

Table S2 Marker genes for identifying cell types in ornamental plants.

Species	Tissue	Cell types	Marker genes	Description	Author [Ref.]
<i>Amygdalus persica</i>	flower buds	Stamen and filament	Prupe.1G152300	Probable aquaporin NIP7-1	Zhao et al.[1]
			Prupe.4G126600	(E,E)-alpha-farnesene synthase	
		Style	Prupe.5G232600	WUSCHEL-related homeobox 1	
			Prupe.3G284800	2-methylene-furan-3-one reductase	
		Sepal	Prupe.1G497800	GDSL-like Lipase	
			Prupe.2G295700	Cytochrome P450	
		Petal	Prupe.6G257500	WRKY DNA-binding protein 49	
<i>Camptotheca acuminata</i>	shoot apices and leaves	Mesophyll cells	gene-CSD56_pgp001	50S ribosomal protein L2-A, chloroplastic	Wang et al.[2]
			gene-CSD56_pgp065	Photosystem I P700 chlorophyll a apoprotein A2	
			gene-CSD56_pgp025	30S ribosomal protein S3, chloroplastic	
			gene-CSD56_pgp063	Photosystem I assembly protein Ycf3	
			Cac0016136.1	Carbonic anhydrase, chloroplastic	
			Cac0005810.1	Cytochrome b6-f complex iron-sulfur subunit, chloroplastic	
		Epidermal cells	Cac0004961.1	Homeobox-leucine zipper protein PROTODERMAL FACTOR 2	
			Cac0008322.1	3-ketoacyl-CoA synthase 10	
			Cac0022301.1	Very-long-chain aldehyde decarbonylase CER1	
			Cac0022972.1	Homeobox-leucine zipper protein ROC2	
			Cac0030130.1	CASP-like protein 2A1	
			Cac0022435.1	Very-long-chain aldehyde decarbonylase CER3	
			Cac0028886.2	Homeobox-leucine zipper protein GLABRA 2	
		Vascular cells	Cac0001865.1	Leucine-rich repeat receptor-like protein kinase TDR	
			Cac0003586.2	Callose synthase 7	
			Cac0020215.1	Thermospermine synthase ACAULIS5	
			Cac0007447.1	Protein NRT1/ PTR FAMILY 1.2	
			Cac0011890.1	Cysteine protease XCP1	
			Cac0003474.1	Thermospermine synthase ACAULIS5	
			Cac0023757.1	Auxin transporter-like protein 5	
			Cac0009688.1	FT-interacting protein 1	
			Cac0021118.1	Leucine-rich repeat receptor-like serine/threonine-protein kinase BAM3	

		Proliferating cells	Cac0021674.1	Histone H4	
			Cac0017124.1	Probable histone H2B.1	
			Cac0029360.1	Probable histone H2A.1	
			Cac0009025.1	Histone H4	
			Cac0019264.1	Probable histone H2A.5	
		Central zone	Cac0026291.1	Protein argonaute 5	
			Cac0003425.1	Probable helicase MAGATAMA 3	
		Shoot apical meristem	Cac0017149.1	Homeobox-leucine zipper protein ATHB-15	
			Cac0017976.1	Protein argonaute 10	
			Cac0007411.1		
			Cac0000069.1		
		Peripheral zone	Cac0006624.1	3-ketoacyl-CoA synthase 6	
			Cac0028401.1	Protein argonaute 10	
	leaves	Mesophyll cells	EVM0005631	ATP synthase subunit a	Sun et al.[3]
			EVM0003293	Photosystem II reaction center protein Z	
			EVM0003007	Ribulose biphosphate carboxylase large chain	
			EVM0004596	ATP synthase subunit b	
			EVM0012653	Photosystem II CP47 reaction center protein	
			EVM0011613	Ribulose biphosphate carboxylase small subunit 2B	
			EVM0013845	Chlorophyll a-b binding protein 2.1	
			EVM0017264	Cytochrome b6-f complex iron-sulfur subunit	
			EVM0030212	Beta carbonic anhydrase 1	
			EVM0006721	Ribulose biphosphate carboxylase/oxygenase activase 2	
		Idioblast cells	EVM0009000	Deacetylvindoline O-acetyltransferase	
			EVM0034553	Deacetoxyvindoline 4-hydroxylase	
			EVM0025879	Dehydrin Rab18	
		Internal phloem-associated parenchyma	EVM0006370	Geraniol synthase	
			EVM0025655	Geraniol 8-hydroxylase	
			EVM0013196	Salicylic acid-binding protein 2	
		Epidermal cells	EVM0029598	Homeobox-leucine zipper protein MERISTEM L1	
			EVM0034768	Homeobox-leucine zipper protein HDG5	
			EVM0026652	Non-specific lipid-transfer protein 2	
			EVM0009371	Cytochrome P450	
			EVM0025066	Very-long-chain aldehyde decarbonylase CER3	
			EVM0012121	Cytochrome P450 77A3	
		Guard cells	EVM0017755	Transcription factor FAMA	
			EVM0031057	Syntaxin-related protein KNOLLE	
			EVM0033625	Kinesin-like protein KIN-5C	

