Supplemental Materials

Tables

Table S1. Raw data of sequencing sample in study.

sample_name	total_raw_read (M)	total_clean_read (M)	total_clean_base (Gb)	clean_read_ratio (%)	Total Mapping to genome (%)	Total Mapping to gene (%)
F0_1	46.2	42.21	6.33	91.38	82.06	71.23
F0_2	46.2	42.47	6.37	91.94	81.93	71.81
F0_3	46.2	42.67	6.4	92.36	81.8	71.48
F1_1	47.79	43.11	6.47	90.2	82.54	71.73
F1_2	47.79	42.16	6.32	88.23	81.9	70.16
F1_3	47.79	42.47	6.37	88.87	80.48	69.12
M0_1	47.79	43.36	6.5	90.74	83.85	71.82
M0_2	46.2	42.31	6.35	91.58	84.24	71.91
M0_3	47.79	43.4	6.51	90.81	84.74	72.96
M1_1	46.2	42.42	6.36	91.82	85.76	74.32
M1_2	46.2	42.71	6.41	92.44	86.29	74.24
M1_3	46.2	42.41	6.36	91.81	85.11	72.93

Table S2. Level 2 Gene Ontology annotation of highly expression genes in four floral buds.

Term type	Term type level 2	GO Term	F0			F1			M0			M1		
			Term Candidate Gene Num	Rich Ratio	P value	Term Candidate Gene Num	Rich Ratio	P value	Term Candidate Gene Num	Rich Ratio	P value	Term Candidate Gene Num	Rich Ratio	P value
biological_process	cellular process	amide biosynthetic process	67	0.071811	8.13E-26	66	0.07074	3.56E-23	59	0.063237	1.12E-24	41	0.043944	1.04E-11
	cellular process	cellular amide metabolic process	70	0.066986	3.10E-25	71	0.067943	5.58E-24	64	0.061244	3.83E-26	46	0.044019	3.97E-13
	cellular process	translation	64	0.07248	8.00E-25	63	0.071348	2.80E-22	56	0.06342	2.04E-23	38	0.043035	1.25E-10
	cellular process	peptide metabolic process	67	0.068789	9.61E-25	68	0.069815	1.39E-23	61	0.062628	2.41E-25	43	0.044148	2.49E-12
	cellular process	peptide biosynthetic process	64	0.07119	2.15E-24	63	0.070078	7.22E-22	38	0.042269	2.10E-10	56	0.062291	4.90E-23
	metabolic process	organonitrogen compound biosynthetic process	85	0.046347	4.10E-20	83	0.045256	7.65E-17	74	0.040349	1.89E-19	55	0.029989	4.32E-09
	cellular process	cellular nitrogen compound biosynthetic process	95	0.038214	6.07E-17	95	0.038214	1.12E-14	79	0.031778	8.78E-15	65	0.026146	2.56E-08
	metabolic process	organic substance biosynthetic process	121	0.030556	1.19E-14	122	0.030808	2.36E-12	102	0.025758	1.28E-13			
	metabolic process	biosynthetic process	124	0.029301	1.10E-13				104	0.024575	1.42E-12			
	cellular process	cellular biosynthetic process							101	0.025778	1.82E-13			
	metabolic process	organonitrogen compound metabolic process										85	0.02301	2.57E-08
cellular_component	cell	ribosome	62	0.086713	5.62E-32	62	0.086713	5.81E-30	55	0.076923	2.72E-30	38	0.053147	3.70E-15
	cell part	intracellular ribonucleoprotein complex	69	0.060105	5.38E-26	67	0.058362	1.86E-22	61	0.053136	5.96E-25	42	0.036585	2.99E-11

	organelle	non-membrane-bounded organelle	83	0.049701	5.67E-26	85	0.050898	8.37E-25	74	0.044311	9.15E-26	56	0.033533	2.29E-13
	cell	intracellular non-membrane-bounded organelle	83	0.049701	5.67E-26	85	0.050898	8.37E-25	74	0.044311	9.15E-26	56	0.033533	2.29E-13
	macromolecular complex	ribonucleoprotein complex	69	0.060105	5.38E-26	61	0.053136	5.96E-25	42	0.036585	2.99E-11	67	0.058362	1.86E-22
	organelle part	ribosomal subunit	29	0.128889	8.05E-20	26	0.115556	7.10E-16	24	0.106667	1.23E-16	17	0.075556	1.31E-09
	macromolecular complex	macromolecular complex	99	0.032534	1.33E-17	107	0.035163	5.62E-19	85	0.027933	1.23E-16	73	0.023989	2.88E-10
	cell	cytosolic ribosome	19	0.188119	1.69E-16	16	0.158416	2.30E-12	15	0.148515	5.94E-13			
	cell	cytosolic part	20	0.15873	8.49E-16	17	0.134921	6.84E-12						
	organelle part	nucleosome										11	0.1375	2.24E-09
	macromolecular complex	DNA packaging complex										11	0.11828	1.14E-08
	macromolecular complex	protein-DNA complex										11	0.11	2.47E-08
molecular_function	structural molecule activity	structural constituent of ribosome	61	0.094281	2.81E-32	62	0.095827	4.81E-31	54	0.083462	2.70E-30	38	0.058733	7.46E-16
	structural molecule activity	structural molecule activity	65	0.082383	5.94E-31	67	0.084918	2.12E-30	56	0.070976	8.00E-28	40	0.050697	1.64E-14

Table S3. KEGG enrichment analysis of highly expressed genes in four floral buds

	Pathway ID	Pathway Name	Level 1	Level 2	Term Candidate Gene Num	Total Candidate Gene Num	Term Gene Num	Total Gene Num	Rich Ratio	P value	Q value
	ko03010	Ribosome	Genetic Information Processing	Translation	68	364	1200	27882	0.056667	7.45E-25	7.82E-23
	ko00941	Flavonoid biosynthesis	Metabolism	Biosynthesis of other secondary metabolites	11	364	314	27882	0.035032	0.002984	0.156664
	ko04145	Phagosome	Cellular Processes	Transport and catabolism	11	364	342	27882	0.032164	0.005632	0.197128
	ko00250	Alanine, aspartate and glutamate metabolism	Metabolism	Amino acid metabolism	6	364	177	27882	0.033898	0.029141	0.339979
	ko00270	Cysteine and methionine metabolism	Metabolism	Amino acid metabolism	13	364	491	27882	0.026477	0.013095	0.339979
	ko00480	Glutathione metabolism	Metabolism	Metabolism of other amino acids	10	364	374	27882	0.026738	0.025989	0.339979
	ko00630	Glyoxylate and dicarboxylate metabolism	Metabolism	Carbohydrate metabolism	8	364	275	27882	0.029091	0.028738	0.339979
	ko00710	Carbon fixation in photosynthetic organisms	Metabolism	Energy metabolism	7	364	225	27882	0.031111	0.028928	0.339979
	ko00944	Flavone and flavonol biosynthesis	Metabolism	Biosynthesis of other secondary metabolites	2	364	18	27882	0.111111	0.022654	0.339979
	ko00591	Linoleic acid metabolism	Metabolism	Lipid metabolism	6	364	198	27882	0.030303	0.046167	0.446224
	ko00592	alpha-Linolenic acid metabolism	Metabolism	Lipid metabolism	8	364	309	27882	0.02589	0.050997	0.446224
	ko00910	Nitrogen metabolism	Metabolism	Energy metabolism	5	364	153	27882	0.03268	0.050744	0.446224
	ko00195	Photosynthesis	Metabolism	Energy metabolism	6	364	221	27882	0.027149	0.07071	0.503931
F0	ko01200	Carbon metabolism	Metabolism	Global and overview maps	19	364	1018	27882	0.018664	0.076789	0.503931

	ko01230	Biosynthesis of amino acids	Metabolism	Global and overview maps	22	364	1205	27882	0.018257	0.072411	0.503931
	ko04075	Plant hormone signal transduction	Environmental Information Processing	Signal transduction	26	364	1472	27882	0.017663	0.07374	0.503931
	ko00290	Valine, leucine and isoleucine biosynthesis	Metabolism	Amino acid metabolism	4	364	129	27882	0.031008	0.089089	0.550258
	ko00660	C5-Branched dibasic acid metabolism	Metabolism	Carbohydrate metabolism	2	364	55	27882	0.036364	0.161334	0.891583
	ko00900	Terpenoid backbone biosynthesis	Metabolism	Metabolism of terpenoids and polyketides	5	364	217	27882	0.023041	0.155543	0.891583
	ko03010	Ribosome	Genetic Information Processing	Translation	68	415	1200	27882	0.056667	1.62E-21	1.76E-19
	ko00480	Glutathione metabolism	Metabolism	Metabolism of other amino acids	18	415	374	27882	0.048128	1.50E-05	0.000819
	ko00195	Photosynthesis	Metabolism	Energy metabolism	11	415	221	27882	0.049774	0.000513	0.018372
	ko04145	Phagosome	Cellular Processes	Transport and catabolism	14	415	342	27882	0.040936	0.000674	0.018372
	ko00941	Flavonoid biosynthesis	Metabolism	Biosynthesis of other secondary metabolites	13	415	314	27882	0.041401	0.000936	0.020404
	ko00196	Photosynthesis - antenna proteins	Metabolism	Energy metabolism	5	415	57	27882	0.087719	0.001582	0.028734
	ko00250	Alanine, aspartate and glutamate metabolism	Metabolism	Amino acid metabolism	7	415	177	27882	0.039548	0.017116	0.266525
	ko00710	Carbon fixation in photosynthetic organisms	Metabolism	Energy metabolism	8	415	225	27882	0.035556	0.01998	0.27223
	ko00944	Flavone and flavonol biosynthesis	Metabolism	Biosynthesis of other secondary metabolites	2	415	18	27882	0.111111	0.028892	0.349919
	ko00270	Cysteine and methionine metabolism	Metabolism	Amino acid metabolism	13	415	491	27882	0.026477	0.033589	0.366122
F1	ko00010	Glycolysis / Gluconeogenesis	Metabolism	Carbohydrate metabolism	14	415	576	27882	0.024306	0.051137	0.506719

	ko01200	Carbon metabolism	Metabolism	Global and overview maps	21	415	1018	27882	0.020629	0.08396	0.687269
	ko01230	Biosynthesis of amino acids	Metabolism	Global and overview maps	24	415	1205	27882	0.019917	0.091886	0.687269
	ko03050	Proteasome	Genetic Information Processing	Folding, sorting and degradation	7	415	253	27882	0.027668	0.085243	0.687269
	ko04146	Peroxisome	Cellular Processes	Transport and catabolism	10	415	416	27882	0.024038	0.094578	0.687269
	ko00190	Oxidative phosphorylation	Metabolism	Energy metabolism	12	415	531	27882	0.022599	0.101394	0.690744
	ko00290	Valine, leucine and isoleucine biosynthesis	Metabolism	Amino acid metabolism	4	415	129	27882	0.031008	0.126899	0.768444
	ko00020	Citrate cycle (TCA cycle)	Metabolism	Carbohydrate metabolism	5	415	182	27882	0.027473	0.136328	0.782093
	ko00051	Fructose and mannose metabolism	Metabolism	Carbohydrate metabolism	6	415	249	27882	0.024096	0.168552	0.88895
	ko00591	Linoleic acid metabolism	Metabolism	Lipid metabolism	5	415	198	27882	0.025253	0.17398	0.88895
	ko03010	Ribosome	Genetic Information Processing	Translation	60	311	1200	27882	0.05	8.12E-23	7.79E-21
	ko00591	Linoleic acid metabolism	Metabolism	Lipid metabolism	7	311	198	27882	0.035354	0.007011	0.224351
	ko04145	Phagosome	Cellular Processes	Transport and catabolism	10	311	342	27882	0.02924	0.005339	0.224351
	ko00480	Glutathione metabolism	Metabolism	Metabolism of other amino acids	10	311	374	27882	0.026738	0.009715	0.233163
	ko00250	Alanine, aspartate and glutamate metabolism	Metabolism	Amino acid metabolism	6	311	177	27882	0.033898	0.014744	0.269849
	ko00944	Flavone and flavonol biosynthesis	Metabolism	Biosynthesis of other secondary metabolites	2	311	18	27882	0.111111	0.016866	0.269849
M0	ko00910	Nitrogen metabolism	Metabolism	Energy metabolism	5	311	153	27882	0.03268	0.028814	0.345771

	ko00941	Flavonoid biosynthesis	Metabolism	Biosynthesis of other secondary metabolites	8	311	314	27882	0.025478	0.025329	0.345771
	ko00270	Cysteine and methionine metabolism	Metabolism	Amino acid metabolism	10	311	491	27882	0.020367	0.049988	0.533209
	ko03050	Proteasome	Genetic Information Processing	Folding, sorting and degradation	6	311	253	27882	0.023715	0.065084	0.624802
	ko00190	Oxidative phosphorylation	Metabolism	Energy metabolism	10	311	531	27882	0.018832	0.075623	0.65998
	ko00900	Terpenoid backbone biosynthesis	Metabolism	Metabolism of terpenoids and polyketides	5	311	217	27882	0.023041	0.096534	0.77227
	ko00592	alpha-Linolenic acid metabolism	Metabolism	Lipid metabolism	6	311	309	27882	0.019417	0.133159	0.983324
	ko00010	Glycolysis / Gluconeogenesis	Metabolism	Carbohydrate metabolism	6	311	576	27882	0.010417	0.62331	0.999751
	ko00020	Citrate cycle (TCA cycle)	Metabolism	Carbohydrate metabolism	1	311	182	27882	0.005495	0.871027	0.999751
	ko00030	Pentose phosphate pathway	Metabolism	Carbohydrate metabolism	1	311	260	27882	0.003846	0.946607	0.999751
	ko00040	Pentose and glucuronate interconversions	Metabolism	Carbohydrate metabolism	3	311	807	27882	0.003717	0.994453	0.999751
	ko00051	Fructose and mannose metabolism	Metabolism	Carbohydrate metabolism	1	311	249	27882	0.004016	0.939527	0.999751
	ko00053	Ascorbate and aldarate metabolism	Metabolism	Carbohydrate metabolism	3	311	514	27882	0.005837	0.927941	0.999751
	ko00071	Fatty acid degradation	Metabolism	Lipid metabolism	1	311	228	27882	0.004386	0.923308	0.999751
	ko03010	Ribosome	Genetic Information Processing	Translation	44	329	1200	27882	0.036667	2.78E-11	2.78E-09
	ko00195	Photosynthesis	Metabolism	Energy metabolism	10	329	221	27882	0.045249	0.000318	0.015887
M1	ko00480	Glutathione metabolism	Metabolism	Metabolism of other amino acids	12	329	374	27882	0.032086	0.00176	0.058673

ko00196	Photosynthesis - antenna proteins	Metabolism	Energy metabolism	4	329	57	27882	0.070175	0.004599	0.114981
ko00250	Alanine, aspartate and glutamate metabolism	Metabolism	Amino acid metabolism	6	329	177	27882	0.033898	0.018901	0.233164
ko00270	Cysteine and methionine metabolism	Metabolism	Amino acid metabolism	12	329	491	27882	0.02444	0.014416	0.233164
ko00710	Carbon fixation in photosynthetic organisms	Metabolism	Energy metabolism	7	329	225	27882	0.031111	0.01786	0.233164
ko00944	Flavone and flavonol biosynthesis	Metabolism	Biosynthesis of other secondary metabolites	2	329	18	27882	0.111111	0.018749	0.233164
ko04145	Phagosome	Cellular Processes	Transport and catabolism	9	329	342	27882	0.026316	0.020985	0.233164
ko00591	Linoleic acid metabolism	Metabolism	Lipid metabolism	6	329	198	27882	0.030303	0.030565	0.304307
ko00941	Flavonoid biosynthesis	Metabolism	Biosynthesis of other secondary metabolites	8	329	314	27882	0.025478	0.03371	0.304307
ko04120	Ubiquitin mediated proteolysis	Genetic Information Processing	Folding, sorting and degradation	16	329	824	27882	0.019417	0.036517	0.304307
ko00010	Glycolysis / Gluconeogenesis	Metabolism	Carbohydrate metabolism	11	329	576	27882	0.019097	0.081325	0.625577
ko00910	Nitrogen metabolism	Metabolism	Energy metabolism	4	329	153	27882	0.026144	0.107888	0.770631
ko00051	Fructose and mannose metabolism	Metabolism	Carbohydrate metabolism	5	329	249	27882	0.02008	0.172613	0.914335
ko00190	Oxidative phosphorylation	Metabolism	Energy metabolism	9	329	531	27882	0.016949	0.178322	0.914335
ko00592	alpha-Linolenic acid metabolism	Metabolism	Lipid metabolism	6	329	309	27882	0.019417	0.160086	0.914335
ko01230	Biosynthesis of amino acids	Metabolism	Global and overview maps	18	329	1205	27882	0.014938	0.182867	0.914335
ko03050	Proteasome	Genetic Information Processing	Folding, sorting and degradation	5	329	253	27882	0.019763	0.18048	0.914335

ko00290	Valine, leucine and isoleucine biosynthesis	Metabolism	Amino acid metabolism	3	329	129	27882	0.023256	0.195725	0.932026

Table S4. Level 2 gene ontology annotation of middlingly expressed genes in four floral buds.

	Term type	Term type level 2	GO Term	Term Candidate Gene Num	Rich Ratio	P value
F0	biological_process	metabolic process	organonitrogen compound metabolic process	500	0.135355	2.99E-08
		metabolic process	small molecule metabolic process	250	0.148633	2.04E-07
		cellular process	organic acid metabolic process	157	0.149952	3.01E-05
		cellular process	oxoacid metabolic process	156	0.15	3.14E-05
		cellular process	carboxylic acid metabolic process	152	0.148148	7.49E-05
		biological regulation	regulation of translational initiation	15	0.319149	0.000101
		metabolic process	organonitrogen compound biosynthetic process	249	0.135769	0.000184
		cellular process	nucleobase-containing small molecule metabolic process	75	0.165929	0.000197
	cellular_component	cell	intracellular	1177	0.120755	5.05E-07
		cell	cytoplasm	698	0.127071	1.25E-06
		cell	intracellular part	1120	0.120872	1.44E-06
		cell	endomembrane system	164	0.150597	1.55E-05
		cell	cytosol	94	0.165202	3.69E-05
		cell	cell	1275	0.117609	5.09E-05
		cell	cytoplasmic part	530	0.126221	0.000104
		macromolecular complex	peptidase complex	26	0.234234	0.000145
		cell	cell part	1253	0.117179	0.000162
	molecular_function	binding	translation initiation factor activity	41	0.241176	4.19E-07
		binding	translation factor activity, RNA binding	52	0.185714	5.04E-05
		catalytic activity	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	40	0.19802	8.55E-05
F1	biological_process	metabolic process	small molecule metabolic process	256	0.1522	1.04E-07
		biological regulation	regulation of translational initiation	16	0.340426	3.12E-05

	cellular process	organic acid metabolic process	159	0.151862	3.96E-05
	cellular process	oxoacid metabolic process	158	0.151923	4.11E-05
	cell	intracellular	1203	0.123423	2.74E-08
	cell	intracellular part	1141	0.123138	2.62E-07
	cell	cell	1312	0.121022	4.57E-07
	cell	cytoplasm	707	0.128709	1.08E-06
	cell	endomembrane system	172	0.157943	1.12E-06
cellular_component	cell	cell part	1290	0.12064	1.88E-06
	cell	cytosol	98	0.172232	7.51E-06
	cell	cytoplasmic part	544	0.129555	1.88E-05
	macromolecular complex	macromolecular complex	403	0.132435	4.99E-05
	macromolecular complex	protein complex	209	0.143939	4.70E-05
	macromolecular complex	peptidase complex	27	0.243243	6.83E-05
	cell	endoplasmic reticulum	78	0.171429	7.31E-05
	binding	translation initiation factor activity	40	0.235294	1.27E-06
molecular_function	catalytic activity	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	42	0.207921	1.93E-05
	binding	coenzyme binding	126	0.150718	4.86E-05
	catalytic activity	oxidoreductase activity, acting on CH-OH group of donors	50	0.185185	8.38E-05
	metabolic process	organonitrogen compound metabolic process	432	0.116946	7.32E-07
	cellular process	nucleobase-containing small molecule metabolic process	75	0.165929	1.69E-06
biological_process	cellular process	cellular nitrogen compound biosynthetic process	300	0.120676	5.67E-06
	metabolic process	small molecule metabolic process	213	0.126635	8.28E-06
	cellular process	ribose phosphate metabolic process	49	0.176259	2.12E-05
M0	cellular process	purine-containing compound metabolic process	46	0.179688	2.28E-05

	metabolic process	organic cyclic compound biosynthetic process	214	0.124854	2.02E-05
	cellular process	pyruvate metabolic process	19	0.267606	2.77E-05
	cellular process	nucleotide metabolic process	57	0.163793	4.26E-05
	cellular process	nucleoside phosphate metabolic process	57	0.163324	4.62E-05
	cellular process	heterocycle biosynthetic process	200	0.124069	5.73E-05
	cellular process	purine ribonucleotide metabolic process	39	0.182243	6.76E-05
	cellular process	purine nucleotide metabolic process	39	0.179724	9.24E-05
	cell	cytoplasm	606	0.110322	2.39E-05
cellular_component	cell	intracellular part	975	0.105223	2.94E-05
	cell	intracellular	1020	0.104648	3.75E-05
	binding	translation initiation factor activity	35	0.205882	5.44E-06
molecular_function	binding	protein heterodimerization activity	24	0.230769	2.23E-05
	binding	translation factor activity, RNA binding	46	0.164286	9.83E-05
	catalytic activity	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	36	0.178218	0.000104
	cellular process	cellular nitrogen compound biosynthetic process	284	0.11424	1.89E-05
	metabolic process	organonitrogen compound metabolic process	404	0.109367	1.44E-05
biological_process	metabolic process	small molecule metabolic process	201	0.119501	2.99E-05
	metabolic process	biosynthetic process	450	0.106333	6.84E-05
	cellular component organization or biogenesis	formation of translation preinitiation complex	13	0.276596	0.000221
	cellular process	cytoplasmic translational initiation	13	0.276596	0.000221
	cell	cytoplasm	593	0.107956	1.13E-06
cellular_component	cell	proteasome complex	22	0.23913	2.42E-05
	cell	intracellular	979	0.100441	2.14E-05
M1	cell	cell	1082	0.099806	9.12E-06

	cell	cytoplasmic part	456	0.108597	2.27E-05
	macromolecular complex	peptidase complex	25	0.225225	2.11E-05
	macromolecular complex	endopeptidase complex	22	0.23913	2.42E-05
	cell	cell part	1061	0.099224	5.19E-05
	cell	cytosol	80	0.140598	8.93E-05
	cell	eukaryotic translation initiation factor 3 complex	13	0.276596	0.000236
	binding	translation initiation factor activity	35	0.205882	2.08E-06
molecular_function	structural molecule activity	structural molecule activity	105	0.13308	1.82E-05
	binding	protein heterodimerization activity	22	0.211538	0.000102
	catalytic activity	threonine-type endopeptidase activity	11	0.297297	0.000259

Table S5. KEGG enrichment analysis of middlingly expressed genes in four floral buds.

Pathway ID	Pathway Name	Level 1	Level 2	Term Candidate Gene Num	Total Candidate Gene Num	Term Gene Num	Total Gene Num	Rich Ratio	P value
ko03050	Proteasome	Genetic Information Processing	Folding, sorting and degradation	49	2638	253	27882	0.193676	1.00E-06
ko01200	Carbon metabolism	Metabolism	Global and overview maps	137	2638	1018	27882	0.134578	1.50E-05
ko01230	Biosynthesis of amino acids	Metabolism	Global and overview maps	151	2638	1205	27882	0.125311	0.000203
ko03010	Ribosome	Genetic Information Processing	Translation	146	2638	1200	27882	0.121667	0.000907
ko00860	Porphyrin and chlorophyll metabolism	Metabolism	Metabolism of cofactors and vitamins	33	2638	203	27882	0.162562	0.001481
ko00250	Alanine, aspartate and glutamate metabolism	Metabolism	Amino acid metabolism	28	2638	177	27882	0.158192	0.004771
ko04075	Plant hormone signal transduction	Environmental Information Processing	Signal transduction	168	2638	1472	27882	0.11413	0.005772
ko00010	Glycolysis / Gluconeogenesis	Metabolism	Carbohydrate metabolism	72	2638	576	27882	0.125	0.009017
ko00620	Pyruvate metabolism	Metabolism	Carbohydrate metabolism	45	2638	330	27882	0.136364	0.008167
ko04145	Phagosome	Cellular Processes	Transport and catabolism	46	2638	342	27882	0.134503	0.009624
ko04136	Autophagy - other	Cellular Processes	Transport and catabolism	26	2638	173	27882	0.150289	0.012198
ko03060	Protein export	Genetic Information Processing	Folding, sorting and degradation	32	2638	226	27882	0.141593	0.013854
ko04146	Peroxisome	Cellular Processes	Transport and catabolism	53	2638	416	27882	0.127404	0.016048
ko00020	Citrate cycle (TCA cycle)	Metabolism	Carbohydrate metabolism	26	2638	182	27882	0.142857	0.022219
ko00030	Pentose phosphate pathway	Metabolism	Carbohydrate metabolism	35	2638	260	27882	0.134615	0.021356
ko00710	Carbon fixation in photosynthetic organisms	Metabolism	Energy metabolism	31	2638	225	27882	0.137778	0.021665
ko00280	Valine, leucine and isoleucine degradation	Metabolism	Amino acid metabolism	36	2638	271	27882	0.132841	0.023771
ko03015	mRNA surveillance pathway	Genetic Information Processing	Translation	107	2638	945	27882	0.113228	0.028908
ko01212	Fatty acid metabolism	Metabolism	Global and overview maps	37	2638	286	27882	0.129371	0.031715
ko04712	Circadian rhythm - plant	Organismal Systems	Environmental adaptation	52	2638	425	27882	0.122353	0.03313

ko03050	Proteasome	Genetic Information Processing	Folding, sorting and degradation	47	2608	253	27882	0.185771	3.99E-06
ko01200	Carbon metabolism	Metabolism	Global and overview maps	137	2608	1018	27882	0.134578	8.53E-06
ko01230	Biosynthesis of amino acids	Metabolism	Global and overview maps	150	2608	1205	27882	0.124481	0.000172
ko00860	Porphyrin and chlorophyll metabolism	Metabolism	Metabolism of cofactors and vitamins	35	2608	203	27882	0.172414	0.000293
ko00280	Valine, leucine and isoleucine degradation	Metabolism	Amino acid metabolism	41	2608	271	27882	0.151292	0.001463
ko04075	Plant hormone signal transduction	Environmental Information Processing	Signal transduction	171	2608	1472	27882	0.116168	0.00166
ko00071	Fatty acid degradation	Metabolism	Lipid metabolism	35	2608	228	27882	0.153509	0.002434
ko00010	Glycolysis / Gluconeogenesis	Metabolism	Carbohydrate metabolism	73	2608	576	27882	0.126736	0.00478
ko00250	Alanine, aspartate and glutamate metabolism	Metabolism	Amino acid metabolism	28	2608	177	27882	0.158192	0.004078
ko00620	Pyruvate metabolism	Metabolism	Carbohydrate metabolism	46	2608	330	27882	0.139394	0.004109
ko01212	Fatty acid metabolism	Metabolism	Global and overview maps	41	2608	286	27882	0.143357	0.003967
ko03010	Ribosome	Genetic Information Processing	Translation	139	2608	1200	27882	0.115833	0.004771
ko01040	Biosynthesis of unsaturated fatty acids	Metabolism	Lipid metabolism	21	2608	124	27882	0.169355	0.00542
ko04145	Phagosome	Cellular Processes	Transport and catabolism	46	2608	342	27882	0.134503	0.007903
ko04712	Circadian rhythm - plant	Organismal Systems	Environmental adaptation	55	2608	425	27882	0.129412	0.008678
ko00604	Glycosphingolipid biosynthesis - ganglio series	Metabolism	Glycan biosynthesis and metabolism	19	2608	114	27882	0.166667	0.009361
ko04136	Autophagy - other	Cellular Processes	Transport and catabolism	26	2608	173	27882	0.150289	0.010632
ko03015	mRNA surveillance pathway	Genetic Information Processing	Translation	109	2608	945	27882	0.115344	0.012849
ko04122	Sulfur relay system	Genetic Information Processing	Folding, sorting and degradation	9	2608	42	27882	0.214286	0.014069
ko00630	Glyoxylate and dicarboxylate metabolism	Metabolism	Carbohydrate metabolism	37	2608	275	27882	0.134545	0.015773
ko03050	Proteasome	Genetic Information Processing	Folding, sorting and degradation	40	2285	253	27882	0.158103	4.52E-05
ko00250	Alanine, aspartate and glutamate metabolism	Metabolism	Amino acid metabolism	28	2285	177	27882	0.158192	0.00058

