyc04g080690.1	-	0.227	down	697	Solyc04g057940.2	RING-type E3 ubiquitin transferase	2.281	up

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206	Solyc03g007570.2	domain-containing protein At5g52790	3.272	up	698	Solyc02g065480.2	-	0.441	down
207	Solyc08g048370.2	-	3.096	up	699	Solyc02g083280.2	-	2.353	up
208	Solyc04g050620.2	-	2.273	up	700	Solyc04g016290.2	-	0.407	down
209	Solyc03g113840.1	-	3.421	up	701	Solyc09g015140.2	-	0.358	down
210	Solyc09g008910.1	-	0.312	down	702	Solyc12g008660.1	-	0.48	down
211	Solyc09g065430.2	-	2.995	up	703	Solyc02g084780.2	Peroxidase	2.046	up
212	Solyc06g072880.1	Glycosyltransferase	3.669	up	704	Solyc01g008650.2	-	2.111	up
213	Solyc07g042400.2	-	0.223	down	705	Solyc07g063020.1	-	2.139	up
214	Solyc05g005850.2	WAT1-related protein	3.123	up	706	Solyc04g071580.2	ABA-and ripening-induced protein	2.14	up
215	Solyc07g005390.2	-	0.303	down	707	Solyc02g082960.2	-	0.398	down
216	Solyc01g081270.2	-	3.046	up	708	Solyc11g006570.1	-	2.737	up
217	Solyc05g005750.2	-	2.124	up	709	Solyc03g098710.1	-	0.397	down
218	Solyc03g032080.2	-	3.832	up	710	Solyc09g082270.2	-	2.167	up
219	Solyc11g045460.1	-	3.241	up	711	Solyc03g059270.2	-	0.431	down
220	Solyc09g075870.1	Lipoxygenase	2.879	up	712	Solyc01g073810.2	-	2.615	up
221	Solyc06g059880.2	Acetolactate synthase	2.967	up	713	Solyc01g080460.2	-	0.462	down
222	Solyc11g007200.1	Copper transport protein CCH	2.148	up	714	Solyc11g011500.1	-	2.22	up
223	Solyc06g006110.2	-	0.289	down	715	Solyc11g065720.1	-	0.479	down
224	Solyc09g008430.2	-	2.162	up	716	Solyc04g017670.2	-	2.716	up
225	Solyc03g025720.2	-	2.547	up	717	Solyc02g063410.2	-	2.271	up
226	Solyc01g009430.2	-	0.416	down	718	Solyc08g075320.2	-	2.236	up

227	Solyc09g011500.2	-	3.005	up	719	Solyc12g098850.1	-	0.46	down
		Phosphomethylpyrimid							
228	Solyc06g006080.2	ine synthase, chloroplastic	0.472	down	720	Solyc07g006290.1	WAT1-related protein	2.717	up
229	Solyc02g031750.2	-	0.376	down	721	Solyc08g075880.2	-	0.491	down
230	Solyc09g072690.1	Cation/calcium exchanger 1	0.27	down	722	Solyc07g065500.1	-	2.558	up
231	Solyc08g008200.1	-	0.248	down	723	Solyc01g110100.2	-	0.498	down
232	Solyc01g005520.2	-	0.378	down	724	Solyc01g109740.2	Putative pectinesterase 11	2.759	up
233	Solyc10g006740.2	-	0.331	down	725	Solyc11g011110.1	-	2.449	up
234	Solyc04g007030.2	-	3.325	up	726	Solyc10g055680.1	Methyltransferase	0.475	down
235	Solyc07g018070.2	-	0.425	down	727	Solyc11g069970.1	-	0.491	down
236	Solyc07g056420.2	-	2.23	up	728	Solyc03g122360.2	-	0.456	down
237	Solyc06g035960.2	-	2.117	up	729	Solyc08g014360.1	-	2.747	up
238	Solyc05g015520.2	-	2.004	up	730	Solyc07g065900.2	Fructose-bisphosphate aldolase	2.32	up
239	Solyc05g006740.2	-	3.444	up	731	Solyc10g086100.1	-	2.743	up
240	Solyc08g077630.2	-	2.292	up	732	Solyc10g080260.1	-	2.231	up
241	Solyc01g098140.2	-	3.023	up	733	Solyc01g090340.2	-	0.464	down
242	Solyc01g100020.2	-	0.315	down	734	Solyc03g096350.2	-	0.463	down
243	Solyc03g114360.2	-	2.066	up	735	Solyc10g083210.1	-	2.334	up
244	Solyc01g105080.2	-	3.488	up	736	Solyc06g075550.2	-	2.111	up
245	Solyc10g011940.1	-	0.371	down	737	Solyc03g093930.2	-	2.321	up
246	Solyc03g013340.2	Nodulin26-like intrinsic protein 21	3.314	up	738	Solyc02g088270.2	-	0.385	down

247	Solyc01g073800.2	-	3.407	up	739	Solyc07g055260.2	-	0.497	down
248	Solyc01g005390.2	-	2.393	up	740	Solyc03g005330.1	Non-specific serine/threonine protein kinase	2.138	up
249	Solyc08g008050.2	-	3.816	up	741	Solyc08g061060.1	-	2.043	up
250	Solyc06g068040.2	-	0.281	down	742	Solyc08g080560.1	-	2.189	up
251	Solyc03g007290.2	Trehalose 6-phosphate phosphatase	2.987	up	743	Solyc04g014470.2	-	0.413	down
252	Solyc01g104800.2	-	3.586	up	744	Solyc07g042460.1	-	2.137	up
253	Solyc09g074570.1	-	0.294	down	745	Solyc05g010650.2	RING-type E3 ubiquitin transferase	2.608	up
254	Solyc01g017600.2	-	0.319	down	746	Solyc07g051930.1	-	0.37	down
255	Solyc07g052670.2	-	3.007	up	747	Solyc01g098790.1	-	2.212	up
256	Solyc05g011970.2	-	2.921	up	748	Solyc08g067300.1	F-box only protein 13	0.463	down
257	Solyc09g074850.2	-	3.557	up	749	Solyc09g066270.2	-	0.392	down
258	Solyc06g050790.2	-	2.064	up	750	Solyc08g083230.1	-	2.123	up
259	Solyc01g102300.2	-	0.47	down	751	Solyc01g102260.2	-	0.4	down
260	Solyc02g070900.1	-	2.638	up	752	Solyc03g071850.1	Glycosyltransferase	2.498	up
261	Solyc09g090210.2	-	2.383	up	753	Solyc03g097500.2	-	2.022	up
262	Solyc03g097410.1	Inositol-tetrakisphosph ate 1-kinase	2.317	up	754	Solyc07g007930.2	Probable galactinol-sucrose galactosyl transferase 6	2.18	up
263	Solyc01g087150.2	Protein Detoxification 43	2.98	up	755	Solyc12g094690.1	-	0.391	down
264	Solyc09g011630.2	Putative glutathione	2.744	up	756	Solyc07g009230.2	-	2.062	up

