

Exhibit 1 Primer information for quantitative fluorescence analysis

Primer name	Unigenes ID	Primer sequence	Temperature(°C)	Product size(bp)
<i>PAL1</i>	TRINITY-DN40299-c0-g1	TATTGAGCTAGCGGAAGCCG	60	109
		GCCAAATCCGGTGGTTACAC	59	
<i>PAL2</i>	TRINITY-DN10112-c0-g1	CCACTTCTCACC GGAGAACC	60	183
		CGAATCGGATGCCGGAGTAA	60	
<i>TYR</i>	TRINITY-DN71019-c1-g1	GTCCAGATGCGGTCGATCAT	60	143
		GGCTACCTCGGTGACAACAA	60	
<i>BZ1</i>	TRINITY-DN35977-c0-g1	CTCTTCTTGTGGCGGTGTTA	56	146
		TCAATGTCGGACCATTCTTT	55	
<i>ANS</i>	TRINITY-DN103233-c0-g1	ACTGCCCAAGAGAACCTCAC	60	150
		CGAGGGCAAATGGGTCATTG	60	
<i>ANR</i>	TRINITY-DN14134-c0-g1	AGCCAAAGTCTTAGAAACAGG	54	208
		AATTGAGGGAATAACCAACG	55	
<i>6GT</i>	TRINITY-DN629-c0-g1	GGTCCCATTTTGGAGCTGGA	60	214
		TGCGTAGGGACCACAAGAAC	60	
<i>CDOPA5GT</i>	TRINITY-DN3701-c1-g1	CCACTACCACCCTAACTCCG	57	232
		AACCCAGCCAAAGAAGACAT	56	
<i>4CL</i>	TRINITY-DN5155-c1-g1	ATCGAAAGGGTCTTGAGGGC	60	143
		GCCGAGTACGAAAGACGTGA	60	
<i>DOPA</i>	TRINITY-DN26707-c0-g1	GGCACCCTACCACCCTAAC	60	276
		AAGCAATACCAGTGGAGCCC	60	
<i>FLS</i>	TRINITY-DN8599-c0-g1	ACGGCATCCACTTGAACCAT	60	106
		TGGCTAGGTTGCCTTGTCAG	60	
<i>CHS1</i>	TRINITY-DN3508-c1-g1	CCCGTCCATTCAACCTAC	53	113
		GAACCCATTTGCCACTTA	51	
<i>CHS2</i>	TRINITY-DN18996-c0-g1	TGCAGAAGATGACGTGGGTG	60	156
		AGAACCCTCACTTGTGCGAC	60	
<i>crtB</i>	TRINITY-DN4940-c0-g2	TCCTGACCCGAGTAGAACCT	56	374
		CCTATCACAACCCAAACGAG	55	
<i>F3H1</i>	TRINITY-DN22992-c0-g1	GCTTCTTAAGGCGAGCAAGC	60	136
		CCAGACCCAGAAGCAATCGT	60	
<i>F3H2</i>	TRINITY-DN5155-c1-g1	GGAAGCATGTGAGAATTGGGG	59	128
		CAAAGCGAAGCTTGTCTCTGA	59	
<i>5GT</i>	TRINITY-DN12266-c0-g1	GCTTCTAGTGCCGAGTTCCA	60	212
		ATGGCTTTAGAAGCCTCGGG	60	
<i>LAR</i>	TRINITY-DN46704-c0-g1	AAGGCCCATGCCATCCATAG	60	130
		CCCCAACAGCCGATATCACA	60	
<i>CYP73A</i>	TRINITY-DN3143-c0-g1	ACCAAGTCATCCAGCAACA	54	487
		AACCACCAGGCATTACC	56	
<i>atp1</i>		ACGAGATTCAAGCTGGGGAA	59	152
		CCACAATAGATCCAGTGCGC	59	
<i>18S</i>		TTCTATGGGTGGTGGTGCAT	59	169
		ATTGCCTCAAACCTCCGTGG	59	
<i>26S</i>		GTAGCGATTGGACAGAAACG	57	152
		CCCATAGCACACCCAGAAT	57	

Note: In each pair of primer sequences, the top one is the upper primer (5' → 3') and the bottom one is the lower primer (3' → 5').