Catharanthus roseus	leaves	Proliferating cells	EVM0004978	Cell division control protein 2 homolog D	
			EVM0009632	Histone H3.2	
			EVM0019115	Histone H2A	
		Vascular cells	EVM0020471	Sucrose transport protein SUC2	
			EVM0033622	Dof zinc finger protein DOF2.1	
			EVM0001919	Myb family transcription factor APL	
			EVM0034564	Pathogenesis-related protein STH-2	
			EVM0006293		
		Mesophyll	CRO_01G002860	Like SEX4	
			CRO_04G022750	Photosystem II light harvesting complex gene 2.1	
			CRO_03G015510	Light-harvesting chlorophyll B-binding protein	
			CRO_08G000160	Light harvesting complex of photosystem II	
			CRO_04G027610	Light-harvesting chlorophyll-protein complex I subunit A4	
			CRO_03G024120	Light harvesting complex photosystem II subunit	
			CRO_02G029000	Photosystem I light harvesting complex gene	
		Epidermis	CRO_04G032540	3-ketoacyl-CoA synthase	
			CRO_06G026070	Myb domain protein	
			CRO_05G019570	Hypothetical protein	
		Guard cells	CRO_06G007040	Basic helix-loop-helix (bHLH) DNA-binding superfamily protein	
		Vasculature	CRO_02G021880	Basic helix-loop-helix (bHLH) DNA-binding superfamily protein	
			CRO_01G030870	Basic helix-loop-helix (bHLH) DNA-binding superfamily protein	
			CRO_07G006930	WUSCHEL related homeobox	
			CRO_06G015830	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	

			CRO_01G029560	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	Li et al.[4]
			CRO_05G004470	Homeodomain-like superfamily protein	
			CRO_01G021080	Sucrose-proton symporter	
		Ploem CC	CRO_02G029480	Senescence-associated gene	
		Internal phloem-associated parenchyma	CRO_03G004950	Cytochrome P450, family 76, subfamily G, polypeptide	
			CRO_03G018360	Cytochrome P450, family 72, subfamily A, polypeptide	
		Idioblast	CRO_06G013360	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	
			CRO_02G001090	HXXXD-type acyl-transferase family protein	
	roots	Meristem	CRO_03G014370	GRAS family transcription factor	
			CRO_01G001550	Integrase-type DNA-binding superfamily protein	
			CRO_05G008350	Integrase-type DNA-binding superfamily protein	
			CRO_06G016450	Integrase-type DNA-binding superfamily protein	
			CRO_02G019190	GRAS family transcription factor	
		Root cap	CRO_07G004780	Organic cation/carnitine transporter	
			CRO_06G009680	Root cap 1 (RCP1)	
			CRO_06G020680	Dual specificity protein phosphatase (DsPTP1) family protein	
		Endodermis/cortex	CRO_08G007220	Protein kinase superfamily protein	
			CRO_07G009480	Eukaryotic aspartyl protease family protein	
		Attrichoblast	CRO_03G000120	WRKY family transcription factor family protein	

