

**Supplementary Table I - W7 induced calcium-responsive 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
AT1G03220	H76724	extracellular dermal glycoprotein (EDGP)	5.07	0.56	9.34	2.41	2.32	0.35	1.36	0.11
	N96972		4.99	1.01	6.70	1.53	1.74	0.43	1.30	0.18
AT1G03730	H37232	unknown protein	1.87	0.41	1.97	0.15	2.21	0.32	1.17	0.18
AT1G03740	T20464	cdc2-like protein kinase	2.34	0.41	2.36	0.57	2.06	0.21	1.32	0.06
AT1G08930	T22578	zinc finger protein ATZF1 -ERD6	3.56	0.99	3.63	0.50	1.73	0.38	1.34	0.22
AT1G09070	T21700	Similar to Glycine SRC2	3.41	0.36	4.62	1.44	2.33	0.55	1.54	0.08
AT1G11530	R65313	thioredoxin h	1.46	0.10	2.38	0.26	2.38	0.50	1.04	0.17
AT1G18470	T76213	unknown protein	1.31	0.39	1.69	0.21	1.89	0.18	1.04	0.10
AT1G18570	T22593	myb51 - R2R3 myb like transcription factor	4.92	1.15	6.84	0.46	3.13	0.54	1.68	0.25
AT1G19180	T42340	unknown protein	5.35	1.47	11.72	2.47	3.21	0.49	1.57	0.34
AT1G20440	N96946	COR47 - ERD10	1.76	0.59	5.39	1.44	4.81	1.56	1.31	0.08
AT1G21110	T75823	O-methyltransferase 1, putative	4.22	0.99	5.72	1.51	3.59	1.17	1.50	0.21
AT1G21730	N38368	kinesin-related protein	2.10	0.05	2.08	0.13	1.78	0.31	1.00	0.09
AT1G22360	W43072	UDP-glucose glucosyltransferase	2.05	0.34	2.61	0.50	1.51	0.20	1.02	0.09
AT1G23490	T46050	putative ADP-ribosylation factor - RAB GTPase	1.48	0.29	1.55	0.26	2.09	0.16	1.04	0.11
AT1G27130	T42273	GST12	1.84	0.10	2.39	0.24	1.74	0.42	0.94	0.04
AT1G27730	R29923	ZAT10 - salt induced zinc finger protein	5.34	0.35	8.60	0.53	2.63	0.29	2.17	0.45
	R90419		4.86	1.71	5.79	1.14	2.31	0.65	1.79	0.34
AT1G28380	R30143	unknown protein	1.65	0.24	1.79	0.29	2.29	0.37	1.05	0.04
AT1G30360	W43679	unknown protein	1.14	0.07	1.67	0.21	1.96	0.21	1.04	0.12
AT1G31130	T20423	unknown protein	3.26	0.48	2.92	0.37	2.60	0.17	1.41	0.18
AT1G33600	T20493	LRR protein family	2.62	0.83	2.45	0.84	2.20	0.30	1.25	0.09
AT1G35140	H37666	phi1 - phosphate induced protein	2.39	0.55	2.29	0.04	1.57	0.22	0.91	0.12
AT1G36310	R65236	unknown protein	2.26	0.58	2.46	0.09	2.03	0.18	1.06	0.09
AT1G36580	T43614	unknown protein	4.86	2.01	6.01	0.50	3.17	0.22	1.20	0.31
AT1G42990	N97053	bZIP family transcription factor	3.41	0.55	3.28	0.47	2.01	0.10	0.89	0.08
	T88194		4.43	1.19	3.13	0.54	1.61	0.24	1.06	0.15
AT1G47380	T44777	protein phosphatase 2C (PP2C) -related	1.52	0.12	1.79	0.17	2.05	0.31	1.03	0.06
AT1G49480	T21005	expressed protein	1.13	0.15	2.17	0.48	1.95	0.17	1.08	0.17
AT1G51805	T20591	LRR protein kinase, putative, similar to light repressible receptor protein kinase	1.42	0.14	1.92	0.13	1.70	0.07	1.16	0.02
AT1G52890	N65888	unknown protein	2.01	0.09	2.85	0.28	1.87	0.09	1.24	0.25