Exhibit 2 Specific module GO enrichment

brochure	GO ID	Term Type	Description	Pvalue_corrected	Gene number
A	GO:0051213	MF	dioxygenase activity	0.003327339	9
	GO:0004793	MF	threonine aldolase activity	0.017013954	2
	GO:0016491	MF	oxidoreductase activity	0.026030997	49
	GO:0010158	BP	abaxial cell fate specification	0.038245526	2
	GO:0045165	BP	cell fate commitment	0.078818347	2
	GO:0006833	BP	water transport	0.093368818	2
	GO:0042044	BP	fluid transport	0.093368818	2
	GO:0003922	MF	GMP synthase (glutamine-hydrolyzing) activity	0.096603805	2
	GO:0005797	CC	Golgi medial cisterna	0.104611843	2
	GO:0005795	CC	Golgi stack	0.104611843	2
	GO:0006567	BP	threonine catabolic process	0.110144743	2
	GO:0020037	MF	heme binding	0.114204905	12
	GO:0050513	MF	glycoprotein 2-beta-D-xylosyltransferase activity	0.115634061	2
	GO:0031985	CC	Golgi cisterna	0.143345628	2
	GO:0031204	BP	posttranslational protein targeting to membrane, translocation	0.148803345	2
	GO:0006273	BP	lagging strand elongation	0.16884949	2
	GO:0016702	MF	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	0.212479007	4
	GO:0001708	BP	cell fate specification	0.237246188	2
	GO:0046906	MF	tetrapyrrole binding	0.248700496	12
	GO:0035252	MF	UDP-xylosyltransferase activity	0.248700496	2
	GO:0045491	BP	xylan metabolic process	1.49E-07	11
	GO:0045492	BP	xylan biosynthetic process	8.22E-07	9
	GO:0009834	BP	plant-type secondary cell wall biogenesis	1.43E-06	9
	GO:0009832	BP	plant-type cell wall biogenesis	1.45E-06	11
C	GO:0042744	BP	hydrogen peroxide catabolic process	4.12E-06	14
	GO:0010383	BP	cell wall polysaccharide metabolic process	4.45E-06	16
	GO:0070592	BP	cell wall polysaccharide biosynthetic process	4.70E-06	11
	GO:0042743	BP	hydrogen peroxide metabolic process	5.45E-06	14
	GO:0044038	BP	cell wall macromolecule biosynthetic process	7.15E-06	11
	GO:0070589	BP	cellular component macromolecule biosynthetic process	7.15E-06	11
	GO:0044036	BP	cell wall macromolecule metabolic process	8.06E-06	17
	GO:0017001	BP	antibiotic catabolic process	1.33E-05	14
	GO:0010410	BP	hemicellulose metabolic process	1.60E-05	14

E	GO:0051187	BP	cofactor catabolic process	1.80E-05	15
	GO:0071669	BP	plant-type cell wall organization or biogenesis	2.51E-05	13
	GO:0042546	BP	cell wall biogenesis	4.98E-05	13
	GO:0016684	MF	oxidoreductase activity, acting on peroxide as acceptor	6.49E-05	21
	GO:0016209	MF	antioxidant activity	8.13E-05	23
	GO:0046983	MF	protein dimerization activity	0.000103317	58
	GO:0044085	BP	cellular component biogenesis	0.000121121	19
	GO:0005794	CC	Golgi apparatus	4.84E-17	51
	GO:0030312	CC	external encapsulating structure	3.16E-14	39
	GO:0005618	CC	cell wall	3.16E-14	39
	GO:0071554	BP	cell wall organization or biogenesis	7.73E-13	51
	GO:0045229	BP	external encapsulating structure organization	1.84E-12	50
	GO:0042546	BP	cell wall biogenesis	1.08E-11	21
	GO:0071555	BP	cell wall organization	2.28E-10	45
	GO:0071669	BP	plant-type cell wall organization or biogenesis	2.99E-10	19
	GO:0009833	BP	plant-type primary cell wall biogenesis	1.11E-09	10
	GO:0030243	BP	cellulose metabolic process	1.80E-09	25
	GO:0005874	CC	microtubule	4.56E-09	28
	GO:0099513	CC	polymeric cytoskeletal fiber	4.79E-09	28
	GO:0099081	CC	supramolecular polymer	4.79E-09	28
	GO:0099512	CC	supramolecular fiber	4.79E-09	28
	GO:0099080	CC	supramolecular complex	5.82E-09	28
	GO:0044036	BP	cell wall macromolecule metabolic process	2.39E-08	21
	GO:0010383	BP	cell wall polysaccharide metabolic process	4.81E-08	19
	GO:0005881	CC	cytoplasmic microtubule	9.42E-08	9
	GO:0010410	BP	hemicellulose metabolic process	1.36E-07	17
	GO:0010411	BP	xyloglucan metabolic process	1.36E-07	14
	GO:0004148	MF	dihydrolipoyl dehydrogenase activity	0.002444792	3
	GO:0010608	BP	posttranscriptional regulation of gene expression	0.026796276	8
	GO:0030244	BP	cellulose biosynthetic process	0.063757534	6
	GO:0047274	MF	galactinol-sucrose galactosyltransferase activity	0.091713903	2
F	GO:1901681	MF	sulfur compound binding	0.12889772	4
	GO:0008135	MF	translation factor activity, RNA binding	0.12889772	11
	GO:0090079	MF	translation regulator activity, nucleic acid binding	0.12889772	11
	GO:0045182	MF	translation regulator activity	0.12889772	11
	GO:0009749	BP	response to glucose	0.130944159	3
	GO:0030976	MF	thiamine pyrophosphate binding	0.132040165	3
	GO:0009405	BP	pathogenesis	0.136200027	2

