

Table S3. A list of up-regulated genes identified by heterologous hybridization of RNA from Brunfelsia flowers (from days 1 and 0) onto potato microarray. Genes were identified as significantly ($P = 0.05$) regulated in at least one of the time points (day 0 or 1) and had a more than 2- fold increase in day 1 versus day 0. The clone name (Systematic name), the mean fold change of day 1 versus day 0 (Time 1 normalized), gene annotation (Annotation) and suggested function (Function) are presented. Suggested functional categories are presented under Systematic name, highlighted in blue. t-test (ANOVA) $p=0.05$ and Benjamini multiple testing correction were performed for identification of significantly regulated genes. Annotations of the regulated genes were based on the potato microarray data (<http://www.tigr.org/tdb/potato/>) and on annotation of Petunia homologues (<http://www.sgn.cornell.edu/>).

Systematic Name	Average fold change (range)	Annotation	Function
Metabolism			
STMEN57	6.232 (3.192 to 14.72)	68418.m06158 ferric reductase-like transmembrane component family protein similar to ferric-chelate	Iron homeostasis/Iron acquisition from soil and metabolism/Electron transport/oxidoreductase/transporter/ in the flower
STMGZ48	4.432 (2.033 to 7.647)	(Q6XP48) UDP-Glc-4-epimerase (EC 5.1.3.2)	Galactose metabolism/ in solanum tuberosum flower
STMJC15	4.048 (1.651 to 9.547)	(Q82001) Tomato invertase inhibitor precursor	Sucrose metabolism-Sucrose transportation from petals to other flower parts/senescence
STMIA83	3.985 (2.167 to 10.32)	(Q6XP48) UDP-Glc-4-epimerase (EC 5.1.3.2)	Galactose metabolism
STMCD65	3.79 (1.382 to 8.976)	(Q9T0P6) Ss-galactosidase precursor (EC 3.2.1.23)	Hydrolysis of terminal non-reducing beta-D-galactose residues in beta-D-galactosides/Galactose metabolism
STMIR51	3.65 (1.874 to 8.782)	(Q9T0P6) Ss-galactosidase precursor (EC 3.2.1.23)	Hydrolysis of terminal non-reducing beta-D-galactose residues in beta-D-galactosides/Galactose metabolism
STMJC34	3.383 (1.875 to 6.701)	(Q9LRI2) Cysteine protease precursor	Cysteine-type endopeptidase activity/ proteolysis/Circadian and senescence
STMIX65	2.92 (1.315 to 4.88)	(Q8RHT6) Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	Phosphate metabolism
STMIC96	2.824 (1.71 to 4.919)	(Q6MMW1) PiS sensor protein precursor (EC 2.7.3.-)	Nitrogen fixation regulatory protein

STMGQ32	2.815 (1.496 to 6.093)	68415.m01944 UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile:	Catalysis of the transfer of a glycosyl group from one compound (donor) to another (acceptor)
STMCV68	2.666 (1.014 to 6.084)	(Q6RHX8) Xyloglucan endotransglucosylase-hydrolase XTH7	Hydrolase activity, hydrolyzing O-glycosyl compounds/ripening
STMIS49	2.628 (1.475 to 4.102)	68416.m05666 SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Phosphate metabolism
STMER62	2.614 (1.507 to 4.23)	AT4g12290/T4C9_130 (Arabidopsis thaliana)	Diverse functions-cell wall, defense..
STMGS26	2.607 (1.667 to 4.602)	(Q40158) Metallothionein-like protein type 2 B	High content of cysteine residues that bind various heavy metals/ Mainly expressed in flowers and first leaves/ Strongly up regulated by heavy metals
STMIV90	2.472 (1.573 to 4.22)	68417.m01946 copper amine oxidase family protein contains Pfam domain PF01179: Copper amine	Diverse functions-cell wall, defense..
