

Supplementary material:

Molecular targets of elevated [CO₂] in leaves and stems of *Populus deltoides*: implications for future tree growth and carbon sequestration

Nathalie Druart^{A,B}, Marisa Rodríguez-Buey^A, Greg Barron-Gafford^C, Andreas Sjödin^A,
Rishikesh Bhalerao^B and Vaughan Hurry^{A,D}

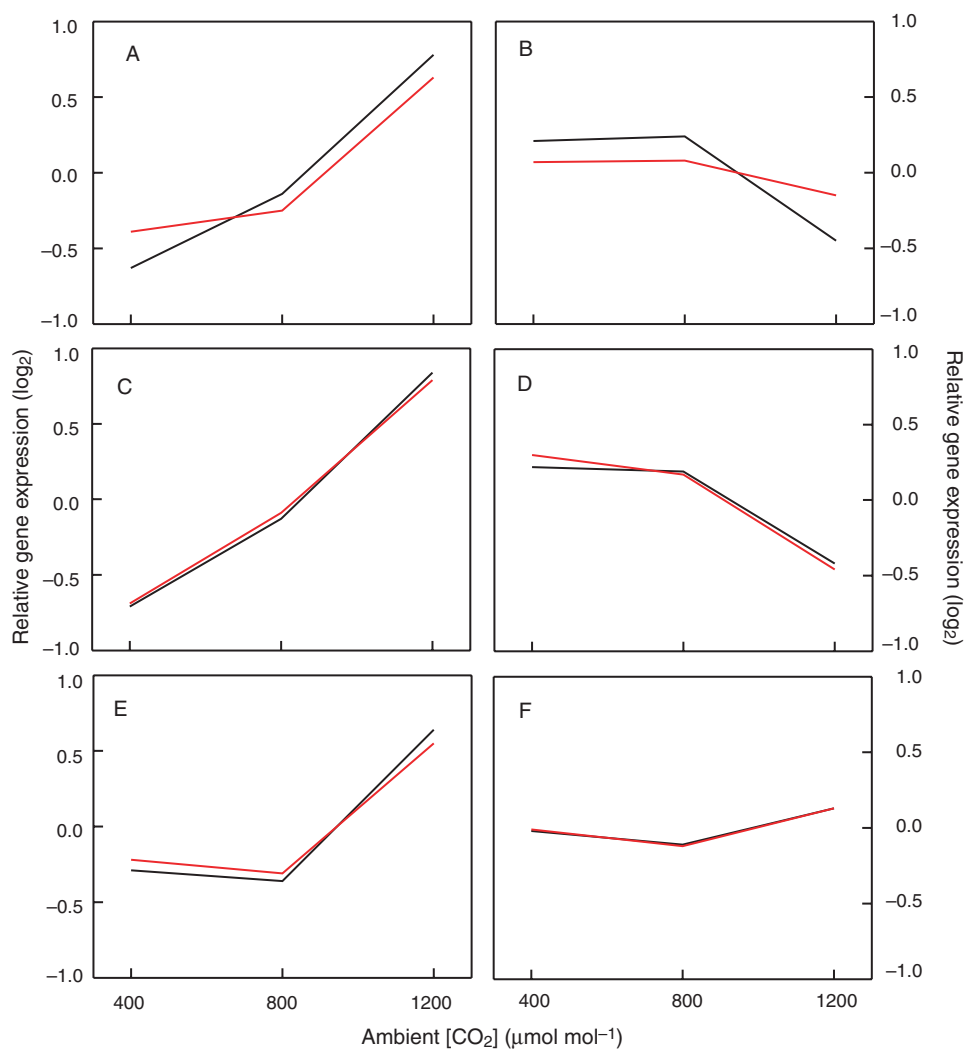
^AUmeå Plant Science Centre, Department of Plant Physiology, Umeå University, S-901 87 Umeå, Sweden.

^BUmeå Plant Science Centre, Department of Forest Genetics and Plant Physiology,
Swedish University of Agricultural Sciences, S-901 83 Umeå, Sweden.

^CBiosphere 2 Laboratory, Columbia University, Oracle AZ 85623 USA. Current address: Ecology and Evolutionary
Biology, University of Arizona, Tucson, AZ 85719, USA.

^DCorresponding author. Email: Vaughan.Hurry@plantphys.umu.se

Appendix S1



Validation of reproducibility of the hybridisations by comparing the hybridisation results of three genes for which two independent cDNA clones had been spotted on the array. (A, C, E leaves; B, D, F stems). (A, B) Protein phosphatase 2A, 65 kDa subunit. (C, D) Elicitor-inducible cytochrome P450. (E, F) Major storage protein.

Appendix S2. [CO₂]-responsive genes in leaves sorted according to functional categories, selected up-regulated clones under 800 or 1200 μmol mol⁻¹ [CO₂]

Values are fold-change and those printed in bold are statistically significant with B-statistic ≥10

Function	Clone ID	At gene ID	800/400	1200/400	1200/800
Metabolism (01)					
Cytochrome P-450	PU03116	At1g13710	4.34	2.29	7.60
Cytochrome P-450	PU03121	At1g13710	4.18	2.44	8.67
Cytochrome P-450 (CYP78A9)	PU05505	At3g61880	1.34	2.19	1.60
Dihydroflavonol 4-reductase	PU12089	At1g61720	4.80	2.22	2.15
Naringenin 3-dioxygenase	PU01480	At3g51240	-1.01	1.70	1.71
Chalcone synthase	PU10149	At5g13930	1.34	1.67	1.23
Chalcone synthase	PU12625	At5g13930	1.18	1.49	1.25
Chalcone synthase 1	PU04294	At5g13930	2.07	1.49	1.25
Chalcone isomerase	PU04986	At3g55120	1.23	1.45	1.28
Elicitor-inducible cytochrome P450	PU08702	At1g01280	4.49	4.26	3.12
Elicitor-inducible cytochrome P450	PU12599	At5g07990	8.84	4.74	2.57
Elicitor-inducible cytochrome P450	PU12470	At5g07990	1.80	4.43	2.50
Glucosyltransferase NTGT3	PU12170	At1g07250	1.39	2.04	1.46
IPP transferase-like protein	PU04004	At5g20040	-1.17	1.83	2.14
Major storage protein	PU03068	At4g24340	-9.1	2.05	2.18
Major storage protein	PU03117	At4g24340	-1.11	2.34	2.53
Major storage protein	PU03474	At4g24340	-1.22	2.09	2.28
Major storage protein	PU03508	At4g24340	-5.86	2.48	2.58
Major storage protein	PU03510	At4g24340	-2.23	2.51	2.51
Major storage protein	PU03513	At4g24340	-1.77	2.42	2.73
Major storage protein	PU03548	At4g24340	-1.07	2.44	2.63
Major storage protein	PU03698	At4g24340	-7.79	2.50	2.64
Major storage protein	PU03708	At4g24340	-1.17	2.35	2.55
Major storage protein	PU03743	At4g24340	-1.56	2.36	2.63
Major storage protein	PU03784	At4g24340	-7.19	2.49	2.62
Major storage protein	PU03820	At4g24340	-7.61	2.36	2.49
Major storage protein	PU03824	At4g24340	-4.04	2.34	2.41
Major storage protein	PU04029	At4g24340	-8.11	2.35	2.48
Thioredoxin H	PU01940	At1g59730	1.87	1.89	1.01
Xyloglucan endotransglycosylase	PU02379	At4g03210	-1.49	2.09	2.32
Xyloglucan endotransglycosylase	PU07373	At4g03210	2.11	2.40	2.07
Endo-xyloglucan transferase	PU11514	At5g65730	1.17	2.00	1.70
3-deoxy-D-arabino-heptulosonate 7-phosphate synthase precursor	PU02218	At1g22410	1.06	2.21	2.28
Cell growth, cell division, DNA synthesis (03)					
Microtubule-associated protein EB1-like protein	PU03283	At5g62500	-1.08	2.52	2.72
Protein phosphatase 2A 65 kDa regulatory subunit	PU05097	At3g25800	1.18	2.65	2.23
Protein phosphatase 2A 65 kDa regulatory subunit	PU12228	At3g25800	1.55	3.75	2.39
Protein phosphatase 2A 65 kDa regulatory subunit	PU12736	At3g25800	1.59	4.11	2.56
RGA1, gibberellin response modulation protein	PU03640	At2g01570	-1.11	2.20	2.44
RING zinc finger ankyrin protein-related	PU03201	At2g28840	-1.12	1.85	2.08
Transcription (04)					
CCAAT-binding factor B subunit	PU03099	At1g72830	-1.09	2.12	2.30
Probable coproporphyrinogen oxidase	PU03696	At3g20740	-1.09	2.30	2.51
Protein destination (06)					
Peptidylprolyl isomerase	PU11811	At5g48570	1.24	3.68	2.94
Ubiquitin fusion-degradation protein	PU03741	At2g21270	-1.04	2.24	2.32
18.5 kDa class I heat shock protein (HSP 18.5)	PU04831	At5g59720	1.28	3.77	2.93
Cell rescue, defense, cell death and ageing (11)					
Disease resistance response protein-related	PU03542	At1g58170	-1.10	2.01	2.20
Cellular organisation (30)					
Pollen allergen	PU06328	At4g38400	1.91	-1.21	2.32

Appendix S2 continued

Function	Clone ID	At gene ID	800/400	1200/400	1200/800
Classification not yet clear-cut (98)					
Expressed protein	PU08410	At1g49750	1.93	1.60	-1.19
Expressed protein	PU03138	At3g08780	-1.11	2.11	2.33
Expressed protein	PU03140	At1g71430	-1.03	2.33	2.39
Expressed protein	PU03233	At1g71080	-1.09	2.46	2.69
Expressed protein	PU03245	At5g19260	-1.15	2.16	2.47
Expressed protein	PU03333	At4g22920	1.05	2.29	2.17
Expressed protein	PU03435	At4g01650	-1.12	2.02	2.26
Expressed protein	PU03543	At4g39140	-1.07	2.13	2.28
Expressed protein	PU03670	At2g21180	1.06	2.10	1.96
Expressed protein	PU05874	At3g24100	1.12	2.10	1.87
Expressed protein	PU06017	At4g24220	1.35	2.28	1.68
Expressed protein	PU11113	At5g41080	-1.09	2.15	2.01
Expressed protein	PU13336	At1g61720	2.09	2.93	2.54
Expressed protein	PU07779	At5g11090	-1.31	1.76	2.32
Expressed protein	PU11064	At5g41080	-7.97		2.01
Unknown protein	PU03835	At1g71010	-1.07	2.09	2.22
Unclassified proteins (99)					
Boiling stable protein A	PU00350	At3g17210	8.76	3.66	3.45
Boiling stable protein A	PU01134	At3g17210	8.76	3.78	3.56
Cellulase, putative	PU03243	At3g26130	-1.02	2.42	2.47
Cytochrome c oxidase polypeptide VIII	PU09960	At5g23100	1.15	1.99	1.73
Expressed protein	PU03457	At1g69050	-1.09	2.44	2.65
Expressed protein	PU03578	At1g22420	-1.10	2.51	2.77
Expressed protein	PU11117	At4g29200	1.50	-1.70	1.99
GDSL-motif lipase/hydrolase-like protein	PU10319	At5g45670	2.65	1.99	9.64
GDSL-motif lipase/hydrolase-like protein	PU12148	At5g45670	1.27	2.42	2.21
GDSL-motif lipase/hydrolase-like protein	PU12188	At5g45670	9.55	2.49	2.33
GDSL-motif lipase/hydrolase-like protein	PU12468	At5g45670	2.96	2.64	2.15
HEN1	PU12175	At4g20910	-1.06	2.18	2.30
Major storage protein	PU03509	At3g17650	-1.09	2.34	2.57
Possibly polygalacturonase inhibiting protein	PU08796	At5g06870	4.93	-1.20	-5.94
Polyphenol oxidase	PU12604	At1g08170	3.92	2.73	-1.44
Protease inhibitor II	PU03669	At2g02130	2.57	2.57	2.88
ORFs (Putative primordial protein)	PU11210	At5g40260	-1.50	1.36	2.05

Appendix S3. [CO₂]-responsive genes in leaves sorted according to functional categories, selected down-regulated clones under 800 or 1200 $\mu\text{mol mol}^{-1}$ [CO₂]

Values are fold-change and those printed in bold are statistically significant with B-statistic ≥ 10

Function	Clone ID	At gene ID	800/400	1200/400	1200/800
Metabolism (01)					
GDP-mannose pyrophosphorylase	PU07331	At2g39770	-4.58	-1.79	2.55
Inositol-3-phosphate synthase	PU13206	At5g10170	1.50	-1.31	-1.98
Transcription (04)					
DNA-binding protein, putative	PU10896	At1g01060	5.90	-4.68	-2.18
DNA-binding protein, putative	PU13388	At1g01060	7.60	-5.66	-2.51
Protein destination (06)					
DnaJ-like protein	PU10218	At2g17880	-2.02	-8.67	1.46
DnaJ-like protein	PU12884	At2g17880	-1.99	-7.49	2.46
DnaJ-like protein	PU13066	At2g17880	-1.93	-8.53	9.26
Cell fate (14)					
Floricaula/leafy homolog (PTLF)	PU00007	At5g61850	1.25	-2.50	-2.63
Floricaula/leafy homolog (PTLF)	PU00843	At5g61850	7.42	-2.39	-2.52
Floricaula/leafy homolog (PTLF)	PU03491	At5g61850	1.76	-2.14	-2.42
Floricaula/leafy homolog (PTLF)	PU03680	At5g61850	1.95	-2.33	-2.37
Floricaula/leafy homolog (PTLF)	PU03755	At5g61850	1.21	-2.38	-2.40
Floricaula/leafy homolog (PTLF)	PU05650	At5g61850	3.41	-2.20	-2.26
Floricaula/leafy homolog (PTLF)	PU12065	At5g61850	1.18	-2.62	-2.85
Floricaula/leafy homolog (PTLF)	PU12438	At5g61850	3.78	-2.43	-2.50
Floricaula/leafy homolog (PTLF)	PU13110	At5g61850	1.69	-2.35	-2.64
Cellular communication/signal transduction (10)					
Protein kinase	PU13475	At2g30360	1.27	-1.54	-1.96
Cellular organisation (30)					
GAB3. Possibly expansin-like protein	PU09319	At1g69530	-1.51	-2.06	-1.36
Classification not yet clear-cut (98)					
Expressed protein	PU01650	At1g26800	1.26	-1.68	-2.12
Expressed protein	PU08923	At1g10560	1.09	-1.97	-1.80
Unclassified proteins (99)					
Possibly polygalacturonase inhibiting protein	PU08796	At5g06870	4.93	-1.20	-5.94
Ribonucleoside-diphosphate reductase α -chain	PU09892	At1g10330	-1.09	-1.80	-2.02