		Anticodon	CRO_06G000190	HD-ZIP IV family of homeobox-leucine zipper protein with lipid-binding START domain	
		Stele	CRO_01G021080	Sucrose-proton symporter	
		Stele/phloem	CRO_07G008710	Sucrose transporter	
			CRO_05G004470	Homeodomain-like superfamily protein	
		Stele/xylem	CRO_08G029490	COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family	
<i>Dendrobium devonianum</i>	flower buds	Epidermal cell	<i>DCR</i>	DEFECTIVE IN CUTICULAR RIDGES	Wang et al.[5]
			<i>GSTF1</i>	GLUTATHIONE S-TRANSFERASE F SUBUNIT 1	
			<i>LACS1/2</i>	LONG-CHAIN ACYL-COA SYNTHETASE 1/2	
			<i>PDF1</i>	PROTODERMAL FACTOR 1	
			<i>FDH</i>	FIDDLEHEAD	
			<i>KCS4</i>	3-KETOACYL-COA SYNTHASE 4	
		Vascular bundle	<i>PIN1C</i>	PIN-FORMED 1C	
			<i>THA2</i>	THREONINE ALDOLASE 2	
			<i>EXL2</i>	EXORDIUM-like 2	
		Mesophyll cell	<i>RBCS1</i>	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL SUBUNIT 1	
			<i>LHCAA</i>	LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM I 4	
			<i>LHCB3</i>	LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 3	
			<i>CAB40</i>	CHLOROPHYLL A/B BINDING PROTEIN 40	
		Xylem	<i>LAX2</i>	LIKE AUXIN RESISTANT 2	
			<i>PHO1</i>	PHOSPHATE 1	
			<i>WAT1</i>	WALLS ARE THIN 1	
		Phloem	<i>WOX8</i>	WUSCHEL-RELATED HOMEODOMAIN 8	
			<i>HSP18</i>	HEAT SHOCK PROTEIN 18	
			<i>PP2A15</i>	PHLOEM PROTEIN 2-LIKE A15	
		Ovule	<i>SPT</i>	SPATULA	
			<i>AG2</i>	AGAMOUS 2	
		Anther	<i>CYP704B1</i>	CYTOCHROME P450 704B1	
			<i>CYP703A3</i>	CYTOCHROME P450 703A3	
			<i>PKSA</i>	POLYKETIDE SYNTHASE A	
			<i>TKPR</i>	TETRAKETIDE α -PYRONE REDUCTASE	

		Guard cell	<i>MPK10</i>	MITOGEN-ACTIVATED PROTEIN KINASE 10	
			<i>OST1A</i>	OPEN STOMATA 1A	
		Proliferating cell	<i>AUR1</i>	AURORA KINASE 1	
			<i>CDKB2-1</i>	CYCLIN-DEPENDENT KINASE B2-1	
			<i>CYC2-1</i>	CYCLIN 2-1	
			<i>CYCB2-4</i>	CYCLIN B2-4	
		Trichome	<i>GL1</i>	GLABRA1	
			<i>GL3</i>	GLABRA3	
<i>Euryale ferox</i>	leaves	Epidermis cells	EF07G016500	Major extracellular endoglucanase	Liu et al.[6]
			EF27G002500	Very-long-chain aldehyde decarboxylase CER3-like	
			EF20G006120	3-ketoacyl-CoA synthase 6	
			EF21G006740	3-ketoacyl-CoA synthase 10	
			EF15G002970	Transcription factor MUTE isoform X1	
			EF11G006580	Transcription factor SPEECHLESS	
			EF18G008130	Protodermal factor 1-like	
		Mesophyll cells	EF02G005690	Homeobox-leucine zipper protein	
			EF09G011360	Chlorophyll a-b binding protein CP29.2, chloroplastic-like	
			EF18G003800	Photosystem I subunit O	
			EF27G002540	Fructose-bisphosphate aldolase 1, chloroplastic-like	
			EF04G013650	Chlorophyll a-b binding protein CP24 10B, chloroplastic	
			EF13G000900	ACT domain-containing protein ACR11	
			EF21G006480	Photosystem I chlorophyll a/b-binding protein 6, chloroplastic isoform X2	
			EF08G001770	Axial regulator YABBY 5-like	
		Proliferating cells	EF07G002500	LOB domain-containing protein 38	
			EF11G003850	Auxin response factor 19-like isoform X1	
		Bundle sheath cells	EF07G010390	Protein EXORDIUM-like	
			EF23G005130	3-ketoacyl-CoA synthase 11-like	
		Xylem cells	EF02G012090	Homeobox-leucine zipper protein ATHB-15-like	
			EF12G010760	Thermospermine synthase ACAULIS5-like	
		Phloem cells	EF02G014760	NAC transcription factor 56-like	
			EF19G003830	bZIP transcription factor RISBZ5-like isoform X1	
		Procambium cells	EF04G002250	Histone H2A.6	
			EF21G005580	Histone H2A	
			EF29G009470	Kinesin-related protein	
			EF15G005430	Cyclin-A1-4-like	
		Hydathode cells	EF23G009790	Endochitinase EP3-like	
			Lb1G03631	Probable WRKY transcription factor 41	