STMIO10	2.456 (1.62 to 3.194)	(Q40158) Metallothionein-like protein type 2 B	High content of cysteine residues that bind various heavy metals/ Mainly expressed in flowers and first leaves/ Strongly up regulated by heavy metals
STMES24	2.432 (1.346 to 4.239)	(Q6JJ29) Prephenate dehydratase	L-phenylalanine biosynthetic process
STMIV80	2.364 (1.442 to 4.823)	68418.m08223 ripening-responsive protein putative similar to ripening regulated protein DDTFR18	Membrane protein/ transporter/ ripening
STMHX70	2.325 (1.476 to 3.77)	68414.m09419 kelch repeat-containing F-box family protein similar to SPIQ9ER30 Kelch-related	Motif in many proteins/ circadin clock/ protein degradation
STMER30	2.252 (1.21 to 4.054)	(P10967) 1-aminocyclopropane-1-carboxylate oxidase homolog (Protein E8)	Acc oxidase/ Ethylene/ ripening
STMET80	2.239 (1.488 to 3.912)	68418.m06449 sorbitol dehydrogenase putative / L-iditol 2-dehydrogenase putative similar to	Fructose and Manose metabolism
STMEM11	2.238 (1.203 to 4.698)	(Q6PXE1) Auxin-repressed protein	
STMIF26	2.216 (1.389 to 3.291)	(Q40410) Metallothionein-like protein type 2	High content of cysteine residues that bind various heavy metals/ Mainly expressed in flowers and first leaves/ Strongly up regulated by heavy metals
STMIT03	2.143 (1.085 to 3.772)	68416.m03350 phosphoglycerate/bisphosphoglycerate mutase family protein similar to X4 protein G1:	Carbohydrate metabolism
STMGS74	2.078 (1.005 to 3.667)	68416.m06260 alpha-galactosidase putative / melibiase putative / alpha-D-galactoside	Carbohydrate metabolism
STMIH73	2.073 (1.396 to 3.603)	(Q8GTJ0) Xyloglucan endotransglycosylase	Hydrolase activity, hydrolyzing O-glycosyl compounds/ripening
STMHT08	2.06 (1.704 to 2.772)	68414.m02678 2-oxoisovalerate dehydrogenase putative / 3-methyl-2-oxobutanoate dehydrogenase	Lysin metabolism
STMGV93	2.046 (1.457 to 3.63)	(Q8RXA4) Putative glucosyltransferase	Carbohydrate metabolism
STMIJ72	2.03 (1.241 to 3.296)	68418.m05290 enoyl-CoA hydratase/isomerase family protein similar to Delta 3 5-delta2 4-dienoyl-CoA	Fatty acids and amino acids metabolism

STMEF73	2.019 (1.495 to 3.049)	68417.m03425 glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Pectin hydrolysis in cell wall/ ripening
Oxidation			
STMIZ53	4.702 (1.88 to 14.37)	(Q42701) Cytochrome P450 (Fragment)	
STMHX09	2.917 (2.059 to 5.106)	68417.m01588 oxidoreductase family protein similar to AX110P [Daucus carota] GI:285739; contains	
STMGR77	2.627 (1.626 to 6.471)	(Q6RJZ7) Thioredoxin	
STMHK40	2.3 (1.325 to 4.5)	(Q8LGM8) Cytochrome P450 monooxygenase CYP72A5	
STMII09	2.243 (1.181 to 4.533)	68416.m01855 cytochrome P450 putative similar to GB:Q05047 from [Catharanthus roseus]	
STMID59	2.139 (1.166 to 3.782)	68416.m01858 cytochrome P450 putative similar to GB:Q05047 from [Catharanthus roseus]	
STMCU85	2.128 (1.229 to 3.382)	68416.m01850 cytochrome P450 putative similar to GB:Q05047 from [Catharanthus roseus]	