AT1G55450	T76836	similar to embryo-abundant protein	2.50	0.30	3.07	0.58	1.68	0.46	1.22	0.06
AT1G55670	T43953	putative photosystem I subunit V precursor	2.08	0.19	2.58	0.18	1.89	0.09	1.22	0.12
AT1G55810	T46383	uracil phosphoribosyltransferase	5.03	1.00	6.14	1.45	1.69	0.26	1.33	0.26
AT1G59820	N96155	similar to Potential phospholipid-transporting ATPase	1.37	0.06	1.92	0.21	2.57	0.48	1.02	0.13
AT1G59870	H37610	ABC transporter family protein	3.95	0.75	4.25	0.80	2.05	0.44	1.23	0.22
AT1G62660	W43492	glycosyl hydrolase family 32, identical to beta-fructosidase	1.65	0.26	2.24	0.11	1.92	0.40	0.99	0.14
AT1G62870	R30034	unknown protein	4.99	0.52	7.49	0.72	3.08	0.31	2.45	0.36
AT1G65310	N37583	xyloglucan endotransglycosylase TCH4-like	2.57	0.10	3.57	0.92	2.34	0.22	1.20	0.15

AT1G66260	T45888	export factor RNA binding protein, putative	1.91	0.23	2.29	0.40	2.08	0.34	1.10	0.07
AT1G69080	N38009	unknown protein	2.16	0.19	2.05	0.25	1.82	0.34	1.10	0.02
AT1G69840	R90080	unknown protein	3.50	0.86	4.39	0.77	2.66	0.50	1.17	0.11
AT1G69890	N37850	unknown protein	3.81	1.30	4.04	0.88	2.27	0.62	1.55	0.17
AT1G70090	N38288	glycosyltransferase family 8	2.14	0.29	4.17	0.32	2.97	0.51	1.01	0.11
AT1G72450	T44776	unknown protein	1.34	0.19	1.80	0.22	1.96	0.24	1.08	0.15
AT1G72910	R29891	disease resistance protein (TIR-NBS class), putative	3.08	0.22	3.11	0.52	1.74	0.59	1.37	0.03
AT1G72930	N65692	TIR - TOLL/INTERLEUKIN-1 RECEPTOR-LIKE	4.10	0.73	6.00	0.66	2.74	0.20	0.93	0.05
AT1G73540	T44808	contains similarity to diphosphoinositol polyphosphate phosphohydrolase	5.92	1.92	5.30	1.50	4.24	2.17	1.43	0.08
AT1G74100	T44722	putative flavonol sulfotransferase	3.37	0.66	5.85	2.31	4.23	1.16	1.29	0.22
AT1G74950	R65457	unknown protein	2.91	0.58	3.20	0.12	1.77	0.07	1.28	0.25
AT1G76180	T41665	dehydrin, putative	1.12	0.15	2.07	0.96	1.90	0.08	1.15	0.17
AT1G76680	T44208	12-oxophytodiene reductase (OPR1)	4.69	1.68	12.37	5.73	3.36	1.06	1.60	0.08
AT1G78850	W43262	curculin-like (mannose-binding) lectin family	2.88	0.03	2.67	0.24	2.30	0.65	0.99	0.08
AT1G79900	T46024	mitochondrial carrier protein family	3.78	0.05	3.09	0.26	2.15	0.37	1.31	0.21
AT2G01270	T22047	thioredoxin	1.55	0.06	2.65	0.63	2.81	0.21	1.20	0.12
AT2G01450	N96333	ATMPK17 - mitogen-activated protein kinase	1.99	0.54	2.34	0.33	1.54	0.12	1.00	0.10
AT2G01670	T20807	unknown protein	2.52	0.55	1.98	0.34	2.21	0.04	1.16	0.07
AT2G05710	T44218	cytoplasmic aconitate hydratase	2.81	0.26	3.26	0.82	3.07	0.38	1.21	0.16
AT2G05940	H76238	putative protein kinase	10.86	2.03	7.28	2.52	3.03	0.65	1.87	0.50
AT2G16530	T21016	expressed protein	1.08	0.12	2.14	0.47	1.84	0.14	1.09	0.18
