

Supplemental Table 1. GO terms for the Flavonoid biosynthesis pathway and genes identified through pathway-level co-expression analysis. The ranking is sorted for descending counts within the pathway. The last two columns give the number of genes within or outside the pathway that are annotated with the term listed in the second column.

GO id	GO term	Genes within pathway	Genes outside pathway
GO:0008372	cellular component unknown	13	28
GO:0016207	4-coumarate-CoA ligase activity	12	0
GO:0008152	metabolism	8	7
GO:0019350	teichoic acid biosynthesis	8	0
GO:0009234	menaquinone biosynthesis	8	0
GO:0009698	phenylpropanoid metabolism	7	0
GO:0009813	flavonoid biosynthesis	7	0
GO:0008299	isoprenoid biosynthesis	6	0
GO:0009507	chloroplast	5	24
GO:0009411	response to UV	4	0
GO:0016706	"oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors"	4	0
GO:0009058	biosynthesis	3	2
GO:0009699	phenylpropanoid biosynthesis	3	1
GO:0008415	acyltransferase activity	3	1
GO:0004315	3-oxoacyl-[acyl-carrier protein] synthase activity	3	0
GO:0006633	fatty acid biosynthesis	3	0
GO:0005739	mitochondrion	2	7
GO:0005783	endoplasmic reticulum	2	1
GO:0009695	jasmonic acid biosynthesis	2	1
GO:0009611	response to wounding	2	1
GO:0005506	iron ion binding	2	1
GO:0016216	isopenicillin-N synthase activity	2	0
GO:0005777	peroxisome	2	0
GO:0045430	chalcone isomerase activity	2	0
GO:0009705	vacuolar membrane (sensu Magnoliophyta)	2	0
GO:0004321	fatty-acyl-CoA synthase activity	2	0
GO:0009621	response to pathogenic fungi	2	0
GO:0000004	biological process unknown	1	41
GO:0005554	molecular function unknown	1	34
GO:0003824	catalytic activity	1	7
GO:0016210	naringenin-chalcone synthase activity	1	0
GO:0016208	AMP binding	1	0
GO:0045486	naringenin 3-dioxygenase activity	1	0
GO:0005727	extrachromosomal circular DNA	1	0
GO:0042406	extrinsic to endoplasmic reticulum membrane	1	0
GO:0009715	chalcone biosynthesis	1	0
GO:0016405	CoA-ligase activity	1	0
GO:0047473	D-alanine-poly(phosphoribitol) ligase activity	1	0
GO:0008756	o-succinylbenzoate-CoA ligase activity	1	0
GO:0019748	secondary metabolism	1	0
GO:0016874	ligase activity	1	0
GO:0012505	endomembrane system	0	30
GO:0003677	DNA binding	0	16
GO:0005634	nucleus	0	14
GO:0003700	transcription factor activity	0	14
GO:0016020	membrane	0	9
GO:0005524	ATP binding	0	8

GO:0006355	"regulation of transcription, DNA-dependent"	0	7
GO:0006869	lipid transport	0	7
GO:0008289	lipid binding	0	7
GO:0031225	anchored to membrane	0	6
GO:0004497	monooxygenase activity	0	4
GO:0016757	"transferase activity, transferring glycosyl groups"	0	4
GO:0006118	electron transport	0	4
GO:0005737	cytoplasm	0	4
GO:0004674	protein serine/threonine kinase activity	0	4
GO:0004672	protein kinase activity	0	4
GO:0009908	flower development	0	4
GO:0006468	protein amino acid phosphorylation	0	4
GO:0005975	carbohydrate metabolism	0	4
GO:0051287	NAD binding	0	3
GO:0016021	integral to membrane	0	3
GO:0005525	GTP binding	0	3
GO:0003676	nucleic acid binding	0	3
GO:0006810	transport	0	3
GO:0004553	"hydrolase activity, hydrolyzing O-glycosyl compounds"	0	3
GO:0016491	oxidoreductase activity	0	3
GO:0009556	microsporogenesis	0	3
GO:0019825	oxygen binding	0	3
GO:0005509	calcium ion binding	0	3
GO:0009405	pathogenesis	0	3
GO:0016301	kinase activity	0	3
GO:0045449	regulation of transcription	0	3
GO:0006499	N-terminal protein myristoylation	0	3
GO:0005576	extracellular region	0	3
GO:0006418	tRNA aminoacylation for protein translation	0	3
GO:0006012	galactose metabolism	0	2
GO:0003854	3-beta-hydroxy-delta5-steroid dehydrogenase activity	0	2
GO:0004812	tRNA ligase activity	0	2
GO:0016999	antibiotic metabolism	0	2
GO:0016740	transferase activity	0	2
GO:0030599	pectinesterase activity	0	2
GO:0016758	"transferase activity, transferring hexosyl groups"	0	2
GO:0008460	"dTDP-glucose 4,6-dehydratase activity"	0	2
GO:0004043	L-aminoadipate-semialdehyde dehydrogenase activity	0	2
GO:0009225	nucleotide-sugar metabolism	0	2
GO:0016789	carboxylic ester hydrolase activity	0	2
GO:0006952	defense response	0	2
GO:0004685	calcium- and calmodulin-dependent protein kinase activity	0	2
GO:0006694	steroid biosynthesis	0	2
GO:0009793	embryonic development (sensu Magnoliophyta)	0	2
GO:0009809	lignin biosynthesis	0	2
GO:0042773	ATP synthesis coupled electron transport	0	2
GO:0005507	copper ion binding	0	2
GO:0003913	DNA photolyase activity	0	2
GO:0006725	aromatic compound metabolism	0	2
GO:0019866	inner membrane	0	2
GO:0048443	stamen development	0	2
GO:0048481	ovule development	0	2
GO:0003978	UDP-glucose 4-epimerase activity	0	2
GO:0004650	polygalacturonase activity	0	2
GO:0009505	cell wall (sensu Magnoliophyta)	0	2
GO:0006486	protein amino acid glycosylation	0	2
GO:0015031	protein transport	0	2

