Supplemental Table 1. List of differentially regulated genes upon arabinose induced Adr1 expression in HE140*.

Probeset	um-Number**	Annotation**	0 min		75 min		180 min		Experimental means					
			Fold change	Adj. p-value	Fold change	Adj. P-value	Fold change	Adj. P-value	FB1_0min	FB1_75min	FB1_180min	HE140_0min	HE140_75min	HE140_180min
W55um190G_at	um00330	- related to UTR2 - cell wall protein	-1,17	9,78E-01	2,3	1,58E-04	-2,2	3,31E-04	290,10	448,73	1164,33	257,90	1034,53	530,67
W100um222G_at	um01424	- related to Cytochrome P450 83A1	-3,05	1,74E-01	2,7	7,62E-04	-2,1	6,88E-03	26,75	446,70	1111,13	7,95	1194,13	541,70
C55um211G_at	um04571	- Ssp1 - putative dioxygenase Ssp1	1,33	9,78E-01	3,0	5,32E-05	-2,2	8,44E-04	114,50	330,73	729,17	156,10	993,77	331,77
W5um026G_at	um02390	- related to alpha,alpha-trehalose-phosphate synth	1,07	9,98E-01	2,4	9,79E-04	-1,1	7,57E-01	188,70	142,67	163,13	202,00	324,83	152,97
C25um106G_at	um01025	- hypothetical protein	1,16	9,91E-01	3,8	4,89E-04	1,2	6,75E-01	10,50	9,67	9,70	12,30	40,30	13,27
W10um155G_at	um04954	- hypothetical protein	1,06	9,91E-01	2,2	4,34E-05	1,0	8,81E-01	65,40	59,77	60,70	69,50	131,37	62,30
W15um279G_at	um05654	- probable ras-related GTP-binding protein	1,11	9,78E-01	2,1	1,68E-05	1,3	2,66E-02	181,85	331,97	249,63	206,15	709,07	327,63
W115um227G_at	um11672	- related to Protein farnesyltransferase alpha subur	-1,09	9,83E-01	3,1	4,09E-07	2,2	1,03E-05	157,95	296,47	150,30	145,60	916,50	335,23
C70um145G_at***	um04386	- hypothetical protein	1,24	9,78E-01	3,6	2,11E-04	1,6	9,62E-02	48,80	72,23	43,80	61,55	253,67	67,43
W60um232G_at	um04526	- hypothetical protein	-1,10	9,91E-01	7,0	5,43E-07	-1,1	6,59E-01	48,10	39,90	32,87	41,80	283,90	30,03
W60um167G_at	um04248	- putative protein	1,21	9,91E-01	12,1	6,73E-06	-1,2	6,24E-01	9,30	12,37	7,67	10,85	137,53	6,17
C100um020G_at	um00860	- conserved hypothetical protein	1,11	9,78E-01	2,6	7,61E-07	1,2	5,77E-02	55,75	62,60	48,93	61,95	166,10	60,37
C20um110G_at	um00578	- bW1 - b locus protein W1	-1,31	9,78E-01	4,7	1,06E-04	2,3	1,02E-02	33,80	38,83	15,13	25,55	183,73	31,87
UG16-16l20-80e12_RC_a	um06510	- conserved hypothetical Ustilago-specific protein	-1,02	9,98E-01	4,4	1,03E-06	1,2	3,94E-01	343,45	318,20	331,57	340,60	1409,90	377,03
W25um110G_at	um00577	- Mating-type locus allele B1 protein	-1,25	9,91E-01	18,0	2,43E-05	1,6	2,90E-01	7,00	17,53	6,03	5,05	322,27	10,73
CLUSTER67_RC_at	um11658	- hypothetical protein	-1,03	9,98E-01	4,1	6,72E-06	1,1	7,88E-01	16,60	25,47	21,67	16,30	106,23	23,87
C20um077G_at	um03317	- related to PRM1 - Pheromone-regulated multispa	1,24	8,90E-01	4,4	2,15E-08	1,7	1,65E-04	54,70	88,53	56,43	68,15	389,90	96,77
W70um083G_at	um03144	- probable clathrin-associated adaptor complex me	-1,13	9,78E-01	3,8	7,18E-08	1,5	1,64E-03	209,80	222,57	158,97	186,05	842,73	240,53
W120um091G_at	um02410	- hypothetical protein	1,06	9,91E-01	5,7	1,61E-08	2,2	2,43E-05	173,65	290,73	143,67	184,35	1670,90	311,87
C85um132G_at	um05182	- hypothetical protein	1,11	9,78E-01	2,8	1,67E-07	1,0	8,02E-01	53,55	56,87	53,03	59,70	159,67	54,47
C25um007G_at***	um05356	- hypothetical protein	1,18	9,78E-01	12,1	5,41E-08	2,8	1,30E-04	42,75	58,57	21,03	52,25	717,47	62,90
W51um130G_at	um10491	- putative protein	1,34	9,78E-01	18,0	5,45E-08	1,6	4,22E-02	34,85	45,57	28,73	47,75	831,07	46,77
W15um280G_at	um00384	- hypothetical protein	1,23	9,78E-01	32,3	1,24E-08	-1,7	3,26E-02	41,70	33,00	43,60	52,35	1091,47	27,77
W10um286G_at	um00530	- hypothetical protein	1,33	9,78E-01	12,9	3,49E-06	1,4	3,56E-01	5,95	9,10	10,53	8,30	127,00	16,07
C140um075G_at	um06071	- related to Para-nitrobenzyl esterase	1,08	9,98E-01	14,4	5,36E-07	1,7	4,89E-02	56,90	224,57	165,50	62,85	3099,47	305,87
C145um075G_at	um06072	- conserved hypothetical protein	-1,11	9,78E-01	2,1	1,37E-05	1,1	2,77E-01	194,75	199,47	194,33	177,15	414,40	219,57
W160um054G_at	um11450	- Hgl1 - Hgl1p, required for dimorphism and teliosp	-1,03	9,98E-01	2,5	7,10E-06	1,3	6,48E-02	320,55	382,20	352,13	315,25	944,53	444,70
W55um065G_at	um10886	- conserved hypothetical protein	-1,03	9,98E-01	2,2	1,29E-05	-1,0	9,11E-01	737,10	671,20	776,40	728,75	1462,77	765,10
W50um041G_at	um05386	- hypothetical protein	1,21	9,78E-01	5,1	5,45E-07	1,2	2,76E-01	270,05	188,60	222,53	330,80	963,53	265,00
W55um007G_at	um05348	- related to RAM1 - protein farnesyltransferase, be	1,02	9,98E-01	4,0	3,25E-08	3,5	9,15E-08	264,10	291,17	119,13	270,40	1166,83	422,47
C112um175G_at	um02713	- Prf1 - pheromone response factor Prf1	1,28	8,94E-01	3,1	7,51E-07	4,1	1,43E-07	363,45	719,67	212,73	471,40	2212,13	876,97
W40um026G_at	um02383	- Pra1 - a2-pheromone receptor Pra1	1,63	1,85E-01	3,5	1,12E-07	3,8	8,64E-08	428,45	1046,17	367,07	693,60	3643,93	1406,00
W40um030G_at	um10528	- related to STE6 - ABC transporter	1,57	9,78E-01	5,3	7,66E-04	17,6	1,36E-05	36,90	150,20	13,17	68,45	797,40	220,77
W35um026G_at	um10139	- probable pantoate--beta-alanine ligase	1,37	3,56E-01	2,5	1,08E-07	1,8	4,53E-06	248,65	286,90	183,17	341,00	708,67	339,40
UG14-15c10-91c8_RC_at	um11679	- related to STE14 - farnesyl cysteine carboxyl-me	1,02	9,98E-01	3,0	1,48E-08	2,0	9,88E-07	466,10	374,60	212,60	474,20	1136,43	432,73
W71um079G_at	none	- no annotation available	1,18	9,91E-01	2,8	4,86E-04	1,2	4,72E-01	89,35	80,30	60,40	105,70	219,37	74,40
C44um147G_at	um11199	- related to CDC28 - cyclin-dependent protein kina	-1,02	9,98E-01	2,2	1,02E-05	-1,2	1,58E-01	160,00	139,70	147,87	158,50	309,20	125,83
W30um110G_at	um00576	- conserved hypothetical protein	1,33	9,88E-01	14,8	1,01E-05	-2,4	3,12E-02	49,15	8,43	31,63	66,50	131,73	14,57
W150um054G_at	um00644	- hypothetical protein	-1,07	9,78E-01	3,0	4,97E-08	-1,2	2,82E-02	333,50	235,80	270,43	311,95	713,60	221,57
EST01um006_at***	um02304	- putative protein	1,00	1,00E+00	3,1	7,16E-09	-1,4	4,58E-04	468,65	301,37	423,17	469,60	924,30	309,70
C25um258G_at	um10519	- putative protein	-1,04	9,91E-01	2,2	1,17E-06	-1,0	9,09E-01	676,75	454,73	502,10	651,00	1009,50	495,93
W20um276G_at	um05997	- hypothetical protein	1,10	9,78E-01	3,5	9,41E-09	-1,2	7,31E-02	114,55	68,07	66,03	126,75	243,40	56,87
W20um256G_at	um05781	- hypothetical protein	-1,01	1,00E+00	5,1	8,86E-05	-1,6	1,12E-01	8,15	6,13	10,73	8,00	35,73	5,37
W80um091G_at	um10152	- Don1 - cytokinesis protein Don1	-1,04	9,94E-01	2,0	7,08E-06	-1,3	7,65E-03	173,05	142,83	194,47	167,40	292,53	145,03
C75um055G_at	um03982	- hypothetical protein	1,04	9,98E-01	2,7	3,29E-06	-2,2	3,00E-05	65,95	49,10	93,40	69,15	135,87	41,87
C15um206G_at	um06497	- putative protein	1,22	9,78E-01	3,9	1,42E-06	-1,7	2,32E-03	78,00	52,93	116,10	96,20	209,63	66,47
C45um029G_at	um03843	- putative protein	1,05	9,98E-01	3,4	1,45E-05	-1,6	1,32E-02	65,65	62,23	97,27	68,85	206,77	58,83
C75um007G_at	um05344	- conserved hypothetical protein	1,07	9,91E-01	5,2	6,30E-09	-2,8	4,00E-07	250,30	222,83	697,57	266,95	1155,43	248,07
W60um280G_at	um00375	- hypothetical protein	1,29	9,78E-01	5,2	8,80E-07	-3,7	8,94E-06	58,25	56,60	196,53	75,90	292,50	52,63
W82um185G_at	um05483	- hypothetical protein	-1,05	9,98E-01	3,5	8,80E-06	-2,1	6,00E-04	34,80	43,03	84,13	33,55	153,03	38,93
W40um269G_at	um05411	- probable quinate permease	1,06	9,91E-01	3,7	4,61E-07	-1,9	1,78E-04	448,50	733,07	1438,07	485,40	2659,57	744,13
W16um206G_at	um00826	- hypothetical protein	1,45	8,33E-01	3,4	4,08E-06	-1,5	1,27E-02	47,65	53,07	93,63	71,60	184,10	60,83
C87um130G_at	um03694	- conserved hypothetical protein	1,13	9,78E-01	4,2	1,48E-08	-1,3	6,91E-03	142,95	167,57	269,03	163,00	699,50	201,00
C61um244G_at	um11223	- conserved hypothetical protein	-1,26	9,78E-01	1,2	1,59E-01	-2,1	2,44E-04	684,20	413,57	629,13	539,20	508,10	297,10
W145um002G_at	um03929	- conserved hypothetical protein	1,21	9,90E-01	2,9	7,15E-04	-1,1	6,58E-01	904,95	249,53	361,50	1097,45	740,17	323,13
W115um107G_at	um01042	- putative protein	-1,17	9,91E-01	5,0	5,83E-05	1,1	7,72E-01	132,15	14,87	50,13	115,75	77,17	53,10
C145um076G_at	um03325	- probable general amino acid permease	-1,28	9,78E-01	5,3	5,26E-07	-3,6	6,59E-06	1050,45	93,07	282,37	852,40	493,13	77,17
C65um222G_at	um01432	- conserved hypothetical protein	-1,59	9,78E-01	6,5	1,06E-04	-4,7	5,44E-04	2880,65	211,83	1284,33	2061,25	1412,10	259,70
W70um222G_at	um01431	- related to ATP-binding cassette transporter prote	-1,47	9,78E-01	10,0	9,74E-06	-7,2	4,78E-05	2340,00	91,57	857,13	1775,80	951,47	111,07
C158um132G_at***	um10189	- Sid2 - Ferrichrome siderophore peptide synthetas	-1,67	9,78E-01	10,4	9,15E-05	-3,3	1,30E-02	834,60	40,67	187,27	647,40	436,63	54,20
W170um132G_at	um10188	- L-Ornithine N5-oxygenase	-2,39	9,61E-01	9,8	3,92E-04	-3,1	3,47E-02	2393,55	79,87	292,03	1541,55	837,00	86,60
W60um222G_at	um01433	- related to Enoyl-CoA hydratase, mitochondrial pr	-1,87	9,78E-01	9,7	1,46E-04	-5,5	1,59E-03	2105,90	60,70	481,10	1481,80	605,50	81,80
C55um222G_at	um01434	- related to Ferrichrome siderophore peptide synth	-2,07	9,78E-01	64,2	2,42E-06	-25,3	2,87E-05	2121,95	10,20	431,57	1489,00	731,90	15,03
C80um006G_at	um02285	- related to Na+/H+ antiporter CNH1	-1,04	9,98E-01	2,2	2,01E-04	-1,4	6,89E-02	181,00	80,93	127,90	176,50	180,83	92,43
W66um013G_at	um03535	- hypothetical protein	-1,07	9,98E-01	4,4	3,22E-04	-1,5	2,22E-01	36,15	8,17	16,07	33,70	37,47	10,60
W5um018G_at	um01213	- conserved hypothetical protein	-1,11	9,91E-01	3,3	2,67E-05	-1,7	1,48E-02	2398,55	335,73	641,23	2164,95	1134,90	386,83
C20um006G_at	um02300	- related to alpha-amylase	1,26	9,78E-01	1,6	3,38E-02	-2,9	2,83E-04	684,70	46,73	105,80	901,25	75,83	36,87
C50um184G_at	um10346	- related to RRP1 - involved in processing rRNA pre	1,13	9,91E-01	1,3	2,52E-01	-4,0	2,49E-05	79,85	25,83	41,40	90,45	34,30	9,77
W15um043G_at	um02803	- related to beta-1,3-glucan binding protein	1,17	9,91E-01	-2,0	1,89E-02	-3,6	4,96E-04	536,45	19,00	81,83	628,75	8,03	22,77
W115um074G_at	um01812	- conserved hypothetical protein	-1,00	9,99E-01	1,7	5,51E-05	-2,5	7,32E-07	426,30	94,70	211,83	424,35	161,83	83,47
W75um049G_at	um00096	- probable ZRT2 - Zinc transporter II	1,01	9,99E-01	2,4	3,63E-05	-2,0	3,09E-04	3058,50	431,40	708,10	3104,90	1007,10	361,50
W75um161G_at	um11409	- probable 6-phosphofructokinase	-1,03	9,98E-01	2,6	3,79E-06	-2,6	4,53E-06	646,35	86,30	209,40	629,40	224,40	79,67
C140um175G_at	um02707	- hypothetical protein	1,22	9,78E-01	1,5	5,62E-02	-3,0	1,54E-04	1016,70	249,40	622,47	1255,60	375,97	207,80
C5um027G_C100um167G	um04239	- probable TIF11 - translation initiation factor eIF1a	1,20	9,78E-01	1,6	5,17E-03	-2,1	2,05E-04	1091,80	375,20	714,80	1341,60	598,73	335,60
W35um013G_at	um03542	- conserved hypothetical protein	1,09	9,98E-01	3,9	6,03E-04	-4,4	4,41E-04	74,35	5,20	27,70	83,00	26,33	5,53
W5um085G_at	um11236	- probable arginine-specific carbamoyl-phosphate s	-1,45	9,78E-01	1,6	7,55E-02	-3,1	3,86E-04	1872,25	611,87	1298,20	1362,65	973,17	410,17
W7um037G_at	um11284	- related to glycogenin-2 beta	-1,27	9,44E-01	1,6	1,20E-03	-2,7	4,53E-06	1187,25	396,77	924,77	963,15	646,30	336,50
W40um066G_at	um04190	- conserved hypothetical protein	-1,40	9,78E-01	1,8	1,55E-02	-3,0	2,57E-04	368,15	79,93	238,83	274,60	143,37	79,80
C55um052G_at	um04445	- related to IST2 - Plasma membrane protein that	-1,10	9,91E-01	1,8	7,05E-03	-2,2	7,51E-04	140,35	39,00	82,23	126,65	68,77	35,87
W110um192G_at	um00207	- related to mitochondrial carrier family protein	-1,07	9,91E-01	1,6	4,42E-03	-2,1	2,77E-04	390,15	210,10	327,03	364,45	341,50	154,90
C40um227G_at	um11664	- related to arginyl-tRNA synthetase, cytosolic	1,05	9,98E-01	1,6	3,69E-03	-2,1	1,36E-04	1053,70	446,83	869,27	1107,95	713,67	404,03
W60um144G_at	um04050	- probable GUA1 - GMP synthase (glutamine-hydro	1,02	9,98E-01	2,1	2,23E-05	-2,5	5,98E-06	1673,05	580,97	1242,63	1713,65	1237,47	499,20
W115um012G_at	um02083	- probable Rad54 homolog MUS-25	-1,09	9,78E-01	1,6	1,18E-04	-2,4	1,49E-06	220,70	100,57	191,77	202,50	164,60	81,10
C15um172G_at	um11500	- probable COT1 - Vacuolar zinc (and possibly othe	-1,15	9,78E-01	2,2	3,48E-05	-2,5	1,32E-05	686,75	225,53	474,17	599,25	498,80	188,90
W30um023G_at	um02942	- probable MET16 - 3^-phosphoadenylylsulfate red	-1,26	9,78E-01	3,1	4,68E-05	-2,8	1,39E-04	232,20	45,33	131,20	187,20	146,83	45,57
UG15-2c19-55f2_RC_at	um06285	- related to carbamoyl-phosphate synthase small c	-1,09	9,96E-01	2,7	5,74E-04	-3,5	1,52E-04	821,35	240,67	679,03	757,10	672,47	190,67
W5um251G_at	um01233	- probable 3-phosphoglycerate dehydrogenase	-1,05	9,98E-01	1,7	1,44E-02	-2,4	4,11E-04	2656,60	1062,17	2097,57	2540,00	1786,93	852,03
C80um023G_at	um02953	- conserved hypothetical protein	-1,09	9,91E-01	1,9	3,86E-03	-2,8	1,31E-04	432,20	150,10	333,53	395,45	282,23	116,10
C25um241G_at	um10971	- related to transcription factor hap3	-1,43	4,18E-01	1,2	6,20E-02	-2,4	1,83E-06	335,65	119,83	206,67	234,50	144,30	86,27
C60um164G_at	um00465	- hypothetical protein	-1,34	9,02E-01	1,6	2,69E-03	-2,6	2,12E-05	137,95	42,90	105,37	103,60	72,40	39,43
C45um244G_at	um11225	- conserved hypothetical protein	-1,19	9,78E-01	1,5	5,08E-03	-2,6	1,27E-05	467,10	205,73	387,93	392,80	311,10	148,60
W25um085G_at	um06224	- probable GTPase/general translation initiation fac	-1,12	9,78E-01	1,2	1,52E-01	-2,2	3,94E-06	1278,70	597,83	919,97	1146,50	688,50	410,37
C185um086G_at	um06156	- probable RPO31 - DNA-directed RNA polymerase	-1,07	9,91E-01	1,2	1,16E-01	-2,2	2,16E-05	625,75	322,90	452,97	585,40	385,23	206,97
W65um244G_at	um06195	- related to EMG1 - Protein required for ribosome b	-1,18	9,78E-01	1,4	2,42E-02	-2,0	1,85E-04	888,60	425,13	642,43	759,95	586,90	317,33
C55um086G_at	um06183	- related to RNA-binding protein rnp24	-1,14	9,91E-01	1,7	1,12E-02	-3,0	1,19E-04	421,60	142,50	265,37	380,95	245,07	89,27
W75um241G_at	um06228	- related to DBP7 - RNA helicase required for 60S r	-1,10	9,94E-01	2,0	1,51E-02	-3,2	6,00E-04	100,40	35,13	67,37	92,20	67,00	21,90
C52um088G_at	um05671	- related to ACETYLORNITHINE AMINOTRANSFERA	-1,05	9,94E-01	1,3	2,98E-02	-2,0	1,03E-04	1001,90	418,33	701,67	951,15	557,23	344,90
W90um257G_at	um05766	- probable YHM2 - Protein of the mitochondrial carr	1,03	9,98E-01	1,6	2,84E-03	-3,1	4,71E-06	2268,50	652,20	1778,17	2324,40	1064,57	571,63
W5um064G_at	um00637	- related to triacylglycerol lipase	-1,07	9,91E-01	1,4	7,54E-03	-2,1	8,92E-06	936,40	367,93	711,10	878,75	497,50	332,03
W70um051G_at	um03807	- hypothetical protein	1,08	9,88E-01	1,7	1,59E-04	-2,1	8,71E-06	1480,65	560,23	1160,47	1601,95	933,77	548,47
W10um040G_at	um00747	- hypothetical protein	-1,02	9,98E-01	2,3	1,47E-05	-2,4	1,39E-05	259,15	75,10	190,43	257,20	173,30	79,30
W25um008G_at	um04362	- related to Cytochrome P450 8B1	-1,10	9,89E-01	2,0	1,13E-04	-2,1	5,98E-05	185,20	63,73	155,90	168,40	127,40	71,30
C25um274G_s_at	um11497	- related to UDP-N-acetylglucosamine pyrophosphc	-1,08	9,88E-01	2,0	1,48E-05	-2,2	5,98E-06	516,05	172,20	410,60	477,60	347,17	181,43
C20um102G_at	um11507	- conserved hypothetical protein	1,37	9,56E-01	2,5	1,30E-04	-2,2	6,81E-04	331,35	166,83	313,60	476,90	421,53	143,70
W102um094G_at	um11839	- hypothetical protein	1,08	9,91E-01	2,0	7,38E-04	-2,0	1,15E-03	222,20	76,90	147,40	238,75	156,47	73,93
W20um161G_at	um11413	- hypothetical protein	1,01	9,99E-01	2,2	1,49E-04	-1,3	7,66E-02	91,60	38,43	49,73	92,40	83,17	37,60
