

Supplementary Table II - W7 induced calcium independent upregulated ESTs

Loci	ESTs	description	fold upregulation average TFP/control	standard error TFP/control	fold upregulation average W7/control	standard error W7/control	fold upregulation average W7/W7 - Ca	standard error W7/W7 - Ca	fold upregulation average W7 - Ca/control - Ca	standard error W7 - Ca/control - Ca
AT1G02880	T21911	thiamin pyrophosphokinase, putative	1.57	0.04	1.76	0.05	0.83	0.09	0.98	0.05
AT1G02920	R90187	GST	2.46	0.48	4.18	1.13	1.13	0.31	1.09	0.13
	W43242		2.07	0.17	4.54	1.16	0.94	0.18	1.00	0.08
AT1G03220	R65072	extracellular dermal glycoprotein (EDGP)	5.34	1.04	5.45	0.95	1.44	0.24	1.33	0.19
AT1G03230	R84105	extracellular dermal glycoprotein (EDGP)	4.63	0.57	4.77	1.25	1.24	0.18	1.41	0.07
AT1G04140	N65081	unknown protein	5.09	1.96	5.32	0.81	0.91	0.20	1.17	0.30
AT1G05150	N37173	putative O-GlcNAc transferase	1.15	0.14	1.99	0.26	1.05	0.11	1.07	0.08
AT1G08940	T44436	unknown protein	2.44	0.37	2.19	0.09	1.07	0.16	1.13	0.13
AT1G10370	H36275	GST	2.63	0.72	2.28	0.29	0.99	0.10	0.96	0.19
AT1G13210	T45045	potential phospholipid-transporting ATPase 11	2.24	0.85	1.98	0.19	0.70	0.04	1.08	0.11
AT1G15210	N97039	ABC transporter family protein	1.58	0.21	1.96	0.17	1.63	0.52	1.04	0.17
AT1G20500	H77072	unknown protein	1.88	0.35	2.43	0.35	1.69	0.39	0.85	0.17
AT1G21750	H36733	putative protein disulfide isomerase precursor	5.64	2.65	4.04	0.81	0.73	0.22	1.12	0.26
AT1G25500	N37553	unknown protein	2.70	0.84	3.69	0.16	1.02	0.08	1.09	0.24
AT1G29910	N64973	photosystem II type I chlorophyll a/b binding protein, putative	4.25	1.95	4.76	0.43	0.78	0.11	1.07	0.22
AT1G62300	T43869	WRKY family transcription factor	3.02	0.85	2.76	0.62	0.91	0.14	1.39	0.10
AT1G65260	N37557	contains similarity to chloroplast membrane-associated protein IM30	2.37	0.70	3.33	0.07	1.18	0.02	0.99	0.19
AT1G68580	H77084	unknown protein	1.39	0.24	1.89	0.11	1.03	0.03	0.95	0.10
AT1G72770	T43928	protein phosphatase 2C (AtP2C-HA)	1.44	0.31	2.05	0.17	1.33	0.21	0.98	0.17
AT1G75680	W43406	glycosyl hydrolase family 9 / similar to endo-beta-1,4-glucanase	0.96	0.17	1.77	0.14	1.21	0.07	1.07	0.12
AT1G75860	R65061	unknown protein	1.51	0.35	2.88	0.53	1.72	0.58	0.93	0.09
AT1G76970	N97071	contains similarity to seed protein B32E	2.65	0.25	2.41	0.32	1.34	0.12	0.97	0.12
AT1G80110	N96461	contains similarity to PP2 lectin polypeptide	2.40	0.60	1.79	0.20	1.26	0.14	0.78	0.03
AT2G02960	T76663	unknown protein	1.87	0.48	2.20	0.09	1.24	0.12	1.05	0.21
AT2G05990	R90100	enoyl-ACP reductase (enr-A)	2.24	0.46	2.17	0.21	1.43	0.10	1.06	0.14
AT2G07688	N37414	unknown protein	3.23	1.22	1.92	0.25	0.73	0.26	0.90	0.12
AT2G18690	R65079	unknown protein	3.71	0.13	5.21	1.68	1.48	0.36	1.16	0.16
AT2G18970	N37609	unknown protein	2.36	0.59	3.11	0.43	1.04	0.12	0.94	0.15
AT2G22900	T76358	unknown protein	3.38	1.73	2.67	0.14	0.77	0.13	1.24	0.26
