

**Table S1. Differentially expressed genes with a Log2 fold >1.0.** Green: upregulated genes. Red: downregulated genes. Genes with no differential expression significant (when p>0.01) are indicated with a dash (—).

Gen	Accession	Protein	Na 12h	Pc12h	NaPc 12h	Na 24h	Pc 24h	NaPc 24h
T459_31962	PHT62618.1	(-)camphene/tricyclene synthase, chloroplastic	-9.430	—	-7.681	—	—	—
T459_23877	PHT80291.1	(R,S)-reticuline 7-O-methyltransferase	—	—	—	1.143	—	1.558
T459_30792	PHT80700.1	1-aminocyclopropane-1-carboxylate oxidase	—	—	—	—	-1.589	—
T459_22418	PHT79051.1	1-aminocyclopropane-1-carboxylate oxidase-like protein 12	—	—	—	—	—	1.548
T459_07849	PHT84153.1	1-aminocyclopropane-1-carboxylate oxidase-like protein 3	-1.365	—	-2.275	—	—	-0.596
T459_07844	PHT70956.1	1-aminocyclopropane-1-carboxylate oxidase-like protein 6	-0.630	—	-0.453	-1.408	-1.570	-2.173
T459_35076	PHT86395.1	1-aminocyclopropane-1-carboxylate oxidase 1	-3.635	—	-4.114	—	—	—
T459_19927	PHT63698.1	1-aminocyclopropane-1-carboxylate oxidase 1	-3.368	—	-3.609	—	—	—
T459_05822	PHT87603.1	1-aminocyclopropane-1-carboxylate oxidase 4	-6.780	—	-6.883	—	—	—
T459_25142	PHT94958.1	1-aminocyclopropane-1-carboxylate synthase	—	—	—	—	-6.219	—
T459_00560	PHT77183.1	14 kDa proline-rich protein DC2.15	1.348	—	—	0.653	—	1.174
T459_11007	PHT92318.1	17.4 kDa class III heat shock protein	-1.563	—	-1.734	—	—	—
T459_23181	PHT82934.1	17.5 kDa class I heat shock protein	-3.947	—	-3.952	-2.923	—	-3.902
T459_07500	PHT87552.1	2-alkenal reductase (NADP(+)-dependent)	—	—	—	—	-1.173	—
T459_06445	PHT62495.1	2-hydroxyacyl-CoA lyase	-1.670	—	-1.739	-0.743	0.819	—
T459_29869	PHT78523.1	22.0 kDa class IV heat shock protein	-1.965	—	-1.818	—	—	-2.065
T459_32175	PHT62916.1	24-methylenesterol C-methyltransferase 2	0.704	—	—	—	—	1.178
T459_01627	PHT85223.1	26.5 kDa heat shock protein, mitochondrial	-2.966	—	-3.307	-1.638	—	-2.944
T459_04178	PHT68484.1	3-hydroxy-3-methylglutaryl-coenzyme A reductase 2	-0.755	—	-1.002	—	—	-0.587
T459_03286	PHT63578.1	3-hydroxyisobutyryl-CoA hydrolase-like protein 1, mitochondrial	-0.931	—	-0.749	-0.959	—	-1.069

T459_26846	PHT93380.1	3-ketoacyl-CoA synthase 6	—	—	0.733	1.176	—	1.380
T459_23220	PHT85709.1	30S ribosomal protein S31, chloroplastic	—	—	—	—	-1.131	-0.968
T459_10634	PHT93829.1	4-coumarate-CoA ligase 1	—	—	-0.489	—	0.590	1.152
T459_00968	PHT82466.1	4-coumarate-CoA ligase-like 3	—	—	—	—	1.480	1.011
T459_03221	PHT85771.1	4,5-DOPA dioxygenase extradiol	-1.023	—	-0.794	-0.849	—	-0.854
T459_09385	PHT84484.1	60S ribosomal protein L19	—	—	—	—	-2.292	-0.744
T459_24847	PHT68980.1	8-hydroxyquercetin 8-O-methyltransferase	—	—	—	—	2.759	1.968
T459_24830	PHT79991.1	9-divinyl ether synthase	-3.445	—	-2.707	—	1.743	—
T459_31777	PHT86960.1	9-divinyl ether synthase	-1.960	-1.434	-2.586	-1.727	-1.272	-2.292
T459_31778	PHT79477.1	9-divinyl ether synthase	—	—	-1.770	—	-2.014	-1.968
T459_13672	PHT82638.1	ABC transporter A family member 1	-0.745	—	-1.367	-0.626	—	—
T459_04214	PHT71879.1	ABC transporter B family member 12	—	—	—	—	—	5.399
T459_00886	PHT89123.1	ABC transporter B family member 19	—	—	—	—	1.374	—
T459_32008	PHT65561.1	ABC transporter G family member 11	-1.435	—	-1.454	-1.455	—	-1.376
T459_32009	PHT69904.1	ABC transporter G family member 13	—	—	—	—	-6.594	—
T459_03848	PHT77851.1	ABC transporter G family member 14	—	—	—	—	—	1.046
T459_17544	PHT83542.1	ABC transporter I family member 17	—	—	0.595	—	-1.407	0.957
T459_13057	PHT72549.1	Abscisic acid 8'-hydroxylase 3	-3.879	—	-3.714	—	—	—
T459_06386	PHT71175.1	Abscisic acid and environmental stress-inducible protein TAS14	—	—	—	—	—	-1.546
T459_09526	PHT63415.1	Acidic endochitinase	—	—	—	—	—	2.069
T459_06172	PHT69094.1	Acidic endochitinase pcht28	—	—	—	-1.548	—	-1.976
T459_06173	PHT86239.1	Acidic endochitinase Q	-1.562	—	—	-1.850	—	-2.064
T459_06174	PHT81228.1	Acidic endochitinase Q	—	—	—	—	—	-2.217
T459_20984	PHT81885.1	Actin-related protein 8	-1.609	—	-1.768	-1.172	—	-1.008
T459_33381	PHT79292.1	Adenosylhomocysteinase	-1.030	—	-1.110	-0.532	0.656	—
T459_31286	PHT75836.1	Adenosylhomocysteinase	-0.851	—	-0.831	—	1.157	—
T459_02769	PHT94221.1	Adenylate isopentenyltransferase 5, chloroplastic	—	—	—	—	—	1.201
T459_26440	PHT64320.1	Adenylyl-sulfate kinase 1, chloroplastic	—	—	—	—	—	1.361