ko03010	Ribosome	Genetic Information Processing	Translation	131	2285	1200	27882	0.109167	0.000437
ko01200	Carbon metabolism	Metabolism	Global and overview maps	112	2285	1018	27882	0.11002	0.000841
ko00860	Porphyrin and chlorophyll metabolism	Metabolism	Metabolism of cofactors and vitamins	29	2285	203	27882	0.142857	0.002375
ko04075	Plant hormone signal transduction	Environmental Information Processing	Signal transduction	149	2285	1472	27882	0.101223	0.004021
ko03015	mRNA surveillance pathway	Genetic Information Processing	Translation	99	2285	945	27882	0.104762	0.00686
ko04122	Sulfur relay system	Genetic Information Processing	Folding, sorting and degradation	9	2285	42	27882	0.214286	0.006123
ko00710	Carbon fixation in photosynthetic organisms	Metabolism	Energy metabolism	29	2285	225	27882	0.128889	0.010154
ko00440	Phosphonate and phosphinate metabolism	Metabolism	Metabolism of other amino acids	7	2285	32	27882	0.21875	0.013369
ko04136	Autophagy - other	Cellular Processes	Transport and catabolism	23	2285	173	27882	0.132948	0.014514
ko04145	Phagosome	Cellular Processes	Transport and catabolism	40	2285	342	27882	0.116959	0.014584
ko01230	Biosynthesis of amino acids	Metabolism	Global and overview maps	119	2285	1205	27882	0.098755	0.018912
ko00071	Fatty acid degradation	Metabolism	Lipid metabolism	28	2285	228	27882	0.122807	0.020651
ko00190	Oxidative phosphorylation	Metabolism	Energy metabolism	57	2285	531	27882	0.107345	0.022094
ko01040	Biosynthesis of unsaturated fatty acids	Metabolism	Lipid metabolism	17	2285	124	27882	0.137097	0.024764
ko00062	Fatty acid elongation	Metabolism	Lipid metabolism	15	2285	110	27882	0.136364	0.034909
ko00010	Glycolysis / Gluconeogenesis	Metabolism	Carbohydrate metabolism	59	2285	576	27882	0.102431	0.044808
ko00943	Isoflavonoid biosynthesis	Metabolism	Biosynthesis of other secondary metabolites	16	2285	124	27882	0.129032	0.046617
ko00770	Pantothenate and CoA biosynthesis	Metabolism	Metabolism of cofactors and vitamins	20	2285	165	27882	0.121212	0.050295
ko03010	Ribosome	Genetic Information Processing	Translation	135	2208	1200	27882	0.1125	2.03E-05
ko03050	Proteasome	Genetic Information Processing	Folding, sorting and degradation	39	2208	253	27882	0.15415	4.70E-05
ko04145	Phagosome	Cellular Processes	Transport and catabolism	46	2208	342	27882	0.134503	0.000294
ko03015	mRNA surveillance pathway	Genetic Information Processing	Translation	103	2208	945	27882	0.108995	0.000586
ko01200	Carbon metabolism	Metabolism	Global and overview maps	108	2208	1018	27882	0.10609	0.001118

ko04075	Plant hormone signal transduction	Environmental Information Processing	Signal transduction	149	2208	1472	27882	0.101223	0.001082
ko00440	Phosphonate and phosphinate metabolism	Metabolism	Metabolism of other amino acids	8	2208	32	27882	0.25	0.002865
ko00250	Alanine, aspartate and glutamate metabolism	Metabolism	Amino acid metabolism	25	2208	177	27882	0.141243	0.003401
ko01040	Biosynthesis of unsaturated fatty acids	Metabolism	Lipid metabolism	19	2208	124	27882	0.153226	0.004072
ko04122	Sulfur relay system	Genetic Information Processing	Folding, sorting and degradation	9	2208	42	27882	0.214286	0.004897
ko01212	Fatty acid metabolism	Metabolism	Global and overview maps	35	2208	286	27882	0.122378	0.006821
ko04136	Autophagy - other	Cellular Processes	Transport and catabolism	23	2208	173	27882	0.132948	0.009942
ko00190	Oxidative phosphorylation	Metabolism	Energy metabolism	57	2208	531	27882	0.107345	0.011917
ko00280	Valine, leucine and isoleucine degradation	Metabolism	Amino acid metabolism	32	2208	271	27882	0.118081	0.015244
ko00860	Porphyrin and chlorophyll metabolism	Metabolism	Metabolism of cofactors and vitamins	25	2208	203	27882	0.123153	0.018442
ko00780	Biotin metabolism	Metabolism	Metabolism of cofactors and vitamins	11	2208	70	27882	0.157143	0.021172
ko00061	Fatty acid biosynthesis	Metabolism	Lipid metabolism	22	2208	182	27882	0.120879	0.031023
ko00630	Glyoxylate and dicarboxylate metabolism	Metabolism	Carbohydrate metabolism	31	2208	275	27882	0.112727	0.029729
ko00710	Carbon fixation in photosynthetic organisms	Metabolism	Energy metabolism	26	2208	225	27882	0.115556	0.033578
ko00071	Fatty acid degradation	Metabolism	Lipid metabolism	26	2208	228	27882	0.114035	0.03859

Table S6. Level 2 gene ontology annotation of the DEGs between M0 vs. F0, M1 vs. F1, and 7029 DEGs of the two compared groups in ontologies.

Group	Term type	Term type level 2	GO Term	Term Candidate Gene Num	Rich Ratio	P value
M0 vs. F0	biological_process	cellular process	photosynthetic electron transport in photosystem II	11	0.34375	2.08E-05
		response to stimulus	response to toxic substance	17	0.236111	3.70E-05
		cellular process	photosynthetic electron transport chain	11	0.275	0.000206
		response to stimulus	response to herbicide	8	0.333333	0.000363
		cellular process	malonyl-CoA metabolic process	3	1	0.000502
		cellular process	malonyl-CoA biosynthetic process	3	1	0.000502
		cellular process	toxin metabolic process	7	0.333333	0.000851
	cellular_component	cell	cytoplasmic part	430	0.102405	1.56E-08
		cell	cytoplasm	534	0.097215	2.14E-07
		cell	cytosol	77	0.135325	6.21E-06
		organelle part	plastoglobule	9	0.36	9.35E-05
		cell junction	cell-cell junction	21	0.169355	0.000997
	molecular_function	catalytic activity	electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity	11	0.423077	1.57E-06
		catalytic activity	peptidyl-prolyl cis-trans isomerase activity	19	0.17757	0.000553
		catalytic activity	dihydrolipoyllysine-residue succinyltransferase activity	3	1	0.000469
		catalytic activity	electron transfer activity	36	0.138996	0.000486
		catalytic activity	oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor	12	0.230769	0.000518
		catalytic activity	succinyltransferase activity	3	1	0.000469
		catalytic activity	S-succinyltransferase activity	3	1	0.000469
		catalytic activity	cis-trans isomerase activity	19	0.17757	0.000553
M1 vs. F1	biological_process	biological regulation	positive regulation of response to stimulus	10	0.238095	0.002648
		cellular process	threonyl-tRNA aminoacylation	3	0.6	0.005728
		cellular process	aspartate family amino acid metabolic process	14	0.184211	0.005395
	cellular_component	cell	cytosol	79	0.13884	4.86E-05
		cell	cytoplasm	547	0.099581	0.000714
		cell	cytoplasmic part	426	0.101453	0.000911
		cell	clathrin coat	9	0.25	0.003576
		cell	AP-type membrane coat adaptor complex	9	0.230769	0.006317

		cell	clathrin adaptor complex	7	0.291667	0.003937
		cell	dihydrolipoyl dehydrogenase complex	3	0.6	0.006166
	molecular_function	catalytic activity	quercetin 3-O-glucosyltransferase activity	16	0.296296	6.90E-06
		catalytic activity	quercetin 7-O-glucosyltransferase activity	16	0.296296	6.90E-06
		catalytic activity	dihydrolipoyllysine-residue succinyltransferase activity	3	1	0.000622
		catalytic activity	succinyltransferase activity	3	1	0.000622
		catalytic activity	S-succinyltransferase activity	3	1	0.000622
		catalytic activity	ubiquitin-ubiquitin ligase activity	4	0.571429	0.001503
		transporter activity	ammonium transmembrane transporter activity	5	0.416667	0.002146
		binding	mRNA binding	17	0.168317	0.005104
		catalytic activity	6-phosphofructokinase activity	5	0.357143	0.004694
		catalytic activity	threonine-tRNA ligase activity	3	0.6	0.005451
all 7029 DEGs	biological_process	cellular process	protein-chromophore linkage	23	0.277108	9.41E-05
		response to stimulus	response to toxic substance	19	0.263889	0.000724
		cellular process	photosynthetic electron transport in photosystem II	11	0.34375	0.000912
		response to stimulus	response to chemical	108	0.161435	0.001007
		cellular process	malonyl-CoA metabolic process	3	1	0.001778
		cellular process	malonyl-CoA biosynthetic process	3	1	0.001778
	cellular_component	cell	cytoplasm	750	0.136537	0.000136
		cell	cytosol	103	0.181019	3.00E-05
		cell	cytoplasmic part	585	0.139319	0.000141
		organelle part	plastoglobule	10	0.4	0.000436
		organelle part	post-mRNA release spliceosomal complex	6	0.5	0.001632
	molecular_function	catalytic activity	electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity	11	0.423077	8.76E-05
		catalytic activity	quercetin 3-O-glucosyltransferase activity	17	0.314815	0.000104
		catalytic activity	quercetin 7-O-glucosyltransferase activity	17	0.314815	0.000104
		binding	chlorophyll binding	21	0.2625	0.000306
		catalytic activity	electron transfer activity	48	0.185328	0.001047
		catalytic activity	peptidyl-prolyl cis-trans isomerase activity	24	0.224299	0.001397
		catalytic activity	dihydrolipoyllysine-residue succinyltransferase activity	3	1	0.001653
		catalytic activity	succinyltransferase activity	3	1	0.001653

catalytic activity	S-succinyltransferase activity	3	1	0.001653
catalytic activity	cis-trans isomerase activity	24	0.224299	0.001397

Table S7. List of DEGs enriched in plant hormone synthesis and the signal transduction pathway.

Gene ID	Gene name	Hormone	Nr annotation
MR3G014767.1	PP2CA	ABA	XP_018810490.1//PREDICTED: protein phosphatase 2C 37-like [Juglans regia]
MR5G022121.1	SAPK10	ABA	XP_018856710.1//PREDICTED: serine/threonine-protein kinase SAPK10-like isoform X2 [Juglans regia]
MR6G000783.1	SAPK7	ABA	XP_018811162.1//PREDICTED: serine/threonine-protein kinase SAPK7-like [Juglans regia]
MR6G029272.1	PP2C	ABA	XP_018846386.1//PREDICTED: probable protein phosphatase 2C 8 [Juglans regia]
MR6G029273.1	PP2C	ABA	XP_018846386.1//PREDICTED: probable protein phosphatase 2C 8 [Juglans regia]
MR7G007481.1	ABF4	ABA	XP_018817895.1//PREDICTED: ABSCISIC ACID-INSENSITIVE 5-like protein 7 [Juglans regia]
MR7G011459.2	SRK2E	ABA	XP_021285698.1//serine/threonine-protein kinase SRK2E isoform X1 [Herrania umbratica]
MR7G014396.1	PP2C	ABA	XP_018810781.1//PREDICTED: probable protein phosphatase 2C 51 [Juglans regia]
MR1G009013.1	SAUR	Auxin	XP_018853693.1//PREDICTED: auxin-responsive protein SAUR36-like [Juglans regia]
MR1G014923.1	GH3.1	Auxin	XP_011001484.1//PREDICTED: probable indole-3-acetic acid-amido synthetase GH3.1 [Populus euphratica]
MR2G004927.1	AUX15A	Auxin	XP_018817449.1//PREDICTED: auxin-induced protein 15A [Juglans regia]
MR2G006882.2	TIR1-L	Auxin	XP_018815703.1//PREDICTED: protein TRANSPORT INHIBITOR RESPONSE 1-like [Juglans regia]
MR2G006999.1	SPL	Auxin	CAD90156.1//squamosa promoter binding like-protein [Betula pendula]
MR2G027556.1	ARF6	Auxin	XP_018847680.1//PREDICTED: auxin response factor 6 isoform X1 [Juglans regia]
MR3G001167.1	IAA13	Auxin	XP_018820113.1//PREDICTED: auxin-responsive protein IAA13-like isoform X2 [Juglans regia]
MR3G011095.1	ARF	Auxin	XP_018818379.1//PREDICTED: auxin response factor 18 [Juglans regia]
MR3G014514.1	IAA4	Auxin	XP_018838419.1//PREDICTED: auxin-responsive protein IAA4-like [Juglans regia]
MR3G014515.1	IAA14	Auxin	XP_018818667.1//PREDICTED: auxin-responsive protein IAA14-like [Juglans regia]
MR3G018668.1	ARF18	Auxin	XP_018853662.1//PREDICTED: auxin response factor 18-like [Juglans regia]
MR3G026193.1	SAUR41	Auxin	XP_018839908.1//PREDICTED: auxin-responsive protein SAUR41-like [Juglans regia]
MR3G026487.1	IAA6	Auxin	XP_012573044.1//PREDICTED: auxin-induced protein IAA6-like isoform X1 [Cicer arietinum]
MR4G010547.2	ARF9	Auxin	XP_018824358.1//PREDICTED: auxin response factor 9 [Juglans regia]
MR4G016064.1	SAUR	Auxin	XP_008372027.1//PREDICTED: auxin-responsive protein SAUR71-like [Malus domestica]
MR4G020436.1	GH3.1	Auxin	XP_007042570.2//PREDICTED: probable indole-3-acetic acid-amido synthetase GH3.1 [Theobroma cacao]
MR4G021266.1	SAUR	Auxin	XP_018848064.1//PREDICTED: auxin-responsive protein SAUR36-like [Juglans regia]
MR4G025315.1	MAKR2	Auxin	XP_018858742.1//PREDICTED: probable membrane-associated kinase regulator 2 [Juglans regia]
MR5G024618.1	ARF19	Auxin	XP_018820293.1//PREDICTED: auxin response factor 19-like [Juglans regia]
MR5G027067.1	ARG7	Auxin	XP_015874543.1//PREDICTED: indole-3-acetic acid-induced protein ARG7 [Ziziphus jujuba]
MR6G011287.1	AUX22	Auxin	XP_018827349.1//PREDICTED: auxin-induced protein 22D-like isoform X2 [Juglans regia]
MR6G011335.1	GH3.6	Auxin	XP_018821933.1//PREDICTED: indole-3-acetic acid-amido synthetase GH3.6-like [Juglans regia]
MR6G022742.1	bZIP53	Auxin	XP_018808498.1//PREDICTED: bZIP transcription factor 53 [Juglans regia]
MR7G007520.1	ARF	Auxin	XP_018840018.1//PREDICTED: auxin response factor 2-like isoform X1 [Juglans regia]
MR7G017780.1	IAA32	Auxin	XP_021824179.1//auxin-responsive protein IAA32 [Prunus avium]
MR7G018915.1	IAA16	Auxin	XP_015875440.1//PREDICTED: auxin-responsive protein IAA16 [Ziziphus jujuba]

MR7G022672.1	IAA	Auxin	XP_018827784.1//PREDICTED: probable indole-3-acetic acid-amido synthetase GH3.1 [Juglans regia]
MR7TCONS_00006944.1	SAUR21	Auxin	MR7TCONS_00006944.1//1Herrania umbratica auxin-responsive protein SAUR21-like (LOC110417626), mRNA
MR8G002059.1	GH3.9	Auxin	XP_018811497.1//PREDICTED: putative indole-3-acetic acid-amido synthetase GH3.9 [Juglans regia]
MR8G016437.1	IAA33	Auxin	XP_018820838.1//PREDICTED: auxin-responsive protein IAA33 [Juglans regia]
MR8G025878.1	ARG7	Auxin	XP_018843039.1//PREDICTED: indole-3-acetic acid-induced protein ARG7-like [Juglans regia]
MR1G018614.1	SERK2	BR	XP_013682256.1//PREDICTED: somatic embryogenesis receptor kinase 2-like [Brassica napus]
MR2G000226.1	BZR1	BR	XP_018805853.1//PREDICTED: BES1/BZR1 homolog protein 4-like [Juglans regia]
MR3G009824.1	BKI1	BR	XP_018853245.1//PREDICTED: BRI1 kinase inhibitor 1-like [Juglans regia]
MR5G011874.1	BIM1	BR	XP_018823964.1//PREDICTED: transcription factor BIM1-like [Juglans regia]
MR5G013073.1	ASK7	BR	XP_002522231.1//PREDICTED: shaggy-related protein kinase eta [Ricinus communis]
MR7G008146.2	BAK1/SERK3	BR	XP_018842160.1//PREDICTED: BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1-like [Juglans regia]
MR7G009280.1	PSKR1	BR	XP_018841053.1//PREDICTED: phytosulfokine receptor 1 [Juglans regia]
MR1G029229.1	ARR	CK	XP_018819177.1//PREDICTED: two-component response regulator ARR10-like [Juglans regia]
MR2G023469.1	ARR	CK	XP_018848410.1//PREDICTED: two-component response regulator ARR9 [Juglans regia]
MR2G024054.1	CYCD3-1	CK	XP_018827983.1//PREDICTED: cyclin-D3-3-like [Juglans regia]
MR3G019062.1	CYCD3-1	CK	XP_018811124.1//PREDICTED: cyclin-D3-3-like [Juglans regia]
MR4G018351.1	ARR	CK	XP_018831695.1//PREDICTED: two-component response regulator ARR5 [Juglans regia]
MR5G017155.1	ARR	CK	XP_018825709.1//PREDICTED: two-component response regulator ARR1 isoform X1 [Juglans regia]
MR7G022722.1	CYCD3-1	CK	XP_018831439.1//PREDICTED: cyclin-D3-1-like [Juglans regia]
MR7G022723.1	CYCD3-1	CK	XP_018831439.1//PREDICTED: cyclin-D3-1-like [Juglans regia]
MR7G024824.1	ARR	CK	XP_018844398.1//PREDICTED: two-component response regulator ARR5-like [Juglans regia]
MR7G028512.1	CYCD3-1	CK	XP_018831439.1//PREDICTED: cyclin-D3-1-like [Juglans regia]
MR8G012754.1	ARR	CK	XP_018850232.1//PREDICTED: two-component response regulator ARR12-like [Juglans regia]
MR8G019008.1	AHP1	CK	XP_018860221.1//PREDICTED: histidine-containing phosphotransfer protein 1-like [Juglans regia]
MR8G026761.1	CKI1	CK	XP_018846142.1//PREDICTED: histidine kinase CKI1-like [Juglans regia]
MR1G018593.1	EIN3	ET	XP_018850150.1//PREDICTED: ETHYLENE INSENSITIVE 3-like 1 protein [Juglans regia]
MR2G016675.1	EIN2	ET	XP_018851486.1//PREDICTED: ethylene-insensitive protein 2-like isoform X1 [Juglans regia]
MR3G008397.1	ETR	ET	XP_018810721.1//PREDICTED: ethylene receptor 2-like [Juglans regia]
MR7G007527.1	ERS	ET	XP_018824791.1//PREDICTED: probable ethylene response sensor 1 [Juglans regia]
MR8G004987.1	EIN3	ET	XP_018858626.1//PREDICTED: ETHYLENE INSENSITIVE 3-like 1 protein [Juglans regia]
MR8G012695.1	EBF1/2	ET	XP_018822226.1//PREDICTED: EIN3-binding F-box protein 1-like [Juglans regia]
MR1G002326.1	RPPL1	GA	XP_018817575.1//PREDICTED: putative disease resistance RPP13-like protein 1 isoform X2 [Juglans regia]
MR1G022996.1	RPPL1	GA	XP_018811278.1//PREDICTED: putative disease resistance RPP13-like protein 1 isoform X1 [Juglans regia]
MR1G029366.2	RPPL1	GA	XP_018830884.1//PREDICTED: putative disease resistance RPP13-like protein 1 [Juglans regia]

MR4G018381.1	CIGR1	GA	XP_018852274.1//PREDICTED: chitin-inducible gibberellin-responsive protein 1-like [Juglans regia]
MR6G010478.1	SLN1	GA	XP_018841073.1//PREDICTED: DELLA protein SLN1-like [Juglans regia]
MR6G021506.1	GAI	GA	XP_018816848.1//PREDICTED: DELLA protein GAI-like [Juglans regia]
MR7G017861.1	bHLH48	GA	XP_018858223.1//PREDICTED: transcription factor bHLH48-like [Juglans regia]
MR7G028053.1	GAIP-like	GA	XP_018814727.1//PREDICTED: DELLA protein GAIP-like [Juglans regia]
MR3G009918.1	MYC2	JA	XP_018824308.1//PREDICTED: transcription factor MYC2-like [Juglans regia]
MR3G014474.2	TIFY 4B	JA	XP_018839402.1//PREDICTED: protein TIFY 4B-like isoform X1 [Juglans regia]
MR5G024985.1	TIFY 6B	JA	XP_018823646.1//PREDICTED: protein TIFY 6B isoform X1 [Juglans regia]
MR6G007069.1	bHLH3	JA	XP_018827271.1//PREDICTED: transcription factor bHLH3 [Juglans regia]
MR6G022827.1	TIFY10A	JA	XP_018814737.1//PREDICTED: protein TIFY 10A-like [Juglans regia]
MR6G022829.1	TIFY 10A	JA	XP_018814737.1//PREDICTED: protein TIFY 10A-like [Juglans regia]
MR7G002983.1	TIFY 10A	JA	XP_018859193.1//PREDICTED: protein TIFY 9-like [Juglans regia]
MR7G002984.2	TIFY 10A	JA	XP_018859193.1//PREDICTED: protein TIFY 9-like [Juglans regia]
MR7G012609.1	TIFY 10A	JA	XP_018859193.1//PREDICTED: protein TIFY 9-like [Juglans regia]
MR8G021808.1	TIFY 10A	JA	XP_018845751.1//PREDICTED: protein TIFY 8-like isoform X2 [Juglans regia]
MR2G026920.1	PR1	SA	XP_018808966.1//PREDICTED: pathogenesis-related protein 1C-like [Juglans regia]
MR4G022374.1	PYL8-L	ABA	XP_018846392.1//PREDICTED: abscisic acid receptor PYL8-like [Juglans regia]
MR4G029081.1	TIR1-L	Auxin	XP_018829906.1//PREDICTED: protein TRANSPORT INHIBITOR RESPONSE 1-like [Juglans regia]
MR4G029089.1	TIR1-L	Auxin	XP_018829906.1//PREDICTED: protein TRANSPORT INHIBITOR RESPONSE 1-like [Juglans regia]
MR4G029093.1	TIR1-L	Auxin	XP_018829906.1//PREDICTED: protein TRANSPORT INHIBITOR RESPONSE 1-like [Juglans regia]
MR0G006960.1	SAPK2	ABA	XP_015890760.1//PREDICTED: serine/threonine-protein kinase SAPK2 isoform X1 [Ziziphus jujuba]
MR0G018446.1	ARR12	CK	XP_018850345.1//PREDICTED: two-component response regulator ARR12-like isoform X1 [Juglans regia]
MR0G024267.1	IAA29	Auxin	XP_018826739.1//PREDICTED: auxin-responsive protein IAA29-like [Juglans regia]

Table S8. List of hormone-related genes identified in the 7029 DEGs

Gene ID	Hormone	Involved process	Gene name	Type	log2(M0/F0)	log2(M1/F1)
MR6G029272.1	Abscisic acid	Hormone signal transduction	PP2C	Female-biased	-9.471	-6.5372
MR6G029273.1	Abscisic acid	Hormone signal transduction	PP2C	Female-biased	-4.1742	-5.2316
MR3G011095.1	Auxin	Hormone signal transduction	ARF	Female-biased	-7.2393	-13.697
MR7G007520.1	Auxin	Hormone signal transduction	ARF	Female-biased	-7.3132	-7.9621
MR4G010547.2	Auxin	Hormone signal transduction	ARF9	Female-biased	-8.7051	-9.5325
MR1G027448.1	Auxin	Hormone biosynthesis	YUC	Female-biased	-7.8526	-2.8105
MR6G021603.1	Auxin	Hormone biosynthesis	YUC	Male-biased	1.3741	1.34733
MR8G021802.1	Auxin	Hormone biosynthesis	YUCCA		-0.6731	-1.3875
MR8G025878.1	Auxin	Hormone response	ARG7	Female-biased	-8.7814	-5.2316
MR6G004324.1	Auxin	Hormone biosynthesis	TDC		-1.6422	-0.7362
MR1G018614.1	Brassinosteroid	Hormone signal transduction	SERK2	Male-biased	2.5924	2.21814
MR2G000226.1	Brassinosteroid	Hormone signal transduction	BZR1		-1.0583	-0.4134
MR5G011874.1	Brassinosteroid	Hormone signal transduction	BIM1	Female-biased	-2.5267	-2.0144
MR5G011875.1	Brassinosteroid	Hormone signal transduction	BIM1	Male-biased	4.04855	7.58352
MR5G013073.1	Brassinosteroid	Hormone signal transduction	ASK7	Male-biased	3.36837	3.13138
MR7G008146.2	Brassinosteroid	Hormone signal transduction	BAK1/SERK3	Female-biased	-5.2789	-4.3219
MR3G026318.1	Brassinosteroid	Hormone biosynthesis	CYP90C1	Female-biased	-2.3108	-2.1396
MR3G019062.1	Cytokinin	Hormone signal transduction	CYCD3-1	Female-biased	-7.9965	-5.7408
MR0G027265.2	Cytokinin	Hormone biosynthesis	LOG	Female-biased	-6.3152	-5.5112
MR3G012354.1	Cytokinin	Hormone signal transduction	CRF5	Female-biased	-1.5747	-1.3338
MR8G026761.1	Cytokinin	Hormone signal transduction	CKI1	Female-biased	-1.0268	-1.189
MR8G019008.1	Cytokinin	Hormone signal transduction	AHP1	Female-biased	-1.0486	-1.2711
MR0TCONS_00017483.1	Ethylene	Hormone biosynthesis	ACO	Male-biased	18.2093	18.2085
MR3G008397.1	Ethylene	Hormone signal transduction	ETR		-2.0674	6.31688
MR7G012066.1	Ethylene	Hormone response	ADH1	Female-biased	-1.2797	-3.4387
MR1G003948.1	Ethylene	Hormone biosynthesis	ETO1	Female-biased	-8.4895	-8.5941
MR2G007010.1	Ethylene	Hormone signal transduction	ERF4	Female-biased	-14.221	-9.4565
MR2G016358.1	Ethylene	Hormone biosynthesis	ETO1	Female-biased	-10.579	-10.344
MR4G016016.1	Ethylene	Hormone signal transduction	ERF5	Female-biased	-3.0617	-2.7395
MR2G016675.1	Ethylene	Hormone signal transduction	EIN2	Male-biased	5.05627	5.35994

