

Supplemental data I

**Fold variations of DTT upregulated genes passing the 1,000-5P-2.5 criteria
(217 genes + 7 nulls)**

(D#), number of entries passing the restriction for this gene.

Affymetrix code	Description	hours	0	2+	2	5+	5
12081_at	unknown protein	0.853	1.997	1	5.322	0.916	
12092_at	unknown protein	0.866	1.645	0.895	2.973	1	
12128_at	unknown protein	1	2.628	0.785	1.188	0.475	
12198_at	unknown protein	1	1.71	0.545	2.603	0.606	
12216_at	unknown protein	0.733	1.752	0.881	4.167	1	
12226_at	unknown protein	0.994	3.389	1	0.637	2.312	
12227_at	unknown protein	0.835	2.201	1	7.919	0.868	
12293_at	putative beta-glucosidase	1.031	3.196	0.806	1	0.968	
12500_s_at	IAA-Ala hydrolase; IAA-amino acid hydrolase	0.904	2.419	0.833	15.359	1	
12505_s_at	putative CONSTANS-like B-box zinc finger protein	0.983	2.291	0.973	6.844	1	
12539_s_at	putative gamma-glutamyltransferase	0.979	3.322	0.912	5.701	1	
12571_s_at	ferrochelatase-I	1	2.44	0.646	5.814	0.601	
12645_at	fibrillin precursor-like protein	0.768	2.27	0.801	3.481	1	
12760_g_at	similar to extracellular dermal glycoprotein (EDGP) precursor	0.778	1.953	1	3.395	0.764	
12764_f_at	putative glutathione S-transferase	1	1.259	0.695	3.311	0.637	
12772_at	similar to extracellular dermal glycoprotein (EDGP) precursor	0.959	2.95	0.842	4.548	1	
12790_s_at	cytochrome P450 like protein	0.904	3.317	1	3.557	0.98	
12842_s_at	unknown protein (null)	0.948	3.308	1	4.192	0.937	
12843_s_at	unknown protein (null)	1	3.916	0.676	6.235	0.598	
12846_s_at	unknown protein (null)	0.872	2.159	1	2.845	0.836	
12880_at	AIG2	0.947	1.926	1	10.752	0.711	
12916_at	coronatine-induced protein 1	0.733	2.145	1	3.076	0.825	
12951_at	unknown protein	0.931	5.681	0.812	5.156	1	
12966_s_at	bZIP transcription factor ATB2	0.983	1.734	0.739	3.107	1	
13014_at	putative lipase	0.862	1.384	0.902	6.838	1	
13115_at	unknown protein	1	19.664	0.045	49.328	0	
13123_at	unknown protein	1	2.011	0.967	2.565	0.91	
13128_at	protein phosphatase 2C-like protein	1	1.934	0.846	13.034	0.841	
13136_at	unknown protein	0.909	1.843	1	3.564	0.863	
13158_at	putative cinnamoyl-CoA reductase	1	1.46	0.853	4.128	0.855	
13176_at	unknown protein	0.722	1.454	0.791	3.563	1	
13177_at	growth factor like protein	1	8.13	0.727	14.375	0.657	
13189_s_at	thioredoxin h	2.268	1	0.395	4.188	0.85	
13246_at	putative protein kinase	0.795	2.765	0.371	2.749	1	
13256_s_at	gamma-glutamyl transpeptidase	0.936	2.487	1	5.603	0.951	
13267_at	glutathione transferase	0.842	2.032	0.898	4.01	1	
13270_at	heat shock transcription factor 21 (D2)	1	1.863	0.246	4.34	0.54	
13273_at	heat shock transcription factor 4	1	1.475	0.768	3.455	0.478	
13284_at	heat shock protein 70	0.721	1.656	0.853	4.684	1	
13285_at	heat shock protein 83	0.773	1.965	1	10.688	0.98	
13461_at	unknown protein	0.85	3.989	1.483	1	0.832	
13538_at	calcium-binding protein-like	0.964	3.962	0.916	3.223	1	