<i>Limonium bicolor</i>	young leaves	Xylem cells	Lb3G17142	NEP1-interacting protein-like 2	Zhao et al.[7]
			Lb5G27540	Sodium/hydrogen exchanger 7	
			Lb2G12446	Receptor-like protein kinase HSL1	
			Lb5G27930	Receptor-like cytochrome serine/threonine-protein kinase RBK1	
		Vascular tissue cells	Lb1G07587	Flavin-containing monooxygenase FMO GS-OX5	
			Lb4G21869	Protein ZINC INDUCED FACILITATOR-LIKE 1	
			Lb2G09311	Glutathione S-transferase U8	
			Lb1G01422	Acidic leucine-rich nuclear phosphoprotein 32-related protein	
			Lb2G11263	Omega-hydroxypalmitate O-feruloyl transferase	
		Tracheid cells	Lb0G37535	Biotin carboxyl carrier protein of acetyl-CoA carboxylase 1, chloroplastic	
			Lb1G00338	Beta-D-xylanase 1	
			Lb1G01967	COBRA-like protein 4	
			Lb1G03387	Sulfotransferase 17	
			Lb1G03593	Xylem cysteine proteinase 2	
		Sieve cells and companion cells	Lb4G22849	Nuclear transport factor 2	
			Lb0G37360	Desiccation-related protein At2g46140	
			Lb5G29244	Early nodulin-like protein 2	
			Lb6G30362	HVA22-like protein f	
			Lb1G06503	Probable transmembrane ascorbate ferrireductase 3	
		Protoderm cells	Lb0G37216	Quercetin 3-O-methyltransferase 1	
			Lb0G37630	Golgi SNAP receptor complex member 1-2	
			Lb0G38349	Kinesin-1	
			Lb1G00233	GDSL esterase/lipase At5g45670	
			Lb1G00320	Cyclin-dependent kinases regulatory subunit 1	
		Promeristem cells	Lb3G15684	Ubiquitin-conjugating enzyme E2 20	
			Lb3G17660	Probable aquaporin PIP2-8	
			Lb4G26317	Serine/threonine-protein kinase Aurora-1	
			Lb5G27754	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase, chloroplastic	
			Lb2G11957	CDT1-like protein a, chloroplastic	
		Pavement cells	Lb6G32080	Protein HOTHEAD	
			Lb6G30031	Transcription factor GLABRA 3	
			Lb3G17987	Transcription factor MYB98	
			Lb2G13956	3-ketoacyl-CoA synthase 13	
			Lb5G27781	Transcription factor GLABRA 3	
			Lb2G13792	Receptor protein kinase CLAVATA1	
			Lb2G11669	Transcription repressor MYB4	

		Mesophyll cells	Lb1G03950	BAHD acyltransferase DCR	
			Lb1G01913	3-ketoacyl-CoA synthase 5	
			Lb0G37616	Desiccation-related protein At2g46140	
			Lb0G37630	Golgi SNAP receptor complex member 1-2	
			Lb1G00835	Cytokinin rib ide 5'-monophate ph phoribohydrolase LOG3	
			Lb1G06336	Peptide methionine sulfoxide reductase B2, chloroplastic	
			Lb2G09750	Heat stress transcription factor A-3	
			Lb2G12349	In itol transporter 4	
			Lb3G21033	Histone-lysine N-methyltransferase ATXR6	
			Lb1G01893	Ran-binding protein 1 homolog b	
<i>Phalaenopsis</i>	inflorescences	Inflorescence meristem	PAXXG117100		Liu et al.[8]
			PAXXG054350	Auxin.perception and signal transduction.transcriptional repressor (IAA/AUX)	
			PAXXG051950	AP2/ERF transcription factor superfamily.transcription factor (AP2)	
		Floral meristem	PAXXG086750	RNA-directed DNA methylation (RdDM) pathway.siRNA-integrating factor (AGO)	
			PAXXG345890	Homologous to AtLFY related to expression regulation of AP3 family genes	
		Tepal	PAXXG301780	Transcription factor (MADS/AGL)	
			PAXXG046700	Fatty acid desaturation.methyl-end desaturation.delta-12/delta-15 fatty acid desaturase (FAD2/3/6-8)	
			PAXXG237140		
		Lip primordium	PAXXG198660	AGL6-like	
		Lip projection	PAXXG226660		
			PAXXG134180		
		Column primordium	PAXXG070630	Transcription factor (MADS/AGL)	
			PAXXG182380	Transcription factor (MADS/AGL)	
		Anther primordium	PAXXG137640	Transcription factor (C3H-ZF)	
		Pollinium		Meiotic double strand break processing.MRE11-RAD50-NBS1 (MRN) complex.component RAD50	
			PAXXG041370		
			PAXXG242310		
		Bract	PAXXG044060	Photosynthesis.photophosphorylation.photosystem II.LHC-II complex.component LHCb1/2/3	
			PAXXG010560	Transcription factor (HD-ZIP IV)	
		Root cap cells	PH02Gene17668	Zinc finger protein	
			PH02Gene46694	Hypothetical protein GQ55_7G094600	
			PH02Gene15627		