MR3G008350.2	Ethylene	Hormone biosynthesis	ACO	Female-biased	-1.1769	-1.068
MR3G008356.1	Ethylene	Hormone biosynthesis	ACO	Female-biased	-3.1296	-4.5493
MR3G008357.1	Ethylene	Hormone biosynthesis	ACO	Female-biased	-8.0572	-8.2154
MR8G021808.1	Jasmonic acid	Hormone response	TIFY 10A	Female-biased	-9.1291	-10.756
MR5G017092.1	Jasmonic acid	Hormone biosynthesis	MFP2	Female-biased	-2.8516	-3.7161
MR6G007069.1	Jasmonic acid	Hormone signal transduction	bHLH3		-0.8699	-1.0583
MR6G022827.1	Jasmonic acid	Hormone response	TIFY10A		0.97303	2.73698
MR0G007890.1	Jasmonic acid	Hormone signal transduction	MYB108	Male-biased	1.16324	1.98043
MR0TCONS_00032219.1	Salicylic acid	Hormone biosynthesis	UGT		1.46425	0.3629
MR7G015242.1	Salicylic acid	Hormone biosynthesis	UGT	Female-biased	-1.3401	-1.4132
MR8G002372.1	Salicylic acid	Hormone biosynthesis	SAMT		1.70216	0.40129
MR8G010075.1	Salicylic acid	Hormone biosynthesis	UGT	Male-biased	1.27143	1.73038
MR8G027413.1	Salicylic acid	Hormone biosynthesis	UGT		-1.2715	0.70812
MR1G005704.1	Salicylic acid	Hormone biosynthesis	UGT	Female-biased	-1.2621	-2.153
MR2G009173.1	Salicylic acid	Hormone biosynthesis	UGT	Female-biased	-9.4838	-6.7737
MR2G009177.1	Salicylic acid	Hormone biosynthesis	UGT	Female-biased	-5.9632	-5.7835
MR2G025731.1	Salicylic acid	Hormone biosynthesis	UGT	Female-biased	-6.8916	-6.6193
MR3G026042.1	Salicylic acid	Hormone biosynthesis	UGT		-1.1643	-0.9663
MR4G020673.1	Salicylic acid	Hormone biosynthesis	UGT	Male-biased	9.66069	8.26327
MR5G011885.1	Salicylic acid	Hormone biosynthesis	UGT		-1.5007	-0.6195
MR5G027230.1	Salicylic acid	Hormone biosynthesis	UGT	Male-biased	5.33241	6.1863
MR7G010685.1	Salicylic acid	Hormone response	PR1-like	Female-biased	-5.5395	-6.3663
MR3G026572.1	Abscisic acid	Hormone signal transduction	WIN1	Male-biased	2.11979	1.00137
MR7G012917.1	Abscisic acid	Hormone signal transduction	WIN1	Male-biased	1.54707	1.41088
MR1G027085.1	Abscisic acid	Hormone biosynthesis	NCED		-1.757	2.73235
MR0G027092.1	Abscisic acid	Hormone biosynthesis	NCED		-1.757	2.73235
MR4G022374.1	Abscisic acid	Hormone receptor	PYL8-L	Female-biased	-1.4883	-1.6179
MR5G003275.1	Abscisic acid	Hormone biosynthesis	ABA1/ZEP1		-1.8828	-0.733
MR0G006960.1	Abscisic acid	Hormone signal transduction	SAPK2		0.1635	1.07846
MR5G022121.1	Abscisic acid	Hormone signal transduction	SAPK10	Female-biased	-4.2816	-6.8864
MR7G007481.1	Abscisic acid	Hormone signal transduction	ABF4		-2.426	0.83586
MR7G011459.2	Abscisic acid	Hormone signal transduction	SRK2E	Female-biased	-1.3472	-1.2869
MR8G011177.1	Abscisic acid	Hormone biosynthesis	NCED	Male-biased	1.71017	2.32974

MR3G014767.1	Abscisic acid	Hormone metabolism	PP2CA	Female-biased	-1.0772	-1.0295
MR4G024721.1	Abscisic acid	Hormone response	ASR2	Male-biased	5.84906	2.78529
MR6G019840.1	Abscisic acid	Hormone biosynthesis	ABA3		-0.7602	-1.8383
MR7G014396.1	Abscisic acid	Hormone signal transduction	PP2C51		-1.0285	0.76367
MR3G018668.1	Auxin	Hormone signal transduction	ARF18	Female-biased	-1.0601	-1.2453
MR5G024618.1	Auxin	Hormone signal transduction	ARF19		-0.0425	1.07621
MR2G027556.1	Auxin	Hormone signal transduction	ARF6		-0.1926	-1.4381
MR5G027067.1	Auxin	Hormone response	ARG7		0.05367	-1.4755
MR7G012941.1	Auxin	Hormone signal transduction	AUX1	Female-biased	-8.6144	-3.3923
MR7G028105.1	Auxin	Hormone signal transduction	AUX1	Female-biased	-8.6144	-3.3923
MR2G004927.1	Auxin	Hormone response	AUX15A		4.66653	-0.0857
MR6G011287.1	Auxin	Hormone response	AUX22D		4.13945	-0.4541
MR6G022742.1	Auxin	Hormone signal transduction	bZIP53		0.93988	1.63194
MR3G001277.1	Auxin	Hormone response	CRY1		1.21193	0.14179
MR1G014923.1	Auxin	Hormone signal transduction	GH3.1	Male-biased	1.6289	2.07012
MR4G020436.1	Auxin	Hormone signal transduction	GH3.1	Male-biased	1.23024	1.61889
MR7G022672.1	Auxin	Hormone signal transduction	GH3.1		-0.51	1.12008
MR6G011335.1	Auxin	Hormone signal transduction	GH3.6	Female-biased	-1.5274	-1.5018
MR8G002059.1	Auxin	Hormone signal transduction	GH3.9	Male-biased	7.64035	8.5394
MR3G001167.1	Auxin	Hormone signal transduction	IAA13	Female-biased	-3.5826	-2.9732
MR3G014515.1	Auxin	Hormone signal transduction	IAA14	Male-biased	1.49823	1.40291
MR0G024267.1	Auxin	Hormone signal transduction	IAA29		-0.7131	-1.5284
MR7G018915.1	Auxin	Hormone signal transduction	IAA16		1.85383	0.20599
MR7G017780.1	Auxin	Hormone signal transduction	IAA32		-0.6464	1.12119
MR8G016437.1	Auxin	Hormone signal transduction	IAA33	Male-biased	3.21402	1.85207
MR3G014514.1	Auxin	Hormone signal transduction	IAA4		0.59864	-3.3042
MR3G026487.1	Auxin	Hormone response	IAA6		-1.2876	1.36125
MR4G025315.1	Auxin	Hormone signal transduction	MAKR2	Female-biased	-1.5195	-1.2605
MR1G009013.1	Auxin	Hormone signal transduction	SAUR	Female-biased	-4.7779	-2.7188
MR4G016064.1	Auxin	Hormone signal transduction	SAUR		1.05235	0.26303
MR4G021266.1	Auxin	Hormone signal transduction	SAUR	Female-biased	-1.3459	-1.1642
MR7TCONS_00006944.1	Auxin	Hormone signal transduction	SAUR21		4.42552	
MR3G026193.1	Auxin	Hormone signal transduction	SAUR41		-0.4516	-1.2633

MR2G006882.2	Auxin	Hormone signal transduction	TIR1-L		-1.1933	-0.9051
MR4G029081.1	Auxin	Hormone signal transduction	TIR1-L		0.03768	1.1505
MR4G029089.1	Auxin	Hormone signal transduction	TIR1-L		0.03768	1.1505
MR4G029093.1	Auxin	Hormone signal transduction	TIR1-L		0.03405	1.11793
MR0G002592.1	Auxin	Hormone biosynthesis	YUCCA		-0.2176	-1.6657
MR3G009824.1	Brassinosteroid	Hormone signal transduction	BKI1		-0.3452	-1.2274
MR1G029229.1	Cytokinin	Hormone signal transduction	ARR		-1.4144	-0.2622
MR0G018446.1	Cytokinin	Hormone signal transduction	ARR12		-0.4344	-1.3707
MR2G005198.1	Cytokinin	Hormone biosynthesis	CKX1	Female-biased	-2.1184	-3.7545
MR2G024054.1	Cytokinin	Hormone signal transduction	CYCD3-1	Female-biased	-1.5986	-2.2838
MR8G002759.1	Cytokinin	Hormone biosynthesis	LOG	Female-biased	-1.5709	-2.927
MR4G018351.1	Cytokinin	Hormone signal transduction	ARR		-1.0445	0.53653
MR5G017155.1	Cytokinin	Hormone signal transduction	ARR		-1.0024	-0.3559
MR7G022722.1	Cytokinin	Hormone signal transduction	CYCD3-1	Male-biased	9.23437	8.2527
MR7G022723.1	Cytokinin	Hormone signal transduction	CYCD3-1	Female-biased	-1.1435	-2.807
MR7G024824.1	Cytokinin	Hormone signal transduction	ARR	Male-biased	6.14066	5.74429
MR7G028512.1	Cytokinin	Hormone signal transduction	CYCD3-1	Male-biased	2.38431	1.89896
MR7G015191.1	Cytokinin	Hormone signal transduction	CRF4	Female-biased	-1.2553	-1.8152
MR8G022212.1	Cytokinin	Hormone signal transduction	CRF2	Female-biased	-1.0704	-1.8954
MR0G003179.1	Cytokinin	Hormone signal transduction	CRF5-LIKE	Female-biased	-1.5564	-1.3338
MR8G027691.1	Cytokinin	Hormone biosynthesis	LOG		-2.0339	-0.8745
MR1G003950.1	Ethylene	Hormone biosynthesis	ETO1	Female-biased	-1.9647	-3.0776
MR1G018593.1	Ethylene	Hormone signal transduction	EIN3	Female-biased	-1.1486	-1.1046
MR3G009444.1	Ethylene	Hormone signal transduction	RTE1	Female-biased	-1.0206	-1.0027
MR3G026169.1	Ethylene	Hormone signal transduction	RAP2-12		-1.1834	-0.0861
MR3G026789.1	Ethylene	Hormone response	ADH1	Male-biased	1.04701	1.09747
MR6G009324.1	Ethylene	Hormone biosynthesis	ACO	Male-biased	2.43294	2.80401
MR6G029280.1	Ethylene	Hormone signal transduction	ERF4		-1.7151	0.1293
MR7G007527.1	Ethylene	Hormone response	ERS	Female-biased	-1.1656	-1.0688
MR7G012067.1	Ethylene	Hormone response	ADH1		1.63141	-0.102
MR8G012695.1	Ethylene	Hormone signal transduction	EBF1/2		-1.4529	-0.0554
MR8G026853.1	Ethylene	Hormone response	ERF		-1.7151	0.1293
MR3G008378.1	Ethylene	Hormone biosynthesis	ACO		-0.4396	-1.4025

MR8G004987.1	Ethylene	Hormone signal transduction	EIN3		-0.3139	2.05285
MR2G005456.1	Ethylene	Hormone biosynthesis	ACO		-0.8253	-1.2361
MR3G008359.1	Ethylene	Hormone biosynthesis	ACO		-0.5659	-1.1052
MR7G004138.1	Gibberellin	Hormone signal transduction	ESR2		1.16306	0.4397
MR6G021506.1	Gibberellin	Hormone signal transduction	GAI	Male-biased	1.51504	1.12346
MR1G002326.1	Gibberellin	Hormone response	RPPL1		-1.8261	-0.4073
MR1G022996.1	Gibberellin	Hormone response	RPPL1	Female-biased	-1.8642	-1.17
MR1G029366.2	Gibberellin	Hormone response	RPPL1	Female-biased	-1.7274	-1.2982
MR2G005641.1	Gibberellin	Hormone biosynthesis	GA2ox2	Female-biased	-1.1717	-1.2116
MR4G018381.1	Gibberellin	Hormone response	CIGR1		-1.4363	0.87884
MR5G010169.1	Gibberellin	Hormone response	GASA14		4.48588	
MR6G010478.1	Gibberellin	Hormone signal transduction	SLN1		1.29238	0.55386
MR6G019831.1	Gibberellin	Hormone biosynthesis	GA20ox		1.15402	-1.4537
MR7G017861.1	Gibberellin	Hormone signal transduction	bHLH48		-1.1139	-0.6303
MR1G027577.1	Gibberellin	Hormone biosynthesis	KAO		-0.826	-1.1782
MR7G028053.1	Gibberellin	Hormone signal transduction	GAIP-like		-0.0062	-1.1663
MR5G010168.1	Gibberellin	Hormone response	**GASA4**		0.74582	1.23166
MR6G013934.1	Gibberellin	Hormone response	**GASA14**		-0.395	-1.4872
MR6G022829.1	Jasmonic acid	Hormone response	TIFY 10A		-2.2416	7.60924
MR7G002983.1	Jasmonic acid	Hormone response	TIFY 10A	Female-biased	-9.231	-6.905
MR7G011529.1	Jasmonic acid	Hormone biosynthesis	AOS		-1.448	0.16378
MR3G009918.1	Jasmonic acid	Hormone signal transduction	MYC2		-1.1506	-0.0368
MR3G014474.2	Jasmonic acid	Hormone response	TIFY 4B	Male-biased	3.23893	3.59722
MR5G021935.1	Jasmonic acid	Hormone signal transduction	MYB108		-1.4256	-0.1038
MR5G024985.1	Jasmonic acid	Hormone response	TIFY 6B	Female-biased	-1.2017	-1.2068
MR6G021641.1	Jasmonic acid	Hormone biosynthesis	AOC	Male-biased	11.3976	11.7652
MR7G002984.2	Jasmonic acid	Hormone response	TIFY 10A	Female-biased	-2.4903	-1.2019
MR7G012609.1	Jasmonic acid	Hormone response	TIFY 10A	Female-biased	-8.583	-8.2747
MR8G002373.1	Salicylic acid	Hormone biosynthesis	SAMT	Male-biased	7.39831	10.1464
MR8G010072.1	Salicylic acid	Hormone biosynthesis	UGT	Female-biased	-1.3994	-2.8599
MR8G010076.1	Salicylic acid	Hormone biosynthesis	UGT	Male-biased	2.52582	5.24179
MR2G026920.1	Salicylic acid	Hormone response	PR1		-0.0466	3.1083

Table S9. List of hormone-related genes specifically expressed in males and females.

Gene ID	F0	F1	M0	M1	Hormone	Involved process	Gene name	Specific expressed	log2(M0/F0)	log2(M1/F1)
MR6G029272.1	6.91	5.95	0	0	Abscisic acid	Hormone signal transduction	PP2C	Female	-9.471	-6.5372
MR6G029273.1	4.24	2.93	0	0	Abscisic acid	Hormone signal transduction	PP2C	Female	-4.1742	-5.2316
MR3G011095.1	73.05	55.63	0	0	Auxin	Hormone signal transduction	ARF	Female	-7.2393	-13.697
MR7G007520.1	22.86	33.53	0	0	Auxin	Hormone signal transduction	ARF	Female	-7.3132	-7.9621
MR4G010547.2	35.01	52.79	0	0	Auxin	Hormone signal transduction	ARF9	Female	-8.7051	-9.5325
MR1G027448.1	3.33	1.00	0	0	Auxin	Hormone biosynthesis	YUC	Female	-7.8526	-2.8105
MR3G026318.1	1.56	1.44	0	0	Brassinosteroid	Hormone biosynthesis	CYP90C1	Female	-2.3108	-2.1396
MR3G019062.1	5.62	7.34	0	0	Cytokinin	Hormone signal transduction	CYCD3-1	Female	-7.9965	-5.7408
MR0G027265.2	6.59	6.69	0	0	Cytokinin	Hormone biosynthesis	LOG	Female	-6.3152	-5.5112
MR1G003948.1	1.10	1.18	0	0	Ethylene	Hormone biosynthesis	ETO1	Female	-8.4895	-8.5941
MR2G007010.1	357.13	259.87	0	0	Ethylene	Hormone signal transduction	ERF4	Female	-14.221	-9.4565
MR2G016358.1	6.19	5.23	0	0	Ethylene	Hormone biosynthesis	ETO1	Female	-10.579	-10.344
MR3G008357.1	2.97	3.30	0	0	Ethylene	Hormone biosynthesis	ACO	Female	-8.0572	-8.2154
MR8G021808.1	16.66	15.98	0	0	Jasmonic acid	Hormone response	TIFY10A	Female	-9.1291	-10.756
MR2G009173.1	7.52	11.71	0	0	Salicylic acid	Hormone biosynthesis	UGT	Female	-9.4838	-6.7737
MR2G009177.1	1.87	1.63	0	0	Salicylic acid	Hormone biosynthesis	UGT	Female	-5.9632	-5.7835
MR2G025731.1	2.89	2.28	0	0	Salicylic acid	Hormone biosynthesis	UGT	Female	-6.8916	-6.6193
MR7G010685.1	14.21	17.07	0	0	Salicylic acid	Hormone response	PR1-like	Female	-5.5395	-6.3663
MR5G011875.1	0	0	3.24	1.98	Brassinosteroid	Hormone signal transduction	BIM1	Male	4.04855	7.58352
MR0TCONS_00017483.1	0	0	30.31	30.29	Ethylene	Hormone biosynthesis	ACO	Male	18.2093	18.2085
MR2G016675.1	0	0	11.32	10.17	Ethylene	Hormone signal transduction	EIN2	Male	5.05627	5.35994
MR4G020673.1	0	0	6.75	2.60	Salicylic acid	Hormone biosynthesis	UGT	Male	9.66069	8.26327
MR5G027230.1	0	0	2.26	2.08	Salicylic acid	Hormone biosynthesis	UGT	Male	5.33241	6.1863
MR8G002059.1	0	0	1.33	2.54	Auxin	Hormone signal transduction	GH3.9	Male	7.64035	8.5394
MR7G022722.1	0	0	6.68	3.44	Cytokinin	Hormone signal transduction	CYCD3-1	Male	9.23437	8.2527
MR7G024824.1	0	0	3.21	3.31	Cytokinin	Hormone signal transduction	ARR	Male	6.14066	5.74429
MR6G009324.1	0	0	2.71	1.67	Ethylene	Hormone biosynthesis	ACO	Male	2.43294	2.80401
MR6G021641.1	0	0	45.12	59.29	Jasmonic acid	Hormone biosynthesis	AOC	Male	11.3976	11.7652

Table S10. List of transcription factors identified in the 7029 DEGs

Gene ID	Family	log2(M0/F0)	log2(M1/F1)	Type
MR8G002609.1	ABI3VP1	-1.85153	-3.25403	Female-biased
MR8G002610.1	ABI3VP1	-1.38193	-1.44051	Female-biased
MR7G011421.1	ABI3VP1	6.784478	6.631908	Male-biased
MR1TCONS_00049818.1	ABI3VP1	2.043654	0.47063	
MR6G025263.1	Alfin-like	-5.26195	-10.1966	Female-biased
MR7G011647.1	Alfin-like	-3.00529	-3.21342	Female-biased
MR7G011644.1	Alfin-like	-2.41654	-3.08635	Female-biased
MR2G028929.1	Alfin-like	-2.28369	-1.59667	Female-biased
MR6G016510.1	Alfin-like	1.626387	0.290219	
MR8G022041.1	AP2-EREBP	-7.99849	-9.65651	Female-biased
MR2G007010.1	AP2-EREBP	-14.2213	-9.4565	Female-biased
MR0G006452.1	AP2-EREBP	-8.50078	-8.64802	Female-biased
MR0G003706.1	AP2-EREBP	-5.79265	-5.70814	Female-biased
MR1G017646.1	AP2-EREBP	-5.7735	-4.40464	Female-biased
MR7G010715.1	AP2-EREBP	-1.20645	-2.86898	Female-biased
MR4G016016.1	AP2-EREBP	-3.06168	-2.73949	Female-biased
MR8G022212.1	AP2-EREBP	-1.07036	-1.89537	Female-biased
MR7G015191.1	AP2-EREBP	-1.25528	-1.81519	Female-biased
MR8G004033.1	AP2-EREBP	-1.85512	-1.69751	Female-biased
MR8G016432.1	AP2-EREBP	-1.47117	-1.58423	Female-biased
MR6G019855.1	AP2-EREBP	-2.42212	-1.56417	Female-biased
MR3G026243.1	AP2-EREBP	-0.40715	-1.49168	
MR3G012354.1	AP2-EREBP	-1.57469	-1.33377	Female-biased
MR0G003179.1	AP2-EREBP	-1.57469	-1.33377	Female-biased
MR6G011327.1	AP2-EREBP	-1.02542	-1.24461	Female-biased
MR7G013560.1	AP2-EREBP	-1.23729	-1.14375	Female-biased
MR3G026572.1	AP2-EREBP	2.119789	1.001365	Male-biased
MR6G011303.1	AP2-EREBP	1.45236	1.300009	Male-biased
MR6G022510.1	AP2-EREBP	1.45236	1.300009	Male-biased
MR1TCONS_00000352.1	AP2-EREBP	-1.78163	1.410138	
MR7G012917.1	AP2-EREBP	1.547074	1.41088	Male-biased
MR4G028420.1	AP2-EREBP	-0.875	1.512286	
MR8G002354.1	AP2-EREBP	1.020806	2.108017	Male-biased
MR8G012748.1	AP2-EREBP	1.539975	2.523333	Male-biased
MR5G020824.1	AP2-EREBP	-0.46613	2.645597	
MR3G017004.1	AP2-EREBP	-0.96864	2.958566	
MR0G007153.1	AP2-EREBP	3.940433	4.132536	Male-biased
MR4G021147.1	AP2-EREBP	0.247381	4.259619	
MR4G021148.1	AP2-EREBP	-1.73725	-0.15486	
MR6G029280.1	AP2-EREBP	-1.71506	0.129297	
MR8G026853.1	AP2-EREBP	-1.71506	0.129297	
MR6G019672.2	AP2-EREBP	-1.6737	-0.03261	
MR4G016017.1	AP2-EREBP	-1.59949	-0.57003	
MR6G019607.1	AP2-EREBP	-1.39414	-0.6713	
MR3G026169.1	AP2-EREBP	-1.18337	-0.08615	
MR8G003355.1	AP2-EREBP	-1.01315	-0.83199	
MR7G004138.1	AP2-EREBP	1.163057	0.4397	
MR3G011095.1	ARF	-7.23927	-13.6966	Female-biased

MR4G010547.2	ARF	-8.70508	-9.5325	Female-biased
MR7G007520.1	ARF	-7.31323	-7.96211	Female-biased
MR2G027556.1	ARF	-0.19262	-1.43813	
MR3G018668.1	ARF	-1.06015	-1.24527	Female-biased
MR5G024618.1	ARF	-0.04247	1.076211	
MR4G010937.1	ARR-B	-7.8639	-10.8964	Female-biased
MR8G012754.1	ARR-B	-1.98753	-1.6918	Female-biased
MR0G018446.1	ARR-B	-0.42555	-1.37074	
MR5G017155.1	ARR-B	-1.00243	-0.35593	
MR2G000226.1	BES1	-1.05833	-0.41339	
MR5G023951.1	BET	-0.80877	-1.37107	
MR6G025606.1	BET	-1.30478	-1.09809	Female-biased
MR1G020885.1	bHLH	-7.51928	-10.4511	Female-biased
MR6G026964.1	bHLH	-4.53719	-4.79464	Female-biased
MR7G020473.2	bHLH	-4.28014	-3.86179	Female-biased
MR4G016077.1	bHLH	3.420044	-3.77364	
MR4G016082.1	bHLH	3.420044	-3.77364	
MR2G024394.1	bHLH	-3.27877	-3.15063	Female-biased
MR4G009030.1	bHLH	-2.52658	-3.07265	Female-biased
MR8TCONS_00067952.1	bHLH	-3.04209	-2.83773	Female-biased
MR4G026989.1	bHLH	-1.38959	-2.18507	Female-biased
MR5G013412.3	bHLH	-1.61887	-2.16854	Female-biased
MR7G000141.1	bHLH	-0.08694	-2.11803	
MR5G011874.1	bHLH	-2.52672	-2.01443	Female-biased
MR8TCONS_00046257.1	bHLH	0.343365	-1.39784	
MR0G008506.1	bHLH	-1.05339	-1.32361	Female-biased
MR2G024128.1	bHLH	0.528519	-1.20542	
MR3TCONS_00023541.1	bHLH	0.454939	-1.16054	
MR7G017853.1	bHLH	-1.34199	-1.07496	Female-biased
MR7G011614.1	bHLH	-0.31229	-1.06354	
MR6G007069.1	bHLH	-0.86988	-1.05825	
MR0G006365.1	bHLH	0.541709	-1.00642	
MR4G027355.1	bHLH	-0.78755	1.144246	
MR0G004582.1	bHLH	-0.89038	1.289587	
MR5G010392.1	bHLH	1.126448	1.949002	Male-biased
MR3G008418.1	bHLH	-0.61478	2.147814	
MR5G025391.1	bHLH	-0.43229	2.164366	
MR5G011875.1	bHLH	4.04855	7.583524	Male-biased
MR5G004903.1	bHLH	4.245559	7.881823	Male-biased
MR6G001563.1	bHLH	8.662568	8.17448	Male-biased
MR8G020751.1	bHLH	8.662568	8.17448	Male-biased
MR8G004382.1	bHLH	-3.30958	-0.77409	
MR0G007712.1	bHLH	-1.83178	-0.46116	
MR8G004392.1	bHLH	-1.29377	-0.44012	
MR3G009918.1	bHLH	-1.15065	-0.03676	
MR7G017861.1	bHLH	-1.11395	-0.63029	
MR2G019409.1	bHLH	-1.02304	-0.88356	
MR0G002577.1	bHLH	3.708077	-0.03248	
MR5G027234.1	BSD	-2.0332	-2.22949	Female-biased
MR6G022953.1	BSD	2.985551	3.405452	Male-biased

MR5G024502.1	BSD	2.696995	0.701965	
MR0G027044.1	BSD	2.696995	0.701965	
MR1G015007.1	bZIP	-1.95842	-2.0696	Female-biased
MR7G012492.1	bZIP	-0.76276	1.354133	
MR1G009147.1	bZIP	0.678651	1.623851	
MR6G022742.1	bZIP	0.939883	1.631941	
MR8G020207.1	bZIP	-0.97954	2.351967	
MR1G007787.1	bZIP	4.77322	4.647635	Male-biased
MR8G028135.1	bZIP	-1.38524	-0.64738	
MR6G011275.1	bZIP	1.690333	0.745053	
MR8G001953.1	bZIP	3.392352	0.549983	
MR6G018079.1	C2C2-CO-like	-8.17679	-10.1009	Female-biased
MR3G018958.1	C2C2-CO-like	-11.4287	-8.96822	Female-biased
MR1G003361.1	C2C2-CO-like	0.036681	1.361655	
MR0G022997.1	C2C2-CO-like	1.413074	1.781265	Male-biased
MR8G027384.1	C2C2-CO-like	11.98149	11.90509	Male-biased
MR8G028280.1	C2C2-CO-like	-1.03577	-0.27221	
MR5G011870.1	C2C2-Dof	-6.81564	-7.94453	Female-biased
MR7G014897.1	C2C2-Dof		-6.78764	
MR3G009872.2	C2C2-Dof	-7.1337	-6.12078	Female-biased
MR5G022127.1	C2C2-Dof	-1.18097	-1.81652	Female-biased
MR7G016761.1	C2C2-Dof	-0.44849	-1.43448	
MR2G021710.1	C2C2-Dof	-6.74898	#NUM!	
MR6G010822.1	C2C2-GATA	-8.81252	-8.47872	Female-biased
MR8G003329.4	C2C2-GATA	-0.5853	-1.54669	
MR4G001510.1	C2C2-GATA	-0.19898	1.520769	
MR3G018666.1	C2C2-GATA	6.93141	8.539027	Male-biased
MR0G018656.1	C2C2-GATA	6.93141	8.539027	Male-biased
MR7G007143.1	C2C2-GATA	10.5785	11.4618	Male-biased
MR7G007144.1	C2C2-GATA	-1.57326	-0.29709	
MR3G009449.2	C2C2-GATA	-1.46801	-0.81531	
MR1G005677.1	C2C2-YABBY	2.222573	-4.50244	
MR1G005676.1	C2C2-YABBY	-9.37387	-3.23821	Female-biased
MR4G021270.1	C2C2-YABBY	0.021283	-1.07775	
MR2G002020.1	C2H2	-5.1245	-5.5756	Female-biased
MR7G011412.1	C2H2	-5.21421	-4.11575	Female-biased
MR0G008582.1	C2H2	-2.16517	-2.24179	Female-biased
MR6G013676.1	C2H2	-0.82261	-1.59921	
MR0TCONS_00064383.1	C2H2	-0.23704	-1.47525	
MR6G019724.1	C2H2	-1.33122	-1.41996	Female-biased
MR7G000378.1	C2H2	-0.51363	-1.1949	
MR7G000383.1	C2H2	-0.51363	-1.1949	
MR3G026299.1	C2H2	-0.0362	-1.09431	
MR6G009098.1	C2H2	-0.41087	-1.0717	
MR2G000513.1	C2H2	1.359404	3.50234	Male-biased
MR7G001351.1	C2H2	-1.21315	0.174025	
MR4TCONS_00019216.1	C2H2	-1.03391	-0.71573	
MR5G017611.1	C2H2	-1.01505	-0.51375	
MR2G025885.1	C3H	-8.1073	-8.34203	Female-biased
MR6G019909.1	C3H	-8.1073	-8.34203	Female-biased

