

Expression profiling of potato germplasm differentiated in quality traits leads to the identification of candidate flavour and texture genes

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Figure S1. Gene expression profiles of other genes possibly affecting tuber quality traits in Phureja (333-16, Mayan Gold) and Tuberosum (Desiree, Maris Piper) cultivars during tuber development (harvest stages H1 to H4-see methods for details) as determined by microarray analysis. Values are the means of three replicates and error bars represent standard error of the mean.

Figure S2. Scatter plot of mean probe intensities of gDNA hybridisations to POCI microarray. Data (intensity values >100) was combined from Tuberosum (Desiree and Maris Piper, X-axis) and Phureja (333-37 and 333-16, Y-axis) genotypes and plotted on log₁₀ scale.

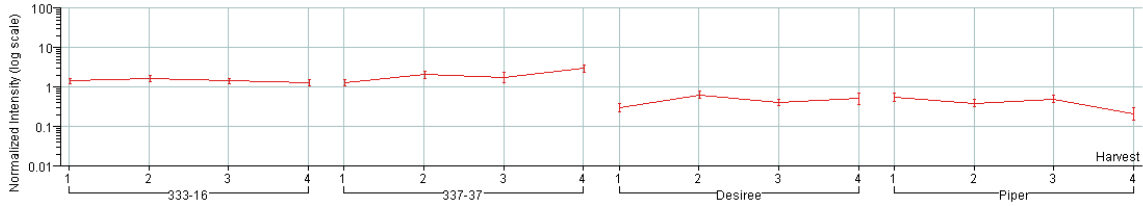
Table S1. Genes differentially expressed between tubers of group Phureja and Tuberosum based on ANOVA analysis: a) probes with significantly higher levels of expression in Phureja; b) probes with significantly higher levels of expression in Tuberosum. Sampling (Harvest 1-4) is detailed in Materials and Methods for the 2005 trial. Probes were designed to target unigenes, (Probe ID; http://pgrc-35.ipk-gatersleben.de/pls/htmldb_pgrc/f?p=194) and are shown with their putative function

(Description) based upon BLAST searches. Fold-change (Normalized) is relative to median values of that gene for all samples. Significance of the differential expression is indicated by the t-test P-value.

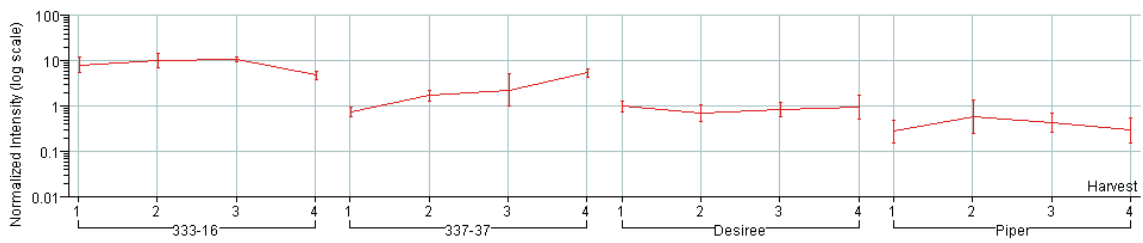
Table S2. Genes differentially expressed in tubers between harvest time points based on ANOVA analysis. Sampling (Harvest 1-4) is detailed in Materials and Methods for the 2005 trial. Probes were designed to target unigenes, (Probe ID; http://pgrc-35.ipk-gatersleben.de/pls/htmldb_pgrc/f?p=194) and are shown with their putative function (Description) based upon BLAST searches. Fold-change (Normalized) is relative to median values of that gene for all samples. Significance of the differential expression is indicated by the t-test P-value.

FIGURE S1.

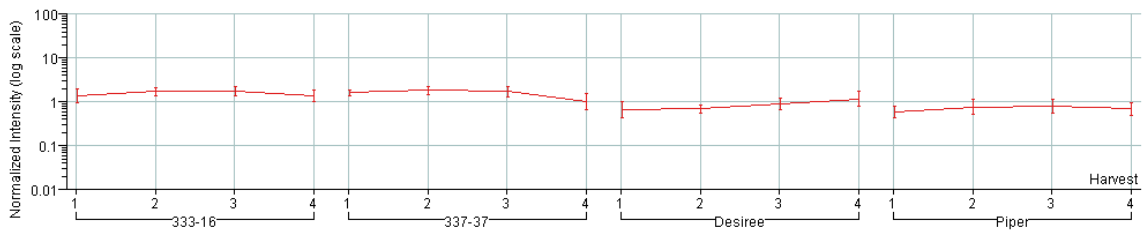
A. Higher in Phureja



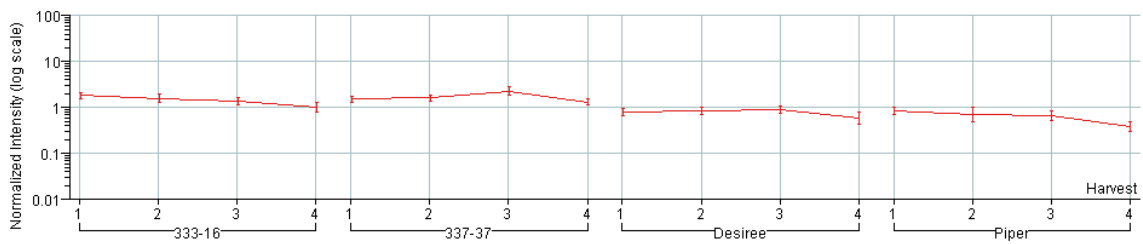
Branched chain amino acid aminotransferase (MICRO.2772.C2_1399)



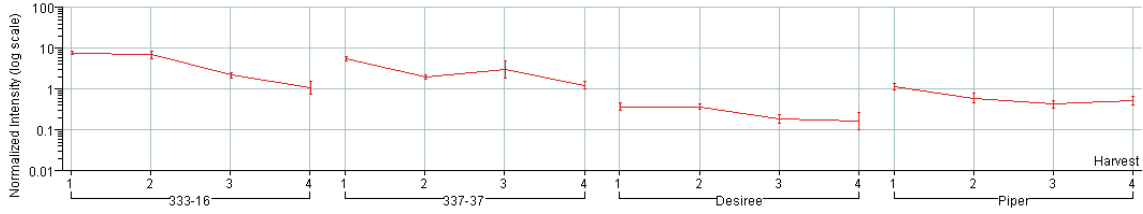
Sesquiterpene synthase (MICRO.8755.C3_977)



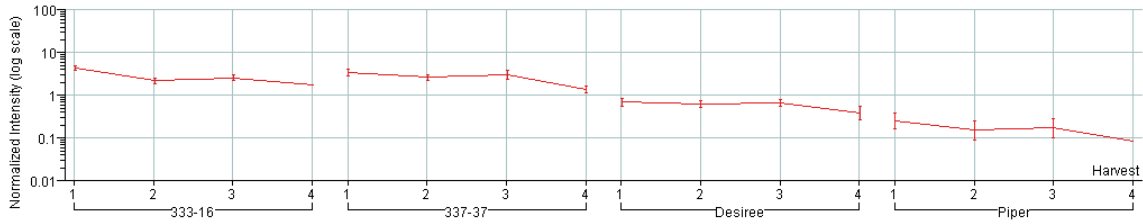
Glutamate ammonia ligase (MICRO.3959.C1_623)



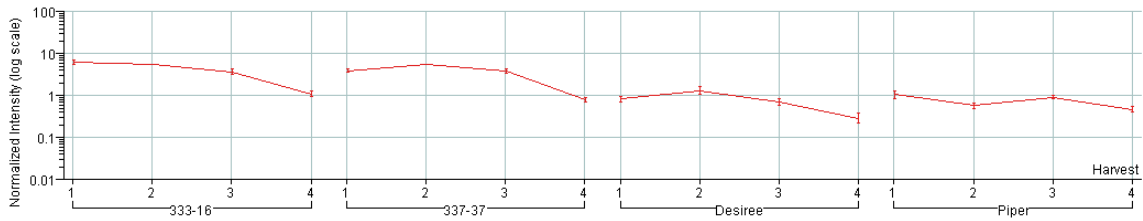
Glutamate synthetase I (STMDI41TV_515)



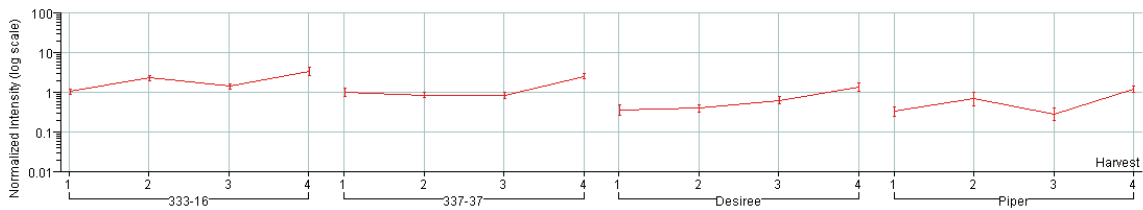
Ribonuclease (MICRO.5716.C1_596)