C50um007G_at	um05349	- conserved hypothetical protein	1,01	9,98E-01	4,6	9,20E-08	-1,8	2,85E-04	460,90	90,43	170,90	469,65	417,90	92,43
C35um032G_at	um04936	- hypothetical protein	1,14	9,91E-01	2,3	3,01E-04	-2,0	1,74E-03	157,00	65,00	119,17	177,95	150,73	61,00
W110um033G_at	um02439	- conserved hypothetical protein	1,09	9,98E-01	4,1	2,59E-04	-4,4	2,29E-04	380,45	99,30	312,70	429,40	396,80	75,63
W44um163G_at	um00689	- related to low-temperature viability protein LTV1	1,29	9,78E-01	3,2	1,07E-03	-3,5	7,06E-04	138,00	40,30	119,70	180,10	124,63	34,63
W75um015G_at	um04625	- hypothetical protein	-1,12	9,91E-01	2,9	4,77E-05	-1,9	3,53E-03	334,15	89,37	187,87	301,75	266,33	101,03
C25um166G_at	um00410	- hypothetical protein	-1,00	9,99E-01	2,1	7,01E-05	-2,1	6,84E-05	241,05	99,87	180,77	242,10	210,30	84,17
W30um152G_at	um05278	- conserved hypothetical protein	1,33	9,78E-01	2,4	3,36E-04	-2,2	1,03E-03	371,05	149,30	308,70	508,25	354,60	141,07
C67um139G_at	um01341	- probable to iron inhibited ABC transporter 2	1,27	9,56E-01	1,8	3,48E-04	-2,2	7,05E-05	1613,85	723,17	1296,33	2089,00	1327,77	594,23
W20um167G_at	um04253	- probable mrna export factor elf1	1,39	9,78E-01	4,5	8,79E-06	-4,3	1,57E-05	280,35	56,53	231,13	421,00	259,30	53,77
W60um027G_at	um04230	- related to MOT1 - transcriptional accessory protei	1,11	9,78E-01	2,0	1,44E-04	-2,1	8,78E-05	258,00	106,70	203,70	287,65	210,73	95,77
W5um170G_at	um04997	- probable SUV3 - ATP-dependent RNA helicase, m	1,16	9,91E-01	3,8	4,53E-04	-2,1	2,46E-02	177,00	42,50	110,50	206,10	148,80	54,23
C10um050G_at	um11641	- conserved hypothetical protein	1,24	9,78E-01	3,4	1,27E-05	-2,4	2,29E-04	464,15	115,90	281,77	573,35	394,07	115,47
C60um083G_at	um03146	- related to TIM54 (component of the mitochondria	1,17	9,78E-01	2,1	3,25E-05	-1,4	1,66E-02	206,65	85,03	120,50	241,45	177,97	87,43
W70um088G_at	um10736	- probable NUC1 - dna/rna non-specific nuclease, r	1,15	9,78E-01	2,8	1,09E-05	-1,9	5,91E-04	807,70	226,67	454,47	932,10	632,83	236,33
C80um127G_at	um04878	- related to MDN1 - Huge dynein-related AAA-type	1,23	9,78E-01	5,0	7,91E-08	-3,0	3,10E-06	603,85	95,23	288,03	745,30	477,27	95,57
C15um112G_at	um04665	- related to ECM16 - putative DEAH-box RNA helica	1,06	9,92E-01	2,6	1,38E-05	-1,9	5,82E-04	173,85	54,70	97,50	186,25	144,37	51,30
W20um232G_at	um11757	- hypothetical protein	-1,01	9,98E-01	2,2	1,44E-05	-1,8	1,35E-04	304,65	108,03	187,87	301,80	233,43	101,57
W41um245G_at	um05921	- conserved hypothetical protein	1,03	9,98E-01	2,4	8,17E-05	-1,9	8,69E-04	252,45	80,60	151,00	261,55	193,33	77,67
W20um218G_at	um04519	- probable HCA4 - can suppress the U14 snoRNA r	1,21	9,78E-01	2,8	2,31E-04	-3,1	1,36E-04	237,20	61,30	160,53	292,95	172,03	52,43
W75um286G_at	um00516	- related to Nucleolar protein NOP4	1,20	9,91E-01	4,0	1,00E-03	-4,8	5,17E-04	161,35	28,47	111,83	198,20	115,07	25,67
W20um105G_at	um02274	- conserved hypothetical protein	1,10	9,91E-01	2,0	6,91E-04	-1,7	5,62E-03	135,45	48,53	76,70	150,90	97,80	44,90
W10um288G_at	um02561	- probable NOP58 - required for pre-18S rRNA proc	1,05	9,98E-01	2,3	1,84E-04	-2,0	9,65E-04	651,90	215,63	391,40	690,95	489,23	193,97
W35um010G_at	um01273	- related to ubiquitin carboxyl-terminal hydrolase 3	1,23	9,78E-01	2,7	7,10E-05	-2,5	1,94E-04	188,40	54,53	122,73	235,45	151,10	48,33
W40um280G_at	um00379	- probable Int-6 protein	1,25	9,44E-01	2,1	3,25E-05	-1,8	1,92E-04	1028,95	419,63	697,40	1290,30	855,67	383,43
W35um205G_at	um04472	- conserved hypothetical protein	1,30	9,78E-01	2,6	1,72E-04	-2,2	8,48E-04	100,55	33,33	68,13	132,25	84,40	30,87
C115um188G_at	um04809	- related to EBP2 - required for pre-rRNA processin	1,10	9,91E-01	2,8	3,10E-04	-2,6	6,24E-04	507,60	109,43	246,30	575,90	294,10	93,50
C5um207G_at	um00266	- related to Rpa34 - 34 kD subunit of DNA-directed	1,18	9,78E-01	2,6	1,35E-04	-2,5	2,33E-04	416,60	103,97	208,13	502,80	266,90	81,63
W40um029G_at	um03844	- related to SSF1 - Nucleolar protein involved in th	1,24	9,78E-01	2,2	4,46E-04	-1,9	1,83E-03	208,40	65,73	132,40	263,20	141,93	67,77
C145um144G_at	um04067	- related to MAK11 protein (maintenance of killer t	1,27	9,78E-01	2,8	2,41E-04	-2,7	4,42E-04	361,00	76,07	192,73	468,20	215,67	71,67
W80um047G_at	um03584	- related to RPA49 - 49 kD subunit of DNA-directec	1,27	9,78E-01	3,3	1,89E-05	-2,9	6,27E-05	627,10	132,97	373,37	811,50	443,70	126,77
W105um076G_at	um03339	- hypothetical protein	1,25	9,78E-01	2,7	2,40E-05	-2,5	5,81E-05	1074,80	299,03	651,37	1362,65	796,30	261,27
C75um119G_at	um01732	- probable DBP3 - putative RNA helicase required f	1,27	9,78E-01	4,1	1,23E-06	-3,1	1,25E-05	708,00	129,23	395,60	911,95	534,93	126,70
W5um079G_at	um10827	- related to ENP1 - required for pre-rRNA processin	1,32	9,78E-01	3,6	7,09E-05	-2,7	5,95E-04	334,20	76,33	191,07	454,20	265,07	69,90
W30um096G_at	um03939	- conserved hypothetical protein	1,28	9,78E-01	3,3	4,25E-05	-2,2	1,11E-03	416,60	102,63	224,70	543,55	331,77	99,97
W110um054G_at	um00652	- probable HCA4 - can suppress the U14 snoRNA r	1,28	9,78E-01	4,5	1,03E-05	-3,1	1,46E-04	758,30	118,30	355,70	1012,15	523,50	113,23
C5um191G_at	um00369	- hypothetical protein	1,16	9,89E-01	2,5	2,81E-04	-2,1	2,22E-03	149,75	39,03	85,20	176,10	100,83	40,60
W145um010G_at	um01252	- probable NOG1 - similarity to M.jannaschii GTP-b	1,22	9,78E-01	4,2	5,43E-05	-4,3	6,91E-05	305,20	47,37	164,37	384,25	204,57	38,27
W15um070G_at	um10166	- probable Rpc40 - 40 kD subunit of DNA-directed	1,11	9,91E-01	3,4	4,44E-05	-3,2	9,00E-05	413,95	83,43	218,77	475,50	279,67	68,97

UG16-17e14-82d11_RC_a	um11690	- related to KEL3 - similarity to Kel2p and Kel1p	1,02	9,98E-01	3,6	2,84E-05	-2,6	3,81E-04	113,80	19,93	61,20	120,55	73,80	23,17
C10um086G_at	um06193	- related to NSR1 - nuclear localization sequence b	1,05	9,98E-01	4,2	6,02E-06	-5,1	2,62E-06	909,10	128,97	474,87	995,30	542,53	89,77
W60um029G_at	um03840	- hypothetical protein	1,15	9,78E-01	1,9	9,50E-05	-2,1	6,27E-05	198,95	78,90	131,07	229,80	154,17	63,60
W110um099G_at	um05900	- probable HMT1 - hnRNP arginine N-methyltransfe	1,13	9,78E-01	2,2	2,06E-05	-1,7	6,63E-04	1615,35	585,20	1023,20	1834,35	1275,60	606,13
W105um129G_at	um03724	- related to LHP1 - RNA binding protein	1,14	9,78E-01	3,9	4,62E-07	-3,1	3,38E-06	1158,85	188,97	585,77	1344,05	750,60	187,30
C110um131G_at	um05214	- probable DEAD box protein (putative RNA helicas	1,03	9,98E-01	2,1	4,77E-05	-1,8	6,18E-04	385,25	136,37	228,67	399,60	291,73	130,63
W30um148G_at	um00802	- probable RRB1 - involved in the regulation of ribc	1,09	9,91E-01	5,1	1,43E-06	-3,9	9,90E-06	847,30	106,07	372,10	927,25	545,17	95,27
W15um225G_at	um10063	- conserved hypothetical protein	1,11	9,91E-01	2,8	9,79E-05	-3,0	8,27E-05	390,20	72,87	178,07	435,40	202,67	59,77
W105um098G_at	um00157	- probable pyruvate kinase	1,11	9,78E-01	3,1	3,09E-08	-3,3	2,20E-08	3133,75	629,00	1847,33	3479,15	1939,40	553,57
C30um008G_at	um04361	- related to KRI1 - KRRI-Interacting protein 1	1,09	9,91E-01	2,5	1,22E-05	-3,2	2,65E-06	183,85	46,20	121,43	200,75	117,30	38,07
W20um007G_at	um05357	- related to SSZ1 - regulator protein involved in ple	1,13	9,78E-01	2,5	3,84E-06	-2,4	8,10E-06	1392,15	375,43	922,30	1586,40	942,40	382,73
W80um020G_at	um00864	- probable ZUO1 - zuotin	1,12	9,78E-01	2,7	1,27E-06	-2,3	8,32E-06	829,55	206,50	519,73	933,40	553,93	227,10
W165um010G_at	um01247	- related to 60s ribosomal protein l7, mitochondria	1,13	9,78E-01	2,1	1,06E-04	-1,7	9,70E-04	626,30	281,43	462,83	705,20	576,63	265,63
C115um099G_at	um05899	- conserved hypothetical protein	1,21	9,78E-01	3,1	6,73E-06	-2,6	3,10E-05	313,10	96,70	192,90	393,55	297,10	72,43
C15um018G_at	um01211	- conserved hypothetical protein	1,19	9,89E-01	4,2	3,37E-05	-2,8	5,31E-04	521,70	108,13	279,10	646,25	451,10	97,83
W50um080G_at	um03241	- probable KRR1 - required for 40S ribosome bioge	1,02	9,98E-01	2,2	6,11E-04	-2,2	8,90E-04	356,70	137,73	238,80	367,40	298,77	107,97
C90um118G_at	um04021	- probable NMD3 - nonsense-mediated mRNA deca	1,22	9,91E-01	8,8	2,50E-04	-7,5	5,70E-04	256,50	27,77	170,40	320,85	216,93	24,90
W75um186G_at	um04751	- related to RRS1 - regulator of ribosome biogenes	1,09	9,98E-01	8,0	2,20E-04	-5,2	1,44E-03	266,75	32,87	183,97	296,80	212,97	36,97
UG23-1p18-134g5_RC_at	um00328	- putative protein	1,11	9,88E-01	2,7	1,05E-05	-2,8	1,31E-05	178,80	53,67	121,37	199,40	148,87	43,90
CLUSTER30_RC_at	um04291	- conserved hypothetical protein	1,24	9,78E-01	3,7	3,80E-05	-3,4	8,78E-05	333,20	91,20	266,40	422,90	330,83	80,30
C60um283G_at	um00310	- related to WD-repeat protein crb3	1,13	9,88E-01	2,1	3,33E-04	-2,0	4,86E-04	444,05	182,83	297,07	504,85	374,53	146,73
C100um076G_at	um03340	- probable NHP2 - nucleolar rRNA processing prote	1,17	9,78E-01	2,2	1,89E-04	-1,8	2,76E-03	687,95	271,80	460,00	816,75	602,73	256,50
C120um003G_at	um01954	- conserved hypothetical protein	1,14	9,91E-01	2,1	8,93E-04	-1,6	1,87E-02	123,20	55,87	92,33	143,10	117,83	57,13
W85um136G_at	um02564	- conserved hypothetical protein	1,20	9,78E-01	2,5	4,04E-04	-1,8	9,52E-03	222,85	87,17	143,93	273,00	213,43	80,33
W55um249G_at	um02983	- putative protein	1,11	9,91E-01	3,3	2,46E-05	-3,1	4,33E-05	158,05	35,40	95,23	178,95	116,63	30,27
C25um041G_at	um05392	- Npi3 - putative protein	1,10	9,91E-01	2,4	3,41E-04	-2,8	1,69E-04	363,20	121,17	249,23	414,90	296,90	90,37
W120um056G_at	um01867	- conserved hypothetical protein	1,19	9,78E-01	2,7	1,52E-05	-3,0	7,13E-06	187,75	56,93	142,47	226,55	153,80	45,97
CLUSTER60_RC_at	um01606	- related to importin beta homolog Kap119p	1,13	9,78E-01	3,2	3,08E-06	-3,6	1,95E-06	818,35	214,23	644,57	935,15	679,67	180,60
UG19-11f6-125b6_RC_at	um03376	- conserved hypothetical protein	1,30	9,78E-01	6,1	4,67E-07	-5,3	1,49E-06	379,10	56,43	260,43	499,55	350,80	47,70
C70um284G_at	um11577	- related to translation initiation factor eIF-3	1,26	8,33E-01	2,4	2,33E-06	-1,8	8,27E-05	1287,50	521,50	996,97	1639,65	1222,03	558,57
C80um165G_at	um10112	- hypothetical protein	1,06	9,91E-01	2,4	1,90E-05	-1,9	3,07E-04	271,10	90,00	176,50	288,60	214,10	93,20
C90um139G_at	um10241	- related to DBP8 - ATP-dependent RNA helicase	1,06	9,94E-01	2,3	1,16E-04	-2,1	3,12E-04	247,10	83,43	160,43	265,90	191,83	73,97
C75um105G_at	um02262	- probable MAK21 - protein required for 60S riboso	1,28	9,78E-01	4,6	3,04E-05	-4,0	9,30E-05	256,35	46,97	156,63	330,85	214,90	40,43
C15um188G_at	um04789	- conserved hypothetical protein	1,11	9,94E-01	3,9	1,10E-04	-4,1	1,09E-04	179,15	35,93	112,43	202,30	139,03	27,47
W30um124G_at	um01305	- conserved hypothetical protein	1,15	9,91E-01	3,7	1,13E-04	-3,3	2,87E-04	224,60	52,73	143,00	263,15	191,50	43,63
CLUSTER46_RC_at	um00835	- putative protein	1,16	9,78E-01	2,8	4,72E-06	-2,5	1,52E-05	528,15	163,87	365,67	614,70	461,20	144,57
W90um138G_at	um02628	- related to DNA-directed RNA polymerase I	1,33	9,78E-01	5,9	2,35E-06	-4,9	8,04E-06	890,55	143,17	632,03	1210,85	825,87	128,93
W125um209G_at	um00026	- related to FK506-binding protein (FKBP)	1,21	9,78E-01	2,8	8,45E-06	-2,4	4,16E-05	1349,10	433,93	1000,83	1661,60	1193,90	416,10
C14um227G_at	um01467	- probable NOP2 - nucleolar protein	1,27	9,78E-01	4,1	1,52E-05	-3,4	6,51E-05	507,70	104,70	341,20	662,70	430,93	99,90
W51um113G_at	um03495	- probable PNO1 protein	1,14	9,88E-01	5,0	1,22E-06	-4,5	3,22E-06	506,90	75,10	305,50	593,85	374,20	67,90
W90um163G_at	um00678	- probable RRP5 - processing of pre-ribosomal RNA	1,24	9,78E-01	5,1	1,24E-06	-4,4	3,91E-06	295,30	45,20	192,37	378,05	228,23	42,70
C65um008G_at	um04356	- conserved hypothetical protein	1,11	9,78E-01	2,9	2,26E-06	-2,9	3,10E-06	228,85	66,00	147,40	259,05	193,07	50,00
W90um038G_at	um04158	- related to RRP12 - Protein required for normal pr	1,14	9,91E-01	4,6	3,21E-05	-3,8	1,24E-04	285,55	50,60	178,00	330,25	224,77	46,73
C75um251G_at	um10593	- conserved hypothetical protein	1,09	9,94E-01	6,0	6,08E-06	-4,2	5,03E-05	167,90	20,73	92,53	186,60	125,00	21,70
C50um179G_at	um01372	- related to nuclear GTPase	1,04	9,98E-01	3,8	2,14E-05	-3,2	9,26E-05	444,20	91,77	250,97	470,95	346,33	79,77
C75um208G_at	um00292	- related to WD repeat protein PWP1	1,08	9,91E-01	4,5	1,28E-06	-4,0	3,62E-06	664,70	114,30	380,43	727,55	509,87	93,70
EST01um044_at	um02337	- conserved hypothetical protein	1,12	9,78E-01	2,4	9,74E-06	-2,1	5,99E-05	303,55	108,80	213,50	342,15	262,53	102,27
C30um134G_at	um05110	- related to UTP13 - U3 snoRNP protein	1,07	9,91E-01	3,6	2,17E-06	-3,2	6,94E-06	540,05	128,67	345,97	588,85	462,17	108,40
C40um151G_at	um05714	- related to ERB1 - Protein required for maturation	1,15	9,91E-01	4,0	8,31E-06	-2,9	1,08E-04	590,80	137,63	384,80	692,00	542,37	132,77
C94um174G_at	um11725	- conserved hypothetical protein	1,16	9,90E-01	3,6	3,41E-05	-3,5	5,03E-05	322,75	73,60	209,10	381,60	256,00	60,40
C40um207G_at***	um00275	- related to DNA polymerase V	1,18	9,78E-01	3,3	5,49E-06	-3,2	8,71E-06	495,50	122,73	330,33	596,10	403,57	101,90
C45um108G_at	um01175	- probable TRF4 - topoisomerase I-related protein	1,12	9,78E-01	2,5	1,38E-05	-2,7	9,46E-06	194,75	64,23	138,07	220,15	159,83	51,17
W7um072G_at***	um00964	- related to NOG2 - GTPase involved in ribosomal la	1,10	9,91E-01	4,2	4,64E-06	-3,7	1,39E-05	372,15	71,53	239,10	415,35	297,90	64,57
C35um089G_at	um01551	- probable BUD23 - Protein involved in bud-site sel	1,07	9,91E-01	2,0	2,03E-05	-2,0	3,74E-05	545,90	214,03	349,60	586,85	434,37	176,23
W105um250G_at	um03058	- conserved hypothetical protein	1,06	9,91E-01	2,9	1,48E-06	-2,7	4,16E-06	462,10	109,80	250,17	494,80	321,93	92,10
W5um169G_at	um11707	- hypothetical protein	1,06	9,94E-01	3,1	7,00E-06	-2,9	1,39E-05	280,40	66,73	156,60	303,95	207,80	52,43
C35um027G_at	um10410	- probable HAS1 - helicase associated with Set1p	1,13	9,91E-01	4,6	9,08E-06	-3,8	3,90E-05	564,15	93,03	303,37	655,30	414,23	80,20
W50um137G_at	um10283	- related to MTD1 - methylenetetrahydrofolate deh	1,07	9,91E-01	2,4	3,03E-06	-2,1	2,04E-05	822,50	260,90	537,07	890,60	622,87	261,27
W95um153G_at	um02662	- probable periodic tryptophan protein PWP2	1,02	9,98E-01	3,0	3,41E-05	-2,8	8,65E-05	316,80	73,27	184,77	328,65	219,10	67,47
W65um057G_at	um06090	- related to Probable RNA-binding protein sce3	1,11	9,78E-01	2,1	1,83E-05	-1,9	5,38E-05	1689,30	662,33	1203,70	1879,35	1365,73	626,07
W10um073G_at	um05722	- probable BMS1 - GTP-binding protein, required fo	1,12	9,91E-01	3,7	4,19E-05	-2,8	3,81E-04	287,20	58,40	155,57	324,30	208,43	56,70
C27um013G_at	um11730	- probable URA2 - multifunctional pyrimidine biosyı	1,19	9,78E-01	2,7	1,42E-06	-2,3	8,67E-06	1490,25	487,57	1090,50	1775,40	1320,70	468,80
W40um267G_at	um11213	- related to RRP6 - Exonuclease component of the	1,07	9,94E-01	2,9	2,63E-05	-2,7	6,91E-05	210,65	56,23	141,80	226,60	163,87	53,33
W60um216G_at	um06035	- probable ADE4 - amidophosphoribosyltransferase	1,06	9,91E-01	3,6	3,50E-07	-3,3	9,32E-07	1269,45	275,70	826,40	1353,70	984,33	249,27
C25um163G_at	umd18-10	- hypothetical protein	1,13	9,94E-01	6,7	4,76E-05	-5,8	1,23E-04	241,65	28,17	157,90	274,95	189,77	29,90
W35um218G_at	um04516	- conserved hypothetical protein	1,08	9,98E-01	9,6	6,83E-04	-13,0	3,33E-04	201,30	18,67	120,20	221,35	158,40	12,10
W60um213G_at	um03654	- related to poly(rC)-binding protein 3	1,14	9,78E-01	2,5	3,80E-06	-2,3	1,13E-05	2006,60	697,03	1463,00	2308,60	1749,27	624,93