T459_28932	PHT70983.1	Allene oxide synthase, chloroplastic	-0.896	—	-1.049	—	—	—
T459_30799	PHT79644.1	Amino acid permease 1	-1.756	—	-1.883	—	1.853	—
T459_05411	PHT62563.1	Aquaporin NIP1-1	—	—	—	—	—	-2.207
T459_15163	PHT63662.1	Aquaporin PIP1-1	—	—	—	—	—	1.878
T459_28400	PHT68034.1	Aquaporin TIP1-2	—	—	—	—	—	2.394
T459_17446	PHT86056.1	Aquaporin TIP2-3	—	—	—	0.851	—	1.531
T459_01418	PHT71685.1	Arginine decarboxylase	-0.972	—	-1.124	—	0.587	—
T459_16555	PHT89340.1	Asparagine synthetase [glutamine-hydrolyzing]	-1.306	—	-1.007	—	1.212	—
T459_05829	PHT92347.1	ATP synthase gamma chain, chloroplastic	—	—	1.182	—	—	—
T459_19615	PHT85908.1	ATP synthase subunit alpha, mitochondrial	—	—	—	—	6.922	—
T459_03987	PHT88192.1	Auxin-responsive protein SAUR32	—	—	—	—	—	2.104
T459_29197	PHT68344.1	Auxin-responsive protein SAUR65	—	—	—	—	-5.553	—
T459_29241	PHT88714.1	Auxin-responsive protein SAUR65	—	—	—	—	-3.565	—
T459_29211	PHT79476.1	Auxin-responsive protein SAUR67	—	—	—	—	-3.423	—
T459_29218	PHT73530.1	Auxin-responsive protein SAUR67	—	—	—	—	-4.603	—
T459_27340	PHT90180.1	Auxin-responsive protein SAUR68	—	—	—	—	-2.334	—
T459_10183	PHT74373.1	Basic blue protein	-1.152	—	-1.201	-1.059	—	-1.013
T459_06785	PHT70992.1	Basic leucine zipper 43	—	1.367	—	—	—	—
T459_30566	PHT85358.1	Beta-amylase	—	—	—	—	—	3.040
T459_00795	PHT70203.1	Beta-amylase 3, chloroplastic	—	—	-1.662	—	—	-1.339
T459_14534	PHT68221.1	Beta-amyrin 28-oxidase	-1.830	—	-2.116	—	—	-0.833
T459_17179	PHT82493.1	Beta-amyrin 28-oxidase	—	—	—	—	3.086	—
T459_24088	PHT63147.1	Beta-amyrin synthase	-3.483	—	-3.499	-2.871	—	-3.647
T459_09971	PHT66581.1	Beta-galactosidase 3	—	—	0.810	—	—	1.070
T459_02484	PHT64678.1	Beta-glucosidase 12	—	—	—	—	—	1.705
T459_02487	PHT62201.1	Beta-glucosidase 24	—	—	—	—	—	1.414
T459_11337	PHT90632.1	Beta-glucosidase 46	—	—	1.203	—	—	—
T459_14130	PHT90814.1	Beta-xylosidase/alpha-L-arabinofuranosidase 2	—	—	1.108	—	—	—

T459_09851	PHT91512.1	Bidirectional sugar transporter SWEET14	—	—	—	—	—	—	1.704
T459_17918	PHT70255.1	Bidirectional sugar transporter SWEET14	—	—	—	—	—	1.467	—
T459_09849	PHT87656.1	Bidirectional sugar transporter SWEET15	—	—	—	—	—	1.349	—
T459_34760	PHT77655.1	Bidirectional sugar transporter SWEET1b	—	—	—	—	—	—	1.287
T459_00351	PHT71855.1	Bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1	-0.700	—	—	-1.168	—	—	-1.035
T459_12903	PHT63098.1	Branched-chain-amino-acid aminotransferase 1, mitochondrial	-1.145	—	-1.145	—	—	—	—
T459_15027	PHT63077.1	BTB/POZ domain-containing protein DOT3	—	—	—	—	—	—	5.629
T459_01136	PHT84956.1	BTB/POZ domain-containing protein NPY1	—	—	—	—	—	—	1.365
T459_04044	PHT69858.1	Calcineurin B-like protein 1	-1.730	—	-1.697	—	—	—	—
T459_19832	PHT87661.1	Calcium permeable stress-gated cation channel 1	—	—	—	—	—	—	1.221
T459_04672	PHT84982.1	Calcium uniporter protein 1, mitochondrial	-1.543	—	-1.543	—	—	1.507	—
T459_24555	PHT90240.1	Calmodulin-like protein 5	—	—	—	—	—	—	1.158
T459_33174	PHT78256.1	Calnexin-like protein	—	—	—	—	—	3.136	—
T459_15649	PHT86688.1	Calvin cycle protein CP12-2, chloroplastic	—	—	1.086	—	—	—	—
T459_32834	PHT76310.1	Carbonic anhydrase	-10.522	—	-10.343	-6.327	—	—	-5.338
T459_06784	PHT84040.1	Catechol oxidase B, chloroplastic	-4.747	—	-3.835	—	—	—	-2.663
T459_21942	PHT84212.1	CBL-interacting serine/threonine-protein kinase 5	—	—	—	—	—	—	1.456
T459_14827	PHT87758.1	CBL-interacting serine/threonine-protein kinase 9	—	—	—	—	—	—	-1.236
T459_03722	PHT63456.1	Cellulose synthase-like protein D2	—	—	—	—	—	1.029	—
T459_13403	PHT90434.1	Chaperone protein DNAJ 11, chloroplastic	—	—	—	—	—	1.555	—
T459_15287	PHT96022.1	Chaperone protein DNAJ 20, chloroplastic	-1.011	—	-0.802	—	—	—	—
T459_24634	PHT77229.1	Chloride channel protein CLC-f	—	—	—	—	—	1.024	—
T459_05315	PHT90573.1	Chlorophyll a-b binding protein 3C, chloroplastic	—	—	—	—	—	-4.052	—
T459_05321	PHT93463.1	Chlorophyll a-b binding protein 3C, chloroplastic	—	—	—	—	—	—	2.144

T459_24689	PHT66656.1	Chlorophyll a-b binding protein 7, chloroplastic	—	—	1.606	—	—	—
T459_32045	PHT80829.1	Chlorophyll a-b binding protein CP24 10B, chloroplastic	—	—	2.381	—	—	—
T459_23373	PHT92535.1	Chlorophyll a-b binding protein CP29.1, chloroplastic	—	—	2.517	—	—	—
T459_10452	PHT88929.1	Chlorophyll a-b binding protein P4, chloroplastic	—	—	2.245	—	—	—
T459_19808	PHT85478.1	Chlorophyll a-b binding protein, chloroplastic	—	—	2.288	—	—	—
T459_20683	PHT95367.1	Chlorophyll a-b binding protein, chloroplastic	—	—	1.836	—	—	—
T459_17973	PHT65060.1	Chloroplast stem-loop binding protein of 41 kDa b, chloroplastic	—	—	—	—	—	1.313
T459_14044	PHT87216.1	Coleoptile phototropism protein 1	—	—	6.590	—	—	—
T459_29596	PHT77010.1	Costunolide synthase	-2.525	—	-2.713	-1.204	—	-1.264
T459_05850	PHT81035.1	CRIB domain-containing protein RIC10	—	—	1.187	—	—	—
T459_31457	PHT64152.1	CRIB domain-containing protein RIC10	—	—	—	—	1.316	—
T459_15800	PHT68040.1	CRIB domain-containing protein RIC6	—	—	—	—	—	1.449
T459_13485	PHT68818.1	Cyclin-B2-3	—	—	—	—	—	1.080
T459_06187	PHT90522.1	Cyclin-B2-4	—	—	—	—	—	1.140
T459_26492	PHT67033.1	Cycloartenol-C-24-methyltransferase 1	—	—	—	—	—	1.153
T459_26300	PHT80447.1	Cysteine-rich receptor-like protein kinase 25	—	—	—	-2.770	—	-2.662
T459_05880	PHT92708.1	Cysteine-rich receptor-like protein kinase 26	—	1.175	—	—	—	—
T459_07667	PHT90491.1	Cysteine-rich repeat secretory protein 3	—	—	—	—	—	1.326
T459_07313	PHT72201.1	Cytochrome	—	—	—	—	—	6.010
T459_13858	PHT86021.1	Cytochrome	—	—	—	—	-3.726	—
T459_19946	PHT90565.1	Cytochrome	—	—	-1.856	—	—	—
T459_20294	PHT77932.1	Cytochrome	—	—	—	-2.411	—	-2.841
T459_29792	PHT76846.1	Cytochrome 71D6	—	—	—	—	—	1.587
T459_17087	PHT80133.1	Cytochrome 71D7	-2.007	—	-2.074	-1.723	—	-1.534
T459_17086	PHT77444.1	Cytochrome 71D7	-1.699	—	-1.698	-1.683	—	-1.614
T459_26145	PHT75439.1	Cytochrome 76A2	-7.448	—	-7.288	—	—	—