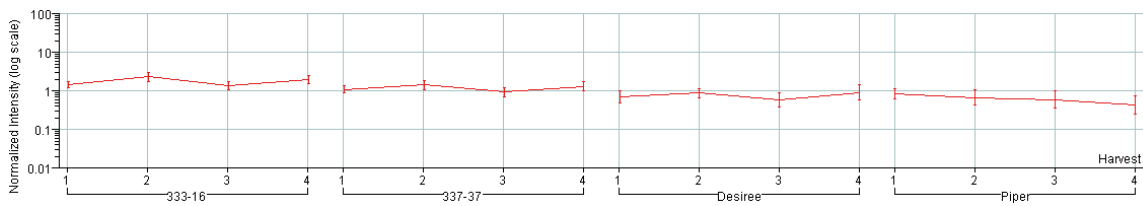
Carotene beta-hydroxylase (MICRO.7880.C2_1119)



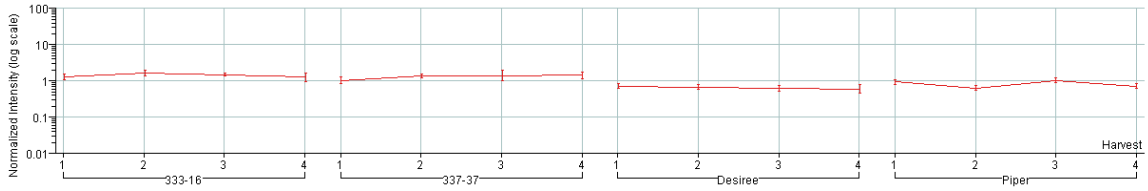
Pectin acetyltransferase (MICRO.4427.C3_1465)



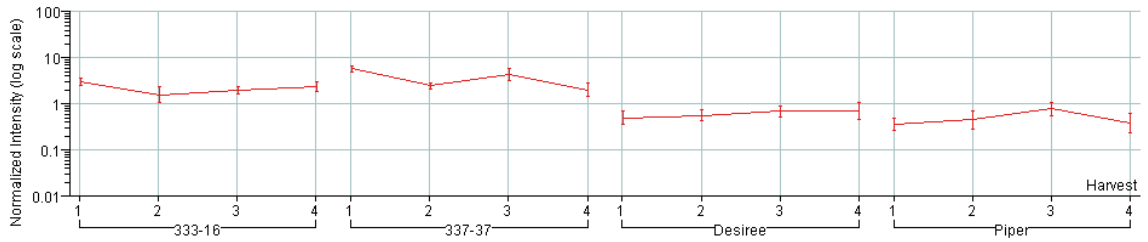
Xyloglucan endotransglycosylase (MICRO.4152.C1_825)



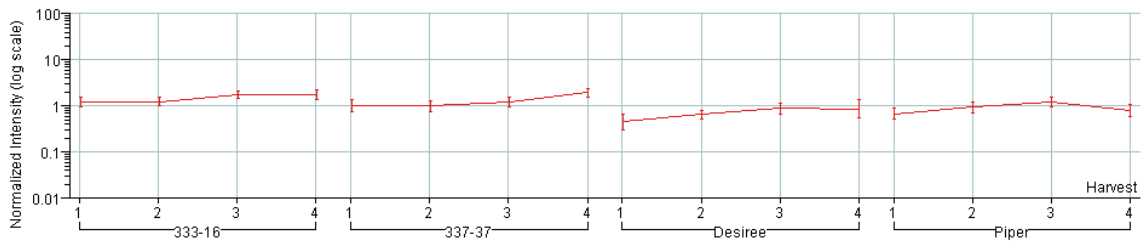
NAD-dependent epimerase (bf_arrayxxx_0046b02.t7m.scf_638)



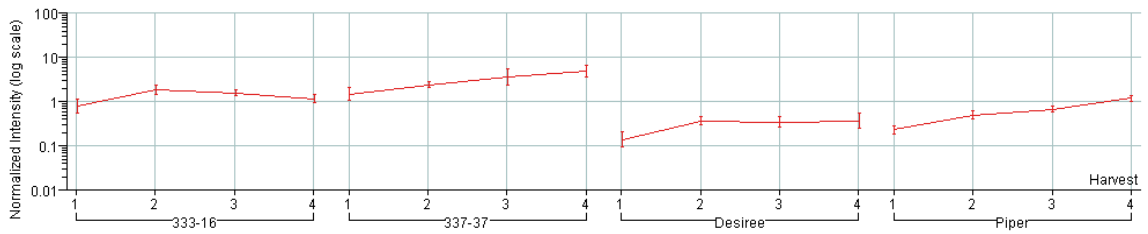
Nucleotide-rhamnose synthase (MICRO.444.C1_634)



Chitinase (MICRO.15095.C1_874)

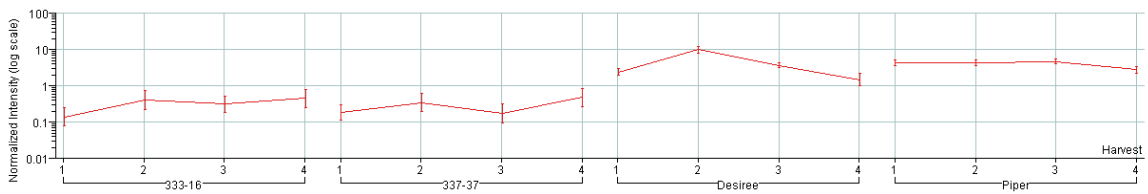


FRIGIDA (MICRO.1851.C1_1)

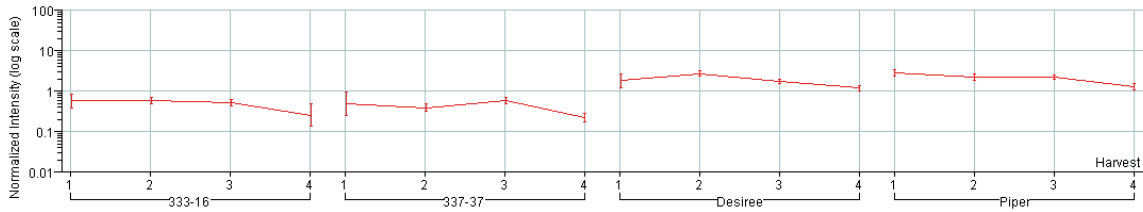


Beta-amylase (MICRO.13823.C1_1872)

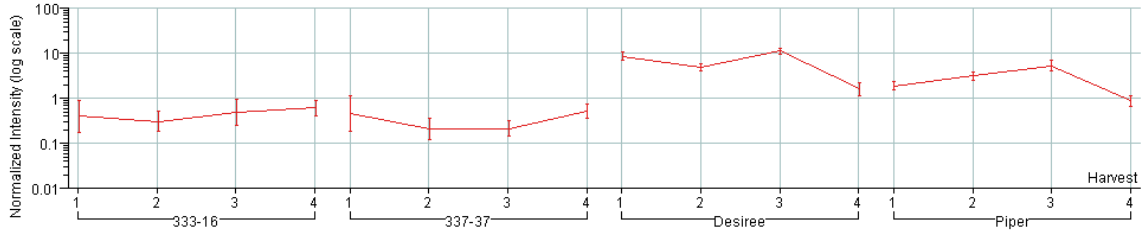
B. Higher in Tuberosum



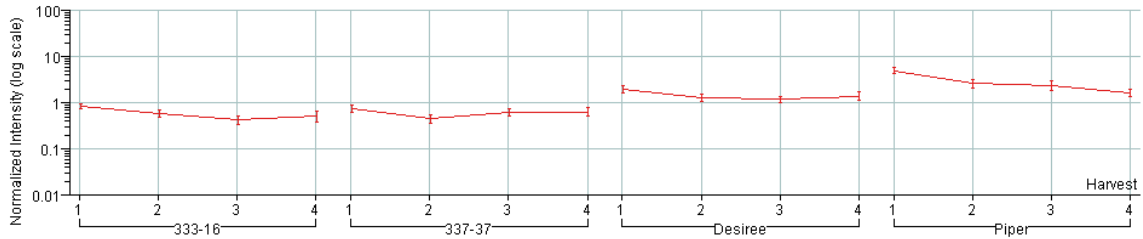
GABA transaminase subunit 3 (MICRO.15425.C2)