AT2G17840	T43413	putative senescence-associated protein 12	1.48	0.26	2.47	0.79	4.29	1.38	1.21	0.36
AT2G20240	N96062	unknown protein	2.63	0.45	2.72	0.20	1.84	0.08	1.39	0.16
AT2G20810	N65415	unknown protein	1.45	0.12	2.13	0.19	1.53	0.30	1.06	0.20
AT2G22500	AA067581 T44564	mitochondrial carrier protein family	4.16 2.87	1.08 0.62	3.43 2.85	0.30 0.38	2.80 2.62	0.24 0.34	1.33 1.26	0.11 0.08
AT2G23120	T21007	unknown protein	1.94	0.42	7.77	3.52	4.41	0.37	1.23	0.22
AT2G23810	N97214	unknown protein	1.62	0.29	3.92	0.95	2.44	0.55	1.26	0.10
AT2G26190	H76031 R90092	unknown protein	1.86 1.47	0.04 0.22	2.31 2.34	0.13 0.25	1.67 2.34	0.13 0.16	1.24 0.89	0.07 0.03
AT2G28840	T22042	putative RING zinc finger ankyrin protein	2.25	0.38	1.96	0.30	2.14	0.14	1.27	0.14
AT2G29960	T46293	cyclophilin	1.77	0.32	2.07	0.49	2.25	0.39	1.15	0.13
AT2G30470	T22510	transcriptional factor B3 family	4.98	0.33	6.97	0.90	5.28	0.28	1.20	0.05
AT2G30740	T76002	serine/threonine protein kinase	3.36	0.37	3.62	0.57	2.40	0.46	1.26	0.22
AT2G30870	R65251 T43250	GST - ERD13	1.39 1.55	0.24 0.04	2.91 2.95	0.58 0.53	2.54 3.11	0.51 0.81	1.14 1.05	0.18 0.11
AT2G32240	H76467 W43372	myosin heavy chain -related	2.48 1.94	0.71 0.37	2.99 2.12	0.29 0.18	2.72 2.13	0.52 0.09	1.07 0.96	0.19 0.16
AT2G39770	AA067512	GDP-mannose pyrophosphorylase	1.41	0.14	3.64	1.78	3.41	0.41	1.15	0.11
AT2G40000	N65731 R90434	nematode-resistance protein -related	3.91 3.63	1.26 0.22	5.99 3.04	1.21 0.28	2.43 1.87	0.58 0.35	1.43 1.21	0.08 0.06
AT2G40140	T43596	CCCH-type zinc finger protein -related, also an ankyrin-repeat protein	10.78	2.02	11.95	0.62	4.86	0.48	2.06	0.46

AT2G41100	N38224 N97207	ATCAL5 - TCH3 -CaM related protein	6.06 4.69	0.62 0.82	12.58 12.12	3.88 3.25	3.03 3.83	0.08 0.14	1.45 1.54	0.19 0.31
AT2G41110	H77078	ATCAL4	1.78	0.18	2.21	0.18	1.60	0.19	1.17	0.08
AT2G41430	AA042759 AA067594 N38398 R90595 T76301 W43612	ERD15	2.21 1.98 1.60 1.38 2.13 2.57	0.30 0.20 0.15 0.25 0.38 0.48	2.98 2.04 1.94 2.67 2.48 2.32	0.85 0.56 0.25 0.19 0.53 0.55	2.11 2.56 2.02 3.30 1.92 2.77	0.28 0.17 0.18 0.56 0.05 0.32	1.35 1.19 1.02 1.17 1.20 1.20	0.11 0.06 0.07 0.20 0.03 0.07
AT2G41640	N64958 T44801	unknown protein	1.72 2.22	0.43 0.36	2.26 1.67	0.27 0.47	1.76 1.78	0.34 0.14	1.16 1.16	0.14 0.09
AT2G45300	T43742	5-enolpyruvylshikimate-3-phosphate (EPSP) synthase	1.07	0.18	1.92	0.07	1.78	0.46	1.23	0.16
AT2G45820	T76318 W43082	remorin - a non-specific DNA binding protein	1.23 1.10	0.05 0.02	2.78 3.08	1.21 1.21	2.14 2.77	0.12 0.50	1.26 1.17	0.05 0.05
AT2G46330	T46678	arabinogalactan-protein (AGP16)	2.79	1.12	2.07	0.25	1.60	0.42	1.32	0.08
AT3G02880	T43104	leucine-rich repeat transmembrane protein kinase	1.79	0.24	2.31	0.29	1.61	0.12	0.98	0.08