STMHS70	2.108 (1.273 to 2.986)	(Q39684) AX110P	
STMIX70	2.058 (1.001 to 3.533)	68417.m03685 cytochrome B561 family protein contains Pfam domain PF03188: Cytochrome b561	
STMEQ24	2.057 (1.183 to 3.687)	Cytochrome b561	
Transcription/RNA processing			
STMCU81	4.007 (2.24 to 9.227)	(Q941L7) BZIP transcription factor BZI-2	Flower development
STMIU33	2.321 (1.654 to 4.847)	(Q8SLI2) Maturase K (Fragment)	Cellular componenet of the chloroplast/ rna splicing/ mrna processing
STMIU43	2.226 (1.372 to 3.239)	68418.m05713 16S rRNA processing protein RimM family contains weak similarity to Swiss-Prot:O74933	
STMJK91	2.084 (1.641 to 2.798)	Myb-like protein {Oryza sativa (japonica cultivar-group);}	
STMDC51	2.063 (1.584 to 2.79)	(Q9SP54) LIM domain protein WLIM1	Transcription factor/ zinc/ cytoskeleton
Translation/Post translation			
STMJN87	3.463 (1.879 to 8.815)	(O04679) Farnesyl-protein transferase beta subunit (EC 2.5.1.-)	Post translation modification
STMEH80	3.014 (1.932 to 4.032)	(P56337) Eukaryotic translation initiation factor 5A-5 (eIF-5A 5) (eIF-4D)	
Protein destination ,storage and degradation			
STMHX44	3.518 (1.618 to 9.012)	68416.m06250 copper homeostasis factor / copper chaperone (CCH) (ATX1) identical to gi:3168840 Pfam	
STMHW51	3.339 (1.702 to 8.595)	(Q84KJ2) Copper chaperone	
STMCG40	2.898 (1.189 to 5.721)	68418.m06883 trigger factor type chaperone family protein contains Pfam profiles PF05697: Bacterial	

STMCX50	2.703 (1.381 to 6.049)	(Q6J338) Copper chaperone	
STMCJ27	2.224 (1.174 to 3.415)	68418.m06172 ATP-dependent Clp protease ATP-binding subunit ClpX putative similar to CLP protease	Protein degradation in plastids
STMIF70	2.125 (1.056 to 3.907)	(Q6V8R2) Putative DnaJ protein (Fragment)	Chaperon/ taking proteins to peroxisome
Transporters			
STMGJ46	4.21 (2.238 to 10.73)	sulfate transporter (Arabidopsis thaliana;)	
STMIH60	2.469 (1.498 to 4.067)	(Q8PI19) Cationic amino acid transporter	
STMGU60	2.185 (1.108 to 4.238)	68415.m03201 nitrate transporter (NTP2) identical to nitrate transporter (ntp2)	Wounding/ Jasmonic acid
Defense			
STMHY32	4.771 (1.645 to 11.06)	(Q7XJE7) Putative xyloglucanase inhibitor	
STMHX25	3.421 (2.58 to 4.652)	68414.m09182 pathogenesis-related family protein contains similarity to pathogen-related protein	
STMEW74	3.325 (2.215 to 5.084)	(Q9ZRB6) Ci21A protein	Cold regulated gene in potato
STMDB42	2.949 (1.951 to 4.774)	(Q8L9B0) Pathogenesis-related protein-like protein	
STMHZ25	2.943 (1.971 to 4.484)	(Q9ZRB5) Ci21B protein	Cold regulated gene in potato
STMIO81	2.923 (1.581 to 5.573)	Trypsin putative	
STMID92	2.706 (1.622 to 5.288)	68416.m06514 universal stress protein (USP) family protein contains Pfam PF00582: universal stress	
STMEW11	2.59 (1.837 to 3.731)	(Q8H0L9) DS2 protein	Stress induced protein
STMIW38	2.281 (1.251 to 5.192)	(Q9LW93) Nicotiana tabacum wound inducive mRNA complete cds	
STMIS93	2.239 (1.622 to 3.669)	(P05315) Endochitinase precursor (EC 3.2.1.14 EC 3.2.1.14 EC 3.2.1.14)	Defence again fungal pathogens with chitin