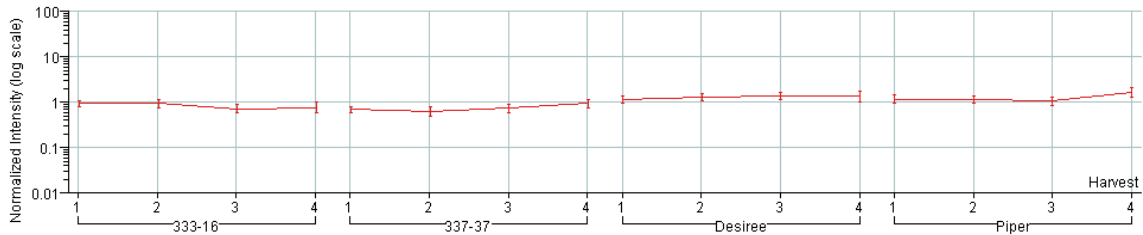
Cystathione gamma synthase I (MICRO.1118.C2_1798)



Pectin methylesterase (MICRO.4403.C1_728)



Ent-kaurene oxidase (MICRO.10720.C2_566)



Dimethylallyl transferase (MICRO.2151.C3_724)

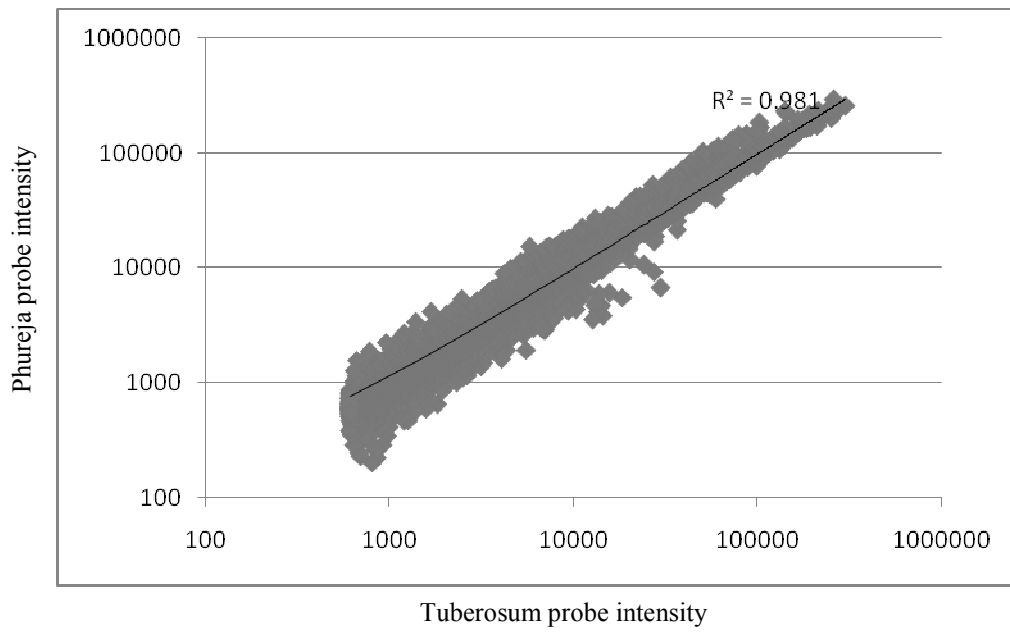


Figure S2

Probe ID	Phage				Tubercosm				Genbank	Description					
	Normalized	t-test P-value	Normalized	t-test P-value	Normalized	t-test P-value	Normalized	t-test P-value							
MCR01851.C1	1.12	0.54	1.12	0.58	1.44	0.02	0.55	0.07	0.78	0.21	1.03	0.87	0.83	0.53	NA
SDN001142cd_455	3.85	0.03	4.13	0.00	3.85	0.00	4.07	0.00	4.11	0.00	4.11	0.00	4.11	0.00	CG1451804
MCR00663.C1_461	1.11	0.54	1.39	0.24	1.74	0.02	1.84	0.00	0.65	0.06	0.70	0.11	0.73	0.19	0.03
STN02174_674	1.29	0.37	1.29	0.37	1.29	0.37	1.29	0.37	1.29	0.37	1.29	0.37	1.29	0.37	NA
MCR00683.C1_1167	1.52	0.07	1.69	0.01	1.67	0.01	0.91	0.30	1.02	0.93	0.82	0.13	0.52	0.00	BT014497
MCR02016.C2_1484	1.03	0.88	1.42	0.05	2.03	0.00	2.23	0.00	0.89	0.39	0.69	0.07	0.94	0.65	0.30
POC02917P_872	1.31	0.07	1.31	0.07	2.32	0.00	2.29	0.00	0.73	0.13	0.62	0.01	0.79	0.01	NA
ACD00661B01_Thm sfd_308	1.37	0.08	1.10	0.49	1.15	0.32	1.18	0.24	0.64	0.02	0.61	0.02	0.71	0.06	0.62
MCR01391.C1_18	1.83	0.01	1.83	0.01	1.83	0.01	1.83	0.01	1.83	0.01	1.83	0.01	1.83	0.01	NA
MCR01160.C1_694	0.98	0.86	1.42	0.10	1.34	0.07	1.47	0.07	0.63	0.11	0.88	0.58	0.98	0.62	0.71
STN02174_519	1.68	0.01	1.69	0.03	1.75	0.02	1.77	0.02	0.83	0.18	0.78	0.27	0.77	0.15	0.48
BF_TUBSXXX_003505_Thm SFCF_378	1.79	0.05	1.96	0.01	1.93	0.02	2.33	0.00	0.47	0.03	0.68	0.06	0.68	0.05	1.14
MCR04000.C1_948	1.28	0.21	1.17	0.44	1.15	0.40	1.36	0.12	0.22	0.11	0.69	0.18	0.79	0.38	0.74
MCR03073.C1_563	1.46	0.02	1.46	0.02	1.46	0.02	1.46	0.02	0.90	0.61	0.58	0.16	0.67	0.22	NA
MCR02456.C3_1305	1.77	0.05	1.61	0.02	1.41	0.02	1.03	0.81	0.00	0.95	0.77	0.08	0.75	0.04	0.47
SDN001142cd_193	1.31	0.29	1.62	0.20	1.98	0.03	2.00	0.00	0.60	0.08	0.80	0.47	0.76	0.23	1.06
MCR01933.C1_757	1.13	0.01	1.13	0.01	1.46	0.08	1.44	0.00	0.70	0.08	0.68	0.02	0.76	0.18	0.46
MCR012781.C1_486	2.02	0.00	1.03	0.87	1.07	0.09	1.78	0.02	0.78	0.24	0.43	0.03	0.77	0.36	0.61
POC02917P_565	1.45	0.03	2.00	0.01	1.78	0.02	1.55	0.05	0.58	0.00	0.28	0.00	0.47	0.09	0.45
TBKS0088FA12_0m sfd_327	2.73	0.00	1.52	0.04	1.64	0.02	1.53	0.56	0.83	0.35	0.75	0.16	0.73	0.20	0.65
MCR02730.C2_1293	2.28	0.01	1.27	0.35	1.55	0.02	2.28	0.00	0.25	0.00	0.28	0.01	0.28	0.01	0.35
DI_000000_000012_0m sfd_245	1.47	0.04	1.47	0.04	1.75	0.01	1.49	0.02	0.52	0.01	0.43	0.01	0.68	0.02	0.47
STN02174_236	1.24	0.24	1.17	0.34	1.44	0.03	1.38	0.09	0.59	0.04	0.79	0.19	1.04	0.80	0.81
MCR03903.C2_798	1.38	0.14	1.40	0.05	1.77	0.01	2.45	0.01	0.50	0.01	0.36	0.00	0.51	0.01	0.52
MCR03678.C2_1237	1.21	0.16	1.34	0.23	1.48	0.09	1.84	0.23	0.51	0.05	0.54	0.04	0.68	0.21	0.40
MCR01700.C1_1002	1.49	0.05	1.00	0.99	1.18	0.37	2.75	0.00	0.39	0.04	0.64	0.13	0.64	0.17	0.90
MCR01729.C1_1244	2.10	0.00	1.97	0.00	1.60	0.01	1.91	0.06	0.75	0.15	0.74	0.42	0.51	0.04	0.35
MCR013196.C4_1228	0.95	0.75	3.58	0.00	3.71	0.05	8.28	0.00	0.37	0.00	0.36	0.00	0.33	0.01	0.12
STN02174_874	2.11	0.06	3.11	0.04	1.39	0.33	1.71	0.04	0.68	0.18	0.73	0.37	0.87	0.26	0.46
MCR0605.C1_2183	3.30	0.00	1.55	0.02	1.87	0.00	1.35	0.08	0.62	0.04	0.49	0.01	0.50	0.02	0.68
MCR014302.C1_1112	1.15	0.11	3.22	0.11	2.20	0.26	1.12	0.51	0.76	0.13	0.85	0.29	0.71	0.12	0.67
MCR01328.C1_611	1.01	0.96	1.91	0.06	1.79	0.03	1.81	0.02	0.72	0.01	0.84	0.02	0.73	0.36	0.70
MCR015096.C1_874	4.18	0.00	1.98	0.01	2.90	0.01	2.21	0.00	0.42	0.02	0.51	0.06	0.74	0.22	0.48