S-transferase T2									
265	Solyc12g008530.1	Pectinesterase	3.097	up	757	Solyc03g112220.1	-	0.442	down
266	Solyc04g063370.1	-	0.362	down	758	Solyc10g086690.1	-	2.069	up
267	Solyc08g007460.2	-	2.173	up	759	Solyc09g089890.1	-	0.435	down
268	Solyc06g072650.1	-	2.219	up	760	Solyc04g083140.1	-	2.478	up
269	Solyc01g056850.2	CTP synthase	2.506	up	761	Solyc05g051940.2	-	0.412	down
270	Solyc03g095510.2	-	0.498	down	762	Solyc10g006640.2	-	0.41	down
271	Solyc03g112100.2	-	3.106	up	763	Solyc12g057100.1	-	2.279	up
272	Solyc09g014300.2	-	0.415	down	764	Solyc02g069190.2	Iron-regulated transporter 2	2.648	up
273	Solyc11g072800.1	-	0.425	down	765	Solyc11g010700.1	-	0.437	down
274	Solyc07g055350.2	-	3.226	up	766	Solyc11g069570.1	Cytokinin riboside 5'-monophosphate phosphoribohydrolase	0.48	down
275	Solyc02g092420.2	-	2.524	up	767	Solyc08g006020.2	-	2.127	up
276	Solyc01g099180.2	Lipoxygenase	0.307	down	768	Solyc07g009080.2	-	2.303	up
277	Solyc02g070090.1	-	0.372	down	769	Solyc08g007270.2	-	0.419	down
278	Solyc09g097930.2	-	2.395	up	770	Solyc01g080150.2	Isopentenyltransferase 2	0.485	down
279	Solyc12g010170.1	-	2.257	up	771	Solyc05g044490.2	-	2.243	up
280	Solyc04g078860.2	Glutamate receptor	3.078	up	772	Solyc04g011970.1	-	2.628	up
281	Solyc10g076210.1	Peroxidase	2.653	up	773	Solyc06g062550.2	-	0.378	down
282	Solyc01g100600.2	-	0.448	down	774	Solyc05g007640.2	-	2.075	up
283	Solyc02g065220.2	-	0.358	down	775	Solyc01g108320.2	Peroxidase	2.004	up
284	Solyc10g076660.1	-	3.897	up	776	Solyc05g050220.2	-	2.077	up
285	Solyc09g005260.2	-	0.4	down	777	Solyc03g117150.2	ATPase 9, plasma	2.654	up

							membrane-type		
286	Solyc09g082760.2	-	0.348	down	778	Solyc02g066960.2	UDP-glycosyltransferase 83A1	2.446	up
287	Solyc04g079480.2	-	0.37	down	779	Solyc02g091050.2	Protein Detoxification	2.05	up
288	Solyc02g063330.2	-	2.156	up	780	Solyc06g060830.2	-	0.471	down
289	Solyc03g096540.2	-	2.52	up	781	Solyc08g077440.2	Lon protease homolog 2, peroxisomal	2.059	up
290	Solyc01g095450.2	-	0.303	down	782	Solyc11g069900.1	-	0.455	down
291	Solyc07g065660.2	-	2.898	up	783	Solyc03g078690.2	-	2.32	up
292	Solyc01g099910.2	-	0.43	down	784	Solyc03g020070.2	-	2.022	up
293	Solyc04g072310.2	-	2.255	up	785	Solyc11g011330.1	-	2.085	up
294	Solyc07g047740.2	Peroxidase	3.843	up	786	Solyc05g048820.2	-	2.366	up
295	Solyc07g064020.2	21.7 kDa class VI heat shock protein	0.378	down	787	Solyc09g089990.2	-	0.492	down
296	Solyc04g054450.1	-	0.356	down	788	Solyc03g113460.1	-	0.423	down
297	Solyc03g121300.2	-	0.383	down	789	Solyc01g081280.2	-	2.128	up
298	Solyc06g074710.1	-	3.546	up	790	Solyc11g069030.1	Blind	2.404	up
299	Solyc03g111120.2	-	0.326	down	791	Solyc08g076400.2	-	0.443	down
300	Solyc05g050090.2	-	0.333	down	792	Solyc07g052190.1	-	2.625	up
301	Solyc07g063930.2	-	0.388	down	793	Solyc07g053900.2	-	0.462	down
302	Solyc12g015920.1	-	3.63	up	794	Solyc12g057070.1	Glycosyltransferase	2.339	up
303	Solyc08g068390.2	-	0.401	down	795	Solyc08g061640.1	-	0.394	down
304	Solyc02g069730.2	CASP-like protein	3.275	up	796	Solyc11g010930.1	HVA22-like protein	2.097	up
305	Solyc04g080010.2	Glycosyltransferase	0.365	down	797	Solyc02g094110.1	-	2.193	up
306	Solyc12g005790.1	Peroxidase	3.358	up	798	Solyc10g017510.2	-	0.45	down
307	Solyc09g061890.2	Pectate lyase	2.656	up	799	Solyc04g055100.1	-	2.445	up

308	Solyc09g008660.2	-	0.43	down	800	Solyc03g116390.2	Late embryogenesis abundant protein	2.505	up
309	Solyc02g084590.2	GATA transcription factor 5	0.43	down	801	Solyc05g007240.1	-	0.47	down
310	Solyc01g008220.2	-	2.625	up	802	Solyc12g099580.1	WAT1-related protein	0.437	down
311	Solyc04g078340.2	-	3.434	up	803	Solyc05g010060.2	Phosphate transporter PHO1 homolog 1	0.449	down
312	Solyc02g083020.1	-	3.764	up	804	Solyc01g109100.2	-	0.488	down
313	Solyc05g011940.2	-	3.105	up	805	Solyc12g049070.1	Extensin-like protein Ext1	2.591	up
314	Solyc03g097240.2	-	2.114	up	806	Solyc10g076500.1	-	2.275	up
315	Solyc08g081480.2	-	0.453	down	807	Solyc01g108220.2	-	2.139	up
316	Solyc04g007050.2	-	3.09	up	808	Solyc07g042430.1	-	2.544	up
317	Solyc12g009930.1	Glycosyltransferase	0.499	down	809	Solyc01g111900.2	-	2.287	up
318	Solyc09g009560.1	Protein Terminal	0.275	down	810	Solyc11g071580.1	-	2.403	up
319	Solyc10g079150.1	-	0.306	down	811	Solyc01g102880.1	-	2.022	up
320	Solyc03g006080.2	-	0.449	down	812	Solyc10g005460.2	-	2.282	up
321	Solyc12g043040.1	-	0.327	down	813	Solyc01g006300.2	Peroxidase	0.487	down
322	Solyc10g049280.1	-	3.633	up	814	Solyc07g006740.2	Protein detoxification	2.118	up
323	Solyc07g055060.2	-	0.385	down	815	Solyc02g043810.2	-	2.08	up
324	Solyc12g010940.1	-	0.381	down	816	Solyc03g020050.2	-	2.177	up
325	Solyc02g089650.2	-	0.428	down	817	Solyc07g051820.2	-	0.471	down
326	Solyc01g059900.2	Dirigent protein	3.176	up	818	Solyc08g078200.1	Plasma membrane ATPase	0.449	down
327	Solyc07g041940.2	-	2.108	up	819	Solyc02g079350.2	-	2.197	up
328	Solyc06g060560.2	-	0.403	down	820	Solyc04g080530.2	Pectinesterase	0.412	down