T459_13159	PHT89622.1	Cytochrome 82A3	—	—	-1.329	—	—	—
T459_09769	PHT82344.1	Cytochrome 89A9	—	—	—	—	1.334	—
T459_10062	PHT77043.1	Cytochrome 94B1	—	—	-6.749	—	—	—
T459_07154	PHT85509.1	Cytochrome 94B3	-0.857	—	-1.089	—	—	-1.243
T459_32673	PHT96156.1	Cytochrome 98A2	-1.144	—	-1.378	—	—	—
T459_32675	PHT92456.1	Cytochrome 98A3	—	—	—	-4.543	—	-4.404
T459_21992	PHT93292.1	Cytochrome and DOMON domain-containing protein	—	—	2.202	—	—	—
T459_21731	PHT70411.1	Cytochrome c oxidase subunit 1	—	—	—	—	-1.098	—
T459_09447	PHT90877.1	Cytochrome P450 71A6	-7.303	—	-6.929	-6.609	—	-6.936
T459_00834	PHT91507.1	Cytochrome P450 87A3-like	—	—	—	—	—	1.859
T459_00823	PHT67028.1	Cytochrome P450 Monooxygenase	1.059	—	—	—	—	1.184
T459_20434	PHT79473.1	CytochromeB1	—	—	—	—	—	1.340
T459_02699	PHT89839.1	Cytokinin dehydrogenase 1	-1.765	—	-1.652	—	—	—
T459_13306	PHT72323.1	Cytokinin dehydrogenase 5	—	—	—	—	1.063	—
T459_24347	PHT62652.1	Cytokinin dehydrogenase 5	—	-1.144	—	—	-0.804	—
T459_00935	PHT63516.1	Cytokinin dehydrogenase 7	—	—	—	—	—	-1.508
T459_19053	PHT73542.1	Defensin-like protein	-2.460	—	-1.339	-2.666	—	-2.154
T459_09275	PHT76477.1	Dehydration-responsive element-binding protein 1A	—	—	1.702	—	—	—
T459_09274	PHT61238.1	Dehydration-responsive element-binding protein 1D	—	—	2.517	—	—	3.326
T459_21559	PHT87705.1	Dehydration-responsive element-binding protein 3	—	—	—	—	—	1.001
T459_04167	PHT80746.1	Dehydrin DHN2	—	—	—	—	—	-3.994
T459_32288	PHT92915.1	Delta(24)-sterol reductase	—	—	—	—	2.189	—
T459_25183	PHT88949.1	Delta(8)-fatty-acid desaturase	—	—	—	—	-2.428	—
T459_31801	PHT93486.1	DeSI-like protein	—	—	—	—	—	1.268
T459_35454	PHT61476.1	Desiccation protectant protein Lea14-like protein	—	—	—	—	2.013	—



T459_26269	PHT64725.1	Exocyst complex component EXO70A1	—	—	—	—	—	6.043
T459_31144	PHT93921.1	Exocyst complex component SEC15A	—	—	—	—	—	1.044
T459_07000	PHT84123.1	Expansin-A14	—	—	—	—	—	-0.686
T459_20643	PHT89319.1	Expansin-A15	—	—	—	—	—	1.241
T459_22940	PHT57596.1	Expansin-A16	—	—	—	—	—	1.548
T459_20160	PHT83412.1	Expansin-B1	—	—	—	—	—	2.270
T459_24891	PHT82022.1	Expansin-B3	—	—	—	—	—	1.751
T459_04037	PHT90981.1	Expansin-like B1	-7.879	—	-8.284	—	—	-5.063
T459_12270	PHT80029.1	F-box protein SKP2A	—	—	—	—	—	-0.448
T459_22663	PHT69034.1	Fasciclin-like arabinogalactan protein 11	1.293	—	1.526	1.063	—	1.359
T459_12404	PHT67101.1	Fructose-1,6-bisphosphatase, cytosolic	—	—	—	—	—	1.520
T459_21289	PHT63287.1	Fruit-specific protein	—	—	—	—	—	1.554
T459_20693	PHT82119.1	G-type lectin S-receptor-like serine/threonine-protein kinase	-1.016	—	-1.427	-0.970	—	-1.002
T459_20705	PHT90713.1	G-type lectin S-receptor-like serine/threonine-protein kinase	-0.945	—	-1.141	—	0.932	—
T459_10867	PHT88670.1	G-type lectin S-receptor-like serine/threonine-protein kinase	—	—	-3.594	—	—	-0.785
T459_20027	PHT64034.1	G-type lectin S-receptor-like serine/threonine-protein kinase	—	—	-1.505	—	—	—
T459_20701	PHT84587.1	G-type lectin S-receptor-like serine/threonine-protein kinase	—	—	-1.553	—	—	-1.203
T459_20703	PHT90644.1	G-type lectin S-receptor-like serine/threonine-protein kinase	—	—	-2.953	—	—	-1.481
T459_28612	PHT92432.1	G-type lectin S-receptor-like serine/threonine-protein kinase	—	—	—	—	—	-1.999
T459_33265	PHT63008.1	G-type lectin S-receptor-like serine/threonine-protein kinase	—	—	—	—	—	-1.393
T459_05748	PHT92016.1	G-type lectin S-receptor-like serine/threonine-protein kinase RKS1	—	—	—	—	2.834	—
T459_32785	PHT73696.1	G2/mitotic-specific cyclin S13-6	—	—	—	—	—	1.167

T459_11510	PHT66755.1	G2/mitotic-specific cyclin-1	—	—	—	—	—	—	1.192
T459_30162	PHT68909.1	GDSL esterase/lipase	—	—	—6.063	—	—	—	—
T459_31003	PHT64945.1	GDSL esterase/lipase EXL1	—	—	—	1.025	—	—	1.051
T459_07814	PHT61944.1	Germin-like protein 12-2	—	—	—	—	—4.646	—	—
T459_24753	PHT95312.1	Gibberellin 2-beta-dioxygenase 1	1.805	—	1.313	—	—	—	1.680
T459_28385	PHT80328.1	Gibberellin 20 oxidase 3	—	—	4.403	—	—	—	—
T459_17693	PHT91499.1	Gibberellin-regulated protein 6	—	—	—	—	—2.520	—	—
T459_32208	PHT66719.1	Gibberellin-regulated protein 8	—	—	—	—	—	—	3.148
T459_01745	PHT87112.1	Glucan endo-1,3-beta-glucosidase	—	—	—1.213	—	—	—	—0.747
T459_13623	PHT85098.1	Glucan endo-1,3-beta-glucosidase, basic vacuolar isoform	—1.796	—	—2.390	—3.711	—	—	—4.697
T459_18086	PHT88129.1	Glucomannan 4-beta-mannosyltransferase 2	—	—	—	—	1.099	—	—
T459_08278	PHT75035.1	Glucose-6-phosphate/phosphate translocator 2, chloroplastic	—	—	—	2.015	—	—	1.513
T459_09938	PHT62319.1	Glutamate decarboxylase	—	—	—	—	1.946	—	—
T459_00062	PHT67073.1	Glutamine-dependent NAD(+) synthetase	—	—	—	—	1.013	—	—
T459_27594	PHT91544.1	Glyceraldehyde-3-phosphate dehydrogenase 3, cytosolic	—	—	—	—	—	—	6.051
T459_19777	PHT64071.1	Guanine nucleotide-binding protein subunit gamma 3	—	—	—	—	—	—	—1.145
T459_14938	PHT79706.1	Heavy metal-associated isoprenylated plant protein 26	—	—	6.441	—	—	—	—
T459_33443	PHT63491.1	Heptahelical transmembrane protein 2	—	—	—	1.005	—	—	1.995
T459_14202	PHT79109.1	High mobility group B protein 7	0.624	—	—	—	—	—	1.076
T459_10131	PHT62034.1	Histone deacetylase 1	—1.405	—	—1.823	—	—	—	—1.515
T459_01563	PHT78937.1	Homeobox-leucine zipper protein ATHB-4	—	—	—	—	—1.199	—	—
T459_08616	PHT71956.1	Homeobox-leucine zipper protein ATHB-8	—	—	—	—	—1.335	—	—
T459_04151	PHT94599.1	Homeobox-leucine zipper protein HOX14	—	—	—	—	—1.041	—	—
T459_11638	PHT84949.1	Homeobox-leucine zipper protein HOX14	—	—	—7.282	—	—	—	—
T459_04774	PHT67370.1	Homeobox-leucine zipper protein HOX21	—	—	—	—	—	—	2.417