MCR01498.C1_1263	2.88	0.00	1.14	0.20	1.18	0.44	0.60	0.00	0.47	0.18	0.44	0.08	0.54	0.08	0.54
MCR04742.C1_1112	1.37	0.05	1.09	0.01	1.01	2.62	0.00	0.41	0.00	0.55	0.05	0.51	0.01	0.69	0.05
MCR02997.C2_625	1.47	0.02	1.29	0.10	1.35	0.07	1.31	0.08	0.77	0.12	0.57	0.02	0.76	0.15	0.64
MCR03305.C2_862	1.83	0.07	1.59	0.13	1.72	0.07	1.76	0.02	0.63	0.09	0.62	0.17	0.76	0.28	0.83
MCR008191.C1_609	1.07	0.15	1.27	0.40	1.18	0.35	1.29	0.22	0.74	0.17	0.61	0.06	0.76	0.28	0.64
MCR01891.C1_41	1.46	0.00	1.46	0.00	1.46	0.00	1.46	0.00	1.46	0.00	1.46	0.00	1.46	0.00	NA
DI_000000_003405_0m sfd_48	1.85	0.00	1.52	0.03	1.84	0.02	0.97	0.80	0.14	0.87	0.54	0.66	0.61	0.65	0.02
BF_TUBSXXX_005296_Thm SFCF_259	1.24	0.08	1.84	0.00	2.12	0.02	2.83	0.00	0.63	0.08	0.50	0.01	0.67	0.19	0.55
MCR01663.C4_1077	1.73	0.02	1.73	0.02	1.73	0.02	1.73	0.02	0.24	0.03	0.45	0.03	0.45	0.03	0.45
MCR01196.C1_1290	1.18	0.38	2.43	0.00	2.17	0.02	5.08	0.00	0.65	0.02	0.66	0.06	0.56	0.02	0.70
MCR01498.C1_1263	2.87	0.00	1.14	0.20	1.18	0.44	0.60	0.00	0.47	0.18	0.44	0.08	0.53	0.09	0.53
DI_000000_003401_0m sfd_543	2.18	0.00	1.18	0.27	1.53	0.06	1.11	0.45	0.88	0.35	0.61	0.53	0.94	0.65	0.91
STN02174_519	3.30	0.05	1.56	0.02	1.65	0.01	1.30	0.05	0.93	0.68	0.42	0.03	0.70	0.05	0.66
MCR01722.C1_792	1.13	0.02	1.11	0.12	1.93	0.12	1.13	0.13	0.13	0.13	0.13	0.13	0.13	0.13	0.13
BF_TUBSXXX_001409_Thm SFCF_121	1.70	0.02	1.05	0.78	1.38	0.05	1.59	0.02	0.47	0.07	0.63	0.24	0.65	0.03	0.86
MCR0223.C1_723	1.08	0.81	1.08	0.81	1.08	0.81	1.08	0.81	1.08	0.81	1.08	0.81	1.08	0.81	1.08
DI_000000_004303_0m sfd_142	1.77	0.24	1.47	0.07	1.48	0.06	1.90	0.00	0.29	0.03	0.48	0.01	0.32	0.04	0.38
MCR015406.C1_800	3.36	0.00	1.31	0.13	1.43	0.21	1.08	0.63	0.89	0.65	0.83	0.23	0.68	0.09	0.89
MCR010905.C1_952	1.92	0.02	1.92	0.02	1.92	0.02	2.07	0.01	0.19	0.01	0.26	0.01	0.26	0.01	0.26
MCR016732.C1_686	1.58	0.01	1.24	0.20	1.47	0.01	1.13	0.13	0.69	0.16	0.68	0.02	0.61	0.39	0.00
MCR01568.C1_770	1.89	0.08	1.89	0.08	1.89	0.08	1.89	0.08	1.89	0.08	1.89	0.08	1.89	0.08	1.89
DI_000000_001260_0m sfd_28	1.05	0.64	1.14	0.48	1.41	0.05	1.34	0.05	0.84	0.25	0.78	0.27	0.82	0.13	0.91
MCR01722.C1_1015	1.05	0.68	1.18	0.29	1.26	0.17	2.03	0.00	0.64	0.04	0.73	0.09	0.69	0.08	1.18
MCR0333.C2_667	1.15	0.02	1.15	0.02	1.18	0.27	1.15	0.42	0.71	0.09	1.00	0.09	1.00	0.09	1.00
DI_000000_003401_0m sfd_321	1.38	0.04	1.59	0.02	1.80	0.01	1.11	0.53	0.67	0.17	0.70	0.09	0.79	0.19	0.63
DI_000000_001869_0m sfd_670	1.13	0.40	1.42	0.03	2.63	0.04	3.53	0.00	0.42	0.03	0.46	0.05	0.91	0.58	0.02
DI_000000_003401_0m sfd_536	1.27	0.00	0.84	0.36	1.34	0.05	1.41	0.03	0.83	0.39	0.50	0.01	0.75	0.13	0.81
MCR014732.C1_1111	1.04	0.84	1.04	0.84	1.04	0.84	1.04	0.84	1.04	0.84	1.04	0.84	1.04	0.84	1.04
MCR0232.C2_1689	2.97	0.00	1.81	0.01	2.04	0.00	2.26	0.01	0.28	0.00	0.29	0.01	0.28	0.00	0.13
DI_000000_000612_0m sfd_726	1.23	0.03	2.45	0.00	1.89	0.06	1.84	0.00	0.53	0.08	0.56	0.07	0.45	0.01	0.17
DI_000000_000612_0m sfd_475	1.66	0.04	1.66	0.04	1.66	0.04	1.66	0.04	1.66	0.04	1.66	0.04	1.66	0.04	1.66
MCR03479.C1_1392	1.12	0.28	1.53	0.02	1.99	0.02	1.17	0.54	0.21	0.44	0.60	0.02	0.72	0.08	1.18
MCR03773.C1_698	1.48	0.07	1.44	0.24	1.40	0.25	1.13	0.41	0.83	0.26	0.63	0.03	0.73	0.18	0.81
MCR0303.C1_368	1.20	0.40	1.12	0.61	1.76	0.01	1.82	0.01	0.50	0.28	0.30	0.01	0.82	0.34	0.77
POC02917P_872	1.47	0.01	1.37	0.01	1.84	0.01	2.42	0.12	0.65	0.03	0.74	0.13	0.69	0.07	0.47
MCR03678.C2_1018	2.42	0.02	1.93	0.03	2.05	0.01	1.13	0.13	0.63	0.24	0.39	0.29</			