13564_at	putative glutathione S-transferase	0.914	1.14	0.868	3.238	1	
13575_at	putative pre-mRNA splicing factor	1.117	1	0.611	2.896	0.666	
13591_at	unknown protein (D2)	1	4.104	0.69	5.779	0.889	
13617_at	putative mitochondrial dicarboxylate carrier protein	1	7.629	0.793	3.588	0.672	
13645_at	unknown protein	0.993	10.068	1	90.858	0.639	
13653_at	unknown protein	0.544	1.022	1	2.991	0.354	
13656_at	unknown protein	0.733	32.274	1	51.283	0.857	
13666_s_at	putative indole-3-glycerol phosphate synthase	1	1.285	0.607	4.403	0.792	
13706_at	putative trehalose-6-phosphate synthase	1	2.693	0.691	3.859	0.424	
13908_s_at	berberine bridge enzyme - like protein	1	3.196	0.511	7.179	0.285	
14026_at	similar to Mg-dependent ATPase	0.91	1	0.688	2.677	1.054	
14030_at	putative protein kinase	0.848	5.683	1	12.027	0.727	
14037_at	similar to cinnamyl alcohol dehydrogenase	0.93	1.565	1	4.253	0.941	
14068_s_at	putative farnesylated protein	1	6.316	0.841	6.324	0.964	
14077_at	putative phi-1-like phosphate-induced protein	1	1.226	0.488	3.398	0.597	
14078_at	unknown protein	0.939	2.616	0.814	3.339	1	
14089_at	putative hydrolase	1	1.854	0.527	4.612	0.523	
14090_i_at	unknown protein (D2)	0.869	0.615	1.175	2.397	1	

14116_at	similar to sugar transporters	1	5.54	0.861	18.444	0.757
14249_i_at	unknown protein	1	3.176	0.769	4.762	0.698
14381_at	unknown protein	0.949	6.608	1	6.816	0.964
14391_at	RING-H2 finger protein RHF1a (D2)	0.912	1.663	1	3.016	0.563
14468_at	unknown protein	1	1.148	0.422	4.156	0.244
14487_at	HSP like protein	1	2.865	0.708	4.258	0.38
14489_at	sperm protein homolog	0.873	2.143	1	3.071	0.94
14490_at	unknown protein	1	1.667	0.964	3.31	0.887
14591_at	unknown protein	0.962	1.38	0.826	2.709	1
14608_at	similar to E1-E2 ATPase family	0.911	2.811	1	2.615	0.702
14614_at	putative glucosyltransferase	0.759	4.556	1	9.161	0.91
14643_s_at	putative steroid sulfotransferase	0.792	5.934	0.707	12.794	1
14667_at	tryptophan synthase beta subunit	0.977	1.866	1	2.766	0.966
14672_at	tryptophan synthase alpha chain	1	1.158	0.818	2.828	0.817
14686_at	similar to receptor-like protein kinase	0.954	1.786	1	2.701	0.9
14697_g_at	unknown protein	0.842	1.682	1	6.149	0.953
14900_at	unknown protein	1	2.279	0.6	2.971	0.866
14937_at	unknown protein	0.481	1.442	1	2.094	0.693
15026_at	unknown protein	1	2.195	0.774	2.764	0.813
15032_at	secretory carrier membrane protein	1	0.666	1.364	3.665	0.909
15040_g_at	drought-induced-19-like 1 (D2)	0.92	3.105	0.973	2.853	1
15143_s_at	phospholipase D-gamma-2	0.994	2.095	1	2.606	0.86
15171_s_at	protein phosphatase-1	0.853	1.518	1	2.505	0.814
15172_s_at	BiP	0.976	4.254	1	4.614	0.752
15190_s_at	epoxide hydrolase (ATsEH)	1	1.806	0.942	2.827	0.844
15192_at	ATP-dependent Clp protease ATP-binding subunit	0.817	3.602	0.856	8.125	1
15392_at	unknown protein	0.917	5.035	0.715	8.297	1
15431_at	unknown protein	1	9.873	0.433	11.862	0.371