329	Solyc04g064630.2	Bidirectional sugar transporter	2.214	up	821	Solyc04g008470.2	-	2.306	up
330	Solyc08g048390.1	-	2.778	up	822	Solyc05g014590.2	-	2.452	up
331	Solyc01g107400.2	-	2.681	up	823	Solyc03g005670.2	-	2.129	up
332	Solyc12g077370.1	-	2.96	up	824	Solyc01g087200.2	-	0.489	down
333	Solyc06g083080.2	-	0.448	down	825	Solyc07g045040.2	-	2.164	up
334	Solyc03g005320.2	3-ketoacyl-CoA synthase	2.545	up	826	Solyc07g006410.1	-	0.391	down
335	Solyc04g011440.2	Heat shock protein 70 isoform 3	0.453	down	827	Solyc01g109470.2	-	0.457	down
336	Solyc07g063690.1	-	0.324	down	828	Solyc11g072930.1	-	2.263	up
337	Solyc03g005280.2	-	0.293	down	829	Solyc12g088830.1	-	0.481	down
338	Solyc01g088830.2	-	3.147	up	830	Solyc06g059990.2	Alkyl transferase	0.449	down
339	Solyc01g096820.2	-	2.706	up	831	Solyc10g050730.1	-	0.413	down
340	Solyc07g062530.2	-	0.444	down	832	Solyc10g006440.2	-	0.419	down
341	Solyc08g077300.2	UMP-CMP kinase	0.435	down	833	Solyc01g079170.2	Galactinol synthase	0.492	down
342	Solyc07g054220.1	-	0.48	down	834	Solyc07g056210.2	-	2.408	up
343	Solyc09g066410.1	-	0.309	down	835	Solyc03g082790.2	-	2.484	up
344	Solyc01g010250.2	-	0.304	down	836	Solyc07g018180.1	-	0.434	down
345	Solyc02g032030.1	Dirigent protein SPX	3.718	up	837	Solyc10g044880.1	-	2.541	up
346	Solyc12g009480.1	domain-containing protein 2	0.367	down	838	Solyc08g082640.2	-	2.272	up
347	Solyc06g008760.1	-	0.275	down	839	Solyc03g005210.2	-	2.055	up
348	Solyc03g097940.2	-	0.398	down	840	Solyc04g009910.2	-	0.464	down
349	Solyc01g092950.2	-	2.072	up	841	Solyc03g111860.1	-	2.06	up

350	Solyc09g014480.1	-	0.488	down	842	Solyc10g018780.1	-	0.418	down
351	Solyc06g082240.2	Laccase	2.684	up	843	Solyc06g075450.1	-	2.243	up
352	Solyc09g010540.2	-	0.448	down	844	Solyc01g100390.2	-	2.497	up
353	Solyc08g079200.1	-	0.393	down	845	Solyc02g036440.2	-	2.529	up
354	Solyc03g111690.2	Pectate lyase	0.479	down	846	Solyc03g112010.2	-	0.396	down
355	Solyc09g089830.2	-	2.872	up	847	Solyc03g005650.1	-	2.342	up
356	Solyc02g062890.1	-	2.226	up	848	Solyc07g008420.2	-	2.264	up
357	Solyc04g014510.2	Glutamine synthetase	2.888	up	849	Solyc10g081790.1	-	2.384	up
358	Solyc06g051550.2	BHLH transcriptional regulator	3.123	up	850	Solyc06g069590.2	-	2.129	up
359	Solyc12g014010.1	-	3.034	up	851	Solyc08g006850.2	Patatin	2.535	up
360	Solyc09g014160.1	-	0.491	down	852	Solyc09g015450.2	-	2.06	up
361	Solyc04g078770.2	Heat stress transcription factor B-4	0.401	down	853	Solyc09g059460.2	-	2.013	up
362	Solyc08g029000.2	Lipoxygenase	2.971	up	854	Solyc12g094400.1	-	0.418	down
363	Solyc02g065190.2	-	2.888	up	855	Solyc08g079690.2	-	0.452	down
364	Solyc06g031710.2	WAT1-related protein	2.92	up	856	Solyc05g043360.1	Laccase	2.521	up
365	Solyc08g005640.2	-	0.383	down	857	Solyc07g026680.2	-	2.064	up
366	Solyc05g054210.2	-	0.491	down	858	Solyc01g094870.1	-	0.399	down
367	Solyc03g113580.1	-	2.623	up	859	Solyc11g066700.1	-	2.509	up
368	Solyc08g077910.2	-	2.809	up	860	Solyc08g048400.2	-	2.491	up
369	Solyc02g089190.1	-	3.828	up	861	Solyc06g051260.2	-	0.47	down
370	Solyc06g064620.2	-	2.94	up	862	Solyc02g077570.1	-	2.435	up
371	Solyc01g066880.2	-	0.409	down	863	Solyc05g015060.2	-	2.165	up
372	Solyc12g013700.1	-	2.425	up	864	Solyc06g066160.2	-	2.236	up
373	Solyc04g054740.2	-	0.337	down	865	Solyc04g007200.2	Methylketone synthase	2.474	up

					IIb				
374	Solyc10g085880.1	-	3.653	up	866	Solyc12g007290.1	-	2.427	up
375	Solyc01g102680.2	-	2.891	up	867	Solyc12g044840.1	-	0.48	down
376	Solyc01g098130.2	-	0.434	down	868	Solyc05g054650.1	-	2.431	up
Meiotic recombination									
377	Solyc09g082790.2	protein DMC1 homolog	0.471	down	869	Solyc04g081770.2	-	0.455	down
378	Solyc08g065380.2	-	2.174	up	870	Solyc02g086530.2	-	2.121	up
379	Solyc05g014550.1	-	0.314	down	871	Solyc07g053360.2	-	2.037	up
380	Solyc08g006730.1	-	2.407	up	872	Solyc11g012220.1	-	0.424	down
381	Solyc09g065590.2	VAN3-binding protein	0.456	down	873	Solyc02g090150.1	-	0.404	down
382	Solyc12g008930.1	-	3	up	874	Solyc01g107220.2	-	2.371	up
383	Solyc07g065920.2	-	0.4	down	875	Solyc05g056440.1	-	0.465	down
384	Solyc11g068370.1	-	2.564	up	876	Solyc01g107780.2	Glycosyltransferase	2.224	up
385	Solyc06g050530.2	Laccase	2.609	up	877	Solyc09g090790.2	-	2.214	up
386	Solyc03g006030.2	-	0.363	down	878	Solyc08g078930.1	-	2.102	up
387	Solyc10g079640.1	IAA-amino acid hydrolase ILR1-like 6	0.397	down	879	Solyc02g086700.2	-	0.428	down
388	Solyc11g072140.1	-	3.369	up	880	Solyc10g083300.1	-	2.271	up
389	Solyc01g098190.2	Sodium/hydrogen exchanger	0.455	down	881	Solyc03g097510.1	-	2.446	up
390	Solyc02g082910.2	-	2.927	up	882	Solyc03g114750.2	-	2.227	up
391	Solyc11g065930.1	-	0.499	down	883	Solyc05g024260.2	Bidirectional sugar transporter SWEET15	0.437	down
392	Solyc01g057260.2	-	0.301	down	884	Solyc10g076680.1	-	2.429	up
393	Solyc03g119740.2	-	0.458	down	885	Solyc06g051060.2	-	2.382	up