Appendix S4. [CO₂]-responsive genes in stems sorted according to functional categories, selected up-regulated clones under 800 or 1200 μmol mol⁻¹ [CO₂]

Values are fold-change and those printed in bold are statistically significant with B-statistic ≥10

Function	Clone ID	At gene ID	800/400	1200/400	1200/800
Metabolism (01)					
Aminopeptidase like protein	PU05176	At4g33090	1.97	2.09	1.06
Caffeic acid 3- <i>O</i> -methyltransferase	PU00567	At5g54160	1.34	2.27	1.69
Caffeic acid 3- <i>O</i> -methyltransferase	PU07978	At5g54160	1.45	2.41	1.63
Caffeoyl-CoA <i>O</i> -methyltransferase	PU01811	At4g34050	1.41	2.07	1.47
Caffeoyl-CoA <i>O</i> -methyltransferase	PU02461	At4g34050	1.85	2.37	1.29
Cellulose synthase	PU02217	At5g44030	1.33	2.16	1.63
Cinnamyl alcohol dehydrogenase	PU00508	At3g19450	1.49	2.38	1.59
Ethylene-inducible protein	PU04727	At3g16050	2.23	2.70	1.21
Isoflavone reductase	PU00516	At1g75280	1.24	2.52	2.03
Isoflavone reductase	PU02555	At1g75280	1.43	2.30	1.61
Laccase	PU02804	At2g38080	-1.17	2.10	2.46
Mitochondrial dicarboxylate carrier protein	PU07562	At2g22500	1.26	2.14	1.70
Mitochondrial dicarboxylate carrier protein	PU12663	At2g22500	1.50	2.35	1.56
Mitochondrial dicarboxylate carrier protein	PU12705	At2g22500	1.47	2.30	1.56
Myo-inositol-1-phosphate synthase	PU13206	At5g10170	1.63	2.05	1.26
PAPS-reductase-like protein precursor	PU03982	At4g04610	1.55	2.67	1.72
Plastidial w-3 fatty acid desaturase	PU06720	At1g07430	1.79	3.28	1.84
Protein phosphatase 2C	PU12652	At2g30020	2.01	2.86	1.42
Putative basic chitinase	PU01517	At3g16920	1.43	2.61	1.82
Putative basic chitinase	PU06113	At3g16920	1.28	3.37	2.63
Putative polygalacturonase PG1	PU02788	At1g48100	1.92	2.11	1.10
SRC2	PU04157	At1g09070	1.65	2.02	1.22
Energy (02)					
Alcohol dehydrogenase 2	PU10963	At1g77120	3.06	6.16	2.01
Alcohol dehydrogenase 2	PU03309	At1g77120	1.98	2.84	1.43
Alcohol dehydrogenase 2	PU03813	At1g77120	1.87	2.48	1.33
Dicyanin	PU12528	At2g32300	1.21	2.09	1.73
Heat shock protein	PU05022	At5g56000	2.50	2.58	1.03
Cell growth, cell division and DNA synthesis (03)					
CCCH-type zinc finger protein	PU10193	At2g40140	2.28	4.38	1.92
CCCH-type zinc finger protein	PU03961	At2g40140	1.61	3.27	2.03
Chaperonin 60 beta-like protein	PU02810	At3g13470	2.03	2.01	-1.01
DnaJ protein homolog atj3	PU05956	At3g44110	1.83	2.26	1.23
GTP-binding protein	PU03770	At5g55190	2.12	2.56	1.20
GTP-binding protein	PU08983	At5g55190	2.00	2.75	1.37
Heat-shock protein 80	PU02135	At5g56010	2.13	2.18	1.03
Heat-shock protein	PU09805	At2g20560	1.84	2.05	1.11
Hypothetical 19.3 kDa protein	PU09764	At1g01490	2.09	4.84	2.32
Hypothetical 19.3 kDa protein	PU11568	At1g01490	1.27	2.23	1.76
PtxA protein precursor	PU03793	At4g15160	2.09	-1.42	-2.97
SOS2-like protein kinase PKS2	PU07078	At5g58380	1.78	3.10	1.74
Transcription factor BHLH12	PU06496	At4g00480	-1.93	1.28	2.47
Transcription (04)					
bZip transcription factor (AtbZip60)	PU13464	At1g42990	1.40	2.46	1.76
CONSTANS B-box zinc finger family protein	PU08816	At3g21150	1.72	2.70	1.57
CONSTANS B-box zinc finger family protein	PU10524	At3g21150	1.99	2.47	1.24
DNA-binding protein, putative	PU10896	At1g01060	2.22	2.04	-1.09
DNA-binding protein, putative	PU13388	At1g01060	2.57	2.35	-1.09
Ethylene responsive element binding factor 4	PU05186	At3g15210	1.82	2.15	1.18
Ethylene responsive element binding factor 4	PU07741	At3g15210	1.93	3.39	1.75
Ethylene responsive element binding factor-like protein	PU13199	At4g17490	3.50	5.33	1.52
Ethylene-responsive transcriptional coactivator-like protein	PU03794	At3g24500	4.67	7.39	1.58
Heat shock protein	PU03264	At1g74310	3.50	3.56	-1.10
High mobility group protein 2-like	PU03103	At3g51880	1.29	2.64	2.05
Homeobox-leucine zipper protein ATHB-12	PU09347	At3g61890	1.30	4.15	3.19

Appendix S4 *continued*

Function	Clone ID	At gene ID	800/400	1200/400	1200/800
Pirin-like protein	PU07375	At3g59220	-1.15	1.91	2.21
SCARECROW gene regulator-like	PU07055	At5g48150	1.05	2.14	2.03
Transcription factor WRKY4	PU09504	At1g80840	1.22	2.05	1.68
WRKY-type DNA binding protein	PU09430	At2g46400	3.81	9.23	2.42
Protein synthesis (05)					
Low-molecular-weight heat shock protein-like	PU05265	At5g37670	3.11	2.28	-1.36
Translation initiation factor-like protein	PU05388	At5g54940	2.81	3.15	1.12
Translation initiation factor-like protein	PU10245	At5g54940	2.99	3.16	1.06
Protein destination (06)					
Heat shock protein 70 (HSC70)	PU00640	At3g12580	2.06	1.58	-1.30
Heat shock protein 70 (HSC70)	PU01142	At3g12580	2.09	1.60	-1.31
Heat shock protein 70	PU06774	At3g12580	4.34	3.74	-1.16
Peptidylprolyl isomerase	PU11811	At5g48570	8.00	6.75	-1.18
18.5 kDa class I heat shock protein (HSP 18.5)	PU04831	At5g59720	4.84	4.05	-1.20
Cellular communication/signal transduction (10)					
Calcium-binding protein-like	PU10452	At5g39670	1.89	4.05	2.15
Protein kinase	PU13475	At2g30360	1.77	2.41	1.36
Receptor-like protein kinase	PU10533	At2g31880	2.10	2.14	1.02
Regulator of gene silencing	PU08510	At5g42380	3.82	5.21	1.36
Regulator of gene silencing	PU12278	At5g42380	2.66	3.72	1.40
Cell rescue, defense, cell death and ageing (11)					
Disease resistance like protein	PU00248	At5g36930	1.01	2.19	2.17
Disease resistance protein (NBS-LRR class)	PU06573	At4g27220	1.20	2.76	2.30
Disease resistance protein (NBS-LRR class)	PU10612	At4g27220	1.19	2.68	2.25
Hs1pro-1-like receptor	PU03751	At2g40000	2.79	4.00	1.43
Pathogenesis-related protein	PU04923	At4g25780	2.59	2.79	1.08
Sn-1 protein	PU05856	At5g28010	-1.60	1.68	2.68
Cell fate (14)					
Hypothetical 39.1 kDa protein.	PU03120	At3g07090	3.37	4.87	1.44
Hypothetical 39.1 kDa protein.	PU12190	At3g07090	2.49	3.16	1.27
Development (25)					
Aquaporin PIP1-1	PU02521	At4g00430	2.03	2.36	1.16
Cellular organisation (30)					
Reversibly glycosylated polypeptide	PU13470	At5g15650	-1.16	1.81	2.09
Classification not yet clear-cut (98)					
Expressed protein	PU00265	At3g61490	1.80	2.23	1.24
Expressed protein	PU00599	At3g57540	1.59	2.16	1.36
Expressed protein	PU00607	At4g32020	1.49	2.01	1.35
Expressed protein	PU00630	At1g60420	1.35	2.13	1.58
Expressed protein	PU01055	At1g10560	2.22	1.27	-1.75
Expressed protein	PU01369	At3g61490	2.03	2.43	1.19
Expressed protein	PU01908	At1g09310	1.72	2.00	1.16
Expressed protein	PU02796	At3g01680	1.71	2.44	1.43
Expressed protein	PU03447	At2g15960	-3.25	-1.63	2.00
Expressed protein	PU03458	At4g24220	-1.32	1.60	2.11
Expressed protein	PU03484	At5g42050	1.54	2.34	1.51
Expressed protein	PU04714	At5g51190	1.56	3.23	2.07
Expressed protein	PU04936	At3g01680	1.79	3.02	1.68
Expressed protein	PU05076	At1g32700	1.45	2.00	1.38
Expressed protein	PU05525	At3g01680	1.40	2.26	1.61
Expressed protein	PU05813	At5g51190	1.90	3.66	1.93
Expressed protein	PU05874	At3g24100	3.28	3.37	1.03
Expressed protein	PU06343	At5g42050	1.79	3.00	1.67
Expressed protein	PU06842	At5g38070	2.06	1.12	-1.85
Expressed protein	PU07391	At1g09750	2.27	1.34	-1.70
Expressed protein	PU08533	At3g21570	1.35	2.23	1.65
Expressed protein	PU08876	At5g11090	1.97	3.00	1.52
Expressed protein	PU08923	At1g10560	3.94	6.01	1.53

Appendix S4 continued

Function	Clone ID	At gene ID	800/400	1200/400	1200/800
Expressed protein	PU09113	At5g11090	2.74	3.05	1.11
Expressed protein	PU09474	At1g60420	-1.09	2.04	2.24
Expressed protein	PU09971	At1g60420	1.35	2.12	1.56
Expressed protein	PU10173	At5g17350	1.31	2.30	1.76
Expressed protein	PU10597	At3g07600	1.72	4.51	2.62
Expressed protein	PU10629	At1g05575	1.56	2.90	1.86
Expressed protein	PU11800	At1g59710	1.72	2.75	1.60
Expressed protein	PU12036	At5g42050	1.92	3.20	1.67
Expressed protein	PU12149	At4g27280	1.20	2.19	1.83
Similar to senescence-associated protein	PU08184	At2g23810	1.58	2.30	1.45
Similar to senescence-associated protein	PU12080	At2g23810	1.80	2.42	1.34
Unclassified proteins (99)					
Ankyrin-repeat protein HBP1	PU04347	At2g17390	2.22	2.37	1.07
CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase	PU09672	At5g05650	4.04	1.19	1.21
ORF YLL020C.	PU02350	At1g02816	2.22	2.15	-1.03
Expressed protein	PU04190	At5g48250	1.25	2.06	1.66
Expressed protein	PU09267	At3g61710	-1.10	2.10	2.31
Expressed protein	PU10116	At1g30260	2.08	4.90	2.36
Expressed protein	PU10334	At1g72650	1.47	2.11	1.44
Expressed protein	PU10429	At5g67250	1.96	2.70	1.38
Non-specific lipid transfer-like protein	PU00488	At5g48490	2.18	1.76	-1.23
Non-specific lipid transfer-like protein	PU01768	At5g48490	2.69	2.00	-1.35
Non-specific lipid transfer-like protein	PU02501	At5g48490	2.24	1.68	-1.33
Ubiquitin-like protein	PU09006	At5g42300	2.01	2.86	1.43

Appendix S5. [CO₂]-responsive genes in stems sorted according to functional categories, selected down-regulated clones under 800 or 1200 μmol mol⁻¹ [CO₂]

Values are fold-change and those printed in bold are statistically significant with B-statistic ≥10