T459_25056	PHT63031.1	Homeobox-leucine zipper protein MERISTEM L1	—	—	—	—	5.871	—
T459_09322	PHT62187.1	Homeobox-leucine zipper protein ROC5	—	—	—	—	-1.828	—
T459_34013	PHT86013.1	Homocysteine S-methyltransferase 2	-1.166	—	-1.311	—	—	—
T459_27347	PHT93946.1	HVA22-like protein c	—	—	1.399	—	—	—
T459_09833	PHT76424.1	HVA22-like protein d	—	—	—	—	5.797	—
T459_15225	PHT93726.1	Hydroxyethylthiazole kinase	—	—	—	—	—	-1.138
T459_00714	PHT90802.1	Hypothetical protein, cell division cycle 7-related protein kinase	—	—	—	—	—	1.076
T459_00825	PHT96155.1	Hypothetical protein, Fe2OG dioxygenase domain-containing protein	—	—	—	—	—	1.388
T459_00723	PHT80335.1	Hypothetical protein, Flavin-containing monooxygenase	—	—	-1.215	—	—	—
T459_00503	PHT76405.1	Hypothetical protein, flavonoid 3'-monooxygenase-like	—	—	—	—	—	5.514
T459_00024	PHT76378.1	Hypothetical protein, Glutaredoxin domain-containing protein	—	—	—	—	—	1.265
T459_00278	PHT71282.1	Hypothetical protein, homeobox-leucine zipper protein HDG1-like isoform X1	—	—	—	—	-5.834	—
T459_00647	PHT88436.1	Hypothetical protein, inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase	—	—	-3.194	—	—	—
T459_00340	PHT91671.1	Hypothetical protein, OS07G0672600 protein	—	1.167	—	—	—	—
T459_00973	PHT74840.1	Hypothetical protein, protein kinase domain-containing protein	—	—	—	—	1.630	—
T459_00348	PHT78984.1	Hypothetical protein, protein P21 (DEFENSE)	—	—	—	-5.113	—	-6.637
T459_00549	PHT72833.1	Hypothetical protein, T28K15.14 protein	—	—	—	—	—	1.227
T459_00188	PHT89976.1	Hypothetical proteinial=true	-1.613	—	-1.927	—	—	—

T459_27537	PHT90601.1	IAA-amino acid hydrolase ILR1-like 1	-5.202	—	-4.151	—	—	—
T459_17405	PHT69536.1	Inositol oxygenase 4	-1.498	—	-1.059	-1.484	—	—
T459_26178	PHT65452.1	Kaempferol 3-O-beta-D-galactosyltransferase	—	—	—	—	—	2.726
T459_29309	PHT61566.1	Kinase-interacting protein 1	—	—	—	—	—	1.107
T459_33681	PHT86260.1	Kinesin-4	—	—	—	—	—	1.145
T459_10292	PHT85729.1	Kinesin-like protein KIF19	—	—	—	—	—	1.297
T459_29377	PHT76283.1	Kirola	—	—	—	—	—	1.259
T459_21680	PHT69537.1	L-gulonolactone oxidase 3	1.498	—	1.241	—	—	1.079
T459_25901	PHT77132.1	Laccase-16	1.115	—	—	1.010	—	1.330
T459_12559	PHT80383.1	Laccase-21	-2.098	—	-2.247	-2.127	—	-2.502
T459_20654	PHT93620.1	LanC-like protein GCR2	—	—	—	—	-6.111	—
T459_10498	PHT89006.1	Late embryogenesis abundant protein Dc3	-7.201	—	-7.822	-7.954	—	-7.117
T459_03214	PHT84140.1	Leucine-rich repeat receptor-like protein kinase PXL2	—	—	—	—	—	1.032
T459_26521	PHT69885.1	Lichenase	—	—	—	—	—	-8.943
T459_01453	PHT77518.1	LOB domain-containing protein 18	—	—	—	2.268	—	1.508
T459_18397	PHT92574.1	LOB domain-containing protein 25	1.451	—	1.597	—	—	—
T459_32282	PHT63223.1	LOB domain-containing protein 3	—	—	—	—	2.030	—
T459_30381	PHT87299.1	Lycopene epsilon cyclase, chloroplastic	—	—	—	—	-1.600	—
T459_32698	PHT85225.1	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic	—	—	1.145	—	—	—
T459_10592	PHT85022.1	Major allergen Pru ar 1	—	—	—	—	—	1.899
T459_10041	PHT72486.1	Malate synthase, glyoxysomal	—	—	—	—	1.266	—
T459_11734	PHT62013.1	Mannose-6-phosphate isomerase 2	—	—	—	—	2.000	—
T459_35419	PHT84882.1	Meiotic nuclear division protein 1-like protein	—	—	—	—	-1.999	—
T459_35496	PHT71744.1	Meiotic nuclear division protein 1-like protein	—	—	—	—	-4.036	—
T459_32022	PHT79004.1	Metacaspase-3	—	—	—	—	—	-1.670
T459_10467	PHT89874.1	Mini zinc finger protein 1	—	—	-1.043	—	—	0.904
T459_14922	PHT88724.1	Mitochondrial uncoupling protein 4	—	—	—	—	—	1.239
T459_14793	PHT93086.1	Mitogen-activated protein kinase 4	—	—	—	1.845	—	2.122