394	Solyc10g009350.2	-	0.325	down	886	Solyc03g005560.1	Inorganic phosphate transporter	0.483	down
395	Solyc06g071130.2	-	3.022	up	887	Solyc03g005530.1	Inorganic phosphate transporter	0.483	down
396	Solyc01g107840.2	-	3.767	up	888	Solyc11g067320.1	Sulfotransferase	2.147	up
397	Solyc03g033410.2	UBC11	0.378	down	889	Solyc10g050880.1	-	0.496	down
398	Solyc04g080710.2	-	0.478	down	890	Solyc12g005710.1	-	2.252	up
399	Solyc04g007590.1	WAT1-related protein	0.296	down	891	Solyc07g044750.2	-	2.012	up
400	Solyc02g088560.2	-	0.426	down	892	Solyc02g072570.1	-	2.158	up
401	Solyc01g105660.2	-	0.485	down	893	Solyc03g006090.2	-	0.477	down
402	Solyc02g092060.1	-	0.275	down	894	Solyc10g009430.2	-	0.41	down
403	Solyc06g076770.2	-	0.46	down	895	Solyc03g043640.2	-	0.412	down
404	Solyc03g096780.1	-	0.29	down	896	Solyc06g075970.2	-	2.427	up
405	Solyc12g005720.1	-	0.43	down	897	Solyc07g063210.2	-	2.36	up
406	Solyc05g053970.2	-	0.44	down	898	Solyc11g073150.1	-	2.388	up
407	Solyc05g021390.2	-	0.461	down	899	Solyc10g079410.1	-	0.414	down
408	Solyc01g080570.2	-	3.146	up	900	Solyc08g067620.2	-	2.347	up
409	Solyc07g062060.2	-	0.444	down	901	Solyc04g080560.2	-	2.043	up
410	Solyc11g012930.1	WAT1-related protein	2.638	up	902	Solyc05g007170.2	-	2.301	up
411	Solyc04g080640.1	-	0.37	down	903	Solyc10g078670.1	-	2.384	up
412	Solyc06g082770.2	-	2.644	up	904	Solyc09g010230.1	-	2.015	up
413	Solyc05g015350.2	-	3.646	up	905	Solyc12g006860.1	Cytochrome P450 734A1	2.177	up
414	Solyc10g078600.1	-	0.391	down	906	Solyc02g092820.2	Putative indole-3-acetic acid amido synthetase	2.204	up
415	Solyc02g087440.2	-	0.41	down	907	Solyc05g005040.2	-	2.315	up

416	Solyc03g077920.1	-	0.404	down	908	Solyc08g062220.2	Glycosyl transferase	2.313	up
417	Solyc02g091800.2	-	3.108	up	909	Solyc08g078520.2	-	0.47	down
418	Solyc01g091870.2	-	2.924	up	910	Solyc08g079850.1	p69F protein	0.472	down
419	Solyc02g081600.2	-	0.422	down	911	Solyc01g095830.2	-	2.384	up
420	Solyc05g055270.1	-	2.668	up	912	Solyc02g081180.1	-	2.126	up
421	Solyc02g063020.1	-	2.407	up	913	Solyc01g066560.2	Protein detoxification	0.46	down
422	Solyc08g079890.1	-	0.33	down	914	Solyc02g070410.1	-	2.394	up
423	Solyc04g076150.2	-	0.276	down	915	Solyc11g072560.1	-	2.113	up
424	Solyc06g067870.2	-	2.783	up	916	Solyc06g066560.1	-	2.131	up
425	Solyc06g074360.2	-	0.467	down	917	Solyc08g007480.1	-	2.334	up
426	Solyc04g007330.1	-	0.371	down	918	Solyc09g065440.2	-	2.256	up
		Myb family							
427	Solyc12g017370.1	transcription factor	0.454	down	919	Solyc03g093890.2	-	2.024	up
		APL							
428	Solyc12g098780.1	-	3.159	up	920	Solyc10g008810.2	-	2.37	up
429	Solyc04g078170.1	-	2.858	up	921	Solyc09g061700.2	-	0.49	down
430	Solyc03g116530.2	-	2.041	up	922	Solyc03g120020.2	-	2.025	up
431	Solyc02g081050.2	-	2.343	up	923	Solyc11g010810.1	-	0.423	down
432	Solyc02g083730.2	-	2.868	up	924	Solyc08g008430.2	Bidirectional sugar transporter	2.076	up
433	Solyc09g011580.2	-	2.22	up	925	Solyc07g008520.2	-	2.35	up
434	Solyc02g084930.2	-	2.924	up	926	Solyc12g096240.1	-	2.19	up
435	Solyc01g097470.2	-	2.695	up	927	Solyc03g007700.1	-	0.436	down
		Bidirectional sugar transporter							
436	Solyc03g097590.2		0.314	down	928	Solyc10g055190.1	Dirigent protein	2.351	up
437	Solyc08g042010.2	-	2.427	up	929	Solyc04g008190.1	-	2.057	up