Function	Clone ID	At gene ID	800/400	1200/400	1200/800
Metabolism (01)					
Chalcone-flavonone isomerase	PU04986	At3g55120	-1.52	-2.07	-1.45
Chalcone synthase 1	PU04294	At5g13930	-2.11	-2.81	-1.33
Chalcone synthase	PU10149	At5g13930	-1.50	-3.12	-2.08
Chalcone synthase	PU12625	At5g13930	-1.35	-4.03	-2.99
Dihydroflavonol 4-reductase	PU12089	At5g42800	-1.59	-4.23	-2.66
Dihydroflavonol 4-reductase	PU12348	At5g42800	-1.17	-2.29	-1.95
Elicitor-inducible cytochrome P450	PU08702	At1g01280	1.06	-1.98	-2.10
Elicitor-inducible cytochrome P450	PU12470	At1g01280	-1.14	-2.13	-1.87
Flavanone 3-hydroxylase (FH3)	PU01480	At3g51240	-1.48	-3.16	-2.14
Flavonoid 3-hydroxylase	PU11503	At3g07990	-1.45	-2.40	-1.65
Flavonoid 3-hydroxylase	PU12061	At5g07990	-1.53	-2.75	-1.80
GDP-mannose pyrophosphorylase	PU03161	At2g39770	-1.36	-2.25	-1.66
Glucosyltransferase NTGT3	PU12170	At1g07250	-1.33	-2.28	-1.71
Leucoanthocyanidin dioxygenase (LDOX)	PU12098	At4g22880	-1.66	-3.51	-2.12
Leucoanthocyanidin dioxygenase (LDOX)	PU12918	At4g22880	-1.66	-3.44	-2.07
Pectinesterase-like protein	PU01896	At3g49220	-1.17	-2.40	-2.06
Phenylcoumaran benzylic ether reductase homolog	PU08497	At1g75290	-1.60	-2.72	-1.70
Seed imbibition protein	PU01324	At3g57520	1.56	-1.32	-2.05
Thioredoxin H	PU11831	At1g59730	-1.45	-2.01	-1.39
Xyloglucan endotransglycosylase	PU02379	At4g03210	-2.30	-2.00	1.15
Xyloglucan endotransglycosylase	PU05203	At4g03210	-2.16	-2.40	-1.11
Xyloglucan endotransglycosylase	PU07448	At4g03210	-2.52	-1.96	1.29
Cell growth, cell division and DNA synthesis (03)					
Protein phosphatase 2A 65 kDa regulatory subunit	PU12228	At3g25800	1.01	-2.04	-2.06
Protein phosphatase 2A 65 kDa regulatory subunit	PU12736	At3g25800	1.04	-1.92	-2.00
PtxA protein precursor	PU03692	At4g15160	1.98	-1.36	-2.69
PtxA protein precursor	PU03793	At4g15160	2.09	-1.42	-2.97
PtxA protein precursor	PU12497	At4g15160	1.62	-1.23	-2.00
Protein destination (06)					
Calcium sensor homolog	PU04805	At5g24270	-1.82	-2.60	-1.43
Protein transport protein SEC61 gamma subunit	PU05824	At4g24920	-1.80	-2.50	-1.39
Cell rescue, defense, cell death and ageing (11)					
Peroxidase	PU01171	At2g22420	-1.55	-2.35	-1.51
Cellular organisation (30)					
Pollen allergen	PU01133	At4g38400	-2.09	-2.42	-1.16
Pollen allergen	PU06328	At4g38400	-3.66	-2.80	1.31
Possibly expansin-like protein	PU05915	At1g69530	1.97	-1.14	-2.24
Classification not yet clear-cut (98)					
Expressed protein	PU00022	At3g15430	-2.29	-2.20	1.04
Expressed protein	PU00768	At3g15430	-2.47	-2.14	1.15
Expressed protein	PU01431	At3g15430	-2.43	-2.04	1.19
Expressed protein	PU01755	At3g15430	-2.24	-2.23	1.01
Expressed protein	PU02181	At4g37300	-2.50	-2.53	-1.01
Expressed protein	PU02241	At5g51550	-1.05	-2.09	-2.00
Expressed protein	PU02279	At3g15430	-2.20	-2.35	-1.07
Expressed protein	PU03447	At2g15960	-3.25	-1.63	1.99
Expressed protein	PU05109	At5g51550	-1.15	-2.02	-1.76
Expressed protein	PU06567	At1g78060	1.52	-1.51	-2.30
Expressed protein	PU06812	At5g51550	-1.09	-2.12	-1.95
Expressed protein	PU07693	At2g17230	-2.40	-2.44	-1.02
Expressed protein	PU07716	At3g15430	-2.38	-1.96	1.22
Expressed protein	PU07779	At5g11090	-1.62	-2.10	-1.29
Expressed protein	PU08808	At5g05270	-1.79	-3.22	-1.80
Expressed protein	PU08856	At5g05270	-1.69	-3.41	-2.02
Expressed protein	PU12444	At2g15960	-2.55	-1.63	1.57

Appendix S5 continued

Function	Clone ID	At gene ID	800/400	1200/400	1200/800
Expressed protein	PU12229	At1g05350	1.40	-1.83	-2.56
Expressed protein	PU13336	At1g61720	-1.62	-3.02	-1.87
Expressed protein	PU13400	At3g08030	1.40	-1.74	-2.44
Pseudo-response regulator 5 (APRR5)	PU00695	At5g24470	-2.29	-1.61	1.42
Unclassified proteins (99)					
Boiling stable protein A	PU00350	At3g17210	-1.54	-2.08	-1.35
Boiling stable protein A	PU01134	At3g17210	-1.43	-2.08	-1.46
Conserved hypothetical protein	PU00175	At1g34650	-1.61	-2.54	-1.58
GDSL-motif lipase/hydrolase-like protein	PU12468	At5g45670	1.48	-1.63	-2.40
Hypothetical protein yncM	PU05373	At5g35650	-1.48	-2.40	-1.62
Populus x generosa pop3 peptide	PU05523	At3g17210	-2.00	-2.70	-1.36
Populus x generosa pop3 peptide	PU12666	At3g17210	-1.81	-2.93	-1.62
Possibly glycine-rich RNA binding protein	PU02308	At2g21660	-2.13	-2.01	1.06
Proline-rich cell wall protein	PU08800	At2g14890	-1.35	-2.17	-1.60
Wound-induced protein	PU05421	At4g10270	-1.70	-2.08	-1.22

Appendix S6. Effect of long-term stable increases in [CO₂] on the expression profile of energy-related genes in leaf and stem tissue
Relative expression refers to fold changes between the two samples. Values printed in bold are statistically significant with B-statistic ≥ 10

Function	Clone ID	Gene ID	Relative expression					
			Leaves			Stems		
			800/400	1200/400	1200/800	800/400	1200/400	1200/800
Energy								
GTP-binding protein	PU03856	At1g02280	-1.15	-1.19	-1.04	-1.11	-1.21	-1.09
GTP-binding protein	PU07129	At1g02280	-1.02	1.01	1.03	-1.09	-1.13	-1.03
Cytochrome b-561, putative	PU03011	At1g26100	1.14	-0.96	-1.10	1.07	1.36	1.27
Nodulin-like protein	PU03199	At1g80530	-1.08	0.95	1.03	-1.06	-1.03	1.02
Nodulin-like protein	PU05979	At1g80530	1.02	1.12	1.10	1.03	-1.06	-1.10
NADH dehydrogenase subunit 6 (EC 1.6.5.3)	PU10445	At2g29990	-1.14	-1.15	-1.01	1.09	1.14	1.05
NADH dehydrogenase subunit 6 (EC 1.6.5.3)	PU10493	At2g29990	-1.30	-1.43	-1.10	-1.41	-1.03	1.36
Expressed protein	PU01329	At2g38710	-1.05	-1.19	-1.13	1.07	-1.04	-1.11
Expressed protein	PU02141	At2g38710	1.03	0.98	-1.05	-1.46	-1.79	-1.22
Expressed protein	PU07776	At2g38710	1.07	-0.98	-1.05	1.14	1.13	1.00
Expressed protein	PU09022	At3g13200	0.93	1.01	1.09	-1.02	1.00	1.02
Copper chaperone COX17-1	PU01971	At3g15352	-1.15	-1.02	1.13	-1.30	1.01	1.32
Heat shock transcription factor 29	PU06279	At3g15352	-1.03	-1.83	-1.77	1.48	1.83	1.23
Expressed protein	PU06918	At3g59650	-1.06	1.03	1.09	-1.03	-1.14	-1.10
NADH dehydrogenase	PU00242	At4g05020	1.00	1.00	-1.01	-1.49	-1.01	1.47
NADH dehydrogenase	PU06352	At4g05020	1.01	1.05	1.04	-1.21	-1.40	-1.16
NADH dehydrogenase	PU12467	At4g05020	1.08	1.11	1.02	1.16	-1.15	-1.34
NADH dehydrogenase	PU13025	At4g05020	1.05	-1.01	-1.06	-1.08	-1.15	0.94
Expressed protein	PU03072	At4g25570	-1.11	-1.04	1.07	-1.14	-1.14	1.00
Cytochrome	PU05666	At4g25570	-1.04	1.06	1.11	1.19	1.29	1.08
Expressed protein	PU08772	At4g30480	1.03	1.09	1.06	1.32	1.20	-1.10
Expressed protein	PU11656	At4g30480	-1.04	-1.02	1.02	1.17	1.44	1.23
Expressed protein	PU01515	At4g37830	1.06	-1.04	-1.10	1.04	-1.08	-1.12
Cytochrome b-561	PU04189	At5g38630	-1.05	-1.00	1.05	-1.06	-1.23	-1.16
NADH dehydrogenase 10.5K chain-like protein	PU07349	At5g47890	-1.06	-1.07	1.00	1.04	-1.18	-1.23
NADH dehydrogenase 10.5K chain-like protein	PU11338	At5g47890	-1.07	-1.02	1.05	-2.43	-1.05	2.31
Electron transport								
Expressed protein	PU03523	At1g02890	-1.10	-1.02	1.08	-1.15	1.02	1.17
Expressed protein	PU07912	At1g02890	1.04	1.05	1.01	1.03	1.11	1.08
Expressed protein	PU05615	At1g02890	-1.06	-1.01	1.05	-1.07	1.00	1.07
Expressed protein	PU09034	At1g07180	1.12	-1.11	-1.25	-1.16	1.04	1.21
Ascorbate peroxidase	PU00482	At1g07890	1.13	1.06	-1.07	1.20	1.03	-1.16
Expressed protein	PU04224	At1g07960	1.24	-1.12	-1.39	1.15	1.38	1.19
Thioredoxin	PU11159	At1g08570	-1.58	-1.92	-1.22	1.54	1.80	1.17
Thioredoxin	PU09808	At1g08570	-1.51	-1.75	-1.16	1.41	1.52	1.07
Ferredoxin-like protein	PU11735	At1g10960	1.07	-1.05	-1.12	1.25	1.64	1.31
Ferredoxin-like protein	PU08371	At1g10960	1.03	-1.08	-1.11	-1.06	-1.24	-1.17
Mandelonitrile lyase	PU11698	At1g14190	-1.03	-1.04	-1.01	-1.17	1.08	1.27
Thioredoxin, putative	PU13348	At1g15020	1.12	1.16	1.03	-1.19	-1.11	1.07
Expressed protein	PU07348	At1g17130	-1.21	-1.10	1.10	-1.24	1.10	1.37
Expressed protein	PU00596	At1g17130	-1.02	-1.03	-1.02	-1.12	-1.21	-1.09
Plastocyanin B, chloroplast precursor	PU06425	At1g20340	1.02	1.05	1.03	1.46	1.35	-1.08
Protein disulfide isomerase precursor (PDI) (EC 5.3.4.1)	PU07520	At1g21750	-1.02	1.06	1.08	-1.27	-1.23	1.04
Protein disulfide isomerase precursor (PDI) (EC 5.3.4.1)	PU06743	At1g21750	-1.03	1.06	1.09	-1.21	-1.18	1.02
Protein disulfide isomerase precursor (PDI) (EC 5.3.4.1)	PU06399	At1g21750	1.01	1.12	1.10	-1.18	-1.17	1.01
Protein disulfide isomerase precursor (PDI) (EC 5.3.4.1)	PU03931	At1g21750	-1.04	1.16	1.20	-1.22	-1.21	1.00
Protein disulfide isomerase precursor (PDI) (EC 5.3.4.1)	PU07569	At1g21750	-1.04	1.05	1.09	-1.17	-1.24	-1.06