MR1G014006.2	C3H	-5.89959	-5.45397	Female-biased
MR5G003404.2	C3H	-5.173	-4.30782	Female-biased
MR8G007629.3	C3H	-0.87872	-1.60592	
MR1G008453.1	C3H	-1.20007	-1.33837	Female-biased
MR5G001015.1	C3H	2.318869	-1.2475	
MR7G007732.1	C3H	-0.74937	-1.05784	
MR5G010200.1	C3H	1.33161	1.085875	Male-biased
MR6G029282.1	C3H	-0.45107	1.165781	
MR4G021029.1	C3H	1.384982	1.489071	Male-biased
MR1G007794.2	C3H	1.844099	1.939494	Male-biased
MR1G017406.1	C3H	-1.90408	-0.99476	
MR0G007920.1	C3H	-1.70241	-0.97331	
MR1G021678.3	C3H	-1.63341	-0.91876	
MR1G017680.1	C3H	-1.39075	-0.73318	
MR3G012196.1	C3H	-1.07733	-0.04131	
MR3G014865.1	C3H	-1.07733	-0.04131	
MR3G012175.1	C3H	-1.07653	-0.08154	
MR6G013360.1	CAMTA	-1.26577	-0.84189	
MR8G014168.2	CPP	-0.47032	-1.74021	
MR6G016114.2	CPP	-1.47233	-1.14124	Female-biased
MR0G023365.1	CSD	-0.4685	-1.05741	
MR7G010688.2	CSD	-0.8202	-1.03882	
MR2G021709.1	E2F-DP	-1.54117	-1.01852	Female-biased
MR8G027687.2	E2F-DP	1.126094	0.284927	
MR1G018593.1	EIL	-1.14857	-1.10458	Female-biased
MR8G004987.1	EIL	-0.3139	2.052851	
MR7G000999.2	FAR1	-3.36617	-2.20343	Female-biased
MR8G002126.2	FAR1	-1.49519	-1.3579	Female-biased
MR6G019872.2	FAR1	-0.77964	-1.07737	
MR1G018598.1	FAR1	-0.54842	-1.0725	
MR5G017147.1	FAR1	-0.40329	-1.04187	
MR6G010304.1	FAR1	-0.21825	1.528206	
MR1G023372.1	FAR1	1.759519	1.858298	Male-biased
MR6G010302.1	FAR1	1.816574	-0.26978	
MR8G005830.2	FHA	-4.07811	-3.95207	Female-biased
MR0G008594.3	FHA	-2.60268	-3.402	Female-biased
MR8G002044.2	FHA	1.247741	1.906657	Male-biased
MR5G003275.1	FHA	-1.88277	-0.73296	
MR3G015153.1	FHA	-1.19393	-0.98928	
MR5G010378.3	FHA	-1.11601	-0.89543	
MR6G018105.1	FHA	1.34144	0.495006	
MR4G026977.1	G2-like	-1.70795	-2.22892	Female-biased
MR6G021459.1	G2-like	-0.29305	-1.76242	
MR1G006382.1	G2-like	-1.46215	-1.54047	Female-biased
MR5G016215.1	G2-like	-0.56207	-1.32259	
MR3G026136.1	G2-like	-0.24101	-1.23208	
MR5G022401.1	G2-like	-0.28262	-1.18032	
MR5G016214.1	G2-like	1.580672	1.098846	Male-biased
MR6G021390.2	G2-like	6.604213	8.738729	Male-biased
MR1G029229.1	G2-like	-1.41441	-0.26218	

MR1G022975.2	G2-like	1.165309	0.611891	
MR4G014241.1	G2-like	2.55105	-11.1033	
MR6G021504.1	GeBP	-1.31507	-1.36985	Female-biased
MR6G010752.1	GRAS	-2.22396	-2.73894	Female-biased
MR5G017608.1	GRAS	-1.81065	-1.77192	Female-biased
MR0G027758.1	GRAS	-0.91852	-1.52675	
MR0G027776.1	GRAS	-0.91852	-1.52675	
MR2G023232.1	GRAS	-1.93178	-1.50894	Female-biased
MR8G007080.2	GRAS	-1.27184	-1.17202	Female-biased
MR7G028053.1	GRAS	-0.00617	-1.16634	
MR4G021295.1	GRAS	-0.27981	-1.06905	
MR4G018381.1	GRAS	-1.43633	0.878844	
MR7G027609.1	GRAS	-1.35167	-0.45257	
MR2G024216.1	GRAS	1.055204	-0.23884	
MR1G005476.1	GRAS	1.197386	-1.11247	
MR6G010478.1	GRAS	1.29238	0.553858	
MR6G021506.1	GRAS	1.515037	1.123464	Male-biased
MR7G021983.1	GRF	-0.95824	-1.81704	
MR4G021188.1	GRF	-2.49099	-1.76062	Female-biased
MR2G005670.1	GRF	-0.16217	-1.7502	
MR6G018847.1	GRF	-0.75895	-1.46888	
MR8G004272.1	HB	-1.1612	-1.32566	Female-biased
MR8G012738.1	HB	-1.29316	-1.25553	Female-biased
MR7G024235.1	HB	1.638543	-0.71307	
MR6TCONS_00015131.1	HRT		-7.89553	
MR1G027453.1	HSF	-0.18982	-2.18553	
MR0G006901.1	HSF	-2.60802	-2.13523	Female-biased
MR6G016551.1	HSF	-1.30693	-1.87181	Female-biased
MR0G005153.1	HSF	1.11624	2.756218	Male-biased
MR3G009468.1	HSF	-0.078	3.180277	
MR7G027933.1	HSF	-1.52891		
MR8G019532.1	LIM		-5.84666	
MR8G019487.1	LIM	-2.53035	-3.07264	Female-biased
MR1G017663.1	LIM	-1.36431	-2.13001	Female-biased
MR6G015557.1	LOB	-1.41076	-4.34938	Female-biased
MR2G016185.1	LOB	-3.14501	-2.99114	Female-biased
MR6G026951.1	LOB	1.688554	-2.19091	
MR1G023921.1	LOB	-0.12673	-1.04671	
MR2G028940.1	LOB	2.229122	2.108295	Male-biased
MR2G011937.1	LOB	0.410933	2.569527	
MR7G001353.1	LOB	-1.16667	2.925592	
MR8G007624.1	MADS	-2.09504	-2.23055	Female-biased
MR6G019836.1	MADS	0.07371	-1.61132	
MR0G004520.1	MADS	-1.12733	-1.40343	Female-biased
MR7G008266.1	MADS	-0.65643	-1.22568	
MR1G028353.2	MADS	0.956644	1.286294	
MR2G024877.1	MADS	-1.03562	2.693258	
MR2G028804.3	MADS	4.498093	3.687309	Male-biased
MR0G005926.1	MADS	10.99077	11.55486	Male-biased
MR7G013040.1	MADS	-1.05235	-0.37322	

MR8G019281.1	MADS	1.537994	1.178597	Male-biased
MR6G009344.1	mTERF	-9.08681	-8.90392	Female-biased
MR7G021960.1	mTERF	-1.11935	-1.51166	Female-biased
MR4G015437.1	mTERF	-0.80804	-1.44181	
MR8G006280.1	mTERF	-0.74854	-1.16045	
MR1G005382.1	mTERF	0.264536	-1.12492	
MR2G002677.1	mTERF	-0.65585	-1.10964	
MR8G023496.1	mTERF	-0.4138	1.051961	
MR5TCONS_00011163.1	mTERF	-1.48875	-3.76457	Female-biased
MR4G006409.1	mTERF	1.133605	0.484122	
MR6G025618.1	mTERF	2.224694	0.893085	
MR4G023331.1	MYB	-6.12077	-8.51967	Female-biased
MR4G009025.1	MYB	-7.05628	-8.20118	Female-biased
MR3G001271.1	MYB	-2.09488	-5.9862	Female-biased
MR2G012875.1	MYB	-4.00775	-4.70921	Female-biased
MR1G002331.1	MYB	-6.11414	-3.40067	Female-biased
MR5G002495.2	MYB	-1.06134	-2.95374	Female-biased
MR2G023221.1	MYB	-2.53232	-2.93501	Female-biased
MR2G005739.1	MYB	0.100929	-2.83422	
MR2G000645.1	MYB	-3.13503	-2.5825	Female-biased
MR2G000192.1	MYB	-1.56439	-2.04467	Female-biased
MR1G029309.1	MYB	0.14691	-1.843	
MR2G016448.1	MYB	-0.70452	-1.82621	
MR6G018838.1	MYB	0.12705	-1.68035	
MR2G000910.2	MYB	-1.12385	-1.64385	Female-biased
MR0G011028.3	MYB	-1.83136	-1.6229	Female-biased
MR5G025086.1	MYB	-0.94429	-1.6092	
MR6G021516.3	MYB	0.128226	-1.60812	
MR6G018839.1	MYB	-0.17587	-1.49344	
MR6TCONS_00015422.1	MYB	0.703873	-1.44692	
MR3G014811.1	MYB	-0.51523	-1.41933	
MR1G027074.1	MYB	-0.49442	-1.40329	
MR5G025027.1	MYB	-0.89639	-1.3256	
MR3G026244.1	MYB	0.626353	-1.32466	
MR0G003835.1	MYB	-0.67035	-1.32404	
MR5G003799.1	MYB	-0.40979	-1.24668	
MR6TCONS_00014817.1	MYB	0.119181	-1.24575	
MR7G007545.1	MYB	-0.05968	-1.24528	
MR6G027697.1	MYB	-0.6581	-1.18333	
MR1G005480.1	MYB	-0.98118	-1.16236	
MR6G016540.1	MYB	-0.2122	-1.14325	
MR1TCONS_00013823.1	MYB	-0.92228	-1.10045	
MR2G027101.3	MYB	-0.99332	-1.07362	
MR3G011069.1	MYB	0.045973	-1.03963	
MR3G011076.1	MYB	0.045973	-1.03963	
MR2G024869.2	MYB	-0.43304	-1.00646	
MR7G000808.1	MYB	-1.11446	-1.00202	Female-biased
MR7G013056.1	MYB	-0.45705	1.022744	
MR5G025085.1	MYB	-0.68849	1.08952	
MR2G006874.1	MYB	-0.89511	1.115388	

MR8G007383.1	MYB	1.203707	1.124883	Male-biased
MR3TCONS_00039020.1	MYB	-0.17365	1.170437	
MR7TCONS_00051920.1	MYB	-0.19193	1.197105	
MR8TCONS_00067993.1	MYB	-0.38162	1.255227	
MR3G014734.2	MYB	1.283921	2.500156	Male-biased
MR6G004331.1	MYB	1.955658	2.773777	Male-biased
MR0G006573.1	MYB	1.172715	3.113033	Male-biased
MR1TCONS_00020658.1	MYB	8.830645	6.819302	Male-biased
MR3G001142.1	MYB	-2.30394	-0.97857	
MR1G014064.1	MYB	-1.86021	-0.40091	
MR5G021935.1	MYB	-1.42563	-0.10385	
MR1G019297.1	MYB	-1.3299	-0.16994	
MR4G021334.1	MYB	-1.13664	-0.6627	
MR7TCONS_00061960.1	MYB	-1.06554	-0.37751	
MR8TCONS_00002049.1	MYB	-1.04001	-0.42747	
MR7G022705.1	MYB	-1.01856	0.009964	
MR6G021487.1	MYB	1.134898	-0.49812	
MR0G007890.1	MYB	1.163236	1.905003	Male-biased
MR1G020571.1	MYB	3.246224	0.030861	
MR7G001983.1	NAC	-8.36097	-6.46387	Female-biased
MR8G028131.1	NAC	-7.17086	-5.35971	Female-biased
MR4G003861.1	NAC	-2.82577	-3.35836	Female-biased
MR4G021267.1	NAC	-1.95145	-1.81652	Female-biased
MR3G017020.2	NAC	-1.1783	-1.06115	Female-biased
MR0G006218.1	NAC	-1.01683	1.018694	
MR7G013515.1	NAC	1.091916	1.078244	Male-biased
MR8G024965.1	NAC	-1.5734	1.388872	
MR7TCONS_00049269.1	NAC	-0.75795	1.638381	
MR4G021102.1	NAC	0.144171	1.906867	
MR2G027638.1	NAC	0.497503	2.004013	
MR2G027639.1	NAC	9.813781	3.868021	Male-biased
MR6G010794.1	NAC	9.68301	8.789061	Male-biased
MR7TCONS_00049466.1	NAC	11.08518	10.27494	Male-biased
MR3G015792.1	NAC	-1.88176	-0.80953	
MR7G013031.1	NAC	-1.88106	-0.5313	
MR7G008137.1	NAC	1.374302	-0.58227	
MR0G007465.1	NFYA	-3.22629	-3.80126	Female-biased
MR1G027429.1	NFYA	3.700775	4.31231	Male-biased
MR6TCONS_00015260.1	NFYA	1.110074	0.37722	
MR2TCONS_00053201.1	NFYA	1.133382	0.784611	
MR1G004770.1	NFYA	1.374178	0.724366	
MR4G016280.1	*NF-YB*	-1.00803	-0.21838	
MR1G019312.1	OFP	0.33098	-1.4505	
MR2G027683.1	OFP	-1.46566	1.40114	
MR6TCONS_00056704.1	PBF-2-like	-0.89295	-1.75383	
MR7G000798.1	PBF-2-like	-0.6833	-1.13872	
MR0G008511.1	PLATZ	-0.57647	-1.20397	
MR4G023632.1	PLATZ	-0.10523	2.126219	
MR8G029140.1	RWP-RK	-5.15885	-4.12747	Female-biased
MR3G001101.1	RWP-RK	-3.22596	-2.59418	Female-biased

MR0G004808.1	RWP-RK	0.169316	-1.4768	
MR8G015360.1	RWP-RK	-0.88394	-1.06601	
MR2G006999.1	SBP	-1.62787	-1.50019	Female-biased
MR5G021895.2	SBP	-1.59857	-1.00064	Female-biased
MR8G007406.1	SBP	1.195964	1.074178	Male-biased
MR1G013974.1	Sigma70-like	-0.74538	-1.72627	
MR8G014224.1	Sigma70-like	-0.34423	-1.28674	
MR7G015183.3	Sigma70-like	-1.84619	0.065646	
MR5G003816.1	SWI/SNF	-1.71197	0.834414	
MR5G024537.1	TAZ	-4.765	-5.9094	Female-biased
MR4G021037.1	TAZ	-1.55079	-0.44955	
MR6TCONS_00004269.1	TCP	1.567073	-1.85264	
MR2G000403.1	TCP	-0.63615	-1.22299	
MR7G011414.1	TCP	-0.30586	-1.15976	
MR0G005919.1	TCP	-1.4997	-1.15836	Female-biased
MR0G005918.1	TCP	-1.0991	-0.93656	
MR8G021808.1	Tify	-9.1291	-10.7563	Female-biased
MR7G012609.1	Tify	-8.58303	-8.27472	Female-biased
MR7G002983.1	Tify	-9.23098	-6.90502	Female-biased
MR3G014475.1	Tify	-8.10048	-6.43062	Female-biased
MR5G024985.1	Tify	-1.2017	-1.20678	Female-biased
MR7G002984.2	Tify	-2.49034	-1.20189	Female-biased
MR6G022827.1	Tify	0.973033	2.736979	
MR3G014474.2	Tify	3.238931	3.597219	Male-biased
MR6G022829.1	Tify	-2.24165	7.609239	
MR6G013367.1	TIG	1.865275	1.894734	Male-biased
MR5G021904.1	TIG	2.837571	2.861517	Male-biased
MR3G023980.1	Trihelix	-10.3626	-10.7322	Female-biased
MR7G000174.1	Trihelix	-0.25756	-1.62714	
MR4G001657.1	Trihelix	-1.10361	-1.61853	Female-biased
MR6G010891.1	Trihelix	-1.32913	-1.30636	Female-biased
MR2G020369.1	Trihelix	-0.43995	-1.20656	
MR1G015648.1	Trihelix	-0.25627	-1.17452	
MR1TCONS_00011999.1	Trihelix	0.239268	-1.1087	
MR1TCONS_00012000.1	Trihelix	0.239268	-1.1087	
MR2G006754.1	Trihelix	-2.07404	-1.05041	Female-biased
MR5G021897.1	Trihelix	-0.84705	-1.02881	
MR5G025093.1	Trihelix	-2.29559	-0.90108	
MR7G005491.2	Trihelix	-1.64212	-0.80735	
MR2G002673.2	Trihelix	1.680352	0.294116	
MR4G018573.1	TUB	-8.57684	-11.363	Female-biased
MR3G023986.1	TUB	-2.68255	-3.61068	Female-biased
MR5G002508.1	TUB	5.845237	4.878932	Male-biased
MR6G008503.1	ULT	-1.12093	-1.00349	Female-biased
MR2G018504.1	VOZ	-1.10918	-1.19351	Female-biased
MR8G004639.1	WRKY	-10.8075	-12.994	Female-biased
MR5G017510.1	WRKY	-12.2154	-11.904	Female-biased
MR6G022939.1	WRKY	-11.5413	-9.05376	Female-biased
MR8G028163.1	WRKY	-10.7269	-9.01122	Female-biased
MR3G026679.1	WRKY	-9.09225	-8.42398	Female-biased

MR0TCONS_00009688.1	WRKY	-0.6629	-1.06625	
MR7G015184.1	WRKY	-1.41053	1.309454	
MR2G016396.1	WRKY	-0.93533	1.775696	
MR3G012299.1	WRKY	0.928839	2.45221	
MR2G016401.1	WRKY	0.721859	3.097345	
MR4G025295.1	WRKY	6.417628	6.963842	Male-biased
MR6G011302.1	WRKY	9.014792	7.439172	Male-biased
MR8G012766.1	WRKY	-1.84204	-0.93253	
MR4G022367.1	WRKY	-1.6215	0.529258	
MR3G019067.1	WRKY	-1.32689	-0.54868	
MR2G028587.1	WRKY	-1.19888	0.547514	
MR3G011147.1	WRKY	-1.08094	0.353637	
MR1G008927.1	WRKY	-1.0493	-0.10859	
MR6G022509.1	WRKY	1.241645	0.269575	
MR7G000837.1	zf-HD	1.19878	-1.30913	
MR7G023875.1	zf-HD	1.19878	-1.30913	
MR6G013935.1	zf-HD	6.105447	5.347811	Male-biased

Table S11. List of transcription factor genes specifically expressed in males and females.

Gene ID	F0	F1	M0	M1	Family	Specific expressed	log2(M0/F0)	log2(M1/F1)
MR7G011421.1	0	0	1.826667	4.44	ABI3VP1	male	6.784478	6.631908
MR5G011875.1	0	0	3.243333	1.976667	bHLH	male	4.04855	7.583524
MR6G001563.1	0	0	7.35	5.33	bHLH	male	8.662568	8.17448
MR8G020751.1	0	0	7.35	5.33	bHLH	male	8.662568	8.17448
MR1G007787.1	0	0	16.40667	15.97667	bZIP	male	4.77322	4.647635
MR8G027384.1	0	0	50.39333	48.64333	C2C2-CO-like	male	11.98149	11.90509
MR3G018666.1	0	0	1.556667	4.78	C2C2-GATA	male	6.93141	8.539027
MR0G018656.1	0	0	1.556667	4.78	C2C2-GATA	male	6.93141	8.539027
MR7G007143.1	0	0	19.22667	36.12333	C2C2-GATA	male	10.5785	11.4618
MR6G021390.2	0	0	14.35667	16.01667	G2-like	male	6.604213	8.738729
MR0G005926.1	0	0	44.56667	67.31333	MADS	male	10.99077	11.55486
MR1TCONS_00020658.1	0	0	13.44	16.56	MYB	male	8.830645	6.819302
MR6G010794.1	0	0	12.09	23.83667	NAC	male	9.68301	8.789061
MR7TCONS_00049466.1	0	0	39.35667	22.87	NAC	male	11.08518	10.27494
MR1G027429.1	0	0	9.006667	12.10333	NFYA	male	3.700775	4.31231
MR4G025295.1	0	0	1.26	1.84	WRKY	male	6.417628	6.963842
MR6G011302.1	0	0	6.446667	2.203333	WRKY	male	9.014792	7.439172
MR6G013935.1	0	0	37.31667	22.05333	zf-HD	male	6.105447	5.347811
MR6G025263.1	10.09333	12.02667	0	0	Alfin-like	female	-5.26195	-10.1966
MR8G022041.1	26.71	11.24667	0	0	AP2-EREBP	female	-7.99849	-9.65651
MR2G007010.1	357.13	259.87	0	0	AP2-EREBP	female	-14.2213	-9.4565
MR0G006452.1	4.96	5.456667	0	0	AP2-EREBP	female	-8.50078	-8.64802
MR1G017646.1	11.86333	12.35667	0	0	AP2-EREBP	female	-5.7735	-4.40464
MR3G011095.1	73.04667	55.63	0	0	ARF	female	-7.23927	-13.6966
MR4G010547.2	35.00667	52.79333	0	0	ARF	female	-8.70508	-9.5325
MR7G007520.1	22.86	33.53	0	0	ARF	female	-7.31323	-7.96211
MR4G010937.1	17.37	25.75667	0	0	ARR-B	female	-7.8639	-10.8964
MR1G020885.1	35.25	35.35	0	0	bHLH	female	-7.51928	-10.4511

MR6G026964.1	7.60	5.71	0	0	bHLH	female	-4.53719	-4.79464
MR7G020473.2	9.12	6.52	0	0	bHLH	female	-4.28014	-3.86179
MR2G024394.1	9.05	7.84	0	0	bHLH	female	-3.27877	-3.15063
MR4G009030.1	2.57	1.96	0	0	bHLH	female	-2.52658	-3.07265
MR8TCONS_00067952.1	4.46	3.53	0	0	bHLH	female	-3.04209	-2.83773
MR6G018079.1	9.806667	12.41667	0	0	C2C2-CO-like	female	-8.17679	-10.1009
MR3G018958.1	25.43667	4.613333	0	0	C2C2-CO-like	female	-11.4287	-8.96822
MR5G011870.1	39.05333	41.75	0	0	C2C2-Dof	female	-6.81564	-7.94453
MR3G009872.2	59.30333	59.01333	0	0	C2C2-Dof	female	-7.1337	-6.12078
MR6G010822.1	14.17333	11.12	0	0	C2C2-GATA	female	-8.81252	-8.47872
MR2G002020.1	35.21667	44.52667	0	0	C2H2	female	-5.1245	-5.5756
MR7G011412.1	20.77333	14.48667	0	0	C2H2	female	-5.21421	-4.11575
MR2G025885.1	2.763333	3.243333	0	0	C3H	female	-8.1073	-8.34203
MR6G019909.1	2.763333	3.243333	0	0	C3H	female	-8.1073	-8.34203
MR5G003404.2	9.55	9.326667	0	0	C3H	female	-5.173	-4.30782
MR6G009344.1	4.253333	3.743333	0	0	mTERF	female	-9.08681	-8.90392
MR4G023331.1	3.88	4.16	0	0	MYB	female	-6.12077	-8.51967
MR4G009025.1	1.35	2.42	0	0	MYB	female	-7.05628	-8.20118
MR7G001983.1	5.24	1.363333	0	0	NAC	female	-8.36097	-6.46387
MR8G028131.1	4.323333	3.006667	0	0	NAC	female	-7.17086	-5.35971
MR5G024537.1	11.91667	12.81667	0	0	TAZ	female	-4.765	-5.9094
MR8G021808.1	16.66	15.97667	0	0	Tify	female	-9.1291	-10.7563
MR3G014475.1	11.34	88.97	0	0	Tify	female	-8.10048	-6.43062
MR3G023980.1	11.90667	15.34333	0	0	Trihelix	female	-10.3626	-10.7322
MR8G004639.1	127.9633	109.3567	0	0	WRKY	female	-10.8075	-12.994
MR5G017510.1	61.07333	49.08333	0	0	WRKY	female	-12.2154	-11.904
MR6G022939.1	18.55	15.46667	0	0	WRKY	female	-11.5413	-9.05376
MR8G028163.1	65.93333	68.51667	0	0	WRKY	female	-10.7269	-9.01122
MR3G026679.1	121.7	140.6733	0	0	WRKY	female	-9.09225	-8.42398

Table S12. The element enriched in promoter region of hormone-related genes.

| Gene ID | 3-A F1 3-bi AF nd 3 | A | AA | A | | |

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Table S13. List of genes in the light-green and dark-cyan networks.