bl_mfxxx0090933m_scd_283	1.14	0.38	1.68	0.01	1.48	0.10	2.39	0.00	0.48	0.00	0.77	0.16	0.54	0.01	0.92	0.05	NA	unknown protein (Arabidopsis thaliana)
bl_mfxxx0090953m_scd_445	2.11	0.47	1.27	0.01	1.48	0.10	2.39	0.00	0.48	0.00	0.77	0.16	0.54	0.01	0.92	0.05	NA	unknown protein (Arabidopsis thaliana)
IPK011697H_504	1.48	0.03	1.27	0.25	1.56	0.04	1.63	0.06	0.68	0.17	0.48	0.06	0.78	0.37	0.76	0.38	NA	glucose-6-phosphate 4-epimerase (Arabidopsis thaliana)
bl_mfxxx0090953m_scd_435	0.88	0.32	1.33	0.12	1.38	0.08	1.59	0.04	0.75	0.30	0.78	0.33	0.77	0.19	0.80	0.09	AY18665	Phytochrome b-interacting factor (Capsicum chinense)
MCR0177381_303	2.76	0.01	2.49	0.01	2.49	0.01	2.49	0.01	2.49	0.01	2.49	0.01	2.49	0.01	2.49	0.01	NA	NA
ESTB417H_142	2.13	0.00	2.06	0.01	1.70	0.01	1.18	0.25	0.77	0.11	0.78	0.10	0.63	0.01	0.67	0.04	NA	NA
MCR03561C1_899	3.49	0.00	3.49	0.00	3.49	0.00	3.49	0.00	3.49	0.00	3.49	0.00	3.49	0.00	3.49	0.00	NA	hypochlorite protein (Solanum tuberosum)
MCR07734C1_875	3.20	0.00	2.46	0.18	2.46	0.01	2.35	0.00	0.34	0.01	0.38	0.03	0.36	0.04	0.38	0.12	NA11304	Os03g0578000 (Xenopus salvia (african cuttlefish))
MCR01196C1_910	1.38	0.03	1.40	0.19	1.22	0.15	1.76	0.01	0.73	0.09	0.93	0.81	0.65	0.05	0.65	0.09	AM472807	putative protein (Arabidopsis thaliana)
MCR02076C2_1031	1.23	0.02	1.23	0.02	1.23	0.02	1.23	0.02	1.23	0.02	1.23	0.02	1.23	0.02	1.23	0.02	NA	putative protein (Arabidopsis thaliana)
bl_mfxxx0020073m_scd_707	3.81	0.00	3.17	0.00	3.65	0.00	2.21	0.00	0.47	0.01	0.33	0.02	0.42	0.02	0.47	0.01	NA	Lycium lactus beta domain - E class P450, gene1 (Medicago truncatula)
MCR01481C1_1547	0.91	0.17	1.37	0.01	1.37	0.01	1.37	0.01	1.37	0.01	1.37	0.01	1.37	0.01	1.37	0.01	AY093851	cytochrome P450 (Solanum tuberosum)
bl_mfxxx00448063m_scd_523	2.03	0.00	1.69	0.05	2.01	0.01	0.80	0.39	0.72	0.18	0.71	0.12	0.86	0.47	0.44	0.09	NA	NA
MCR02388C1_1095	1.67	0.01	1.24	0.18	1.49	0.05	1.20	0.31	0.62	0.67	0.73	0.09	0.70	0.11	0.71	0.29	NA	gelatinase B (Pisum sativum)
ESTB0000141_413	1.67	0.01	1.30	0.13	1.46	0.02	1.10	0.52	0.71	0.07	0.88	0.41	0.71	0.07	0.81	0.31	AY011131	BDP1 (R. ADE ON FR1042) protein binding (Arabidopsis thaliana)
MCR01707C1_712	1.10	0.53	1.27	0.28	2.04	0.10	1.84	0.02	0.64	0.42	0.48	0.08	0.76	0.39	0.81	0.60	AM70105	kinase (Arabidopsis thaliana)
SSBND01043u_scd_383	1.86	0.01	1.78	0.01	2.49	0.00	1.95	0.01	0.38	0.00	0.48	0.00	0.58	0.01	0.52	0.01	AY22223	cytochrome P450 (Solanum tuberosum)
bl_mfxxx0035053m_scd_99	3.23	0.00	1.69	0.14	2.95	0.03	2.34	0.02	0.61	0.59	0.41	0.52	0.63	0.13	0.37	0.11	NA	NA
MCR01802C1_312	1.57	0.01	1.38	0.08	1.87	0.01	2.01	0.00	0.54	0.03	0.51	0.02	0.72	0.12	0.71	0.29	NA	hypochlorite protein (Arabidopsis thaliana)
ESTB0217V_377	2.36	0.00	1.30	0.14	1.40	0.11	1.14	0.42	0.60	0.33	0.45	0.01	0.42	0.02	0.43	0.04	NA	NA
MCR016623C1_449	2.81	0.00	2.22	0.00	1.65	0.09	0.89	0.88	0.83	0.19	0.77	0.10	0.81	0.49	0.50	0.02	NA	calcium ion binding (Arabidopsis thaliana)
BP_TURE300C_04238m_TAM_SCF_474	3.29	0.00	1.98	0.02	2.24	0.02	0.94	0.65	0.42	0.34	0.23	0.20	0.50	0.19	0.53	0.02	NA	unknown protein (Arabidopsis thaliana)
MCR012893C1_775	1.09	0.49	1.77	0.02	1.54	0.01	1.39	0.05	0.34	0.01	0.53	0.14	0.50	0.01	0.54	0.05	NA	NA
bl_mfxxx0026503m_scd_68	1.69	0.01	1.58	0.03	1.70	0.08	1.52	0.08	0.48	0.01	0.50	0.02	0.60	0.07	0.60	0.08	NA	NA
POCK0097H_101	1.89	0.00	3.93	0.00	2.97	0.00	1.94	0.01	0.32	0.00	0.37	0.00	0.43	0.01	0.42	0.02	AY32223	monosaccharide transporter (Nicotiana glauca)
ESTB0177V_549	0.86	0.32	1.46	0.03	2.00	0.03	3.42	0.00	0.44	0.00	0.48	0.11	0.63	0.19	0.71	0.34	NA	Os06g028300 (Xenopus salvia (african cuttlefish))
SSBND01043u_scd_386	1.97	0.00	1.98	0.01	2.88	0.01	1.61	0.01	0.10	0.00	0.24	0.00	0.10	0.01	0.14	0.02	NA	NA
MCR013373C1_703	2.33	0.00	2.71	0.02	2.34	0.00	0.88	0.50	0.70	0.58	0.86	0.39	0.84	0.25	0.53	0.13	NA	TPA hypochlorite protein (Rice turgor bacilliform virus)
MCR01173C1_1794	1.33	0.05	1.38	0.08	1.35	0.06	1.43	0.06	0.89	0.45	0.85	0.27	0.79	0.16	0.73	0.15	AM48143	lysine (Medicago truncatula)