EST01um279_at***	um05651	- conserved hypothetical protein	1,17	9,78E-01	4,2	8,04E-06	-3,9	1,62E-05	260,85	52,57	181,00	308,00	218,57	46,67
C67um124G_at	um01296	- related to RIX7 - AAA-type ATPase required for bi	1,21	9,78E-01	3,5	3,21E-05	-2,5	4,87E-04	352,10	93,57	222,83	435,90	330,23	90,70
C35um249G_at	um02979	- conserved hypothetical protein	1,26	9,78E-01	2,2	1,13E-04	-1,9	5,91E-04	202,55	85,47	150,40	259,25	189,20	77,73
W20um169G_at	um02327	- hypothetical protein	1,21	9,78E-01	2,5	9,31E-05	-2,4	2,10E-04	171,30	59,57	119,03	210,05	151,33	50,17
C75um097G_at	um03892	- probable ATP dependent RNA helicase	1,24	9,78E-01	2,7	3,80E-04	-3,0	2,57E-04	286,20	95,83	220,00	359,65	261,47	77,10
W10um124G_at	um01310	- related to NOP14 - nuclear and nucleolar protein	1,23	9,78E-01	2,8	6,39E-05	-2,8	8,78E-05	325,25	111,83	263,10	410,70	310,67	95,13
W80um208G_at	um00293	- related to protein RPF2 involved in ribosomal larg	1,33	9,78E-01	5,1	8,09E-06	-4,5	2,29E-05	279,45	50,50	207,40	384,90	260,00	45,23
C45um041G_at	um05387	- probable MAK16 protein	1,40	9,78E-01	5,2	4,28E-04	-5,4	4,51E-04	215,20	42,70	154,20	304,50	220,80	31,90
W90um132G_at	um05180	- related to BRX1 - Essential nucleolar protein requ	1,16	9,91E-01	3,1	2,26E-04	-2,4	1,70E-03	579,80	181,37	433,40	684,50	559,00	177,93
W105um088G_at	um05683	- probable NIP7 - required for efficient 60S ribosom	1,23	9,78E-01	3,7	1,38E-05	-2,4	3,73E-04	620,55	168,13	422,50	782,05	617,33	172,00
W25um189G_at	um00716	- related to NOP6 - protein with possible role in rRI	1,21	9,78E-01	3,3	7,99E-05	-3,1	1,47E-04	156,50	46,17	109,77	193,80	151,33	35,27
C110um093G_at	um00596	- putative protein	1,14	9,88E-01	3,7	5,85E-06	-2,7	8,78E-05	372,60	92,57	228,87	429,75	347,40	85,77
C107um044G_at	um02343	- related to excision repair protein RAD4	1,17	9,78E-01	4,7	2,71E-06	-3,9	1,20E-05	526,35	109,37	345,27	629,95	514,03	89,50
C5um092G_C85um051G_	um11734	- probable NOP1 - fibrillarin	1,19	9,78E-01	2,4	6,34E-05	-2,1	3,28E-04	1695,05	679,07	1291,27	2038,00	1632,10	611,90
W20um265G_at	um05627	- probable xanthine phosphoribosyl transferase	1,17	9,78E-01	4,4	2,33E-06	-3,2	2,82E-05	837,50	180,67	601,97	1002,05	792,47	189,30
C60um157G_at	um10065	- related to ACN9 (protein of gluconeogenesis in m	1,19	9,78E-01	3,3	3,16E-06	-2,7	2,16E-05	404,10	128,07	300,03	481,30	423,13	111,07
W55um140G_at	um03774	- probable positive effector protein GCN20	1,19	9,56E-01	2,1	6,65E-06	-1,7	1,33E-04	413,55	206,97	367,73	493,80	427,73	218,50
C160um015G_at	um04607	- related to Asparaginyl-tRNA synthetase	1,22	9,89E-01	3,6	2,73E-04	-2,7	2,17E-03	148,95	49,83	118,20	183,25	166,60	43,43
W55um031G_at	um03567	- related to LCP5 - U3 small nucleolar ribonucleopr	1,05	9,98E-01	3,1	1,87E-05	-2,6	9,44E-05	248,40	72,83	151,50	263,50	220,77	57,77
W70um218G_at	um04508	- probable BFR2 - involved in protein transport ste	1,08	9,98E-01	4,2	3,17E-04	-3,5	1,07E-03	147,65	36,07	94,67	162,10	141,93	28,33
CLUSTER28_RC_at	um06360	- probable SNU13 - component of the U4/U6.U5 sn	1,11	9,78E-01	2,4	4,03E-06	-1,9	4,92E-05	2111,50	808,03	1541,00	2347,80	1917,80	796,87
W80um136G_at	um10276	- Inosine 5^-monophosphate dehydrogenase	1,15	9,78E-01	3,5	3,43E-07	-2,5	7,11E-06	1749,55	496,93	1157,50	2021,60	1721,77	468,50
W35um050G_at	um01133	- probable RPA135 - DNA-directed RNA polymerase	1,12	9,94E-01	7,7	2,23E-05	-5,5	1,28E-04	369,20	46,20	253,03	419,10	326,90	46,30
C30um226G_at	um11749	- probable translation initiation factor eIF3 p39 sub	1,13	9,78E-01	2,1	4,64E-06	-1,9	2,29E-05	2018,65	920,67	1561,23	2297,35	1887,43	841,33
W35um147G_at	um11200	- putative protein	1,14	9,78E-01	2,8	2,63E-05	-2,2	2,33E-04	1908,90	758,20	1526,03	2190,05	2050,27	696,97
C45um021G_at	um03102	- hypothetical protein	1,12	9,78E-01	3,4	3,77E-07	-2,8	2,46E-06	654,05	187,37	436,93	739,25	630,53	156,53
W65um030G_at	um10524	- related to TIF4631 - mRNA cap-binding protein (ε	1,15	9,78E-01	2,3	6,71E-07	-2,0	3,49E-06	1228,45	560,37	968,70	1421,30	1264,90	480,77
W45um027G_at	um10409	- related to UTP21 - U3 snoRNP protein	1,18	9,78E-01	3,0	4,36E-06	-2,6	1,65E-05	295,75	102,27	224,90	351,30	303,67	86,63
C120um259G_at	um04732	- related to RIO2 protein	1,18	9,78E-01	2,8	8,59E-06	-2,3	7,26E-05	220,50	83,67	180,00	261,35	237,20	77,07
W27um200G_at	um11011	- conserved hypothetical protein	1,09	9,98E-01	5,2	1,15E-03	-6,8	4,89E-04	385,05	69,67	273,27	425,75	357,13	49,13
C130um211G_at	um10900	- conserved hypothetical protein (fragment)	1,08	9,94E-01	4,0	1,62E-05	-3,7	3,41E-05	1697,00	415,77	1282,70	1833,25	1594,30	356,83
C95um044G_at	um02346	- probable RNA-binding protein	1,11	9,91E-01	4,5	8,80E-07	-3,7	4,28E-06	399,85	85,73	294,07	449,95	392,63	78,37
UG16-23e12-113c12_RC_	um03866	- related to UTP6 - U3 snoRNP protein	1,13	9,91E-01	3,9	4,08E-06	-3,2	1,88E-05	334,45	84,73	229,93	377,90	325,47	72,17
W50um203G_at	um04986	- related to TSR1	1,20	9,91E-01	6,0	4,92E-05	-4,3	3,19E-04	394,20	74,43	292,57	475,40	411,90	70,07
C183um119G_at	um01706	- hypothetical protein	1,09	9,91E-01	1,7	1,78E-03	-2,5	3,29E-05	88,75	40,17	64,43	97,15	68,60	25,33
C45um028G_at	um00491	- related to BRF1 - TFIIIB subunit, 70 kD	1,06	9,94E-01	1,8	8,02E-04	-2,1	3,04E-04	111,80	48,27	81,67	119,00	88,60	39,70
C10um197G_at	um10785	- related to RPC34 - DNA-directed RNA polymerase	1,07	9,92E-01	2,1	4,41E-04	-2,4	1,31E-04	160,50	60,37	124,67	173,45	125,20	50,97
C25um152G_at	um10549	- related to Glioma tumor suppressor candidate reg	1,22	9,91E-01	10,4	1,23E-04	-4,9	2,61E-03	165,90	19,33	103,20	205,80	174,90	22,77
C80um033G_at	um02444	- probable rRNA (adenine-N6,N6-)-dimethyltransfe	1,28	9,78E-01	2,7	9,88E-05	-2,1	1,44E-03	299,45	106,07	218,57	389,80	293,77	105,97
C66um074G_at	um10253	- related to MAP1 - methionine aminopeptidase	1,17	9,78E-01	2,4	2,33E-05	-2,2	8,72E-05	305,55	130,47	263,80	363,90	318,23	119,63
C35um106G_at	um01023	- probable ADE17 - 5-aminoimidazole-4-carboxami	1,21	9,78E-01	2,6	2,73E-05	-2,1	1,90E-04	841,10	338,27	744,57	1035,55	872,67	343,77
C55um002G_at	um03911	- probable RIM2 - Protein of the mitochondrial carr	1,09	9,91E-01	2,3	1,29E-04	-1,9	8,69E-04	172,10	73,93	147,77	189,60	168,53	75,87
W5um272G_at	um03617	- conserved hypothetical protein	1,08	9,98E-01	4,7	3,67E-05	-5,9	1,56E-05	306,50	56,27	229,23	335,55	258,00	39,10
C25um040G_at	um11623	- probable KRE35 - similarity to putative human GT	1,08	9,91E-01	2,7	2,80E-05	-2,6	5,79E-05	262,20	85,77	200,70	287,15	228,27	78,23
C20um243G_at	um03681	- conserved hypothetical protein	1,04	9,94E-01	2,0	9,43E-06	-2,2	4,10E-06	165,95	74,77	148,70	172,75	149,83	67,93
C80um005G_at	um05835	- probable SMC2 - chromosome segregation protei	1,05	9,91E-01	2,2	6,13E-06	-2,2	8,38E-06	247,25	101,60	222,97	260,00	227,43	99,30
W50um037G_at	um11281	- probable PRP43 - involved in spliceosome disasse	1,10	9,91E-01	2,2	2,45E-04	-2,4	1,02E-04	614,75	256,47	520,27	684,90	548,80	215,63
C70um033G_at	um02446	- probable DNA-directed RNA polymerase III, 130 l	1,08	9,91E-01	2,3	6,18E-05	-2,8	1,56E-05	404,55	174,67	381,27	439,60	394,90	139,17
C10um147G_at	um00770	- probable URA7 - CTP synthase 1	1,08	9,91E-01	2,8	8,65E-07	-3,0	8,00E-07	1329,65	402,60	1049,73	1441,05	1123,57	354,13
W50um197G_at	um06323	- probable translation initiation factor eIF3	-1,01	9,98E-01	1,9	1,27E-05	-2,0	8,71E-06	1192,45	514,23	893,07	1184,00	992,37	436,77
W10um132G_at	um05200	- related to putative RNA helicase involved in ribos	1,08	9,91E-01	3,0	4,72E-06	-3,1	4,53E-06	266,80	85,57	222,47	289,20	252,73	71,13
W1um105G_at	um11401	- related to Exportin T	1,12	9,91E-01	2,0	5,75E-04	-2,1	4,26E-04	543,35	272,13	479,77	610,85	541,03	227,20
C120um153G_at	um10304	- putative protein	1,11	9,91E-01	2,6	6,87E-05	-3,1	2,16E-05	255,55	95,77	212,83	287,65	241,30	70,00
C55um113G_at	um03494	- probable PAB1 - mRNA polyadenylate-binding prc	1,18	9,78E-01	3,8	1,82E-07	-3,6	4,45E-07	1210,80	278,97	975,90	1433,30	1069,93	273,10
C20um037G_at	um11282	- conserved hypothetical protein	1,18	9,78E-01	2,4	1,62E-05	-2,1	7,78E-05	203,00	86,80	179,47	239,75	206,87	84,23
C65um079G_at	um03267	- conserved hypothetical protein	1,07	9,91E-01	2,4	2,10E-05	-2,4	2,22E-05	154,50	62,37	125,90	165,35	148,17	52,23
W100um227G_at	um11667	- probable MTR4 - involved in nucleocytoplasmic tr	1,12	9,91E-01	2,6	1,12E-04	-2,4	2,94E-04	318,10	115,83	254,67	355,35	296,67	106,77
W15um079G_at	um03277	- related to Ribonucleases P/MRP protein subunit P	1,03	9,98E-01	2,1	8,62E-05	-1,9	4,44E-04	177,25	77,60	145,40	182,40	162,93	77,50
UG14-32n16-122d4_RC_a	um06362	- related to Angio-associated migratory cell protein	-1,02	9,98E-01	2,2	4,25E-05	-2,2	5,95E-05	701,15	276,13	527,93	689,45	596,80	245,43
W125um250G_W1um117	um03062	- related to MPP10 - component of the U3 small nu	1,15	9,85E-01	2,3	3,06E-04	-2,5	2,55E-04	982,20	354,10	786,27	1133,40	807,47	321,37
W125um122G_at	um01673	- related to UTP5 protein	1,04	9,98E-01	7,1	1,28E-04	-7,6	1,32E-04	233,70	24,07	150,17	244,20	175,17	22,73
W25um102G_at	um03608	- conserved hypothetical protein	1,11	9,91E-01	2,3	8,74E-05	-2,3	1,31E-04	132,75	58,53	119,83	150,50	133,40	52,47
C80um193G_at	um10047	- conserved hypothetical protein	1,08	9,98E-01	4,8	1,58E-03	-7,2	3,75E-04	244,40	48,00	186,90	268,25	230,80	30,53
C75um037G_at	um01092	- hypothetical protein	1,02	9,98E-01	2,2	2,17E-02	-4,0	6,72E-04	161,00	53,07	85,67	164,50	115,90	23,40
W30um040G_at	um00743	- conserved hypothetical protein	1,05	9,98E-01	2,4	7,15E-04	-2,5	6,48E-04	307,90	94,77	180,27	322,20	230,90	72,20
C10um278G_at	um04765	- probable TRM8 - part of complex required for 7-n	1,04	9,98E-01	2,1	3,38E-04	-1,7	6,71E-03	209,50	96,20	150,20	225,75	203,73	91,00
W110um029G_at	um10508	- conserved hypothetical protein	1,12	9,91E-01	3,9	9,24E-05	-2,9	8,04E-04	204,20	53,83	152,13	240,60	211,60	54,03
C120um220G_at	um10766	- conserved hypothetical protein	1,05	9,98E-01	3,4	1,78E-05	-1,8	5,84E-03	299,10	102,10	197,90	326,50	349,17	111,70
C90um186G_at	um10683	- probable ROK1 - ATP-dependent RNA helicase	1,14	9,78E-01	2,0	3,23E-04	-1,7	2,47E-03	125,25	72,13	93,57	145,95	144,10	53,90
C15um105G_at	um02275	- probable PET127 - component of mitochondrial tr	1,17	9,78E-01	3,0	4,03E-05	-2,1	8,05E-04	147,00	55,27	100,70	173,15	163,23	47,50
C95um156G_at***	um04260	- conserved hypothetical protein	-1,03	9,98E-01	3,9	8,09E-06	-2,6	1,69E-04	194,10	47,23	120,63	187,90	180,20	46,13
W10um250G_at	um03036	- conserved hypothetical protein	-1,04	9,98E-01	2,3	8,59E-05	-1,6	1,06E-02	253,75	111,57	177,67	243,55	257,30	115,40
W15um047G_at	um03601	- conserved hypothetical protein	1,02	9,98E-01	2,9	1,48E-05	-1,9	8,48E-04	630,55	215,17	416,37	644,05	617,83	215,37
W125um076G_at	um03331	- putative protein	1,13	9,98E-01	6,0	8,45E-04	-2,4	5,71E-02	173,10	35,87	104,47	197,80	176,13	43,30
C77um283G_at	um10095	- probable RNA helicase dbp2 (DEAD box protein)	-1,02	9,98E-01	2,2	4,00E-05	-2,2	4,56E-05	274,80	120,90	201,93	269,95	264,67	90,93
C100um223G_at	um11320	- hypothetical protein	-1,20	9,78E-01	2,2	8,09E-06	-2,0	4,13E-05	299,50	120,43	205,47	249,55	270,10	102,70
W80um029G_at	um10512	- probable 25 kD subunit of DNA-directed RNA poly	1,11	9,89E-01	2,0	1,41E-04	-1,4	3,09E-02	663,95	248,13	393,67	728,40	504,63	285,27
C15um269G_at	um05416	- related to PUS1 - pseudouridine synthase 1	-1,05	9,97E-01	2,1	2,83E-04	-1,8	1,17E-03	416,20	124,13	222,87	402,05	254,77	120,10
W85um127G_at	um10858	- probable RPA12 - 13.7 kD subunit of DNA-directe	1,00	1,00E+00	2,1	6,60E-05	-1,6	1,69E-03	364,15	123,23	183,90	371,45	254,77	112,40
W166um027G_at	um04208	- conserved hypothetical protein	-1,03	9,98E-01	3,0	1,48E-06	-2,0	1,24E-04	192,85	39,03	73,53	188,20	117,87	37,17
C75um163G_at	um11617	- conserved hypothetical protein	1,13	9,78E-01	2,1	3,82E-05	-1,8	2,44E-04	77,55	27,63	43,77	87,20	58,33	23,90
C50um191G_at	um11349	- hypothetical protein	-1,20	9,44E-01	2,1	5,64E-06	-1,9	2,82E-05	475,05	169,57	308,23	396,55	354,40	165,43

C5um268G_at	um04484	- related to choline-sulfatase	-1,09	9,78E-01	2,4	2,30E-06	-1,9	4,33E-05	198,70	70,30	120,63	182,70	167,63	63,70
C95um257G_at	none	- no annotation available	-1,16	9,78E-01	2,2	9,65E-06	-1,8	1,40E-04	183,90	63,23	112,67	158,85	141,40	60,97
W31um188G_at	um04791	- related to to G1/S-specific cyclin	-1,03	9,98E-01	3,9	7,61E-07	-2,2	1,00E-04	381,50	75,20	220,40	372,00	293,00	99,20
C80um161G_at	um11407	- probable PHM7 - similarity to A.thaliana hyp1 pro	1,01	9,98E-01	3,2	2,91E-07	-3,6	1,75E-07	447,20	93,13	280,90	450,35	301,87	77,17
C70um164G_at	um00463	- putative protein	1,04	9,98E-01	2,3	2,40E-04	-2,5	1,46E-04	104,95	31,73	68,17	110,20	71,87	27,40
W20um120G_at	um02997	- related to CHO2 - phosphatidylethanolamine N-m	-1,12	9,91E-01	3,8	7,59E-06	-4,1	6,35E-06	670,25	110,63	367,57	603,85	411,97	90,63
C65um223G_at	um01397	- probable REX4 - strong similarity to X.laevis XPM	-1,03	9,98E-01	14,1	2,34E-06	-6,5	5,98E-05	152,90	6,73	73,80	148,45	107,83	11,90
UG21-14j14-109c11_RC_	um00219	- conserved hypothetical protein	-1,08	9,91E-01	2,5	1,23E-06	-1,7	2,43E-04	797,40	240,03	407,13	740,95	600,90	245,63
CLUSTER17_RC_at	um00812	- probable bifunctional purine biosynthetic protein	1,06	9,91E-01	3,1	9,20E-08	-2,2	3,09E-06	1181,35	337,67	689,97	1246,65	1032,77	312,93
W100um170G_at	um05019	- probable SAM2 - S-adenosylmethionine syntheta:	-1,00	1,00E+00	3,2	4,31E-07	-2,1	2,21E-05	2852,45	712,53	1533,07	2856,45	2266,27	718,13
W25um032G_at	um04934	- related to a component of the yeast U3 snoRNP R	1,03	9,98E-01	2,7	1,83E-04	-2,5	3,55E-04	346,05	88,67	182,40	355,65	233,10	73,20
W70um133G_at	um05126	- related to NCL1 - tRNA (cytosine-5-)-methyltrans	-1,07	9,94E-01	2,8	4,65E-05	-2,5	1,53E-04	446,90	95,40	210,03	418,70	261,53	85,10
W90um129G_at	um03729	- related to para-aminobenzoic acid synthetase	-1,10	9,91E-01	2,2	5,06E-05	-1,8	4,66E-04	224,10	68,30	117,67	203,80	150,60	63,40
W45um031G_at	um03569	- related to KRE6 - beta-1,6-glucan synthetase	-1,03	9,98E-01	2,4	4,57E-06	-2,0	3,29E-05	518,45	143,53	235,63	504,25	337,50	115,83
W40um122G_at	um01694	- hypothetical protein	-1,13	9,91E-01	2,1	8,13E-04	-1,7	1,25E-02	86,85	32,50	50,63	76,60	67,30	30,23
W170um139G_at	um01319	- hypothetical protein	-1,22	9,78E-01	2,3	5,40E-05	-2,0	2,74E-04	267,05	81,00	153,40	219,00	185,63	75,20
W175um175G_at	um11928	- related to PCL1 - cyclin, G1/S-specific	-1,22	9,78E-01	2,1	2,86E-04	-1,4	5,12E-02	422,60	202,93	270,33	359,85	433,93	194,27
W10um232G_at	um04538	- probable DAL5 - Allantoate and ureidosuccinate p	1,04	9,98E-01	3,6	1,48E-05	-1,4	7,20E-02	377,40	120,67	179,07	418,75	433,67	125,90
C120um049G_at	um00105	- probable FET3 - cell surface ferroxidase, high affi	-1,75	9,78E-01	22,5	2,39E-06	-2,5	2,46E-02	3762,70	186,00	731,67	2747,85	4163,80	277,93
W125um049G_at	um10023	- related to high-affinity iron permease	-2,03	9,56E-01	54,0	5,32E-07	-3,2	9,29E-03	3188,45	61,63	509,73	2165,45	3375,63	151,97
EST02um143_at	um03129	- hypothetical protein	1,06	9,94E-01	2,3	6,76E-05	-1,8	1,31E-03	494,70	190,40	318,63	518,05	436,33	179,87
C127um055G_at	um03992	- hypothetical protein	-1,05	9,94E-01	2,0	8,90E-05	-1,2	1,25E-01	159,85	75,90	109,60	152,05	153,47	89,33