MElightgreen network edges			MEdarkcyan network edges		
Source	**Target**	**Weight**	**Source**	**Target**	**Weight**
MR0TCONS_00017483.1	MR6G019729.1	0.472695	MR1G019545.1	MR4G006774.1	0.530353
MR0TCONS_00017483.1	MR7G000813.2	0.467842	MR1G019545.1	MR7G011363.5	0.530615
MR0TCONS_00017483.1	MR5G009737.1	0.462667	MR1G019545.1	MR8G000678.2	0.533582
MR0TCONS_00017483.1	MR2G024219.1	0.478073	MR1G019545.1	MR7G014360.1	0.521973
MR0TCONS_00017483.1	MR6G018085.1	0.462152	MR1G019545.1	MR4G026972.1	0.535006
MR0TCONS_00017483.1	MR6G018093.1	0.490058	MR1G019545.1	MR8G012690.1	0.531392
MR0TCONS_00017483.1	MR2G024440.1	0.48157	MR1G019545.1	MR7G014376.1	0.535668
MR0TCONS_00017483.1	MR2G024131.1	0.474114	MR1G019545.1	MR8G000662.1	0.529448
MR0TCONS_00017483.1	MR5G011953.1	0.487234	MR1G019545.1	MR8G016813.1	0.523919
MR0TCONS_00017483.1	MR0TCONS_00026066.1	0.449195	MR1G019545.1	MR4G026702.1	0.52099
MR0TCONS_00017483.1	MR5G003464.1	0.474372	MR1G019545.1	MR4G009043.1	0.537901
MR0TCONS_00017483.1	MR6G018097.1	0.486165	MR1G019545.1	MR7TCONS_00020974.1	0.535619
MR0TCONS_00017483.1	MR6G025626.1	0.466192	MR1G019545.1	MR6G005848.1	0.527777
MR0TCONS_00017483.1	MR2G020373.1	0.444728	MR1G019545.1	MR4G014243.1	0.533526
MR0TCONS_00017483.1	MR2G022287.1	0.488992	MR1G019545.1	MR4G015995.1	0.536947
MR0TCONS_00017483.1	MR6G018074.1	0.48746	MR1G019545.1	MR4G008724.1	0.527548
MR0TCONS_00017483.1	MR5G011870.1	0.484514	MR1G019545.1	MR8G001590.1	0.523659
MR0TCONS_00017483.1	MR0TCONS_00023638.1	0.4729	MR1G019545.1	MR8G001596.1	0.527655
MR0TCONS_00017483.1	MR7G000148.1	0.466159	MR1G019545.1	MR4G016027.1	0.528404
MR0TCONS_00017483.1	MR0TCONS_00029296.1	0.474483	MR1G019545.1	MR5TCONS_00034061.1	0.531977
MR0TCONS_00017483.1	MR2TCONS_00005123.1	0.471948	MR1G019545.1	MR7G011670.2	0.524342
MR0TCONS_00017483.1	MR3G001179.1	0.490514	MR1G019545.1	MR4G023618.1	0.537393
MR0TCONS_00017483.1	MR3G001245.1	0.440777	MR1G019545.1	MR8G011203.1	0.527833
MR0TCONS_00017483.1	MR6G020073.2	0.487276	MR1G019545.1	MR7G007479.1	0.524569
MR0TCONS_00017483.1	MR5G003617.1	0.462246	MR1G019545.1	MR7G007524.1	0.533887
MR0TCONS_00017483.1	MR6G021647.1	0.465426	MR1G019545.1	MR0G025665.1	0.522876
MR0TCONS_00017483.1	MR5G009648.1	0.488198	MR1G019545.1	MR8G020746.1	0.525507
MR0TCONS_00017483.1	MR5G009689.1	0.489969	MR1G019545.1	MR8G020754.1	0.532128
MR0TCONS_00017483.1	MR1G014018.1	0.461549	MR1G019545.1	MR4G009044.1	0.535816
MR0TCONS_00017483.1	MR0TCONS_00018991.1	0.465868	MR1G019545.1	MR6G004352.1	0.523767
MR0TCONS_00017483.1	MR6TCONS_00003668.1	0.489351	MR1G019545.1	MR8G003125.1	0.529818
MR0TCONS_00017483.1	MR5G025810.1	0.444786	MR1G019545.1	MR8G003345.1	0.531511
MR0TCONS_00017483.1	MR5G012384.1	0.484915	MR1G019545.1	MR8G004551.1	0.526003
MR0TCONS_00017483.1	MR0TCONS_00035048.1	0.491539	MR1G019545.1	MR8G001577.1	0.536081
MR0TCONS_00017483.1	MR0TCONS_00037396.1	0.486234	MR1G019545.1	MR6G003889.1	0.520869
MR0TCONS_00017483.1	MR6G019866.1	0.481042	MR1G019545.1	MR7G016713.1	0.522065
MR0TCONS_00017483.1	MR6G019911.1	0.488566	MR1G019545.1	MR8G010076.1	0.531217
MR0TCONS_00017483.1	MR6G021435.1	0.494329	MR1G019545.1	MR2G000623.1	0.528358
MR0TCONS_00017483.1	MR3G002725.1	0.488576	MR1G019545.1	MR2G006160.1	0.524486
MR0TCONS_00017483.1	MR3G006431.1	0.467835	MR1G019545.1	MR2G009995.1	0.533892
MR0TCONS_00017483.1	MR6G016528.1	0.465699	MR1G019545.1	MR2G011703.1	0.521744
MR0TCONS_00017483.1	MR8G012637.1	0.453043	MR1G019545.1	MR2G011723.1	0.521744
MR0TCONS_00017483.1	MR6G025929.3	0.475683	MR1G019545.1	MR8G019130.1	0.522096
MR0TCONS_00017483.1	MR5G025036.1	0.47007	MR1G019545.1	MR8G019531.1	0.532421

MR0TCONS_00017483.1	MR2G024060.1	0.468873	MR1G019545.1	MR6G010863.1	0.52806
MR0TCONS_00017483.1	MR2G024087.2	0.463476	MR1G019545.1	MR6G013295.1	0.523673
MR0TCONS_00017483.1	MR5G015914.1	0.461509	MR1G019545.1	MR6G013325.1	0.533876
MR0TCONS_00017483.1	MR5G017115.1	0.482252	MR1G019545.1	MR4G021010.1	0.537064
MR0TCONS_00017483.1	MR5G017134.1	0.483385	MR1G019545.1	MR4G021019.1	0.532904
MR0TCONS_00017483.1	MR5G017201.1	0.45717	MR1G019545.1	MR2G005420.4	0.529413
MR0TCONS_00017483.1	MR8G020616.1	0.47464	MR1G019545.1	MR7G022721.1	0.526542
MR0TCONS_00017483.1	MR5G003222.1	0.461414	MR1G019545.1	MR2G006162.1	0.522268
MR0TCONS_00017483.1	MR5G003457.1	0.461668	MR1G019545.1	MR3G021766.1	0.521165
MR0TCONS_00017483.1	MR6G025594.1	0.485874	MR1G019545.1	MR2G022146.2	0.531827
MR0TCONS_00017483.1	MR1G003952.1	0.4635	MR1G019545.1	MR8G002765.1	0.537251
MR0TCONS_00017483.1	MR8G012696.1	0.472083	MR1G019545.1	MR8G002789.1	0.524698
MR0TCONS_00017483.1	MR8G015530.1	0.44582	MR1G019545.1	MR4G016473.3	0.537799
MR0TCONS_00017483.1	MR1G012147.1	0.453971	MR1G019545.1	MR4G021008.1	0.529365
MR0TCONS_00017483.1	MR3G014724.1	0.478088	MR1G019545.1	MR1G028360.1	0.530692
MR0TCONS_00017483.1	MR8G018185.1	0.485219	MR1G019545.1	MR7G022720.1	0.531906
MR0TCONS_00017483.1	MR8G019278.2	0.442798	MR1G019545.1	MR5G024989.2	0.530019
MR0TCONS_00017483.1	MR8G019517.1	0.443497	MR1G019545.1	MR4G023611.1	0.531846
MR0TCONS_00017483.1	MR8G019525.2	0.463006	MR1G019545.1	MR0G014428.1	0.521333
MR0TCONS_00017483.1	MR5G017299.1	0.478958	MR1G019545.1	MR8G022070.1	0.520206
MR0TCONS_00017483.1	MR7G007720.1	0.483596	MR1G019545.1	MR2G024066.1	0.526811
MR0TCONS_00017483.1	MR5G017371.1	0.456278	MR1G019545.1	MR5G024525.1	0.52037
MR0TCONS_00017483.1	MR1G003946.1	0.4635	MR1G019545.1	MR4G016475.1	0.526399
MR0TCONS_00017483.1	MR7G016767.2	0.479855	MR1G019545.1	MR8G006636.1	0.526668
MR0TCONS_00017483.1	MR1G008473.1	0.484447	MR1G019545.1	MR8G007621.1	0.524177
MR0TCONS_00017483.1	MR1G008913.1	0.448723	MR1G019545.1	MR5G017247.1	0.522975
MR0TCONS_00017483.1	MR7G024256.1	0.47191	MR1G019545.1	MR5G018745.1	0.527478
MR0TCONS_00017483.1	MR7G028038.2	0.462208	MR1G019545.1	MR0G024306.1	0.532135
MR0TCONS_00017483.1	MR7G000150.1	0.484082	MR1G019545.1	MR8G028462.1	0.528279
MR0TCONS_00017483.1	MR1G019332.1	0.483024	MR1G019545.1	MR7G024817.1	0.528395
MR0TCONS_00017483.1	MR7G000834.1	0.477033	MR1G019545.1	MR5G010171.1	0.529574
MR0TCONS_00017483.1	MR7G004995.1	0.47243	MR1G019545.1	MR8G022192.1	0.536927
MR0TCONS_00017483.1	MR8G020258.1	0.489902	MR1G019545.1	MR3G011044.1	0.528279
MR0TCONS_00017483.1	MR8G010060.1	0.466389	MR1G019545.1	MR8G027828.1	0.523591
MR0TCONS_00017483.1	MR2G007010.1	0.454479	MR1G019545.1	MR6G022644.1	0.536699
MR0TCONS_00017483.1	MR8G010083.1	0.483132	MR1G019545.1	MR6G025256.1	0.534017
MR0TCONS_00017483.1	MR8G011210.1	0.474825	MR1G019545.1	MR5G010481.1	0.520254
MR0TCONS_00017483.1	MR6G016522.1	0.482652	MR1G019545.1	MR2G027161.1	0.524456
MR0TCONS_00017483.1	MR0TCONS_00017544.1	0.474151	MR1G019545.1	MR0G013397.1	0.526775
MR0TCONS_00017483.1	MR0TCONS_00018067.1	0.459493	MR1G019545.1	MR0G008817.1	0.536209
MR0TCONS_00017483.1	MR4G026749.1	0.453288	MR1G019545.1	MR0G005900.1	0.527376
MR0TCONS_00017483.1	MR4G027358.3	0.44441	MR1G019545.1	MR3G012293.1	0.532055
MR0TCONS_00017483.1	MR8G018182.3	0.44333	MR1G019545.1	MR6G023576.1	0.535173
MR0TCONS_00017483.1	MR8G018183.1	0.485711	MR1G019545.1	MR0G005287.1	0.532593
MR0TCONS_00017483.1	MR4TCONS_00016369.1	0.452956	MR1G019545.1	MR3G014742.1	0.529744
MR0TCONS_00017483.1	MR7G006051.1	0.443093	MR1G019545.1	MR4G021196.1	0.533183
MR0TCONS_00017483.1	MR0TCONS_00037684.1	0.474883	MR1G019545.1	MR3G007323.2	0.534421
MR0TCONS_00017483.1	MR0TCONS_00052571.1	0.466838	MR1G019545.1	MR0G007649.1	0.525951
MR0TCONS_00017483.1	MR1G003944.1	0.488007	MR1G019545.1	MR0G007648.1	0.525951
MR0TCONS_00017483.1	MR7G008145.3	0.444381	MR1G019545.1	MR0G007264.1	0.538374

MR0TCONS_00017483.1	MR8G020751.1	0.445314	MR1G019545.1	MR0G002914.1	0.522428
MR0TCONS_00017483.1	MR8G020766.1	0.454808	MR1G019545.1	MR0G007880.1	0.532747
MR0TCONS_00017483.1	MR3G011063.1	0.492797	MR2G024066.1	MR2G027161.1	0.520497
MR0TCONS_00017483.1	MR3G014650.1	0.466436	MR2G024066.1	MR3G007323.2	0.525727
MR0TCONS_00017483.1	MR8G022503.2	0.469232	MR2G024066.1	MR8G012690.1	0.52246
MR0TCONS_00017483.1	MR1G014145.1	0.441061	MR2G024066.1	MR8G022192.1	0.529221
MR0TCONS_00017483.1	MR1G015692.1	0.463819	MR2G024066.1	MR5G018745.1	0.523794
MR0TCONS_00017483.1	MR1G015702.1	0.474997	MR2G024066.1	MR0G005900.1	0.520407
MR0TCONS_00017483.1	MR4TCONS_00017612.1	0.451866	MR2G024066.1	MR8G020754.1	0.527961
MR0TCONS_00017483.1	MR1G020884.1	0.486851	MR2G024066.1	MR0G024306.1	0.523726
MR0TCONS_00017483.1	MR1G022529.1	0.483721	MR2G024066.1	MR8G019531.1	0.525198
MR0TCONS_00017483.1	MR1G027855.1	0.47009	MR2G024066.1	MR5G024989.2	0.525191
MR0TCONS_00017483.1	MR6G008503.1	0.441617	MR2G024066.1	MR0G005287.1	0.528321
MR0TCONS_00017483.1	MR5G020302.1	0.475735	MR2G024066.1	MR5TCONS_00034061.1	0.524546
MR0TCONS_00017483.1	MR5G020321.1	0.484915	MR2G024066.1	MR6G004352.1	0.520849
MR0TCONS_00017483.1	MR5G021736.1	0.470478	MR2G024066.1	MR4G014243.1	0.528402
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MR0TCONS_00017483.1	MR5G024537.1	0.476263	MR2G024066.1	MR0G008817.1	0.530871
MR0TCONS_00017483.1	MR5G025035.1	0.494069	MR2G024066.1	MR4G015995.1	0.529578
MR0TCONS_00017483.1	MR6G000259.1	0.444918	MR2G024066.1	MR6G025256.1	0.529309
MR0TCONS_00017483.1	MR6G000783.1	0.480504	MR2G024066.1	MR3G012293.1	0.523335
MR0TCONS_00017483.1	MR1G020792.1	0.474273	MR2G024066.1	MR3G014742.1	0.520521
MR0TCONS_00017483.1	MR8G001629.2	0.464934	MR2G024066.1	MR6G022644.1	0.528839
MR0TCONS_00017483.1	MR2G006757.1	0.444574	MR2G024066.1	MR6G023576.1	0.527567
MR0TCONS_00017483.1	MR6G007202.1	0.472187	MR2G024066.1	MR6G010863.1	0.52253
MR0TCONS_00017483.1	MR0G005280.1	0.450192	MR2G024066.1	MR4G009043.1	0.530856
MR0TCONS_00017483.1	MR6G010888.2	0.474599	MR2G024066.1	MR4G009044.1	0.527478
MR0TCONS_00017483.1	MR2G014105.1	0.473622	MR2G024066.1	MR0G007648.1	0.521378
MR0TCONS_00017483.1	MR2G016358.1	0.441022	MR2G024066.1	MR0G007880.1	0.522761
MR0TCONS_00017483.1	MR2G020031.1	0.474745	MR2G024066.1	MR7G014376.1	0.53037
MR0TCONS_00017483.1	MR8G021808.1	0.462043	MR2G024066.1	MR8G011203.1	0.522299
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MR0TCONS_00017483.1	MR4G028396.1	0.450406	MR2G024066.1	MR4G016473.3	0.531383
MR0TCONS_00017483.1	MR4TCONS_00007092.1	0.467096	MR2G024066.1	MR7G022720.1	0.523979
MR0TCONS_00017483.1	MR0G001497.1	0.463496	MR2G024066.1	MR7G022721.1	0.521616
MR0TCONS_00017483.1	MR0G003728.1	0.484166	MR2G024066.1	MR7G024817.1	0.521012
MR0TCONS_00017483.1	MR5G000697.1	0.459128	MR2G024066.1	MR7TCONS_00020974.1	0.526691
MR0TCONS_00017483.1	MR5G001859.1	0.487491	MR2G024066.1	MR8G000662.1	0.522348
MR0TCONS_00017483.1	MR7TCONS_00068913.1	0.461654	MR2G024066.1	MR6G005848.1	0.522243
MR0TCONS_00017483.1	MR0G005933.1	0.494561	MR2G024066.1	MR0G007264.1	0.531009
MR0TCONS_00017483.1	MR7G010648.1	0.442516	MR2G024066.1	MR4G021008.1	0.521088
MR0TCONS_00017483.1	MR7G010680.1	0.471934	MR2G024066.1	MR8G002765.1	0.531468
MR0TCONS_00017483.1	MR7G012054.1	0.453014	MR2G024066.1	MR7G011670.2	0.520616
MR0TCONS_00017483.1	MR7G022891.1	0.473788	MR2G024066.1	MR7G011363.5	0.524822
MR0TCONS_00017483.1	MR1G029232.1	0.460258	MR2G024066.1	MR5G010171.1	0.526775
MR0TCONS_00017483.1	MR8G027384.1	0.482076	MR2G024066.1	MR4G021019.1	0.523793
MR0TCONS_00017483.1	MR0G001496.1	0.490771	MR2G024066.1	MR6G013325.1	0.525004
MR0TCONS_00017483.1	MR1TCONS_00065258.1	0.466849	MR2G024066.1	MR0G007649.1	0.521378
MR0TCONS_00017483.1	MR6G001563.1	0.445314	MR2G024066.1	MR8G003345.1	0.522888
MR0TCONS_00017483.1	MR1G017405.1	0.449327	MR2G024066.1	MR4G016475.1	0.521403

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MR0TCONS_00017483.1	MR3G015834.1	0.451201	MR2G024066.1	MR4G023618.1	0.529901
MR0TCONS_00017483.1	MR4G021335.1	0.475047	MR2G024066.1	MR7G007479.1	0.520864
MR0TCONS_00017483.1	MR2G011234.3	0.477498	MR2G024066.1	MR8G006636.1	0.521804
MR0TCONS_00017483.1	MR4G024734.1	0.454284	MR2G024066.1	MR8G004551.1	0.521361
MR0TCONS_00017483.1	MR4G025266.1	0.443041	MR2G024066.1	MR7G007524.1	0.526827
MR0TCONS_00017483.1	MR4G025779.1	0.492714	MR2G024066.1	MR4G023611.1	0.523027
MR0TCONS_00017483.1	MR4G023328.1	0.484709	MR2G024066.1	MR8G001577.1	0.530571
MR0TCONS_00017483.1	MR1TCONS_00047494.1	0.467581	MR2G024066.1	MR8G003125.1	0.520559
MR0TCONS_00017483.1	MR1TCONS_00056373.1	0.457865	MR2G024066.1	MR8G001596.1	0.521705
MR0TCONS_00017483.1	MR1TCONS_00025928.1	0.463062	MR2G024066.1	MR4G026972.1	0.527714
MR0TCONS_00017483.1	MR0G027022.1	0.443096	MR2G024066.1	MR8G000678.2	0.524837
MR0TCONS_00017483.1	MR6G003925.1	0.468884	MR2G024066.1	MR4G021196.1	0.528696
MR0TCONS_00017483.1	MR6G006799.1	0.447178	MR3G015757.1	MR0G007424.1	0.525208
MR0TCONS_00017483.1	MR2G006156.1	0.455038	MR3G015757.1	MR6G007208.1	0.534927
MR0TCONS_00017483.1	MR3G026361.1	0.442768	MR3G015757.1	MR6G011265.1	0.520559
MR0TCONS_00017483.1	MR3G026562.1	0.468428	MR3G015757.1	MR6G015490.1	0.520719
MR0TCONS_00017483.1	MR0G006220.1	0.486098	MR3G015757.1	MR7G002562.1	0.537489
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MR0TCONS_00017483.1	MR1G028362.1	0.475992	MR3G015757.1	MR8G007621.1	0.540371
MR0TCONS_00017483.1	MR0G007114.1	0.480664	MR3G015757.1	MR0G007917.1	0.536056
MR0TCONS_00017483.1	MR1G029339.2	0.454724	MR3G015757.1	MR6G013325.1	0.536961
MR0TCONS_00017483.1	MR7G015326.1	0.460303	MR3G015757.1	MR0G013397.1	0.539903
MR0TCONS_00017483.1	MR0G022769.1	0.47378	MR3G015757.1	MR6G003659.1	0.52626
MR0TCONS_00017483.1	MR0G025657.1	0.490262	MR3G015757.1	MR6G023576.1	0.528902
MR0TCONS_00017483.1	MR3G014762.1	0.476613	MR3G015757.1	MR7G016713.1	0.540803
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MR0TCONS_00017483.1	MR3G015801.1	0.442965	MR3G015757.1	MR8G002087.1	0.526543
MR0TCONS_00017483.1	MR7TCONS_00002942.1	0.448832	MR3G015757.1	MR6G021640.1	0.52372
MR0TCONS_00017483.1	MR4G021077.5	0.493715	MR3G015757.1	MR4G021019.1	0.537563
MR0TCONS_00017483.1	MR4G022364.1	0.453277	MR3G015757.1	MR7G017822.1	0.525331
MR0TCONS_00017483.1	MR4G023063.1	0.480552	MR3G015757.1	MR7G022720.1	0.524608
MR0TCONS_00017483.1	MR4G023099.1	0.488117	MR3G015757.1	MR4G026972.1	0.530651
MR0TCONS_00017483.1	MR4G007287.2	0.48881	MR3G015757.1	MR3G021766.1	0.537608
MR0TCONS_00017483.1	MR0G007601.1	0.474967	MR3G015757.1	MR6G022644.1	0.531854
MR0TCONS_00017483.1	MR0G008632.2	0.490067	MR3G015757.1	MR4G028681.1	0.539336
MR0TCONS_00017483.1	MR4G007135.1	0.482432	MR3G015757.1	MR8G000679.2	0.52192
MR0TCONS_00017483.1	MR4G021049.1	0.443955	MR3G015757.1	MR8G001578.1	0.524193
MR0TCONS_00017483.1	MR2G001814.1	0.445857	MR3G015757.1	MR0G007264.1	0.530232
MR0TCONS_00017483.1	MR7G028821.1	0.480141	MR3G015757.1	MR8G002789.1	0.522778
MR0TCONS_00017483.1	MR4G018534.1	0.457298	MR3G015757.1	MR8G003125.1	0.540688
MR0TCONS_00017483.1	MR3TCONS_00012160.1	0.469943	MR3G015757.1	MR8G003357.1	0.522194
MR0TCONS_00017483.1	MR4G021219.4	0.450921	MR3G015757.1	MR4G021134.1	0.520525
MR0TCONS_00017483.1	MR4G021076.1	0.49464	MR3G015757.1	MR4G021195.1	0.522508
MR0TCONS_00017483.1	MR3G026615.1	0.480007	MR3G015757.1	MR4G001417.1	0.525443
MR0TCONS_00017483.1	MR4G009026.1	0.490048	MR3G015757.1	MR4G006774.1	0.527886
MR0TCONS_00017483.1	MR4G001427.1	0.480718	MR3G015757.1	MR4G023616.1	0.524015
MR0TCONS_00017483.1	MR4G002293.2	0.469186	MR3G015757.1	MR8G012676.1	0.53375
MR0TCONS_00017483.1	MR4G012554.1	0.452883	MR3G015757.1	MR8G012690.1	0.539385
MR0TCONS_00017483.1	MR4G016029.1	0.469926	MR3G015757.1	MR8G012742.1	0.523338

MR0TCONS_00017483.1	MR1TCONS_00020658.1	0.454865	MR3G015757.1	MR3G023792.1	0.522512
MR1TCONS_00020658.1	MR4G023099.1	0.462815	MR3G015757.1	MR4G008743.1	0.52002
MR1TCONS_00020658.1	MR5G020321.1	0.456762	MR3G015757.1	MR8G000678.2	0.537645
MR1TCONS_00020658.1	MR6G021435.1	0.456179	MR3G015757.1	MR7G007526.1	0.527777
MR1TCONS_00020658.1	MR6G018097.1	0.448233	MR3G015757.1	MR4G021021.3	0.522491
MR1TCONS_00020658.1	MR5G012384.1	0.456762	MR3G015757.1	MR5TCONS_00034061.1	0.526133
MR1TCONS_00020658.1	MR3G011063.1	0.46673	MR3G015757.1	MR8G012788.1	0.524723
MR1TCONS_00020658.1	MR7G024256.1	0.441777	MR3G015757.1	MR5G002859.1	0.523754
MR1TCONS_00020658.1	MR6G018074.1	0.45237	MR3G015757.1	MR4G023618.1	0.529348
MR1TCONS_00020658.1	MR4G021076.1	0.457026	MR3G015757.1	MR8G011209.1	0.522636
MR1TCONS_00020658.1	MR8G010083.1	0.459438	MR3G015757.1	MR8G011218.1	0.524262
MR1TCONS_00020658.1	MR8G020258.1	0.454109	MR3G015757.1	MR5G003500.1	0.534043
MR1TCONS_00020658.1	MR7G000150.1	0.451301	MR3G015757.1	MR4G015995.1	0.527538
MR1TCONS_00020658.1	MR6G018093.1	0.450264	MR3G015757.1	MR4G016473.3	0.521519
MR1TCONS_00020658.1	MR5G009648.1	0.461591	MR3G015757.1	MR8G019130.1	0.540813
MR1TCONS_00020658.1	MR5G009689.1	0.458412	MR3G015757.1	MR8G019531.1	0.527964
MR1TCONS_00020658.1	MR3G014762.1	0.442344	MR3G015757.1	MR5G003521.1	0.522211
MR1TCONS_00020658.1	MR4G009026.1	0.452212	MR3G015757.1	MR0G006455.1	0.520713
MR1TCONS_00020658.1	MR0G003728.1	0.453523	MR3G015757.1	MR8G024955.1	0.529208
MR1TCONS_00020658.1	MR4G007287.2	0.452989	MR3G015757.1	MR5G024481.1	0.524004
MR1TCONS_00020658.1	MR6G021647.1	0.440131	MR3G015757.1	MR5G010483.1	0.525811
MR1TCONS_00020658.1	MR6G025626.1	0.451642	MR3G015757.1	MR4G009044.1	0.534496
MR1TCONS_00020658.1	MR4G021077.5	0.464331	MR3G015757.1	MR5G024525.1	0.533539
MR1TCONS_00020658.1	MR5G011870.1	0.445363	MR3G015757.1	MR4G009043.1	0.526608
MR2G007010.1	MR5G012384.1	0.46137	MR3G015757.1	MR4G009608.1	0.52814
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MR2G007010.1	MR5G009648.1	0.469187	MR3G015757.1	MR0G002914.1	0.541657
MR2G007010.1	MR7G024256.1	0.463148	MR3G015757.1	MR8G022192.1	0.52995
MR2G007010.1	MR3G011063.1	0.452488	MR3G015757.1	MR0G005135.1	0.533756
MR2G007010.1	MR8G019525.2	0.453391	MR3G015757.1	MR8G028457.1	0.525204
MR2G007010.1	MR4G023099.1	0.469444	MR3G015757.1	MR8G028462.1	0.539068
MR2G007010.1	MR6G018074.1	0.443449	MR3G015757.1	MR8G020746.1	0.540459
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MR2G007010.1	MR6G016522.1	0.456606	MR4G023618.1	MR6G015490.1	0.525688
MR2G007010.1	MR4G009026.1	0.46924	MR4G023618.1	MR0G002914.1	0.538662
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MR2G016358.1	MR5G009689.1	0.446725	MR4G023618.1	MR5G018745.1	0.53275
MR2G016358.1	MR5G012384.1	0.466637	MR4G023618.1	MR7G014360.1	0.520059
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MR5G011870.1	MR6G007202.1	0.454813	MR4G023618.1	MR8G002789.1	0.53707
MR5G011870.1	MR8G011210.1	0.442677	MR4G023618.1	MR8G003125.1	0.538397
MR5G011870.1	MR6G000783.1	0.461006	MR4G023618.1	MR8G003345.1	0.536287
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MR5G011870.1	MR6G025929.3	0.463053	MR4G023618.1	MR8G006636.1	0.524108
MR5G011870.1	MR6G016528.1	0.450016	MR4G023618.1	MR8G007621.1	0.539944
MR5G011870.1	MR6G006799.1	0.440989	MR4G023618.1	MR8G010076.1	0.541359
MR5G011870.1	MR6G018085.1	0.452907	MR4G023618.1	MR8G011180.1	0.529939
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MR5G011870.1	MR6G018097.1	0.477099	MR4G023618.1	MR8G011209.1	0.525145
MR5G011870.1	MR6G018074.1	0.469332	MR4G023618.1	MR8G012676.1	0.536155
MR5G011870.1	MR8G018185.1	0.454848	MR4G023618.1	MR5G003500.1	0.535108
MR5G011870.1	MR5G025036.1	0.443103	MR4G023618.1	MR5G003521.1	0.533076
MR5G011870.1	MR6G021435.1	0.485718	MR4G023618.1	MR7G022721.1	0.524097
MR5G011870.1	MR6G021647.1	0.443507	MR4G023618.1	MR7G000279.1	0.52188
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MR5G011870.1	MR8G018183.1	0.47118	MR4G023618.1	MR7G016713.1	0.539706
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MR6G000783.1	MR8G018185.1	0.442295	MR6G021640.1	MR0G007917.1	0.536525
MR6G000783.1	MR0G003728.1	0.466568	MR6G021640.1	MR8G007621.1	0.538128
MR6G000783.1	MR6G021647.1	0.444706	MR6G021640.1	MR7G014911.1	0.530681
MR6G000783.1	MR6G019911.1	0.45073	MR6G021640.1	MR0G005135.1	0.534636
MR6G000783.1	MR0G001496.1	0.46584	MR6G021640.1	MR8G011180.1	0.521396
MR6G001563.1	MR6G020073.2	0.450618	MR6G021640.1	MR8G003125.1	0.537629
MR6G001563.1	MR0G001496.1	0.448847	MR6G021640.1	MR8G000678.2	0.533645
MR6G008503.1	MR0G001496.1	0.452374	MR7G000837.1	MR0G007264.1	0.524313
MR6G008503.1	MR6G019911.1	0.440289	MR7G000837.1	MR8G003125.1	0.523283
MR6G018085.1	MR7G000150.1	0.455636	MR7G000837.1	MR8G002765.1	0.520098
MR6G018085.1	MR7G024256.1	0.458712	MR7G000837.1	MR8G012690.1	0.523035
MR6G018085.1	MR0G025657.1	0.452779	MR7G000837.1	MR8G022192.1	0.523307
MR6G018085.1	MR6G021647.1	0.450705	MR7G000837.1	MR8G000678.2	0.524446
MR6G018085.1	MR8G010083.1	0.455147	MR7G000837.1	MR8G019531.1	0.521985
MR6G018085.1	MR6G021435.1	0.466698	MR7G007524.1	MR8G000678.2	0.536501
MR6G018085.1	MR0G003728.1	0.451408	MR7G007524.1	MR8G001577.1	0.534468
MR6G018085.1	MR6G019911.1	0.471219	MR7G007524.1	MR8G000662.1	0.529195
MR6G018085.1	MR6G018093.1	0.458608	MR7G007524.1	MR8G022192.1	0.537547
MR6G018085.1	MR0G001496.1	0.459988	MR7G007524.1	MR8G020746.1	0.532929
MR6G018085.1	MR8G020258.1	0.460943	MR7G007524.1	MR8G001596.1	0.525999
MR6G018085.1	MR6G018097.1	0.456111	MR7G007524.1	MR8G002765.1	0.535122
MR7G010680.1	MR0G025657.1	0.461538	MR7G007524.1	MR8G016813.1	0.533655
MR7G010680.1	MR0G003728.1	0.448826	MR7G007524.1	MR8G019130.1	0.532336
MR7G010680.1	MR8G010083.1	0.442579	MR7G007524.1	MR8G019531.1	0.533347
MR7G010680.1	MR8G018183.1	0.441572	MR7G007524.1	MR8G006636.1	0.52306
MR7G010680.1	MR8G020258.1	0.459933	MR7G007524.1	MR8G020754.1	0.532877
MR7G010680.1	MR0G001496.1	0.479472	MR7G007524.1	MR7G007526.1	0.532863
MR7G010680.1	MR7G024256.1	0.455577	MR7G007524.1	MR8G012788.1	0.532665
MR7G015326.1	MR0G007601.1	0.446785	MR7G007524.1	MR8G002789.1	0.531893
MR7G015326.1	MR0G003728.1	0.456158	MR7G007524.1	MR8G003125.1	0.534156
MR7G015326.1	MR0G005933.1	0.443643	MR7G007524.1	MR8G003345.1	0.5328
MR7G015326.1	MR8G018183.1	0.451581	MR7G007524.1	MR8G004551.1	0.522253
MR7G015326.1	MR8G020258.1	0.45787	MR7G007524.1	MR8G007621.1	0.532814
MR7G015326.1	MR0G007114.1	0.447258	MR7G007524.1	MR7G024817.1	0.532404

