

Supplementary Table IV - W7 repressed calcium-responsive down regulated ESTs

loci	EST	description	Fold downregulation average TFP/control	standard error TFP/control	Fold downregulation average W7/control	standard error W7/control	Fold downregulation average W7/W7 - Ca	standard error W7/W7 - Ca	Fold downregulation average W7 - Ca/control - Ca	standard error W7 - Ca/control - Ca
AT1G02780	N65309	60S ribosomal protein L19	1.53	0.01	1.74	0.39	2.87	0.37	0.92	0.05
AT1G11580	T88066	pectin methylesterase	1.46	0.36	2.23	0.26	1.77	0.29	1.01	0.14
AT1G15670	T21823	unknown protein	0.60	0.11	2.25	1.16	1.79	0.13	0.87	0.05
AT1G21310	T43479	unknown protein	1.40	0.25	1.83	0.59	3.44	0.31	1.10	0.21
AT1G24040	H37589	unknown protein	1.73	0.40	2.52	0.57	2.12	0.23	0.97	0.04
AT1G35720	H36260 T76739	Ca ²⁺ -dependent membrane-binding protein annexin	2.12 1.98	0.38 0.25	1.82 1.67	0.62 0.19	1.97 2.31	0.07 0.19	1.21 1.24	0.13 0.22
AT1G54000	T88191	myosinase-associated protein, putative	2.70	1.43	2.60	0.29	1.73	0.57	1.14	0.16
AT1G55250	N65499	nuclear zinc finger protein	1.41	0.17	1.58	0.13	1.84	0.20	1.00	0.12
AT1G56220	N64983 T20760 T21186	unknown protein	1.74 1.82 1.83	0.31 0.21 0.25	1.95 1.98 1.94	0.21 0.11 0.15	1.51 1.60 1.44	0.19 0.22 0.28	0.96 0.93 0.91	0.05 0.04 0.07
AT1G62060	T75641	unknown protein	1.44	0.11	2.50	0.10	1.76	0.22	0.91	0.04
AT1G66200	N65571	glutamine synthetase	1.37	0.27	2.72	0.25	1.70	0.17	1.03	0.10
AT1G66270	N64947 N65342 N97158	glycosyl hydrolase family 1, beta-glucosidase	7.25 5.34 5.80	4.43 2.82 2.99	5.45 4.19 4.79	1.58 0.62 0.86	1.81 2.52 2.45	0.50 0.59 0.71	1.45 1.18 1.24	0.39 0.02 0.06
AT1G73260	R30257	putative trypsin inhibitor	1.99	1.04	2.80	1.18	6.41	1.34	0.93	0.11
AT1G80440	T41717	unknown protein	1.10	0.37	1.80	0.24	2.18	0.23	0.94	0.12
AT2G03890	T88580	unknown protein	1.13	0.24	1.87	0.24	2.12	0.49	1.21	0.05
AT2G24260	H36262	bHLH transcription factor	1.37	0.20	1.55	0.20	1.86	0.25	1.05	0.08
AT2G33790	H36027	putative proline-rich protein	1.25	0.14	1.79	0.16	1.62	0.27	0.96	0.13
AT2G33830	N65046 N97310 N64968	auxin-regulated protein	1.71 1.40 1.35	0.69 0.52 0.09	1.87 2.00 1.85	0.21 0.24 0.17	2.31 3.14 3.74	0.64 1.39 0.72	1.04 1.01 1.27	0.09 0.04 0.24
AT2G43150	T41880	putative extensin /	1.23	0.20	1.63	0.31	2.47	0.41	0.97	0.16
AT2G46750	T76287	FAD-linked oxidoreductase family	1.49	0.54	1.86	0.55	2.53	0.25	0.71	0.10
AT3G03470	T45663	cyp89a9 - cytochrome p450	1.49	0.40	1.67	0.09	1.85	0.25	0.91	0.14
AT3G04445	T46435	putative polyribonucleotide phosphorylase	1.96	0.52	2.26	0.42	2.05	0.17	1.14	0.14
AT3G15950	N65234	unknown protein	1.68	0.53	2.50	0.02	1.87	0.61	1.17	0.08
AT3G16420	N65032 N65228 N65775 R65544 W43058	jacalin-like lectin - similar to myosinase binding protein - JA inducible	2.37 2.57 1.40 2.14 2.30	0.83 1.06 0.26 0.49 0.96	2.74 2.67 2.40 2.14 2.11	0.37 0.33 0.30 0.15 0.43	1.74 1.75 1.74 2.03 2.14	0.24 0.30 0.21 0.39 0.32	1.27 1.24 1.16 1.15 1.12	0.11 0.13 0.03 0.15 0.10