W115um178G_at	um02002	- hypothetical protein	1,02	9,98E-01	3,7	5,60E-06	-2,2	3,99E-04	308,90	79,27	195,60	320,35	304,40	88,00
UG24-1d14-47c8_RC_at	um00813	- conserved hypothetical protein	-1,39	9,78E-01	3,3	1,68E-04	-2,0	1,04E-02	472,80	140,83	275,83	378,85	457,13	140,23
UG22-1c18-45f9_RC_at	um10319	- hypothetical protein	-1,25	9,78E-01	3,3	2,54E-04	-1,5	1,33E-01	242,65	66,20	147,17	202,05	208,33	100,07
C85um140G_at	um03761	- related to aldehyde dehydrogenase	-1,46	9,36E-01	2,4	4,78E-04	-1,8	7,50E-03	241,55	76,17	150,07	174,60	179,47	82,60
C205um019G_at	um06434	- conserved hypothetical protein	-1,27	8,90E-01	2,1	1,80E-05	-2,3	1,05E-05	965,05	378,50	707,07	774,75	805,37	309,20
W31um174G_at	um02751	- hypothetical protein	-1,68	8,33E-01	4,7	8,19E-06	-4,2	2,27E-05	50,60	7,13	26,57	30,75	38,17	5,63
W45um097G_at	um03886	- conserved hypothetical protein	1,00	9,99E-01	2,5	9,99E-06	-1,8	3,81E-04	128,50	46,03	97,97	128,35	114,97	54,33
C115um163G_at	um00672	- probable urate oxidase (uricase)	1,00	1,00E+00	2,9	9,80E-05	-2,4	7,03E-04	1120,15	376,13	864,13	1144,80	1113,30	366,47
W45um213G_at	um03658	- conserved hypothetical protein	-1,11	9,91E-01	4,1	3,29E-05	-2,1	5,53E-03	62,15	25,57	61,77	55,65	103,03	28,77
C15um066G_at	um04197	- related to purine-cytosine permease	1,24	8,33E-01	2,5	6,57E-07	-1,3	6,56E-03	363,45	223,77	277,37	454,50	554,03	207,63
C30um182G_at	um05574	- conserved hypothetical protein	1,01	9,99E-01	2,1	3,40E-06	-1,3	5,40E-03	177,65	112,47	156,60	179,25	240,20	116,13
C45um209G_at	um00006	- conserved hypothetical protein	1,05	9,94E-01	2,3	9,46E-06	-1,5	4,94E-03	165,95	91,00	135,00	172,90	214,73	91,10
C105um047G_at	um10572	- related to MET10 - sulfite reductase flavin-binding	1,05	9,98E-01	3,6	1,02E-06	-2,0	2,57E-04	873,15	277,20	528,43	925,70	1001,30	265,93
C140um018G_at	um01184	- probable Rpc19 - 18 kD subunit of DNA-directed	1,03	9,98E-01	4,0	1,67E-07	-2,4	1,34E-05	267,80	83,87	199,40	276,40	343,23	81,33
CLUSTER18_RC_s_at	um04076	- hypothetical protein	-1,10	9,91E-01	3,5	8,05E-07	-1,7	1,29E-03	252,45	93,40	159,90	230,30	326,70	94,17
C30um256G_at	um11585	- related to capsular associated protein	-1,09	9,78E-01	6,7	5,30E-09	-3,3	3,41E-07	425,20	73,80	237,37	388,05	502,23	71,83
W40um256G_at	um05786	- related to UDP N-acetylglucosamine transporter	-1,12	9,78E-01	7,0	4,78E-09	-2,6	2,29E-06	633,50	105,50	353,10	565,60	746,63	135,57
C75um127G_at	um04875	- conserved hypothetical protein	-1,19	9,78E-01	2,0	2,92E-05	-1,3	2,15E-02	574,85	365,13	447,43	487,85	741,20	337,10
W21um256G_at	um05782	- capsule-associated protein-like protein	1,01	9,99E-01	5,9	6,41E-08	-2,1	1,41E-04	767,10	263,73	766,67	766,80	1553,47	367,63
C10um054G_at	um11612	- putative protein	-1,32	9,78E-01	2,7	1,94E-04	-1,8	7,52E-03	335,85	156,00	248,27	261,70	420,07	137,90
W35um256G_at	um05785	- acyl transferase-like protein	-1,13	9,78E-01	8,8	4,31E-09	-3,0	1,50E-06	1105,00	228,77	905,83	983,45	2022,53	302,33
W45um256G_at	um05787	- hypothetical protein	-1,16	9,78E-01	6,1	3,86E-08	-2,8	7,44E-06	1024,45	226,17	757,87	904,50	1390,87	272,67
C25um256G_at	um05783	- related to UDP-galactose transporter	-1,22	9,78E-01	10,0	6,65E-07	-3,6	1,30E-04	265,15	43,90	232,50	225,95	422,10	63,53
C24um071G_at***	um06371	- conserved hypothetical protein	1,10	9,91E-01	1,9	2,00E-03	-2,7	1,32E-04	136,40	77,17	174,87	152,25	149,93	62,87
C90um144G_at	um04056	- probable SNQ2 - ABC transporter involved in mul	1,21	9,78E-01	2,7	3,41E-05	-2,2	2,52E-04	279,15	134,53	335,53	341,20	370,00	148,13
C60um028G_at	um00488	- hypothetical protein	1,09	9,91E-01	2,0	5,05E-04	-1,5	2,71E-02	215,90	121,87	215,30	234,40	245,73	143,93
W20um237G_at	um03281	- putative protein	-1,15	9,78E-01	2,0	7,44E-05	-1,8	3,16E-04	234,80	159,17	261,93	206,40	322,73	143,50
C25um138G_at	um02640	- conserved hypothetical protein	-1,49	7,03E-01	2,9	4,08E-06	-2,7	9,18E-06	299,95	146,17	360,33	207,10	418,77	133,80
W70um213G_at	um03651	- hypothetical protein	-1,23	9,78E-01	4,5	6,33E-06	-4,7	6,36E-06	171,45	83,37	356,40	150,10	373,30	75,27
C15um235G_at	um05153	- related to MNT4 - putative alpha-1,3-mannosyltra	-1,04	9,94E-01	4,2	4,25E-08	-3,3	2,86E-07	602,00	292,43	1049,20	583,85	1220,93	319,07
C150um145G_at	um04368	- related to endo-1,3(4)-beta-glucanase	-1,21	9,78E-01	6,1	1,42E-07	-3,7	3,77E-06	1020,70	354,83	1726,70	879,95	2176,07	472,60
W235um074G_at	um01785	- putative protein	-1,10	9,78E-01	3,0	5,44E-08	-2,7	2,09E-07	675,80	343,67	965,77	617,95	1050,70	360,13
W20um235G_at	um05152	- conserved hypothetical protein	-1,16	9,78E-01	6,6	3,26E-07	-4,5	3,15E-06	245,75	67,17	375,70	221,35	451,17	82,70
C95um210G_at	um02825	- hypothetical protein	1,08	9,78E-01	2,5	4,62E-07	-1,8	3,44E-05	565,40	428,23	868,23	614,95	1086,23	484,03
W35um022G_at	um00118	- probable UDP-glucose 6-dehydrogenase	-1,22	9,78E-01	3,5	2,19E-06	-2,4	6,92E-05	631,40	351,30	907,90	537,95	1239,50	382,07
W75um281G_at	um02242	- related to translation initiation protein SUA5	1,03	9,98E-01	3,2	1,45E-04	-2,8	4,41E-04	146,40	61,27	185,67	148,35	197,23	66,53
W70um226G_at	um04312	- related to alpha-actinin	1,04	9,94E-01	2,1	8,09E-06	-1,8	7,07E-05	166,80	115,03	221,60	173,55	244,30	121,20
W40um164G_at	um00468	- related to glycinamide ribonucleotide transformyl	-1,03	9,98E-01	2,2	2,02E-05	-1,7	4,75E-04	269,05	155,90	278,23	260,30	346,33	160,83
W20um114G_at	um05633	- conserved hypothetical protein	-1,07	9,91E-01	4,3	5,52E-08	-3,2	5,29E-07	510,65	172,67	614,47	475,85	743,80	190,40
C95um158G_at	um01755	- putative protein	1,01	9,99E-01	2,9	1,36E-05	-3,0	1,39E-05	343,60	168,00	439,33	345,80	484,70	148,57
W15um118G_at	um04004	- related to gamma-glutamylcysteine synthetase	1,17	9,78E-01	2,6	4,85E-07	-2,3	1,90E-06	431,75	245,63	552,20	506,20	628,47	239,03
W10um201G_at	um00857	- probable KRE6 - glucan synthase subunit	-1,13	9,78E-01	3,0	2,91E-07	-2,2	7,34E-06	375,05	145,87	363,43	333,85	446,17	161,73
W15um094G_at	um00896	- Kin1 - kinesin motor protein 1	1,01	9,99E-01	2,6	1,96E-06	-2,1	2,12E-05	326,90	164,87	361,43	331,35	430,13	170,73
W165um172G_at	um11487	- conserved hypothetical protein	-1,15	9,78E-01	4,5	4,97E-08	-3,8	1,70E-07	296,65	104,07	368,77	257,95	468,97	95,47
W20um258G_at	um04414	- hypothetical protein	-1,08	9,80E-01	2,7	2,84E-07	-2,4	1,49E-06	1777,25	869,53	2049,90	1649,70	2392,40	851,30
C15um013G_at	um03547	- hypothetical protein	-1,06	9,91E-01	3,2	4,25E-08	-2,8	1,64E-07	704,60	297,37	742,40	667,05	961,43	262,60
W10um208G_at	um00277	- related to M-phase inducer phosphatase	1,03	9,94E-01	2,4	8,10E-08	-1,8	6,05E-06	236,85	135,60	257,27	243,85	329,13	145,80
W20um195G_at	um01851	- conserved hypothetical protein	-1,02	9,98E-01	3,3	3,43E-08	-2,5	4,50E-07	1113,40	484,27	1225,40	1089,15	1612,00	484,57
W35um144G_at	um11063	- conserved hypothetical protein (fragment)	1,02	9,98E-01	3,5	6,26E-06	-2,9	3,00E-05	176,15	67,50	234,40	182,60	234,63	80,10
W124um171G_at	um00072	- conserved hypothetical protein	-1,01	9,99E-01	2,0	4,77E-05	-1,8	3,47E-04	1008,15	683,47	1333,37	1003,20	1385,40	757,27
C5um162G_at	um12127	- hypothetical protein	1,05	9,92E-01	2,2	1,18E-05	-2,2	2,04E-05	135,85	87,70	198,03	142,65	193,37	90,50
W90um158G_at	um01756	- probable Purine Transporter AzgA	-1,00	9,99E-01	2,1	1,57E-06	-2,1	1,94E-06	814,60	531,37	1151,33	812,95	1111,57	541,33
W40um177G_at	um02690	- hypothetical protein	-1,13	9,78E-01	4,7	5,96E-08	-3,8	3,18E-07	156,00	42,83	210,07	138,15	204,67	54,07
W5um226G_at	um11751	- conserved hypothetical protein	-1,13	9,78E-01	2,0	1,02E-05	-2,3	3,33E-06	357,80	222,33	447,73	319,25	441,83	196,70
W90um156G_at	um10419	- Cts1 - Chitinase	-1,00	1,00E+00	2,2	6,19E-06	-2,2	8,10E-06	1605,70	972,83	2212,43	1605,45	2122,30	1019,77
C85um023G_at	um02954	- putative protein	-1,07	9,91E-01	2,7	5,67E-07	-2,7	6,45E-07	224,40	121,50	302,40	210,70	324,17	109,47
C30um020G_at	um00876	- related to cellulase	1,05	9,91E-01	2,1	1,11E-05	-2,1	1,62E-05	2594,20	1822,90	3834,77	2730,00	3804,30	1856,30
UG16-1i3-50e2_RC_at	um10446	- putative protein	1,14	9,78E-01	2,6	1,17E-05	-2,4	3,42E-05	214,55	152,57	405,80	244,85	404,10	167,27
W50um040G_at	um00738	- hypothetical protein	1,38	8,08E-01	2,9	1,50E-06	-3,9	2,13E-07	96,25	67,10	246,27	132,90	195,87	62,30
W105um119G_at	um01725	- hypothetical protein	1,49	4,18E-01	2,9	8,80E-07	-3,3	4,27E-07	479,70	288,13	963,10	722,00	833,27	289,13
C52um092G_at	um10669	- putative protein	-1,13	9,78E-01	2,2	1,29E-05	-2,3	1,19E-05	74,75	55,30	120,80	65,80	124,00	52,00
W95um036G_at	um02758	- hypothetical protein	1,07	9,89E-01	2,4	7,40E-07	-2,4	9,10E-07	947,20	746,10	1875,00	1012,05	1754,70	779,57
C35um232G_at	um04533	- related to 6-HYDROXY-D-NICOTINE OXIDASE	1,11	9,78E-01	2,6	9,72E-08	-2,9	6,84E-08	714,35	484,87	1485,57	795,60	1268,33	510,37
W55um018G_at	um01202	- hypothetical protein	1,05	9,98E-01	2,6	2,62E-04	-2,3	8,27E-04	45,95	28,13	60,50	48,80	72,80	25,70
W10um083G_at	um10384	- related to TATA-binding protein-associated phosp	-1,04	9,98E-01	2,7	2,08E-05	-2,5	4,82E-05	87,80	54,50	121,37	84,75	151,57	47,83
W70um158G_at	um01761	- conserved hypothetical protein	1,08	9,94E-01	1,8	5,43E-03	-2,3	3,85E-04	66,35	37,47	68,60	73,15	66,23	29,43
C45um267G_at	um06133	- conserved hypothetical protein	1,07	9,91E-01	2,0	1,24E-04	-2,0	1,39E-04	310,75	185,40	358,97	333,50	373,77	178,43
W40um095G_at	um01073	- putative protein	-1,24	9,78E-01	2,8	3,14E-04	-2,9	3,39E-04	133,55	50,37	163,83	107,10	135,30	55,67
C85um027G_at	um04224	- related to Myosin-like protein NUF2	-1,17	9,78E-01	1,9	4,11E-04	-2,5	3,54E-05	135,25	59,93	140,97	115,80	113,63	55,97
W95um105G_at	um02259	- hypothetical protein	-1,28	9,78E-01	7,1	6,41E-08	-12,4	1,04E-08	104,40	12,23	150,57	83,65	92,03	11,23
C9um200G_x_at	um11013	- putative protein	-1,04	9,94E-01	2,0	4,60E-05	-1,9	9,26E-05	217,05	130,27	302,37	208,90	260,33	155,27
C75um118G_at	um04016	- hypothetical protein	-1,06	9,91E-01	1,8	5,49E-04	-2,1	1,39E-04	247,90	141,07	296,30	233,20	250,90	142,57
C75um110G_at	um00567	- related to B2-aldehyde-forming enzyme	1,01	9,98E-01	1,9	2,05E-04	-2,3	3,03E-05	416,65	261,43	566,33	420,90	484,23	247,97
C40um131G_at	um05227	- hypothetical protein	-1,26	9,78E-01	1,8	1,13E-03	-2,4	5,29E-05	275,85	123,90	279,63	217,10	218,40	116,30
C97um209G_at	um10002	- related to NADH-dependent flavin oxidoreductase	-1,24	9,78E-01	2,0	2,82E-03	-3,0	1,37E-04	1349,35	541,67	1423,97	1138,40	1090,07	491,73
W95um055G_at	um03987	- related to BRN1 - functional homologue of humar	-1,19	9,78E-01	2,1	4,76E-05	-2,9	3,01E-06	312,25	100,27	290,23	265,35	209,43	100,37
C175um209G_at	um00036	- conserved hypothetical protein	1,04	9,98E-01	2,6	1,16E-04	-3,3	2,61E-05	130,20	60,77	168,70	135,20	159,43	52,17
C5um248G_at	um03025	- probable DNA mismatch repair protein MSH2	-1,06	9,91E-01	2,0	6,27E-06	-1,7	5,99E-05	213,10	99,57	189,83	201,05	201,80	108,40
C50um064G_at	um11446	- conserved hypothetical protein	1,00	1,00E+00	2,1	1,15E-03	-2,9	1,18E-04	176,80	80,03	204,47	178,15	167,50	72,43
C50um055G_at	um03976	- related to PDR16 protein	-1,03	9,98E-01	1,8	7,26E-04	-2,9	1,13E-05	344,65	157,37	375,40	336,20	289,87	131,10
W20um134G_at	um05112	- related to NUG1 - Nuclear GTPase (involved in Ril	-1,13	9,78E-01	2,4	4,52E-05	-3,6	2,80E-06	227,55	68,10	214,47	202,10	167,90	59,03
W40um072G_at	um00957	- related to serine/threonine-protein kinase	1,10	9,89E-01	1,7	6,40E-04	-2,3	3,20E-05	288,55	177,67	324,00	318,15	305,70	141,07
C63um236G_at***	um10401	- related to CHL1 - protein of the DEAH box family	-1,07	9,91E-01	2,3	1,21E-05	-2,7	3,21E-06	176,80	70,93	174,67	164,30	161,63	63,57
C105um044G_at	um02344	- related to translation initiation factor IF-2, mito...	1,04	9,98E-01	2,5	1,30E-03	-2,8	7,63E-04	226,55	95,30	224,40	234,50	229,53	83,40
W60um178G_at	um02018	- conserved hypothetical protein	-1,02	9,98E-01	1,8	4,44E-04	-2,0	1,45E-04	121,85	74,83	134,73	119,20	136,43	65,47
C45um105G_at	um11398	- probable UBP1 - ubiquitin-specific protease	-1,01	9,98E-01	2,2	1,64E-04	-1,9	6,48E-04	203,05	107,27	218,03	200,40	232,53	114,90
C105um039G_at	um01142	- conserved hypothetical protein	-1,01	9,99E-01	1,7	5,67E-04	-2,0	9,47E-05	735,30	400,80	722,27	729,30	685,70	351,10
C45um050G_at	um01129	- hypothetical protein	-1,03	9,98E-01	2,1	5,17E-04	-1,6	1,30E-02	295,75	156,60	262,93	286,20	322,80	165,20
C60um122G_at	um01688	- related to mRNA export factor mex67	1,12	9,78E-01	2,0	5,57E-06	-2,3	2,05E-06	434,55	239,13	399,63	488,10	488,10	174,17
C65um137G_at	um02605	- hypothetical protein	1,17	9,78E-01	3,6	1,02E-05	-3,0	4,74E-05	209,05	78,83	214,27	242,50	290,47	71,80
W30um089G_at	um01550	- conserved hypothetical protein	1,09	9,91E-01	2,1	1,66E-04	-2,2	1,27E-04	294,10	180,97	351,87	323,80	371,93	161,87
W112um148G_at	um00785	- conserved hypothetical protein	1,20	9,78E-01	2,3	4,22E-04	-2,5	2,57E-04	148,60	93,40	174,27	186,25	214,17	69,27
W132um075G_at	um06069	- related to NOL1R protein	1,03	9,98E-01	2,2	1,30E-04	-2,0	5,42E-04	113,90	59,90	109,73	118,10	134,63	53,97
C110um030G_at	um04420	- related to ECM31 - 3-methyl-2-oxobutanoate hy	1,17	9,78E-01	2,4	7,73E-06	-1,8	2,54E-04	189,15	115,70	209,57	222,55	281,23	114,70
W40um116G_at	um10792	- related to S-adenosylmethionine decarboxylase (	1,22	9,78E-01	3,5	1,13E-05	-2,4	2,32E-04	542,20	222,70	490,90	672,35	765,60	204,33
W20um132G_at	um05198	- conserved hypothetical protein	1,08	9,91E-01	2,0	1,05E-04	-1,6	2,65E-03	265,40	156,07	252,37	287,70	314,97	157,17
C140um010G_at	um11855	- hypothetical protein	1,07	9,91E-01	2,6	6,05E-06	-2,3	2,56E-05	326,65	148,10	292,23	350,60	393,07	125,67
W95um015G_at	um04621	- hypothetical protein	-1,24	9,78E-01	3,3	2,03E-04	-2,8	7,66E-04	135,85	34,83	120,90	108,85	114,17	44,67
C35um037G_at	um01102	- putative protein	-1,10	9,91E-01	2,0	6,04E-04	-1,9	1,31E-03	340,75	169,33	299,47	309,20	344,07	158,57
W140um002G_at	um03928	- related to protein kinase Gin4p	1,02	9,98E-01	2,6	6,42E-05	-2,3	2,32E-04	248,00	106,27	262,53	250,35	276,33	115,90
W65um019G_at	um06404	- probable thioredoxin peroxidase	-1,19	9,78E-01	3,9	4,60E-07	-2,9	5,98E-06	2744,15	746,73	2162,23	2369,95	2934,23	751,80
C25um116G_at	um10795	- hypothetical protein	-1,01	9,99E-01	2,3	4,28E-05	-1,9	4,98E-04	72,05	34,13	65,80	71,75	78,90	34,83
W110um188G_at	um04808	- related to serine/threonine protein kinase	1,14	9,78E-01	2,7	3,55E-07	-2,4	1,66E-06	225,35	99,33	259,27	257,15	275,67	106,43
C60um084G_at	um10977	- conserved hypothetical protein	-1,11	9,91E-01	2,1	2,46E-04	-2,9	1,81E-05	352,15	152,60	316,43	319,65	320,07	110,47
C20um191G_at	um00366	- probable MCM6 - involved in replication	-1,08	9,91E-01	2,5	5,32E-05	-2,1	4,48E-04	135,10	51,30	111,47	125,65	127,33	53,37
W50um039G_at	um01153	- probable DIP2 - Dom34p-interacting protein	1,01	9,98E-01	3,2	1,63E-06	-3,2	2,62E-06	408,60	120,00	305,07	413,90	384,00	94,83
W12um235G_at	um10186	- putative protein	1,05	9,91E-01	5,3	8,97E-09	-3,0	4,00E-07	4124,90	984,23	3785,23	4351,65	5173,33	1247,27
W30um219G_at	um02493	- related to RPO41 - DNA-directed RNA polymerase	-1,06	9,94E-01	3,7	2,77E-06	-3,8	3,18E-06	283,40	80,47	249,10	266,20	299,80	65,67
W115um140G_at	um03756	- related to DNA helicase Fdhp	-1,05	9,88E-01	2,5	5,00E-08	-2,2	2,14E-07	194,95	81,30	176,80	184,80	203,00	79,57
C130um144G_at	um04065	- conserved hypothetical protein	-1,03	9,91E-01	2,8	3,25E-08	-2,8	4,17E-08	523,00	193,07	468,10	507,10	535,87	166,53