T459_04605	PHT67074.1	Mitogen-activated protein kinase kinase kinase YODA	—	—	—	—	—	—1.131	—
T459_20194	PHT84802.1	Mitotic checkpoint serine/threonine-protein kinase BUB1	—	—	—	—	—	—	1.043
T459_27755	PHT76228.1	Mitotic spindle checkpoint protein MAD2	—	—	—	—	—	—	1.545
T459_32119	PHT75623.1	Molybdate transporter 2	—	—	1.022	—	—	—	—
T459_06107	PHT94067.1	Monosaccharide-sensing protein 3	—	—	—	—	—	—	1.511
T459_15759	PHT66239.1	Monothiol glutaredoxin-S11	—	—	—	—	—	1.164	—
T459_15612	PHT73394.1	mRNA-decapping enzyme subunit 2	—	—	—	—	—	1.058	—
T459_28006	PHT75410.1	Myb-related protein	—	—	—	—	—	—	1.007
T459_20053	PHT73202.1	Myb-related protein Myb4	—	—	—	1.989	—	—	1.709
T459_30568	PHT81613.1	NAC domain-containing protein	—	—	1.048	—	—	—	—
T459_17011	PHT94931.1	NAC domain-containing protein 45	—	—	—	—	—	2.301	—
T459_06269	PHT60900.1	NAC domain-containing protein 76	—	—	—	1.054	—	—	1.102
T459_12551	PHT67503.1	NAC domain-containing protein 78	—	—	—	—	—	-0.668	-0.611
T459_33809	PHT67293.1	NAC transcription factor	-1.159	—	-1.478	-0.989	—	—	-1.333
T459_02323	PHT77337.1	NAC transcription factor	-0.422	—	—	—	—	—	-0.441
T459_33284	PHT66214.1	NAC transcription factor 25	—	—	—	—	—	—	-5.595
T459_30097	PHT95980.1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2	—	—	—	—	—	-1.331	—
T459_22050	PHT79119.1	NADPH:quinone oxidoreductase	-0.869	—	-1.179	—	—	—	—
T459_11555	PHT84695.1	NEP1-interacting protein 1	—	—	—	—	—	—	-1.266
T459_14471	PHT90488.1	Ninja-family protein AFP3	—	—	—	—	—	—	-1.459
T459_08353	PHT94331.1	Non-specific lipid-transfer protein	—	—	—	—	—	—	1.723
T459_17590	PHT70871.1	Non-specific lipid-transfer protein 2	—	—	—	—	—	1.596	—
T459_32895	PHT92751.1	Nuclear transcription factor Y subunit B-2	—	—	—	—	—	—	2.122
T459_19389	PHT91278.1	Nudix hydrolase 5	—	—	—	—	—	-1.022	—
T459_12846	PHT63481.1	Oligopeptide transporter 6	—	—	—	—	—	1.325	—
T459_31494	PHT91463.1	Omega-6 fatty acid desaturase, endoplasmic reticulum	—	—	-1.126	—	0.711	—	—

T459_03859	PHT92881.1	orig_transcript_id=gnl WGS:AYRZ T459_0385 9_mrna	—	—	—	—	—	—	5.618
T459_04105	PHT70271.1	orig_transcript_id=gnl WGS:AYRZ T459_0410 5_mrna	—	—	—	—	—	—	1.121
T459_09997	PHT88326.1	orig_transcript_id=gnl WGS:AYRZ T459_0999 7_mrna	—	—	—	—	—	—	-3.174
T459_11138	PHT86973.1	orig_transcript_id=gnl WGS:AYRZ T459_1113 8_mrna	—	—	—	—	—	1.346	—
T459_11293	PHT71244.1	orig_transcript_id=gnl WGS:AYRZ T459_1129 3_mrna	—	—	—	—	—	—	-6.288
T459_12955	PHT91440.1	orig_transcript_id=gnl WGS:AYRZ T459_1295 5_mrna	—	—	—	—	—	—	-1.359
T459_15944	PHT65658.1	orig_transcript_id=gnl WGS:AYRZ T459_1594 4_mrna	—	—	—	—	—	-1.272	—
T459_18340	PHT79574.1	orig_transcript_id=gnl WGS:AYRZ T459_1834 0_mrna	—	—	—	—	—	—	-1.084
T459_18815	PHT85591.1	orig_transcript_id=gnl WGS:AYRZ T459_1881 5_mrna	—	—	—	—	—	—	1.363
T459_19812	PHT74284.1	orig_transcript_id=gnl WGS:AYRZ T459_1981 2_mrna	—	—	—	—	—	—	1.122
T459_22118	PHT63583.1	orig_transcript_id=gnl WGS:AYRZ T459_2211 8_mrna	-4.005	—	-4.619	—	—	—	—
T459_23169	PHT88518.1	orig_transcript_id=gnl WGS:AYRZ T459_2316 9_mrna	—	—	—	—	—	1.419	—
T459_24065	PHT71687.1	orig_transcript_id=gnl WGS:AYRZ T459_2406 5_mrna	-2.253	—	-2.077	-1.653	—	—	-2.395
T459_26049	PHT83827.1	orig_transcript_id=gnl WGS:AYRZ T459_2604 9_mrna	—	—	—	—	—	—	-1.440
T459_32652	PHT92155.1	orig_transcript_id=gnl WGS:AYRZ T459_3265 2_mrna	—	—	—	—	—	1.803	—

T459_34045	PHT84316.1	orig_transcript_id=gnl WGS:AYRZ T459_34045_mrna	—	—	—	—	—	—	1.144
T459_35262	PHT61605.1	orig_transcript_id=gnl WGS:AYRZ T459_35262_mrna	—	—	—	—	—	1.659	—
T459_26747	PHT80854.1	Origin of replication complex subunit 4	—	—	—	—	—	—	1.346
T459_00349	PHT96163.1	Osmotin-like protein OSML13	-5.961	—	-6.510	-5.475	—	—	-6.351
T459_13507	PHT86700.1	Outer envelope pore protein 21, chloroplastic	—	-0.456	—	—	—	-1.163	0.438
T459_09338	PHT81602.1	Oxalate-CoA ligase	-1.346	—	-1.503	—	1.497	—	—
T459_06651	PHT92091.1	Oxygen-evolving enhancer protein 1, chloroplastic	—	—	1.791	—	—	—	—
T459_19506	PHT87964.1	Oxygen-evolving enhancer protein 2, chloroplastic	—	—	1.564	—	—	—	—
T459_05720	PHT72295.1	Oxygen-evolving enhancer protein 3-2, chloroplastic	—	—	1.313	—	—	—	—
T459_00426	PHT87566.1	P69F protein	—	—	—	—	1.130	—	—
T459_33694	PHT82885.1	Pantoate-beta-alanine ligase	—	—	—	—	—	—	-1.041
T459_25695	PHT63714.1	partial=true	-1.029	—	-1.285	—	—	—	-1.129
T459_19675	PHT71058.1	partial=true	-0.864	—	-1.075	-1.022	-1.293	-1.636	—
T459_13097	PHT71025.1	Patatin-like protein 2	-2.131	—	-2.130	—	—	—	—
T459_06695	PHT63804.1	Patatin-like protein 2	-1.941	—	-2.333	—	—	—	—
T459_01133	PHT82291.1	Patatin-T5	-1.670	—	-1.532	—	—	—	—
T459_22749	PHT73937.1	Pathogenesis-related protein 1B	—	—	-3.288	-3.026	—	—	-3.949
T459_31889	PHT86635.1	Pathogenesis-related protein 1B	—	—	1.118	—	—	—	—
T459_22169	PHT92608.1	Pathogenesis-related protein PR-4B	—	—	—	-3.700	—	—	-4.634
T459_31175	PHT85045.1	Pathogenesis-related protein STH-21	—	—	-2.246	—	—	—	-2.187
T459_20808	PHT87069.1	Pectinesterase 2.1	—	—	—	—	1.772	—	—
T459_01056	PHT64695.1	Pentatricopeptide repeat-containing protein, mitochondrial	—	—	—	—	-1.090	—	—
T459_35559	PHT87291.1	Peptidyl-prolyl cis-trans isomerase CYP26-2, chloroplastic	—	—	—	—	-2.423	—	—
T459_33490	PHT86080.1	Peptidyl-prolyl cis-trans isomerase FKBP17-1, chloroplastic	—	—	—	—	—	—	1.513