AT3G05320	R30381	unknown protein	1.40	0.39	1.93	0.08	1.92	0.49	0.95	0.09
AT3G07180	R90439	unknown protein	3.64	1.22	6.54	1.37	3.34	0.56	1.34	0.17
AT3G07780	W43216	unknown protein	1.20	0.13	2.11	0.33	2.84	0.47	1.08	0.32
AT3G11820	R90507	SYPI21 - syntaxin-related protein	2.99	0.34	3.48	0.28	2.21	0.30	1.00	0.13
AT3G15210	T76090	ethylene responsive element binding factor 4 (AtERF4)	2.82	0.43	2.67	0.37	2.18	0.52	1.16	0.15
AT3G15356	T43774	similar to putative lectin	2.47	0.28	5.20	1.66	3.61	2.19	1.39	0.21
AT3G16530	T75902	putative lectin	2.99	0.92	7.50	2.57	3.69	1.75	1.34	0.04
AT3G16720	N38413	ATL2 - RING zinc finger protein	2.94	0.28	3.09	0.24	1.95	0.13	1.40	0.24
AT3G17390	AA041124	MTO3 - s-adenosylmethionine synthetase-related - methionine biosynthesis	1.86	0.47	2.62	0.45	2.42	0.44	0.97	0.02
AT3G17650	R90414	unknown protein	3.10	0.80	3.58	0.78	2.02	0.31	1.51	0.20
AT3G19260	T21493	LAG1 HOMOLOG 2, LONGEVITY ASSURANCE GENE1	1.84	0.14	3.53	0.69	2.43	0.13	1.11	0.14
AT3G23030	T44815	auxin-inducible gene (IAA2)	1.50	0.26	1.80	0.10	1.71	0.23	1.06	0.15
AT3G26980	H77004	similar to geranylgeranylated proteins ATGP4	2.61	0.27	2.13	0.74	1.81	0.03	0.94	0.12
AT3G29170	H76592	unknown protein	0.98	0.23	1.61	0.30	2.00	0.28	0.99	0.11
AT3G29360	R30251	UDP-glucose dehydrogenase-related	1.18	0.19	1.80	0.16	1.85	0.12	1.08	0.04
AT3G44720	N96696 T42435	prephenate dehydratase family, similar to bacterial PheA gene products	4.89 5.45	0.16 0.96	6.71 6.01	1.98 1.53	2.75 1.57	0.29 0.40	1.45 1.47	0.16 0.18
AT3G45640	N65559	mitogen-activated protein kinase 3	2.99	0.39	3.22	0.20	2.69	0.65	1.44	0.27
AT3G51550	R64794	receptor-protein kinase-like protein	4.39	1.47	3.06	0.65	4.16	2.02	1.15	0.05
AT3G52800	T41958	zinc finger - like protein	2.69	0.40	2.97	0.37	1.71	0.28	1.42	0.03
AT3G54770	AA067387	contains RNA recognition motif	1.46	0.17	2.10	0.13	2.26	0.65	1.28	0.10
AT3G55430	N97124	glycosyl hydrolase family 17 -beta 1,3 glucanase	3.44	0.16	3.86	0.80	1.64	0.45	1.06	0.03
AT3G55980	T22041	PEI1- CCCH zinc finger transcription factor	12.14	1.16	21.17	1.34	8.35	0.73	1.62	0.05
AT3G56800	N38696	calmodulin like	1.49	0.07	2.22	0.24	1.81	0.25	1.11	0.04

AT3G56880	N37725	unknown protein	1.66	0.31	2.25	0.22	1.58	0.11	1.14	0.20
AT3G57530	N96364	CDPK	2.01	0.19	3.15	0.39	2.30	0.24	1.48	0.27
AT3G58510	T44044	DEAD BOX PROTEIN 3 (RNA HELICASE-LIKE PROTEIN)	4.35	0.91	2.12	0.23	1.62	0.39	1.11	0.06
AT3G59350	H36060	protein kinase-like protein - Pto kinase interactor 1	2.19	0.53	2.40	0.47	1.55	0.36	1.01	0.12
AT3G60220	R89979	RING-H2 zinc finger protein ATL4	1.24	0.34	1.87	0.25	2.34	0.21	1.02	0.06