W160um107G_at	um11854	- related to protein arginine N-methyltransferase	1,07	9,78E-01	2,3	6,57E-07	-1,7	4,12E-05	698,55	337,00	627,77	749,45	772,70	369,37
W140um145G_at	um04371	- conserved hypothetical protein	-1,06	9,91E-01	2,4	7,99E-07	-2,1	4,12E-06	829,55	330,00	690,63	779,65	788,37	325,97
W21um079G_at	um03276	- related to SRP40 - suppressor of mutant AC40 su	-1,12	9,98E-01	6,7	1,77E-04	-5,2	6,72E-04	226,45	36,77	158,70	203,60	217,80	31,33
W142um049G_at	um10025	- conserved hypothetical protein	1,05	9,98E-01	4,2	8,05E-07	-3,3	6,11E-06	343,80	80,67	238,50	359,00	344,37	71,30
W75um222G_at***	um11338	- conserved hypothetical protein	-1,05	9,98E-01	4,6	2,19E-07	-3,0	5,23E-06	5003,40	1011,57	3912,10	4817,25	4660,37	1293,93
W35um258G_at	um04410	- probable siderophore iron transporter mirC	-1,10	9,91E-01	5,0	2,54E-07	-3,8	1,76E-06	4649,15	778,03	2955,33	4276,25	3885,47	776,10
C40um034G_at	um05052	- hypothetical protein	-1,08	9,91E-01	2,1	2,67E-05	-1,7	3,81E-04	249,10	112,67	199,67	231,45	237,47	115,27
W10um164G_at	um10120	- Chs3 - Chitin Synthase 3	1,01	9,98E-01	2,6	8,73E-07	-2,6	1,61E-06	410,45	150,47	355,27	414,90	396,73	137,90
C9um060G_at	um02134	- related to mixed-linked glucanase precursor MLG	-1,22	9,49E-01	2,4	4,05E-06	-2,2	1,39E-05	1270,40	526,53	1063,43	1043,00	1244,77	491,20
C10um226G_at	um11750	- probable ribonucleoside-diphosphate reductase la	-1,06	9,91E-01	2,0	6,88E-06	-1,8	3,03E-05	900,10	448,77	856,57	853,10	897,23	469,17
C50um074G_at	um01826	- hypothetical protein	-1,08	9,91E-01	3,6	4,67E-07	-2,8	3,86E-06	180,70	47,90	172,57	168,20	175,80	59,83
W65um179G_at	um11315	- hypothetical protein	-1,19	9,78E-01	2,9	1,88E-06	-2,3	2,03E-05	786,60	252,10	711,40	673,30	740,93	303,40
W85um164G_at	um00459	- related to Condensin complex subunit 3	-1,11	9,78E-01	2,1	8,44E-06	-2,3	5,49E-06	285,85	125,70	276,57	258,95	265,17	122,43
C115um192G_at	um00208	- related to SRC1 - involved in sister chromatid seç	-1,17	9,52E-01	3,1	4,18E-08	-3,0	7,73E-08	180,80	57,60	188,13	155,70	180,83	62,57
W37um070G_at	um10164	- related to E2 ubiquitin-conjugating enzyme	-1,04	9,94E-01	2,4	1,27E-06	-2,9	3,09E-07	281,00	120,23	287,07	270,00	283,10	99,53
UG15-35a17-116a6_RC_a	um03446	- probable protein kinase DBF2	-1,11	9,78E-01	2,7	3,30E-07	-3,4	7,54E-08	446,05	140,07	453,63	399,90	381,17	130,93
C70um241G_at	um06229	- related to SDA1 - required for normal organizatio	-1,23	9,78E-01	3,0	5,45E-05	-9,7	1,53E-07	203,00	55,93	210,90	164,85	171,17	21,70

C70um167G_at	um10414	- conserved hypothetical protein	-1,10	9,78E-01	2,0	3,11E-05	-2,2	1,15E-05	402,15	208,37	458,13	366,20	407,83	207,77
W65um258G_at	um04403	- conserved hypothetical protein	-1,05	9,92E-01	1,9	6,18E-05	-2,0	3,07E-05	156,70	89,93	174,80	149,40	171,30	84,73
W110um135G_at	um01647	- related to CDC20 - cell division control protein	-1,16	9,78E-01	2,3	2,42E-06	-2,5	1,47E-06	519,50	241,93	560,60	447,70	545,50	227,70
C45um140G_at	um03776	- putative protein	-1,08	9,91E-01	2,6	7,25E-06	-2,8	5,84E-06	1111,80	453,17	1293,27	1032,45	1177,60	468,03
C10um049G_at	um00081	- hypothetical protein	-1,05	9,94E-01	2,1	6,06E-05	-1,9	1,95E-04	595,95	317,43	579,53	569,40	646,13	303,13
C75um174G_at	um02741	- related to serine/threonine protein kinase COT-1	-1,12	9,78E-01	3,2	5,08E-07	-2,7	2,88E-06	190,70	68,60	207,90	170,85	224,13	74,50
C90um079G_at	um03262	- related to Separin	1,08	9,78E-01	2,1	2,08E-06	-2,3	9,88E-07	159,80	89,47	176,33	172,50	187,00	75,87
W5um007G_at	um10206	- related to Serine/threonine-protein kinase mph1	1,03	9,98E-01	2,3	1,84E-04	-2,5	1,16E-04	317,70	145,93	309,53	327,40	329,33	125,90
W25um145G_at	um04393	- putative protein	1,10	9,78E-01	2,4	2,42E-06	-2,1	8,88E-06	250,35	118,30	282,13	276,30	279,93	130,17
W95um117G_at	um03082	- conserved hypothetical protein	1,01	9,98E-01	1,7	3,61E-05	-2,1	4,53E-06	409,75	224,40	400,20	412,95	388,67	193,40
W65um022G_at	um00126	- conserved hypothetical protein	1,08	9,89E-01	2,2	6,71E-06	-2,1	1,11E-05	562,30	277,57	568,00	603,95	596,00	269,50
W35um151G_at	um10937	- conserved hypothetical protein	1,06	9,94E-01	2,4	6,85E-05	-3,0	1,21E-05	186,35	77,63	189,73	198,10	184,07	62,00
W30um113G_at	um03501	- probable DNA topoisomerase II	1,02	9,98E-01	2,3	2,84E-05	-2,2	6,07E-05	247,70	86,97	214,33	252,80	200,17	96,57
W115um083G_at	um03133	- related to SMC4 - Stable Maintenance of Chromo:	1,15	9,78E-01	1,8	1,87E-05	-2,1	4,10E-06	228,35	125,97	247,50	263,30	229,37	117,30
C155um139G_at	um01322	- probable VID27 - involved in Vacuole import and	1,01	9,98E-01	2,0	1,92E-06	-1,9	4,10E-06	426,50	195,23	399,70	429,35	393,30	206,07
W55um098G_at	um00144	- putative protein	1,04	9,98E-01	2,4	4,99E-05	-2,9	1,34E-05	219,10	83,37	222,97	228,15	201,83	76,57
W40um150G_at	um00985	- conserved hypothetical protein	1,20	9,78E-01	2,0	2,82E-04	-1,9	6,12E-04	126,85	61,27	142,23	151,40	126,37	73,03
W6um131G_at***	um11783	- related to N-acetylglucosaminyltransferase SPT14	1,58	9,16E-01	6,5	3,03E-06	-5,6	8,14E-06	53,00	8,70	66,30	84,55	62,87	11,90
W20um166G_at	um00411	- related to metalloprotease MEP1	-1,46	9,78E-01	-1,1	7,75E-01	-4,2	4,13E-05	15,35	14,17	48,73	10,25	13,20	11,63
C110um127G_at	um04884	- conserved hypothetical protein	-1,07	9,98E-01	-2,5	1,17E-03	-3,1	2,90E-04	63,85	247,07	604,57	59,35	95,80	198,63
W130um209G_at	um00027	- putative protein	-1,19	9,78E-01	1,0	9,03E-01	-4,7	7,16E-06	17,10	62,70	263,77	13,95	64,60	54,63
W125um090G_at	um00913	- Glo2 - Glyoxaloxidase 2	1,39	9,56E-01	-1,1	7,53E-01	-2,3	4,89E-04	31,60	64,93	107,20	44,55	62,83	45,57
W55um283G_at	um00309	- conserved hypothetical protein	1,09	9,91E-01	1,5	6,92E-03	-2,2	1,34E-04	230,90	934,97	2468,43	250,90	1455,23	1106,33
C11um259G_at	um10671	- related to Pectin lyase B precursor	-1,03	9,98E-01	1,5	2,76E-02	-2,1	5,10E-04	75,80	53,03	100,97	73,80	78,53	47,07
W75um278G_at	um04782	- probable GUS1 - Glutamyl-tRNA synthetase	-1,17	9,78E-01	1,5	4,42E-03	-2,2	2,82E-05	361,15	249,27	440,27	308,80	368,07	200,27
W65um127G_at	um04872	- probable ARG1 - argininosuccinate synthetase	-1,15	9,91E-01	2,6	2,94E-04	-3,1	1,24E-04	2386,95	863,90	2497,30	2144,65	2336,03	795,53
W80um213G_at	um03648	- related to purine nucleotide binding protein	-1,28	9,78E-01	1,4	7,48E-02	-2,7	2,02E-04	271,75	126,47	268,60	214,65	184,57	97,43
C210um132G_at	um05156	- probable Replication factor-A protein 1	-1,15	9,78E-01	1,7	3,64E-03	-2,6	5,79E-05	266,75	133,67	334,77	231,40	230,30	128,70
C45um043G_at	um02796	- probable ATP-binding multidrug cassette transpor	-1,33	9,91E-01	4,4	3,06E-03	-16,9	3,03E-05	1005,40	102,83	1186,57	753,85	504,03	62,90
C65um135G_at	um01655	- related to lipase family	1,00	1,00E+00	1,5	1,13E-03	-3,2	1,70E-07	239,70	100,70	299,80	240,00	148,57	93,57
C50um148G_at	um00798	- probable RAD5 - DNA helicase	1,04	9,98E-01	1,5	3,17E-03	-2,4	2,46E-05	247,80	138,17	279,30	258,40	215,97	117,57
W30um214G_at	um06443	- probable TIF6 - translation initiation factor 6 (eI..	1,16	9,78E-01	1,6	3,53E-03	-2,2	7,58E-05	814,30	377,90	835,27	956,45	593,73	375,63
C75um079G_at	um03264	- probable xanthine dehydrogenase	1,42	9,20E-01	2,3	3,22E-04	-2,5	2,20E-04	204,75	201,17	478,97	281,05	458,80	196,53
W115um078G_at	um03290	- Rad51 - DNA repair protein RAD51	1,00	1,00E+00	2,1	2,51E-05	-2,9	1,91E-06	129,60	84,63	237,10	131,35	182,40	80,20
W60um154G_at	um02548	- related to Sorting nexin 9	1,36	9,78E-01	4,0	1,98E-04	-6,0	3,01E-05	9,05	4,03	31,27	11,50	18,90	4,50
W35um023G_at	um10329	- related to guanine deaminase	1,01	9,99E-01	1,8	1,66E-03	-2,1	5,42E-04	192,60	177,60	362,60	193,60	326,93	172,67
C40um019G_at	um06399	- conserved hypothetical protein	1,03	9,98E-01	2,1	2,48E-03	-3,0	2,38E-04	184,10	128,00	378,90	189,50	278,73	123,43
W85um189G_at	um00700	- related to Zinc-binding oxidoreductase	-1,41	9,56E-01	1,3	1,81E-01	-2,6	3,22E-04	1955,45	1012,03	2710,23	1496,60	1327,93	1063,40
C78um043G_at	um02787	- hypothetical protein	1,15	9,91E-01	1,3	3,17E-01	-3,8	4,64E-04	6,95	4,80	18,80	8,20	6,87	4,10
C40um084G_at	um06255	- hypothetical protein	1,17	9,91E-01	-1,0	9,25E-01	-4,8	5,91E-04	11,55	9,10	44,57	13,70	8,87	7,07
W26um190G_at	um00336	- putative protein	1,05	9,98E-01	1,3	5,29E-01	-6,5	1,67E-04	125,30	126,83	683,40	132,10	168,83	89,23
UG16-21e9-139e5_RC_at	um05253	- related to ATP-binding multidrug cassette transpo	-1,43	9,78E-01	1,9	1,29E-01	-8,9	1,81E-04	715,35	618,10	3572,67	564,75	1331,40	391,77
W61um152G_at	um05271	- related to Malic acid transport protein	-1,30	9,78E-01	1,7	7,50E-02	-4,3	2,19E-04	226,30	106,03	411,60	174,05	186,93	88,20
C41um217G_at	um04500	- hypothetical protein	-1,46	9,78E-01	1,7	1,28E-01	-9,1	4,16E-05	1255,40	410,93	2372,00	861,35	864,83	252,63
W50um085G_at	um06219	- related to dna excision repair protein ercc-1	-1,35	9,78E-01	1,2	3,39E-01	-2,8	2,40E-04	139,35	144,10	239,57	103,10	175,60	85,10
C25um036G_at	um02775	- hypothetical protein	1,22	9,78E-01	1,6	2,82E-02	-3,7	4,27E-05	6,95	6,97	23,70	8,70	12,10	5,23
W105um021G_at	um03114	- conserved hypothetical protein	-1,30	8,08E-01	-2,9	2,56E-07	-1,2	1,50E-01	496,65	512,30	488,30	381,80	177,03	422,70
C52um065G_at	um04145	- putative protein	-1,47	9,37E-01	-1,6	2,52E-02	-2,5	4,85E-04	164,85	79,20	181,53	114,35	49,97	72,63
W125um018G_at	um01187	- hypothetical protein	-1,06	9,91E-01	-4,3	3,43E-08	-2,2	8,69E-06	2156,45	1361,70	2273,60	2043,25	315,80	1033,90
W75um267G_at	um06140	- related to programmed cell death protein (calciur	-1,26	9,78E-01	-2,7	3,14E-04	-1,5	8,96E-02	176,35	124,33	155,20	140,30	46,50	105,53
W25um259G_at	um04712	- related to N-methyltransferase	1,34	8,33E-01	-2,0	5,38E-05	1,9	2,29E-04	341,25	299,83	197,30	464,15	147,03	367,23
W85um192G_at	um10053	- related to carbonic anhydrase	1,08	9,89E-01	-2,4	3,08E-06	1,2	1,26E-01	456,95	296,87	243,23	499,85	124,23	287,97
W20um231G_at	um06152	- hypothetical protein	-1,12	9,78E-01	-2,4	1,83E-05	1,0	8,54E-01	358,75	321,37	226,23	320,90	134,90	231,73
W5um052G_at	um10537	- "Adr1 - Protein kinase A, catalytic subunit; requir	-1,03	9,98E-01	1,6	1,54E-04	3,2	9,77E-08	410,95	511,73	428,40	398,95	828,13	1395,03
W130um013G_at	um03523	- probable aldehyde dehydrogenase	1,19	9,91E-01	-4,0	3,79E-04	1,1	8,20E-01	23,25	49,03	40,37	25,95	11,53	44,93
C64um147G_at	um00757	- conserved hypothetical protein	-1,16	9,78E-01	-2,3	2,34E-04	1,2	3,99E-01	193,30	498,20	398,67	167,95	217,50	473,00
C61um123G_at	um00542	- conserved hypothetical protein	1,08	9,94E-01	-2,1	9,90E-04	-1,0	9,49E-01	54,20	105,53	90,00	58,35	50,20	90,83
W120um002G_at	um03924	- Rep1 - repellent protein 1 precursor	-1,01	9,99E-01	-3,6	5,56E-04	-2,0	2,49E-02	28,70	183,47	182,20	28,90	47,77	90,10
W10um109G_at	um11143	- probable phenol 2-monooxygenase	-1,24	9,88E-01	-4,1	1,73E-04	-1,2	4,98E-01	40,30	72,57	76,67	32,35	18,93	61,90
W120um099G_at	um05898	- conserved hypothetical protein	-1,14	9,78E-01	-2,1	2,98E-04	-1,2	2,06E-01	147,95	231,30	242,90	129,90	108,27	196,20
W130um021G_at	um10636	- conserved hypothetical protein	-1,52	8,43E-01	-3,1	4,36E-05	-1,6	1,74E-02	125,65	583,60	899,13	83,45	187,70	549,90
C10um163G_at	um00695	- putative exochitinase	-2,01	7,94E-01	-4,0	9,50E-05	-1,5	1,34E-01	51,85	154,40	164,27	26,25	40,53	111,20
W20um158G_at	um01772	- related to Aldose 1-epimerase precursor	1,10	9,98E-01	-7,2	7,55E-04	-2,0	1,50E-01	17,30	1037,23	1909,87	16,85	148,20	937,50
C65um167G_at	um04247	- related to Cholinesterase precursor	-1,22	9,78E-01	-4,8	2,56E-05	-2,1	6,74E-03	16,95	150,07	178,27	14,50	30,67	82,27
C25um119G_at	um10866	- related to canalicular multispecific organic anion .	1,23	9,91E-01	-3,4	7,71E-04	-1,1	8,73E-01	38,95	215,20	206,93	48,20	64,17	180,60
C15um143G_at	um10483	- conserved hypothetical protein	1,24	9,78E-01	-2,2	2,51E-04	1,0	9,34E-01	57,65	147,90	141,47	72,30	66,73	138,80
C110um021G_at	um03115	- related to Sge1 - drug resistance protein	-1,53	7,29E-01	-6,2	7,23E-08	1,0	9,26E-01	147,15	573,83	528,70	97,40	92,37	536,17
C120um021G_at	um03117	- conserved hypothetical protein	-1,12	9,78E-01	-4,5	8,10E-08	-1,0	7,99E-01	68,50	238,43	228,03	61,30	52,10	222,50
C25um195G_at	um01850	- conserved hypothetical protein	-1,20	9,78E-01	-2,5	6,18E-05	1,0	8,56E-01	44,15	456,90	457,17	37,15	186,03	473,67
C45um186G_at	um04742	- related to stomatin	1,23	9,78E-01	-2,1	1,66E-04	-1,1	6,07E-01	177,50	542,90	567,20	224,60	262,90	521,60
C100um173G_at	um11482	- related to E2 ubiquitin-conjugating enzyme	1,11	9,97E-01	-4,8	1,57E-04	1,2	5,63E-01	3,20	51,57	47,67	3,65	11,33	57,17
C70um043G_at	um10605	- probable ADH3 - alcohol dehydrogenase III	-1,06	9,98E-01	-4,8	2,43E-05	-1,1	6,73E-01	8,80	83,97	102,80	8,25	18,37	91,50
W115um119G_at	um01723	- related to Cytochrome P450 94A1	1,17	9,91E-01	-2,6	8,13E-04	-1,2	4,02E-01	27,20	569,47	676,73	32,80	225,23	538,80
C30um217G_at	um04503	- related to Alpha-N-acetylgalactosaminidase precu	-1,41	9,78E-01	-7,4	5,68E-05	-1,1	7,69E-01	31,60	1931,97	2105,13	27,70	261,90	1822,87
W5um146G_at	um05964	- related to esterase	1,14	9,78E-01	-4,7	4,87E-07	-1,2	2,99E-01	51,95	403,17	525,77	59,75	84,57	435,67
W155um044G_at	um02331	- Kpp6 - MAP kinase	-1,05	9,98E-01	-1,1	6,03E-01	3,8	1,47E-04	47,30	94,23	30,03	47,40	82,60	108,73
W35um030G_at	um10529	- conserved hypothetical protein	1,10	9,91E-01	-1,1	6,02E-01	2,4	2,87E-05	103,90	163,17	70,33	113,70	152,73	172,03
C60um055G_at	um03978	- hypothetical protein	-2,36	7,45E-01	-3,4	8,09E-04	1,9	3,83E-02	33,80	41,57	13,30	14,25	11,33	24,60
C130um257G_at	um05774	- related to metalloprotease MEP1	-1,37	9,91E-01	-6,1	1,15E-03	14,1	8,45E-05	32,05	203,50	11,07	24,10	27,43	189,97
C91um047G_at	um03580	- related to annexin XIV	1,02	9,98E-01	-2,5	2,43E-04	1,7	9,77E-03	125,15	239,93	126,10	130,20	93,97	226,73
C25um084G_at	um06258	- conserved hypothetical protein	-1,23	9,78E-01	-2,1	5,07E-05	-1,0	8,54E-01	228,15	345,53	244,73	185,85	166,07	237,43
W90um157G_at	um02170	- conserved hypothetical protein	-1,26	9,78E-01	-2,0	6,74E-04	1,3	1,20E-01	93,70	149,17	82,13	76,10	72,57	109,07
C17um145G_s_at	um10514	- conserved hypothetical protein	-1,26	9,78E-01	-2,2	8,78E-05	1,5	1,14E-02	86,20	90,47	66,03	67,90	41,03	99,40
W95um133G_at	um10175	- probable sphingosine-1-phosphate lyase	-1,01	9,99E-01	-2,4	1,38E-06	1,6	3,99E-04	246,15	248,93	157,53	244,90	103,00	248,60
W120um209G_at	um10008	- conserved hypothetical protein	-1,27	9,91E-01	-6,6	5,66E-04	3,0	1,98E-02	92,85	102,03	37,00	72,55	16,90	95,83
C70um286G_at	um00517	- related to Tripeptidyl-peptidase II	-1,06	9,91E-01	-2,2	8,44E-06	1,6	4,46E-04	597,50	684,10	394,50	566,65	313,27	645,50
C125um222G_at	um11335	- hypothetical protein	-1,22	9,52E-01	-2,0	1,87E-05	1,6	8,66E-04	163,70	157,70	95,83	134,90	75,83	151,07
W40um112G_at	um04659	- related to GUT1 - glycerol kinase	-1,03	9,98E-01	-2,1	7,79E-05	2,0	1,57E-04	564,55	581,63	296,13	551,80	276,03	601,13
W5um098G_at***	um00132	- hypothetical protein	-1,13	9,91E-01	-2,8	8,28E-05	3,2	4,58E-05	140,95	141,63	51,47	123,80	49,53	165,03
C10um228G_at	um10452	- related to channel protein	-1,11	9,91E-01	-2,2	8,43E-04	2,0	2,48E-03	174,85	164,33	85,50	154,05	72,50	179,47
W15um216G_at	um06022	- probable RIB7 - HTP reductase	-1,06	9,94E-01	-1,4	1,26E-02	2,2	5,99E-05	408,60	448,50	243,10	392,20	309,03	544,87
