

Supplementary Table III - W7 repressed calcium independent 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
AT1G02205	N38051	contains similarity to lipid transfer protein	1.09	0.16	1.80	0.11	1.27	0.32	0.93	0.06
AT1G03090	H36836	putative 3-methylcrotonyl-CoA carboxylase	1.05	0.16	1.79	0.19	1.38	0.15	1.27	0.16
AT1G04410	N96490	putative malate dehydrogenase	1.41	0.31	1.76	0.07	1.08	0.15	1.03	0.12
	T42329		1.21	0.13	1.81	0.19	1.22	0.10	1.12	0.13
AT1G09740	T43334	putative ER6 protein	1.34	0.42	1.83	0.16	1.90	0.57	1.75	0.66
AT1G56220	N65433	unknown protein	1.36	0.11	2.05	0.11	1.44	0.28	1.09	0.09
AT1G61740	H36406	unknown protein	1.21	0.20	1.78	0.11	1.22	0.13	1.24	0.11
AT1G62080	AA067506	unknown protein	2.30	0.78	1.81	0.22	1.00	0.06	0.96	0.07
AT1G68560	N37141	glycosyl hydrolase family 31 (alpha-xylosidase)	2.08	0.67	2.18	0.30	1.23	0.04	1.22	0.03
AT1G80460	T43219	similar to GLYCEROL KINASE	1.09	0.14	1.92	0.11	1.42	0.17	1.40	0.18
AT2G30620	T42725	histone H1	1.63	0.11	2.08	0.25	1.26	0.09	1.25	0.10
AT2G37130	N96395	peroxidase, putative (ATP2a)	1.76	0.31	1.84	0.22	1.24	0.07	1.13	0.10
AT2G43610	T22039	glycosyl hydrolase family 19 (chitinase)	1.73	0.17	1.87	0.14	1.70	0.53	1.08	0.16
AT2G45960	N65882	aquaporin (plasma membrane intrinsic protein 1B)	1.58	0.35	1.79	0.12	1.27	0.06	1.26	0.07
AT3G09260	N96636	glycosyl hydrolase family 1 / almost identical to beta-glucosidase	1.54	0.38	2.48	0.31	1.29	0.15	1.33	0.16
	W43104		3.19	1.75	2.23	0.36	0.91	0.07	1.16	0.23
AT3G13750	W43678	glycosyl hydrolase family 35 (beta-galactosidase) / similar to beta-galactosidase precursor	1.52	0.32	1.95	0.10	1.20	0.13	1.18	0.14
AT3G21510	T46792	two-component phosphorelay mediator, putative / similar to ATP2	1.24	0.08	2.02	0.04	1.27	0.08	1.11	0.15
AT3G26740	N65532	light regulated protein, putative	2.16	0.26	2.49	0.29	1.62	0.26	1.35	0.05
AT3G53430	T42421	60S RIBOSOMAL PROTEIN L12 -like	1.29	0.27	1.86	0.25	1.33	0.17	1.27	0.21
AT4G12550	H77253	putative cell wall-plasma membrane disconnecting CLCT protein (AIR1A)	2.66	1.11	6.30	2.12	3.02	2.08	1.22	0.36
AT4G15390	T21211	similar to alcohol acyltransferase	1.49	0.16	2.19	0.31	1.09	0.30	0.76	0.07
AT4G21960	N65901	peroxidase, putative	1.42	0.26	1.99	0.19	1.43	0.13	1.18	0.16
	N97208		1.57	0.15	1.88	0.07	1.42	0.25	1.11	0.14
AT4G26130	T20837	unknown protein	1.10	0.18	2.00	0.27	1.15	0.26	1.09	0.27

AT4G30190	N65613 N65849 T22206 W43684	H ⁺ -transporting ATPase type 2, plasma membrane	1.96 1.86 1.70 1.41	0.44 0.46 0.19 0.22	2.17 2.01 2.34 1.79	0.29 0.20 0.27 0.11	0.86 0.90 1.08 1.30	0.11 0.17 0.06 0.08	0.96 1.02 1.06 1.25	0.10 0.15 0.09 0.13
AT4G31910	R30296	anthranilate N- hydroxycinnamoyl/benzoyl transferase	1.25	0.34	1.90	0.17	1.16	0.10	1.20	0.10
AT4G32420	T44369	putative protein / CDC28/cdc2-like kinase associating arginine- serine cyclophilin	1.62	0.19	1.82	0.15	1.25	0.03	1.18	0.05
AT4G34870	N37554	peptidylprolyl isomerase (cyclophilin)	3.14	1.13	2.84	0.50	1.24	0.38	0.98	0.12
AT4G36850	H77118	putative protein	1.76	0.37	2.48	0.17	1.02	0.21	1.02	0.21
AT4G37980	N65902	cinnamyl-alcohol dehydrogenase ELI3-1	1.81	0.34	1.91	0.26	1.11	0.13	1.08	0.12
AT5G11420	N65468	unknown protein	0.89	0.22	1.84	0.22	1.12	0.24	1.00	0.13
AT5G23010	N65307	2-isopropylmalate synthase-like; homocitrate synthase-like	2.51	1.12	1.95	0.03	1.02	0.05	1.01	0.06
AT5G26260	N37424 R84203	unknown protein	2.53 3.07	0.69 0.89	3.28 3.28	0.61 0.77	1.29 1.35	0.19 0.33	1.14 1.31	0.14 0.32
AT5G26280	N65011	unknown protein	2.13	0.67	2.06	0.22	1.10	0.20	1.02	0.18
AT5G39530	T44194	putative protein	1.86	0.46	2.28	0.30	1.27	0.10	1.12	0.08
AT5G42180	T43249	peroxidase, putative	1.96	0.38	2.20	0.12	1.50	0.13	1.34	0.25
AT5G44020	AA042539	vegetative storage protein- like	0.96	0.14	1.81	0.11	1.49	0.25	1.17	0.08
AT5G57660	N65050	CONSTANS-like B-box zinc finger protein-like	1.63	0.26	1.79	0.16	1.48	0.27	1.44	0.28
AT5G61590	N65166	Ethylene responsive element binding factor 5	1.55	0.31	1.86	0.03	1.48	0.30	1.47	0.30
AT5G64100	T21726	identical to peroxidase ATP3a	1.91	0.15	1.96	0.09	1.32	0.10	1.12	0.21
no hits found	N96675		1.85	0.67	2.19	0.24	1.44	0.16	1.47	0.14
average			1.73		2.16		1.31		1.17	