AT3G62680	R90421	proline-rich protein	4.03	1.12	4.66	0.68	2.88	0.95	1.52	0.25
AT4G02380	H37120	ERD1 - SAG21 -clp protease	2.65	0.81	3.08	0.80	2.15	0.11	1.16	0.08
AT4G17490	T43246	ethylene-responsive element binding factor(ATERF6)	6.33	0.77	6.35	0.52	1.94	0.28	2.57	0.85
AT4G17500	T42394	ATERF-1, ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1	2.92	0.54	2.56	0.30	1.66	0.25	1.27	0.07
AT4G21850	T75897	unknown protein	4.52	1.72	5.62	0.93	2.16	1.00	1.42	0.23
AT4G22710	N65907	CYP706A2 - cytochrome p450	8.90	1.21	9.33	0.54	2.58	0.16	1.47	0.34
	T21057		8.34	1.77	7.31	1.34	2.91	0.18	1.67	0.39
	T46193		3.59	0.05	3.24	0.18	2.16	0.44	1.31	0.21
	T46392		4.58	0.75	4.75	0.84	2.22	0.28	1.35	0.23
AT4G24160	T76500	unknown protein	2.49	0.45	3.23	0.74	1.80	0.33	1.53	0.19
AT4G24570	T76263	mitochondrial carrier protein family	8.38	3.16	5.64	2.80	4.04	0.68	1.60	0.36
AT4G25030	N65831	unknown protein	2.01	0.09	3.04	0.28	2.07	0.34	1.11	0.03
	T41814		2.67	0.35	2.83	0.27	2.13	0.42	1.42	0.32
AT4G30530	T43728	component of aniline dioxygenase	4.94	0.21	4.05	1.63	2.31	0.15	0.96	0.25
AT4G31500	T20600	CYP83B1, CYTOCHROME P450 MONOOXYGENASE	1.77	0.30	2.14	0.32	1.70	0.28	1.21	0.13
	T76397		2.01	0.62	2.32	0.05	2.22	0.46	1.17	0.08
AT4G32020	T75628	unknown protein	2.18	0.05	2.30	0.38	1.57	0.16	1.16	0.12
AT4G33070	N97215	pyruvate decarboxylase-1 (Pdc1)	3.36	2.17	1.81	0.44	2.06	0.17	1.03	0.12
AT4G35480	T45602	RING-H2 finger protein RHA3b	2.87	1.01	4.29	0.95	2.38	0.22	1.19	0.27
AT4G36500	N97118	unknown protein	2.54	0.45	2.56	0.38	2.90	1.04	1.43	0.13
	T43539		3.79	1.16	7.70	0.77	4.23	0.95	1.26	0.32
AT4G38550	R65028	Phospholipase like protein-pEARLI 4	2.27	0.25	3.23	0.56	2.21	0.36	1.20	0.18
AT4G39670	R30050	unknown protein	3.87	0.60	3.98	0.19	2.95	0.52	1.33	0.17
AT4G39940	T42885	adenosine-5-phosphosulfate-kinase	2.92	0.59	2.77	0.36	2.86	0.71	1.35	0.19
AT4G39950	T42902	cytochrome P450	3.07	0.74	4.78	0.80	3.65	0.94	1.55	0.39
AT5G03210	W43163	putative protein	3.53	0.56	2.30	0.36	1.52	0.15	1.23	0.09
AT5G03380	T20408	similar to farnesylated protein ATFP2	2.62	0.34	2.10	0.59	1.81	0.12	1.23	0.07
AT5G03530	AA042493	unknown protein - RAB GTPase	2.06	0.34	2.17	0.35	1.72	0.30	1.13	0.12
AT5G05730	N65620	ASA1 - ANTHRANILATE SYNTHASE ALPHA SUBUNIT - tryptophan biosynthesis	2.49	0.45	2.65	0.38	1.70	0.17	1.01	0.19
AT5G06320	H37034	NDR1/HIN1-like protein 3 (NHL3)	7.32	0.91	12.81	5.49	2.50	0.56	1.41	0.14
AT5G09850	T43948	unknown protein	2.50	0.37	1.68	0.15	1.88	0.17	1.18	0.11
AT5G11670	N65762	NADP dependent malic enzyme - like protein	3.16	0.32	3.87	0.05	1.94	0.22	1.14	0.14
AT5G11740	N97068	AGP15 - ARABINOGALACTAN PROTEIN	2.37	0.77	2.74	0.59	2.08	0.31	0.97	0.04