438	Solyc07g055470.2	-	0.476	down	930	Solyc12g096620.1	-	2.201	up
439	Solyc02g082900.2	-	2.045	up	931	Solyc04g006940.2	Phospholipid-transporting ATPase	2.033	up
440	Solyc05g009620.2	-	3.143	up	932	Solyc11g042580.1	-	2.128	up
441	Solyc04g076950.2	Protein detoxification	0.366	down	933	Solyc12g094410.1	-	2.236	up
442	Solyc09g082530.1	Leucine-rich repeat extensin-like protein 6	2.715	up	934	Solyc02g089450.1	-	0.429	down
443	Solyc09g011190.1	-	2.226	up	935	Solyc10g007750.1	-	0.444	down
444	Solyc12g098790.1	-	3.182	up	936	Solyc02g090600.1	-	0.43	down
445	Solyc04g080250.2	Deoxyuridine 5'-triphosphate nucleotidohydrolase	2.189	up	937	Solyc05g018820.1	-	2.207	up
446	Solyc08g007060.2	-	2.964	up	938	Solyc09g015850.2	-	2.219	up
447	Solyc06g005130.2	Dof zinc finger protein DOF2.1	0.421	down	939	Solyc04g011480.2	CASP-like protein	2.174	up
448	Solyc02g077370.1	Pathogenesis-related genes transcriptional activator PTI5	2.044	up	940	Solyc02g021430.1	-	0.46	down
449	Solyc03g046380.1	-	2.785	up	941	Solyc11g051150.1	-	2.317	up
450	Solyc04g050440.2	Ammonium transporter	2.681	up	942	Solyc03g083500.2	-	2.104	up
451	Solyc01g100920.2	WAT1-related protein	2.164	up	943	Solyc04g014830.1	-	0.48	down
452	Solyc03g097570.2	Bidirectional sugar transporter	0.321	down	944	Solyc01g102380.2	Germin-like protein	2.201	up
453	Solyc07g042510.2	-	2.197	up	945	Solyc03g118900.1	WAT1-related protein	2.13	up
454	Solyc01g065980.2	ERF6	2.358	up	946	Solyc04g082000.2	Phospholipase D	2.185	up
455	Solyc02g089860.1	-	0.44	down	947	Solyc04g074880.2	-	0.498	down

456	Solyc04g058150.2	Metallothionein-like protein type 2 A	0.414	down	948	Solyc03g098260.1	-	0.487	down
457	Solyc07g006600.1	-	0.406	down	949	Solyc06g072670.2	-	2.086	up
458	Solyc01g105770.2	-	2.577	up	950	Solyc09g074040.1	-	0.461	down
459	Solyc01g009760.2	-	0.465	down	951	Solyc06g035980.2	-	2.283	up
460	Solyc01g088530.2	-	0.468	down	952	Solyc01g099590.2	Glutathione-S-transferase	0.442	down
461	Solyc02g092410.2	Adenylyl-sulfate kinase	2.659	up	953	Solyc10g076440.1	-	2.238	up
462	Solyc09g089790.2	-	2.495	up	954	Solyc06g050760.1	-	2.023	up
463	Solyc01g111820.2	-	2.565	up	955	Solyc11g007490.1	Glycosyl transferase	2.187	up
464	Solyc10g085350.1	-	0.326	down	956	Solyc10g008330.2	-	2.036	up
465	Solyc06g061280.2	-	0.5	down	957	Solyc08g078360.1	-	0.444	down
466	Solyc02g032910.1	Glycine rich protein	3.263	up	958	Solyc05g021580.2	-	2.257	up
467	Solyc08g007070.2	-	3.18	up	959	Solyc03g093940.1	-	2.215	up
468	Solyc12g096840.1	-	3.443	up	960	Solyc03g113150.2	Pectate lyase	2.262	up
469	Solyc03g020010.1	Lemir	2.214	up	961	Solyc01g009410.2	Peroxidase	2.253	up
470	Solyc01g102850.1	-	0.354	down	962	Solyc12g100080.1	-	2.266	up
471	Solyc07g045160.2	ATP-dependent 6-phosphofructokinase	0.41	down	963	Solyc09g098610.1	-		up
472	Solyc01g091830.2	-	2.355	up	964	Solyc02g071070.2	-		up
473	Solyc09g011620.1	-	3.354	up	965	Solyc11g007500.1	-		up
474	Solyc02g089630.2	-	2.398	up	966	Solyc08g079190.1	-		up
475	Solyc07g054560.1	-	0.488	down	967	Solyc07g044710.1	-		up
476	Solyc08g077900.2	Expansin-like B1	2.618	up	968	Solyc04g078350.1	-		up
477	Solyc02g090210.2	-	2.64	up	969	Solyc02g091600.1	-		down
478	Solyc12g056920.1	-	2.264	up	970	Solyc03g116290.1	-		up

479	Solyc03g114800.1	Sulfotransferase	0.494	down	971	Solyc09g065420.2	-	up
480	Solyc02g071750.2	-	0.455	down	972	Solyc03g006150.2	-	up
481	Solyc01g090210.2	-	0.468	down	973	Solyc03g026120.2	-	up
482	Solyc06g076800.2	Cytochrome P450 86A1	2.855	up	974	Solyc04g014450.1	-	up
483	Solyc08g048290.2	-	0.407	down	975	Solyc08g007780.2	-	up
484	Solyc11g072920.1	Peroxidase	2.145	up	976	Solyc06g083020.1	Carboxypeptidase	up
485	Solyc12g044420.1	-	0.318	down	977	Solyc06g076550.2	-	up
486	Solyc11g006900.1	-	0.403	down	978	Solyc01g100980.2	-	down
487	Solyc09g097990.1	-	2.155	up	979	Solyc12g096310.1	-	up
488	Solyc04g054500.2	-	2.019	up	980	Solyc06g051830.1	Potassium transporter	up
489	Solyc02g088210.2	-	0.406	down	981	Solyc06g065970.1	-	up
490	Solyc05g041140.2	-	3.257	up	982	Solyc01g104870.2	-	up
491	Solyc02g086890.2	-	2.866	up	983	Solyc04g051270.1	CASP-like protein	up
492	Solyc09g010800.2	Metallothionein-like protein type 2 B	0.433	down	984	Solyc01g093980.2	Gibberellin 20-oxidase 4	down

Appendix C The 984 differentially expressed genes (DEGs) were significantly enriched in 44 terms among biological process, cellular component and molecular function categories based on Gene ontology (GO) analysis (FDR < 0.05)

GO id	GO description	Term type	DEGs number	DEGs percent
GO:0032501	multicellular organismal process	Biological process	34	34/984
GO:0050789	regulation of biological process	Biological process	165	165/984
GO:0040007	growth	Biological process	4	4/984
GO:0022414	reproductive process	Biological process	14	14/984
GO:0098754	detoxification	Biological process	30	30/984
GO:0050896	response to stimulus	Biological process	158	158/984
GO:0009987	cellular process	Biological process	433	433/984
GO:0071840	cellular component organization or biogenesis	Biological process	59	59/984
GO:0000003	reproduction	Biological process	14	14/984
GO:0065007	biological regulation	Biological process	205	205/984
GO:0048519	negative regulation of biological process	Biological process	12	12/984
GO:0051179	localization	Biological process	139	139/984
GO:0032502	developmental process	Biological process	53	53/984
GO:0044699	single-organism process	Biological process	422	422/984
GO:0008152	metabolic process	Biological process	477	477/984
GO:0048518	positive regulation of biological process	Biological process	12	12/984
GO:0023052	signaling	Biological process	54	54/984
GO:0002376	immune system process	Biological process	6	6/984
GO:0051704	multi-organism process	Biological process	10	10/984
GO:0005623	cell	Cellular component	390	390/984
GO:0043226	organelle	Cellular component	203	203/984
GO:0044422	organelle part	Cellular component	42	42/984