Appendix S6 continued

Function	Clone ID	Gene ID	Relative expression					
			Leaves			Stems		
			800/400	1200/400	1200/800	800/400	1200/400	1200/800
Subunit 6b of cytochrome c oxidase	PU05707	At1g22450	-1.04	-1.05	-1.02	1.10	1.24	1.12
POSSIBLY Subunit 6b of cytochrome c oxidase	PU06811	At1g22450	-1.03	-1.05	-1.02	-1.13	-1.02	1.11
Subunit 6b of cytochrome c oxidase	PU09162	At1g22450	1.05	1.03	-1.02	-1.12	-1.15	-1.03
Subunit 6b of cytochrome c oxidase	PU07566	At1g22450	1.03	-1.09	-1.12	1.13	1.01	-1.12
Subunit 6b of cytochrome c oxidase	PU04711	At1g22450	1.00	1.16	1.15	1.02	-1.10	-1.12
Superoxide-generating NADPH oxidase flavocytochrome	PU00451	At1g23020	-1.12	-1.18	-1.06	-1.04	1.55	1.60
Thylakoid structural protein	PU08928	At1g23040	1.02	-1.03	-1.05	-1.13	1.01	1.15
Expressed protein	PU01489	At1g25682	-1.08	-1.05	1.03	-1.38	-1.63	-1.18
Unknown protein (At1g34780; F21H2.1)	PU07900	At1g34780	-1.05	1.01	1.06	-1.32	1.23	1.62
Unknown protein (At1g34780; F21H2.1)	PU03267	At1g34780	-1.03	1.07	1.11	-1.05	-1.12	-1.06
Protein disulfide isomerase, putative (At1g35620)	PU04229	At1g35620	-1.07	-1.05	1.03	1.03	-1.23	-1.27
Hypothetical protein, 5 partial	PU06485	At1g50140	-1.02	1.05	1.07	-1.25	-1.18	1.06
Thioredoxin like protein	PU09242	At1g50320	-1.06	-1.25	-1.18	-1.13	1.04	1.17
Electron transport flavo protein-related	PU06854	At1g50940	1.00	1.04	1.04	-1.11	-1.00	1.10
ATP synthase epsilon chain, mitochondrial (EC 3.6.3.14)	PU06522	At1g51650	1.02	1.01	-1.01	1.04	1.01	-1.04
ATP synthase epsilon chain, mitochondrial (EC 3.6.3.14)	PU00785	At1g51650	1.03	-1.01	-1.04	1.20	-1.12	-1.34
Protein disulfide isomerase precursor, putative	PU06713	At1g52260	1.04	-1.01	-1.05	-1.04	1.09	1.14
Expressed protein	PU09474	At1g60420	-1.26	-1.36	-1.08	-1.09	2.04	2.24
Expressed protein	PU00630	At1g60420	1.06	1.33	1.25	1.35	2.13	1.58
Expressed protein	PU09971	At1g60420	-1.05	1.18	1.24	1.35	2.12	1.56
Expressed protein	PU08865	At1g60420	1.04	-1.22	-1.27	-1.07	1.09	1.17
Expressed protein	PU04090	At1g60420	-1.09	-1.02	1.07	1.04	-1.04	-1.08
Blue copper protein precursor	PU00078	At1g72230	1.25	-1.05	-1.31	1.39	2.41	1.74
Blue copper protein precursor	PU00221	At1g72230	1.03	1.01	-1.02	1.24	1.83	1.47
Blue copper protein precursor	PU06349	At1g72230	1.35	1.17	-1.16	1.07	1.40	1.31
Blue copper protein precursor	PU01792	At1g72230	1.11	1.09	-1.01	1.02	1.29	1.26
Blue copper protein precursor	PU01814	At1g72230	1.17	1.10	-1.06	1.31	1.63	1.24
Blue copper protein precursor	PU01766	At1g72230	1.08	1.06	-1.02	-1.28	-1.04	1.24
Blue copper protein precursor	PU07720	At1g72230	1.31	1.13	-1.16	1.37	1.66	1.22
Blue copper protein precursor	PU02148	At1g72230	1.11	1.04	-1.07	1.69	1.65	-1.03
Expressed protein	PU12038	At1g72970	1.02	1.03	1.01	-1.18	1.45	1.72
Alcohol dehydrogenase 2 (EC 1.1.1.1)	PU10963	At1g77120	1.22	-1.60	-1.95	3.06	6.16	2.01
Alcohol dehydrogenase 2 (EC 1.1.1.1)	PU03309	At1g77120	1.29	-1.48	-1.90	1.98	2.84	1.43
Alcohol dehydrogenase 2 (EC 1.1.1.1)	PU03813	At1g77120	1.31	-1.47	-1.92	1.87	2.48	1.33
Alcohol dehydrogenase 2 (EC 1.1.1.1)	PU03141	At1g77120	1.31	1.08	-1.21	-1.40	-1.12	1.25
Alcohol dehydrogenase 2 (EC 1.1.1.1)	PU04010	At1g77120	1.14	1.32	1.16	1.49	1.34	-1.12
Alcohol dehydrogenase 2 (EC 1.1.1.1)	PU00686	At1g77120	1.07	1.19	1.12	1.41	1.18	-1.19
Cytochrome c oxidase subunit-related	PU00816	At1g80230	1.04	1.02	-1.02	-1.05	-1.15	-1.10
Cytochrome c oxidase subunit-related	PU09005	At1g80230	-1.00	-1.04	-1.04	-1.07	-1.31	-1.22
Expressed protein	PU04246	At2g01270	-1.02	1.11	1.13	1.03	1.20	1.17
Expressed protein	PU13431	At2g01270	-1.10	1.01	1.11	-1.09	-1.06	1.03
Expressed protein	PU11983	At2g01270	1.04	1.00	-1.03	-1.29	-1.30	-1.01
Expressed protein	PU12007	At2g01270	-1.07	1.03	1.10	1.11	1.10	-1.01
Ferredoxin-thioredoxin reductase	PU03626	At2g04700	-1.03	-1.10	-1.06	1.05	1.05	1.00
AAA-type ATPase	PU07903	At2g18190	1.03	1.05	1.01	-1.05	1.10	1.16
AAA-type ATPase	PU08086	At2g18190	1.17	1.07	-1.09	1.55	1.22	-1.27
ATP binding protein	PU02621	At2g18990	1.11	1.06	-1.04	-1.04	-1.03	1.01
ATP binding protein	PU03028	At2g18990	1.16	1.16	-1.00	1.07	1.00	-1.07
Expressed protein	PU02323	At2g25950	-1.06	1.16	1.22	-1.16	1.01	1.17
Expressed protein	PU12566	At2g26070	-1.01	-1.06	-1.05	-1.33	1.28	1.70
Post-floral-specific protein (PPF-1 protein)	PU10280	At2g28800	-1.14	-1.18	-1.04	1.11	1.18	1.06

Appendix S6 continued

Function	Clone ID	Gene ID	Relative expression					
			Leaves			Stems		
			800/400	1200/400	1200/800	800/400	1200/400	1200/800
Dicyanin	PU12528	At2g32300	1.06	1.21	1.13	1.21	2.09	1.73
Dicyanin	PU08771	At2g32300	1.13	-1.17	-1.32	-1.20	1.28	1.54
ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14)	PU08227	At2g33040	1.06	1.05	-1.01	1.04	1.17	1.13
ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14)	PU00245	At2g33040	1.10	-1.02	-1.12	1.10	1.21	1.09
ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14)	PU07178	At2g33040	1.07	1.07	-1.00	1.09	-1.23	-1.34
Expressed protein	PU01082	At2g35760	1.02	1.12	1.09	1.00	-1.00	-1.01
Expressed protein	PU13187	At2g38000	-1.30	-1.40	-1.08	-1.30	-1.14	1.14
Expressed protein	PU08168	At2g38270	-1.08	1.05	1.14	-1.08	-1.00	1.08
Expressed protein	PU09202	At2g46620	-1.12	-1.06	1.06	-1.09	1.10	1.20
Cytochrome c oxidase subunit 5c	PU03822	At2g47380	-1.01	1.11	1.12	1.00	1.07	1.06
Cytochrome c oxidase subunit 5c	PU13166	At2g47380	1.02	1.03	1.01	-1.04	-1.32	-1.27
Protein disulfide-isomerase	PU01124	At2g47470	-1.10	-1.23	-1.12	-1.08	1.33	1.43
Protein disulfide-isomerase	PU03843	At2g47470	-1.24	-1.19	1.04	-1.23	-1.38	-1.12
Protein disulfide-isomerase	PU00220	At2g47470	1.08	1.16	1.08	1.13	-1.07	-1.21
Protein disulfide-isomerase	PU00748	At2g47470	1.05	1.12	1.06	1.13	-1.12	-1.27
AAA ATPase	PU04682	At3g01610	-1.00	-1.05	-1.05	-1.09	-1.12	-1.03
Thioredoxin F-type, chloroplast precursor (TRX-F)	PU10314	At3g02730	1.03	-1.00	-1.04	1.18	1.05	-1.12
Expressed protein	PU04016	At3g03100	1.09	1.08	-1.01	-1.36	-1.50	-1.10
Expressed protein	PU04675	At3g04340	1.03	-1.06	-1.09	-1.08	-1.13	-1.05
Expressed protein	PU02721	At3g04780	1.01	-1.01	-1.03	-1.21	-1.19	1.02
Expressed protein	PU07387	At3g04780	1.11	1.03	-1.07	1.47	1.36	-1.08
Phytochrome B2	PU12031	At3g06310	1.03	-1.06	-1.09	-1.02	-1.12	-1.11
Expressed protein	PU09291	At3g06390	1.05	-1.23	-1.28	-1.19	1.04	1.24
Thioredoxin-like protein	PU03807	At3g08710	-1.14	1.01	1.15	-1.18	1.05	1.24
Ascorbate peroxidase 2	PU02971	At3g09640	-1.20	1.06	1.27	-1.07	1.17	1.25
Ascorbate peroxidase 3	PU06690	At3g09640	1.18	1.20	1.02	1.14	1.08	-1.05
Expressed protein	PU09520	At3g12260	-1.02	-1.04	-1.02	1.13	1.36	1.20
Expressed protein	PU07694	At3g12260	1.09	1.04	-1.05	-1.06	-1.06	1.00
Expressed protein	PU02427	At3g12260	1.03	-1.06	-1.09	-1.13	-1.14	-1.01
Expressed protein	PU12169	At3g12260	-1.26	-1.04	1.21	-1.02	-1.07	-1.05
Hypothetical protein	PU02278	At3g15140	1.01	1.00	1.07	1.15	1.58	1.37
Hypothetical protein	PU12294	At3g15140	1.05	1.03	-1.02	-1.30	-1.22	1.06
Hypothetical protein	PU00118	At3g15140	-1.07	1.03	1.10	-1.19	-1.20	-1.01
Thioredoxin M-type, chloroplast precursor (TRX-M)	PU09582	At3g15360	-1.04	-1.10	-1.05	1.07	1.32	1.23
Thioredoxin m2	PU02636	At3g15360	-1.25	-1.06	1.18	1.05	1.25	1.20
Thioredoxin M-type, chloroplast precursor (TRX-M)	PU10123	At3g15360	-1.01	-1.04	-1.03	-1.32	-1.13	1.16
Glutathione reductase, cytosolic (EC 1.8.1.7)	PU05036	At3g24170	1.10	1.13	1.03	-1.16	1.04	1.20
Glutathione reductase, cytosolic	PU09132	At3g24170	1.08	1.05	-1.03	-1.10	-1.10	-1.00
MRP protein (ATP/GTP-binding protein)	PU08754	At3g24430	1.15	-1.07	-1.24	1.20	1.14	-1.06
Rubisco expression protein-related	PU05851	At3g24530	-1.05	1.08	1.14	-1.28	-1.06	1.21
Rubisco expression protein-related	PU07539	At3g24530	-1.12	1.15	1.29	1.13	1.29	1.14
Expressed protein	PU01533	At3g24730	1.03	1.03	1.00	1.07	-1.07	-1.15
Blue copper protein, putative	PU00311	At3g27200	-1.06	-1.02	1.03	-1.04	1.26	1.31
NADPH:quinone oxidoreductase (NQR)	PU02208	At3g27890	1.22	1.22	1.00	-1.25	-1.22	1.02
Expressed protein	PU05692	At3g28540	1.07	1.03	-1.04	-1.21	-1.18	1.02
Expressed protein	PU02639	At3g44370	-1.01	-1.07	-1.06	-1.22	-1.18	1.03
Expressed protein	PU08438	At3g48200	-1.16	-1.35	-1.16	-1.08	1.02	1.10
Thioredoxin H	PU08713	At3g51030	1.06	-1.00	-1.06	1.05	1.24	1.18
Thioredoxin H	PU01266	At3g51030	1.09	1.04	-1.06	1.28	1.36	1.06
Thioredoxin H	PU02305	At3g51030	1.00	1.02	1.01	1.32	1.31	-1.01