T459_06392	PHT77598.1	Peroxidase 15	-1.813	—	-1.742	-0.589	0.848	-0.431
T459_31688	PHT69263.1	Peroxidase 21	-1.599	—	-1.590	—	—	—
T459_13424	PHT75441.1	Peroxidase 3	—	—	—	—	—	1.412
T459_19850	PHT89289.1	Peroxidase 39	—	—	—	1.021	—	1.355
T459_33232	PHT66372.1	Peroxidase 4	-3.535	—	-3.322	-2.845	—	-2.947
T459_14811	PHT67048.1	Peroxidase 4	-2.196	—	-2.039	-1.509	—	-1.097
T459_14090	PHT88152.1	Peroxidase 4	-1.179	—	-1.384	-1.437	-1.667	-1.935
T459_14088	PHT74902.1	Peroxidase 4	—	—	-1.742	—	-1.859	-2.580
T459_14089	PHT88464.1	Peroxidase 4	—	—	-1.291	—	-1.517	-2.078
T459_06151	PHT65521.1	Peroxidase 66	1.383	—	1.791	—	1.316	—
T459_09245	PHT64880.1	Peroxidase 66	—	—	—	—	—	1.631
T459_05984	PHT91818.1	Peroxidase 7	—	—	—	—	—	1.358
T459_31719	PHT61362.1	Peroxidase N	—	—	—	—	—	-7.061
T459_00407	PHT77439.1	PGR5-like protein 1A, chloroplastic	—	—	—	—	—	1.948
T459_17535	PHT88042.1	Phosphatidylcholine:diacylglycerol cholinephosphotransferase 1	—	—	—	—	-1.083	—
T459_32715	PHT88506.1	Phosphatidylinositol/phosphatidylcholine transfer protein SFH6	—	—	—	—	—	-5.959
T459_20584	PHT75365.1	Phosphoenolpyruvate carboxylase 2	—	—	—	—	1.313	—
T459_33236	PHT63910.1	Phosphoenolpyruvate carboxylase kinase 1	—	—	—	—	-2.288	—
T459_06848	PHT86196.1	Phosphoenolpyruvate/phosphate translocator 2, chloroplastic	—	—	—	—	2.389	—
T459_22330	PHT65568.1	Phosphoglycerate mutase-like protein AT74	—	—	—	—	1.131	—
T459_05088	PHT84392.1	Phospholipase A1-II 1	-5.234	—	-4.761	-4.433	—	-2.878
T459_03600	PHT94476.1	Phospholipase A1-II 1	—	—	—	—	1.178	—
T459_12216	PHT90078.1	Phosphoribosylformylglycinamide cyclo-ligase	—	—	—	—	-1.487	—
T459_00963	PHT90609.1	Phosphoribulokinase, chloroplastic	—	—	4.703	—	—	—
T459_16774	PHT82204.1	Photosystem I reaction center subunit II, chloroplastic	—	—	1.775	—	—	—

T459_32283	PHT66286.1	Photosystem I reaction center subunit III, chloroplastic	—	—	1.525	—	—	—	-0.940
T459_18456	PHT85589.1	Photosystem I reaction center subunit IV, chloroplastic	—	—	1.881	—	—	—	—
T459_03540	PHT93439.1	Photosystem I reaction center subunit psaK, chloroplastic	—	—	1.984	—	—	—	—
T459_10915	PHT91059.1	Photosystem I reaction center subunit VI, chloroplastic	—	—	2.046	—	—	—	—
T459_18379	PHT87497.1	Photosystem I reaction center subunit XI, chloroplastic	—	—	3.376	—	—	—	—
T459_18050	PHT81385.1	Photosystem I subunit O	—	—	2.848	—	—	—	—
T459_16891	PHT87650.1	Photosystem II 22 kDa protein, chloroplastic	—	—	—	3.968	—	—	2.013
T459_22488	PHT88131.1	Photosystem II reaction center W protein, chloroplastic	—	—	2.050	—	—	—	—
T459_01678	PHT90904.1	Phytoene synthase, chloroplastic	—	—	—	—	—	—	9.331
T459_21172	PHT91719.1	Phytosulfokine receptor 1	—	—	-0.520	—	—	—	1.104
T459_20865	PHT62170.1	Pirin-like protein	-0.957	—	-1.216	—	—	—	-1.261
T459_11820	PHT91040.1	plasmodesmata callose-binding protein 3	—	—	—	—	—	—	1.736
T459_31503	PHT71016.1	Pleiotropic drug resistance protein 1	-6.326	—	-7.394	—	—	—	—
T459_18327	PHT80966.1	Pleiotropic drug resistance protein 12	—	—	—	—	—	—	-1.060
T459_29579	PHT73407.1	Pleiotropic drug resistance protein 2	-2.845	—	-3.575	—	—	—	-2.824
T459_28645	PHT89501.1	Pleiotropic drug resistance protein 4	-3.407	—	-4.235	-1.223	—	—	-2.120
T459_30824	PHT94024.1	Pollen-specific protein SF3	—	—	1.190	—	—	—	—
T459_32172	PHT62359.1	Polyamine transporter PUT1	—	—	—	—	—	1.386	—
T459_02540	PHT85424.1	Polygalacturonase	-2.148	—	-2.280	—	—	—	-2.513
T459_29749	PHT71255.1	Polygalacturonase	—	—	—	—	—	—	2.886
T459_17948	PHT88304.1	Polygalacturonase inhibitor	—	-0.876	—	—	—	-3.885	—
T459_27656	PHT93132.1	Polygalacturonase non-catalytic subunit AroGP3	—	—	—	—	1.489	—	—
T459_04865	PHT77347.1	Polygalacturonase QRT3	—	—	—	—	—	—	1.017
T459_35776	PHT93501.1	Polyneuridine-aldehyde esterase	-1.269	—	-1.105	—	—	—	-1.175

T459_04157	PHT69261.1	Polyol transporter 5	—	—	—	—	1.439	—
T459_06889	PHT64509.1	Protein altered xyloglucan 4-like	—	—	—	—	—	1.246
T459_01421	PHT61110.1	Protein basic pentacysteine4	—	—	—	—	2.047	-0.712
T459_20612	PHT91522.1	Protein cup-shaped cotyledon 2	-7.010	—	-6.346	-6.410	—	—
T459_01344	PHT68885.1	Protein eceriferum 1	—	—	-7.853	—	—	—
T459_24481	PHT68996.1	Protein eceriferum 3	—	—	—	—	—	1.008
T459_12696	PHT90195.1	Protein exordium	1.780	—	1.830	1.121	—	1.034
T459_12692	PHT67595.1	Protein exordium-like 1	1.607	—	1.686	1.523	0.922	1.439
T459_12695	PHT76179.1	Protein exordium-like 1	2.125	—	1.689	1.405	0.944	1.782
T459_12693	PHT80067.1	Protein exordium-like 2	1.911	—	2.425	—	—	—
T459_12691	PHT85997.1	Protein exordium-like 2	—	-1.266	—	0.813	—	0.513
T459_24116	PHT84613.1	Protein kinase pinoid 2	—	—	—	—	-1.090	—
T459_34151	PHT93577.1	Protein light-dependent short hypocotyls 5	—	—	—	—	1.105	—
T459_13941	PHT84110.1	Protein light-dependent short hypocotyls 6	—	—	—	—	1.892	—
T459_00840	PHT66861.1	Protein LSD1	—	—	1.444	—	—	—
T459_18197	PHT88238.1	Protein NRT1/ PTR FAMILY 2.7	—	—	—	—	—	1.627
T459_10228	PHT77105.1	Protein NRT1/ PTR FAMILY 2.9	—	—	—	—	1.955	—
T459_17301	PHT64697.1	Protein NRT1/ PTR FAMILY 5.1	—	—	—	1.304	—	1.095
T459_07683	PHT93604.1	Protein NRT1/ PTR FAMILY 5.2	-1.153	—	-1.601	—	—	—
T459_03151	PHT85015.1	Protein NRT1/ PTR FAMILY 7.3	0.987	-1.530	—	1.094	—	1.498
T459_01481	PHT62480.1	Protein NRT1/ PTR FAMILY 7.3	—	—	—	—	-1.403	—
T459_07112	PHT62864.1	Protein ODORANT1	—	—	—	—	—	1.354
T459_15576	PHT95381.1	Protein PHR1-LIKE 1	—	—	—	—	1.046	—
T459_10911	PHT64158.1	Protein plant cadmium resistance 8	—	—	—	—	—	1.232
T459_33203	PHT63251.1	Protein PMR5	—	—	—	—	—	1.399
T459_07652	PHT77179.1	Protein proton gradient regulation 5, chloroplastic	—	—	—	—	—	1.872