STMCA80	2.211 (1.221 to 3.569)	(Q9LW93) Nicotiana tabacum wound inducive mRNA complete cds	
STMJA36	2.206 (1.583 to 3.672)	68418.m07876 band 7 family protein strong similarity to hypersensitive-induced response protein	
STMJI19	2.151 (1.294 to 3.283)	68414.m09182 pathogenesis-related family protein contains similarity to pathogen-related protein	
STMIX53	2.116 (1.219 to 3.508)	68418.m07876 band 7 family protein strong similarity to hypersensitive-induced response protein	
STMIN77	2.109 (1.423 to 3.525)	(O81144) Class I chitinase (EC 3.2.1.14 EC 3.2.1.14)	
STMCK62	2.053 (1.043 to 4.449)	68416.m01522 serine carboxypeptidase S10 family protein contains Pfam profile: PF00450 serine	Wounding and protein degradation
STMIU20	2.031 (1.279 to 2.728)	68417.m00172 CAAX protease putative (STE24) contains Pfam domain PF01435: Peptidase family M48	Heat shock protein

Cell structure			
STMIF12	3.027 (1.437 to 4.603)	68418.m01103 hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains	
STMJK93	2.541 (1.427 to 3.52)	(Q9W596) Microtubule-associated protein futsch	
STMIH61	2.291 (1.163 to 3.626)	68418.m01103 hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains	
STMJJ12	2.229 (1.351 to 4.128)	68418.m01103 hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains	
STMIX33	2.092 (1.476 to 3.084)	(Q40142) Cell wall protein precursor	
STMIG95	2.034 (1.183 to 3.567)	68418.m01101 hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains	
Signal transduction			
STMFA19	2.355 (1.432 to 3.759)	(Q41342) Ethylene receptor 1 (LeETR1) (EC 2.7.3.- EC 2.7.3.-)	
Secondary metabolism			
STMHW02	5.39 (3.246 to 10.18)	(P15004) Suberization-associated anionic peroxidase 2 precursor (TMP2)	Suberization
STMCL66	5.271 (4.096 to 7.023)	(Q9M527) Phenylcoumaran benzylic ether reductase homolog Fi2	Lignification
STMDQ29	4.608 (3.016 to 9.118)	(Q41242) Alcohol dehydrogenase ADH	
STMCC79	3.475 (2.195 to 4.905)	(Q42958) Catechol O-methyltransferase (EC 2.1.1.6 EC 2.1.1.6)	Lignification
STMJL95	3.387 (1.797 to 5.991)	(Q8H9B6) Caffeoyl-CoA O-methyltransferase (Trans-caffeoyl-CoA 3-O-methyltransferase) (CCoAMT)	Lignification
STMIC60	3.361 (2.379 to 4.822)	(Q42945) Caffeoyl-CoA O-methyltransferase 6 (Trans-caffeoyl-CoA 3-O-methyltransferase 6) (CCoAMT-6)	Lignification
STMCL31	3.037 (0.936 to 5.418)	(Q9AVG9) S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase	Scent/ enzymatic activity that catalyzes the formation of methylsalicylate from salicylic acid
STMER77	3.023 (1.58 to 7.432)	(P15004) Suberization-associated anionic peroxidase 2 precursor (TMP2)	Suberization
STMCK29	2.867 (2.037 to 4.372)	(Q9XH50) 1-D-deoxyxylulose 5-phosphate synthase	Terpenoids/ IPP synthesis
STMCY65	2.745 (1.409 to 5.622)	(Q82676) 1-deoxyxylulose 5-phosphate synthase	Terpenoids/ IPP synthesis
STMHZ50	2.586 (1.723 to 3.886)	(Q8H9B6) Caffeoyl-CoA O-methyltransferase (Trans-caffeoyl-CoA 3-O-methyltransferase) (CCoAMT)	Lignification