<i>Phyllostachys edulis</i>	basal root tips		PH02Gene28681	PREDICTED: glutathione S-transferase F10-like	Cheng et al.[9]
			PH02Gene10382	Hypothetical protein SETIT_9G191400v2	
		Epidermis cells	PH02Gene14566		
			PH02Gene10382	Hypothetical protein SETIT_9G191400v2	
			PH02Gene49134	Germin-like protein 12-2	
			PH02Gene29592	PREDICTED: translationally-controlled tumor protein homolog	
		Ground tissue cells	PH02Gene45651	Hypothetical protein OsI_30931	
			PH02Gene04869	PREDICTED: endoglucanase 7	
			PH02Gene29708	LEC14B protein	
			PH02Gene15920	PREDICTED: uncharacterized protein LOC102716106	
			PH02Gene32823	Putative lipid-transfer protein DIR1	
			PH02Gene17676	Ubiquitin-like	
			PH02Gene02396	60S ribosomal protein L30	
			PH02Gene36445	Uncharacterized protein LOC111473462 isoform X8	
			PH02Gene41070	Hypothetical protein SORBI_3001G039400	
		Meristematic initial cells	PH02Gene04325	Hypothetical protein GQ55_3G103500	
			PH02Gene30509	Phenylalanine ammonia-lyase	
		Epidermal cells	evm.TU.Chr1.1863	Non-specific lipid-transfer protein 1-like	
			evm.TU.Chr2.3078	MLP-like protein 423	
			evm.TU.Chr2.1703	3-ketoacyl-CoA synthase 10	
			evm.TU.Chr2.2101	GDSL esterase/lipase EXL3-like	
			evm.TU.Chr1.1597	Neutral ceramidase	
		Parenchyma cells	evm.TU.Chr5.1087	Beta-D-glucosyl crocetin beta-1,6-glucosyltransferase-like	
			evm.TU.Chr6.2277	Myosin heavy chain kinase	
			evm.TU.Chr5.1923	LRR receptor-like serine/threonine-protein kinase GSO1	
			evm.TU.Chr3.796	Chlorophyll a-b binding protein of LHCII type 1	
			evm.TU.Chr1.2459	LOW QUALITY PROTEIN: ammonium transporter 1 member 2	

<i>Prunus mume</i>	petals	Xylem parenchyma cells	evm.TU.Chr2.2442	MLP-like protein 328	Guo et al.[10]
			evm.TU.Chr1.1295	Zinc finger protein JACKDAW	
			evm.TU.Chr2.4181	Ubiquinol oxidase, mitochondrial-like	
			evm.TU.Chr2.2358	U-box domain-containing protein 21-like	
			evm.TU.Chr2.1628	Probable WRKY transcription factor 40	
		Phloem parenchyma cells	evm.TU.Chr6.827	ABC transporter C family member 14	
			evm.TU.Chr7.2525	Acid beta-fructofuranosidase-like	
			evm.TU.Chr4.2659	AP2/ERF and B3 domain-containing transcription repressor RAV2-like	
			evm.TU.Chr4.2595	Sodium-coupled neutral amino acid transporter 2	
			evm.TU.Chr1.760	Hypothetical protein PRUPE_6G182600	
		Xylem vessels and fibers	evm.TU.Chr2.2367	Vacuolar iron transporter 1	
			evm.TU.Chr6.1883	UDP-glycosyltransferase 74G1-like	
			evm.TU.Chr3.243	Pectinesterase	
			evm.TU.Chr5.2338	Auxin-responsive protein SAUR32	
			evm.TU.Chr2.1828	Chitotriosidase-1-like	
		Sieve element companion cell complex	evm.TU.Chr8.3091	Uncharacterized protein LOC103338947 isoform X1	
			evm.TU.Chr2.3010	CLAVATA3/ESR (CLE)-related protein 25	
			evm.TU.Chr6.874	Monothiol glutaredoxin-S1	
			evm.TU.Chr2.1937	RADIALIS-like 6	