T459_03387	PHT91489.1	Protein QUIRKY	—	—	—	—	—	—	2.239
T459_05495	PHT65642.1	Protein RALF-like 34	—	—	—	—	—	—	1.764
T459_34381	PHT84290.1	Protein reveille 1	-1.840	—	-1.918	—	—	—	-0.984
T459_05942	PHT77242.1	Protein reveille 2	-1.626	—	-1.404	1.005	0.632	0.746	
T459_02260	PHT80240.1	Protein self-pruning	—	—	—	-3.573	—	—	-3.220
T459_03562	PHT88616.1	Protein short-root	—	1.591	—	—	—	—	—
T459_08676	PHT94091.1	Protein strictosidine synthase-like 13	—	—	—	—	—	-1.149	—
T459_00876	PHT78841.1	Protein tornado 2	—	—	1.386	—	—	—	—
T459_21964	PHT84954.1	Protein trichome birefringence-like 25	—	—	—	—	—	—	1.289
T459_23761	PHT80679.1	Protein trichome birefringence-like 31	—	—	1.335	—	—	—	—
T459_24837	PHT62479.1	Protein trichome birefringence-like 43	—	—	—	—	—	—	2.188
T459_22119	PHT89889.1	Protein zinc induced facilitator-like 1	—	—	-3.634	—	—	—	—
T459_17036	PHT75743.1	Proteinase inhibitor PSI-1.2	-9.056	—	-8.852	—	—	—	—
T459_33285	PHT93053.1	Protochlorophyllide reductase, chloroplastic	—	—	4.672	—	—	—	2.184
T459_29465	PHT93483.1	Pumilio-like protein 2	—	—	—	—	—	—	5.689
T459_05258	PHT73041.1	putative 2-oxoglutarate/Fe(II)-dependent dioxygenase	-1.048	—	-1.042	—	—	—	-0.779
T459_11395	PHT70196.1	putative acyl-activating enzyme 5, peroxisomal	—	—	—	—	—	—	1.011
T459_07143	PHT84199.1	putative adenylate kinase 7, mitochondrial	—	—	-1.713	—	—	—	—
T459_20969	PHT66183.1	putative amino acid permease 7	-7.053	—	-6.802	-8.015	—	—	-7.659
T459_23171	PHT74102.1	putative anion transporter 3, chloroplastic	-1.212	—	-1.557	—	—	—	-0.616
T459_16939	PHT84205.1	putative aquaporin TIP-type RB7-5A	—	—	—	1.637	—	—	1.168
T459_12630	PHT73297.1	putative beta-D-xylosidase 7	—	—	—	—	—	—	3.977
T459_10296	PHT79611.1	putative calcium-binding protein CML12	—	—	—	—	—	—	1.171
T459_04072	PHT79732.1	putative calcium-binding protein CML18	—	—	1.019	—	—	—	—
T459_07899	PHT75401.1	putative calcium-transporting ATPase 13, plasma membrane-type	—	—	—	—	—	—	1.410
T459_01424	PHT90094.1	putative carbohydrate esterase	—	—	—	—	—	—	2.109

T459_01425	PHT91654.1	putative carbohydrate esterase	—	—	—	—	—	1.822
T459_01301	PHT89342.1	putative carboxylesterase 8	—	—	—	—	-0.592	2.176
T459_34124	PHT63753.1	putative CCR4-associated factor 1-like protein 11	—	—	—	—	—	-1.002
T459_12487	PHT64691.1	putative choline kinase 1	-0.532	—	-0.481	—	1.041	—
T459_19320	PHT69616.1	putative flavin-containing monooxygenase 1	—	—	-1.169	—	—	—
T459_27491	PHT66262.1	putative galacturonosyltransferase-like 8	—	—	—	—	—	1.074
T459_20467	PHT66301.1	putative glutathione S-transferase	-6.533	—	-6.145	-7.425	—	-7.789
T459_01150	PHT64075.1	putative glycosyltransferase	—	—	—	—	—	1.358
T459_04558	PHT73899.1	putative indole-3-acetic acid-amido synthetase GH3.8	—	—	—	—	—	-6.360
T459_26874	PHT67135.1	putative inorganic phosphate transporter 1-4	—	—	—	—	-1.900	—
T459_13512	PHT70619.1	putative inorganic phosphate transporter 1-9	—	—	—	—	1.570	-0.838
T459_06203	PHT65004.1	putative L-ascorbate peroxidase 3	—	—	—	—	-1.218	—
T459_16516	PHT94045.1	putative leucine-rich repeat receptor-like protein kinase IMK3	—	—	—	—	1.070	—
T459_13934	PHT86853.1	putative low-specificity L-threonine aldolase 1	-1.109	—	-1.562	—	—	—
T459_03489	PHT69865.1	putative mannitol dehydrogenase	—	—	—	—	—	1.810
T459_04401	PHT64067.1	putative mannitol dehydrogenase	—	—	—	—	—	1.450
T459_29287	PHT72525.1	putative mannitol dehydrogenase	—	—	—	1.483	—	2.000
T459_33880	PHT76976.1	putative methylesterase 12, chloroplastic	—	—	—	—	-1.355	—
T459_20033	PHT60964.1	putative NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5, mitochondrial	—	—	—	—	-1.039	—
T459_18447	PHT79974.1	putative pectate lyase 8	—	—	—	—	—	1.878
T459_00597	PHT71450.1	putative pectinesterase 11	—	—	—	—	—	2.014
T459_06419	PHT75537.1	putative pectinesterase 53	—	—	1.769	—	—	—
T459_08239	PHT93001.1	putative pectinesterase/pectinesterase inhibitor 40	—	—	—	—	—	1.489
T459_13528	PHT75509.1	Pyrophosphate-fructose 6-phosphate 1-phototransferase subunit alpha	—	—	—	—	-1.765	1.171