GO:0044464	cell part	Cellular component	384	384/984
GO:0016020	membrane	Cellular component	324	324/984
GO:0099080	supramolecular complex	Cellular component	2	2/984
GO:0055044	symplast	Cellular component	16	16/984
GO:0031974	membrane-enclosed lumen	Cellular component	5	5/984
GO:0044425	membrane part	Cellular component	282	282/984
GO:0005576	extracellular region	Cellular component	58	58/984
GO:0032991	macromolecular complex	Cellular component	15	15/984
GO:0044421	extracellular region part	Cellular component	3	3/984
GO:0030054	cell junction	Cellular component	16	16/984
GO:0000988	transcription factor activity, protein binding	Molecular function	16	16/984
GO:0001071	nucleic acid binding transcription factor activity	Molecular function	48	48/984
GO:0009055	electron carrier activity	Molecular function	13	13/984
GO:0005215	transporter activity	Molecular function	102	102/984
GO:0005488	binding	Molecular function	377	377/984
GO:0003824	catalytic activity	Molecular function	418	418/984
GO:0004871	signal transducer activity	Molecular function	13	13/984
GO:0005198	structural molecule activity	Molecular function	4	4/984
GO:0098772	molecular function regulator	Molecular function	15	15/984
GO:0045735	nutrient reservoir activity	Molecular function	8	8/984
GO:0016209	antioxidant activity	Molecular function	30	30/984
GO:0060089	molecular transducer activity	Molecular function	13	13/984

Appendix D The 984 differentially expressed genes (DEGs) were significantly enriched in 206 pathways in Kyoto Encyclopedia of Genes and Genomes (KEGG) database (FDR < 0.05)

Gene number	Pathway id	KEGG description	Ratio in study	Ratio in population
31	map00940	Phenylpropanoid biosynthesis	31/401	290/12870
16	map00480	Glutathione metabolism	16/401	127/12870
4	map00905	Brassinosteroid biosynthesis	4/401	17/12870
4	map00750	Vitamin B6 metabolism	4/401	16/12870
7	map00052	Galactose metabolism	7/401	63/12870
2	map04911	Insulin secretion	2/401	4/12870
2	map04725	Cholinergic synapse	2/401	3/12870
3	map04012	ErbB signaling pathway	3/401	12/12870
4	map04066	HIF-1 signaling pathway	4/401	23/12870
5	map00980	Metabolism of xenobiotics by cytochrome P450	5/401	41/12870
5	map00910	Nitrogen metabolism	5/401	36/12870
5	map00983	Drug metabolism - other enzymes	5/401	40/12870
5	map05204	Chemical carcinogenesis	5/401	40/12870
4	map00290	Valine, leucine and isoleucine biosynthesis	4/401	31/12870
2	map04740	Olfactory transduction	2/401	7/12870
2	map04713	Circadian entrainment	2/401	7/12870
2	map04971	Gastric acid secretion	2/401	7/12870
5	map05225	Hepatocellular carcinoma	5/401	47/12870
3	map04912	GnRH signaling pathway	3/401	18/12870
3	map05214	Glioma	3/401	18/12870
3	map05205	Proteoglycans in cancer	3/401	20/12870
2	map04925	Aldosterone synthesis and secretion	2/401	9/12870

6	map00410	beta-Alanine metabolism	6/401	73/12870
4	map00982	Drug metabolism - cytochrome P450	4/401	36/12870
7	map00561	Glycerolipid metabolism	7/401	94/12870
7	map05200	Pathways in cancer	7/401	94/12870
3	map04024	cAMP signaling pathway	3/401	22/12870
6	map00330	Arginine and proline metabolism	6/401	77/12870
4	map00591	Linoleic acid metabolism	4/401	41/12870
10	map00500	Starch and sucrose metabolism	10/401	170/12870
2	map04745	Phototransduction - fly	2/401	10/12870
2	map04750	Inflammatory mediator regulation of TRP channels	2/401	10/12870
2	map05031	Amphetamine addiction	2/401	11/12870
2	map04916	Melanogenesis	2/401	11/12870
2	map04934	Cushing syndrome	2/401	12/12870
5	map00592	alpha-Linolenic acid metabolism	5/401	66/12870
5	map00030	Pentose phosphate pathway	5/401	67/12870
2	map04720	Long-term potentiation	2/401	13/12870
7	map00620	Pyruvate metabolism	7/401	115/12870
14	map04626	Plant-pathogen interaction	14/401	288/12870
3	map04922	Glucagon signaling pathway	3/401	34/12870
1	map00232	Caffeine metabolism	1/401	3/12870
2	map04261	Adrenergic signaling in cardiomyocytes	2/401	15/12870
2	map00830	Retinol metabolism	2/401	15/12870
7	map00270	Cysteine and methionine metabolism	7/401	121/12870
3	map04921	Oxytocin signaling pathway	3/401	32/12870
5	map05418	Fluid shear stress and atherosclerosis	5/401	76/12870
2	map04360	Axon guidance	2/401	16/12870

8	map00040	Pentose and glucuronate interconversions	8/401	145/12870
4	map00250	Alanine, aspartate and glutamate metabolism	4/401	57/12870
3	map00565	Ether lipid metabolism	3/401	36/12870
3	map00901	Indole alkaloid biosynthesis	3/401	36/12870
3	map00770	Pantothenate and CoA biosynthesis	3/401	39/12870
3	map00220	Arginine biosynthesis	3/401	39/12870
3	map00073	Cutin, suberine and wax biosynthesis	3/401	40/12870
5	map00945	Stilbenoid, diarylheptanoid and gingerol biosynthesis	5/401	83/12870
1	map00333	Prodigiosin biosynthesis	1/401	4/12870
1	map00401	Novobiocin biosynthesis	1/401	4/12870
2	map04728	Dopaminergic synapse	2/401	20/12870
4	map01524	Platinum drug resistance	4/401	60/12870
5	map00280	Valine, leucine and isoleucine degradation	5/401	87/12870
3	map05231	Choline metabolism in cancer	3/401	38/12870
3	map04910	Insulin signaling pathway	3/401	38/12870
3	map00100	Steroid biosynthesis	3/401	42/12870
4	map00380	Tryptophan metabolism	4/401	66/12870
1	map04670	Leukocyte transendothelial migration	1/401	5/12870
5	map00630	Glyoxylate and dicarboxylate metabolism	5/401	90/12870
2	map00740	Riboflavin metabolism	2/401	23/12870
3	map01040	Biosynthesis of unsaturated fatty acids	3/401	46/12870
3	map04612	Antigen processing and presentation	3/401	46/12870
2	map00780	Biotin metabolism	2/401	25/12870
5	map00710	Carbon fixation in photosynthetic organisms	5/401	99/12870
1	map05221	Acute myeloid leukemia	1/401	7/12870
1	map05146	Amoebiasis	1/401	7/12870