AT3G16460	T46036 W43253	jacalin-like lectin - similar to myrosinase binding protein - JA inducible	1.35 1.97	0.20 0.48	1.99 2.16	0.25 0.11	2.60 2.38	0.37 0.22	1.06 1.09	0.07 0.11
AT3G22280	W43476	unknown protein	1.62	0.17	1.69	0.28	1.80	0.12	0.87	0.10
AT3G23190	T20932	unknown protein	2.67	0.31	3.84	0.59	2.69	1.00	1.33	0.18
AT3G26510	N65790 T22188	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	1.55 1.64	0.51 0.49	2.13 2.16	0.39 0.57	4.08 3.41	0.49 0.33	1.11 1.06	0.08 0.07
AT3G26520	AA042125 AA067532 N37491 N65442 T46091 T88331	GAMMA-TIP2 aquaporin	1.47 1.33 1.46 1.33 1.36 1.47	0.01 0.09 0.28 0.20 0.20 0.12	1.97 2.60 1.59 2.09 1.87 2.23	0.12 0.77 0.33 0.22 0.26 0.33	1.68 2.31 1.80 2.10 1.43 1.88	0.08 0.43 0.12 0.46 0.18 0.29	1.10 0.97 1.17 0.96 1.05 1.06	0.03 0.02 0.03 0.05 0.12 0.11
AT3G26740	N37331 N65056 N65497 N65560 N96961 N97032 T44738	light regulated protein	1.36 1.89 2.17 2.03 1.58 2.35 1.91	0.13 0.05 0.09 0.34 0.22 0.31 0.17	1.86 3.08 3.41 3.02 2.77 2.43 2.73	0.27 1.22 0.97 0.58 0.48 0.26 0.63	2.26 1.86 2.09 1.75 2.24 1.50 1.97	0.31 0.22 0.29 0.15 0.37 0.13 0.26	0.96 0.94 0.93 1.02 1.03 1.21 0.90	0.15 0.12 0.12 0.12 0.05 0.19 0.14
AT3G27260	N96279	unknown protein	1.36	0.10	2.04	0.34	1.82	0.18	1.08	0.09
AT3G28550	N38107	unknown protein	2.24	0.38	4.85	1.64	10.27	6.77	1.44	0.26
AT3G49070	N65390	unknown protein	2.06	0.65	2.60	1.03	2.73	0.43	1.08	0.18
AT3G49100	T45597	signal recognition particle subunit 9 - like	1.81	0.42	2.31	0.21	1.51	0.08	1.07	0.31
AT3G51370	T46496	protein phosphatase 2C - related protein	1.48	0.27	2.27	0.12	2.26	0.37	1.15	0.12
AT3G51730	T43972	unknown protein	1.57	0.52	1.96	0.22	2.45	0.43	0.85	0.08
AT3G52060	R90105 T44083	unknown protein	1.24 1.06	0.29 0.28	2.63 1.60	0.27 0.32	1.88 2.12	0.31 0.14	1.13 1.11	0.09 0.07
AT3G53420	AA067484 N65114 N96511 N97303 T42727 T44097 W43194	PIP2A - aquaporin	1.63 1.21 1.33 1.45 1.61 1.39 1.52	0.16 0.08 0.11 0.19 0.05 0.17 0.08	1.71 2.19 1.63 1.81 2.27 2.67 1.68	0.31 0.29 0.21 0.54 0.34 0.45 0.18	2.11 1.78 1.91 1.89 2.17 2.16 2.02	0.16 0.35 0.27 0.18 0.22 0.43 0.31	1.21 1.07 1.05 1.12 1.09 1.02 0.95	0.14 0.09 0.04 0.07 0.06 0.03 0.23
AT3G61430	N95974	PIP1A - Aquaporin	1.50	0.22	1.87	0.03	1.77	0.03	1.12	0.05
AT4G11650	H76850 N97229	osmotin precursor	1.77 1.70	0.85 0.89	3.14 3.54	1.27 1.51	5.06 5.64	1.58 1.98	0.82 0.81	0.04 0.07
AT4G14060	T43693	major latex protein (MLP)-related	1.59	0.26	1.83	0.21	1.63	0.09	1.27	0.07
AT4G16260	N65329	glycosyl hydrolase family 17 - glucan endo-1,3-beta-glucosidase	2.19	0.81	1.99	0.86	3.86	0.37	0.99	0.12
AT4G16360	N96609	kinase like protein	1.53	0.17	1.82	0.09	1.58	0.11	1.08	0.03
AT4G26090	T88149	disease resistance protein RPS2 (CC-NBS-LRR class), putative	1.71	0.75	2.78	1.12	5.69	0.57	0.98	0.08
AT4G30170	T21036	peroxidase ATP8a	3.64	1.23	4.22	0.82	2.30	0.57	1.42	0.14