Appendix S6 continued

Function	Clone ID	Gene ID	Relative expression					
			Leaves			Stems		
			800/400	1200/400	1200/800	800/400	1200/400	1200/800
Expressed protein	PU04399	At3g51040	-1.14	-1.10	1.04	1.25	1.12	-1.11
Expressed protein	PU00636	At3g51040	1.03	1.05	1.02	-1.07	-1.39	-1.30
Cell division cycle protein 48 homolog	PU06260	At3g53230	1.10	-1.06	-1.16	1.02	1.01	-1.01
Cell division cycle protein 48 homolog	PU08037	At3g53230	1.11	-1.03	-1.14	1.06	1.02	-1.03
Cell division cycle protein 48 homolog	PU01047	At3g53230	1.09	-1.02	-1.11	1.19	-1.03	-1.23
Cell division cycle protein 48 homolog	PU00805	At3g53230	1.11	-1.06	-1.18	1.12	-1.13	-1.26
Expressed protein	PU07658	At3g54900	-1.08	-1.08	-1.01	1.09	1.26	1.16
Protein disulfide-isomerase-like protein	PU06421	At3g54960	1.14	-1.02	-1.16	-1.11	1.64	1.83
Protein disulfide-isomerase-like protein	PU04109	At3g54960	1.15	-1.08	-1.23	-1.01	1.45	1.47
Protein disulfide-isomerase-like protein	PU11184	At3g54960	1.13	-1.04	-1.18	1.06	1.39	1.31
Protein disulfide-isomerase-like protein	PU11662	At3g54960	1.18	1.05	-1.12	-1.02	-1.17	-1.14
Quinone reductase-like protein	PU09353	At3g56460	1.05	-1.17	-1.23	1.01	1.42	1.41
Quinone reductase-like protein	PU04749	At3g56460	1.03	-1.10	-1.13	-1.91	-1.80	1.06
Uclacyanin 3	PU00579	At3g60280	1.03	-1.13	-1.16	1.12	-1.00	-1.13
Uclacyanin 3	PU09517	At3g60280	-1.12	-1.22	-1.08	-1.15	-1.52	-1.32
Uclacyanin 3-like protein	PU07655	At3g60280	-1.04	-1.03	1.01	1.55	1.12	-1.38
ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14)	PU11720	At4g04640	-1.08	-1.16	-1.07	1.04	1.44	1.38
N-ethylmaleimide sensitive fusion protein	PU10622	At4g04910	-1.08	-1.04	1.04	-1.06	-1.07	-1.01
Thioredoxin	PU04768	At4g04950	1.23	-1.08	-1.32	-1.06	1.04	1.11
Thioredoxin	PU11601	At4g04950	1.07	-1.02	-1.09	1.01	1.08	1.07
Oxygen-evolving enhancer protein 3, chloroplast	PU09326	At4g05180	-1.08	1.00	1.08	-1.02	1.21	1.23
Oxygen-evolving enhancer protein 3, chloroplast	PU08604	At4g05180	-1.07	-1.04	1.03	1.29	1.19	-1.08
Ferredoxin-NADP reductase, root isozyme, chloroplast precursor(EC 1.18.1.2)	PU09707	At4g05390	-1.14	1.06	1.20	-1.01	-1.01	-1.00
Ferredoxin-NADP reductase, root isozyme, chloroplast precursor(EC 1.18.1.2)	PU11991	At4g05390	-1.07	1.14	1.22	-1.06	-1.15	-1.09
Blue copper-binding protein, 15K (lamin)	PU02010	At4g12880	1.07	1.11	1.04	-1.20	-1.13	1.07
Ferredoxin	PU10882	At4g14890	1.07	1.00	-1.07	-1.03	1.19	1.23
ATP binding protein-like	PU06010	At4g19540	-1.00	-1.00	1.00	-1.11	-1.14	-1.03
ATP binding protein-like	PU11721	At4g19540	1.00	1.05	1.04	1.74	1.19	-1.47
Expressed protein	PU02280	At4g25650	-1.01	-1.29	-1.27	1.06	1.25	1.18
Zinc-finger protein zfs1	PU04450	At4g25650	-1.13	-1.04	1.09	1.29	1.36	1.05
Hypothetical 10.4 kDa protein	PU11317	At4g25650	-1.16	-1.16	-1.00	-1.19	-1.24	-1.04
Expressed protein	PU06126	At4g25650	-1.06	-1.19	-1.12	1.02	-1.24	-1.27
Expressed protein	PU02475	At4g27680	1.02	-1.07	-1.08	-1.03	-1.22	-1.18
Thioredoxin-like protein	PU05816	At4g29670	-1.10	-1.14	-1.03	-1.20	-1.08	1.11
Expressed protein	PU05086	At4g29720	-1.01	1.24	1.26	-1.14	-1.02	1.11
Thiol-disulfide interchange like protein	PU10918	At4g37200	-1.10	-1.21	-1.10	-1.18	-1.07	1.11
Thiol-disulfide interchange like protein	PU08989	At4g37200	-1.11	-1.19	-1.07	-1.08	-1.01	1.07
Hypothetical membrane-spanning protein FN0587	PU11785	At5g06430	-1.14	1.07	1.22	1.09	1.09	1.00
Expressed protein	PU02378	At5g08290	-1.01	1.18	1.19	-1.05	1.06	1.11
Expressed protein	PU12251	At5g08290	-1.08	1.15	1.24	1.07	1.12	1.05
Ubiquinol-cytochrome C reductase iron-sulfur subunit 2, mitochondrial precursor (EC 1.10.2.2)	PU02083	At5g13430	1.05	1.03	-1.03	-1.06	1.06	1.12
Ubiquinol-cytochrome C reductase iron-sulfur subunit 2, mitochondrial precursor (EC 1.10.2.2)	PU01640	At5g13430	1.05	1.01	-1.04	-1.05	-1.26	-1.20
Expressed protein	PU01070	At5g14240	1.06	1.07	1.01	-1.10	-1.13	-1.03
Ubiquinol-cytochrome C reductase complex ubiquinone-binding protein QP-C	PU10802	At5g15350	-1.06	-1.22	-1.16	-1.22	1.03	1.26
Lamin	PU00874	At5g15350	1.02	1.20	1.18	-1.06	1.01	1.07
Stellacyanin	PU10974	At5g20230	1.01	-1.22	-1.23	-1.04	-1.06	-1.02

Appendix S6 continued

Function	Clone ID	Gene ID	Relative expression					
			800/400	Leaves		Stems		1200/800
				1200/400	1200/800	800/400	1200/400	
Copper binding protein-like, predicted GPI-anchored protein	PU07669	At5g26330	-1.03	1.14	1.17	-1.35	-1.08	1.24
Copper binding protein-like, predicted GPI-anchored protein	PU06849	At5g26330	-1.08	-1.21	-1.11	-1.04	-1.03	1.01
Copper binding protein-like, predicted GPI-anchored protein	PU01898	At5g26330	1.13	1.02	-1.11	-1.01	-1.13	-1.11
Expressed protein	PU11927	At5g26940	-1.03	-1.18	-1.14	-1.10	-1.13	-1.03
Expressed protein	PU11208	At5g26940	-1.01	-1.09	-1.08	1.14	1.04	-1.10
Unknown protein (A_TM021B04.14)	PU02512	At5g27280	-1.16	1.03	1.20	1.18	-1.04	-1.22
Thioredoxin	PU05726	At5g39950	1.05	1.21	1.16	-1.31	-1.10	1.19
Thioredoxin	PU10821	At5g39950	-1.09	1.05	1.15	-1.33	-1.13	1.18
Expressed protein	PU11815	At5g40010	-1.17	-1.06	1.11	1.17	2.04	1.74
Expressed protein	PU01068	At5g40010	-1.08	1.11	1.20	-1.34	1.06	1.42
Expressed protein	PU09009	At5g49580	1.05	-1.00	-1.05	1.03	1.04	1.01
DNA repair protein-like	PU12831	At5g50340	-1.06	-1.19	-1.13	1.03	1.22	1.19
Expressed protein	PU00787	At5g52840	1.05	1.07	1.02	-1.06	-1.18	-1.11
Predicted GPI-anchored protein	PU07706	At5g53870	-1.08	-1.11	-1.03	-1.31	1.01	1.32
Dihydropteroate synthase	PU02143	At5g53870	1.14	-1.40	-1.59	-1.21	-1.06	1.14
Predicted GPI-anchored protein	PU13084	At5g53870	1.01	1.09	1.08	-1.21	-1.10	1.10
Hypothetical 31.5 kDa protein	PU13079	At5g53870	-1.14	-1.12	1.01	-1.52	-1.40	1.09
Expressed protein	PU06536	At5g56090	-1.14	-1.05	1.09	1.02	1.17	1.14
Expressed protein	PU13308	At5g56090	-1.04	1.03	1.06	-1.15	-1.21	-1.05
Expressed protein	PU06222	At5g57815	1.07	-1.07	-1.14	1.15	-1.11	-1.28
Protein disulfide isomerase precursor-like	PU01054	At5g60640	-1.11	-1.16	-1.05	1.10	1.15	1.05
Ferredoxin-NADP reductase, chloroplast precursor (EC 1.18.1.2)	PU09343	At5g66190	1.02	1.01	-1.01	1.29	1.76	1.36
Chloroplast ferredoxin-NADP+ oxidoreductase precursor (EC 1.18.1.2)	PU08844	At5g66190	1.02	-1.03	-1.05	1.24	1.51	1.22
Ferredoxin-NADP reductase, chloroplast precursor (EC 1.18.1.2)	PU09345	At5g66190	1.01	1.03	1.02	1.51	1.70	1.12
Expressed protein	PU02633	At5g66410	-1.07	-1.03	1.04	-1.45	-1.63	-1.13
Respiration								
AAA-metalloprotease FtsH	PU04020	At1g07510	-1.04	-1.08	-1.04	-1.32	1.18	1.57
AAA-metalloprotease FtsH	PU04056	At1g07510	1.11	1.00	-1.10	-1.16	1.28	1.49
Unknown protein (At1g07510)	PU08044	At1g07510	1.10	-1.01	-1.11	-1.02	1.02	1.04
AAA-metalloprotease FtsH	PU01723	At1g07510	1.05	1.03	-1.02	-1.07	-1.12	-1.05
Response regulator (two component phosphotransfer signalling)	PU01865	At1g74890	1.04	1.63	1.57	-1.21	1.08	1.31
Expressed protein	PU00494	At2g11000	-1.08	-1.00	1.08	1.07	-1.03	-1.10
Ethylene receptor	PU09099	At3g23150	1.14	1.21	1.07	1.18	-1.06	-1.25
Ethylene receptor	PU01195	At3g23150	-1.07	1.03	1.10	-1.28	-1.66	-1.29
Response regulator 5	PU06571	At3g57040	1.08	1.44	1.33	1.26	1.31	1.04
Response regulator	PU04052	At3g57040	-1.09	-1.22	-1.11	-1.33	-2.07	-1.55
Predicted protein	PU00870	At4g31920	-1.07	1.02	1.10	1.02	-1.09	-1.11
Expressed protein	PU06238	At5g42870	-1.03	-1.03	1.00	-1.12	1.25	1.40
Phytocyanin/early nodulin-like protein	PU12582	At5g57920	-1.58	-1.11	1.43	-1.59	-1.53	1.04
Fermentation								
FtsH-like protein Pftf precursor	PU01020	At1g06430	-1.03	-1.04	-1.01	1.08	-1.23	-1.32
Chloroplast FtsH protease, putative	PU03119	At1g50250	1.02	-1.01	-1.03	1.06	1.08	1.02
Chloroplast FtsH protease, putative	PU10600	At1g50250	1.01	-1.13	-1.14	1.21	1.42	1.18
Chloroplast FtsH protease, putative	PU05638	At1g50250	-1.03	-1.12	-1.09	1.08	1.11	1.03
FtsH like cell division protein	PU06109	At1g79560	-1.14	-1.00	1.14	-1.03	-1.15	-1.12
Photosynthesis								
Photosystem I reaction centre subunit II, chloroplast precursor	PU10316	At1g03130	-1.05	1.07	1.12	1.19	1.33	1.12

Appendix S6 continued

Function	Clone ID	Gene ID	Relative expression					
			Leaves		Stems			
			800/400	1200/400	1200/800	800/400	1200/400	1200/800
Photosystem I reaction centre subunit II, chloroplast precursor	PU08452	At1g03130	-1.05	-1.03	1.02	1.21	1.32	1.10
Photosystem I reaction centre subunit II, chloroplast precursor	PU10272	At1g03130	-1.01	1.05	1.07	1.14	1.20	1.05
Photosystem I reaction centre subunit II, chloroplast precursor	PU08974	At1g03130	-1.12	1.00	1.12	1.32	1.21	-1.09
Photosystem I reaction centre subunit II, chloroplast precursor	PU09496	At1g03130	1.14	1.01	-1.13	1.14	-1.10	-1.25
Expressed protein	PU09899	At1g06150	1.03	1.05	1.02	1.02	-1.02	-1.04
Oxygen-evolving enhancer protein 2, chloroplast [Precursor]	PU08552	At1g06680	-1.06	-1.03	1.03	1.03	1.19	1.15
Oxygen-evolving enhancer protein 2, chloroplast [Precursor]	PU01695	At1g06680	-1.11	-1.06	1.05	1.27	1.24	-1.02
PsbQ domain protein family extrinsic pII protein	PU09569	At1g14150	-1.10	-1.15	-1.05	1.25	1.11	-1.13
(Putative DNA-binding protein)	PU08018	At1g15480	-1.16	1.10	1.28	-1.01	-1.21	-1.20
Chlorophyll a/b-binding protein CP24	PU12865	At1g15820	1.03	-1.08	-1.11	-1.30	1.07	1.39
Chlorophyll a/b-binding protein CP24	PU09300	At1g15820	1.08	1.17	1.08	1.01	1.21	1.20
Chlorophyll a/b-binding protein CP24	PU12094	At1g15820	-1.06	-1.19	-1.13	1.11	1.16	1.05
Chlorophyll a/b-binding protein CP24	PU10089	At1g15820	1.02	1.00	-1.02	1.03	1.04	1.01
Light-harvesting chlorophyll a/b binding protein	PU08870	At1g19150	-1.08	-1.08	1.00	1.24	1.19	-1.04
Photosystem I subunit X precursor	PU08421	At1g30380	1.04	-1.07	-1.11	1.38	1.49	1.08
Photosystem I subunit X precursor	PU07325	At1g30380	-1.00	-1.07	-1.07	1.29	1.36	1.06
Photosystem I reaction centre subunit III	PU01658	At1g31330	1.01	-1.04	-1.05	-1.07	1.05	1.13
Photosystem I reaction centre subunit III	PU08515	At1g31330	1.01	1.01	-1.00	1.07	1.08	1.02
Pyruvate kinase isozyme G, chloroplast (EC 2.7.1.40)	PU08246	At1g32440	1.09	-1.31	-1.44	-1.31	1.01	1.32
PSII K protein	PU09437	At1g33000	1.12	-1.39	-1.55	1.03	-1.01	-1.04
Photosystem II 22 kDa protein, chloroplast precursor (CP22)	PU11626	At1g44575	-1.08	-1.05	1.03	1.19	1.49	1.25
Photosystem II 22 kDa protein, chloroplast precursor (CP22)	PU08493	At1g44575	-1.09	-1.05	1.04	-1.03	1.19	1.22
Photosystem I reaction center subunit V, chloroplast precursor	PU08897	At1g55670	-1.07	-1.06	1.01	1.35	1.18	-1.15
PSI type III chlorophyll a/b-binding protein	PU09129	At1g61520	-1.04	-1.02	1.02	1.63	1.53	-1.07
PSI type III chlorophyll a/b-binding protein	PU11127	At1g61520	1.01	1.03	1.02	1.54	1.34	-1.15
PSI type III chlorophyll a/b-binding protein	PU09641	At1g61520	1.03	1.02	-1.01	1.68	1.45	-1.16
PSI type III chlorophyll a/b-binding protein	PU04287	At1g61520	1.05	-1.10	-1.16	1.57	1.35	-1.17
Protein psbY-1 (psbY-A1); Photosystem II protein psbY-2 (psbY-A2)	PU09897	At1g67740	-1.07	-1.02	1.05	-1.02	1.16	1.19
Protein psbY-1 (psbY-A1); Photosystem II protein psbY-2 (psbY-A2)	PU08423	At1g67740	-1.02	-1.14	-1.12	1.25	1.23	-1.02
Protein psbY-1 (psbY-A1); Photosystem II protein psbY-2 (psbY-A2)	PU09945	At1g67740	-1.03	-1.16	-1.13	1.33	1.29	-1.03
Unknown protein	PU09225	At1g77090	1.01	-1.11	-1.12	1.99	2.08	1.04
Photosystem II 10 kDa polypeptide, chloroplast precursor	PU10192	At1g79040	-1.01	-1.00	1.01	-1.17	1.32	1.54
Photosystem II 10 kDa polypeptide, chloroplast precursor	PU08701	At1g79040	-1.09	-1.02	1.07	-1.60	-1.08	1.47
Photosystem II 10 kDa polypeptide, chloroplast precursor	PU09470	At1g79040	-1.10	1.05	1.16	-1.17	1.20	1.40
Photosystem II 10 kDa polypeptide, chloroplast precursor	PU09038	At1g79040	-1.03	-1.00	1.03	-1.03	1.25	1.29
Photosystem II 10 kDa polypeptide, chloroplast precursor	PU09360	At1g79040	-1.07	-1.02	1.05	-1.00	1.26	1.26