GO:0005788	endoplasmic reticulum lumen	0	1
GO:0008378	galactosyltransferase activity	0	1
GO:0008270	zinc ion binding	0	1
GO:0006824	cobalt ion transport	0	1
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	0	1
GO:0016628	"oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor"	0	1
GO:0016998	cell wall catabolism	0	1
GO:0000160	two-component signal transduction system (phosphorelay)	0	1
GO:0006308	DNA catabolism	0	1
GO:0004713	protein-tyrosine kinase activity	0	1
GO:0003988	acetyl-CoA C-acyltransferase activity	0	1
GO:0004089	carbonate dehydratase activity	0	1
GO:0005794	Golgi apparatus	0	1
GO:0016168	chlorophyll binding	0	1
GO:0015846	polyamine transport	0	1
GO:0005792	microsome	0	1
GO:0015725	gluconate transport	0	1
GO:0003924	GTPase activity	0	1
GO:0046409	p-coumarate 3-hydroxylase activity	0	1
GO:0004386	helicase activity	0	1
GO:0003841	1-acylglycerol-3-phosphate O-acyltransferase activity	0	1
GO:0008171	O-methyltransferase activity	0	1
GO:0007155	cell adhesion	0	1
GO:0006839	mitochondrial transport	0	1
GO:0046487	glyoxylate metabolism	0	1
GO:0009765	photosynthesis light harvesting	0	1
GO:0008679	2-hydroxy-3-oxopropionate reductase activity	0	1
GO:0000719	photoreactive repair	0	1
GO:0004064	arylesterase activity	0	1
GO:0005829	cytosol	0	1
GO:0004828	serine-tRNA ligase activity	0	1
GO:0000151	ubiquitin ligase complex	0	1
GO:0008677	2-dehydropantoate 2-reductase activity	0	1
GO:0016567	protein ubiquitination	0	1
GO:0045551	cinnamyl-alcohol dehydrogenase activity	0	1
GO:0009877	nodulation	0	1
GO:0016563	transcriptional activator activity	0	1
GO:0019861	flagellum	0	1
GO:0006457	protein folding	0	1
GO:0015706	nitrate transport	0	1
GO:0017004	cytochrome complex assembly	0	1
GO:0019656	heterolactate fermentation	0	1
GO:0005489	electron transporter activity	0	1
GO:0005488	binding	0	1
GO:0004831	tyrosine-tRNA ligase activity	0	1
GO:0004830	tryptophan-tRNA ligase activity	0	1
GO:0008565	protein transporter activity	0	1
GO:0009941	chloroplast envelope	0	1
GO:0042626	"ATPase activity, coupled to transmembrane movement of substances"	0	1
GO:0006573	valine metabolism	0	1
GO:0019430	removal of superoxide radicals	0	1
GO:0006206	pyrimidine base metabolism	0	1
GO:0016597	amino acid binding	0	1
GO:0006886	intracellular protein transport	0	1
GO:0004664	prephenate dehydratase activity	0	1