ESTB0241H_150	1.74	0.00	2.24	0.01	2.79	0.00	1.14	0.30	0.97	0.04	0.98	0.01	0.61	0.03	0.68	0.04	NA	NA
ESTB0207H_566	1.92	0.00	2.06	0.07	2.58	0.00	1.17	0.24	0.68	0.12	0.62	0.04	0.61	0.03	0.70	0.15	AM48951	similar to wvs absent protein (Arabidopsis thaliana)
BP_TURE300C_04238m_TAM_SCF_317	3.83	0.00	3.00	0.00	2.77	0.07	3.16	0.00	0.32	0.01	0.31	0.04	0.29	0.01	0.48	0.04	AC11987	NA
MCR013054C2_589	3.05	0.00	3.47	0.00	3.92	0.00	7.06	0.00	0.40	0.01	0.44	0.02	0.60	0.03	0.63	0.05	AY498119	disulfide oxidoreductase/m monooxygenase/oxidoreductase (Arabidopsis thaliana)
POCK0097H_74	2.34	0.00	2.33	0.00	2.79	0.08	2.18	0.01	0.50	0.02	0.56	0.02	0.43	0.01	0.39	0.01	AY224824	NA
MCR01222C1_476	3.81	0.00	3.51	0.00	3.63	0.00	3.62	0.00	2.92	0.00	2.92	0.00	2.92	0.00	2.92	0.00	NA	NA
POCK0097H_773	1.57	0.05	1.85	0.02	1.94	0.01	1.60	0.13	0.18	0.06	0.48	0.14	0.37	0.11	0.40	0.21	NA	NA
MCR01118C1_738	1.89	0.00	2.81	0.00	1.88	0.01	1.87	0.06	0.24	0.00	0.24	0.00	0.24	0.00	0.24	0.00	NA	glucanase class 3 (Medicago truncatula)
MCR04318C2_655	1.73	0.01	1.53	0.01	2.01	0.01	1.31	0.09	0.61	0.56	0.66	0.64	0.64	0.64	0.64	0.64	AM48861	similar to wvs absent protein (Arabidopsis thaliana)
MCR01367C1_477	1.23	0.17	1.48	0.09	1.33	0.13	1.12	0.61	0.82	0.37	0.72	0.18	0.93	0.75	0.88	0.33	AC129230	NA
ESTB0107V_894	1.12	0.21	1.89	0.01	1.89	0.01	0.53	0.03	0.73	0.13	0.77	0.13	0.83	0.09	0.83	0.09	AY324884	carbohydrate transporter/sugar porter (Arabidopsis thaliana)
MCR02624C1_1133	1.83	0.00	1.56	0.03	1.58	0.04	1.30	0.16	0.77	0.18	0.63	0.06	0.71	0.13	0.60	0.05	BT014055	RNA binding motif RNP-1 (RNA recognition motif) (Medicago truncatula)
MCR01462C1_124	1.28	0.00	1.24	0.01	1.24	0.01	1.24	0.01	1.24	0.01	1.24	0.01	1.24	0.01	1.24	0.01	NA	NA
MCR011293C1_622	1.77	0.01	1.59	0.19	1.21	0.30	1.55	0.07	0.69	0.15	0.69	0.26	0.86	0.52	0.22	0.24	NA	NA
MCR02821C1_737	1.50	0.02	1.67	0.09	1.37	0.18	1.81	0.01	0.39	0.00	0.84	0.41	0.87	0.04	0.81	0.03	AP092939	Os06g0125400 (Xenopus salvia (african cuttlefish))
MCR011605C1_495	1.07	0.00	1.59	0.00	1.59	0.00	1.59	0.00	0.81	0.00	0.72	0.07	0.71	0.14	0.73	0.03	AY224824	hypochlorite protein (Arabidopsis thaliana)
MCR011274C2_403	1.58	0.01	1.51	0.06	1.88	0.05	1.52	0.11	0.59	0.06	0.79	0.14	0.69	0.10	0.63	0.02	NA	NA
MCR02007C1_1289	1.11	0.11	0.64	0.07	1.19	0.03	1.19	0.03	0.69	0.00	0.69	0.00	0.69	0.00	0.69	0.00	BT013014	endoneurite/serum ion binding (Arabidopsis thaliana)
MCR011003C1_714	1.83	0.01	1.18	0.30	1.43	0.04	1.47	0.06	0.62	0.04	0.58	0.02	0.77	0.17	0.95	0.48	AM454907	RNA binding / oxidoreductase III (Arabidopsis thaliana)
MCR011202C1_3562	2.52	0.00	2.36	0.00	2.13	0.00	0.78	0.12	0.92	0.54	0.92	0.48	0.90	0.32	0.55	0.02	AM47963	ATPase/E1ATZMP: metalloendopeptidase (Arabidopsis thaliana)
ESTB0131H_343	1.38	0.02	1.95	0.02	1.90	0.01	1.90	0.01	0.27	0.00	0.27	0.00	0.27	0.00	0.27	0.00	CT100458	unknown protein (Arabidopsis thaliana)
MCR01196C1_1044	0.90	0.33	3.55	0.00	3.38	0.04	13.49	0.00	0.20	0.00	0.23	0.00	0.30	0.00	1.12	0.42	NA	unknown (Solanum tuberosum)
MCR0164C1_610	1.89	0.00	4.89	0.01	2.13	0.01	0.69	0.07	0.69	0.13	1.12	0.12	0.65	0.07	0.65	0.12	AY42179	lysine isomerase 2
MCR0807C1_503	1.33	0.15	1.47	0.04	1.56	0.01	1.16	0.54	0.84	0.23	0.61	0.02	0.77	0.17	0.75	0.12	U69633	NA
MCR01180C2_1138	1.47	0.01	1.11	0.45	1.99	0.09	1.50	0.40	0.72	0.10	0.44	0.07	0.72	0.14	0.47	0.05	NA	hypochlorite protein (Arabidopsis thaliana)
bl_mfxxx00100053m_scd_85	2.11	0.02	1.91	0.02	1.91	0.02	0.99	0.90	0.80	0.42	0.67	0.02	0.67	0.02	0.72	0.22	NA	NA2 superfamily tyrosinase subfamily A, member 3 (Medicago truncatula)
171509AF_scd_272	2.69	0.00	2.18	0.10	1.95	0.01	1.33	0.40	0.78	0.40	0.54	0.39	0.69	0.33	0.56	0.33	NA	NA
bl_mfxxx0054107m_scd_18	1.89	0.00	2.48	0.01	2.48	0.01	2.48	0.01	0.42	0.00	0.42	0.00	0.42	0.00	0.42	0.00	NA	NA
MCR0287C1_53	1.04	0.74	1.30	0.14	1.67	0.02	2.00	0.00	0.69	0.03	0.63	0.05	0.78	0.05	0.81	0.29	AC140022	hypochlorite protein MDRAF1_AC140022/230 (Medicago truncatula)
MCR01645C1_450	1.16	0.18	1.22	0.														