			evm.TU.Chr2.2663	Phosphate	
<i>Rosa hybrida</i>	petals	Epidermis cell	ncbi_112198227	3-ketoacyl-CoA synthase 6	Li et al.[11]
			ncbi_112176978	Long chain acyl-CoA synthetase 4	
			ncbi_112193531	Glycerol-3-phosphate acyltransferase 2	
			ncbi_112194775	Glycerol-3-phosphate 2-O-acyltransferase 6	
		Petal mesophyll cells	ncbi_112166194	Photosystem II 5 kDa protein, chloroplastic	
			ncbi_112170093	Photosystem II reaction center W protein	
			ncbi_112165518	Photosystem I reaction c	
			ncbi_112191879	Light harvesting complex photosystem II	
			ncbi_112168431	Chlorophyll A/B binding protein 3	
		Epidermis/Fra cell	ncbi_112200569	Major strawberry allergen Fra a 1.08	
			ncbi_112201102	Major strawberry allergen Fra a 1.08	
			ncbi_112195753	Major strawberry allergen Fra a 1.08	
			ncbi_112196660	UDP-glucose flavonoid 3-O-glucosyltransferase 3	
			ncbi_112178635	Glutathione S-transferase	
		Bundle sheath	ncbi_112194865	NDR1/HIN1-like protein 10	
			ncbi_112201562	Scarecrow-like protein 13, transcript variant X1	
			ncbi_112203403	Scarecrow-like protein 21	
			ncbi_112187288	Transcription factor MYBS3	
			ncbi_112197799	Sulfate transporter 3.1	
		Guard cell	ncbi_112176172	Aluminum-activated malate transporter 9	
			ncbi_112178591	HMG1/2-like protein, transcript variant X1	
		Phloem	ncbi_112190051	Protein GAST1	
			ncbi_112173221	Lipid-transfer protein DIR1	
			ncbi_112166083	Xyloglucan endotransglucosylase/hydrolase protein 8	
		Xylem	ncbi_112172425	Bidirectional sugar transporter SWEET1	
			ncbi_112188461	Cinnamoyl-CoA reductase 1	
			ncbi_112197670	Xyloglucan endotransglucosylase/hydrolase protein 23	
			ncbi_112173540	Auxin transporter-like protein 3	
	leaves	Leaf mesophyll cell	ctg1820_gene.5	Light harvesting complex photosystem II subunit 6	Zhan et al.[12]
			ctg18492_gene.1	Light harvesting complex photosystem II subunit 6	
		Leaf stomatal complex	ctg9019_gene.2	Duplicated homeodomain-like superfamily protein	
			ctg9664_gene.1	HD-ZIP IV family of homeobox-leucine zipper protein with lipid-binding START domain-containing protein	
		Vascular/procambium cell	ctg3593_gene.5	Leucine-rich repeat protein kinase family protein	
		Phloem	ctg8447_gene.3	ALTERED PHLOEM DEVELOPMENT	

		Leaf guard cell	ctg4435_gene.11	MAP kinase 9	
		Leaf epidermis cell	ctg560_gene.1	ABA responsive trichome formation regulator	
			ctg4709_gene.1	Fatty acid hydroxylase superfamily	
		leaf pavement cell	ctg596_gene.10	Ribulose biphosphate carboxylase small chain 1A	
		Bundle sheath and vein	ctg2007_gene.6	1-Amino-cyclopropane-1-carboxylic acid oxidase 3	
		Photosynthetic cell	ctg1754_gene.5	PHOTOSYSTEM I LIGHT HARVESTING COMPLEX GENE 1 (LHCA1)	
			ctg63_gene.1	PHOTOSYSTEM I LIGHT HARVESTING COMPLEX GENE 2 (LHCA2)	
			ctg11154_gene.1		
			ctg2247_gene.10	PHOTOSYSTEM I LIGHT HARVESTING COMPLEX GENE 3 (LHCA3)	
			ctg388_gene.2	PHOTOSYSTEM I SUBUNIT D-2 (PSAD-2)	
			ctg684_gene.8	PHOTOSYSTEM I SUBUNIT G (PSAG)	
			ctg17766_gene.1	PHOTOSYSTEM I SUBUNIT H2 (PSAH2)	
			ctg1219_gene.1	PHOTOSYSTEM I SUBUNIT K (PSAK)	
			ctg129_gene.2	PHOTOSYSTEM I SUBUNIT L (PSAL)	
			ctg22737_gene.1	PHOTOSYSTEM I SUBUNIT O (PSAO)	
			ctg4975_gene.5	PHOTOSYSTEM II BY (PSBY)	
			ctg8753_gene.1	PHOTOSYSTEM II LIGHT HARVESTING COMPLEX GENE 2.2 (LHCB2.2)	
			ctg3909_gene.38	PHOTOSYSTEM II SUBUNIT O-2 (PSBO2)	
			ctg4222_gene.2	PHOTOSYSTEM II SUBUNIT P-1 (PSBP-1)	
			ctg5584_gene.2	PHOTOSYSTEM II SUBUNIT Q-2 (PSBQ-2)	
			ctg1372_gene.2	PHOTOSYSTEM II SUBUNIT R (PSBR)	
			ctg2632_gene.14	PHOTOSYSTEM II SUBUNIT X (PSBX)	
		Cambium region	ctg4363_gene.1	AINTEGUMENTA (ANT)	
			ctg8286_gene.1	AINTEGUMENTA-LIKE 5 (AIL5)	
			ctg4695_gene.2		
			ctg1335_gene.9	PHLOEM INTERCALATED WITH XYLEM (PXY)	
			ctg3593_gene.5		
			ctg8245_gene.1	PIN-FORMED 1 (PIN1)	
			ctg17881_gene.1		
			ctg3024_gene.11		
			ctg564_gene.13	SCARFACE (SFC)	
			ctg11798_gene.1	WUSCHEL RELATED HOMEBOX 4 (WOX4)	
			ctg1401_gene.10	USUALLY MULTIPLE ACIDS MOVE IN AND OUT TRANSPORTERS 21 (UMAMIT21)	