C51um169G_at	um02320	- hypothetical protein	-1,10	9,91E-01	-1,3	4,11E-02	2,0	1,88E-04	257,55	238,13	141,53	235,45	177,73	290,27
W10um074G_at	um01834	- hypothetical protein	-1,30	9,78E-01	-2,1	3,08E-03	3,0	2,44E-04	52,60	73,60	31,93	41,35	34,67	91,43
W15um113G_at	um03504	- related to Purine-nucleoside phosphorylase	1,00	1,00E+00	-2,0	9,24E-06	1,8	7,41E-05	185,45	212,60	123,83	186,35	105,00	218,97
W90um060G_at	um02113	- hypothetical protein	-1,00	9,98E-01	-1,6	7,25E-06	2,1	3,36E-07	128,35	158,00	76,63	127,80	96,07	159,93
W230um074G_at	um01786	- putative protein	1,08	9,78E-01	-2,6	1,24E-07	3,4	2,20E-08	139,00	241,00	79,77	149,70	92,63	269,83
W70um129G_at	um10502	- probable aminopeptidase P, cytoplasmic	1,09	9,78E-01	-1,9	1,52E-05	2,4	1,14E-06	938,30	1319,77	588,83	1024,75	702,43	1428,47
EST01um036_at	none	- no annotation available	-1,31	9,78E-01	-2,4	2,70E-04	3,5	2,16E-05	36,80	49,83	15,23	28,45	20,37	56,10
C11um184G_at	um05520	- conserved hypothetical protein	-1,06	9,91E-01	-1,9	2,34E-04	2,5	1,41E-05	197,85	241,47	103,30	187,45	129,20	257,87
C70um019G_at	um06405	- related to amme syndrome candidate gene 1 prot	1,00	1,00E+00	-2,1	2,44E-04	1,2	2,43E-01	230,70	352,13	287,23	235,80	169,30	346,20
C35um178G_at	um02023	- related to GMC-type oxidoreductase Y4NJ	-1,19	9,78E-01	-2,1	5,91E-04	2,2	3,35E-04	155,85	529,00	325,83	131,90	257,27	744,13
W130um119G_at	um11365	- hypothetical protein	1,02	9,98E-01	-1,7	2,13E-02	2,7	3,80E-04	18,85	35,10	11,97	19,25	20,47	34,10
W15um026G_at	um02389	- conserved hypothetical protein	-1,15	9,91E-01	-1,7	5,82E-02	3,3	4,29E-04	57,50	146,30	50,93	55,05	85,70	173,83
CLUSTER35_RC_at	um06492	- related to NMA2 - nicotinate-nucleotide adenylylt	-1,11	9,91E-01	-2,8	8,76E-06	2,0	3,09E-04	446,00	1037,93	427,40	402,60	368,20	857,90
W111um003G_at	um01958	- hypothetical protein	1,03	9,98E-01	-2,2	1,46E-04	1,9	8,32E-04	123,15	290,67	119,10	127,90	132,67	225,03
W20um109G_at	um04347	- probable isp4 - oligopepteide transporter	1,03	9,98E-01	-3,7	3,81E-06	1,6	1,05E-02	91,75	367,70	140,80	94,40	97,93	229,97
W15um034G_at	um10713	- conserved hypothetical protein	-1,06	9,94E-01	-2,7	1,87E-05	1,4	5,66E-02	30,60	67,80	38,00	28,85	24,20	50,83
C15um163G_at	um00694	- related to Acyl-CoA dehydrogenase	2,15	4,18E-01	-1,7	1,08E-02	2,4	7,66E-04	11,30	152,83	85,27	25,85	87,37	201,33
C95um161G_at	um02508	- Iad1 - indole-3-acetaldehyde dehydrogenase	-1,13	9,78E-01	-1,9	1,66E-04	2,0	1,37E-04	527,35	6360,57	3359,80	474,35	3312,67	6766,63
C55um171G_at	um00058	- hypothetical protein	1,03	9,98E-01	-1,7	1,50E-02	2,5	6,49E-04	3,70	150,33	74,53	4,00	88,20	184,00
C60um256G_at	um05791	- related to Cytochrome P450 67	1,16	9,78E-01	-1,5	1,63E-02	2,2	1,45E-04	57,05	2674,10	1414,10	66,55	1846,43	3059,80
C50um256G_at	um11586	- hypothetical protein	-1,01	9,98E-01	-1,4	3,44E-03	2,5	2,03E-06	77,35	231,00	102,60	76,85	163,13	259,50
W54um256G_at	um05789	- conserved hypothetical protein	-1,31	9,78E-01	-1,3	7,59E-02	2,1	3,55E-04	324,30	702,63	349,30	254,10	527,50	737,43
W5um190G_at	um00343	- probable amino acid transport protein GAP1	-1,21	9,49E-01	-1,2	1,18E-01	2,1	1,21E-05	808,95	3240,97	1617,17	670,90	2751,57	3422,13
C165um175G_at	um02703	- probable FBP1 - fructose-1,6-bisphosphatase	1,05	9,98E-01	-1,4	1,20E-01	3,6	1,21E-04	236,80	2062,97	644,63	265,60	1443,93	2286,03
W65um063G_at	um05366	- conserved hypothetical protein	1,09	9,91E-01	-1,2	1,39E-01	2,8	1,99E-05	209,30	889,67	394,57	230,75	724,17	1093,30
C95um025G_s_at	um10518	- related to Copia protein	1,21	9,78E-01	-1,7	1,63E-03	2,1	1,91E-04	49,45	105,30	45,23	59,95	60,33	96,77
W15um178G_at	um11392	- hypothetical protein	-1,12	9,91E-01	-2,1	4,01E-04	2,4	1,58E-04	205,30	618,67	279,63	185,50	291,13	684,20
C135um119G_at	um01718	- related to glucosamine-6-phosphate deaminase	-1,48	9,78E-01	-5,3	1,41E-04	4,5	3,94E-04	16,30	54,53	10,63	10,70	9,50	49,67
C40um184G_at	um05514	- putative protein	1,07	9,98E-01	-3,4	3,06E-04	4,9	5,77E-05	127,50	213,23	42,23	136,95	58,10	224,27
W45um055G_at	um03975	- related to Carboxypeptidase Y precursor	-1,14	9,78E-01	-2,0	2,63E-04	2,1	1,94E-04	661,45	1055,40	508,20	572,65	528,57	1058,47
W146um171G_at	um00077	- conserved hypothetical protein	1,13	9,78E-01	-1,8	7,79E-05	2,0	3,03E-05	218,45	338,17	167,93	246,40	184,70	341,53
C15um268G_at	um04482	- hypothetical protein	-1,32	9,78E-01	-2,8	3,22E-04	3,8	5,44E-05	152,15	267,53	68,43	112,40	93,60	267,20
W20um138G_at	um02641	- related to PEX10 - peroxisomal assembly protein	-1,04	9,98E-01	-2,2	6,53E-05	2,5	2,81E-05	129,25	204,60	91,93	124,40	90,80	237,63
W42um165G_at	um00440	- conserved hypothetical protein	1,13	9,89E-01	-2,1	6,15E-04	2,6	9,43E-05	274,70	544,40	218,00	311,35	262,13	578,07
C105um281G_at	um02234	- conserved hypothetical protein	-1,11	9,91E-01	-2,2	5,78E-04	2,2	6,18E-04	50,15	87,10	43,17	45,05	38,80	99,83
C175um003G_at	um01941	- conserved hypothetical protein	-1,06	9,98E-01	-4,0	4,45E-05	6,8	3,76E-06	113,30	480,53	81,17	106,70	113,30	577,90
C10um178G_at	um02028	- related to Acyl-coenzyme A oxidase 1, peroxisom	-1,05	9,98E-01	-3,8	1,84E-04	5,3	3,67E-05	90,90	392,07	88,40	88,40	98,77	497,03
C22um79G_at	um10825	- related to 3-hydroxyacyl-CoA dehydrogenase	-1,05	9,98E-01	-2,1	2,28E-04	2,3	1,26E-04	493,10	720,63	377,47	469,10	336,17	874,80
C15um203G_at	um11558	- putative protein	-1,07	9,91E-01	-2,0	2,94E-04	2,1	2,67E-04	277,80	416,47	219,50	259,95	204,93	453,23
W35um259G_at	um04715	- conserved hypothetical protein	-1,10	9,78E-01	-2,6	2,50E-07	3,1	8,33E-08	841,00	1264,77	490,43	761,45	476,00	1548,67
W180um281G_at	um02217	- related to glutamate carboxypeptidase II	-1,11	9,91E-01	-4,7	5,26E-07	2,7	3,53E-05	414,30	838,83	322,57	381,45	176,00	873,10
C117um228G_at	um01902	- conserved hypothetical protein	-1,08	9,91E-01	-2,4	5,57E-06	1,9	6,23E-05	959,70	1318,73	781,67	894,55	558,80	1519,13
W125um228G_at	um01900	- conserved hypothetical protein	-1,09	9,91E-01	-2,1	3,85E-04	2,0	8,20E-04	1292,20	1700,73	945,43	1189,20	798,90	1916,27
C92um006G_at	um02282	- conserved hypothetical protein	-1,01	9,98E-01	-2,1	1,05E-04	2,4	3,29E-05	292,45	418,63	214,13	289,55	194,77	523,13
C20um183G_at	um05548	- related to L-ascorbate oxidase precursor	-1,02	9,98E-01	-2,7	1,10E-03	3,4	3,22E-04	21,45	99,53	38,10	21,05	33,10	134,03
W110um171G_at	um10016	- hypothetical protein	-1,11	9,91E-01	-2,0	1,27E-03	2,1	7,73E-04	69,60	167,10	77,87	62,50	81,70	167,73
W35um024G_at	um01515	- related to ECM4 - protein involved in cell wall bi.	-1,14	9,78E-01	-2,1	8,09E-05	1,9	2,61E-04	485,10	771,43	413,33	435,00	373,80	783,90
amd1_at	um03417	- Amd1 - putative acetamidase	1,17	9,78E-01	-2,3	7,97E-05	4,1	1,47E-06	81,70	685,60	268,77	97,90	295,37	1101,03
W121um079G_at	um03254	- hypothetical protein	1,16	9,78E-01	-2,2	1,97E-05	1,6	1,70E-03	75,55	133,90	87,03	88,55	60,23	138,13
W95um250G_at	um10370	- conserved hypothetical protein	1,12	9,78E-01	-2,3	1,14E-07	1,6	1,61E-05	205,15	355,90	197,23	229,70	152,50	325,23
C149um157G_at	um02158	- conserved hypothetical protein	1,04	9,94E-01	-2,7	2,48E-07	2,0	4,89E-06	1171,55	2114,60	1108,13	1219,90	796,97	2273,00
W50um087G_at	um05869	- probable carnitine/acyl carnitine carrier	1,23	9,78E-01	-2,4	2,23E-05	2,5	1,95E-05	988,10	2239,10	952,47	1249,40	925,57	2419,33
C30um186G_at	um04739	- conserved hypothetical protein	-1,03	9,98E-01	-2,1	9,65E-05	1,8	6,59E-04	343,60	967,80	587,00	341,70	463,47	1066,63
W70um147G_at	um00756	- probable GDI1 - GDP dissociation inhibitor	1,00	1,00E+00	-2,1	5,21E-05	1,9	2,02E-04	792,55	1595,20	975,37	794,75	785,50	1832,27
C40um284G_at	um10746	- conserved hypothetical protein	-1,19	9,78E-01	-2,5	8,09E-06	2,2	2,79E-05	168,25	332,60	160,57	141,65	133,83	363,83
W40um261G_at	um11935	- hypothetical protein	1,00	1,00E+00	-3,4	5,14E-05	2,3	1,04E-03	66,00	325,53	121,80	66,10	96,27	275,90
W67um178G_at	um02016	- related to C.elegans LIM homeobox protein	-1,22	8,33E-01	-2,2	8,05E-07	1,7	2,66E-05	185,70	287,63	170,97	152,10	129,37	297,93
W55um036G_at	um02769	- conserved hypothetical protein	1,06	9,91E-01	-5,5	1,06E-08	2,4	3,99E-06	264,00	1716,67	674,33	279,35	310,13	1649,97

W50um117G_at	um10373	- probable RIB4 - 6,7-dimethyl-8-ribityllumazine sy	-1,08	9,91E-01	-2,4	3,22E-05	1,6	2,94E-03	1088,20	2054,70	1295,73	1019,50	872,80	2079,47
W145um054G_at	um00645	- hypothetical protein	-1,32	9,08E-01	-2,5	1,83E-05	1,7	1,43E-03	120,95	228,80	128,70	92,80	90,50	219,57
C85um106G_at	um01014	- conserved hypothetical protein	-1,29	7,03E-01	-2,2	9,30E-07	1,5	1,90E-04	203,90	373,40	237,73	157,85	170,53	366,90
C100um029G_at	um03830	- conserved hypothetical protein	-1,07	9,91E-01	-2,1	4,97E-06	1,7	8,27E-05	140,30	215,67	126,67	131,35	102,57	220,20
C60um007G_at	um05347	- conserved hypothetical protein	-1,28	9,78E-01	-4,4	4,60E-05	2,8	9,70E-04	255,05	589,33	232,67	214,60	128,93	658,57
C60um056G_at	um01878	- conserved hypothetical protein	-1,31	9,78E-01	-2,8	3,28E-04	2,1	4,58E-03	170,75	331,77	169,13	132,85	122,13	342,90
W95um130G_at	um03692	- probable alpha-glucosidase (maltase)	-1,31	9,61E-01	-3,5	3,29E-06	1,9	7,90E-04	97,65	235,23	114,80	76,15	66,00	223,63
C45um122G_at	um01692	- probable CHA1 - L-serine/L-threonine deaminase	-1,05	9,98E-01	-2,8	3,72E-05	1,8	2,86E-03	74,75	156,47	80,43	71,20	55,43	144,97
W10um103G_at	um11382	- conserved hypothetical protein	1,00	1,00E+00	-4,4	3,94E-04	2,7	8,35E-03	99,60	419,97	187,83	101,40	99,10	461,73
W25um055G_at	um03971	- related to E.coli thermoresistant gluconokinase	-1,11	9,91E-01	-2,9	2,57E-04	2,3	2,04E-03	188,90	520,83	230,53	171,20	184,07	523,10
C65um250G_at	um03049	- related to neutral amino acid permease	1,21	9,88E-01	-6,9	4,56E-06	7,9	3,38E-06	3,30	56,30	4,47	4,20	8,00	42,10
UG21-15g23-101e12_RC_	um00583	- conserved hypothetical protein	1,01	9,99E-01	-12,8	5,11E-07	7,1	6,86E-06	94,30	1670,23	177,20	95,50	131,50	1273,97
W51um284G_at	um05463	- hypothetical protein	-1,26	9,78E-01	-3,2	5,02E-05	2,8	1,67E-04	9,60	36,57	11,03	7,70	10,77	32,80
CLUSTER62_RC_at	um03620	- related to Regulatory protein alcR	1,03	9,98E-01	-2,9	1,98E-05	3,3	1,07E-05	104,75	906,47	253,97	108,10	308,70	854,90
C65um081G_at	um03221	- conserved hypothetical protein	-1,07	9,91E-01	-1,9	1,01E-05	2,1	4,10E-06	287,85	695,07	317,13	270,20	365,60	669,50
C65um074G_at	um10254	- conserved hypothetical protein	1,13	9,78E-01	-3,0	3,41E-06	3,5	1,53E-06	254,65	1013,70	390,77	285,90	331,17	1389,83
C70um192G_at	um00197	- related to TAD2 - tRNA-specific adenosine deamir	-1,02	9,98E-01	-4,0	5,51E-07	1,9	4,64E-04	81,90	309,20	175,03	80,00	76,63	326,87
W55um110G_at	um10467	- related to RAD16 - nucleotide excision repair prot	-1,15	9,78E-01	-2,0	2,99E-06	1,4	1,82E-03	198,15	373,57	260,30	173,05	183,27	361,00
W25um285G_at	um11434	- hypothetical protein	-1,17	9,91E-01	-3,7	2,81E-04	1,9	2,74E-02	22,05	87,80	44,40	20,00	23,77	87,03
C10um229G_at	um10268	- putative protein	-1,05	9,91E-01	-2,3	6,19E-06	1,6	7,27E-04	418,70	962,83	600,13	395,70	421,83	962,93
C20um146G_at	um05961	- probable alpha-methylacyl-coa racemase	1,37	9,78E-01	-4,1	5,21E-05	2,3	2,97E-03	41,05	251,43	107,23	59,20	60,73	250,93
C160um019G_at	um11241	- related to aldehyde dehydrogenase [NAD(P)]	1,27	7,29E-01	-2,2	8,44E-07	1,7	4,31E-05	174,35	461,83	272,43	222,35	212,97	451,80
W35um146G_at	um10864	- related to GNA1 - essential acetyltransferase	1,02	9,98E-01	-5,8	8,05E-07	3,5	2,12E-05	15,00	197,63	74,30	15,40	33,53	256,67
C94um144G_at	um04057	- related to dihydroflavonol reductase	-1,18	9,78E-01	-2,2	1,02E-04	2,0	4,22E-04	493,60	1119,50	613,80	433,50	496,80	1224,43
W40um248G_at	um03034	- conserved hypothetical protein	1,05	9,91E-01	-8,1	1,67E-09	2,6	9,30E-07	136,25	1644,63	701,17	143,80	202,33	1788,87
C85um220G_at	um10769	- probable potassium channel beta subunit protein	-1,47	9,78E-01	-4,3	5,45E-05	1,9	1,63E-02	400,35	2137,27	1124,77	314,25	498,37	2180,17
W21um227G_at***	um11662	- related to ECM4 - involved in cell wall biogenesis	-1,08	9,91E-01	-2,7	1,05E-06	2,1	1,77E-05	457,85	1728,20	936,73	425,45	649,40	1926,70
C60um177G_at	um06495	- putative protein	1,06	9,91E-01	-2,3	8,45E-06	2,0	6,46E-05	159,90	422,77	251,20	169,25	186,20	487,57
W90um013G_at	um03532	- hypothetical protein	1,11	9,78E-01	-5,6	1,41E-08	3,0	1,15E-06	14,15	107,27	32,77	15,85	18,27	97,97
W45um010G_at	um01270	- probable aminopeptidase P, cytoplasmic	1,01	9,99E-01	-2,9	4,97E-08	2,3	6,72E-07	171,00	597,23	271,37	171,90	207,63	612,90
W85um037G_at	um01090	- probable POT1 - acetyl-CoA C-acyltransferase, pe	-1,07	9,94E-01	-4,0	2,64E-06	3,5	8,04E-06	179,05	1760,80	562,70	167,50	446,17	1935,67
C100um112G_at	um04641	- probable PRC1 - carboxypeptidase y, serine-type	-1,23	9,78E-01	-4,3	7,46E-06	2,4	6,62E-04	394,65	1724,40	770,93	339,25	405,80	1805,70
C55um066G_at	um04187	- conserved hypothetical protein	-1,72	9,36E-01	-8,9	4,25E-06	3,0	1,19E-03	36,45	387,47	131,57	22,10	45,47	399,10
W75um193G_at	um00177	- conserved hypothetical protein	-1,11	9,91E-01	-6,0	4,28E-07	3,1	3,03E-05	166,05	1643,07	552,63	150,45	277,30	1684,80
W60um060G_at	um02118	- putative protein	-1,76	8,41E-01	-3,2	3,16E-04	2,1	8,97E-03	16,55	187,00	87,43	7,75	57,43	184,10
W30um057G_at	um06082	- related to NIPSNAP protein	-1,20	9,78E-01	-2,7	2,68E-05	1,9	7,90E-04	332,35	1453,77	757,90	284,75	548,80	1446,93
W175um086G_at	um06158	- related to glutaminase A	1,03	9,98E-01	-4,9	6,28E-05	2,4	5,55E-03	37,85	587,87	261,47	38,90	122,63	587,40
C25um178G_at	um11391	- hypothetical protein	-1,14	9,88E-01	-2,4	1,66E-04	1,9	1,64E-03	346,15	1552,77	873,30	310,00	669,20	1648,17
C42um003G_at	um11378	- hypothetical protein	-1,08	9,91E-01	-2,4	2,89E-05	2,4	3,74E-05	71,65	414,27	197,30	67,65	170,33	474,70
C35um117G_at	um03069	- probable acetyl-CoA synthetase	1,34	7,03E-01	-2,0	8,54E-06	1,9	1,84E-05	1308,35	4660,73	2489,67	1780,60	2300,47	4844,60
W30um240G_at	um03169	- probable CAR2 - ornithine aminotransferase	2,19	7,58E-01	-2,7	1,95E-03	5,1	6,64E-05	58,40	2508,17	552,63	145,60	929,27	2748,40
C40um209G_at	um00005	- probable benzoate 4-monooxygenase cytochrome	1,55	9,49E-01	-3,2	2,22E-04	3,7	1,31E-04	55,35	2998,70	932,67	88,40	969,37	3290,93
W75um036G_at	um02763	- conserved hypothetical protein	-1,01	9,98E-01	-1,9	4,40E-05	2,6	2,69E-06	1207,20	4776,87	2122,13	1193,10	2480,90	5457,80
W10um227G_at	um01466	- related to ACYL-COA DEHYDROGENASE, LONG-CI	1,48	9,49E-01	-2,4	7,04E-04	2,6	4,99E-04	172,75	1481,30	645,20	284,15	618,40	1655,67
C5um022G_C145um049G	um10026	- related to membrane protein, peroxisomal	-1,07	9,88E-01	-2,7	2,37E-07	3,1	9,77E-08	391,40	1880,50	726,33	366,55	701,43	2242,30
W60um103G_at	um01984	- probable ALCOHOL DEHYDROGENASE I - ADH1	1,12	9,78E-01	-5,7	6,30E-09	3,9	7,07E-08	12,15	5584,20	1585,47	13,85	980,57	6148,13
C95um165G_at	um00428	- conserved hypothetical protein	-1,18	9,91E-01	-4,7	6,56E-05	3,2	7,33E-04	34,50	580,10	192,00	31,40	122,63	610,70
W50um257G_at	um05757	- conserved hypothetical protein	-1,12	9,78E-01	-2,2	2,98E-05	2,7	5,93E-06	221,30	695,43	305,27	196,00	316,93	818,70
W30um268G_at	um04479	- related to 4-coumarate--CoA ligase 1	1,18	9,78E-01	-2,1	3,25E-05	3,0	1,37E-06	106,85	687,20	294,27	126,60	327,37	894,87
W75um209G_at	um00014	- related to 4-coumarate--CoA ligase 1 (fragment)	1,13	9,78E-01	-2,3	3,29E-06	2,7	9,54E-07	63,00	1204,83	523,37	70,90	523,90	1410,47