MCR04866.C2_731	1.10	0.43	1.22	0.17	1.43	0.03	1.33	0.07	0.74	0.16	0.61	0.02	0.61	0.17	0.69	0.09	BT013298	zinc finger protein LSD1 (Brassica oleracea)
MCR01081.C5_616	2.18	0.01	2.29	0.00	2.29	0.02	2.29	0.26	0.48	0.01	0.72	0.09	0.59	0.17	0.69	0.35	NA	
STRMS20V_344	1.55	0.01	1.51	0.06	1.56	0.00	1.56	0.08	0.76	0.21	0.55	0.01	0.75	0.07	0.64	0.02	NA	hydroethereal protein BmatM064 (Brassica napus)
bf_ncdxxxx_0031a0503m.scf_517	1.18	0.11	1.18	0.26	2.00	0.00	1.24	0.18	0.54	0.08	0.36	0.00	0.76	0.24	0.52	0.04	BA000042	hypothetical protein NtAmB04 (Nicotiana glauca)
MCR01874.C1_882	0.82	0.07	1.29	0.06	1.27	0.03	1.27	0.00	0.66	0.04	0.76	0.07	0.71	0.04	1.07	0.68	NA	hypothetical protein Os_100906 (Oryza sativa japonica cultivar-group)
MCR02793.C1_804	1.13	0.45	1.30	0.09	1.68	0.00	2.81	0.00	0.62	0.02	1.03	0.89	0.59	0.00	0.50	0.00	AB212933	NA
CR034827M_482	1.60	0.01	1.51	0.08	1.39	0.07	1.59	0.08	0.48	0.05	0.49	0.11	0.61	0.20	0.54	0.27	DQ245385	unknown protein (Arabidopsis thaliana)
POCAF10V_554	1.07	0.64	2.31	0.01	2.06	0.03	7.01	0.00	0.38	0.00	0.37	0.01	0.41	0.00	0.99	0.95	NA	
MCR04911.C1_1244	4.08	0.00	5.86	0.00	4.40	0.00	3.15	0.01	0.23	0.00	0.32	0.01	0.39	0.00	0.29	0.00	NA	
STRMS20V_441	1.13	0.27	1.10	0.31	1.42	0.01	1.76	0.01	0.46	0.08	0.45	0.10	0.38	0.04	0.56	0.00	NA	isoprenyl resistance protein E (Lycopersicon esculentum)
MCR02042.C2_664	1.20	0.08	1.25	0.23	1.24	0.14	1.12	0.45	0.86	0.35	0.84	0.33	0.91	0.54	0.74	0.97	NA	
bf_ncdxxxx_00517a0413m.scf_365	1.84	0.00	1.70	0.01	1.37	0.05	1.05	0.71	0.52	0.02	0.58	0.03	0.51	0.01	0.54	0.11	NA	unknown protein (Arabidopsis thaliana)
MCR08878.C5_322	1.80	0.04	1.39	0.07	2.13	0.00	1.20	0.13	0.54	0.03	0.40	0.01	0.56	0.03	0.35	0.02	BT012792	cutinase glucosylase (Datura innoxiosa)
MCR01649.C1_251	3.31	0.02	3.81	0.00	2.75	0.00	0.98	0.89	0.73	0.29	0.75	0.11	0.81	0.25	0.37	0.03	NA	
MCR01081.C1_1	1.53	0.05	1.32	0.25	1.86	0.00	1.64	0.02	0.99	0.08	0.56	0.01	0.74	0.33	0.79	0.10	AM72509	hypothetical protein MtGRAFT_AC1466834702 (Medicago truncatula)
bf_ncdxxxx_00570a0413m.scf_616	1.30	0.04	1.50	0.32	1.54	0.02	1.97	0.01	0.67	0.10	0.72	0.36	0.76	0.21	0.77	0.49	AM75541	carbohydrate transporter/sugar cofactor (Arabidopsis thaliana)
MCR01878.C1_603	1.80	0.29	1.80	0.01	3.85	0.00	4.34	0.00	0.66	0.21	0.45	0.03	0.78	0.18	0.61	0.02	DQ26252	ATP binding / RNA ligase / trypsin-RNA ligase (Arabidopsis thaliana)
MCR016148.C1_460	1.45	0.02	1.50	0.01	1.77	0.01	1.15	0.42	0.49	0.52	0.72	0.13	0.73	0.15	0.89	0.62	NA	
MCR02427.C3_1465	4.92	0.00	5.48	0.01	3.81	0.00	0.95	0.62	0.94	0.60	0.87	0.61	0.80	0.09	0.36	0.00	AK228936	acetate/methyltransferase precursor (Vigna radiata var. radiata)
MCR017629_1	2.48	0.00	3.00	0.00	3.10	0.00	1.75	0.01	0.44	0.01	0.48	0.01	0.48	0.02	0.48	0.01	NA	hypothetical protein MtGRAFT_AC131510a17 (Medicago truncatula)
MCR0347.C31_670	1.20	0.21	1.36	0.34	1.71	0.07	1.87	0.03	0.40	0.01	0.48	0.01	0.63	0.08	1.00	1.00	NA	Et/Som-like transposon proteins- Putative chlamy transposon protein (Medicago truncatula)
STRMS20V_212	1.80	0.88	1.29	0.63	1.22	0.46	2.00	0.01	0.72	0.17	0.78	0.36	0.80	0.25	0.85	0.69	BT013831	putative protein (Arabidopsis thaliana)
MCR03285.C1_1812	2.58	0.01	2.43	0.00	2.61	0.00	1.51	0.03	0.44	0.03	0.44	0.03	0.45	0.03	0.32	0.05	AB050509	BtA1/Spo11-like protein BS14 (Nicotiana glauca)
MCR013823.C1_1872	1.08	0.78	2.13	0.00	2.43	0.04	2.41	0.13	0.18	0.00	0.43	0.00	0.48	0.02	0.67	0.34	AF038447	beta-amylase PCT-BMW (Solanum tuberosum)
MCR01081.C1_1	1.41	0.04	2.92	0.00	1.84	0.01	1.39	0.02	0.48	0.01	0.66	0.01	0.68	0.02	0.61	0.10	AP009300	NA
MCR010128.C1_668	1.26	0.10	1.95	0.01	2.11	0.00	2.02	0.00	0.71	0.08	0.83	0.27	0.89	0.34	0.64	0.07	NA	unassigned protein (Arabidopsis thaliana)
MCR01786.C2_1118	3.83	0.03	2.41	0.00	2.87	0.00	1.49	0.06	0.42	0.02	0.28	0.03	0.34	0.03	0.17	0.08	Y14810	carotene beta-hydroxylase (Lycopersicon esculentum)
MCR07821.C1_682	1.20	0.23	1.55	0.03	1.29	0.12	1.35	0.16	0.78	0.24	0.77	0.14	0.84	0.35	0.54	0.21	NA	
MCR02345.C2_1350	1.21	0.18	1.76	0.02	1.11	0.53	1.07	0.73	0.80	0.35	0.86	0.53	0.62	0.50	0.61	0.21	BA000042	NA
STRMS20V_607	1.14	0.32	1.28	0.36	1.53	0.37	1.72	0.00	0.87	0.49	0.78	0.41	0.81	0.48	0.84	0.97	NA	Protein kinase (Medicago truncatula)
MCR013762.C1_634	1.78	0.00	1.91	0.03	1.44	0.05	1.99	0.69	0.42	0.03	0.35	0.04	0.34	0.05	0.20	0.07	NA	Os07g0538800 (Oryza sativa japonica cultivar-group)
STRMS20V_478	2.68	0.10	2.88	0.14	1.39	0.04	1.55	0.04	0.58	0.03	0.75	0.15	0.69	0.09	0.71	0.16	BT014027	Shim-char, deoxyribose/ribose/uracilase SCW (Medicago truncatula)
ACDAD041009.T3m.scf_101	2.08	0.08	1.63	0.06	2.05	0.00	2.05	0.00	0.47	0.13	0.46	0.04	0.22	0.01	0.59	0.08	AK224664	NA
SDNN0812a.scf_262	1.34	0.14	1.88	0.01	1.61	0.01	1.80	0.02	0.38	0.01	0.47	0.08	0.52	0.06	0.53	0.00	DQ773980	cutinase RNA-binding protein (Anemone nemorosa)
MCR014878.C1_863	1.74	0.01	1.33	0.04	1.44	0.02	0.93	0.56	1.00	1.00	0.93	0.62	0.74	0.77	0.51	0.04	AY055596	unknown protein (Arabidopsis thaliana)
MCR018930.C1_469	2.27	0.00	1.05	0.77	2.39	0.02	1.26	0.19	0.53	0.02	0.52	0.02	0.71	0.15	0.43	0.11	AM113866	Os03g0360700 (Oryza sativa japonica cultivar-group)
MCR013688.C1_616	1.43	0.04	2.48	0.00	2.49	0.03	5.11	0.00	0.49	0.10	0.61	0.01	0.68	0.07	0.69	0.05	DQ284486	putative protein (Nicotiana glauca)
MCR03374.C2_630	2.04	0.00	1.63	0.02	1.58	0.02	1.30	0.19	0.59	0.56	0.87	0.16	0.60	0.07	0.45	0.10	NA	PS01_12 (Arabidopsis thaliana)
MCR02926.C1_1237	1.49	0.01	1.10	0.71	1.65	0.01	1.97	0.00	0.87	0.29	0.66	0.19	0.78	0.10	0.65	0.02	BT013818	MS15C1.4 (Oryza sativa indica cultivar-group)
STRMS20V_201	1.64	0.01	1.47	0.12	1.85	0.01	1.51	0.07	0.56	0.06	0.74	0.22	0.69	0.21	0.73	0.26	NA	Protein kinase (Medicago truncatula)
MCR01781.C1_621	1.26	0.20	1.39	0.10	1.50	0.01	1.76	0.01	0.54	0.02	0.70	0.09	0.73	0.10	0.84	0.40	AP009287	unassigned protein (Arabidopsis thaliana)
MCR027208.C2_222	1.23	0.13	1.75	0.03	1.29	0.14	1.29	0.00	0.35	0.02	0.72	0.28	0.52	0.08	0.30	0.25	BT012787	hypothetical protein Os_100906 (Oryza sativa indica cultivar-group)
bf_ncdxxxx_003a00303m.scf_581	1.29	0.05	1.46	0.05	1.47	0.02	1.14	0.32	0.69	0.03	0.80	0.21	0.75	0.10	0.63	0.04	NA	disease resistance protein BS2 (Nicotiana glauca)
MCR02775.C1_862	2.52	0.00	2.14	0.01	1.22	0.08	1.18	0.65	0.45	0.04	0.88	0.28	0.45	0.02	0.27	0.12	DQ284473	cytochrome P450 (Solanum tuberosum)
MCR01081.C1_88	1.16	0.24	1.53	0.06	1.21	0.18	1.17	0.30	0.51	0.01	0.66	0.16	0.62	0.06	0.80	0.31	NA	NA
BF_TUBSXXX_0021FD1_T3M_SCF_160	1.31	0.30	1.55	0.02	1.68	0.02	1.68	0.00	0.60	0.02	0.68	0.01	0.56	0.00	0.62	0.13	AM686279	NA
bf_ncdxxxx_0007G11_03m.scf_524	1.83	0.01	2.29	0.01	1.88	0.01	1.14	0.36	0.51	0.02	0.44	0.01	0.60	0.09	0.48	0.02	NA	
MCR018106.C1_502	1.98	0.00	1.69	0.02	1.61	0.01	0.90	0.63	0.86	0.58	0.97	0.80	0.64	0.08	0.24	0.00	AB211520	similar to ATP synthase subunit H protein (Solanum tuberosum)
MCR02772.C2_1399	1.36	0.07	1.85	0.01	1.68	0.01	1.86	0.04	0.41	0.00	0.50	0.01	0.44	0.00	0.32	0.01	AF193845	branched-chain amino acid aminotransferase (Solanum tuberosum)
SDNN0506u.scf_606	1.24	0.12	1.13	0.51	1.64	0.01	2.40	0.00	0.52	0.06	0.68	0.01	0.77	0.26	0.71	0.30	NA	NA
MCR04501.C1_671	0.94	0.67	1.22	0.26	1.53	0.02	1.66	0.01	0.56	0.01	0.78	0.15	0.79	0.20	0.63	0.03	NA	isocontig resistance protein C beta (Lycopersicon esculentum)
MCR013308.C1_1493	2.34	0.04	2.28	0.01	1.87	0.04	0.88	0.67	0.91	0.71	0.90	0.63	0.71	0.38	0.39	0.16	Y10839	hypothetical protein Os_100814 (Oryza sativa indica cultivar-group)
MCR012202.C1_803	0.97	0.82	1.14	0.47	1.14	0.38	1.27	0.36	0.72	0.27	0.93	0.69	0.99	0.87	0.87	0.56	CU010621	AAA1Phase (Medicago truncatula)
MCR04876.C2_1351	1.06	0.66	1.43	0.04	1.27	0.06	1.80	0.01	0.41	0.00	0.46	0.00	0.51	0.00	1.08	0.75	NA	expressed protein (Arabidopsis thaliana)