MR7G024824.1	MR0G025657.1	0.448245
MR8G020751.1	MR0G001496.1	0.448847
MR8G021808.1	MR0G001496.1	0.449382
MR8G021808.1	MR8G022503.2	0.448402
MR8G021808.1	MR0G007601.1	0.460024
MR8G021808.1	MR0G003728.1	0.455608
MR8G021808.1	MR0G007114.1	0.448266
MR8G027384.1	MR0G001496.1	0.466679
MR8G027384.1	MR0G022769.1	0.440792
MR8G027384.1	MR0G025657.1	0.481543
MR8G027384.1	MR0G003728.1	0.446691
MR8G027384.1	MR0G005933.1	0.45634

MR7G007524.1	MR7TCONS_00020974.1	0.534238
MR7G007524.1	MR0G024306.1	0.532831
MR7G007524.1	MR8G012676.1	0.527399
MR7G007524.1	MR0G002914.1	0.531184
MR7G007524.1	MR7G011363.5	0.533178
MR7G007524.1	MR8G012690.1	0.534565
MR7G007524.1	MR0G007648.1	0.521997
MR7G007524.1	MR0G007649.1	0.521997
MR7G007524.1	MR0G005135.1	0.528117
MR7G007524.1	MR0G008817.1	0.534037
MR7G007524.1	MR0G013397.1	0.533432
MR7G007524.1	MR0G014428.1	0.520921
MR7G007524.1	MR8G028462.1	0.533497
MR7G007524.1	MR0G007880.1	0.533984
MR7G007524.1	MR0G005900.1	0.527209
MR7G007524.1	MR0G007264.1	0.538765
MR7G007524.1	MR7G016747.1	0.520138
MR7G007524.1	MR0G007917.1	0.528177
MR7G007524.1	MR0G005287.1	0.533071
MR7G007524.1	MR8G010076.1	0.537752
MR7G007524.1	MR8G011180.1	0.520369
MR7G007524.1	MR8G011203.1	0.525241
MR7G007524.1	MR7G016713.1	0.532324
MR7G007524.1	MR7G022720.1	0.534779
MR7G007524.1	MR7G014911.1	0.523144
MR7G007524.1	MR7G022721.1	0.523135
MR7G007524.1	MR7G014376.1	0.534451
MR7G023875.1	MR8G000678.2	0.524446
MR7G023875.1	MR8G019531.1	0.521985
MR7G023875.1	MR8G012690.1	0.523035
MR7G023875.1	MR8G002765.1	0.520098
MR7G023875.1	MR8G003125.1	0.523283
MR7G023875.1	MR8G022192.1	0.523307
MR7G023875.1	MR0G007264.1	0.524313
MR8G001578.1	MR8G003125.1	0.536478
MR8G001578.1	MR8G028462.1	0.534865
MR8G001578.1	MR8G012690.1	0.534664
MR8G001578.1	MR8G007621.1	0.537178
MR8G001578.1	MR0G002914.1	0.539009
MR8G001578.1	MR0G005135.1	0.53445
MR8G001578.1	MR8G012676.1	0.533492
MR8G001578.1	MR8G024955.1	0.52013
MR8G001578.1	MR0G007264.1	0.522738
MR8G001578.1	MR8G011180.1	0.521821
MR8G001578.1	MR0G007917.1	0.536206
MR8G001578.1	MR0G013397.1	0.536152
MR8G001578.1	MR8G020746.1	0.537023
MR8G001578.1	MR8G022192.1	0.522691
MR8G001578.1	MR8G012788.1	0.523719
MR8G001578.1	MR8G019130.1	0.538093

MR8G001578.1	MR8G019531.1	0.521154
MR8G010076.1	MR8G016813.1	0.526733
MR8G010076.1	MR8G019130.1	0.530289
MR8G010076.1	MR8G012690.1	0.53721
MR8G010076.1	MR8G012788.1	0.522893
MR8G010076.1	MR0G007264.1	0.541778
MR8G010076.1	MR0G007880.1	0.529744
MR8G010076.1	MR0G008817.1	0.537016
MR8G010076.1	MR0G013397.1	0.534407
MR8G010076.1	MR0G024306.1	0.52582
MR8G010076.1	MR8G019531.1	0.537166
MR8G010076.1	MR8G020746.1	0.533029
MR8G010076.1	MR8G020754.1	0.531865
MR8G010076.1	MR8G022192.1	0.541091
MR8G010076.1	MR8G028462.1	0.535022
MR8G010076.1	MR0G002914.1	0.530204
MR8G010076.1	MR0G005287.1	0.532358

Table S14. Annotation of genes in light-green module

Gene ID	Nr annotation
MR0TCONS_00017483.1	MR0TCONS_00017483.1//1Carya illinoinensis 1-aminocyclopropane-1-carboxylate oxidase homolog 4-like (LOC122314425), mRNA
MR5G011870.1	XP_018856839.1//PREDICTED: dof zinc finger protein DOF5.4-like [Juglans regia]
MR1TCONS_00020658.1	PREDICTED: Juglans regia transcription repressor MYB5-like (LOC108982488), mRNA
MR6G000783.1	XP_018811162.1//PREDICTED: serine/threonine-protein kinase SAPK7-like [Juglans regia];XP_022157841.1//serine/threonine-protein kinase SRK2H-like [Momordica charantia]
MR2G007010.1	XP_018810380.1//PREDICTED: ethylene-responsive transcription factor 4-like [Juglans regia]
MR5G024537.1	XP_018809309.1//PREDICTED: BTB/POZ and TAZ domain-containing protein 4-like isoform X2 [Juglans regia];XP_018809308.1//PREDICTED: BTB/POZ and TAZ domain-containing protein 4-like isoform X1 [Juglans regia];XP_018809310.1//PREDICTED: BTB/POZ and TAZ domain-containing protein 4-like isoform X3 [Juglans regia]
MR2G016358.1	XP_018826227.1//PREDICTED: ethylene-overproduction protein 1 [Juglans regia]
MR6G018085.1	XP_018834937.1//PREDICTED: nascent polypeptide-associated complex subunit beta-like [Juglans regia];XP_018834144.1//PREDICTED: LOW QUALITY PROTEIN: auxin response factor 8-like [Juglans regia]
MR0G001496.1	ABW06959.1//isopentenyl pyrophosphate isomerase [Corylus avellana];XP_016488563.1//PREDICTED: isopentenyl-diphosphate Delta-isomerase I [Nicotiana tabacum];XP_009608528.1//PREDICTED: isopentenyl-diphosphate Delta-isomerase I [Nicotiana tomentosiformis]
MR0G003728.1	XP_018835416.1//PREDICTED: uncharacterized protein LOC109002223 [Juglans regia];XP_017183988.1//PREDICTED: 30S ribosomal protein S18-like [Malus domestica]
MR7G024256.1	XP_018815083.1//PREDICTED: phosphatidylinositol 3-kinase, root isoform isoform X3 [Juglans regia]
MR7G010680.1	XP_018852422.1//PREDICTED: cytosolic sulfotransferase 5-like [Juglans regia];XP_021824417.1//cytosolic sulfotransferase 12-like [Prunus avium]
MR6G021435.1	XP_022009881.1//ras-related protein RHN1-like [Helianthus annuus];XP_002272169.1//PREDICTED: ras-related protein Rab5 [Vitis vinifera]
MR8G020258.1	XP_004495676.1//PREDICTED: syntaxin-41 isoform X1 [Cicer arietinum];XP_018848003.1//PREDICTED: syntaxin-41-like [Juglans regia]
MR7G015326.1	EOY23226.1//Alpha/beta-Hydrolases superfamily protein isoform 1 [Theobroma cacao];XP_018859358.1//PREDICTED: uncharacterized protein At3g49055 [Juglans regia]
MR6G018093.1	XP_018825951.1//PREDICTED: 40S ribosomal protein S21-2-like [Juglans regia]
MR8G010083.1	CBI28434.3//unnamed protein product, partial [Vitis vinifera];XP_022154866.1//transcription initiation factor TFIID subunit 15b [Momordica charantia]
MR8G021808.1	XP_018845751.1//PREDICTED: protein TIFY 8-like isoform X2 [Juglans regia]
MR8G027384.1	XP_018833641.1//PREDICTED: zinc finger protein CONSTANS-LIKE 4-like [Juglans regia]
MR0G025657.1	OMO84962.1//hypothetical protein CCACVL1_10519 [Corchorus capsularis];XP_018809182.1//PREDICTED: protein trichome birefringence-like 35 [Juglans regia]
MR6G018097.1	XP_018834942.1//PREDICTED: probable metal-nicotianamine transporter YSL7 [Juglans regia]
MR6G018074.1	XP_018834139.1//PREDICTED: ribosomal RNA-processing protein 7 homolog A [Juglans regia]
MR6G021647.1	XP_018834113.1//PREDICTED: protein CROWDED NUCLEI 1-like [Juglans regia]
MR6G019911.1	XP_018844883.1//PREDICTED: non-specific phospholipase C1-like [Juglans regia]
MR7G000150.1	XP_004136918.1//PREDICTED: DUF21 domain-containing protein At2g14520-like [Cucumis sativus]
MR8G018183.1	XP_016480921.1//PREDICTED: FACT complex subunit SPT16-like [Nicotiana tabacum];XP_018816427.1//PREDICTED: FACT complex subunit SPT16-like [Juglans regia]

MR5G009689.1	XP_018825404.1//PREDICTED: protein ASPARTIC PROTEASE IN GUARD CELL 1-like [Juglans regia]
MR5G012384.1	XP_018844074.1//PREDICTED: chaperone protein dnaJ 20, chloroplastic-like [Juglans regia]
MR6G016522.1	XP_018844750.1//PREDICTED: WD repeat-containing protein VIP3 [Juglans regia]
MR5G020321.1	XP_018844074.1//PREDICTED: chaperone protein dnaJ 20, chloroplastic-like [Juglans regia]
MR0G022769.1	XP_018818044.1//PREDICTED: pentatricopeptide repeat-containing protein At5g48730, chloroplastic [Juglans regia]
MR0G007601.1	XP_018809559.1//PREDICTED: ER membrane protein complex subunit 3-like [Juglans regia]
MR6G025626.1	CBI40053.3//unnamed protein product, partial [Vitis vinifera];XP_018849247.1//PREDICTED: ribulose-phosphate 3-epimerase, cytoplasmic isoform [Juglans regia]
MR5G009648.1	XP_018813119.1//PREDICTED: uncharacterized protein LOC108985314 [Juglans regia]
MR6G025594.1	XP_018814333.1//PREDICTED: probable carboxylesterase 11 [Juglans regia]
MR0G005933.1	XP_018857760.1//PREDICTED: phosphoglycerate mutase-like protein 4 [Juglans regia]
MR0G007114.1	XP_018832001.1//PREDICTED: Golgi apparatus membrane protein-like protein ECHIDNA isoform X1 [Juglans regia]
MR4G023099.1	XP_018849388.1//PREDICTED: dol-P-Man:Man(6)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase [Juglans regia]
MR4G021076.1	XP_018811726.1//PREDICTED: elongation factor Tu, chloroplastic [Juglans regia]
MR4G009026.1	XP_018835191.1//PREDICTED: uncharacterized protein LOC109002062 [Juglans regia];XP_006476326.1//PREDICTED: WD repeat-containing protein YMR102C-like [Citrus sinensis]
MR4G021188.1	XP_018847281.1//PREDICTED: growth-regulating factor 7-like [Juglans regia]
MR6G020073.2	KHN31394.1//Histone H3.3 [Glycine soja];KOM39698.1//hypothetical protein LR48_Vigan03g308000 [Vigna angularis]
MR8G018185.1	XP_018816525.1//PREDICTED: ATP-citrate synthase alpha chain protein 3 [Juglans regia]
MR8G019525.2	XP_018831555.1//PREDICTED: protease Do-like 9 [Juglans regia]
MR3G011063.1	XP_018846745.1//PREDICTED: bifunctional fucokinase/fucose pyrophosphorylase isoform X1 [Juglans regia];XP_018846747.1//PREDICTED: bifunctional fucokinase/fucose pyrophosphorylase isoform X3 [Juglans regia]
MR8G022503.2	XP_009418690.1//PREDICTED: probable protein phosphatase 2C 60 isoform X1 [Musa acuminata subsp. malaccensis];XP_021604217.1//probable protein phosphatase 2C 46 [Manihot esculenta]
MR6G008503.1	XP_018808737.1//PREDICTED: protein ULTRAPETALA 1-like [Juglans regia]
MR5G025035.1	XP_018806781.1//PREDICTED: ERAD-associated E3 ubiquitin-protein ligase component HRD3A [Juglans regia]
MR6G010888.2	XP_018827742.1//PREDICTED: protein starmaker isoform X1 [Juglans regia]
MR6G001563.1	XP_018851434.1//PREDICTED: transcription factor bHLH106-like isoform X3 [Juglans regia]
MR4G021077.5	XP_018850913.1//PREDICTED: choline transporter-like protein 2 [Juglans regia];XP_021288033.1//choline transporter protein 1 [Herrania umbratica]
MR4G007287.2	OMO79913.1//Ribosomal protein L11 [Corchorus capsularis]
MR0G008632.2	OVA12420.1//SecY/SEC61-alpha family [Macleaya cordata]
MR7G000813.2	XP_018857020.1//PREDICTED: peptidyl-prolyl cis-trans isomerase CYP23 [Juglans regia];XP_012478677.1//PREDICTED: peptidyl-prolyl cis-trans isomerase CYP23 isoform X2 [Gossypium raimondii]
MR5G011953.1	XP_018822108.1//PREDICTED: KH domain-containing protein HEN4-like [Juglans regia]

MR7G000148.1	XP_018847079.1//PREDICTED: LL-diaminopimelate aminotransferase, chloroplastic-like [Juglans regia]
MR3G001179.1	XP_018820114.1//PREDICTED: oxidation resistance protein 1-like [Juglans regia];XP_020411452.1//TLD domain-containing protein 2 isoform X2 [Prunus persica]
MR6G019866.1	XP_018830700.1//PREDICTED: probable transcriptional regulator SLK2 isoform X2 [Juglans regia]
MR6G016528.1	XP_018844863.1//PREDICTED: mitogen-activated protein kinase kinase 2 [Juglans regia]
MR8G012637.1	XP_002528798.1//PREDICTED: ATP synthase subunit delta', mitochondrial [Ricinus communis]
MR6G025929.3	CAN75406.1//hypothetical protein VITISV_010510, partial [Vitis vinifera];XP_018837505.1//PREDICTED: ras-related protein Rab7-like [Juglans regia]
MR5G025036.1	XP_018806781.1//PREDICTED: ERAD-associated E3 ubiquitin-protein ligase component HRD3A [Juglans regia]
MR5G015914.1	XP_002511419.1//PREDICTED: serine/threonine-protein kinase HT1 [Ricinus communis];XP_012481903.1//PREDICTED: serine/threonine-protein kinase HT1 [Gossypium raimondii];XP_017191584.1//PREDICTED: serine/threonine-protein kinase STY8-like [Malus domestica]
MR5G017115.1	XP_018811557.1//PREDICTED: probable bifunctional TENA-E protein [Juglans regia]
MR5G017134.1	XP_018809451.1//PREDICTED: acetate/butyrate--CoA ligase AAE7, peroxisomal [Juglans regia]
MR8G020616.1	XP_018812868.1//PREDICTED: uncharacterized protein LOC108985139 [Juglans regia]
MR8G012696.1	XP_018822229.1//PREDICTED: protein WVD2-like 6 isoform X2 [Juglans regia]
MR8G015530.1	XP_018829633.1//PREDICTED: proteasome subunit alpha type-7 [Juglans regia]
MR5G017299.1	XP_016507994.1//PREDICTED: probable serine/threonine-protein phosphatase 2A regulatory subunit B" subunit TON2 [Nicotiana tabacum];XP_021607790.1//probable serine/threonine-protein phosphatase 2A regulatory subunit B" subunit TON2 [Manihot esculenta];XP_021679543.1//probable serine/threonine-protein phosphatase 2A regulatory subunit B" subunit TON2 [Hevea brasiliensis]
MR7G007720.1	XP_018855654.1//PREDICTED: survival of motor neuron-related-splicing factor 30 isoform X1 [Juglans regia];XP_018855766.1//PREDICTED: survival of motor neuron-related-splicing factor 30 isoform X3 [Juglans regia]
MR5G017371.1	XP_018838973.1//PREDICTED: uncharacterized protein LOC109004757 [Juglans regia]
MR7G016767.2	AFY26894.1//RNA-binding protein with multiple splicing [Morella rubra]
MR7G000834.1	XP_010044743.1//PREDICTED: 60S ribosomal protein L34 [Eucalyptus grandis]
MR7G004995.1	XP_018857675.1//PREDICTED: PITH domain-containing protein At3g04780-like, partial [Juglans regia];XP_012089246.1//PITH domain-containing protein At3g04780 [Jatropha curcas];GAV90642.1//PITH domain-containing protein [Cephalotus follicularis]
MR8G010060.1	XP_018828531.1//PREDICTED: exocyst complex component EXO70B1-like [Juglans regia]
MR8G011210.1	XP_021659332.1//V-type proton ATPase 16 kDa proteolipid subunit [Hevea brasiliensis];KJB17312.1//hypothetical protein B456_003G010900 [Gossypium raimondii]
MR8G018182.3	XP_018816462.1//PREDICTED: protein transport protein Sec24-like At3g07100 [Juglans regia];XP_018857395.1//PREDICTED: protein transport protein Sec24-like At3g07100 [Juglans regia]
MR7G008145.3	XP_018851016.1//PREDICTED: protein TIC 40, chloroplastic-like [Juglans regia]
MR8G020751.1	XP_018851434.1//PREDICTED: transcription factor bHLH106-like isoform X3 [Juglans regia]
MR8G020766.1	XP_018812759.1//PREDICTED: uncharacterized protein LOC108985063 isoform X1 [Juglans regia];XP_018812757.1//PREDICTED: pentatricopeptide repeat-containing protein At5g18475 isoform X1 [Juglans regia]
MR5G020302.1	XP_018844084.1//PREDICTED: uncharacterized protein LOC109008446 isoform X2 [Juglans regia]

MR5G021736.1	XP_018849298.1//PREDICTED: E3 ubiquitin-protein ligase RING1-like [Juglans regia]
MR6G007202.1	XP_018846418.1//PREDICTED: acid phosphatase 1-like [Juglans regia]
MR0G005280.1	XP_018809258.1//PREDICTED: uncharacterized protein LOC108982363 [Juglans regia];XP_018848469.1//PREDICTED: fatty acid hydroperoxide lyase, chloroplastic [Juglans regia]
MR0G001497.1	XP_019176544.1//PREDICTED: putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 2 [Ipomoea nil]
MR7G012054.1	XP_018849558.1//PREDICTED: V-type proton ATPase subunit H-like [Juglans regia];XP_021816170.1//V-type proton ATPase subunit H [Prunus avium]
MR7G022891.1	XP_018823837.1//PREDICTED: eukaryotic translation initiation factor 4B3 [Juglans regia]
MR0G004687.1	XP_018820232.1//PREDICTED: very-long-chain 3-oxoacyl-CoA reductase 1 [Juglans regia]
MR0G027022.1	XP_018807444.1//PREDICTED: pectin acetylesterase 12-like isoform X1 [Juglans regia]
MR6G003925.1	XP_021602735.1//60S ribosomal protein L8 [Manihot esculenta]
MR6G006799.1	XP_018827274.1//PREDICTED: uncharacterized protein LOC108996014 [Juglans regia]
MR0G006220.1	XP_018831272.1//PREDICTED: uncharacterized protein LOC108998955 [Juglans regia]
MR0G006609.1	XP_018834277.1//PREDICTED: nuclear cap-binding protein subunit 2-like [Juglans regia]
MR3G014762.1	XP_021654626.1//ARF guanine-nucleotide exchange factor GNOM [Hevea brasiliensis];XP_012067704.1//ARF guanine-nucleotide exchange factor GNOM [Jatropha curcas]
MR7G028821.1	XP_011045964.1//PREDICTED: beta-galactosidase-like isoform X1 [Populus euphratica];XP_018820458.1//PREDICTED: beta-galactosidase-like isoform X1 [Juglans regia]
MR6G019729.1	XP_018840105.1//PREDICTED: leucine-rich repeat receptor-like protein kinase TDR isoform X1 [Juglans regia]
MR5G009737.1	XP_018821067.1//PREDICTED: probable U3 small nucleolar RNA-associated protein 11 isoform X1 [Juglans regia]
MR2G024219.1	XP_018819392.1//PREDICTED: ethanolamine-phosphate cytidylyltransferase [Juglans regia]
MR2G024440.1	XP_018857901.1//PREDICTED: alpha-galactosidase 1-like [Juglans regia];XP_018837465.1//PREDICTED: uncharacterized protein At5g48480-like [Juglans regia]
MR2G024131.1	XP_018814977.1//PREDICTED: methyltransferase-like protein 5 isoform X1 [Juglans regia]
MR0TCONS_00026066.1	XP_018834652.1//PREDICTED: putative disease resistance protein At3g14460 isoform X1 [Juglans regia];MR0TCONS_00026066.1//1
MR5G003464.1	XP_018815792.1//PREDICTED: MACPF domain-containing protein At4g24290-like [Juglans regia]
MR2G020373.1	AFK43072.1//unknown [Lotus japonicus]
MR2G022287.1	XP_018847693.1//PREDICTED: F-box protein SKIP19-like [Juglans regia]
MR0TCONS_00023638.1	XP_018835437.1//PREDICTED: putative disease resistance protein At3g14460 isoform X1 [Juglans regia];MR0TCONS_00023638.1//1
MR0TCONS_00029296.1	XP_018824162.1//PREDICTED: TMV resistance protein N-like isoform X2 [Juglans regia];MR0TCONS_00029296.1//1;XP_018826968.1//PREDICTED: TMV resistance protein N-like [Juglans regia]
MR2TCONS_00005123.1	MR2TCONS_00005123.1//1;XP_018839624.1//PREDICTED: probable calcium-binding protein CML49 [Juglans regia]
MR3G001245.1	XP_018820939.1//PREDICTED: 60S ribosomal protein L14-1 [Juglans regia]
MR5G003617.1	XP_018822624.1//PREDICTED: uncharacterized protein LOC108992488 [Juglans regia]
MR1G014018.1	XP_018817532.1//PREDICTED: ubiquitin carboxyl-terminal hydrolase 24 isoform X2 [Juglans regia];XP_018817528.1//PREDICTED: ubiquitin carboxyl-terminal hydrolase 24 isoform X1 [Juglans regia]
MR5G025810.1	XP_002264828.1//PREDICTED: proteasome subunit beta type-5 [Vitis vinifera]
MR3G002725.1	XP_021828543.1//putative F-box protein At3g16210 [Prunus avium]

MR3G006431.1	P83304.1//RecName: Full=Mannose/glucose-specific lectin
MR2G024060.1	XP_018828037.1//PREDICTED: chaperone protein dnaJ 11, chloroplastic-like [Juglans regia]
MR2G024087.2	XP_018850930.1//PREDICTED: peptidyl-tRNA hydrolase 2, mitochondrial-like [Juglans regia]
MR5G017201.1	XP_018825743.1//PREDICTED: multiple organellar RNA editing factor 3, mitochondrial-like [Juglans regia]
MR5G003222.1	XP_007051874.1//PREDICTED: phosphomannomutase [Theobroma cacao]
MR5G003457.1	XP_018831435.1//PREDICTED: uncharacterized protein LOC108999088 [Juglans regia]
MR1G003952.1	XP_018828488.1//PREDICTED: uncharacterized protein At5g39865-like isoform X2 [Juglans regia]
MR1G012147.1	XP_018850034.1//PREDICTED: 60S ribosomal protein L22-3-like [Juglans regia]
MR3G014724.1	XP_010108756.1//AP3-complex subunit beta-A [Morus notabilis];XP_018814465.1//PREDICTED: AP3-complex subunit beta-A [Juglans regia]
MR8G019278.2	XP_018837044.1//PREDICTED: probable cytosolic oligopeptidase A [Juglans regia];XP_018850785.1//PREDICTED: probable cytosolic oligopeptidase A [Juglans regia]
MR8G019517.1	XP_021294583.1//glycine--tRNA ligase, mitochondrial 1 [Herrania umbratica];XP_018829229.1//PREDICTED: glycine--tRNA ligase, mitochondrial 1-like [Juglans regia]
MR1G003946.1	XP_018828488.1//PREDICTED: uncharacterized protein At5g39865-like isoform X2 [Juglans regia]
MR1G008473.1	XP_018818443.1//PREDICTED: cytochrome P450 734A5-like isoform X1 [Juglans regia]
MR7G028038.2	XP_021593499.1//putative receptor-like protein kinase At4g00960 [Manihot esculenta];XP_018837849.1//PREDICTED: putative receptor-like protein kinase At4g00960 [Juglans regia];XP_015895441.1//PREDICTED: putative receptor-like protein kinase At4g00960 [Ziziphus jujuba]
MR1G019332.1	XP_018847023.1//PREDICTED: zinc finger CCCH domain-containing protein 19-like [Juglans regia];AAX33674.1//plus agglutinin, partial [Chlamydomonas incerta];XP_015892420.1//PREDICTED: zinc finger CCCH domain-containing protein 19 [Ziziphus jujuba]
MR4G026749.1	XP_021685894.1//DDRGK domain-containing protein 1-like [Hevea brasiliensis];XP_018824029.1//PREDICTED: DDRGK domain-containing protein 1 [Juglans regia]
MR4G027358.3	XP_018823765.1//PREDICTED: uncharacterized protein LOC108993338 [Juglans regia]
MR4TCONS_00016369.1	XP_018840086.1//PREDICTED: protein DEHYDRATION-INDUCED 19 homolog 6-like [Juglans regia];MR4TCONS_00016369.1//1
MR7G006051.1	XP_018815515.1//PREDICTED: spermidine synthase 1-like [Juglans regia]
MR0TCONS_00037684.1	XP_018825583.1//PREDICTED: condensin-2 complex subunit H2 isoform X1 [Juglans regia];MR0TCONS_00037684.1//1
MR1G003944.1	XP_018819183.1//PREDICTED: ubiquitin-activating enzyme E1 1-like [Juglans regia]
MR3G014650.1	XP_018831984.1//PREDICTED: actin-depolymerizing factor 2-like [Juglans regia];XP_018814417.1//PREDICTED: pentatricopeptide repeat-containing protein At2g39620 [Juglans regia]
MR1G014145.1	XP_018819535.1//PREDICTED: WD repeat-containing protein 20-like [Juglans regia]
MR1G015692.1	XP_018860033.1//PREDICTED: ankyrin repeat-containing protein ITN1-like isoform X1 [Juglans regia];XP_018812140.1//PREDICTED: uncharacterized protein LOC108984585 isoform X1 [Juglans regia];XP_018807238.1//PREDICTED: uncharacterized protein LOC108980690 isoform X1 [Juglans regia]
MR1G015702.1	XP_018851787.1//PREDICTED: uncharacterized protein LOC109013963 [Juglans regia];XP_018846052.1//PREDICTED: uncharacterized protein LOC109009862 [Juglans regia]
MR4TCONS_00017612.1	XP_021821504.1//5'-adenylylsulfate reductase 3, chloroplastic-like [Prunus avium];MR4TCONS_00017612.1//1;XP_018811788.1//PREDICTED: dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2, mitochondrial-like [Juglans regia]
MR1G020884.1	XP_006433549.1//hypothetical protein CICLE_v10003144mg [Citrus clementina]
MR1G022529.1	XP_018818952.1//PREDICTED: probable glucuronoxylan glucuronosyltransferase IRX7 [Juglans regia]