G	GO:0042550	BP	photosystem I stabilization	0.136200027	2
	GO:0070204	MF	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase activity	0.136305564	2
	GO:0070205	MF	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase activity	0.136305564	2
	GO:0033180	CC	proton-transporting V-type ATPase, V1 domain	0.141027599	3
	GO:0034284	BP	response to monosaccharide	0.141607582	3
	GO:0009746	BP	response to hexose	0.141607582	3
	GO:0035194	BP	posttranscriptional gene silencing by RNA	0.153732198	2
	GO:0010325	BP	raffinose family oligosaccharide biosynthetic process	0.153732198	2
	GO:0016760	MF	cellulose synthase (UDP-forming) activity	0.163522591	5
	GO:0071479	BP	cellular response to ionizing radiation	0.027217143	2
	GO:0044454	CC	nuclear chromosome part	0.040692919	8
	GO:0043399	MF	tRNA A64-2'-O-ribosylphosphate transferase activity	0.062582487	2
	GO:0019988	BP	charged-tRNA amino acid modification	0.068315984	2
	GO:0044427	CC	chromosomal part	0.114926927	19
	GO:0051336	BP	regulation of hydrolase activity	0.135733708	5
	GO:0000724	BP	double-strand break repair via homologous recombination	0.187295821	5
	GO:0000725	BP	recombinational repair	0.194068405	5
	GO:0005504	MF	fatty acid binding	0.203122353	3
	GO:0046556	MF	alpha-L-arabinofuranosidase activity	0.204607509	3
	GO:0050468	MF	reticuline oxidase activity	0.204607509	2
	GO:0046993	MF	oxidoreductase activity, acting on X-H and Y-H to form an X-Y bond, with oxygen as acceptor	0.204607509	2
	GO:0046992	MF	oxidoreductase activity, acting on X-H and Y-H to form an X-Y bond	0.204607509	2
	GO:0006566	BP	threonine metabolic process	0.222621703	3
	GO:0044774	BP	mitotic DNA integrity checkpoint	0.253983512	2
	GO:0071949	MF	FAD binding	0.301521604	8
	GO:0006302	BP	double-strand break repair	0.332374018	5
	GO:0009627	BP	systemic acquired resistance	0.332374018	2
	GO:0032541	CC	cortical endoplasmic reticulum	0.352940125	1
	GO:0072686	CC	mitotic spindle	0.352940125	1