T459_34590	PHT93500.1	Pyrophosphate-energized vacuolar membrane proton pump 1	-2.016	—	-2.124	-0.695	—	-1.076
T459_31839	PHT57611.1	Ras-related protein RABC2a	—	—	—	—	1.122	—
T459_08395	PHT89432.1	Receptor-like cytosolic serine/threonine-protein kinase RBK2	—	—	-1.162	—	—	-0.544
T459_20382	PHT76371.1	Receptor-like protein kinase feronia	—	—	—	—	1.703	—
T459_05752	PHT83059.1	Receptor-like serine/threonine-protein kinase SD1-8	-0.591	—	-1.134	—	0.693	—
T459_35607	PHT90382.1	Regulator of rDNA transcription protein 15	—	—	—	—	-1.661	—
T459_05020	PHT68082.1	Reticuline oxidase-like protein	-2.021	—	-2.672	-1.379	—	-1.971
T459_25501	PHT79451.1	Rhodanese-like domain-containing protein 10	—	—	—	—	-1.539	—
T459_17006	PHT71208.1	Ribose-phosphate pyrophosphokinase 1	—	—	—	—	2.554	—
T459_33149	PHT76672.1	Ribosomal silencing factor RsfS	—	—	—	—	—	1.191
T459_03410	PHT74323.1	Secoisolariciresinol dehydrogenase	—	—	—	—	—	-1.661
T459_03413	PHT71305.1	Secoisolariciresinol dehydrogenase	—	—	—	—	—	1.435
T459_03414	PHT70305.1	Secoisolariciresinol dehydrogenase	—	—	—	—	—	1.540
T459_12956	PHT77290.1	Serine carboxypeptidase-like 17	—	—	—	-1.584	—	-1.612
T459_02606	PHT64722.1	Serine carboxypeptidase-like 40	—	—	-6.263	—	—	—
T459_33719	PHT71258.1	Serine decarboxylase 2	-1.219	—	-1.381	-0.719	—	-0.981
T459_06519	PHT76585.1	Serine hydroxymethyltransferase, mitochondrial	—	—	1.692	—	—	—
T459_33326	PHT75866.1	Serine/threonine-protein kinase	1.042	—	1.340	—	—	—
T459_21390	PHT73387.1	Serine/threonine-protein kinase Aurora-1	—	—	—	—	—	1.390
T459_22828	PHT93301.1	Serine/threonine-protein kinase PBS1	—	—	—	—	1.247	—
T459_31724	PHT76034.1	Serine/threonine-protein kinase SRK2E	—	—	—	—	0.738	-2.158
T459_13125	PHT89115.1	Serpin-ZX	—	—	—	—	-3.253	—
T459_09386	PHT90561.1	Short-chain dehydrogenase TIC 32, chloroplastic	—	—	0.856	—	—	-1.796
T459_22901	PHT95430.1	Short-chain dehydrogenase TIC 32, chloroplastic	—	—	2.228	—	—	—
T459_13456	PHT84396.1	Signal recognition particle 54 kDa protein 2	—	—	—	—	1.621	—

T459_03836	PHT89789.1	Snakin-1	—	—	—	—	—	—	1.398
T459_12179	PHT84877.1	Snakin-2	1.169	—	—	—	—	—	—
T459_19386	PHT82450.1	SNF1-related protein kinase regulatory subunit beta-2	—	—	—	—	—	—	3.214
T459_32910	PHT94866.1	Sodium/hydrogen exchanger 2	—	—	—	—	—	1.169	—
T459_31642	PHT83094.1	Suberization-associated anionic peroxidase	-0.995	—	-1.072	-1.021	—	—	-1.131
T459_05761	PHT79482.1	Suberization-associated anionic peroxidase 2	-2.109	—	-2.109	-1.837	—	—	-1.792
T459_23724	PHT74869.1	Subtilisin-like protease	-0.496	—	-1.041	-0.762	—	—	-0.629
T459_22081	PHT72453.1	Succinate dehydrogenase cytochrome subunit	—	—	—	—	—	-1.240	—
T459_27389	PHT76675.1	Sulfate transporter 1.1	1.157	—	1.131	—	—	—	—
T459_30564	PHT68328.1	Sulfate transporter 1.3	-1.039	—	-1.672	—	—	—	—
T459_00347	PHT88440.1	Thaumatin-like protein	-4.511	—	-4.714	—	—	—	-3.114
T459_06217	PHT62224.1	Thaumatin-like protein 1	1.429	—	1.081	—	—	—	—
T459_05248	PHT89759.1	Thebaine 6-O-demethylase	—	—	—	-1.981	—	—	-2.649
T459_20809	PHT83497.1	Thiamine thiazole synthase, chloroplastic	—	—	1.517	—	—	—	—
T459_22823	PHT95480.1	Thioredoxin-like protein AAED1, chloroplastic	—	—	—	—	—	-1.408	—
T459_29152	PHT78330.1	Toll/interleukin-1 receptor-like protein	—	—	—	—	—	1.412	—
T459_32938	PHT64854.1	Transcription factor ALC	—	—	—	—	—	—	-1.351
T459_31305	PHT73601.1	Transcription factor bHLH49	—	—	—	—	—	—	2.021
T459_09895	PHT87606.1	Transcription factor bHLH74	—	—	—	—	—	—	3.158
T459_10824	PHT67414.1	Transcription factor divaricata	—	—	—	-1.506	—	—	-1.482
T459_14209	PHT92027.1	Transcription factor divaricata	—	—	1.938	—	—	—	—
T459_16404	PHT88775.1	Transcription factor fer-like iron deficiency-induced transcription factor	—	—	—	—	—	—	1.027
T459_06748	PHT81668.1	Transcription factor MYB24	—	—	—	—	—	5.899	—
T459_25035	PHT77243.1	Transcription factor MYB39	-2.433	—	-2.029	-1.678	—	—	-1.994
T459_00888	PHT62525.1	Transcription factor MYB39	—	—	—	—	—	—	1.327
T459_19043	PHT61287.1	Transcription factor MYB46	—	—	—	—	—	—	1.010

T459_02504	PHT82292.1	Transcription factor MYB86	—	—	—	1.105	—	1.354
T459_25133	PHT70581.1	Transcription factor MYC2	-3.685	—	-3.345	-1.671	1.694	—
T459_23838	PHT67642.1	Transcription factor PCF5	—	—	—	—	2.559	—
T459_17717	PHT89931.1	Transcription factor PRE5	1.368	—	—	—	—	1.663
T459_06350	PHT74467.1	Transcription factor Radialis	—	—	2.051	—	—	1.791
T459_23310	PHT67690.1	Transcription repressor OFP11	—	—	—	—	1.043	—
T459_06307	PHT64471.1	Transcription repressor OFP6	—	—	2.018	1.598	—	1.888
T459_26164	PHT76468.1	Trihelix transcription factor PTL	—	—	2.574	—	—	—
T459_25651	PHT87525.1	Tropinone reductase-like protein	—	—	—	—	—	1.168
T459_03794	PHT74464.1	Tryptophan aminotransferase-related protein 2	—	—	—	—	—	1.900
T459_25165	PHT95960.1	Two-component response regulator-like APRR5	—	—	-1.207	—	0.541	—
T459_31139	PHT81725.1	Tyrosine aminotransferase	-1.204	—	-2.018	-0.863	—	-0.860
T459_23603	PHT89327.1	Ubiquinol oxidase 1, mitochondrial	—	—	—	—	—	1.697
T459_33450	PHT77748.1	UDP-glucuronate 4-epimerase 4	—	—	—	—	—	1.345
T459_04049	PHT83901.1	Vesicle-associated protein 2-1	—	—	—	—	—	1.041
T459_19171	PHT70979.1	VQ motif-containing protein 22	—	—	—	-0.837	—	-1.032
T459_12411	PHT79820.1	WAT1-related protein	—	—	2.864	—	—	—
T459_13901	PHT88898.1	WAT1-related protein	—	—	—	—	-1.464	—
T459_14381	PHT63113.1	WAT1-related protein	—	—	2.455	—	—	—
T459_26411	PHT85061.1	WAT1-related protein	—	—	—	—	—	1.026
T459_33109	PHT96169.1	WAT1-related protein	—	—	—	—	—	6.473
T459_33110	PHT81104.1	WAT1-related protein	—	—	—	—	—	1.872
T459_14070	PHT71453.1	Xyloglucan endotransglucosylase/hydrolase 1	—	—	—	—	—	1.204
T459_18704	PHT87203.1	Xyloglucan endotransglucosylase/hydrolase protein 24	—	—	—	—	—	1.337
T459_34848	PHT70771.1	Xyloglucan endotransglucosylase/hydrolase protein 9	—	—	-1.049	—	—	—
T459_08379	PHT88721.1	Zinc finger CCCH domain-containing protein 32	—	—	—	—	1.469	—

T459_24012	PHT94474.1	Zinc finger protein constans-like 9	—	—	—	—	1.560	-0.969
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