11	map05152	Tuberculosis	11/401	260/12870
3	map04217	Necroptosis	3/401	49/12870
2	map04020	Calcium signaling pathway	2/401	26/12870
1	map05032	Morphine addiction	1/401	8/12870
1	map05033	Nicotine addiction	1/401	8/12870
2	map00650	Butanoate metabolism	2/401	31/12870
2	map00902	Monoterpenoid biosynthesis	2/401	31/12870
1	map01522	Endocrine resistance	1/401	9/12870
1	map04930	Type II diabetes mellitus	1/401	9/12870
2	map04920	Adipocytokine signaling pathway	2/401	33/12870
2	map04931	Insulin resistance	2/401	33/12870
4	map00941	Flavonoid biosynthesis	4/401	84/12870
1	map04380	Osteoclast differentiation	1/401	10/12870
1	map00981	Insect hormone biosynthesis	1/401	10/12870
1	map00140	Steroid hormone biosynthesis	1/401	11/12870
1	map04913	Ovarian steroidogenesis	1/401	11/12870
1	map04630	Jak-STAT signaling pathway	1/401	11/12870
1	map00660	C5-Branched dibasic acid metabolism	1/401	12/12870
1	map01521	EGFR tyrosine kinase inhibitor resistance	1/401	12/12870
2	map04150	mTOR signaling pathway	2/401	39/12870
2	map04213	Longevity regulating pathway - multiple species	2/401	39/12870
1	map00430	Taurine and hypotaurine metabolism	1/401	13/12870
1	map04659	Th17 cell differentiation	1/401	13/12870
1	map04727	GABAergic synapse	1/401	14/12870
1	map05212	Pancreatic cancer	1/401	14/12870
1	map05410	Hypertrophic cardiomyopathy (HCM)	1/401	14/12870

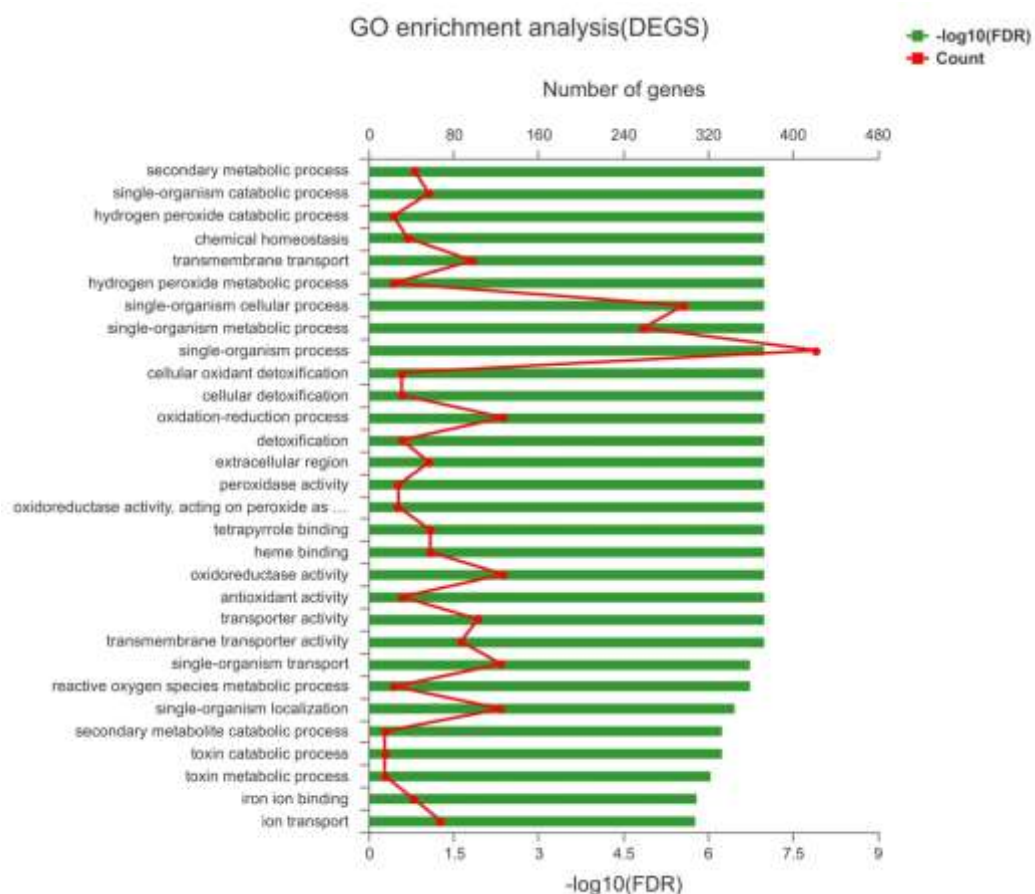
1	map00625	Chloroalkane and chloroalkene degradation	1/401	14/12870
3	map00061	Fatty acid biosynthesis	3/401	68/12870
1	map04137	Mitophagy - animal	1/401	16/12870
1	map05224	Breast cancer	1/401	15/12870
1	map04724	Glutamatergic synapse	1/401	15/12870
1	map05323	Rheumatoid arthritis	1/401	15/12870
2	map00062	Fatty acid elongation	2/401	43/12870
2	map04072	Phospholipase D signaling pathway	2/401	43/12870
2	map04014	Ras signaling pathway	2/401	43/12870
4	map00564	Glycerophospholipid metabolism	4/401	110/12870
1	map05230	Central carbon metabolism in cancer	1/401	17/12870
2	map04211	Longevity regulating pathway	2/401	49/12870
2	map04151	PI3K-Akt signaling pathway	2/401	48/12870
2	map04142	Lysosome	2/401	48/12870
2	map00906	Carotenoid biosynthesis	2/401	46/12870
2	map00909	Sesquiterpenoid and triterpenoid biosynthesis	2/401	46/12870
2	map00904	Diterpenoid biosynthesis	2/401	45/12870
3	map00071	Fatty acid degradation	3/401	75/12870
1	map05210	Colorectal cancer	1/401	18/12870
1	map00903	Limonene and pinene degradation	1/401	18/12870
1	map04216	Ferroptosis	1/401	18/12870
2	map04371	Apelin signaling pathway	2/401	47/12870
8	map04722	Neurotrophin signaling pathway	8/401	241/12870
2	map04152	AMPK signaling pathway	2/401	51/12870
1	map05215	Prostate cancer	1/401	20/12870
1	map00531	Glycosaminoglycan degradation	1/401	20/12870