C110um281G_at	um10077	- probable alcohol dehydrogenase	-1,01	9,98E-01	-1,9	1,37E-05	2,3	1,99E-06	115,45	457,73	243,67	114,05	240,90	561,70
C75um003G_at	um01966	- related to Acyl-coenzyme A oxidase 1, peroxisom	1,23	9,78E-01	-3,6	6,91E-07	3,5	1,22E-06	7,30	594,30	199,53	9,25	165,03	693,93
W45um019G_at	um06400	- conserved hypothetical protein	-1,07	9,91E-01	-3,5	1,73E-07	7,6	4,82E-09	175,25	3107,37	497,30	162,90	878,77	3771,50
C65um098G_at	um00146	- conserved hypothetical protein	-1,02	9,98E-01	-2,9	3,29E-06	3,1	2,84E-06	37,55	335,60	117,37	36,55	113,93	367,53
C155um005G_at	um11191	- related to phenylacetyl-CoA ligase	1,02	9,98E-01	-3,9	3,98E-06	5,4	7,88E-07	50,65	831,43	186,30	53,35	211,93	1024,33
C95um018G_at	um11303	- hypothetical protein	-1,22	9,78E-01	-3,2	1,57E-06	3,4	1,42E-06	209,15	1404,83	469,60	174,75	441,63	1611,63
C145um093G_at	um00589	- related to GLO4 - glyoxalase II (hydroxyacylgluta	1,20	9,56E-01	-1,6	2,48E-04	2,2	8,84E-06	279,05	658,90	353,40	337,95	400,27	767,47
C46um166G_at	um00406	- conserved hypothetical protein	-1,07	9,91E-01	-2,0	2,69E-04	3,3	3,44E-06	74,20	529,37	220,07	69,10	264,07	726,23
W95um139G_at	um10240	- probable glutaryl-CoA dehydrogenase	1,27	9,35E-01	-1,7	4,45E-04	3,0	2,02E-06	197,15	692,47	294,43	251,95	399,40	876,70
W155um281G_at	um02223	- related to acid phosphatase	-1,13	9,91E-01	-4,1	8,79E-06	6,1	1,49E-06	4,95	27,87	5,17	4,40	6,13	36,60
W35um041G_at	um05390	- Npi5 - related to peroxisomal membrane protein	1,07	9,91E-01	-2,8	7,46E-06	4,3	4,64E-07	66,25	234,03	63,57	70,50	82,83	279,43
W155um003G_at	um01945	- probable SUC2 - invertase (sucrose hydrolyzing e	1,04	9,98E-01	-7,0	1,51E-07	4,8	1,56E-06	51,20	246,27	49,03	53,25	34,17	233,70
W125um129G_at***	um03720	- related to OAC1 - similarity to mitochondrial uncc	-1,05	9,94E-01	-2,9	7,47E-07	2,7	1,95E-06	548,30	1145,60	440,33	523,50	401,10	1172,30
W71um089G_at	um10819	- related to aminopeptidase c	1,14	9,49E-01	-3,3	7,03E-09	3,7	4,47E-09	243,35	567,13	153,57	277,65	173,03	571,03
C45um117G_at	um03071	- related to enoyl-CoA-hydratase	1,07	9,94E-01	-8,0	1,22E-07	5,6	9,54E-07	602,35	2402,67	472,27	653,30	302,43	2613,03
W50um088G_at	um10732	- related to dimeric dihydrodiol dehydrogenase	1,06	9,91E-01	-8,6	1,67E-09	6,2	4,47E-09	398,45	1632,70	268,73	421,00	189,93	1653,70
W90um049G_at	um10022	- conserved hypothetical protein	1,08	9,91E-01	-5,4	5,45E-08	5,1	9,77E-08	87,15	284,00	57,97	94,35	52,37	293,03
C30um078G_at	um03308	- probable Cytosol aminopeptidase	1,02	9,98E-01	-4,4	7,13E-09	4,4	9,33E-09	888,85	2300,53	594,20	901,45	522,30	2633,27
C10um237G_at	um03283	- hypothetical protein	1,02	9,98E-01	-2,3	9,30E-07	2,5	5,50E-07	634,15	1174,63	515,73	644,00	516,50	1279,03
W85um258G_at	um04399	- probable succinate-fumarate transporter (mitoch	1,07	9,94E-01	-4,2	4,47E-06	5,5	1,47E-06	162,60	1745,37	320,37	180,50	418,07	1778,53
C20um078G_at	um03310	- conserved hypothetical protein	-1,07	9,93E-01	-23,6	2,97E-09	22,2	4,12E-09	141,75	3378,30	126,70	132,90	142,70	2879,30
C106um003G_at	um11373	- conserved hypothetical protein	1,13	9,78E-01	-6,4	2,28E-08	5,5	7,54E-08	59,05	592,27	101,10	66,75	91,07	569,93
C80um195G_at	um01835	- related to carnitine acetyl transferase FacC	1,07	9,91E-01	-3,8	5,58E-07	3,3	2,24E-06	223,55	1070,63	285,87	243,80	278,80	956,77
C15um170G_at	um04999	- conserved hypothetical protein	-1,10	9,78E-01	-2,4	3,75E-06	2,2	1,46E-05	178,35	415,47	199,27	160,70	171,50	436,50
W140um222G_at	um01415	- hypothetical protein	-1,23	9,49E-01	-3,2	4,01E-07	2,7	1,90E-06	97,20	262,80	99,03	78,85	81,67	273,53
W90um120G_at	um03011	- conserved hypothetical protein	-1,20	9,78E-01	-2,5	3,61E-06	2,4	7,10E-06	153,35	325,70	138,03	128,20	129,53	333,70
C45um088G_at	um10731	- related to PEX19 - required for biogenesis of perc	-1,12	9,78E-01	-4,8	1,44E-07	3,6	1,27E-06	377,35	1184,37	341,87	337,30	244,33	1254,47
W50um235G_at	um10183	- related to SPS19 - peroxisomal 2,4-dienoyl-CoA r	-1,04	9,98E-01	-8,3	1,51E-08	6,2	7,73E-08	165,25	902,53	157,10	159,55	106,53	969,53
C30um191G_at***	um11350	- related to acetyl coenzyme A synthetase	-1,17	9,78E-01	-7,2	7,90E-08	6,6	1,66E-07	254,65	1239,53	189,17	219,45	170,27	1277,90
C45um037G_at	um01099	- probable short chain 3-hydroxyacyl-CoA dehydro	1,00	1,00E+00	-2,5	3,75E-06	3,8	1,95E-07	314,95	824,43	249,13	315,25	331,60	938,83
C37um257G_at	um05754	- probable electron transfer flavoprotein alpha chai	-1,04	9,91E-01	-1,6	7,10E-05	2,1	1,66E-06	1385,40	2426,30	1298,37	1338,70	1546,33	2702,40
C70um074G_at	um10252	- related to 3-oxoacyl-(acyl carrier protein) reducta	-1,13	9,78E-01	-3,3	3,77E-07	3,5	4,06E-07	452,80	2109,30	674,03	404,70	628,17	2328,43
C40um235G_at	um05149	- conserved hypothetical protein	-1,09	9,89E-01	-2,9	8,01E-07	2,7	2,13E-06	239,85	749,73	288,30	221,90	255,43	784,83
W100um028G_at	um00477	- related to Monocarboxylate transporter 1	-1,12	9,78E-01	-3,3	1,27E-06	3,7	8,46E-07	578,20	2026,40	555,13	519,35	622,07	2080,80
C55um013G_at	um03538	- related to aromatic amino acid aminotransferase	-1,13	9,78E-01	-6,6	7,16E-09	7,1	8,62E-09	216,30	2010,13	282,27	192,80	303,03	2017,03
W90um107G_at	um01049	- probable acyl-CoA dehydrogenase, medium-chair	-1,03	9,98E-01	-3,6	1,38E-08	3,2	4,48E-08	293,30	1088,57	371,70	285,45	302,27	1189,17
W250um074G_at	um01782	- related to peroxisomal membrane protein PMP47I	1,02	9,98E-01	-2,9	1,80E-06	4,0	2,40E-07	163,00	589,23	179,60	166,20	204,50	707,93
C165um054G_at	um11449	- related to Phenol 2-monooxygenase	-1,00	1,00E+00	-4,5	7,59E-06	5,8	2,65E-06	173,30	2357,20	478,57	174,65	541,20	2732,93
C105um191G_at	um11344	- conserved hypothetical protein	1,04	9,98E-01	-3,6	3,79E-07	4,8	8,00E-08	207,80	1359,00	336,30	215,50	382,03	1610,07
W115um155G_at	um11556	- probable enoyl-CoA hydratase precursor, mitocho	-1,00	1,00E+00	-10,0	1,44E-09	10,8	9,79E-10	312,05	2472,70	261,50	312,10	245,43	2827,00
W85um098G_at	um10038	- probable multifunctional beta-oxidation protein	-1,08	9,78E-01	-3,1	8,60E-08	3,5	5,81E-08	488,80	1827,47	598,97	455,40	588,50	2105,47
C110um210G_at	um11932	- probable methylcrotonyl-CoA carboxylase beta ch	-1,54	8,26E-01	-7,4	1,06E-07	5,7	5,72E-07	70,70	2243,97	428,00	47,85	305,67	2416,13
C107um175G_at	um02715	- probable POT1 - acetyl-CoA C-acyltransferase, pe	-1,06	9,91E-01	-2,5	2,91E-07	2,7	1,88E-07	1121,20	3084,17	1242,10	1061,05	1236,30	3339,73
C90um145G_at	um04382	- probable methylcrotonoyl-CoA carboxylase biotin	-1,09	9,91E-01	-8,9	4,31E-09	7,8	7,18E-09	145,55	3276,63	465,77	134,95	369,87	3619,57
C155um019G_at	um06422	- conserved hypothetical protein	-1,35	9,78E-01	-8,7	7,18E-07	7,0	2,63E-06	155,90	2364,80	393,93	128,10	271,90	2744,57
C60um254G_at	um04833	- probable isovaleryl-CoA dehydrogenase	-1,04	9,92E-01	-7,8	2,96E-09	7,6	4,12E-09	191,15	3591,93	535,70	182,90	462,20	4057,30
W65um088G_at	um10735	- probable 2-oxoisovalerate dehydrogenase alpha s	-1,79	9,78E-01	-11,7	4,15E-05	9,6	1,06E-04	44,35	1950,27	224,40	35,90	168,47	2151,80
C123um126G_at	um02189	- probable 3-hydroxyisobutyrate dehydrogenase, n	-1,05	9,91E-01	-6,5	7,13E-09	6,3	1,02E-08	287,05	2634,87	458,43	276,15	405,30	2901,07
C95um098G_at	um00154	- related to Para-nitrobenzyl esterase	-1,14	9,91E-01	-4,7	6,69E-06	5,0	6,24E-06	23,30	179,20	42,40	19,30	38,10	214,90
W30um081G_at	um03229	- conserved hypothetical protein	-1,21	9,78E-01	-3,5	1,06E-06	4,0	7,10E-07	384,10	1574,83	470,03	316,00	442,67	1870,43
W90um284G_at	um05450	- related to Long-chain-fatty-acid--CoA ligase 6	-1,07	9,91E-01	-3,7	5,45E-08	5,2	1,02E-08	347,10	2061,87	460,37	326,15	557,17	2386,30
W120um178G_at	um02001	- related to hydroxymethylglutaryl-CoA lyase	-1,11	9,78E-01	-6,3	1,41E-08	6,5	1,43E-08	105,65	1152,67	187,23	94,80	181,97	1226,33
C85um060G_at	um02114	- hypothetical protein	-1,11	9,78E-01	-2,5	1,03E-06	2,8	4,27E-07	316,25	993,00	382,87	285,30	401,03	1081,33
W60um134G_at	um05104	- putative protein	-1,85	8,90E-01	-41,6	5,96E-08	12,8	2,56E-06	35,00	1875,60	164,90	20,55	44,00	2048,43
C45um133G_at	um05131	- probable Acetoacetyl-CoA synthetase	-1,09	9,78E-01	-6,9	1,97E-09	8,3	1,22E-09	192,35	1669,20	226,23	176,70	242,57	1892,17
W25um140G_at	um10665	- related to acyl-CoA dehydrogenase	-1,36	9,49E-01	-17,8	5,32E-09	15,7	9,40E-09	130,50	1087,63	79,67	101,25	59,73	1260,87
W10um171G_at	um00045	- related to quinone reductase	-1,54	8,51E-01	-11,9	7,42E-08	12,0	9,89E-08	165,30	1271,60	122,87	112,15	105,63	1462,13
C75um228G_at	um10273	- related to DELTA3,5-DELTA2,4-DIENOYL-COA ISC	-1,28	9,16E-01	-8,4	5,32E-09	12,1	4,12E-09	175,75	1512,73	148,13	139,55	178,93	1797,83
C30um157G_at	um02182	- probable NADPH-dependent beta-ketoacyl reduct	1,04	9,94E-01	-5,3	2,27E-08	6,9	9,33E-09	222,25	1439,13	251,00	232,15	269,53	1731,53
C46um133G_at	um05131	- probable Acetoacetyl-CoA synthetase	1,00	1,00E+00	-8,8	4,31E-09	8,9	4,12E-09	156,70	1584,03	184,43	156,50	178,33	1644,67
W110um003G_at	um01959	- hypothetical protein	1,33	9,49E-01	-7,1	6,76E-08	7,5	7,73E-08	11,50	89,20	11,03	15,80	11,77	89,67
W180um119G_at	um11363	- related to RIB5 - riboflavin synthase, alpha chain	-1,08	9,78E-01	-3,1	8,40E-08	3,3	7,73E-08	325,20	927,10	302,30	301,40	301,60	998,47
W15um119G_at	um01747	- related to Estradiol 17 beta-dehydrogenase 4	-1,14	9,78E-01	-9,0	4,85E-09	7,9	9,33E-09	100,20	1855,37	261,23	87,30	203,97	2075,33
C15um103G_at	um01992	- related to amidohydrolase AmhX	1,07	9,91E-01	-5,1	1,55E-08	4,9	2,89E-08	666,65	3443,50	750,00	710,25	674,90	3650,60
C100um278G_at	um04787	- related to GLY1 - L-threonine aldolase, low-specif	1,24	9,56E-01	-4,8	4,94E-08	4,8	7,64E-08	214,95	1183,93	264,57	266,55	246,03	1262,63
C95um129G_at	um03728	- conserved hypothetical protein	-1,03	9,98E-01	-5,6	1,82E-07	7,3	7,73E-08	37,60	3155,90	472,33	35,80	565,47	3413,37
W50um103G_at	um01986	- probable sterol carrier protein	-1,04	9,98E-01	-5,0	1,03E-07	6,6	4,48E-08	60,90	2014,90	322,43	59,45	399,27	2101,67
W10um036G_at	um10600	- putative protein	-1,11	9,78E-01	-3,7	1,51E-07	3,2	6,31E-07	242,85	1086,40	342,23	213,95	291,27	1105,87
C60um236G_at	um10402	- related to lipoamide acyltransferase component o	-1,00	1,00E+00	-6,6	4,31E-09	5,2	1,02E-08	84,85	2571,33	506,83	84,45	393,37	2617,03
C80um166G_at	um11610	- related to novobiocin biosynthesis protein novR	1,13	9,78E-01	-5,2	5,44E-08	3,9	4,00E-07	154,90	2539,50	685,47	176,45	485,43	2683,20
C125um060G_at	um02105	- probable 3-hydroxybutyryl-CoA dehydrogenase	-1,55	9,78E-01	-14,8	8,80E-07	12,0	2,65E-06	78,65	1863,60	159,80	55,75	134,77	1928,40
C150um171G_at	um00078	- Pal1 - Phenylalanine ammonia-lyase	-1,38	9,49E-01	-17,2	7,16E-09	15,4	1,31E-08	6,95	1459,77	91,40	4,65	85,33	1423,93
C45um086G_at	um06185	- probable acyl-CoA dehydrogenase short-branchec	-1,28	8,09E-01	-5,4	5,32E-09	4,2	2,20E-08	413,25	2816,10	605,43	321,50	523,13	2568,30
C65um036G_at	um10596	- probable aldehyde dehydrogenase	-1,68	9,78E-01	-18,3	8,54E-06	5,2	9,60E-04	298,85	2028,70	431,07	229,40	113,00	2079,03
W25um022G_at	um00115	- probable BAT2 - branched-chain-amino-acid tran:	-1,01	9,98E-01	-2,1	1,02E-05	2,0	1,96E-05	1178,70	2516,57	1401,40	1169,55	1220,40	2827,73
C15um122G_at	um01699	- conserved hypothetical protein	-1,15	9,78E-01	-2,9	8,79E-06	2,6	2,52E-05	143,65	385,90	165,80	130,00	133,37	435,93
C85um178G_at	um02010	- related to family II 2-keto-3-deoxy-D-arabino-he	-1,07	9,91E-01	-2,6	7,73E-06	2,6	8,92E-06	644,85	1670,67	706,70	608,55	644,47	1855,40
W65um267G_at	um06138	- probable PTR2 - Di- and tripeptide permease	-1,07	9,91E-01	-5,2	1,56E-07	3,5	2,69E-06	637,60	2287,50	722,83	606,70	443,90	2524,90
C70um096G_at	um03947	- related to carboxypeptidase	-1,18	9,78E-01	-4,9	2,87E-07	3,9	1,53E-06	93,35	304,83	91,57	81,20	62,70	359,83
W65um286G_at	um11436	- probable electron transfer flavoprotein beta chain	1,05	9,91E-01	-2,5	4,67E-07	3,0	1,52E-07	1554,45	3464,43	1304,23	1637,35	1377,47	3871,83
C85um078G_at	um03298	- probable ERG10 - acetyl-CoA C-acetyltransferase	1,07	9,91E-01	-4,4	2,27E-08	7,2	4,12E-09	313,15	1338,47	243,17	334,10	300,30	1765,43
W95um148G_at	um00789	- probable carnitine O-acetyltransferase, mitochon	1,24	9,78E-01	-3,7	1,28E-06	7,8	3,85E-08	379,70	1884,33	284,73	471,70	510,37	2221,60
W170um056G_at	um01858	- conserved hypothetical protein	1,19	9,78E-01	-5,3	3,09E-08	3,8	2,86E-07	82,75	645,00	164,47	98,70	121,50	616,17
C15um171G_at	um00046	- related to flavin oxidoreductase	-1,06	9,91E-01	-3,0	3,07E-07	1,9	3,53E-05	166,95	459,17	224,67	158,80	151,93	433,17
W10um251G_at	um01232	- related to LAP3 - member of the GAL regulon	-1,29	9,44E-01	-6,3	3,44E-08	3,1	3,19E-06	218,90	653,50	216,77	171,15	102,77	673,33
W20um090G_at	um10623	- related to Tuberin	-1,05	9,91E-01	-2,2	9,68E-06	2,1	2,13E-05	238,50	457,90	231,13	227,40	212,57	476,10
C36um245G_at	um05923	- related to 2-deoxy-D-gluconate 3-dehydrogenase	-1,07	9,98E-01	-3,1	2,00E-04	3,2	2,33E-04	171,00	1958,77	696,30	159,05	608,53	2144,23
C45um095G_at	um01072	- conserved hypothetical protein	1,05	9,98E-01	-2,1	1,53E-04	2,4	6,29E-05	269,35	1642,97	758,83	282,60	751,77	1842,80
W165um003G_at	um01943	- related to alpha-glucosidase	-1,42	9,78E-01	-4,3	4,00E-04	3,3	2,03E-03	25,70	275,67	91,60	14,95	62,33	308,90
W5um075G_at	um11596	- related to CSR1 - phosphatidylinositol transfer pr	-1,10	9,91E-01	-2,5	1,12E-04	2,2	3,54E-04	333,55	1117,93	591,63	303,00	438,43	1353,20
W7um082G_s_at	um04617	- hypothetical protein	1,06	9,91E-01	-1,9	4,76E-05	2,6	3,44E-06	57,35	140,27	57,47	61,00	71,00	148,30
C20um278G_at	um04769	- hypothetical protein	1,03	9,98E-01	-4,6	7,40E-07	4,7	8,91E-07	193,60	627,97	135,47	198,70	133,53	650,57
W25um069G_at	um05032	- related to NIT3 - nitrilase	-1,02	9,98E-01	-2,3	1,95E-05	2,5	1,30E-05	472,85	889,10	389,30	461,70	388,40	958,77
W160um003G_at	um01944	- related to allantoate permease	-1,30	9,91E-01	-8,6	5,77E-04	8,6	7,23E-04	12,35	151,90	19,90	9,40	21,23	164,90
W145um056G_at	um01863	- related to Cytochrome P450	1,19	9,91E-01	-4,2	2,94E-04	4,9	1,71E-04	5,10	36,30	7,83	6,35	7,60	38,70
W57um276G_at***	um11592	- related to PYC2 - pyruvate carboxylase 2	1,03	9,98E-01	-14,6	1,82E-07	15,2	2,25E-07	4,25	112,60	7,63	4,50	6,37	131,10
C15um083G_at	um03158	- related to probable enoyl-CoA hydratase	1,06	9,98E-01	-11,8	4,64E-06	11,5	7,03E-06	34,40	383,43	40,53	36,65	33,27	480,20
W60um095G_at	um11275	- related to D-lactate dehydrogenase (cytochrome)	-1,06	9,98E-01	-4,1	7,57E-06	3,3	3,79E-05	96,10	395,10	141,73	92,90	94,97	470,73
C13um226G_at***	um04324	- probable POX1 - acyl-CoA oxidase	1,06	9,91E-01	-2,4	1,61E-06	2,2	5,16E-06	408,80	1323,13	613,87	432,30	541,00	1379,23

C60um171G_at	um00059	- related to 3-mercaptopyruvate sulfurtransferase	1,05	9,98E-01	-3,0	1,76E-05	2,4	1,37E-04	238,30	779,20	355,50	256,50	259,33	848,23
C135um003G_at	um01950	- conserved hypothetical protein	1,20	9,91E-01	-10,6	3,29E-06	6,3	3,66E-05	16,85	386,50	70,53	20,25	34,60	413,87
C140um209G_at	um00029	- probable myo-inositol oxygenase	-1,99	9,37E-01	-11,8	1,19E-05	5,0	4,86E-04	30,85	1601,40	356,47	15,65	139,83	1729,40
C55um022G_at	um00123	- related to L-lactate dehydrogenase (cytochrome l	1,49	9,78E-01	-5,8	1,30E-04	4,4	6,50E-04	62,05	1119,00	290,30	101,75	195,13	1230,30