AT4G34030	T75761	3-METHYLCROTONYL-COA CARBOXYLASE, MCCB	1.42	0.54	1.59	0.19	1.83	0.20	1.03	0.03
AT4G35750	T42554	putative protein similar to E1B 19K Bcl-2-interacting protein Nip2, Homo sapiens	1.18	0.36	1.70	0.15	1.87	0.20	1.00	0.08
AT4G37070	T41937	similar to patatin-like latex allergen	1.25	0.26	1.72	0.44	2.66	0.51	1.10	0.17
AT4G37900	N97112	unknown protein	2.08	0.22	1.91	0.26	1.79	0.20	1.13	0.10
AT4G39090	AA042446 N65662 N65892 N96916 T41787	cysteine proteinase RD19A,	1.39 1.77 1.69 1.99 1.35	0.33 0.54 0.49 0.68 0.37	1.69 1.89 2.08 1.85 2.42	0.45 0.67 0.36 0.64 0.77	2.42 2.29 3.07 3.90 4.31	0.27 0.10 0.31 0.66 0.91	1.03 1.16 1.10 1.11 0.99	0.06 0.16 0.09 0.11 0.03
AT5G10300	R84081	alpha-hydroxynitrile lyase HNL4	1.47	0.20	2.70	0.28	1.88	0.31	0.94	0.08
AT5G13180	R30592	hypothetical protein SENU5 - senescence up-regulated	1.25	0.35	1.54	0.11	3.36	0.82	1.16	0.02
AT5G17820	T45353	peroxidase ATP13a	2.05	0.57	2.88	0.31	2.14	0.37	1.26	0.26
AT5G23660	T21006	nodulin MtN3 family protein	1.54	0.19	2.23	0.18	1.97	0.34	1.06	0.14
AT5G26260	H35993 N37539	unknown protein	3.54 2.59	1.58 0.65	3.23 2.92	0.42 0.26	1.44 1.72	0.27 0.32	1.42 1.19	0.21 0.18
AT5G43060	N65542	cysteine proteinase RD21A	1.79	0.07	2.04	0.14	1.85	0.19	1.04	0.18
AT5G43370	T46507	inorganic phosphate transporter (PHT2)	2.07	0.67	2.82	0.54	1.93	0.32	1.01	0.05
AT5G43450	H37619	l-aminocyclopropane-1-carboxylate oxidase	1.53	0.34	1.83	0.12	1.43	0.29	0.90	0.14
AT5G44020	N65745 N96976 T21723	vegetative storage protein-related	1.15 1.56 1.39	0.25 0.21 0.10	2.13 2.58 1.94	0.20 0.44 0.14	1.74 1.84 1.75	0.32 0.08 0.13	1.20 1.26 1.17	0.09 0.01 0.02
AT5G44610	T21724 T22213	unknown protein	1.97 1.67	0.52 0.39	2.74 2.42	0.84 0.73	4.18 4.12	0.34 0.84	1.23 0.94	0.03 0.11
AT5G47560	T42907	sodium-dicarbonic-acid-transporter	2.08	0.06	2.79	0.14	1.76	0.35	0.96	0.05
AT5G49360	H37097 N65441 N96119 T42707 T75638 W43153	glycosyl hydrolase family 3	1.78 1.67 1.70 1.46 1.60 1.94	0.41 0.31 0.46 0.26 0.43 0.31	2.63 3.22 2.55 2.43 2.75 3.05	0.94 0.31 0.53 0.45 0.21 0.02	2.12 2.50 1.77 1.58 1.79 2.10	0.29 0.71 0.17 0.29 0.34 0.52	0.97 0.89 1.05 0.99 1.01 0.95	0.08 0.11 0.09 0.09 0.11 0.08
AT5G50900	W43466	unknown protein	1.77	0.10	2.13	0.23	1.82	0.33	0.95	0.19
AT5G59090	W43482	subtilisin-like serine protease	1.92	0.18	2.16	0.21	1.92	0.35	0.93	0.13
AT5G59780	T42666	putative transcription factor (MYB59)	1.46	0.07	1.79	0.05	1.56	0.07	1.10	0.09
AT5G59870	H76422	histone H2A, putative	1.26	0.33	1.65	0.22	1.92	0.20	0.97	0.02
AT5G64100	N65288 T44766	peroxidase ATP3a	1.90 2.13	0.52 0.61	3.67 5.50	0.80 1.91	2.50 2.83	0.63 0.64	0.88 0.77	0.18 0.10

AT5G65210	R90199	bZIP transcription factor,	1.81	0.40	2.36	0.18	2.12	0.16	1.23	0.15
	T22979	TGA1	1.12	0.04	2.15	0.31	1.48	0.19	1.01	0.14
average(all)			1.81		2.38		2.36		1.06	