STMEM71	2.4 (0.927 to 5.05)	(Q9MB73) Limonoid UDP-glucosyltransferase (Limonoid glucosyltransferase) (Limonoid GTase) (LGTase)	Terpenoids/ glucosylation of limonoids
STMIN59	2.38 (1.399 to 4.517)	(Q8GVE3) Flavonoid 1-2 rhamnosyltransferase	Biosynthesis of flavonoids
STM EU71	2.365 (1.076 to 3.65)	68418.m05207 O-methyltransferase N-terminus domain-containing protein contains Pfam profile PF02409:	Lignification

STMIX91	2.322 (0.126 to 4.496)	(P30359) Cinnamyl-alcohol dehydrogenase (CAD) (EC 1.1.1.195 EC 1.1.1.195 EC 1.1.1.195)	Lignification
STMIJ60	2.267 (1.662 to 3.439)	(Q9SXJ0) Transcription factor Ntlm1	Lignification/ zinc binding
STMHR20	2.151 (1.657 to 3.4)	adenosine monophosphate binding protein 7 AMPBP7	Acyl co-A synthase/ secondary metabolites biosynthesis
STMGM34	2.113 (1.5 to 3.42)	(Q42698) Geranylgeranyl pyrophosphate synthetase chloroplast precursor (GGPP synthetase) (GGPS)	Carotenoids
STMEP23	2.056 (1.16 to 3.063)	(Q41437) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 (HMG-CoA reductase 2) (HMG2.2)	Isoprenoids synthesis/ mevalonate synthesis
STMCB66	2.054 (1.652 to 2.731)	68417.m04881 LytB family protein contains Pfam profile: PF02401 LytB protein	Isoprenoids synthesis/ Enzyme
STMIV38	2.037 (0.684 to 5.894)	(P28554) Phytoene dehydrogenase chloroplast precursor (Phytoene desaturase)	Carotenoids
Photosynthesis			
STMHZ22	5.104 (2.163 to 10.49)	unnamed protein product; ST-LS1 protein (AA 1-138) {Solanum tuberosum;}	
STMFB17	3.586 (1.607 to 6.626)	(P26575) Ribulose bisphosphate carboxylase small chain 2A chloroplast precursor	
STMIZ57	3.497 (1.774 to 5.197)	(P06183) Photosystem II 10 kDa polypeptide chloroplast precursor	
STMET36	3.441 (1.777 to 5.238)	(P26575) Ribulose bisphosphate carboxylase small chain 2A chloroplast precursor	
STMCE25	3.406 (2.027 to 5.015)	(P26575) Ribulose bisphosphate carboxylase small chain 2A chloroplast precursor	
STMCG74	3.247 (0.5 to 7.765)	(P26575) Ribulose bisphosphate carboxylase small chain 2A chloroplast precursor	
STM CJ24	3.117 (1.542 to 5.367)	(P26574) Ribulose bisphosphate carboxylase small chain 1 chloroplast precursor	
STM IW88	3.038 (1.396 to 5.35)	(P26575) Ribulose bisphosphate carboxylase small chain 2A chloroplast precursor	
STM CG51	3.002 (0.912 to 5.399)	(P26575) Ribulose bisphosphate carboxylase small chain 2A chloroplast precursor	
STM ET72	2.996 (1.137 to 6.317)	(P26574) Ribulose bisphosphate carboxylase small chain 1 chloroplast precursor	
STM CG28	2.949 (1.426 to 5.192)	(P26574) Ribulose bisphosphate carboxylase small chain 1 chloroplast precursor	
STM IR27	2.906 (1.551 to 4.716)	(P26575) Ribulose bisphosphate carboxylase small chain 2A chloroplast precursor	

STMIW68	2.898 (1.526 to 5.097)	(P26575) Ribulose biphosphate carboxylase small chain 2A chloroplast precursor	
STMCP20	2.896 (1.455 to 5.121)	(P26577) Ribulose biphosphate carboxylase small chain 2C chloroplast precursor	