C85um074G_at***	um10251	- conserved hypothetical protein	1,12	9,89E-01	-2,9	1,01E-05	3,4	4,01E-06	58,45	290,63	91,47	65,25	97,87	314,50
C95um281G_at	um02236	- putative protein	1,09	9,94E-01	-5,3	4,57E-06	4,2	2,16E-05	8,30	197,83	47,93	9,40	35,70	207,07
W35um047G_at	um03596	- probable PEX7 - peroxisomal import protein - per	-1,12	9,78E-01	-2,3	3,40E-05	2,2	7,63E-05	128,60	299,43	151,63	114,40	128,60	329,90
C200um003G_at	um10454	- related to 4-coumarate-CoA ligase	-1,47	9,78E-01	-11,0	4,63E-07	5,3	1,44E-05	233,30	1017,33	229,20	162,65	89,67	1192,33
C40um137G_at	um02610	- conserved hypothetical protein	1,02	9,98E-01	-6,5	2,17E-06	7,6	1,60E-06	78,20	400,80	63,13	81,25	59,83	482,70
W100um146G_at	um05936	- conserved hypothetical protein	-1,67	9,78E-01	-6,6	4,98E-05	6,6	6,76E-05	88,40	609,47	114,47	56,85	91,07	769,87
C40um228G_at	um01923	- conserved hypothetical protein	-1,10	9,91E-01	-3,1	8,36E-05	4,2	1,32E-05	49,95	240,43	66,80	45,15	75,40	294,63
C206um003G_at	um01935	- probable methylglutaconyl-coa hydratase, mitoch	1,03	9,98E-01	-5,0	1,92E-06	4,5	4,26E-06	43,35	270,13	65,23	45,30	52,43	305,27
C25um217G_at	um04504	- related to CYB2 - lactate dehydrogenase cytochrc	1,18	9,78E-01	-5,0	1,23E-06	5,7	8,91E-07	82,75	476,77	102,23	97,45	93,50	590,63
W120um144G_at	um04063	- related to soluble epoxide hydrolase	1,23	9,78E-01	-4,8	9,43E-06	5,8	4,41E-06	89,65	555,80	113,77	111,45	111,30	681,80
W45um208G_at	um10088	- related to Acetoacetyl-CoA synthetase	-1,07	9,98E-01	-12,5	2,07E-06	21,5	5,29E-07	34,50	454,33	26,07	33,00	33,47	593,07
W16um071G_at	um10996	- conserved hypothetical protein	1,03	9,98E-01	-8,8	1,98E-05	10,2	1,52E-05	34,10	411,60	52,90	33,90	46,97	546,33
W110um228G_at	um01907	- conserved hypothetical protein	-1,00	1,00E+00	-7,4	6,36E-07	11,4	1,60E-07	41,15	675,93	82,90	41,10	85,57	971,80
W30um126G_at	um02208	- probable acyl-CoA oxidase	-1,20	9,78E-01	-6,1	5,58E-07	4,7	3,19E-06	411,45	2162,97	541,57	346,60	355,77	2503,17
W62um108G_at	um01171	- related to 4-coumarate-CoA ligase	-1,07	9,91E-01	-7,4	5,96E-08	7,7	7,73E-08	114,00	699,83	106,00	107,75	91,87	832,63
W25um229G_at	um01892	- probable isocitrate lyase	-1,04	9,98E-01	-5,5	4,01E-08	7,0	1,71E-08	232,40	1209,67	201,03	222,90	214,87	1423,67
W40um012G_at	um11466	- related to enoyl-CoA hydratase	-1,12	9,91E-01	-12,1	5,45E-08	11,2	9,77E-08	101,55	1102,30	113,43	92,35	89,70	1296,23
W10um013G_at	um03548	- related to endo-polygalacturonase 6	-1,16	9,78E-01	-5,5	1,21E-06	5,3	2,19E-06	192,60	890,07	186,97	166,25	160,13	989,37
W100um281G_at	um02235	- related to AMP-binding protein	1,08	9,91E-01	-20,9	4,78E-09	18,7	7,18E-09	36,35	1460,20	91,90	39,25	68,00	1746,10
C69um189G_at	um11164	- conserved hypothetical protein	-1,00	1,00E+00	-3,5	2,33E-06	4,1	1,27E-06	203,55	891,13	240,90	199,40	252,00	986,27
C55um049G_at	um00092	- related to levodione reductase	-1,02	9,98E-01	-3,2	7,34E-07	5,2	5,28E-08	327,60	1184,60	282,77	322,25	364,13	1482,80
W110um010G_at	um01257	- related to peroxisomal ATP carrier	1,13	9,78E-01	-3,6	2,70E-06	7,0	8,64E-08	155,35	993,50	169,87	176,65	272,40	1208,47
W35um081G_at	um03228	- related to 4-coumarate--CoA ligase 1	-1,50	9,10E-01	-4,9	4,03E-06	8,8	3,72E-07	37,85	318,70	49,47	25,10	63,10	438,47
W70um081G_at	um03220	- conserved hypothetical protein	-1,01	9,98E-01	-2,9	3,43E-06	4,9	1,44E-07	171,05	908,20	233,33	169,75	309,27	1148,13
W35um066G_at	um11122	- probable PEX1 - peroxisomal assembly protein - p	-1,05	9,94E-01	-2,4	2,11E-05	2,7	1,00E-05	85,75	199,10	71,50	81,20	80,80	198,07
W85um188G_at	um10691	- related to Long-chain-fatty-acid--CoA ligase	1,17	9,91E-01	-4,1	3,15E-05	4,1	4,15E-05	34,20	168,27	39,90	39,70	40,00	169,13
C31um203G_at	um04982	- probable LEU5 - mitochondrial coenzyme A transp	1,12	9,91E-01	-3,3	5,01E-05	3,7	3,18E-05	110,05	442,27	132,53	124,90	130,93	510,27
W70um039G_at	um01149	- Glo3 - Glyoxaloxidase 3	1,23	9,78E-01	-2,9	3,09E-06	1,8	5,39E-04	43,80	288,80	178,80	54,10	99,87	316,33
W35um190G_at	um00334	- probable peroxisomal acyl-coenzyme A thioester	1,32	9,20E-01	-2,1	1,15E-04	2,2	1,03E-04	105,65	772,27	445,33	140,45	364,77	981,33
W45um228G_at	um01922	- conserved hypothetical protein	1,39	9,44E-01	-2,0	8,43E-04	2,7	8,78E-05	18,05	108,33	42,80	25,35	52,20	118,33
C40um035G_at	um11207	- related to PNP1 - purine-nucleoside phosphorylas	-1,08	9,91E-01	-2,5	1,14E-05	2,2	4,35E-05	163,10	804,60	358,03	152,15	321,43	799,63
W80um225G_at	um02142	- related to muconate cycloisomerase	-1,13	9,88E-01	-2,1	3,68E-04	1,8	2,47E-03	112,05	370,50	208,37	100,10	171,47	382,60
C29um022G_at	um00116	- related to nicotinamide mononucleotide permease	-1,23	9,78E-01	-2,5	8,67E-05	1,7	4,69E-03	49,65	258,87	137,50	38,95	102,67	238,87
C165um119G_at	um01710	- related to N-carbamoyl-L-amino acid hydrolase	1,06	9,94E-01	-2,4	4,05E-05	1,9	6,46E-04	130,20	601,13	309,20	140,15	245,83	592,57
C5um198G_at	um06344	- probable 2-methylcitrate dehydratase	-1,01	1,00E+00	-1,5	1,92E-02	2,0	7,65E-04	1855,45	3899,50	2185,50	1929,55	2602,03	4368,77
W155um054G_at	um11451	- related to Probable 26S proteasome non-ATPase	-1,31	8,94E-01	-1,4	1,11E-02	2,2	6,28E-05	183,10	357,13	191,37	140,95	246,73	417,20
W60um049G_at	um10021	- related to uracil phosphoribosyltransferase	1,05	9,91E-01	-1,4	1,12E-02	2,0	3,65E-05	177,90	334,53	197,37	188,50	246,20	401,17
W75um153G_at	um02667	- probable Succinyl-CoA:3-ketoacid-coenzyme A tr	1,10	9,91E-01	-1,9	9,92E-03	3,0	2,15E-04	328,95	1108,67	443,03	363,45	606,83	1300,17
W245um074G_at	um01783	- related to Inosine-uridine preferring nucleoside h	1,15	9,78E-01	-1,5	5,94E-03	2,2	5,58E-05	185,60	411,23	198,10	212,75	275,97	434,37
W50um079G_at	um11958	- related to MLS1 - malate synthase 1	1,28	9,56E-01	-1,5	1,09E-02	3,2	3,26E-06	918,80	2771,87	925,00	1205,35	1889,57	2992,47
C30um080G_at	um03246	- related to versicolorin b synthase	-1,03	9,98E-01	-2,7	3,31E-04	2,0	4,82E-03	286,35	1526,33	904,47	279,30	579,60	1840,93
W143um119G_at	um11364	- conserved hypothetical protein	1,04	9,98E-01	-2,2	2,78E-04	1,6	9,40E-03	63,05	137,97	89,67	65,60	63,13	146,93
W102um257G_at	um11582	- conserved hypothetical protein	1,13	9,91E-01	-6,4	2,23E-05	2,7	3,22E-03	8,05	45,07	12,03	9,25	6,17	37,60
W50um023G_at	um10330	- related to AVT3 - Vacuolar transporter, involved i	1,07	9,91E-01	-1,8	4,16E-05	2,3	1,95E-06	450,45	826,37	408,60	482,25	468,40	945,40
W84um003G_at	um01964	- related to multidrug resistance proteins	-1,20	9,78E-01	-1,9	7,79E-03	2,5	7,90E-04	64,45	171,23	75,70	56,45	91,13	193,23
W10um213G_at	um03664	- conserved hypothetical protein	1,35	9,78E-01	-4,7	2,51E-04	8,4	2,64E-05	11,75	3303,23	426,63	16,30	706,20	3159,10
W70um097G_at	um11513	- conserved hypothetical protein	-1,35	9,78E-01	-2,5	1,56E-03	4,9	3,03E-05	35,05	309,57	73,67	25,55	123,03	344,13
C70um175G_at	um02720	- conserved hypothetical protein	-1,07	9,91E-01	-2,3	9,77E-06	1,9	1,50E-04	312,75	674,77	360,93	291,80	287,10	688,90
W34um201G_at	um11255	- putative protein	-1,13	9,78E-01	-2,4	3,72E-05	1,8	8,39E-04	58,95	268,97	138,57	52,45	110,17	257,57
W90um276G_at	um06012	- probable general amino acid permease	-1,20	9,78E-01	-7,2	7,53E-07	8,4	5,78E-07	68,40	755,27	67,90	57,60	104,20	576,70
C75um191G_at	um11348	- conserved hypothetical protein	-1,08	9,98E-01	-6,8	2,55E-04	4,2	2,49E-03	7,85	88,30	20,13	7,35	13,13	82,40
W60um156G_at	um04268	- probable saccharopine dehydrogenase (NAD, L-ly	-1,16	9,78E-01	-2,5	1,19E-04	2,1	5,62E-04	1169,60	2707,23	1166,70	1012,90	1100,70	2478,73
W85um165G_at	um00430	- probable GCV1 - glycine decarboxylase, subunit T	1,07	9,91E-01	-2,3	2,07E-05	2,1	6,35E-05	620,60	1033,40	507,77	668,30	450,17	1080,67
C5um096G_at	um03935	- related to fructosyl amino acid oxidase	1,00	1,00E+00	-4,8	1,04E-05	5,5	7,10E-06	367,10	1029,03	171,90	367,75	216,23	917,53
W65um064G_at	um10928	- hypothetical protein	-1,06	9,91E-01	-2,4	2,52E-05	2,1	1,73E-04	88,00	148,23	65,53	82,85	60,13	137,27
W45um057G_at	um06085	- conserved hypothetical protein	1,26	9,78E-01	-2,9	5,64E-04	1,4	2,09E-01	45,85	282,00	190,90	60,40	97,80	266,73
W15um036G_at	um02778	- related to GCY1 - galactose-induced protein of al	-1,03	9,98E-01	-2,2	1,64E-04	1,4	3,02E-02	641,50	2255,40	1455,17	623,35	1055,43	2094,67
W140um132G_at	um05170	- probable formate dehydrogenase	1,12	9,89E-01	-2,4	8,17E-05	2,0	6,11E-04	6,50	1188,17	768,93	7,50	504,33	1510,93
CLUSTER42_RC_at	um05984	- probable glutamate dehydrogenase, NAD(+)-spe	-1,03	9,98E-01	-2,3	1,23E-05	1,6	2,04E-03	1179,10	3597,30	2584,40	1151,85	1579,03	4003,87
W25um089G_at	um10815	- conserved hypothetical protein	-1,10	9,94E-01	-2,5	7,08E-04	1,3	2,73E-01	195,45	2836,70	2208,77	179,55	1176,63	2786,93
W5um166G_at	um10104	- probable GCY1 - galactose-induced protein of ald	-1,25	9,78E-01	-2,4	1,87E-04	1,2	2,41E-01	543,80	3174,97	2835,47	436,55	1359,57	3478,00
C5um103G_at	um01994	- conserved hypothetical protein	-1,25	9,91E-01	-3,6	7,55E-04	1,9	4,39E-02	245,60	944,43	528,57	208,60	271,97	949,10
W125um144G_at	um04064	- related to Glucoamylase precursor	-1,11	9,98E-01	-26,1	6,73E-06	2,7	3,08E-02	6,85	277,13	125,60	6,10	10,03	270,87
C40um196G_at	um05084	- related to lignostilbene alphabeta-dioxygenase I	1,18	9,91E-01	-4,7	1,73E-04	1,7	1,02E-01	19,40	222,80	132,03	21,00	47,03	209,23
C95um157G_at	um02169	- related to aquaporin 3	1,11	9,94E-01	-4,2	5,62E-05	1,9	1,53E-02	117,70	2630,33	1296,07	131,60	632,67	2320,50
C102um055G_at	um03990	- related to 2-(R)-hydroxypropyl-CoM dehydrogena	1,20	9,78E-01	-2,7	8,09E-06	1,4	1,86E-02	32,90	202,60	125,03	39,85	75,63	175,20
C30um201G_at	um11256	- related to D-arabinitol 2-dehydrogenase	1,32	9,02E-01	-2,9	4,64E-06	1,8	6,60E-04	70,35	2417,17	1314,87	93,95	850,63	2360,50
W20um228G_at	um01928	- putative protein	-1,25	9,78E-01	-2,9	8,90E-06	1,4	2,34E-02	19,75	201,03	134,73	15,65	70,93	193,80
CLUSTER21_RC_at	um03398	- related to transesterase	1,09	9,78E-01	-2,5	4,25E-07	1,5	4,88E-04	41,45	3996,03	2760,33	45,45	1577,53	4164,07
W90um211G_at	um04562	- probable aspartate aminotransferase, cytoplasmi	1,00	9,99E-01	-2,2	4,01E-07	1,3	1,64E-03	895,65	2440,10	1743,27	899,95	1103,00	2340,83
C85um097G_at	um11514	- probable HXT15 - strong similarity to Hxt17p and	1,06	9,91E-01	-3,9	2,10E-07	1,5	2,54E-03	113,25	2269,27	1446,83	120,20	588,37	2251,53
C5um216G_at	um06020	- conserved hypothetical protein	-1,05	9,97E-01	-2,2	3,99E-05	1,5	9,84E-03	133,45	503,03	339,93	129,75	224,67	497,03
W160um175G_at	um02704	- related to allantoate permease	1,17	9,78E-01	-3,0	5,19E-05	2,0	2,07E-03	53,30	1193,67	527,93	64,20	402,37	1065,67
W60um066G_at	um04186	- probable general amino acid permease	-1,13	9,78E-01	-2,4	3,05E-06	2,0	3,67E-05	107,15	995,50	508,30	94,95	415,63	995,37
C220um074G_at	um01788	- related to deacetylase	-1,27	9,78E-01	-4,9	7,44E-06	1,7	2,86E-02	25,40	1056,33	580,50	20,20	214,87	976,87
C15um056G_at	um01887	- hypothetical protein	-1,04	9,98E-01	-2,9	1,07E-06	1,4	1,75E-02	55,25	148,20	102,27	53,25	50,50	138,10
W170um074G_at	um01799	- putative protein	-1,04	9,94E-01	-2,9	8,60E-08	1,3	1,02E-02	184,70	643,33	529,83	178,10	218,10	681,57
C50um021G_at	um03103	- related to ribose-5-phosphate isomerase	-1,25	8,08E-01	-2,2	1,15E-06	1,2	4,50E-02	851,90	1805,63	1461,57	678,40	834,73	1750,60
W50um126G_at	um02204	- related to beta-galactosidase	-1,08	9,98E-01	-9,3	1,21E-06	1,6	6,72E-02	41,45	1713,33	1107,80	41,25	183,30	1767,53
W85um175G_at	um11720	- related to Cystathionine beta-lyase	-1,17	9,78E-01	-3,1	6,24E-06	1,7	3,40E-03	273,40	1652,60	1060,00	242,75	526,83	1787,00
W100um056G_at	um01870	- related to glutathione-S-transferase	1,05	9,91E-01	-2,1	4,14E-06	1,5	6,74E-04	118,00	289,70	196,23	124,15	139,77	293,27
C31um005G_at	um05845	- conserved hypothetical protein	-1,19	9,72E-01	-2,1	9,65E-06	1,4	6,20E-03	126,65	201,93	136,40	106,40	95,90	189,90
W15um158G_at	um01773	- conserved hypothetical protein	1,45	8,33E-01	-4,2	7,40E-07	1,6	4,90E-03	153,35	571,40	356,60	222,00	133,63	579,50
C75um165G_at	um00432	- probable proline iminopeptidase	-1,22	9,78E-01	-2,2	1,17E-04	1,2	2,33E-01	1319,60	1819,83	1592,33	1091,15	841,87	1900,60
W70um114G_at	um05644	- related to alcohol dehydrogenase	-1,22	9,78E-01	-2,2	1,10E-04	1,2	1,54E-01	1019,35	1795,67	1586,50	845,05	834,60	1952,90
C155um119G_at	um01712	- conserved hypothetical protein	-1,10	9,78E-01	-2,2	5,71E-06	1,4	4,66E-03	754,30	1055,13	797,40	688,50	480,10	1109,30
C25um158G_at	um01771	- conserved hypothetical protein	-1,25	9,36E-01	-2,2	1,39E-05	1,2	1,96E-01	509,05	688,60	564,07	415,85	311,07	659,10
C15um165G_at	um00446	- probable beta-glucosidase	-1,05	9,98E-01	-4,1	2,34E-06	1,2	2,03E-01	60,35	123,00	91,57	56,80	29,33	112,50
C115um021G_at	um03116	- conserved hypothetical protein	-1,69	7,06E-01	-9,4	6,41E-08	1,3	1,92E-01	578,50	1373,57	1025,37	352,05	147,07	1303,43
C90um022G_at	um00131	- related to NADPH quinone oxidoreductase homolo	-1,15	9,78E-01	-3,9	8,54E-07	1,5	1,23E-02	376,85	858,07	557,63	327,55	218,90	823,83
W35um241G_at	um06236	- probable RIB3 - 3,4-dihydroxy-2-butanone 4-pho	-1,39	4,18E-01	-2,3	8,96E-07	1,3	1,96E-02	505,90	658,47	402,90	363,95	281,70	508,23
C105um086G_at	um11219	- related to TLG2 - member of the syntaxin family	-1,43	8,33E-01	-2,3	9,42E-05	1,2	1,96E-01	257,80	416,60	267,93	180,80	182,87	325,63
W130um086G_at	um06167	- probable PMI40 - mannose-6-phosphate isomera	-1,50	3,79E-01	-2,2	5,57E-06	1,3	1,41E-02	676,30	1160,77	648,53	453,60	517,33	861,40
W80um076G_at	um03344	- conserved hypothetical protein	-1,36	9,03E-01	-2,2	1,73E-04	1,4	3,12E-02	71,35	91,17	60,50	52,85	41,70	85,40
C5um086G_C67um244G_	um06194	- conserved hypothetical protein	-1,24	9,44E-01	-2,4	3,67E-06	1,3	4,04E-02	687,95	947,13	641,00	555,20	388,53	822,90
W50um024G_at	um01518	- putative protein	-1,17	9,78E-01	-3,1	6,92E-06	1,8	1,08E-03	53,35	68,57	36,30	45,55	21,70	68,23
W85um066G_at	um04181	- conserved hypothetical protein	-1,05	9,98E-01	-5,6	1,66E-05	2,1	8,15E-03	398,05	628,17	304,07	378,30	108,10	687,80
C110um056G_at	um01868	- related to GIT1 - Glycerophosphoinositol transpor	-1,17	9,78E-01	-2,1	1,77E-04	1,3	7,06E-02	272,45	342,37	249,90	233,80	159,67	337,10
W145um099G_at	um05892	- related to NAD-dependent histone deacetylase	-1,44	9,78E-01	-3,8	2,19E-04	1,7	5,49E-02	33,90	45,63	24,73	23,30	12,53	43,27
W110um145G_at	um04378	- related to phenylacetaldehyde dehydrogenase	-1,05	9,98E-01	-2,2	6,77E-05	1,8	7,65E-04	68,10	106,80	56,10	65,30	48,87	102,27
C50um146G_at	um05952	- hypothetical protein	1,27	9,78E-01	-2,6	2,02E-04	1,6	2,33E-02	121,45	210,13	123,20	160,00	80,43	198,37
W85um133G_at	um05122	- related to carboxylic acid transport protein JEN1	2,42	8,09E-01	-8,8	2,74E-05	3,6	2,03E-03	12,60	92,57	19,30	38,50	9,30	72,83
C70um146G_at	um10861	- related to Reticuline oxidase precursor	1,45	9,78E-01	-3,9	7,41E-04	1,8	1,04E-01	22,45	88,20	43,53	32,00	22,50	78,57

* Microarray data were submitted to the NCBI GEO database under accession number GSE6039. The probesets corresponding to the 407 coregulated genes are highlighted in orange, iron cluster genes in yellow.

** MUMDB (http://mips.gsf.de/genre/proj/ustilago/), (10/2006)

*** One of two probesets identifying the same gene. The other probeset showed higher adjusted p-values and was not included in this list.