<i>Taxus mairei</i>	young stems	Phloem parenchyma cell	ctg705_gene.1	USUALLY MULTIPLE ACIDS MOVE IN AND OUT TRANSPORTERS 9 (UMAMIT9)	Yu et al.[13]
			ctg13230_gene.1		
			ctg17202_gene.3		
			ctg7223_gene.1	USUALLY MULTIPLE ACIDS MOVE IN AND OUT TRANSPORTERS 12 (UMAMIT12)	
			ctg5263_gene.1		
			ctg10841_gene.1	USUALLY MULTIPLE ACIDS MOVE IN AND OUT TRANSPORTERS 19 (UMAMIT19)	
			ctg7891_gene.1		
			ctg5233_gene.1		
		Xylem cell (fiber&vessel)	ctg4041_gene.2	USUALLY MULTIPLE ACIDS MOVE IN AND OUT TRANSPORTERS 22 (UMAMIT22)	
			ctg6840_gene.1	MYB DOMAIN PROTEIN 83 (MYB83)	
			ctg2410_gene.2	MYB DOMAIN PROTEIN 46 (MYB46)	
			ctg5376_gene.4	KNOTTED-LIKE HOMEBOX OF ARABIDOPSIS THALIANA 7 (KNAT7)	
			ctg10451_gene.2	LACCASE 17 (LAC17)	
			ctg10451_gene.5		
			ctg18102_gene.2		
			ctg2497_gene.9		
			ctg2497_gene.4		
			ctg2497_gene.6		
			ctg2497_gene.12		
			ctg501_gene.11		
			ctg501_gene.14	IRREGULAR XYLEM 12 (IRX12)	
			ctg501_gene.11		
			ctg10628_gene.2		
			ctg2497_gene.6		
			ctg2497_gene.4		
			ctg2497_gene.9		
			ctg501_gene.10		
			ctg2497_gene.12		
			ctg501_gene.12		
			ctg15518_gene.1	IRX3	
			ctg1570_gene.4		
			ctg3909_gene.31		
			ctg1911_gene.13	IRX5	