Exhibit 3 Specific module KEGG enrichment

brochure	Database	Pathway id	Description	Pvalue_corrected	Gene number
A	KEGG PATHWAY	map00592	alpha-Linolenic acid metabolism	0.199569494	5
	KEGG PATHWAY	map01040	Biosynthesis of unsaturated fatty acids	0.265842535	3
	KEGG PATHWAY	map00903	Limonene and pinene degradation	0.275435721	2
	KEGG PATHWAY	map00780	Biotin metabolism	0.275860535	2
	KEGG PATHWAY	map00620	Pyruvate metabolism	0.282039627	5
	KEGG PATHWAY	map00561	Glycerolipid metabolism	0.303561543	4
	KEGG PATHWAY	map00071	Fatty acid degradation	0.305653349	5
	KEGG PATHWAY	map00380	Tryptophan metabolism	0.313250556	3
	KEGG PATHWAY	map00640	Propanoate metabolism	0.313250556	3
	KEGG PATHWAY	map00310	Lysine degradation	0.316452998	3
	KEGG PATHWAY	map00010	Glycolysis / Gluconeogenesis	0.326581526	6
	KEGG PATHWAY	map00906	Carotenoid biosynthesis	0.32805724	3
	KEGG PATHWAY	map00053	Ascorbate and aldarate metabolism	0.32816468	3
	KEGG PATHWAY	map00340	Histidine metabolism	0.334162683	2
	KEGG PATHWAY	map00510	N-Glycan biosynthesis	0.34840724	4
	KEGG PATHWAY	map00480	Glutathione metabolism	0.365173991	4
	KEGG PATHWAY	map00230	Purine metabolism	0.371794196	6
	KEGG PATHWAY	map00270	Cysteine and methionine metabolism	0.382254934	4
	KEGG PATHWAY	map04626	Plant-pathogen interaction	0.387461923	6
	KEGG PATHWAY	map00902	Monoterpenoid biosynthesis	0.407251015	2
C	KEGG PATHWAY	map00940	Phenylpropanoid biosynthesis	0.00843216	22
	KEGG PATHWAY	map03410	Base excision repair	0.187154265	8
	KEGG PATHWAY	map03030	DNA replication	0.202427571	9
	KEGG PATHWAY	map00945	Stilbenoid, diarylheptanoid and gingerol biosynthesis	0.521610593	4
	KEGG PATHWAY	map00531	Glycosaminoglycan degradation	0.643595603	5
	KEGG PATHWAY	map03420	Nucleotide excision repair	0.75972438	8

E

KEGG PATHWAY	map00630	Glyoxylate and dicarboxylate metabolism	0.999317034	1
KEGG PATHWAY	map03010	Ribosome	1	31
KEGG PATHWAY	map05226	Gastric cancer	1	7
KEGG PATHWAY	map03430	Mismatch repair	1	5
KEGG PATHWAY	map03060	Protein export	1	5
KEGG PATHWAY	map03022	Basal transcription factors	1	5
KEGG PATHWAY	map00604	Glycosphingolipid biosynthesis - ganglio series	1	2
KEGG PATHWAY	map02010	ABC transporters	1	8
KEGG PATHWAY	map00514	Other types of O-glycan biosynthesis	1	3
KEGG PATHWAY	map00999	Biosynthesis of various secondary metabolites - part 1	1	1
KEGG PATHWAY	map04146	Peroxisome	1	11
KEGG PATHWAY	map00380	Tryptophan metabolism	1	5
KEGG PATHWAY	map00061	Fatty acid biosynthesis	1	6
KEGG PATHWAY	map00941	Flavonoid biosynthesis	1	5
KEGG PATHWAY	map00520	Amino sugar and nucleotide sugar metabolism	3.25E-05	30
KEGG PATHWAY	map04075	Plant hormone signal transduction	0.000174622	31
KEGG PATHWAY	map00062	Fatty acid elongation	0.000303332	9
KEGG PATHWAY	map00910	Nitrogen metabolism	0.000639797	10
KEGG PATHWAY	map00100	Steroid biosynthesis	0.001025196	9
KEGG PATHWAY	map00073	Cutin, suberine and wax biosynthesis	0.006373763	6
KEGG PATHWAY	map00514	Other types of O-glycan biosynthesis	0.021178511	6
KEGG PATHWAY	map00515	Mannose type O-glycan biosynthesis	0.024085969	2
KEGG PATHWAY	map00940	Phenylpropanoid biosynthesis	0.059250453	17
KEGG PATHWAY	map00460	Cyanoamino acid metabolism	0.061780949	9
KEGG PATHWAY	map00051	Fructose and mannose metabolism	0.064355265	11