Appendix S6 continued

Function	Clone ID	Gene ID	Relative expression					
			Leaves			Stems		
			800/400	1200/400	1200/800	800/400	1200/400	1200/800
Photosystem II 10 kDa polypeptide, chloroplast precursor	PU02413	At1g79040	1.03	1.14	1.12	1.18	1.32	1.12
Photosystem II 10 kDa polypeptide, chloroplast precursor	PU10701	At1g79040	-1.01	-1.01	-1.00	1.31	1.27	-1.03
Unknown protein (At1g80270; F5I6.2)	PU13218	At1g80270	1.03	1.06	1.03	-1.19	-1.18	1.01
Unknown protein (At1g80270; F5I6.2)	PU02399	At1g80270	-1.07	-1.14	-1.07	1.10	-1.05	-1.15
expressed protein	PU08797	At2g04860	-1.01	-1.04	-1.03	-1.83	1.34	2.46
Light harvesting chlorophyll A/B binding protein	PU09118	At2g05070	1.05	-1.20	-1.25	1.00	1.15	1.15
Light harvesting chlorophyll A/B binding protein	PU10691	At2g05070	1.03	-1.04	-1.08	1.02	1.15	1.13
Light harvesting chlorophyll A/B binding protein	PU08637	At2g05070	1.06	-1.13	-1.20	1.01	1.09	1.08
Light harvesting chlorophyll A/B binding protein	PU09362	At2g05070	1.03	-1.16	-1.20	1.07	1.15	1.08
Light harvesting chlorophyll A/B binding protein	PU09175	At2g05070	1.12	-1.17	-1.31	1.07	1.16	1.08
Light harvesting chlorophyll A/B binding protein	PU01826	At2g05070	1.16	-1.19	-1.38	1.01	1.09	1.07
Photosystem II reaction center W protein, chloroplast precursor (PSII6.1 kDa protein)	PU11769	At2g30570	-1.03	-1.08	-1.05	1.01	1.31	1.30
Photosystem II reaction center W protein, chloroplast precursor (PSII6.1 kDa protein)	PU02972	At2g30570	1.01	-1.10	-1.10	-1.21	1.05	1.26
Photosystem II reaction center W protein, chloroplast precursor (PSII6.1 kDa protein)	PU10194	At2g30570	-1.01	1.04	1.05	-1.04	-1.20	-1.15
Expressed protein	PU12277	At2g34400	-1.02	-1.03	-1.01	1.09	-1.36	-1.48
Chlorophyll A/B binding protein precursor	PU08388	At2g34430	-1.03	1.00	1.03	1.08	1.20	1.12
Chlorophyll A/B binding protein 3C, chloroplast precursor (LHCII type I CAB-3C) (LHCP)	PU08563	At2g34430	1.02	-1.05	-1.07	1.04	1.13	1.08
Chlorophyll A/B binding protein 3C, chloroplast precursor (LHCII type I CAB-3C) (LHCP)	PU08740	At2g34430	-1.01	1.07	1.08	1.10	1.17	1.06
Chlorophyll A/B binding protein precursor	PU08473	At2g34430	1.04	-1.01	-1.06	1.14	1.19	1.04
Chlorophyll A/B binding protein 3C, chloroplast precursor (LHCII type I CAB-3C) (LHCP)	PU08999	At2g34430	-1.01	-1.03	-1.02	1.16	1.19	1.03
Chlorophyll A/B binding protein 3C, chloroplast precursor (LHCII type I CAB-3C) (LHCP)	PU09860	At2g34430	1.01	1.05	1.04	1.12	1.15	1.03
Chlorophyll A/B binding protein 3C, chloroplast precursor (LHCII type I CAB-3C) (LHCP)	PU08697	At2g34430	-1.04	-1.02	1.01	1.21	1.21	-1.00
Chlorophyll A/B binding protein 3C, chloroplast precursor (LHCII type I CAB-3C) (LHCP)	PU08514	At2g34430	1.17	-1.09	-1.27	1.36	1.34	-1.01
Chlorophyll A/B binding protein precursor	PU01914	At2g34430	-1.03	1.03	1.06	1.15	1.11	-1.04
Chlorophyll A/B binding protein precursor	PU04291	At2g34430	-1.06	-1.15	-1.09	-1.21	-1.30	-1.08
Chlorophyll A/B binding protein 3C, chloroplast precursor (LHCII type I CAB-3C) (LHCP)	PU08688	At2g34430	-1.00	1.00	1.00	1.39	1.26	-1.10
Chlorophyll A/B binding protein 3C, chloroplast precursor (LHCII type I CAB-3C) (LHCP)	PU08710	At2g34430	1.04	-1.07	-1.12	1.53	1.38	-1.10

Appendix S6 continued

Function	Clone ID	Gene ID	800/400	Relative expression					
				Leaves		Stems			
				800/400	1200/400	1200/800	800/400	1200/400	1200/800
Pyruvate kinase isozyme A, chloroplast precursor (EC 2.7.1.40)	PU06984	At3g22960	-1.05	-1.10	-1.05	1.12	1.12	-1.00	
Pyruvate kinase isozyme A, chloroplast precursor (EC 2.7.1.40)	PU06201	At3g22960	1.05	-1.17	-1.23	1.17	1.06	-1.10	
Pyruvate kinase isozyme A, chloroplast precursor (EC 2.7.1.40)	PU06014	At3g22960	-1.01	-1.04	-1.04	1.46	1.24	-1.18	
Hypothetical 27.6 kDa protein	PU08505	At3g47470	-1.05	1.02	1.08	1.00	1.38	1.38	
Hypothetical 27.6 kDa protein	PU00355	At3g47470	-1.14	1.00	1.14	1.31	1.17	-1.11	
Hypothetical 27.6 kDa protein	PU00827	At3g47470	-1.11	1.00	1.11	1.42	1.22	-1.17	
Hypothetical 27.6 kDa protein	PU08457	At3g47470	-1.08	1.08	1.17	1.54	1.26	-1.22	
Hypothetical 27.6 kDa protein	PU08568	At3g47470	-1.16	-1.06	1.10	1.63	1.31	-1.25	
Oxygen evolving enhancer protein 1 precursor	PU08491	At3g50820	-1.05	-1.04	1.01	1.06	1.15	1.09	
Oxygen evolving enhancer protein 1 precursor	PU00411	At3g50820	-1.10	-1.05	1.04	1.20	1.25	1.05	
Oxygen evolving enhancer protein 1 precursor	PU09125	At3g50820	-1.02	-1.08	-1.06	1.26	1.25	-1.01	
Oxygen evolving enhancer protein 1 precursor	PU04452	At3g50820	-1.02	-1.03	-1.01	1.32	1.24	-1.06	
Pyruvate kinase-like protein	PU03877	At3g52990	1.01	1.14	1.12	-1.20	-1.11	1.08	
Pyruvate kinase-like protein	PU01941	At3g52990	1.17	-1.02	-1.20	-1.12	-1.04	1.08	
Pyruvate kinase-like protein	PU12762	At3g52990	1.07	1.16	1.08	-1.03	1.03	1.06	
Pyruvate kinase-like protein	PU13112	At3g52990	-1.32	-1.31	1.01	-1.15	-1.10	1.05	
Pyruvate kinase-like protein	PU08136	At3g52990	1.16	-1.00	-1.17	1.05	-1.05	-1.11	
Pyruvate kinase-like protein	PU04889	At3g52990	1.02	1.02	-1.00	1.01	-1.17	-1.17	
Photosystem I light-harvesting chlorophyll a/b-binding protein	PU08680	At3g54890	-1.03	1.04	1.07	1.23	1.17	-1.05	
Photosystem I light-harvesting chlorophyll a/b-binding protein	PU09731	At3g54890	-1.04	1.04	1.09	-1.04	-1.12	-1.07	
Photosystem I light-harvesting chlorophyll a/b-binding protein	PU08784	At3g54890	-1.04	1.06	1.10	1.03	-1.08	-1.11	
Chlorophyll A/B binding protein 7, chloroplast precursor (LHCI type IICAB-7)	PU09715	At3g61470	-1.01	1.03	1.03	1.37	1.66	1.21	
Chlorophyll A/B binding protein 7, chloroplast precursor (LHCI type IICAB-7)	PU02558	At3g61470	-1.02	-1.01	1.01	1.30	1.35	1.04	
Chlorophyll a/b-binding protein-like	PU09440	At4g10340	1.00	-1.13	-1.13	-1.56	-1.31	1.19	
Chlorophyll a/b-binding protein-like	PU09468	At4g10340	-1.03	-1.09	-1.05	1.00	1.09	1.08	
Chlorophyll a/b-binding protein-like	PU08995	At4g10340	1.00	-1.03	-1.03	-1.02	-1.00	1.02	
Chlorophyll a/b-binding protein-like	PU02643	At4g10340	-1.02	-1.10	-1.08	1.14	1.15	1.01	
Chlorophyll a/b-binding protein-like	PU09649	At4g10340	-1.05	-1.05	-1.01	1.08	1.06	-1.02	
Chlorophyll a/b-binding protein-like	PU08475	At4g10340	-1.00	1.02	1.02	1.16	1.05	-1.11	
Chlorophyll a/b-binding protein-like	PU08883	At4g10340	-1.12	-1.11	1.00	1.17	1.01	-1.16	
Probable photosystem I chain XI precursor	PU09380	At4g12800	-1.01	1.03	1.05	1.02	1.12	1.10	
Probable photosystem I chain XI precursor	PU10462	At4g12800	-1.06	1.06	1.12	1.09	1.04	-1.05	
Probable photosystem I chain XI precursor	PU10414	At4g12800	-1.02	1.05	1.07	1.09	-1.06	-1.16	
Oxygen-evolving complex 25.6 kD protein, chloroplast precursor	PU09143	At4g15510	-1.14	-1.13	1.01	-1.18	1.01	1.18	
Oxygen-evolving complex 25.6 kD protein, chloroplast precursor	PU09145	At4g15510	-1.11	1.06	1.18	-1.22	-1.25	-1.02	
Expressed protein	PU10952	At4g15510	1.03	-1.16	-1.19	1.11	1.00	-1.10	
Expressed protein	PU10746	At4g17620	-1.13	-1.11	1.02	-1.07	1.22	1.31	
Brain protein 44	PU10976	At4g22310	-1.08	-1.11	-1.03	1.19	1.31	1.10	
Expressed protein	PU04732	At4g22310	-1.06	1.04	1.11	-1.01	-1.11	-1.10	
Expressed protein	PU09759	At4g25270	-1.11	1.01	1.13	-1.02	1.03	1.05	
Y20 protein	PU09568	At4g27270	1.04	-1.00	-1.04	-1.11	1.20	1.33	
Y20 protein	PU11588	At4g27270	-1.17	-1.04	1.12	-1.31	-1.52	-1.17	
Photosystem II protein W-like	PU10357	At4g28660	1.05	-1.15	-1.21	1.19	1.95	1.63	
H ⁺ -transporting ATP synthase chain 9-like protein	PU11501	At4g32260	-1.11	-1.12	-1.01	1.07	1.67	1.56	