MR1G027855.1	ONI29973.1//hypothetical protein PRUPE_1G225000 [Prunus persica];XP_018808222.1//PREDICTED: ranBP2-type zinc finger protein At1g67325-like isoform X2 [Juglans regia]
MR5G021745.1	XP_018808387.1//PREDICTED: uncharacterized protein LOC108981612 [Juglans regia]
MR6G000259.1	XP_018856599.1//PREDICTED: derlin-1 [Juglans regia];XP_021668993.1//profilin-2 [Hevea brasiliensis]
MR1G020792.1	XP_018844177.1//PREDICTED: non-functional NADPH-dependent codeinone reductase 2-like isoform X1 [Juglans regia]
MR8G001629.2	XP_018808099.1//PREDICTED: uncharacterized protein LOC108981407 [Juglans regia]
MR2G006757.1	XP_018825879.1//PREDICTED: selT-like protein [Juglans regia]
MR2G014105.1	XP_018830864.1//PREDICTED: uncharacterized protein LOC108998669 [Juglans regia]
MR2G020031.1	KRG95050.1//hypothetical protein GLYMA_19G126700 [Glycine max];XP_018857670.1//PREDICTED: psbP domain-containing protein 6, chloroplastic [Juglans regia]
MR1TCONS_00041911.1	MR1TCONS_00041911.1//1;XP_009371499.1//PREDICTED: nudC domain-containing protein 2-like [Pyrus x bretschneideri]
MR4G028396.1	XP_021814380.1//long chain base biosynthesis protein 2a [Prunus avium];XP_018832123.1//PREDICTED: long chain base biosynthesis protein 2a [Juglans regia]
MR5G000697.1	XP_018846416.1//PREDICTED: uncharacterized protein LOC109010150 [Juglans regia];XP_018846407.1//PREDICTED: uncharacterized protein LOC109010143 [Juglans regia]
MR5G001859.1	XP_008460096.1//PREDICTED: 50S ribosomal protein L3, chloroplastic [Cucumis melo]
MR7G010648.1	XP_018849622.1//PREDICTED: uncharacterized protein LOC109012442 [Juglans regia];XP_018849623.1//PREDICTED: histone acetyltransferase of the MYST family 1-like isoform X1 [Juglans regia];XP_018849624.1//PREDICTED: histone acetyltransferase of the MYST family 2-like isoform X2 [Juglans regia]
MR1G029232.1	XP_018828598.1//PREDICTED: probable phytol kinase 3, chloroplastic [Juglans regia];XP_007205802.2//probable phytol kinase 3, chloroplastic [Prunus persica]
MR1TCONS_00065258.1	MR1TCONS_00065258.1//1;XP_018812980.1//PREDICTED: copper transporter 1-like [Juglans regia]
MR1G017405.1	XP_018839745.1//PREDICTED: RNA-binding protein 8A-like [Juglans regia]
MR3G015834.1	XP_021285398.1//protein LIKE COV 1-like [Herrania umbratica];XP_018826705.1//PREDICTED: glucan endo-1,3-beta-D-glucosidase-like [Juglans regia];OIW03484.1//hypothetical protein TanjilG_14709 [Lupinus angustifolius]
MR4G021335.1	XP_018825050.1//PREDICTED: 2-oxoglutarate-Fe(II) type oxidoreductase-like isoform X2 [Juglans regia];XP_018819252.1//PREDICTED: E3 ubiquitin-protein ligase HOS1-like isoform X2 [Juglans regia];XP_018819251.1//PREDICTED: E3 ubiquitin-protein ligase HOS1-like isoform X1 [Juglans regia]
MR2G011234.3	XP_018849879.1//PREDICTED: GDSL esterase/lipase At5g45920-like [Juglans regia]
MR4G024734.1	XP_018824266.1//PREDICTED: uncharacterized protein LOC108993715 [Juglans regia]
MR4G025266.1	XP_018852532.1//PREDICTED: BTB/POZ domain-containing protein At1g63850-like [Juglans regia]
MR4G025779.1	XP_018842158.1//PREDICTED: probable splicing factor 3A subunit 1 isoform X1 [Juglans regia]
MR4G023328.1	XP_018858684.1//PREDICTED: uncharacterized protein LOC109020632 [Juglans regia]
MR1TCONS_00025928.1	MR1TCONS_00025928.1//1;KCW50716.1//hypothetical protein EUGRSUZ_J00392, partial [Eucalyptus grandis]
MR2G006156.1	XP_003630811.1//trafficking protein particle complex subunit-like protein [Medicago truncatula];XP_012486075.1//PREDICTED: trafficking protein particle complex subunit 4 isoform X1 [Gossypium raimondii]
MR3G026361.1	XP_018811100.1//PREDICTED: GDSL esterase/lipase APG-like [Juglans regia]
MR3G026562.1	XP_018823521.1//PREDICTED: uncharacterized protein At1g04910-like isoform X1 [Juglans regia];XP_020088947.1//uncharacterized protein At1g04910 isoform X2 [Ananas comosus];XP_018823520.1//PREDICTED: pentatricopeptide repeat-containing protein At1g52640, mitochondrial [Juglans regia]
MR1G028362.1	XP_018825704.1//PREDICTED: uncharacterized protein LOC108994797 [Juglans regia]

MR1G029339.2	XP_018847278.1//PREDICTED: anaphase-promoting complex subunit 13 [Juglans regia];XP_020422273.1//ABC transporter G family member 11 [Prunus persica]
MR0G003971.1	KDO45995.1//hypothetical protein CISIN_1g002232mg [Citrus sinensis];XP_018834046.1//PREDICTED: uncharacterized protein LOC109001286 [Juglans regia]
MR3G015801.1	XP_018821636.1//PREDICTED: arabinosyltransferase RRA3-like [Juglans regia]
MR4G022364.1	XP_018846398.1//PREDICTED: protein SEH1 [Juglans regia]
MR4G023063.1	XP_018824245.1//PREDICTED: acyl-coenzyme A oxidase 3, peroxisomal-like [Juglans regia]
MR4G007135.1	XP_018850746.1//PREDICTED: uncharacterized protein LOC109013191 isoform X2 [Juglans regia]
MR4G021049.1	XP_018833326.1//PREDICTED: protein-L-isoaspartate O-methyltransferase 1-like [Juglans regia]
MR2G001814.1	XP_018817193.1//PREDICTED: ganglioside-induced differentiation-associated protein 2 [Juglans regia]
MR4G018534.1	XP_018825601.1//PREDICTED: phosphatidylinositol/phosphatidylcholine transfer protein SFH9-like isoform X1 [Juglans regia];GAV59666.1//CRAL_TRIO domain-containing protein/CRAL_TRIO_N domain-containing protein [Cephalotus follicularis]
MR3TCONS_00012160.1	MR3TCONS_00012160.1//1;XP_010273654.1//PREDICTED: mannose/glucose-specific lectin-like [Nelumbo nucifera]
MR4G021219.4	XP_018847688.1//PREDICTED: SNARE-interacting protein KEULE isoform X2 [Juglans regia];XP_018847679.1//PREDICTED: SNARE-interacting protein KEULE isoform X1 [Juglans regia]
MR3G026615.1	XP_018839930.1//PREDICTED: pyrophosphate-energized vacuolar membrane proton pump [Juglans regia]
MR4G001427.1	XP_018812266.1//PREDICTED: transcription initiation factor TFIID subunit 6-like [Juglans regia]
MR4G002293.2	XP_018815569.1//PREDICTED: putative E3 ubiquitin-protein ligase UBR7 [Juglans regia]
MR4G012554.1	XP_018828872.1//PREDICTED: protein P21-like [Juglans regia]
MR4G016029.1	XP_006370463.1//hypothetical protein POPTR_0001s42940g [Populus trichocarpa];XP_018827406.1//PREDICTED: uncharacterized protein LOC108996090 [Juglans regia]
MR7G016748.1	XP_018824697.1//PREDICTED: protein phosphatase 2C 57 [Juglans regia]
MR7G024824.1	XP_018844398.1//PREDICTED: two-component response regulator ARR5-like [Juglans regia]

Table S15. Annotation of genes in dark-cyan module.

Gene ID	Nr annotation
MR1G019545.1	XP_018806529.1//PREDICTED: ethylene receptor [Juglans regia]
MR7G007524.1	XP_018824793.1//PREDICTED: ethylene-responsive transcription factor 1-like [Juglans regia]
MR3G008361.1	XP_018814221.1//PREDICTED: 1-aminocyclopropane-1-carboxylate oxidase homolog 1-like [Juglans regia];XP_015887927.1//PREDICTED: 1-aminocyclopropane-1-carboxylate oxidase homolog 1-like [Ziziphus jujuba]
MR8G001578.1	XP_018843080.1//PREDICTED: squamosa promoter-binding-like protein 14 [Juglans regia]
MR7G011514.1	XP_018807978.1//PREDICTED: B3 domain-containing transcription factor VRN1-like isoform X1 [Juglans regia];XP_018807979.1//PREDICTED: B3 domain-containing transcription factor VRN1-like isoform X2 [Juglans regia]
MR8G010076.1	XP_018828595.1//PREDICTED: UDP-glycosyltransferase 87A1-like [Juglans regia]
MR6G011287.1	XP_018827349.1//PREDICTED: auxin-induced protein 22D-like isoform X2 [Juglans regia];XP_018827348.1//PREDICTED: auxin-induced protein 22D-like isoform X1 [Juglans regia]
MR8G002775.1	XP_007017801.1//PREDICTED: gibberellin-regulated protein 1 [Theobroma cacao]
MR7G000279.1	XP_018817886.1//PREDICTED: shaggy-related protein kinase kappa-like [Juglans regia]
MR4G023618.1	XP_017973938.1//PREDICTED: zinc finger CCCH domain-containing protein 12 [Theobroma cacao]
MR7G000837.1	XP_018832014.1//PREDICTED: zinc-finger homeodomain protein 11-like [Juglans regia]
MR7G023875.1	XP_018832014.1//PREDICTED: zinc-finger homeodomain protein 11-like [Juglans regia]
MR2G024066.1	XP_018805348.1//PREDICTED: protein PHR1-LIKE 2-like isoform X1 [Juglans regia]
MR3G015757.1	XP_018857297.1//PREDICTED: cytochrome P450 CYP82D47-like [Juglans regia]
MR6G011265.1	XP_015891497.1//PREDICTED: light-inducible protein CPRF2 isoform X1 [Ziziphus jujuba]
MR6G021640.1	XP_018815487.1//PREDICTED: allene oxide cyclase, chloroplastic-like [Juglans regia]
MR3G015734.1	XP_018846613.1//PREDICTED: cytochrome P450 CYP82D47-like [Juglans regia]
MR2G018522.5	XP_018859835.1//PREDICTED: uncharacterized protein LOC109021631 isoform X1 [Juglans regia];XP_018818511.1//PREDICTED: beta-glucosidase 40-like [Juglans regia]
MR8G020754.1	XP_018851428.1//PREDICTED: AT-hook motif nuclear-localized protein 17-like [Juglans regia]
MR8G019531.1	XP_018831523.1//PREDICTED: uncharacterized protein LOC108999173 [Juglans regia]
MR8G022192.1	XP_018845274.1//PREDICTED: probable nucleolar protein 5-2 [Juglans regia]
MR0G008817.1	XP_018846820.1//PREDICTED: GDSL esterase/lipase EXL3-like [Juglans regia];XP_018847896.1//PREDICTED: GDSL esterase/lipase EXL3-like [Juglans regia]
MR0G005287.1	XP_002273297.1//PREDICTED: uncharacterized protein LOC100246609 [Vitis vinifera];XP_018810077.1//PREDICTED: ubiquitin fusion degradation protein 1 [Juglans regia]
MR0G007264.1	XP_018834537.1//PREDICTED: LOW QUALITY PROTEIN: uncharacterized protein LOC109001639 [Juglans regia];XP_018860339.1//PREDICTED: monoacylglycerol lipase abhd6-A-like [Juglans regia]
MR8G012690.1	XP_018822243.1//PREDICTED: RNA-dependent RNA polymerase 6 [Juglans regia]
MR8G002765.1	XP_018857921.1//PREDICTED: tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit trm6 isoform X2 [Juglans regia]
MR8G028462.1	XP_018814811.1//PREDICTED: ras-related protein RABA3 [Juglans regia]

MR8G000678.2	EOY15140.1//Major facilitator superfamily protein isoform 1 [Theobroma cacao];XP_018807630.1//PREDICTED: phospholipase D delta-like [Juglans regia]
MR8G012676.1	XP_018822222.1//PREDICTED: DEAD-box ATP-dependent RNA helicase 56 [Juglans regia]
MR8G020746.1	XP_018851444.1//PREDICTED: probable ubiquitin-like-specific protease 2B [Juglans regia]
MR8G003125.1	XP_018814681.1//PREDICTED: uncharacterized protein LOC108986499 [Juglans regia];XP_013467208.1//50S ribosomal L24-like protein [Medicago truncatula]
MR8G001577.1	XP_018832979.1//PREDICTED: calponin homology domain-containing protein DDB_G0272472-like [Juglans regia]
MR8G019130.1	XP_018815217.1//PREDICTED: mediator of RNA polymerase II transcription subunit 28-like [Juglans regia]
MR8G002789.1	GAV88627.1//Tubulin domain-containing protein/Tubulin_C domain-containing protein [Cephalotus follicularis];KHG21743.1//Tubulin beta-6 chain [Gossypium arboreum]
MR0G013397.1	XP_018837122.1//PREDICTED: putative wall-associated receptor kinase-like 16 isoform X2 [Juglans regia];XP_018837121.1//PREDICTED: putative wall-associated receptor kinase-like 16 isoform X1 [Juglans regia]
MR0G007917.1	XP_018816202.1//PREDICTED: heterogeneous nuclear ribonucleoprotein H3 [Juglans regia]
MR0G005135.1	XP_018811673.1//PREDICTED: polypyrimidine tract-binding protein homolog 3 [Juglans regia]
MR0G002914.1	XP_018827844.1//PREDICTED: UPF0481 protein At3g47200-like [Juglans regia]
MR7G014376.1	XP_018815945.1//PREDICTED: cyclic nucleotide-gated ion channel 1-like [Juglans regia];XP_018817070.1//PREDICTED: cyclic nucleotide-gated ion channel 1-like [Juglans regia]
MR8G016813.1	XP_018852473.1//PREDICTED: AT-hook motif nuclear-localized protein 5-like [Juglans regia]
MR8G003345.1	XP_007017641.1//PREDICTED: probable ubiquitin-conjugating enzyme E2 18 [Theobroma cacao];XP_021636594.1//probable ubiquitin-conjugating enzyme E2 18 isoform X2 [Hevea brasiliensis]
MR8G012788.1	XP_018848154.1//PREDICTED: thioredoxin Y1, chloroplastic-like [Juglans regia]
MR7G022720.1	XP_018827476.1//PREDICTED: uncharacterized protein LOC108996170 isoform X1 [Juglans regia];XP_018827760.1//PREDICTED: uncharacterized protein LOC108996356 isoform X3 [Juglans regia];XP_018827477.1//PREDICTED: uncharacterized protein LOC108996170 isoform X2 [Juglans regia]
MR8G007621.1	XP_018835920.1//PREDICTED: cysteine desulfurase, mitochondrial [Juglans regia]
MR7G024817.1	XP_018823789.1//PREDICTED: uncharacterized protein LOC108993357 [Juglans regia];XP_018841531.1//PREDICTED: metal-independent phosphoserine phosphatase-like [Juglans regia];XP_018809737.1//PREDICTED: uncharacterized protein LOC108982736 [Juglans regia]
MR8G011180.1	XP_018809682.1//PREDICTED: 3-ketoacyl-CoA thiolase 2, peroxisomal-like [Juglans regia];XP_018817260.1//PREDICTED: 3-ketoacyl-CoA thiolase 2, peroxisomal [Juglans regia]
MR8TCONS_00054106.1	XP_018845568.1//PREDICTED: rhomboid-like protein 11, chloroplastic isoform X1 [Juglans regia];MR8TCONS_00054106.1//1;XP_006450616.1//hypothetical protein CICLE_v10008742mg [Citrus clementina]
MR7G011363.5	XP_018835517.1//PREDICTED: importin-4 [Juglans regia]
MR7G011362.2	XP_018842055.1//PREDICTED: uncharacterized protein LOC109007028 [Juglans regia]
MR8G011209.1	XP_018821156.1//PREDICTED: probable 1-acylglycerol-3-phosphate O-acyltransferase [Juglans regia]
MR7G007526.1	XP_018824789.1//PREDICTED: 60S ribosomal protein L19-3 isoform X1 [Juglans regia]
MR7G016747.1	XP_018824595.1//PREDICTED: protein PLASTID TRANSCRIPTIONALLY ACTIVE 7 isoform X2 [Juglans regia];XP_018824594.1//PREDICTED: protein PLASTID TRANSCRIPTIONALLY ACTIVE 7 isoform X1 [Juglans regia]
MR7G016713.1	XP_018835879.1//PREDICTED: probable pectinesterase/pectinesterase inhibitor 61 [Juglans regia]
MR8G012742.1	XP_018822278.1//PREDICTED: uncharacterized protein LOC108992239 [Juglans regia]

MR0G014428.1	XP_018810780.1//PREDICTED: rust resistance kinase Lr10-like [Juglans regia];XP_018848214.1//PREDICTED: rust resistance kinase Lr10-like [Juglans regia]
MR0G007424.1	XP_018807955.1//PREDICTED: uncharacterized protein LOC108981294 isoform X2 [Juglans regia]
MR0G027783.1	CAN66161.1//hypothetical protein VITISV_008123 [Vitis vinifera];XP_010277194.1//PREDICTED: V-type proton ATPase catalytic subunit A [Nelumbo nucifera]
MR8G011203.1	XP_018809066.1//PREDICTED: protein LTV1 homolog isoform X1 [Juglans regia]
MR0G024306.1	XP_018826762.1//PREDICTED: LOW QUALITY PROTEIN: CBL-interacting serine/threonine-protein kinase 24-like [Juglans regia]
MR6G022644.1	XP_018821485.1//PREDICTED: CLAVATA3/ESR (CLE)-related protein 41-like [Juglans regia]
MR6G025256.1	XP_018848480.1//PREDICTED: endoglucanase 11-like isoform X1 [Juglans regia]
MR0G005900.1	XP_018856092.1//PREDICTED: cyclic nucleotide-gated ion channel 1-like, partial [Juglans regia]
MR6G023576.1	XP_014622642.1//PREDICTED: isocitrate dehydrogenase [NADP] [Glycine max];XP_011014473.1//PREDICTED: isocitrate dehydrogenase [NADP] isoform X2 [Populus euphratica];EOY02462.1//Isocitrate/isopropylmalate dehydrogenase family protein isoform 4 [Theobroma cacao];XP_018830447.1//PREDICTED: isocitrate dehydrogenase [NADP]-like [Juglans regia];XP_011014465.1//PREDICTED: isocitrate dehydrogenase [NADP] isoform X1 [Populus euphratica]
MR0G007649.1	XP_018852998.1//PREDICTED: 60S acidic ribosomal protein P3-like [Juglans regia]
MR0G007648.1	XP_018852998.1//PREDICTED: 60S acidic ribosomal protein P3-like [Juglans regia]
MR0G006455.1	XP_018809141.1//PREDICTED: protein disulfide-isomerase SCO2-like isoform X1 [Juglans regia];OMO63235.1//hypothetical protein COLO4_32660 [Corchorus olitorius];XP_018809147.1//PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At1g67720 isoform X1 [Juglans regia]
MR8G000662.1	XP_018851775.1//PREDICTED: ribonuclease P protein subunit p25-like protein [Juglans regia]
MR8G001590.1	XP_018843096.1//PREDICTED: uncharacterized protein LOC109007741 [Juglans regia];XP_018832963.1//PREDICTED: uncharacterized protein LOC109000515 [Juglans regia]
MR8G001596.1	ACJ38667.1//cellulose synthase [Betula luminifera];XP_018832959.1//PREDICTED: probable cellulose synthase A catalytic subunit 3 [UDP-forming] [Juglans regia]
MR0G025665.1	XP_011019066.1//PREDICTED: uncharacterized protein LOC105121905 isoform X1 [Populus euphratica]
MR8G004551.1	XP_018844209.1//PREDICTED: uncharacterized protein LOC109008540 [Juglans regia]
MR6G013325.1	XP_018845402.1//PREDICTED: acyl-coenzyme A oxidase 2, peroxisomal [Juglans regia]
MR7G014911.1	XP_006486653.1//PREDICTED: coiled-coil domain-containing protein 124 [Citrus sinensis]
MR8G008686.2	XP_018841763.1//PREDICTED: GDSL esterase/lipase At1g54790 isoform X3 [Juglans regia];XP_018841762.1//PREDICTED: GDSL esterase/lipase At1g54790 isoform X2 [Juglans regia];OIV95120.1//hypothetical protein TanjilG_21510 [Lupinus angustifolius]
MR7G002562.1	XP_018834258.1//PREDICTED: uncharacterized protein LOC109001432 [Juglans regia]
MR0G013904.1	XP_012854681.1//PREDICTED: tubulin alpha-3 chain-like [Erythranthe guttata];XP_002532068.1//PREDICTED: tubulin alpha-3 chain [Ricinus communis]
MR8G022070.1	XP_018854753.1//PREDICTED: phytochrome A-associated F-box protein-like [Juglans regia]
MR8G006636.1	XP_018843143.1//PREDICTED: uncharacterized protein LOC109007768 [Juglans regia]
MR8G027828.1	XP_018843670.1//PREDICTED: probable E3 ubiquitin-protein ligase RHC1A [Juglans regia]
MR0G013882.1	XP_018846455.1//PREDICTED: uncharacterized protein LOC109010170 isoform X2 [Juglans regia]
MR7G014360.1	XP_018810725.1//PREDICTED: CWF19-like protein 2 isoform X1 [Juglans regia]
MR8G000663.1	XP_018808145.1//PREDICTED: uncharacterized protein LOC108981433 isoform X2 [Juglans regia]
MR7G011549.1	XP_018858124.1//PREDICTED: probable 1-acyl-sn-glycerol-3-phosphate acyltransferase 5 isoform X1 [Juglans regia]

MR7G012077.1	EMT29211.1//Tocopherol O-methyltransferase, chloroplastic [Aegilops tauschii];XP_018837640.1//PREDICTED: probable tocopherol O-methyltransferase, chloroplastic isoform X4 [Juglans regia]
MR7G022721.1	XP_018851259.1//PREDICTED: DNA-directed RNA polymerases II, IV and V subunit 3-like [Juglans regia]
MR7G024245.1	XP_018805220.1//PREDICTED: signal recognition particle receptor subunit beta-like [Juglans regia]
MR6G029291.1	XP_018852174.1//PREDICTED: probable methyltransferase PMT21 [Juglans regia]
MR0G005136.1	XP_018848151.1//PREDICTED: uncharacterized protein LOC109011402 isoform X8 [Juglans regia];XP_018811676.1//PREDICTED: cold and drought-regulated protein CORA-like [Juglans regia]
MR4G026972.1	XP_018856812.1//PREDICTED: E3 ubiquitin-protein ligase RNF14 [Juglans regia]
MR7G028535.1	XP_012066736.1//40S ribosomal protein S16 [Jatropha curcas]
MR7G012055.1	XP_018849553.1//PREDICTED: uncharacterized protein LOC109012398 [Juglans regia]
MR5TCONS_00034061.1	XP_018817376.1//PREDICTED: uncharacterized protein LOC108988545 isoform X1 [Juglans regia];MR5TCONS_00034061.1//1;XP_018860419.1//PREDICTED: uncharacterized protein LOC109022075 isoform X3 [Juglans regia]
MR7G014900.1	OVA16003.1//Organic solute transporter Ost-alpha [Macleaya cordata]
MR5G010171.1	XP_018833680.1//PREDICTED: uncharacterized protein LOC109001019 [Juglans regia];XP_018815898.1//PREDICTED: uncharacterized protein LOC108987432 [Juglans regia]
MR0G007880.1	XP_018846040.1//PREDICTED: protein translocase subunit SECA2, chloroplastic isoform X2 [Juglans regia]
MR8G011218.1	KQL09126.1//hypothetical protein SETIT_007379mg [Setaria italica];KOM49126.1//hypothetical protein LR48_Vigan07g283000 [Vigna angularis];KQL30138.1//hypothetical protein SETIT_018284mg [Setaria italica]
MR4G006774.1	XP_018837952.1//PREDICTED: cyclin-dependent kinase F-4-like [Juglans regia];XP_018852179.1//PREDICTED: cyclin-dependent kinase F-4-like isoform X1 [Juglans regia]
MR4G009043.1	XP_018859956.1//PREDICTED: UPF0160 protein C27H6.8-like [Juglans regia]
MR7TCONS_00020974.1	XP_018817103.1//PREDICTED: long chain acyl-CoA synthetase 9, chloroplastic [Juglans regia];MR7TCONS_00020974.1//1
MR4G014243.1	XP_018831294.1//PREDICTED: ALA-interacting subunit 3 [Juglans regia];XP_021691142.1//ALA-interacting subunit 3-like [Hevea brasiliensis]
MR4G015995.1	XP_018819594.1//PREDICTED: uncharacterized protein LOC108990167 [Juglans regia]
MR4G009044.1	XP_018859956.1//PREDICTED: UPF0160 protein C27H6.8-like [Juglans regia]
MR4G021010.1	XP_018814785.1//PREDICTED: protein PLASTID TRANSCRIPTIONALLY ACTIVE 10 [Juglans regia]
MR4G016473.3	XP_018860751.1//PREDICTED: uncharacterized protein LOC109022330 isoform X2 [Juglans regia]
MR5G024989.2	XP_018820305.1//PREDICTED: uracil-DNA glycosylase, mitochondrial isoform X2 [Juglans regia]
MR5G024525.1	XP_018860442.1//PREDICTED: adenylyl-sulfate kinase 3-like isoform X1 [Juglans regia]
MR5G017247.1	XP_018810246.1//PREDICTED: kinesin-like protein KIN-13A [Juglans regia]
MR5G018745.1	XP_018858205.1//PREDICTED: lysine-rich arabinogalactan protein 18-like [Juglans regia]
MR4G021196.1	XP_018847370.1//PREDICTED: uncharacterized protein LOC109010875 [Juglans regia]
MR8G002087.1	XP_018835291.1//PREDICTED: protein IWS1 homolog 2-like [Juglans regia]