15496_at	putative glucosyl transferase	0.769	21.15	0.636	34.126	1
15580_at	acyl-CoA oxidase	0.907	1.769	0.821	2.748	1
15582_s_at	alternative oxidase	0.855	7.651	0.794	8.614	1
15586_s_at	ABI1	0.974	3.741	0.948	5.817	1
15594_s_at	glutamate dehydrogenase 2	1	2.789	0.866	8.296	0.607
15612_s_at	G protein alpha subunit 1 (GP-alpha-1)	0.729	1.786	1	3.91	0.694
15614_s_at	xyloglucan endo-1, 4-beta-D-glucanase precursor	0.79	2.174	0.646	3.05	1
15617_s_at	formerly called HAT24; synaptobrevin-related protein	1	1.288	0.974	2.796	0.965
15629_s_at	unknown protein	1	0.748	1.008	3.027	0.721
15646_s_at	serine acetyltransferase	0.851	7.675	0.971	6.884	1
15660_s_at	glutathione peroxidase; ATGP1	1	2.396	0.853	5.177	0.809
15672_s_at	unknown protein	1	2.147	0.845	5.424	0.602
15680_s_at	putative ribosomal-protein S6 kinase (ATPK19)	1	4.94	0.83	8.874	0.852
15774_at	unknown protein	0.828	1.329	0.631	2.999	1
15792_at	unknown protein	1	2.87	0.719	4.135	0.907
15839_at	unknown protein	1	3.435	0.462	10.361	0.509
15866_s_at	unknown protein	1	1.037	0.613	4.765	0.853
15924_at	PITSLRE protein kinase family	0.691	1.147	0.982	2.922	1
15978_at	adenosine nucleotide translocator	1	1.212	0.966	2.509	0.921
16008_i_at	glutathione S-transferase (GST6) (D2)	1	2.609	0.964	6.825	0.785
16054_s_at	glutathione S-transferase (D2)	1	2.39	0.365	5.61	0.529
16064_s_at	ethylene responsive element binding factor 4	0.802	2.604	1	2.625	0.528
16077_s_at	phytochelatin synthase 1	1	2.917	0.857	2.353	0.95
16079_s_at	C2H2 zinc finger protein FZF	0.879	1.376	1	2.57	0.869
16109_s_at	putative protein kinase	1	3.853	0.969	3.936	0.94
16298_at	unknown protein	0.999	2.536	1	3.691	0.837
16335_at	xanthine dehydrogenase-like protein	0.864	1.236	0.921	2.568	1
16393_s_at	putative receptor-like protein kinase	1	1.334	0.68	4.291	0.895
16447_at	HSP90 isolog (D2)	1	2.84	0.969	3.33	0.953
16524_at	similar to aldehyde dehydrogenase	0.896	2.03	0.759	4.227	1
16528_at	unknown protein	0.939	2.302	0.876	3.152	1
16536_at	ethylene responsive element binding factor 5	1	4.717	0.125	2.644	0.206
16539_s_at	EREBP-4 like protein	1	17.841	0.547	12.675	0.533
16570_s_at	calcium-dependent protein kinase 1	0.794	1.893	1	3.357	0.835
16571_s_at	calcium-dependent protein kinase	1	1.095	0.83	2.673	0.871
16603_s_at	UDP-glucose:indole-3-acetate beta-D-glucosyltransferase	1	4.79	0.894	4.319	0.932
16609_at	ethylene responsive element binding factor 2	1	4.423	0.439	6.275	0.46
16620_s_at	xyloglucan endotransglycosylase related protein	1	8.214	0.448	18.305	0.579
16635_s_at	unknown protein	1	1.506	0.897	3.165	0.807

16637_s_at	light induced protein like	0.72	2.834	0.762	3.47	1
16888_at	putative alcohol dehydrogenase	0.482	2.165	1	3.578	0.727
16902_at	unknown protein	0.914	1.353	1	3.45	0.962
16916_s_at	heat shock cognate 70-2	1.142	0.918	0.884	5.181	1
16927_s_at	endo-xyloglucan transferase	0.793	2.649	0.545	4.837	1