Appendix S6 continued

Function	Clone ID	Gene ID	800/400	Relative expression					
				Leaves		Stems			
				800/400	1200/400	1200/800	800/400	1200/400	1200/800
H ⁺ -transporting ATP synthase chain 9-like protein	PU12414	At4g32260	-1.08	-1.15	-1.06	-1.02	-1.10	-1.09	
H ⁺ -transporting ATP synthase chain 9-like protein	PU09475	At4g32260	-1.06	-1.14	-1.08	1.07	-1.02	-1.09	
H ⁺ -transporting ATP synthase chain 9-like protein	PU10343	At4g32260	-1.04	-1.17	-1.12	1.34	1.05	-1.28	
Minor allergen	PU03958	At4g36750	1.42	1.34	-1.06	1.60	2.01	1.25	
Minor allergen	PU07798	At4g36750	-1.00	1.12	1.12	1.06	-1.05	-1.11	
Minor allergen	PU08100	At4g36750	1.02	1.12	1.09	-1.07	-1.20	-1.12	
Chlorophyll a/b-binding protein CP29	PU06076	At5g01530	-1.10	1.05	1.16	1.03	-1.06	-1.09	
Chlorophyll a/b-binding protein CP30	PU09088	At5g01530	-1.09	1.12	1.23	1.25	1.13	-1.11	
Chlorophyll a/b-binding protein CP31	PU09368	At5g01530	-1.10	1.04	1.15	1.19	1.05	-1.14	
One helix protein (OHP)	PU11714	At5g02120	-1.19	-1.12	1.06	1.37	1.24	-1.11	
Pyruvate kinase, cytosolic isozyme (EC 2.7.1.40)	PU06775	At5g08570	1.08	-1.00	-1.08	-1.13	1.07	1.21	
Pyruvate kinase, cytosolic isozyme (EC 2.7.1.40)	PU05377	At5g08570	1.03	-1.10	-1.13	-1.13	1.02	1.14	
Pyruvate kinase, cytosolic isozyme (EC 2.7.1.40)	PU03187	At5g08570	1.05	-1.03	-1.08	1.23	1.29	1.05	
Pyruvate kinase, cytosolic isozyme (EC 2.7.1.40)	PU10936	At5g08570	1.07	-1.04	-1.12	1.09	1.04	-1.04	
Pyruvate kinase, cytosolic isozyme (EC 2.7.1.40)	PU06747	At5g08570	1.03	-1.09	-1.12	1.12	1.05	-1.07	
Oxygen-evolving complex related protein 23 kDa polypeptide	PU08709	At5g11450	-1.16	-1.09	1.06	1.19	1.21	1.01	
Expressed protein	PU02075	At5g20090	-1.01	-1.12	-1.12	-1.14	-1.16	-1.01	
LHCII type III chlorophyll a/b-binding protein	PU03295	At5g54270	-1.08	-1.03	1.06	-1.26	1.34	1.69	
LHCII type III chlorophyll a/b-binding protein	PU08450	At5g54270	1.10	-1.02	-1.12	1.15	1.28	1.11	
LHCII type III chlorophyll a/b-binding protein	PU00298	At5g54270	1.17	-1.02	-1.20	1.29	1.40	1.09	
1,4-benzoquinone reductase-like; Trp repressor binding protein-like	PU02254	At5g54500	1.14	1.28	1.11	-1.11	1.20	1.32	
Hypothetical 21.7 kDa protein	PU01283	At5g54500	1.03	-1.10	-1.13	1.23	1.55	1.26	
1,4-benzoquinone reductase-like; Trp repressor binding protein-like	PU01800	At5g54500	1.05	1.03	-1.03	1.10	1.35	1.23	
Hypothetical 21.7 kDa protein	PU01588	At5g54500	-1.05	1.04	1.09	-1.07	-1.07	1.00	
Hypothetical 21.7 kDa protein	PU11705	At5g54500	-1.01	-1.08	-1.08	-1.33	-1.50	-1.13	
Pyruvate kinase	PU05921	At5g56350	-1.13	-1.03	1.10	-1.25	1.18	1.46	
Pyruvate kinase	PU01181	At5g56350	1.00	-1.11	-1.12	-1.38	-1.04	1.32	
Pyruvate kinase	PU11807	At5g56350	1.03	-1.05	-1.08	-1.21	-1.19	1.01	
Photosystem I reaction centre subunit psaN precursor	PU09419	At5g64040	1.01	-1.14	-1.14	1.31	1.18	-1.11	
Photosystem I reaction centre subunit psaN precursor	PU10257	At5g64040	1.10	-1.16	-1.27	1.39	1.20	-1.16	
Rubisco and Calvin cycle									
Sucrose-phosphate synthase, putative	PU03569	At1g04920	1.02	1.01	-1.01	-1.20	-1.17	1.03	
Glyceraldehyde 3-phosphate dehydrogenase B, chloroplast	PU08978	At1g12900	1.07	-1.07	-1.15	-1.44	-1.12	1.29	
UDP-glycosyltransferase family	PU08910	At1g22360	1.07	1.24	1.16	-1.12	-1.09	1.03	
Phosphoglucomutase, cytoplasmic (EC 5.4.2.2)	PU13421	At1g23190	1.04	-1.02	-1.06	-1.05	1.02	1.07	
Phosphoglucomutase, cytoplasmic (EC 5.4.2.2)	PU00915	At1g23190	1.06	1.01	-1.05	-1.01	1.01	1.03	
Phosphoglucomutase, cytoplasmic (EC 5.4.2.2)	PU06231	At1g23190	1.10	1.01	-1.09	1.12	1.15	1.03	
Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19)	PU11066	At1g32060	-1.04	-1.08	-1.04	1.29	1.11	-1.16	

Appendix S6 continued

Function	Clone ID	Gene ID	Relative expression					
			Leaves		Stems			
			800/400	1200/400	1200/800	800/400	1200/400	1200/800
POSSIBLY putative glyceraldehyde-3-phosphate dehydrogenase (At1g42970)	PU08785	At1g42970	1.01	1.04	1.03	1.12	1.11	-1.01
D-ribulose-5-phosphate 3-epimerase (EC 5.1.3.1)	PU02541	At1g63290	-1.00	1.03	1.04	-1.11	-1.13	-1.01
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU09239	At1g67090	-1.02	-1.02	1.01	1.11	1.41	1.27
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU12328	At1g67090	-1.00	1.06	1.07	1.21	1.50	1.25
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU08898	At1g67090	1.04	1.02	-1.02	1.10	1.33	1.21
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU09041	At1g67090	1.04	-1.01	-1.05	1.19	1.44	1.21
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU08803	At1g67090	1.03	-1.00	-1.03	1.46	1.76	1.21
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU06295	At1g67090	1.01	-1.02	-1.03	1.19	1.43	1.20
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU09462	At1g67090	1.00	1.03	1.03	1.14	1.35	1.19
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU09374	At1g67090	-1.03	1.05	1.08	1.18	1.37	1.16
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU09089	At1g67090	1.03	1.03	1.01	1.06	1.22	1.15
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU08633	At1g67090	-1.00	1.02	1.02	1.21	1.39	1.15
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU09264	At1g67090	1.02	1.02	-1.00	1.13	1.29	1.14
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU08825	At1g67090	1.02	1.04	1.02	1.24	1.40	1.13
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU08913	At1g67090	1.01	1.09	1.08	1.15	1.29	1.12
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU09043	At1g67090	-1.00	1.07	1.08	1.22	1.36	1.12
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU10298	At1g67090	1.01	1.03	1.02	1.23	1.38	1.12
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU12369	At1g67090	-1.05	-1.01	1.04	1.01	1.13	1.12
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU09553	At1g67090	1.02	1.02	1.00	1.16	1.27	1.10

Appendix S6 continued

Function	Clone ID	Gene ID	Relative expression					
			Leaves			Stems		
			800/400	1200/400	1200/800	800/400	1200/400	1200/800
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU08428	At1g67090	1.01	1.08	1.07	1.40	1.53	1.10
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU08539	At1g67090	1.02	-1.03	-1.05	1.33	1.45	1.09
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU10119	At1g67090	1.05	1.04	-1.01	1.31	1.42	1.09
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU09232	At1g67090	1.05	1.05	-1.00	1.41	1.50	1.07
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU09363	At1g67090	1.02	1.03	1.01	1.20	1.28	1.07
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU08779	At1g67090	1.05	-1.24	-1.31	1.11	1.18	1.06
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU08492	At1g67090	1.01	-1.04	-1.05	1.22	1.29	1.05
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU10250	At1g67090	1.02	1.07	1.05	1.31	1.38	1.05
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU11603	At1g67090	1.03	1.01	-1.02	1.22	1.27	1.04
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU10817	At1g67090	1.04	-1.08	-1.12	-1.15	-1.11	1.04
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU09012	At1g67090	-1.07	1.04	1.11	1.16	1.20	1.03
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU08560	At1g67090	1.01	1.01	-1.00	1.22	1.24	1.02
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU10714	At1g67090	1.02	-1.03	-1.05	1.26	1.26	1.00
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU11281	At1g67090	1.02	-1.01	-1.03	1.28	1.27	-1.01
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU03769	At1g67090	1.02	-1.07	-1.10	1.27	1.14	-1.12
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU08993	At1g67090	1.03	1.03	-1.01	1.04	-1.08	-1.12
Ribulose biphosphate carboxylase small chain 3, chloroplast precursor (EC 4.1.1.39)	PU08765	At1g67090	-1.03	1.03	1.06	1.42	1.14	-1.24
similar to glucoronosyl transferase-like protein	PU10937	At1g78270	1.14	-1.01	-1.15	-1.51	-1.37	1.10
Triosephosphate isomerase, chloroplast precursor (EC 5.3.1.1)	PU07742	At2g21170	1.00	1.01	1.01	-1.09	1.11	1.20
Triosephosphate isomerase, chloroplast precursor (EC 5.3.1.1)	PU05808	At2g21170	-1.05	-1.02	1.03	-1.13	1.06	1.20

Appendix S6 continued

Function	Clone ID	Gene ID	800/400	Relative expression					
				Leaves		Stems			
				800/400	1200/400	1200/800	800/400	1200/400	1200/800
Triosephosphate isomerase, chloroplast precursor (EC 5.3.1.1)	PU06653	At2g21170	1.01	-1.01	-1.02	-1.04	1.03	1.08	
(Glyceraldehyde-3-phosphate dehydrogenase [NADP+]) (Triosephosphatedehydrogenase)	PU08451	At2g24270	1.17	-1.22	-1.42	-1.08	1.51	1.63	
(Glyceraldehyde-3-phosphate dehydrogenase [NADP+]) (Triosephosphatedehydrogenase)	PU09033	At2g24270	1.22	-1.20	-1.47	1.06	1.57	1.48	
(Glyceraldehyde-3-phosphate dehydrogenase [NADP+]) (Triosephosphatedehydrogenase)	PU09037	At2g24270	1.26	-1.19	-1.50	1.23	1.51	1.23	
Rubisco activase	PU11445	At2g39730	1.17	1.00	-1.16	1.21	1.60	1.33	
Rubisco activase	PU11249	At2g39730	1.05	-1.06	-1.11	-1.04	1.06	1.10	
Rubisco activase	PU08719	At2g39730	1.04	-1.05	-1.10	1.68	1.81	1.08	
Transketolase, chloroplast (EC 2.2.1.1)	PU07838	At2g45290	1.08	-1.18	-1.28	-1.04	-1.12	-1.08	
Transketolase, chloroplast (EC 2.2.1.1)	PU02587	At2g45290	1.09	-1.14	-1.24	1.12	-1.03	-1.16	
Beta-amylase	PU13041	At2g45880	-1.09	-1.47	-1.34	-1.46	-1.18	1.24	
Sucrose synthase	PU02568	At3g43190	1.17	1.20	1.03	1.49	1.40	-1.07	
Sucrose synthase	PU06267	At3g43190	1.04	-1.03	-1.07	1.52	1.15	-1.32	
Sucrose synthase	PU07712	At3g43190	1.14	1.21	1.06	1.22	-1.09	-1.33	
Sucrose synthase	PU07980	At3g43190	1.13	-1.10	-1.25	1.74	1.25	-1.39	
Sucrose synthase	PU07545	At3g43190	1.21	-1.28	-1.54	1.82	1.31	-1.39	
Sucrose synthase	PU00401	At3g43190	1.09	-1.05	-1.14	2.11	1.41	-1.50	
Sucrose synthase	PU01211	At3g43190	1.08	-1.37	-1.47	1.47	-1.07	-1.57	
Sedoheptulose-1,7-bisphosphatase, chloroplast precursor (EC 3.1.3.37)	PU09289	At3g55800	1.05	-1.20	-1.26	-1.24	1.28	1.58	
Sedoheptulose-1,7-bisphosphatase, chloroplast precursor (EC 3.1.3.37)	PU10917	At3g55800	1.06	-1.26	-1.33	1.08	1.47	1.36	
Sedoheptulose-1,7-bisphosphatase, chloroplast precursor (EC 3.1.3.37)	PU01501	At3g55800	1.00	-1.20	-1.21	-1.01	-1.04	-1.02	
Sedoheptulose-1,7-bisphosphatase, chloroplast precursor (EC 3.1.3.37)	PU09166	At3g55800	-1.02	-1.13	-1.11	1.24	1.12	-1.11	
Sucrose synthase	PU03976	At4g02280	-1.15	-1.07	1.08	-1.38	1.05	1.45	
Sucrose synthase	PU01379	At4g02280	-1.00	-1.10	-1.09	1.03	1.28	1.24	
Sucrose synthase	PU12928	At4g02280	-1.20	-1.06	1.13	-1.02	1.17	1.19	
Sucrose synthase	PU12930	At4g02280	-1.06	1.09	1.16	1.03	1.20	1.16	
Sucrose synthase	PU09676	At4g02280	-1.06	1.01	1.07	1.44	1.33	-1.08	
Sucrose-phosphate synthase-like protein	PU09723	At4g10120	1.11	1.02	-1.09	-1.47	-1.38	1.07	
Beta-amylase (EC 3.2.1.2)	PU03585	At4g15210	-1.34	1.10	1.48	-1.62	1.11	1.81	
Beta-amylase (EC 3.2.1.2)	PU03653	At4g15210	-1.37	-1.01	1.35	-1.69	-1.01	1.66	
Beta-amylase PCT-BMYI (EC 3.2.1.2)	PU09978	At4g17090	-1.17	-1.03	1.14	-1.14	-1.13	1.00	
Starch branching enzyme I precursor	PU06428	At5g03650	-1.05	1.06	1.11	1.10	1.39	1.27	
Starch branching enzyme I precursor	PU08471	At5g03650	-1.01	-1.04	-1.04	1.09	1.28	1.18	
Hypothetical 41.9 kDa protein	PU05543	At5g13420	1.09	1.24	1.14	-1.19	-1.13	1.05	
Hypothetical 41.9 kDa protein	PU07440	At5g13420	1.03	1.19	1.15	-1.08	-1.15	-1.07	
Beta-amylase-like proten	PU04549	At5g18670	1.05	1.11	1.06	1.81	1.89	1.05	
Sucrose-phosphate synthase 1 (EC 2.4.1.14)	PU09622	At5g20280	1.07	1.06	-1.02	-1.08	1.32	1.42	
Sucrose-phosphate synthase 1 (EC 2.4.1.14)	PU07499	At5g20280	-1.01	-1.03	-1.02	1.07	1.17	1.10	
Sucrose synthase	PU07221	At5g20830	-1.02	1.09	1.11	-1.33	-1.14	1.17	
Sucrose synthase	PU07957	At5g20830	1.11	-1.23	-1.37	1.66	1.33	-1.25	
Phosphoglucomutase	PU02739	At5g51820	-1.12	-1.14	-1.01	1.51	1.56	1.03	
Phosphoglucomutase	PU04213	At5g51820	-1.11	-1.08	1.03	1.20	1.05	-1.15	
Nilulose-5-phosphate-3-epimerase	PU06579	At5g61410	-1.10	-1.09	1.01	-1.13	1.01	1.14	