MR8G028457.1	XP_018847437.1//PREDICTED: BTB/POZ and MATH domain-containing protein 2-like [Juglans regia];XP_010652109.1//PREDICTED: BTB/POZ and MATH domain-containing protein 2 [Vitis vinifera]
MR6G005848.1	EOX93041.1//DEAD-box ATP-dependent RNA helicase 53 isoform 3 [Theobroma cacao];XP_018843891.1//PREDICTED: DEAD-box ATP-dependent RNA helicase 53-like [Juglans regia]
MR4G008724.1	XP_018827500.1//PREDICTED: acetolactate synthase 2, chloroplastic [Juglans regia]
MR8G016250.3	XP_018832755.1//PREDICTED: putative GPI-anchor transamidase [Juglans regia]
MR7G007479.1	XP_018817813.1//PREDICTED: uncharacterized protein LOC108988884 [Juglans regia]
MR6G010863.1	XP_018844721.1//PREDICTED: probable gamma-secretase subunit PEN-2 [Juglans regia]
MR4G021019.1	XP_007209234.1//26S proteasome non-ATPase regulatory subunit 6 homolog [Prunus persica]
MR3G021766.1	XP_008225280.1//PREDICTED: protein YLS3-like [Prunus mume];XP_012476463.1//PREDICTED: BAG family molecular chaperone regulator 4-like isoform X2 [Gossypium raimondii];XP_015874580.1//PREDICTED: BAG family molecular chaperone regulator 4-like [Ziziphus jujuba]
MR0G024320.1	XP_018822164.1//PREDICTED: protein NETWORKED 3A-like isoform X3 [Juglans regia];XP_018822162.1//PREDICTED: protein NETWORKED 3C-like isoform X1 [Juglans regia]
MR6G007208.1	CBI27972.3//unnamed protein product, partial [Vitis vinifera]
MR4G028681.1	XP_018806918.1//PREDICTED: MND1-interacting protein 1-like [Juglans regia];XP_018824663.1//PREDICTED: MND1-interacting protein 1 [Juglans regia]
MR4G023611.1	XP_018805178.1//PREDICTED: RNA-binding protein 34 [Juglans regia]
MR8G023194.1	XP_018856502.1//PREDICTED: peptidyl-prolyl cis-trans isomerase CYP63 isoform X1 [Juglans regia];AJA29688.1//peptidyl-prolyl cis-trans isomerase [Betula luminifera]
MR5G003500.1	XP_018815791.1//PREDICTED: probably inactive leucine-rich repeat receptor-like protein kinase At3g28040 [Juglans regia]
MR7G000283.1	XP_007041211.1//PREDICTED: uncharacterized protein LOC18607136 [Theobroma cacao]
MR0G013881.1	XP_018850833.1//PREDICTED: aspartic proteinase-like protein 1 isoform X1 [Juglans regia]
MR7G017822.1	XP_002284010.1//PREDICTED: uncharacterized protein LOC100262828 [Vitis vinifera]
MR8G000679.2	XP_018807630.1//PREDICTED: phospholipase D delta-like [Juglans regia];GAV56681.1//C2 domain-containing protein/PLDc domain-containing protein/PLD_C domain-containing protein/PLDc_2 domain-containing protein [Cephalotus follicularis]
MR8G003357.1	XP_018843843.1//PREDICTED: protein WALLS ARE THIN 1-like [Juglans regia];XP_018821147.1//PREDICTED: protein WALLS ARE THIN 1-like [Juglans regia]
MR8G012787.1	XP_018851917.1//PREDICTED: uncharacterized protein LOC109014067 isoform X1 [Juglans regia]
MR8G024955.1	XP_018840959.1//PREDICTED: lipid phosphate phosphatase gamma, chloroplastic [Juglans regia]
MR8G000677.1	XP_015887788.1//PREDICTED: 24-methylenesterol C-methyltransferase 2 [Ziziphus jujuba]
MR4G024559.1	XP_018848220.1//PREDICTED: protein PAT1 homolog 1 isoform X1 [Juglans regia]
MR7G011595.1	XP_018847836.1//PREDICTED: probable receptor-like serine/threonine-protein kinase At4g34500 [Juglans regia]
MR4G026702.1	XP_002304382.1//ankyrin repeat family protein [Populus trichocarpa];XP_018808658.1//PREDICTED: protein phosphatase 1 regulatory subunit 12C-like [Juglans regia]
MR4G026757.1	XP_018828995.1//PREDICTED: ER membrane protein complex subunit 10 [Juglans regia]
MR6G009339.2	XP_018821342.1//PREDICTED: somatic embryogenesis receptor kinase 2 [Juglans regia];XP_015886099.1//PREDICTED: somatic embryogenesis receptor kinase 2 [Ziziphus jujuba]
MR4G016026.1	XP_018827313.1//PREDICTED: renalase isoform X2 [Juglans regia]
MR4G016027.1	XP_018827386.1//PREDICTED: putative serine/threonine-protein kinase isoform X5 [Juglans regia];XP_021663709.1//disease resistance protein At4g27190-like [Hevea brasiliensis]
MR7G002569.1	XP_012082985.1//AP-4 complex subunit epsilon [Jatropha curcas];XP_018834253.1//PREDICTED: AP-4 complex subunit epsilon-like [Juglans regia]

MR8G015375.1	XP_012446789.1//PREDICTED: BTB/POZ domain-containing protein At2g24240 [Gossypium raimondii];XP_010265605.1//PREDICTED: BTB/POZ domain-containing protein At2g24240-like [Nelumbo nucifera];KVI11713.1//BTB/POZ fold [Cynara cardunculus var. scolymus]
MR6G004352.1	XP_018829296.1//PREDICTED: glutamate--tRNA ligase, chloroplastic/mitochondrial [Juglans regia]
MR6G010787.1	XP_018827798.1//PREDICTED: uncharacterized protein LOC108996383 [Juglans regia]
MR6G013343.1	XP_002310569.2//hypothetical protein POPTR_0007s05580g [Populus trichocarpa];XP_018850797.1//PREDICTED: uncharacterized protein LOC109013234 isoform X1 [Juglans regia]
MR6G015490.1	XP_018848760.1//PREDICTED: long chain acyl-CoA synthetase 8 [Juglans regia]
MR3G023792.1	ONH90192.1//hypothetical protein PRUPE_8G039700 [Prunus persica]
MR8G006644.2	XP_018843120.1//PREDICTED: uncharacterized protein C9orf78 [Juglans regia]
MR4G021008.1	XP_018859977.1//PREDICTED: transcription factor GTE10-like isoform X2 [Juglans regia];XP_018859976.1//PREDICTED: transcription factor GTE10-like isoform X1 [Juglans regia]
MR5G024527.1	XP_018840271.1//PREDICTED: 60S ribosomal protein L26-1 [Juglans regia]
MR4G016475.1	XP_018860745.1//PREDICTED: putative invertase inhibitor [Juglans regia]
MR4G021134.1	OWM71998.1//hypothetical protein CDL15_Pgr017881 [Punica granatum];XP_018811956.1//PREDICTED: replication factor C subunit 2 [Juglans regia]
MR8G027539.1	XP_018848181.1//PREDICTED: eukaryotic translation initiation factor 5B [Juglans regia]
MR3G012293.1	XP_018830097.1//PREDICTED: exocyst complex component SEC10-like [Juglans regia]
MR5G003521.1	XP_021608313.1//ATP-dependent DNA helicase 2 subunit KU70 isoform X2 [Manihot esculenta];XP_008222687.1//PREDICTED: ATP-dependent DNA helicase 2 subunit KU70 [Prunus mume];XP_018815795.1//PREDICTED: ATP-dependent DNA helicase 2 subunit KU70 [Juglans regia]
MR0G003829.1	XP_018845643.1//PREDICTED: peroxidase 16-like [Juglans regia]
MR0G008593.1	XP_002866062.1//tryptophan synthase beta chain 1, chloroplastic [Arabidopsis lyrata subsp. lyrata]
MR8G004610.1	XP_018847629.1//PREDICTED: bifunctional 3-dehydroquinate dehydratase/shikimate dehydrogenase, chloroplastic-like [Juglans regia]
MR0G006545.2	XP_018837765.1//PREDICTED: endoplasmin homolog [Juglans regia]
MR8G012806.1	XP_018814709.1//PREDICTED: serine/threonine-protein kinase HT1-like [Juglans regia]
MR8G023204.1	XP_017981486.1//PREDICTED: protein SPIRRIG isoform X1 [Theobroma cacao]
MR0G003764.1	XP_018838089.1//PREDICTED: VIN3-like protein 1 isoform X1 [Juglans regia]
MR7G011382.1	XP_018842032.1//PREDICTED: thiamine biosynthetic bifunctional enzyme TH1, chloroplastic isoform X1 [Juglans regia]
MR4G001651.1	XP_018809368.1//PREDICTED: RING-H2 finger protein ATL79-like [Juglans regia]
MR7G014383.1	XP_018808415.1//PREDICTED: protein PHYLLO, chloroplastic isoform X2 [Juglans regia];KVI10176.1//Cyclic nucleotide-binding domain-containing protein [Cynara cardunculus var. scolymus];XP_018810782.1//PREDICTED: cyclic nucleotide-gated ion channel 1-like [Juglans regia];XP_016686050.1//PREDICTED: cyclic nucleotide-gated ion channel 1-like [Gossypium hirsutum];XP_018808414.1//PREDICTED: protein PHYLLO, chloroplastic isoform X1 [Juglans regia]
MR6G005851.1	XP_018833268.1//PREDICTED: glucose-1-phosphate adenylyltransferase small subunit, chloroplastic/amyloplastic [Juglans regia]
MR4G025821.1	XP_018811143.1//PREDICTED: uncharacterized protein LOC108983821 isoform X2 [Juglans regia];XP_018811137.1//PREDICTED: uncharacterized protein LOC108983821 isoform X1 [Juglans regia]
MR4G024555.1	XP_021634866.1//protein Iojap, chloroplastic [Manihot esculenta];XP_018809326.1//PREDICTED: protein Iojap, chloroplastic-like [Juglans regia];GAV64110.1//Oligomerisation domain-containing protein [Cephalotus follicularis]

MR5TCONS_00064307.1	KCW83875.1//hypothetical protein EUGRSUZ_B00733 [Eucalyptus grandis]
MR6G003889.1	XP_018840689.1//PREDICTED: sterol 3-beta-glucosyltransferase UGT80A2-like [Juglans regia];XP_015892518.1//PREDICTED: sterol 3-beta-glucosyltransferase UGT80A2 [Ziziphus jujuba];XP_018820333.1//PREDICTED: sterol 3-beta-glucosyltransferase UGT80A2 isoform X1 [Juglans regia]
MR4G009608.1	XP_018856515.1//PREDICTED: uncharacterized protein LOC109018784 [Juglans regia]
MR6G011311.1	XP_018827335.1//PREDICTED: fructokinase-1 [Juglans regia]
MR6G013295.1	XP_018857294.1//PREDICTED: uncharacterized protein LOC109019461 [Juglans regia]
MR7G014401.1	XP_018848214.1//PREDICTED: rust resistance kinase Lr10-like [Juglans regia]
MR4G021009.1	XP_018814780.1//PREDICTED: 3-oxoacyl-[acyl-carrier-protein] reductase 4 isoform X2 [Juglans regia];XP_018859977.1//PREDICTED: transcription factor GTE10-like isoform X2 [Juglans regia]
MR3G026510.1	XP_018823517.1//PREDICTED: plastidic ATP/ADP-transporter-like [Juglans regia];XP_018827865.1//PREDICTED: root phototropism protein 3-like [Juglans regia]
MR8G002778.1	XP_018833461.1//PREDICTED: putative ER lumen protein-retaining receptor C28H8.4 isoform X2 [Juglans regia];XP_018833452.1//PREDICTED: probable alkaline/neutral invertase B [Juglans regia]
MR5G002858.1	XP_018830233.1//PREDICTED: uncharacterized protein LOC108998196 [Juglans regia];XP_018826337.1//PREDICTED: uncharacterized protein LOC108995260 isoform X2 [Juglans regia]
MR4G020624.1	XP_018847734.1//PREDICTED: GPI transamidase component PIG-T [Juglans regia]
MR6G006417.1	XP_018838033.1//PREDICTED: beta-hexosaminidase 3 [Juglans regia]
MR5G003466.1	XP_018815757.1//PREDICTED: phosphoglucan, water dikinase, chloroplastic isoform X1 [Juglans regia]
MR5G024481.1	XP_018844184.1//PREDICTED: thiol protease aleurain-like [Juglans regia]
MR4G028683.1	XP_018806922.1//PREDICTED: AT-hook motif nuclear-localized protein 8-like [Juglans regia]
MR6G018059.1	XP_018834126.1//PREDICTED: uncharacterized protein LOC109001335 [Juglans regia]
MR3G011044.1	XP_018814811.1//PREDICTED: ras-related protein RABA3 [Juglans regia]
MR6G025936.1	XP_018857876.1//PREDICTED: mediator of RNA polymerase II transcription subunit 17-like [Juglans regia];KRH14114.1//hypothetical protein GLYMA_14G007400 [Glycine max]
MR3G009348.1	XP_018809497.1//PREDICTED: probable arabinosyltransferase ARAD1 [Juglans regia]
MR6G021566.1	XP_018816897.1//PREDICTED: putative lipid phosphate phosphatase 3, chloroplastic isoform X2 [Juglans regia];XP_018816896.1//PREDICTED: lipid phosphate phosphatase 2-like isoform X1 [Juglans regia];XP_018816899.1//PREDICTED: putative lipid phosphate phosphatase 3, chloroplastic isoform X4 [Juglans regia]
MR6G019772.1	XP_018815843.1//PREDICTED: 21 kDa protein-like [Juglans regia]
MR6G021434.2	XP_018846355.1//PREDICTED: probable polyamine oxidase 4 [Juglans regia]
MR6G021455.1	XP_018816578.1//PREDICTED: universal stress protein PHOS34 [Juglans regia]
MR3G014742.1	XP_018814519.1//PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP20-1 [Juglans regia]
MR3G014770.1	XP_018810496.1//PREDICTED: BTB/POZ and MATH domain-containing protein 3-like isoform X1 [Juglans regia];XP_018821781.1//PREDICTED: BTB/POZ and MATH domain-containing protein 3-like [Juglans regia]
MR6G013865.1	XP_018846455.1//PREDICTED: uncharacterized protein LOC109010170 isoform X2 [Juglans regia]
MR7G013561.1	XP_018855154.1//PREDICTED: anthocyanidin 3-O-glucosyltransferase 7-like [Juglans regia]

MR6G013864.1	XP_018850833.1//PREDICTED: aspartic proteinase-like protein 1 isoform X1 [Juglans regia]
MR7G011439.1	XP_018835593.1//PREDICTED: uncharacterized protein LOC109002347 [Juglans regia]
MR7G028529.1	XP_018817793.1//PREDICTED: polyadenylate-binding protein 8-like [Juglans regia]
MR4G008743.1	XP_018809325.1//PREDICTED: UDP-arabinopyranose mutase 1-like isoform X2 [Juglans regia];XP_002283867.1//PREDICTED: UDP-arabinopyranose mutase 1 isoform X2 [Vitis vinifera]
MR4G023616.1	AIX92145.1//cinnamoyl-CoA reductase 1 [Betula platyphylla]
MR6G011277.1	XP_018827345.1//PREDICTED: tryptophan synthase alpha chain-like isoform X1 [Juglans regia]
MR7G016687.1	XP_018809512.1//PREDICTED: cyclic nucleotide-gated ion channel 1-like [Juglans regia]
MR4G021018.2	XP_018808074.1//PREDICTED: uncharacterized protein LOC108981385 [Juglans regia]
MR5G027232.1	XP_006424909.1//hypothetical protein CICLE_v10029051mg [Citrus clementina];XP_015874042.1//PREDICTED: tropinone reductase homolog At5g06060-like [Ziziphus jujuba]
MR3G026575.1	XP_018850654.1//PREDICTED: uncharacterized protein LOC109013126 [Juglans regia]
MR2G022146.2	XP_018828020.1//PREDICTED: cation-chloride cotransporter 1-like [Juglans regia];KMZ57105.1//Solute carrier family 12 member [Zostera marina]
MR5G023182.1	XP_018826140.1//PREDICTED: endo-1,3;1,4-beta-D-glucanase-like isoform X1 [Juglans regia]
MR3G019030.1	XP_018833902.1//PREDICTED: cytochrome c oxidase subunit 6b-1-like isoform X2 [Juglans regia]
MR2G026847.2	XP_018824705.1//PREDICTED: acetylornithine deacetylase [Juglans regia];XP_021669905.1//mitochondrial carnitine/acylcarnitine carrier-like protein [Hevea brasiliensis]
MR2G027137.1	XP_021276261.1//mitochondrial amidoxime reducing component 2 [Herrania umbratica];XP_018812726.1//PREDICTED: mitochondrial amidoxime-reducing component 1-like [Juglans regia]
MR4G021054.1	XP_018833335.1//PREDICTED: rhodanese-like domain-containing protein 11, chloroplastic [Juglans regia]
MR4G021195.1	XP_018859335.1//PREDICTED: DEAD-box ATP-dependent RNA helicase 35 [Juglans regia]
MR6G021656.1	XP_018834126.1//PREDICTED: uncharacterized protein LOC109001335 [Juglans regia]
MR6G009128.1	XP_021275482.1//signal peptide peptidase-like 1 [Herrania umbratica]
MR3G009415.1	XP_008388058.1//PREDICTED: 3-ketoacyl-CoA synthase 4-like [Malus domestica]
MR2G027161.1	XP_018809112.1//PREDICTED: binding partner of ACD11 1-like [Juglans regia]
MR4G023305.1	XP_018810168.1//PREDICTED: AP-4 complex subunit epsilon-like [Juglans regia]
MR3G007323.2	XP_006493466.1//PREDICTED: uncharacterized protein C1450.15 [Citrus sinensis];XP_018827956.1//PREDICTED: glycosylphosphatidylinositol anchor biosynthesis protein 11-like isoform X1 [Juglans regia];XP_015868139.1//PREDICTED: uncharacterized protein C1450.15 [Ziziphus jujuba]
MR0G006163.1	XP_018818342.1//PREDICTED: DNA-directed RNA polymerase III subunit 2 isoform X1 [Juglans regia];XP_018818353.1//PREDICTED: DNA-directed RNA polymerase III subunit 2 isoform X2 [Juglans regia];XP_010659064.1//PREDICTED: DNA-directed RNA polymerase III subunit 2 [Vitis vinifera];OMO61172.1//hypothetical protein CCACVL1_23713 [Corchorus capsularis]
MR0G007458.1	XP_018806479.1//PREDICTED: cadmium-induced protein AS8 isoform X4 [Juglans regia];XP_018806472.1//PREDICTED: cadmium-induced protein AS8 isoform X2 [Juglans regia]
MR6G020537.1	XP_018859353.1//PREDICTED: calcium-transporting ATPase 9, plasma membrane-type-like isoform X1 [Juglans regia];XP_018859237.1//PREDICTED: calcium-transporting ATPase 9, plasma membrane-type-like isoform X1 [Juglans regia]
MR6G013315.1	XP_018843111.1//PREDICTED: TMV resistance protein N-like isoform X1 [Juglans regia]
MR6G003659.1	GAV68459.1//Thiolase_N domain-containing protein/Thiolase_C domain-containing protein/ABC1 domain-containing protein [Cephalotus follicularis];XP_018848751.1//PREDICTED: acetyl-CoA acetyltransferase, cytosolic 1 isoform X2 [Juglans regia]
MR7G024251.1	XP_018815059.1//PREDICTED: uncharacterized protein LOC108986773 [Juglans regia]

MR4G028678.1	XP_018824669.1//PREDICTED: protein LE25 [Juglans regia]
MR7G008316.1	XP_018833412.1//PREDICTED: cation/calcium exchanger 2 [Juglans regia]
MR5G025131.1	XP_018835514.1//PREDICTED: glutelin type-A 3-like [Juglans regia]
MR5G002859.1	XP_018826334.1//PREDICTED: STS14 protein [Juglans regia]
MR5G010483.1	GAV57497.1//LRR_1 domain-containing protein/NB-ARC domain-containing protein [Cephalotus follicularis]
MR8G002615.1	XP_018833608.1//PREDICTED: phosphoinositide phosphatase SAC1 isoform X2 [Juglans regia];XP_018833609.1//PREDICTED: phosphoinositide phosphatase SAC1 isoform X3 [Juglans regia]
MR8G001626.1	XP_018831155.1//PREDICTED: uncharacterized protein LOC108998873 [Juglans regia]
MR7G009259.2	XP_018840622.1//PREDICTED: uncharacterized protein LOC109005956 isoform X1 [Juglans regia];XP_018840630.1//PREDICTED: uncharacterized protein LOC109005956 isoform X2 [Juglans regia]
MR4G004748.1	XP_018810169.1//PREDICTED: decapping nuclease DXO homolog, chloroplastic isoform X1 [Juglans regia]
MR2G019459.1	XP_018816499.1//PREDICTED: importin subunit alpha-4 [Juglans regia]
MR2G000623.1	XP_018852310.1//PREDICTED: protein MODIFIER OF SNC1 11-like [Juglans regia]
MR2G004713.1	XP_018836272.1//PREDICTED: cell division cycle protein 48 homolog [Juglans regia]
MR2G006160.1	XP_018816513.1//PREDICTED: pentatricopeptide repeat-containing protein At1g56690, mitochondrial [Juglans regia];XP_018816409.1//PREDICTED: GDSL esterase/lipase At1g09390 [Juglans regia]
MR2G009995.1	XP_018819401.1//PREDICTED: WEB family protein At2g38370 [Juglans regia]
MR2G011703.1	XP_018820571.1//PREDICTED: transcription initiation factor TFIID subunit 8 [Juglans regia]
MR2G011723.1	XP_018820571.1//PREDICTED: transcription initiation factor TFIID subunit 8 [Juglans regia]
MR2G012442.1	XP_018811980.1//PREDICTED: kinetochore protein spc25 [Juglans regia]
MR2G013617.1	XP_009113912.1//PREDICTED: alpha N-terminal protein methyltransferase 1-like [Brassica rapa];XP_018813602.1//PREDICTED: alpha N-terminal protein methyltransferase 1 isoform X1 [Juglans regia]
MR2G004727.1	XP_018855383.1//PREDICTED: thiol-disulfide oxidoreductase LTO1-like [Juglans regia]
MR2G005420.4	XP_018859537.1//PREDICTED: la-related protein 6A [Juglans regia]
MR2G006162.1	XP_018816409.1//PREDICTED: GDSL esterase/lipase At1g09390 [Juglans regia]
MR2G006842.1	XP_018824515.1//PREDICTED: 40S ribosomal protein S4-1-like [Juglans regia]
MR1G028360.1	XP_018859181.1//PREDICTED: uncharacterized protein LOC109021088 [Juglans regia]
MR1TCONS_00054219.1	MR1TCONS_00054219.1//1;XP_018835437.1//PREDICTED: putative disease resistance protein At3g14460 isoform X1 [Juglans regia];XP_017984378.1//PREDICTED: putative disease resistance RPP13-like protein 1 [Theobroma cacao]
MR3G019174.2	XP_018858836.1//PREDICTED: GRF1-interacting factor 3-like [Juglans regia]
MR2G012857.1	XP_018832807.1//PREDICTED: velvet complex subunit B [Juglans regia]
MR2G022150.1	XP_018828022.1//PREDICTED: BTB/POZ domain-containing protein At1g30440 [Juglans regia]
MR2G023480.1	XP_018817223.1//PREDICTED: pyrroline-5-carboxylate reductase [Juglans regia];XP_015898143.1//PREDICTED: pyrroline-5-carboxylate reductase-like isoform X1 [Ziziphus jujuba]

MR3G011046.1	XP_018814811.1//PREDICTED: ras-related protein RABA3 [Juglans regia]
MR3G011007.1	XP_018807798.1//PREDICTED: uncharacterized protein LOC108981167 [Juglans regia]
MR1G027563.1	XP_018818917.1//PREDICTED: UMP-CMP kinase 3-like isoform X1 [Juglans regia];XP_018818963.1//PREDICTED: UMP-CMP kinase 3-like isoform X2 [Juglans regia];XP_015886496.1//PREDICTED: UMP-CMP kinase 3 isoform X1 [Ziziphus jujuba];XP_019449659.1//PREDICTED: UMP-CMP kinase 3-like [Lupinus angustifolius]
MR1G019986.1	XP_009350240.1//PREDICTED: pentatricopeptide repeat-containing protein At1g62350 [Pyrus x bretschneideri];XP_018825515.1//PREDICTED: pentatricopeptide repeat-containing protein At1g62350 [Juglans regia]
MR6G023574.1	XP_018850816.1//PREDICTED: protein UPSTREAM OF FLC [Juglans regia]
MR6G013317.5	XP_018835437.1//PREDICTED: putative disease resistance protein At3g14460 isoform X1 [Juglans regia];XP_018826305.1//PREDICTED: TMV resistance protein N-like [Juglans regia]
MR6G001701.1	XP_018820691.1//PREDICTED: protein S-acyltransferase 24 [Juglans regia]
MR4G021194.1	XP_018847359.1//PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At1g12460 [Juglans regia]
MR4G001417.1	XP_015866027.1//PREDICTED: 65-kDa microtubule-associated protein 1 [Ziziphus jujuba];XP_018812214.1//PREDICTED: 65-kDa microtubule-associated protein 1-like [Juglans regia]
MR4G003859.1	XP_018826580.1//PREDICTED: uncharacterized endoplasmic reticulum membrane protein YGL010W-like [Juglans regia]
MR4G015417.1	XP_018852245.1//PREDICTED: lysine-specific demethylase JMJ706-like [Juglans regia]
MR4G010943.1	XP_018842632.1//PREDICTED: tobamovirus multiplication protein 2B-like isoform X2 [Juglans regia]
MR4G021021.3	XP_018814781.1//PREDICTED: telomere length regulation protein TEL2 homolog isoform X1 [Juglans regia]
MR5G013405.1	XP_018820989.1//PREDICTED: mannan endo-1,4-beta-mannosidase 7 [Juglans regia]
MR5G023109.1	XP_018856419.1//PREDICTED: uncharacterized protein LOC109018719 [Juglans regia]
MR7G002567.2	XP_018810176.1//PREDICTED: decapping 5-like protein [Juglans regia]
MR5G003421.1	XP_018844047.1//PREDICTED: crocetin glucosyltransferase, chloroplastic-like [Juglans regia]
MR5G003282.1	OWM66251.1//hypothetical protein CDL15_Pgr013468 [Punica granatum];XP_004288038.2//PREDICTED: caltractin [Fragaria vesca subsp. vesca]

Table S16. List of primers used for qRT-PCR.

Gene name	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')
Actin	AGCCTACATCGCTCTGGACT	GTGGTTTCGTGTATGCCAGC
MR4G016016.1	AGCTCTGAGTCTCTTTCGCA	CCACGTGAGGTTTAGCTTCG
MR4G025315.1	CATTAGTCACTGCCGTCACG	ATTCTCTCTCGCCATCCTCG
MR6G025594.1	CCGGCGGAGTAGTTTACAGA	ACCCAACTGCCAAGACGATA
MR1G012865.1	TGTTGATCCCTACATTGTAGTGG	AAGAGCCGGATCAACATCGA
MR2G007342.1	ATGTCAGAGAAGCAACCCCA	GCCAAGGATCACAACGACAG
MR2G011842.1	TGAAACAGGCTACCACCACT	TTCACACTGGGGTCAATTGG
MR3G015028.1	GAGGTGCTATCAGAGGCCAT	CACCTGATCCTGGAGCAAGA
MR5G022585.3	TACAACACTCCCCAAACCCA	AGAGGAGAAGAGCGAACACC
MR5TCONS_00064963.1	GATCTCACCCACCTCACCTC	GCCACAGCGACACAAAAGTA
MR0TCONS_00017483.1	ACTACTACCCCTACTGCCCA	AACCAACTCCCACCGTACTT