			ctg358_gene.7	
			ctg9749_gene.3	
			ctg3654_gene.4	IRREGULAR XYLEM 1 (IRX1)
			ctg14378_gene.1	IRREGULAR XYLEM 9 (IRX9)
			ctg307_gene.13	IRREGULAR XYLEM 6 (IRX6)
			ctg608_gene.1	
			ctg2674_gene.5	
			ctg5118_gene.1	IRX15-LIKE (IRX15-L)
			ctg773_gene.16	VASCULAR RELATED NAC-DOMAIN PROTEIN 1 (VND1)
			ctg667_gene.2	
			ctg9583_gene.1	NAC DOMAIN CONTAINING PROTEIN 12 (NAC012)
			ctg4371_gene.9	
			ctg4124_gene.2	
			ctg14525_gene.1	ELICITOR-ACTIVATED GENE 3-1 (ELI3-1)
			ctg19005_gene.2	
			ctg21098_gene.1	
		Xylem mother cell	ctg38_gene.16	PttHB8
			ctg12638_gene.1	
			ctg9442_gene.3	
		Phloem mother cell	ctg8351_gene.1	SMAX1-LIKE 5 (SMXL5)
		Endodermal cell	ctg2761_gene.6	NRT1/ PTR FAMILY 3.1 (NPF3.1)
			ctg2761_gene.7	
		Xylem parenchyma cell	ctg14525_gene.1	palCAD7
			ctg19005_gene.2	
			ctg17554_gene.3	
			ctg14525_gene.4	
			ctg17359_gene.1	
			ctg8110_gene.1	ABA REPRESSOR1 (ABR1)
			ctg510_gene.6	
			ctg7698_gene.1	
		Cork cell	ctg18012_gene.3	
			ctg10348_gene.6	ALIPHATIC SUBERIN FERULOYL TRANSFERASE(ASFT)
			ctg12291_gene.1	
			ctg3550_gene.2	
		Epidermal cell	ctg3550_gene.1	
			ctg8332_gene.2	GLABRA 2 (GL2)

		Epidermal cell	ctg5709_gene.2		
		Companion cell	ctg2178_gene.13		
			ctg1436_gene.10		
		Cortex/endodermal cell	ctg735_gene.2	SUCROSE-PROTON SYMPORTER 2 (SUC2)	
			ctg787_gene.9		
		Cortex/endodermis initial cell	ctg1963_gene.2	CYCLIN D6;1 (CYCD6;1)	
			ctg3105_gene.8		
			ctg17233_gene.1		
			ctg10795_gene.3		
			ctg3916_gene.1		
		Sieve element	ctg1793_gene.8	CALLOSE SYNTHASE 7 (CalS7)	
			ctg7963_gene.3		
			ctg5147_gene.1		
			ctg25_gene.22		
			ctg1890_gene.4		
			ctg25_gene.34		
			ctg1793_gene.7		
<i>Tillandsia duratii</i>	leaves	Mesophyll-01	Td13g06080		Lyu et al.[14]
			Td00g23100		
		Mesophyll-02	Td11g12820	Arabinogalactan protein 20	
			Td16g08110		
		Mesophyll-03	Td00g35890		
			Td16g05500	Scarecrow-like protein 33	
		Mesophyll-04	Td12g01380	Jacalin-related lectin 19	
			Td11g03050	AUGMIN subunit 1	
		Trichome-01	Td03g09910		
			Td08g00890	Cytochrome P450 89A2	
		Trichome-02	Td20g02800	Protein BIG GRAIN 1-like B	
			Td03g03810		
		Vascular_m	Td11g12820	Arabinogalactan protein 20	
			Td16g08110		
		Vascular_y	Td13g06080		
			Td05g06150		
		Epidermal cell-y	Td00g20360		
			Td00g27160		
		Epidermal cel-m	Td23g02240	Indole glucosinolate O-methyltransferase 1	
			Td09g01590	Caffeoyl-CoA O-methyltransferase	
		Root cap	Ve07G00627	Fatty acid hydroxylase 1	

<i>Vriesea erythrodactylon</i>	roots	Root cap	Ve09G00600	Hevein-like preproprotein	Lyu et al.[14]
		Meristem-1	Ve12G00575	Mannose/glucose-specific lectin-like	
			Ve12G00574	Protein GOS9-like	
		Meristem-2	Ve06G00146	Dof zinc finger protein DOF4.6-like isoform X1	
			Ve25G00623		
		Endodermis	Ve11G00361		
			Ve01G00560	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin protein	
		Cortex-1	Ve22G00468	Acidic endochitinase-like	
			Ve01G00842	Glucan endo-1,3-beta-glucosidase-like isoform X2	
		Cortex-2	Ve08G00683	Hypothetical protein ACMD2_02874	
			Ve10G00700	Unnamed protein product	
		Cortex-3	Ve06G00592	S-norocclaurine synthase-like	
			Ve12G00404	Mannose-specific lectin-like	
		Cortex-4	Ve0G00005		
			Ve0G00003	Hypothetical protein VNO78_07124	
		Cortex-5	Ve15G00370	Probable lysophospholipase BODYGUARD 2	
			Ve23G00411	Pathogenesis-related protein 1-like	
		Velamen	Ve12G00366	Metallothionein-like protein 4A	
			Ve21G00030	Vacuolar-processing enzyme-like	
	Stele		Ve23G00078	UDP-glucuronic acid decarboxylase 6	
			Ve12G00489	S-adenosylmethionine synthase 3	

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