F

KEGG PATHWAY	map00909	Sesquiterpenoid and triterpenoid biosynthesis	0.136013894	4
KEGG PATHWAY	map00500	Starch and sucrose metabolism	0.13749929	16
KEGG PATHWAY	map00600	Sphingolipid metabolism	0.382237377	4
KEGG PATHWAY	map04130	SNARE interactions in vesicular transport	0.388566045	5
KEGG PATHWAY	map00250	Alanine, aspartate and glutamate metabolism	0.393241078	7
KEGG PATHWAY	map00620	Pyruvate metabolism	0.39998455	11
KEGG PATHWAY	map00901	Indole alkaloid biosynthesis	0.470900944	2
KEGG PATHWAY	map00010	Glycolysis / Gluconeogenesis	0.904616306	13
KEGG PATHWAY	map00564	Glycerophospholipid metabolism	0.94536588	8
KEGG PATHWAY	map00480	Glutathione metabolism	0.447551213	6
KEGG PATHWAY	map04927	Cortisol synthesis and secretion	0.474896715	1
KEGG PATHWAY	map00640	Propanoate metabolism	0.502184082	4
KEGG PATHWAY	map00280	Valine, leucine and isoleucine degradation	0.508915055	4
KEGG PATHWAY	map05225	Hepatocellular carcinoma	0.529323546	5
KEGG PATHWAY	map00620	Pyruvate metabolism	0.568228956	5
KEGG PATHWAY	map01040	Biosynthesis of unsaturated fatty acids	0.576361618	3
KEGG PATHWAY	map00130	Ubiquinone and other terpenoid-quinone biosynthesis	0.578586351	3
KEGG PATHWAY	map04928	Parathyroid hormone synthesis, secretion and action	0.589975978	2
KEGG PATHWAY	map00564	Glycerophospholipid metabolism	0.59069041	5
KEGG PATHWAY	map00590	Arachidonic acid metabolism	0.595883514	2
KEGG PATHWAY	map02010	ABC transporters	0.600362118	4
KEGG PATHWAY	map00260	Glycine, serine and threonine metabolism	0.615786182	6

G

KEGG PATHWAY	map00360	Phenylalanine metabolism	0.621371044	3
KEGG PATHWAY	map00660	C5-Branched dibasic acid metabolism	0.67086073	1
KEGG PATHWAY	map00100	Steroid biosynthesis	0.687659768	2
KEGG PATHWAY	map00902	Monoterpenoid biosynthesis	0.696410347	2
KEGG PATHWAY	map00010	Glycolysis / Gluconeogenesis	0.717509219	6
KEGG PATHWAY	map04146	Peroxisome	0.729571166	5
KEGG PATHWAY	map00052	Galactose metabolism	0.750654005	4
KEGG PATHWAY	map00130	Ubiquinone and other terpenoid-quinone biosynthesis	0.141292054	6
KEGG PATHWAY	map04928	Parathyroid hormone synthesis, secretion and action	0.177780856	4
KEGG PATHWAY	map00945	Stilbenoid, diarylheptanoid and gingerol biosynthesis	0.340173171	3
KEGG PATHWAY	map00520	Amino sugar and nucleotide sugar metabolism	0.374490033	11
KEGG PATHWAY	map03430	Mismatch repair	0.480319235	4
KEGG PATHWAY	map00360	Phenylalanine metabolism	0.693093842	4
KEGG PATHWAY	map03030	DNA replication	0.709128062	4
KEGG PATHWAY	map00430	Taurine and hypotaurine metabolism	0.758381749	2
KEGG PATHWAY	map05167	Kaposi sarcoma-associated herpesvirus infection	0.773051387	4
KEGG PATHWAY	map00965	Betalain biosynthesis	0.792068089	1
KEGG PATHWAY	map04934	Cushing syndrome	0.792111681	1
KEGG PATHWAY	map00270	Cysteine and methionine metabolism	0.799276886	4
KEGG PATHWAY	map01040	Biosynthesis of unsaturated fatty acids	0.808952766	2
KEGG PATHWAY	map04016	MAPK signaling pathway - plant	0.817538726	5
KEGG PATHWAY	map04625	C-type lectin receptor signaling pathway	0.832924524	1
KEGG PATHWAY	map00908	Zeatin biosynthesis	0.839916615	1

KEGG PATHWAY	map03020	RNA polymerase	0.842079234	3
KEGG PATHWAY	map00785	Lipoic acid metabolism	0.84212239	1
KEGG PATHWAY	map00909	Sesquiterpenoid and triterpenoid biosynthesis	0.844232364	1
KEGG PATHWAY	map00940	Phenylpropanoid biosynthesis	0.844632661	8