16950_s_at	sec61 beta-subunit homolog	0.985	2.357	0.788	2.634	1
16951_i_at	calmodulin-like protein (D2)	1	1.862	0.762	3.441	0.675
16981_s_at	thioredoxin h	1.996	1	0.67	7.901	0.454
17104_s_at	phosphoserine aminotransferase	0.969	1.495	0.974	4.001	1
17105_at	respiratory burst oxidase protein D	1	3.039	0.732	3.101	0.579
17119_s_at	OPDA-reductase homolog	0.98	1.852	1	6.464	0.862
17300_at	NADPH-ferrihemoprotein reductase	1	3.623	0.719	3.36	0.843
17352_at	putative protein kinase	0.89	1.767	1	3.924	0.831
17379_at	putative CCCH-type zinc finger protein	1	8.685	0.564	6.875	0.612
17381_at	unknown protein	1	5.187	0.541	5.54	0.606
17391_at	unknown protein	0.859	2.348	0.878	5.775	1
17396_at	similar to NAD-dependent glyceraldehyde-3-phosphate dehydrogenase	0.713	1	1.035	2.581	0.749
17398_at	putative protein disulfide-isomerase	1	1.838	0.939	3.261	0.963
17458_at	unknown protein	0.94	1.314	1	3.291	0.897
17464_at	similar to receptor-like protein kinase	1	1.889	0.736	3.235	0.748
17473_at	calnexin, CNX1	1	5.169	0.938	4.34	0.981
17482_at	GTP-binding RAB1C like protein	0.89	1.514	1	2.898	0.909
17579_s_at	phytochelatin synthase	1	2.533	0.766	2.246	0.888
17627_at	unknown protein	0.598	2.09	0.681	6.912	1
17775_at	similar to glucose-6-phosphate/phosphate-translocator	1	1.614	0.821	4.193	0.677
17832_at	class 1 non-symbiotic hemoglobin	1	1.977	0.62	6.138	0.67
17860_at	unknown protein	1	1.009	0.319	2.581	0.406
17876_at	monooxygenase (D2)	0.934	5.231	0.834	11.104	1
17881_at	AtWRKY-15	0.866	2.698	0.861	6.634	1
17882_at	protein transport protein sec61 gamma subunit-like	1	3.618	0.961	4.216	0.978
17886_at	unknown protein	1	3.935	0.585	3.33	0.808
17899_at	unknown protein	1	1.727	0.756	2.629	0.661
17900_s_at	similar to SRC2, low temperature induced	1	4.287	0.608	7.158	0.854
17924_at	calnexin homolog	0.965	4.007	0.913	3.143	1
17952_at	GTP-binding protein	0.666	1.465	0.837	2.565	1
17955_at	small GTP-binding protein-like	0.95	1.162	1	2.872	0.802
18022_at	glucose-6-phosphate 1-dehydrogenase	1	1.019	0.778	2.777	0.738
18059_i_at	unknown protein (null)	1	1.802	0.738	3.928	0.879
18109_s_at	putative metal ion transporter (NRAMP)	0.858	2.639	0.846	8.304	1
18217_g_at	salt tolerant zinc finger protein (D2)	1	14.968	0.314	16.885	0.302
18228_at	lectin like protein (null)	1	2.073	0.985	3.622	0.914
18253_s_at	12-oxophytodienoate reductase OPR1	0.624	6.119	1	8.703	0.639
18255_at	unknown protein	1	1.224	0.71	6.22	0.703
18284_at	unknown protein	1	5.646	0.872	7.446	0.869
18287_at	unknown protein	1	2.334	0.897	5.319	0.986
18300_at	calmodulin-related protein	1	3.737	0.865	3.884	0.812
18314_i_at	putative beta-glucosidase	0.683	1	1.012	2.809	0.989
18351_at	unknown protein	0.773	2.364	0.844	3.827	1
18544_at	similar to putative UDP-galactose-4-epimerase	1	1.714	0.878	5.319	0.364
18600_at	putative zinc finger protein	1	2.25	0.74	2.518	0.76
18605_s_at	unknown protein	0.934	1.89	0.974	2.918	1