AT5G13420	N38293	transaldolase - like protein - suger metabolism	2.93	1.11	8.01	1.47	6.29	1.72	1.36	0.12

AT5G13650	T44050	GTP-binding protein typA (tyrosine phosphorylated protein A)	1.94	0.13	1.80	0.21	1.85	0.06	1.26	0.06
AT5G14930	N37740	leaf senescence-associated gene SAG101	1.40	0.25	2.02	0.20	1.76	0.18	0.93	0.02
AT5G15970	T21841	cold-regulated protein COR6.6 (KIN2)	2.84	1.48	2.47	1.01	6.31	1.38	1.14	0.47
AT5G18400	T43145	unknown protein	4.02	0.56	7.32	2.09	2.45	0.53	1.18	0.08
AT5G24140	T44667	squalene monooxygenase 2	2.57	0.20	3.39	0.14	2.72	0.11	1.18	0.14
AT5G24300	T22050	strach synthase	2.49	0.31	4.22	0.35	3.36	0.12	1.36	0.11
AT5G25880	N97161	malate dehydrogenase	3.28	0.54	3.35	0.49	2.34	0.55	1.22	0.28
AT5G26030	N38420	ferrochelatase-I	3.53	0.93	4.47	1.34	3.76	0.24	1.63	0.12
AT5G37770	AA067498	CALMODULIN-RELATED PROTEIN 2 (TCH2)	1.98	0.30	3.30	0.27	3.13	1.31	1.27	0.18
AT5G38410	N64949	(RuBisCO small subunit 3b)	2.33	0.61	5.56	2.69	2.99	0.24	1.26	0.42
AT5G42050	T21358	unknown protein	4.87	0.37	5.12	1.12	3.00	0.74	1.34	0.13
	T44501		3.70	0.66	4.34	1.05	2.58	0.57	1.37	0.11
AT5G42380	R30557	calmodulin-related protein	5.29	1.33	6.35	0.89	5.17	0.81	1.17	0.17
AT5G42500	R89967	similar to disease resistance response protein	1.72	0.31	2.02	0.10	1.85	0.28	0.86	0.10
AT5G42650	N65720	AOS - Allene oxide synthase - JA biosynthesis	3.00	0.45	4.53	0.64	3.14	0.48	1.27	0.21
AT5G45280	T41817	pectinacetyltransferase, putative	2.14	0.48	2.58	0.23	1.56	0.23	1.16	0.13
AT5G45350	AA067411	unknown protein	1.36	0.20	1.93	0.23	1.86	0.18	1.15	0.11
	T42791		1.77	0.24	2.39	0.29	2.25	0.08	1.16	0.18
AT5G46500	T22187	unknown protein	1.37	0.20	1.72	0.28	1.79	0.23	1.00	0.09
AT5G53350	T20819	ATP-dependent Clp protease ATP-binding subunit ClpX1	2.89	0.86	2.88	1.00	2.08	0.15	0.96	0.23
AT5G56870	T42972	glycosyl hydrolase family 35 (beta-galactosidase)	3.31	0.25	4.21	0.27	2.49	0.53	1.29	0.06
AT5G56980	T21530	unknown protein	2.01	0.52	3.51	0.21	2.67	0.70	0.98	0.13
AT5G57220	T88150	CYP81F2 cytochrome p450	5.54	1.30	7.29	1.55	3.37	1.28	1.51	0.28
AT5G59550	R30129	COP1-interacting protein CIP8	2.92	0.52	3.32	0.79	2.50	0.55	1.43	0.18
AT5G62570	H37503	calmodulin-binding protein	1.88	0.16	2.04	0.21	1.98	0.82	1.17	0.05
AT5G64310	T46733	arabinogalactan-protein (AGP1)	8.03	2.45	9.05	1.90	1.82	0.43	1.31	0.16
AT5G65630	T42826	unknown protein	1.50	0.48	1.67	0.21	2.10	0.19	1.05	0.12
unknown	N97187		1.95	0.08	2.88	1.02	2.71	0.31	1.21	0.08
unknown	N97200		4.00	0.27	4.49	1.73	2.50	0.34	1.41	0.20
unknown	T45312		1.88	0.52	2.82	0.13	2.00	0.33	1.15	0.13
average			3.02		3.89		2.48		1.25	