GO:0008643	carbohydrate transport	0	1
GO:0005528	FK506 binding	0	1
GO:0045036	protein-chloroplast targeting	0	1
GO:0008757	S-adenosylmethionine-dependent methyltransferase activity	0	1
GO:0007186	G-protein coupled receptor protein signaling pathway	0	1
GO:0015144	carbohydrate transporter activity	0	1
GO:0016149	"translation release factor activity, codon specific"	0	1
GO:0006811	ion transport	0	1
GO:0006817	phosphate transport	0	1
GO:0048497	maintenance of floral organ identity	0	1
GO:0015627	type II protein secretion system complex	0	1
GO:0019395	fatty acid oxidation	0	1
GO:0004842	ubiquitin-protein ligase activity	0	1
GO:0042545	cell wall modification	0	1
GO:0015071	protein phosphatase type 2C activity	0	1
GO:0009707	chloroplast outer membrane	0	1
GO:0003743	translation initiation factor activity	0	1
GO:0006434	seryl-tRNA aminoacylation	0	1
GO:0006437	tyrosyl-tRNA aminoacylation	0	1
GO:0006436	tryptophanyl-tRNA aminoacylation	0	1
GO:0008026	ATP-dependent helicase activity	0	1
GO:0006730	one-carbon compound metabolism	0	1
GO:0006865	amino acid transport	0	1
GO:0044249	cellular biosynthesis	0	1
GO:0008704	5-carboxymethyl-2-hydroxyruconate delta-isomerase activity	0	1
GO:0009650	UV protection	0	1
GO:0045226	extracellular polysaccharide biosynthesis	0	1
GO:0006461	protein complex assembly	0	1
GO:0007264	small GTPase mediated signal transduction	0	1
GO:0009554	megasporogenesis	0	1
GO:0008194	UDP-glycosyltransferase activity	0	1
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	0	1
GO:0004757	sepiapterin reductase activity	0	1
GO:0008831	dTDP-4-dehydrorhamnose reductase activity	0	1
GO:0004616	phosphogluconate dehydrogenase (decarboxylating) activity	0	1
GO:0004103	choline kinase activity	0	1
GO:0015450	protein translocase activity	0	1
GO:0005351	sugar porter activity	0	1
GO:0009408	response to heat	0	1
GO:0008200	ion channel inhibitor activity	0	1
GO:0009094	L-phenylalanine biosynthesis	0	1
GO:0009522	photosystem I	0	1
GO:0016853	isomerase activity	0	1
GO:0005515	protein binding	0	1
GO:0004519	endonuclease activity	0	1
GO:0008654	phospholipid biosynthesis	0	1
GO:0005743	mitochondrial inner membrane	0	1
GO:0009933	meristem organization	0	1
GO:0003723	RNA binding	0	1
GO:0008382	iron superoxide dismutase activity	0	1
GO:0048440	carpel development	0	1
GO:0015628	type II protein secretion system	0	1
GO:0006098	pentose-phosphate shunt	0	1
GO:0042597	periplasmic space	0	1
GO:0004871	signal transducer activity	0	1
GO:0009543	thylakoid lumen (sensu Viridiplantae)	0	1

GO:0000103	sulfate assimilation	0	1
GO:0009103	lipopolysaccharide biosynthesis	0	1
GO:0008446	"GDP-mannose 4,6-dehydratase activity"	0	1
GO:0016844	strictosidine synthase activity	0	1
GO:0008442	3-hydroxyisobutyrate dehydrogenase activity	0	1
GO:0009821	alkaloid biosynthesis	0	1
GO:0019871	sodium channel inhibitor activity	0	1
GO:0006281	DNA repair	0	1
GO:0015758	glucose transport	0	1
GO:0015698	inorganic anion transport	0	1
GO:0048533	sporocyte differentiation	0	1
GO:0015757	galactose transport	0	1
GO:0006857	oligopeptide transport	0	1
GO:0046423	allene-oxide cyclase activity	0	1
GO:0006464	protein modification	0	1
GO:0003904	deoxyribodipyrimidine photo-lyase activity	0	1
GO:0009052	"pentose-phosphate shunt, non-oxidative branch"	0	1
GO:0008191	metalloendopeptidase inhibitor activity	0	1
GO:0009051	"pentose-phosphate shunt, oxidative branch"	0	1
GO:0005618	cell wall	0	1
GO:0005478	intracellular transporter activity	0	1
GO:0006415	translational termination	0	1
GO:0006413	translational initiation	0	1
GO:0045941	positive regulation of transcription	0	1