18623_at	unknown protein	0.838	1.785	0.669	5.46	1
18659_at	unknown protein	0.85	1.406	1	3.398	0.885
18662_s_at	unknown protein	1	8.481	0.986	17.008	0.689
18672_s_at	chloroplast envelope Ca2+-ATPase precursor	1	2.057	0.903	2.507	0.88
18673_at	unknown protein (null)	1	1.147	0.92	2.613	0.995
18675_at	GPT (D2)	0.828	1.548	1	3.085	0.949
18681_at	ER lumen protein retaining receptor	1	1.433	0.779	3.345	0.877
18885_at	putative protein kinase	0.76	2.664	0.935	2.345	1
18936_at	protein phosphatase 2C	0.885	1.891	0.765	3.522	1
18948_s_at	putative ubiquitin conjugating enzyme (D2)	0.77	1.669	1	4.168	0.843
18966_at	putative glutathione S-transferase	0.533	8.694	0.728	20.694	1
19132_at	putative NADPH quinone oxidoreductase	0.96	1.549	1	2.874	0.996
19137_at	ATAF1	0.946	7.062	0.749	7.808	1
19176_at	unknown protein	1	3.115	0.851	3.317	0.874
19178_at	blue copper binding protein	1	5.962	0.52	14.943	0.743
19181_s_at	late embryogenesis abundant protein homolog	1	2.244	0.804	2.699	0.922

19212_at	similar to vesicle trafficking protein	1	1.819	0.83	3.212	0.82
19366_at	carnitine racemase like protein	0.94	1.767	0.979	2.564	1
19411_at	unknown protein	0.916	2.21	0.94	6.895	1
19457_at	putative protein disulfide isomerase	0.984	3.898	0.822	5.57	1
19591_at	IAA-amino acid hydrolase, putative	0.878	1.183	0.784	5.12	1
19597_s_at	lactate dehydrogenase	0.975	3.271	1	6.548	0.75
19624_at	cytochrome c	0.496	1.615	0.635	3.589	1
19648_at	similar to coatamer alpha subunit (HEPCOP) homolog	0.972	2.884	1	3.505	0.989
19762_at	peptide transporter-like protein	0.857	3.825	0.506	14.96	1
19843_at	unknown protein	0.992	2.815	0.946	5.456	1
19844_at	monooxygenase 2 (MO2) (D2)	0.668	2.011	0.935	3.645	1
19848_s_at	calmodulin-related protein	1	3.806	0.525	5.028	0.532
19946_at	putative senescence-associated protein 5	1	8.544	0.636	16.51	0.686
19956_at	unknown protein	1	1.593	0.619	5.758	0.71
20032_at	unknown protein	0.997	3.82	1	3.983	0.977
20178_at	unknown protein	0.784	8.831	0.897	4.371	1
20194_at	unknown protein	1	0.845	1.03	5.705	0.613
20200_at	unknown protein	0.844	1.799	1	3.986	0.659
20291_at	anthranilate synthase alpha subunit	0.704	2.567	0.808	6.018	1
20294_at	peroxidase ATP17a-like protein	1	2.614	0.652	3.859	0.886
20305_at	similar to UTP-Glucose Glucosyltransferase	0.879	3.434	0.94	4.531	1
20337_at	ubiquitin conjugating enzyme	0.955	1.774	1	5.017	0.996
20372_at	unknown protein	1.147	4.393	0.731	0.742	1
20432_at	xyloglucan endotransglycosylase-related protein	1	1.717	0.712	2.571	0.595
20462_at	putative protein kinase PK1	1	1.963	0.824	2.867	0.989
20480_s_at	cytochrome P450-like protein (D2)	1	1.461	0.578	3.995	0.607
20656_at	unknown protein	0.7	0.655	1	2.767	1.102
20685_at	short-chain alcohol dehydrogenase like protein	0.992	5.33	0.819	18.717	1
20701_s_at	unknown protein	1	1.896	0.834	2.718	0.952
AFFX-Athal-5SrRNA_at (null)		0.704	4.223	0.778	2.268	1