AT2G23320	H36048	WRKY family transcription factor - WRKY15	3.19	1.05	3.70	0.37	1.41	0.29	1.29	0.03
AT2G26560	T42260	patatin, putative / similar to patatin-like latex allergen	1.71	0.33	2.40	0.39	0.90	0.09	1.10	0.09
AT2G26990	W43761	COP9 complex subunit CSN2, putative	3.47	1.16	3.55	0.36	1.00	0.11	1.03	0.22
AT2G27310	T21586	unknown protein / supported by cDNA: gi_13877666	2.05	0.12	1.78	0.04	1.17	0.13	1.13	0.36
AT2G31880	N65616	leucine-rich repeat transmembrane protein kinase, putative	1.92	0.55	2.80	0.29	1.34	0.39	1.28	0.24
AT2G31900	N37543	putative unconventional myosin	1.49	0.25	1.84	0.07	0.96	0.13	1.08	0.04
AT2G34660	N37563	glutathione S-conjugate ABC transporter (AtMRP2) / almost identical to MgATP-energized glutathione S-conjugate pump	2.95	1.49	2.38	0.34	0.72	0.12	1.00	0.05
AT2G38360	T88274	unknown protein	2.23	0.28	2.85	0.27	1.23	0.20	1.35	0.32
AT2G41410	H36575	calmodulin-like protein	1.71	0.27	1.95	0.09	1.29	0.17	1.22	0.15

AT2G41640	T44481	unknown protein	3.29	0.39	2.54	0.33	1.41	0.12	1.54	0.39
AT2G47390	H77233	unknown protein	3.16	1.43	2.15	0.25	0.78	0.20	1.00	0.13
AT2G47730	N65628	GST6	6.41	3.02	3.97	0.46	0.84	0.34	1.23	0.15
AT3G01290	R65336	unknown protein	1.92	0.43	2.09	0.35	1.37	0.16	1.15	0.07
AT3G01570	H76640	oleosin	3.06	0.75	2.25	0.20	1.17	0.08	1.12	0.12
AT3G04240	N96122	putative O-linked GlcNAc transferase	3.02	1.28	2.15	0.28	0.69	0.10	1.09	0.14
AT3G07560	H77117	unknown protein	1.80	0.88	2.29	0.23	1.20	0.08	1.11	0.10
AT3G08760	R65414	putative protein kinase	2.78	0.28	1.93	0.17	0.97	0.11	1.30	0.34
AT3G09260	N65420	glycosyl hydrolase family 1 / almost identical to beta-glucosidase	6.91	3.76	4.58	0.39	0.71	0.10	1.08	0.27
AT3G09390	AA042473	metallothionein-like protein	2.43	0.80	2.48	0.35	0.91	0.12	1.04	0.13
AT3G16640	AA042588	translationally controlled tumor protein-like protein	3.66	1.66	1.93	0.25	0.93	0.04	0.95	0.16
AT3G21720	W43445	putative isocitrate lyase	1.88	0.06	2.32	0.24	1.47	0.19	1.11	0.14
AT3G22310	H76736	putative RNA helicase	4.51	2.69	3.65	0.39	0.87	0.03	1.05	0.17
AT3G23170	N65028	unknown protein	1.66	0.16	1.83	0.14	1.14	0.15	0.68	0.05
AT3G26910	T76738	unknown protein	4.06	0.60	2.60	0.41	1.24	0.06	1.24	0.25
AT3G46510	R87023	arm repeat containing protein homolog	1.53	0.53	2.14	0.28	1.15	0.04	1.11	0.06
AT3G47340	N37610	glutamine-dependent asparagine synthetase	1.81	0.43	1.97	0.29	1.07	0.12	0.96	0.04
AT3G53990	N65857	similar to ER6 protein - Lycopersicon esculentum	1.15	0.18	2.15	0.31	1.47	0.09	1.17	0.10
AT3G54640	T21998	tryptophan synthase alpha chain	2.04	0.10	2.83	0.37	1.48	0.24	1.24	0.27
AT3G55430	R90193	glycosyl hydrolase family 17 (beta-1,3-glucanase)	2.10	0.04	2.11	0.24	1.05	0.09	1.17	0.09
AT4G01870	N37624	unknown protein	1.98	0.28	2.83	0.50	1.16	0.34	1.39	0.13
AT4G08950	N95936	putative phi-1-like phosphate-induced protein	3.24	0.79	2.99	0.57	1.14	0.43	1.12	0.14