STMCM49	2.888 (1.519 to 4.384)	(P06183) Photosystem II 10 kDa polypeptide chloroplast precursor	
STMCB56	2.831 (1.309 to 4.521)	(P26574) Ribulose biphosphate carboxylase small chain 1 chloroplast precursor	
STMCG27	2.791 (1.389 to 4.346)	(P26575) Ribulose biphosphate carboxylase small chain 2A chloroplast precursor	
STMIX84	2.772 (1.385 to 5.094)	(P26574) Ribulose biphosphate carboxylase small chain 1 chloroplast precursor	
STMIP23	2.639 (1.34 to 4.173)	68417.m04615 peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein weak similarity to	
STMCCQ63	2.639 (1.189 to 5.125)	(P26574) Ribulose biphosphate carboxylase small chain 1 chloroplast precursor	
STMIY49	2.467 (1.445 to 4.534)	(P26574) Ribulose biphosphate carboxylase small chain 1 chloroplast precursor	
STMDB96	2.42 (1.341 to 3.84)	(Q41387) Photosystem II reaction center W protein chloroplast precursor (PSII 6.1 kDa protein)	
STMEQ02	2.351 (1.143 to 4.172)	68416.m06426 peptidase S41 family protein similar to PSII D1 protein processing enzyme (GI::7268527)	
STMCB57	2.291 (1.159 to 3.689)	(Q84UU0) Photosystem I subunit XI	
STMCCQ90	2.237 (1.56 to 3.248)	chlorophyll a/b-binding protein type I precursor (cab-6A) - tomato {Lycopersicon esculentum;}	
STMCCX03	2.235 (1.328 to 3.982)	(P26575) Ribulose biphosphate carboxylase small chain 2A chloroplast precursor	
STMIW93	2.189 (1.01 to 4.088)	(P26574) Ribulose biphosphate carboxylase small chain 1 chloroplast precursor	
STMCCZ35	2.156 (1.36 to 4.481)	(Q41228) Photosystem I reaction center subunit IV A chloroplast precursor (PSI-E A)	
STMEW75	2.133 (1.284 to 2.729)	(Q41387) Photosystem II reaction center W protein chloroplast precursor (PSII 6.1 kDa protein)	
STMCL53	2.096 (1.291 to 3.105)	(P06183) Photosystem II 10 kDa polypeptide chloroplast precursor	
Others and unknown			
STMIJ42	3.834 (1.815 to 7.448)	68418.m01845 pollen Ole e 1 allergen and extensin family protein contains Pfam profile PF01190:	

STMHT55	3.495 (2.227 to 7.384)	Nicotiana tabacum 18S rRNA gene	
STMDB78	3.358 (1.914 to 6.599)	(Q94I88) Putative miraculin (Fragment)	
STMIZ92	3.032 (1.38 to 4.949)	(Q6L4A7) Expressed protein	
STMDB95	2.981 (1.179 to 5.769)	68414.m04006 expressed protein	
STMCC47	2.758 (1.647 to 4.54)	(Q94I88) Putative miraculin (Fragment)	
STMIY29	2.671 (1.22 to 5.011)	(Q6H4I2) Brain protein 44-like	
STMIQ48	2.486 (1.38 to 4.057)	68414.m00754 gamma interferon responsive lysosomal thiol reductase family protein / GILT family	
STMEP42	2.315 (1.38 to 3.396)	(Q8H0H5) Hypothetical protein A20	
STMEU74	2.266 (1.337 to 4.054)	(Q942Q2) P0701D05.1 protein (B1189A09.32 protein)	
STMIJ14	2.161 (1.692 to 2.916)	(Q9M614) Hypothetical protein	
STMEQ20	2.136 (1.299 to 4.047)	68415.m01821 expressed protein	
STMJA56	2.103 (1.419 to 3.086)	68418.m01597 expressed protein	
STMEJ62	2.083 (1.173 to 4.549)	(Q9CBP6) Hypothetical protein ML1750	
STMEZ48	2.069 (1.22 to 3.521)	unknown {Populus tremuloides;}	