3	map04310	Wnt signaling pathway	3/401	88/12870
1	map05163	Human cytomegalovirus infection	1/401	21/12870
1	map00730	Thiamine metabolism	1/401	21/12870
2	map04140	Autophagy - animal	2/401	56/12870
3	map00562	Inositol phosphate metabolism	3/401	87/12870
2	map04218	Cellular senescence	2/401	54/12870
1	map00790	Folate biosynthesis	1/401	23/12870
1	map00590	Arachidonic acid metabolism	1/401	23/12870
13	map04075	Plant hormone signal transduction	13/401	409/12870
7	map05140	Leishmaniasis	7/401	221/12870
1	map00999	Biosynthesis of secondary metabolites - unclassified	1/401	22/12870
1	map04933	AGE-RAGE signaling pathway in diabetic complications	1/401	22/12870
2	map04114	Oocyte meiosis	2/401	60/12870
7	map04624	Toll and Imd signaling pathway	7/401	230/12870
1	map05167	Kaposi sarcoma-associated herpesvirus infection	1/401	27/12870
1	map04928	Parathyroid hormone synthesis, secretion and action	1/401	27/12870
1	map04212	Longevity regulating pathway - worm	1/401	29/12870
2	map00053	Ascorbate and aldarate metabolism	2/401	64/12870
2	map00350	Tyrosine metabolism	2/401	66/12870
1	map05226	Gastric cancer	1/401	31/12870
1	map04071	Sphingolipid signaling pathway	1/401	33/12870
1	map04666	Fc gamma R-mediated phagocytosis	1/401	34/12870
1	map04919	Thyroid hormone signaling pathway	1/401	34/12870
1	map00950	Isoquinoline alkaloid biosynthesis	1/401	34/12870
6	map04621	NOD-like receptor signaling pathway	6/401	232/12870
4	map00010	Glycolysis / Gluconeogenesis	4/401	158/12870

1	map04136	Autophagy - other	1/401	46/12870
1	map04068	FoxO signaling pathway	1/401	46/12870
3	map04146	Peroxisome	3/401	112/12870
2	map00360	Phenylalanine metabolism	2/401	88/12870
2	map00051	Fructose and mannose metabolism	2/401	82/12870
1	map00920	Sulfur metabolism	1/401	43/12870
6	map05142	Chagas disease (American trypanosomiasis)	6/401	226/12870
6	map05162	Measles	6/401	240/12870
6	map04010	MAPK signaling pathway	6/401	240/12870
6	map04064	NF-kappa B signaling pathway	6/401	229/12870
1	map04710	Circadian rhythm	1/401	41/12870
1	map04113	Meiosis - yeast	1/401	41/12870
1	map04721	Synaptic vesicle cycle	1/401	40/12870
1	map00960	Tropane, piperidine and pyridine alkaloid biosynthesis	1/401	39/12870
1	map04530	Tight junction	1/401	45/12870
1	map04139	Mitophagy - yeast	1/401	51/12870
1	map00860	Porphyrin and chlorophyll metabolism	1/401	49/12870
1	map02010	ABC transporters	1/401	52/12870
1	map04712	Circadian rhythm – plant	1/401	52/12870
1	map00130	Ubiquinone and other terpenoid-quinone biosynthesis	1/401	52/12870
6	map05133	Pertussis	6/401	225/12870
1	map05166	Human T-cell leukemia virus 1 infection	1/401	50/12870
1	map00340	Histidine metabolism	1/401	50/12870
6	map05145	Toxoplasmosis	6/401	239/12870
1	map00460	Cyanoamino acid metabolism	1/401	55/12870
1	map00400	Phenylalanine, tyrosine and tryptophan biosynthesis	1/401	55/12870

3	map00908	Zeatin biosynthesis	3/401	116/12870
1	map04013	MAPK signaling pathway - fly	1/401	57/12870
6	map04620	Toll-like receptor signaling pathway	6/401	224/12870
6	map05169	Epstein-Barr virus infection	6/401	273/12870
1	map04138	Autophagy - yeast	1/401	60/12870
1	map04723	Retrograde endocannabinoid signaling	1/401	60/12870
7	map04016	MAPK signaling pathway - plant	7/401	307/12870
1	map00640	Propanoate metabolism	1/401	65/12870
1	map05165	Human papillomavirus infection	1/401	64/12870
5	map05164	Influenza A	5/401	248/12870
4	map00240	Pyrimidine metabolism	4/401	218/12870
1	map00310	Lysine degradation	1/401	76/12870
1	map00900	Terpenoid backbone biosynthesis	1/401	74/12870
1	map04932	Non-alcoholic fatty liver disease (NAFLD)	1/401	74/12870
5	map04141	Protein processing in endoplasmic reticulum	5/401	286/12870
2	map03010	Ribosome	2/401	465/12870
2	map03018	RNA degradation	2/401	143/12870
1	map04070	Phosphatidylinositol signaling system	1/401	92/12870
1	map04145	Phagosome	1/401	101/12870
1	map05206	MicroRNAs in cancer	1/401	103/12870
4	map04144	Endocytosis	4/401	259/12870
2	map04714	Thermogenesis	2/401	179/12870
2	map04120	Ubiquitin mediated proteolysis	2/401	196/12870
1	map00970	Aminoacyl-tRNA biosynthesis	1/401	158/12870
1	map00520	Amino sugar and nucleotide sugar metabolism	1/401	171/12870
2	map03040	Spliceosome	2/401	240/12870

2	map00230	Purine metabolism	2/401	249/12870
3	map00190	Oxidative phosphorylation	3/401	319/12870



Appendix E The top 30 Gene Ontology (GO) enrichment terms of the 984 differentially expressed genes (DEGs)

Appendix H List of primer pairs used in qRT-PCR assay

Gene id	Gene description		Primer pairs	Expected size of PCR product (bp)
Solyc06g005060.2	Elongation factor 1-alpha	FWD	CACTTCCCCTTCTTCTGG	86
		REV	GTTGCTGTCGGTGTTGTC	
Solyc03g116910.2	Cinnamoyl-CoA reductase	FWD	CGGTTTCATTGCCTCTTG	84
		REV	ATTTTACCAGGGTTTCTA	
Solyc12g005790.1	Peroxidase	FWD	AAGCAACAATAATCACAT	103
		REV	TAAACCCTTGGGATTCTA	
Solyc09g011630.2	Putative glutathione S-transferase T2	FWD	AATTTGTGAGTCAATGGTG	117
		REV	TCAAAGAACTTAGCCCCAA	
Solyc10g078550.1	Glutamate dehydrogenase	FWD	CTTACGCCTCCCATCCTC	100
		REV	ATGTGCAAGACTCACAAC	
Solyc10g084120.1	Plasmamembrane intrinsic protein 25	FWD	ATTATGTGATCATCATTTTCGTA	86
		REV	AGGATTATCAGGCTCACG	
Solyc01g099590.2	Glutathione-S-transferase	FWD	GTTGATGGCAAGGTAAAA	82
		REV	GTGAGATTAGAATGATGG	
Solyc06g006080.2	Phosphomethylpyrimidine synthase	FWD	CTCCAAGGAATACAGGTC	144
		REV	TTTAGCCATTTCACTCGA	
Solyc04g080010.2	Glycosyltransferase	FWD	ATCTCCTCGTTTCTCACC	109
		REV	CTTTTGGGCGGTTCTTCA	
Solyc04g080660.2	Jasmonate O-methyltransferase	FWD	TTCAACCACAGCCCTAAT	84
		REV	AGCGTTTCTTCAAATCTATCAA	
Solyc10g079640.1	IAA-amino acid hydrolase 1CR1-like 6	FWD	TTGCCCAGAAAACAGAGC	150

REV

CCAACGGAAACCGATAAG