AT4G10020	AA041112	putative oxidoreductase	1.49	0.08	1.85	0.15	1.37	0.22	1.04	0.08
AT4G13860	N37162	RRM-containing protein	1.53	0.24	1.86	0.01	1.76	0.50	0.98	0.05
AT4G15450	T46704	unknown protein	2.14	0.16	2.74	0.48	1.51	0.35	1.17	0.04
AT4G27720	W43316	putative protein	1.46	0.19	1.77	0.05	1.55	0.24	0.90	0.15
AT4G30470	N65754	cinnamoyl-CoA reductase - like protein	1.76	0.19	2.16	0.30	1.24	0.18	0.91	0.09
AT4G32620	N37931	unknown protein	1.77	0.49	1.98	0.24	1.07	0.05	0.95	0.14
AT4G39330	T76074	cinnamyl-alcohol dehydrogenase CAD1	1.90	0.37	1.93	0.24	1.06	0.12	1.19	0.05
AT5G03180	H76914	unknown protein	5.35	2.94	3.29	0.35	0.71	0.06	0.95	0.10
AT5G03630	R90280	monodehydroascorbate reductase, putative	1.78	0.27	2.46	0.49	1.14	0.32	1.03	0.08
AT5G16010	T43852	steroid 5alpha-reductase-like protein	1.27	0.26	1.85	0.11	0.97	0.23	0.76	0.10
AT5G21090	T21150	leucine-rich repeat protein	1.23	0.28	2.07	0.27	1.40	0.25	1.09	0.07
AT5G22000	N96476	Expressed protein	2.95	0.68	2.05	0.30	0.73	0.28	1.19	0.08
AT5G24800	H76930	bZIP protein, G/HBF-1-related / light-induced protein CPRF-2 - Petroselinum crispum	2.40	1.01	2.24	0.39	0.77	0.11	1.00	0.19
AT5G25265	H76923	unknown protein	2.26	0.84	2.30	0.35	0.76	0.08	0.98	0.09
AT5G25350	N38266	leucine-rich repeats containing protein / grr1 - Glycine max	3.59	1.29	5.30	0.60	0.99	0.19	1.01	0.24
AT5G26000	T21685	glycosyl hydrolase family 1, myrosinase precursor	3.31	1.32	2.78	0.29	0.84	0.09	1.00	0.16
AT5G44440	T45555	FAD-linked oxidoreductase family	2.74	0.94	4.89	1.21	0.94	0.27	1.11	0.06
AT5G52540	T88428	unknown protein	1.61	0.26	2.67	0.31	1.55	0.23	0.99	0.16
AT5G52920	N96241	pyruvate kinase	4.10	1.91	2.67	0.60	0.64	0.04	1.08	0.30
AT5G55120	N38393	unknown protein	1.92	0.59	1.98	0.04	1.49	0.23	1.03	0.21
AT5G60530	T45284	late embryonic abundant protein - like	1.80	0.27	2.33	0.41	0.72	0.20	1.19	0.15
AT5G64260	R89938	phi-1-like protein	1.57	0.22	2.05	0.25	1.09	0.16	1.09	0.10
unknown	AA042610		3.01	1.17	2.24	0.17	0.67	0.18	1.09	0.20
unknown	AA042713		1.38	0.21	1.83	0.19	0.95	0.04	1.07	0.31
unknown	AA042749		3.75	1.14	3.69	0.64	1.33	0.40	1.18	0.20

unknown	H76566		4.34	1.81	2.93	0.24	0.60	0.15	1.12	0.22
unknown	H77010		2.46	0.54	2.72	0.38	1.18	0.04	1.03	0.11
unknown	H77014		5.26	3.11	3.64	0.51	0.77	0.13	1.14	0.20
unknown	N37617		4.44	2.14	3.37	0.60	1.01	0.03	1.02	0.20
unknown	N37896		3.22	0.83	2.86	0.17	0.76	0.07	0.95	0.18
unknown	N37911		4.87	2.11	4.49	0.90	0.77	0.25	1.11	0.27
unknown	N38416		2.34	0.63	2.57	0.22	0.77	0.11	1.10	0.20
unknown	N96255		3.17	2.06	1.81	0.21	1.45	0.14	0.87	0.07
unknown	N96775		3.08	0.99	2.86	0.56	0.80	0.20	1.24	0.26
unknown	R90273		2.96	1.13	2.14	0.16	0.81	0.19	1.04	0.16
unknown	T43763		1.24	0.38	1.95	0.14	1.21	0.34	1.06	0.11
unknown	W43205		3.30	0.51	3.98	0.61	0.91	0.15	1.30	0.21
average			2.70		2.73		1.09		1.08	