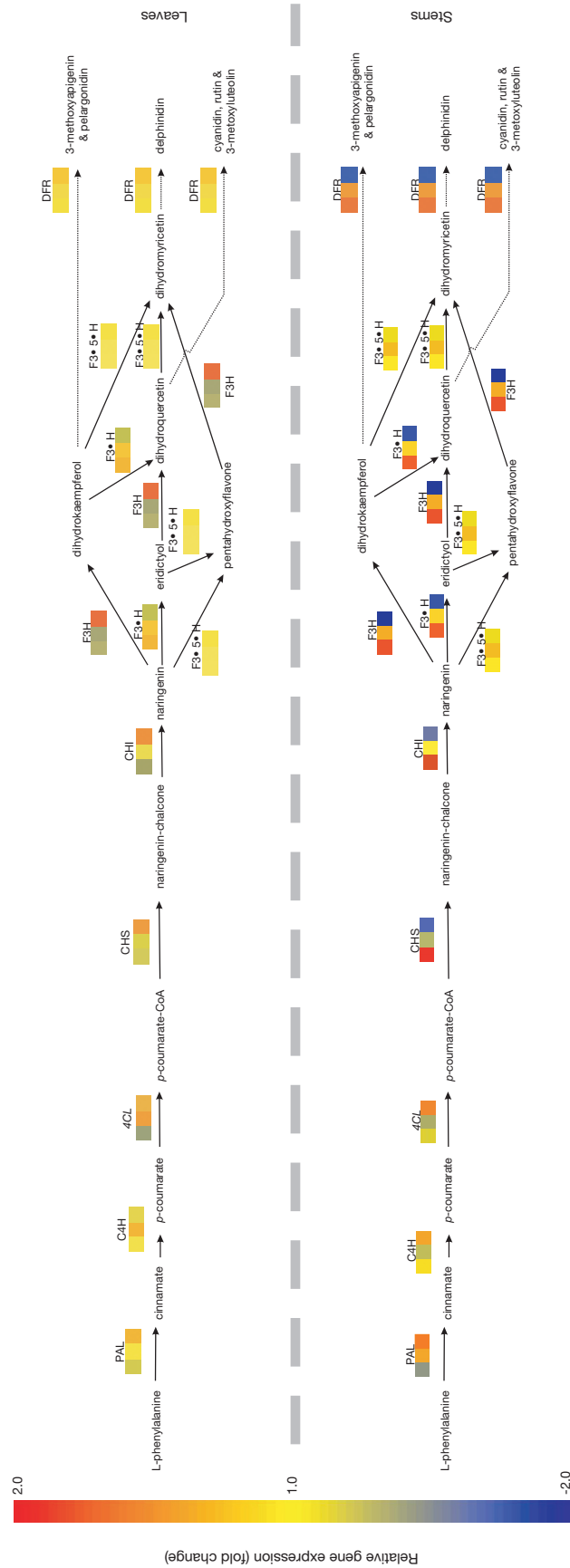
Appendix S6 continued

Function	Clone ID	Gene ID	Relative expression					
			Leaves			Stems		
			800/400	1200/400	1200/800	800/400	1200/400	1200/800
Photorespiration								
Aminomethyltransferase, mitochondrial precursor (EC 2.1.2.10)	PU09074	At1g11860	1.01	-1.13	-1.14	1.23	1.26	1.02
Aminomethyltransferase, mitochondrial precursor (EC 2.1.2.10)	PU07242	At1g11860	1.06	-1.09	-1.15	1.30	1.20	-1.09
Catalase isozyme 1 (EC 1.11.1.6)	PU09186	At1g20630	-1.04	-1.16	-1.11	-1.03	1.02	1.06
Hydroxymethyltransferase like protein	PU04914	At1g36370	1.04	1.17	1.13	-1.39	-1.24	1.11
Hydroxypyruvate reductase (EC 1.1.1.29)	PU10880	At1g68010	1.05	1.01	-1.04	1.04	1.38	1.32
Glycine decarboxylase complex H-protein	PU05496	At2g35120	-1.07	-1.03	1.04	-1.20	-1.07	1.12
Glycine decarboxylase complex H-protein	PU01744	At2g35120	-1.23	-1.20	1.02	-1.11	-1.07	1.03
Glycolate oxidase, putative	PU05752	At3g14150	1.06	1.23	1.17	1.21	1.11	-1.08
Glycolate oxidase (EC 1.1.3.15)	PU08652	At3g14415	1.08	-1.08	-1.17	1.13	1.07	-1.06
Glutamine synthetase (EC 6.3.1.2)	PU11411	At3g17820	1.07	-1.02	-1.08	-1.31	1.45	1.90
Hydroxymethyltransferase	PU00316	At4g13930	1.09	1.01	-1.09	-1.26	-1.07	1.18
Hydroxymethyltransferase	PU02529	At4g13930	1.15	-1.04	-1.20	1.21	1.40	1.16
Hydroxymethyltransferase	PU02209	At4g13930	1.16	-1.01	-1.16	1.20	1.22	1.02
Hydroxymethyltransferase	PU06217	At4g13930	1.19	-1.01	-1.21	1.13	-1.22	-1.37
Glycine hydroxymethyltransferase (EC 2.1.2.1)-like protein	PU03587	At4g32520	-1.08	-1.06	1.02	-1.16	-1.18	-1.02
Catalase isozyme 1 (EC 1.11.1.6)	PU11606	At4g35090	1.06	1.03	-1.03	1.13	1.24	1.11
Catalase isozyme 1 (EC 1.11.1.6)	PU02760	At4g35090	1.01	1.13	1.11	-1.05	1.03	1.07
Serine hydroxymethyltransferase, mitochondrial precursor (EC 2.1.2.1)	PU07376	At4g37930	1.09	-1.07	-1.16	1.02	1.14	1.11
Ferredoxin-dependent glutamate synthase, chloroplast (EC 1.4.7.1)	PU09069	At5g04140	1.04	1.02	-1.02	1.04	-1.05	-1.09
Glutamine synthetase precursor (EC 6.3.1.2)	PU12880	At5g35630	1.02	-1.13	-1.15	-1.50	-1.23	1.22
Glutamine synthetase precursor (EC 6.3.1.2)	PU06395	At5g35630	-1.16	-1.07	1.08	1.32	-1.12	-1.48
Glutamine synthetase nodule isozyme (EC 6.3.1.2)	PU02286	At5g37600	1.04	1.17	1.12	-1.06	1.33	1.41
Glutamine synthetase nodule isozyme (EC 6.3.1.2)	PU02929	At5g37600	1.11	1.19	1.08	1.18	1.43	1.22
Glutamine synthetase nodule isozyme (EC 6.3.1.2)	PU06913	At5g37600	1.02	1.19	1.16	-1.16	-1.00	1.16
Glutamine synthetase nodule isozyme (EC 6.3.1.2)	PU00010	At5g37600	1.24	1.32	1.06	1.09	1.18	1.08
Glutamine synthetase nodule isozyme (EC 6.3.1.2)	PU08292	At5g37600	1.12	1.27	1.13	1.02	-1.03	-1.05
Glutamine synthetase nodule isozyme (EC 6.3.1.2)	PU02327	At5g37600	1.03	1.12	1.09	1.36	1.24	-1.09
Glutamine synthetase nodule isozyme (EC 6.3.1.2)	PU04179	At5g37600	1.02	1.12	1.10	1.22	1.09	-1.12
Glutamine synthetase nodule isozyme (EC 6.3.1.2)	PU01775	At5g37600	1.17	1.09	-1.07	-1.11	-1.36	-1.22
Glutamine synthetase nodule isozyme (EC 6.3.1.2)	PU06292	At5g37600	1.17	1.22	1.04	1.63	1.23	-1.32
Other energy activities								
Cysteine proteinase	PU07286	At1g20850	-1.11	-1.09	1.02	-1.52	-1.08	1.41
Cysteine proteinase	PU02345	At1g20850	1.02	1.48	1.45	-1.08	1.03	1.11
Thiol protease	PU04803	At1g20850	1.10	-1.04	-1.14	1.28	-1.12	-1.43
Expressed protein	PU07961	At1g58110	1.04	1.10	1.06	-1.12	-1.06	1.06
Expressed protein	PU07332	At1g63300	-1.05	1.07	1.13	-1.05	-1.19	-1.13
Expressed protein	PU04956	At1g63300	1.09	-1.09	-1.18	-1.18	-1.42	-1.20
Membrane trafficking factor	PU02895	At4g04210	-1.08	-1.10	-1.01	1.05	1.03	-1.03
ATP synthase delta chain, chloroplast precursor (EC 3.6.3.14)	PU12504	At4g13340	1.04	-1.03	-1.07	1.15	1.19	1.03

Appendix S6 continued

Function	Clone ID	Gene ID	Relative expression					
			Leaves			Stems		
			800/400	1200/400	1200/800	800/400	1200/400	1200/800
Endoplasmic homolog precursor (GRP94 homolog)	PU04411	At4g24190	1.18	1.72	1.46	1.28	1.27	-1.01
Endoplasmic homolog precursor (GRP94 homolog)	PU12289	At4g24190	1.16	1.62	1.40	1.23	1.15	-1.07
Endoplasmic homolog precursor (GRP94 homolog)	PU01841	At4g24190	1.08	1.59	1.47	1.23	1.08	-1.14
Papain-like cysteine proteinase isoform I	PU07684	At4g39090	1.09	1.23	1.13	-1.23	-1.09	1.14
Papain-like cysteine proteinase isoform I	PU02705	At4g39090	1.04	1.07	1.02	1.07	1.14	1.07
Papain-like cysteine proteinase isoform I	PU06015	At4g39090	1.03	1.13	1.10	-1.23	-1.35	-1.10
Papain-like cysteine proteinase isoform I	PU04135	At4g39090	1.11	1.11	-1.00	-1.15	-1.44	-1.26
Papain-like cysteine proteinase isoform I	PU07717	At4g39090	1.00	1.17	1.17	-1.10	-1.39	-1.27
ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)	PU04562	At5g08670	1.01	-1.01	-1.03	-1.24	1.05	1.29
ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)	PU03047	At5g08670	-1.29	1.23	1.59	-1.02	1.13	1.14
ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)	PU00228	At5g08670	1.08	-1.00	-1.08	1.06	-1.14	-1.21
ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)	PU07285	At5g08670	1.14	1.11	-1.03	-1.07	-1.35	-1.26
12-oxophytodienoate reductase 3 (EC 1.3.1.42)	PU05322	At5g55230	1.02	-1.14	-1.17	-1.34	-1.01	1.33
12-oxophytodienoate reductase 3 (EC 1.3.1.42)	PU04474	At5g55230	1.05	-1.10	-1.15	1.05	1.29	1.23
DnaJ-like protein	PU02939	At5g55230	1.02	1.15	1.13	-1.02	-1.06	-1.03
12-oxophytodienoate reductase 3 (EC 1.3.1.42)	PU12490	At5g55230	-1.04	1.02	1.06	1.17	1.02	-1.15
Heat shock protein	PU05022	At5g56000	1.28	1.07	-1.19	2.50	2.58	1.03

Appendix S7



Model of the effects of elevated [CO₂] on the expression of genes of the flavonol biosynthesis pathway in leaves and stems of poplar. The coloured squares represent, from left to right, changes in gene expression at 400, 800 and 1200 μmol mol⁻¹ CO₂ respectively, relative to the *in silico* average of all samples from all treatments. 4CL, 4-coumarate-CoA ligase; C4H, trans-cinnamate 4-monooxygenase; CHI, chalcone isomerase; CHS, naringenin-chalcone synthase; DFR, dihydrokaempferol 4-reductase; F3H, naringenin 3-dioxygenase; F3'5'H, flavonoid 3',5'-hydroxylase; PAL, phenylalanine ammonia-lyase. The colour scale on the left depicts expression ratios in fold change.