Probe ID	Harvest 1		Harvest 2		Harvest 3		Harvest 4		Harvest 5		Harvest 6		Harvest 7		Genebank	Description		
	Normalized	Log2 P-value	Normalized	Log2 P-value	Normalized	Log2 P-value	Normalized	Log2 P-value	Normalized	Log2 P-value	Normalized	Log2 P-value	Normalized	Log2 P-value				
MICRO 8260.C1_490	0.53	0.01	0.62	0.02	0.57	0.02	0.71	0.13	1.18	0.08	1.26	0.19	1.52	0.08	1.32	0.15	TEJ ₁ poly(ADP-ribose) glycohydrolase [Arabidopsis thaliana]	
MICRO 1913.C1_1686	0.21	0.00	0.28	0.01	0.22	0.00	0.43	0.02	2.96	0.00	3.02	0.02	3.15	0.00	1.76	0.02	NU 127791	
MICRO 2286.C2_873	0.17	0.01	0.19	0.01	0.22	0.01	0.15	0.01	1.54	0.03	1.49	0.03	1.94	0.03	1.84	0.03	Os11g0671300 (Oryza sativa [japonica cultivar-group])	
BF_mfxxxx_0054412.13m.scf_33	0.49	0.00	0.81	0.02	0.40	0.01	0.78	0.10	1.93	0.07	1.16	0.28	0.87	0.89	1.44	0.98	AC149801	
MICRO 2317.C1_560	1.00	0.00	0.62	0.03	0.95	0.28	0.96	0.01	1.53	0.04	1.27	0.24	1.84	0.01	1.07	0.64	NA	
BF_mfxxxx_0040903.13m.scf_41	0.34	0.01	0.26	0.01	0.24	0.01	0.72	0.18	1.06	0.26	0.72	0.18	1.70	0.27	1.56	0.27	unknown protein [Arabidopsis thaliana]	
MICRO 14409.C1_894	0.45	0.00	0.51	0.02	0.72	0.21	0.69	0.09	3.65	0.00	2.71	0.00	3.40	0.00	1.67	0.04	NA	
MICRO 438.C1_1653	0.85	0.10	0.66	0.01	0.73	0.01	0.78	0.18	1.43	0.04	1.38	0.11	1.11	0.11	0.57	2.63	0.00	BT013857
MICRO 5059.C1_1144	0.50	0.03	0.69	0.03	0.69	0.11	0.76	0.15	1.90	0.01	1.64	0.01	1.87	0.01	1.87	0.01	NA	
BF_mfxxxx_0031033.13m.scf_102	0.07	0.00	0.05	0.01	0.04	0.01	0.14	0.03	1.37	0.11	2.26	0.04	1.86	0.01	4.55	0.00	NA	
MICRO 7929.C2_136	0.07	0.01	0.12	0.01	0.04	0.01	0.19	0.03	3.79	0.02	4.09	0.00	3.61	0.03	3.18	0.06	NA	
BF_mfxxxx_0052938.13m.scf_68	0.14	0.01	0.27	0.00	0.60	0.00	0.14	0.00	4.07	0.00	2.78	0.07	3.02	0.03	3.73	0.09	NA	
ACDAG436307.13m.scf_562	0.43	0.00	0.61	0.09	0.69	0.06	0.97	1.02	0.89	1.18	0.56	1.44	0.55	1.55	0.95	NA	hypothetical protein Os1_000005 (Oryza sativa [indica cultivar-group])	
MICRO 9106.C7_745	0.65	0.08	0.66	0.03	0.90	0.47	0.57	0.02	2.87	0.00	1.80	0.02	2.47	0.00	1.15	0.43	AB061243	
MICRO 2633.C1_702	0.96	0.04	0.84	0.07	0.89	0.09	0.86	0.46	1.84	0.02	1.39	0.07	1.39	0.14	1.21	0.41	AB040485	
STRK27171_77	0.27	0.00	0.48	0.11	0.43	0.03	0.46	0.29	1.32	0.14	1.78	0.02	1.99	0.70	1.39	0.38	NA	
BF_TUBSXXX_0042003.T3M.SCF_269	0.25	0.01	0.42	0.04	0.24	0.04	1.26	0.14	0.85	0.36	1.43	0.34	1.55	0.38	5.14	0.00	NA	
ACDAG0204906.13m.scf_410	0.82	0.07	0.78	0.19	0.85	0.08	0.62	0.10	1.31	0.14	1.42	0.08	1.19	0.39	1.50	0.41	NA	
STRK2071_432	0.34	0.00	0.42	0.02	0.43	0.10	0.76	0.28	1.06	0.81	1.26	0.12	1.34	0.07	1.32	0.48	NA	
MICRO 5849.C3_725	0.54	0.02	0.71	0.09	0.97	0.86	1.55	0.17	1.40	0.04	1.47	0.04	1.77	0.01	1.77	0.01	AC151801	
POACH7077_81	0.63	0.03	0.86	0.11	0.82	0.29	0.84	0.74	1.06	0.70	1.19	0.30	1.20	0.37	1.69	0.02	NM_102111	
MICRO 1643.C8_866	0.23	0.00	0.29	0.01	0.24	0.00	0.52	0.03	1.98	0.01	3.78	0.00	2.87	0.07	7.04	0.00	NA	
TBRK0203FB05.13m.scf_117	0.81	0.00	0.08	0.00	0.08	0.00	0.26	0.00	2.20	0.00	2.51	0.00	3.82	0.00	10.92	0.00	NA	
BPL5E207H_63	0.02	0.00	0.03	0.00	0.05	0.01	0.09	0.01	2.43	0.00	3.86	0.00	5.07	0.00	11.70	0.00	NA	
MICRO 339.C9_1241	0.07	0.00	0.21	0.02	0.17	0.02	0.58	0.05	1.47	0.08	1.88	0.01	1.73	0.01	3.98	0.01	NA	
MICRO 1081.C57_303	0.33	0.01	0.48	0.32	0.41	0.01	0.31	0.05	2.31	0.02	3.45	0.04	3.22	0.01	3.19	0.00	NA	
POACH7077_369	0.25	0.01	0.26	0.03	0.32	0.01	0.38	0.12	3.68	0.00	2.48	0.00	2.39	0.01	1.65	0.07	NA	
MICRO 10015.C1_1103	0.14	0.01	0.03	0.01	0.42	0.01	0.64	0.15	1.63	0.01	1.55	0.01	1.58	0.01	1.84	0.01	NA	
BF_mfxxxx_0034405.17m.scf_21	0.15	0.01	0.22	0.04	0.02	0.06	0.28	0.06	2.00	0.49	0.00	4.06	0.00	1.77	0.23	AF006079		
MICRO 8096.C3_21	0.26	0.00	0.36	0.01	0.25	0.01	0.36	0.04	1.91	0.01	2.07	0.00	2.09	0.01	1.53	0.09	NA	
MICRO 8098.C1_857	0.37	0.07	0.42	0.02	0.63	0.03	0.62	0.02	3.62	0.01	4.56	0.01	4.56	0.11	3.81	0.11	NA	
STRM327V_509	0.27	0.02	0.34	0.04	0.17	0.04	0.67	0.32	1.95	0.27	1.62	0.04	1.87	0.03	1.84	0.03	NA	
MICRO 3156.C9_1200	0.20	0.02	0.48	0.09	0.42	0.11	0.76	0.87	1.10	0.74	2.11	0.02	1.68	0.08	8.59	0.00	CG284470	
BF_mfxxxx_0045020.13m.scf_202	0.28	0.08	0.49	0.07	0.65	0.03	0.68	0.13	1.57	0.02	1.62	0.02	1.65	0.02	1.62	0.43	NA	
MICRO 8079.C1_751	0.04	0.01	0.15	0.02	0.07	0.01	0.25	0.06	1.78	0.01	2.08	0.00	1.84	0.01	2.06	0.02	AC151801	
MICRO 4618.C1_1396	1.16	0.38	0.64	0.02	0.81	0.14	0.33	0.00	1.83	0.01	1.44	0.08	1.89	0.01	1.67	0.61	AC137360	
BF_mfxxxx_0048024.13m.scf_18	0.02	0.00	0.04	0.00	0.04	0.00	0.18	0.04	1.68	0.01	1.71	0.00	1.70	0.00	2.71	0.00	NA	
MICRO 432.C14_712	0.51	0.12	0.50	0.02	0.49	0.16	0.37	0.05	7.11	0.00	5.27	0.00	2.56	0.00	1.08	0.60	NA	
STRM327V_522	0.83	0.23	0.63	0.08	0.82	0.29	0.82	0.37	3.23	0.00	1.30	0.12	2.00	0.01	0.99	0.97	AY303171	
BF_mfxxxx_0060610.13m.scf_500	0.25	0.00	0.20	0.00	0.17	0.00	0.27	0.00	2.94	0.00	2.36	0.00	2.45	0.00	2.77	0.00	NA	
BF_mfxxxx_0050420.13m.scf_71	0.45	0.01	0.40	0.01	0.40	0.01	0.27	0.00	2.47	0.00	1.24	0.02	1.45	0.01	1.22	0.01	AB124411	
MICRO 11344.C3_354	0.23	0.00	0.41	0.01	0.31	0.02	0.60	0.20	1.78	0.02	2.02	0.01	1.60	0.13	1.72	0.06	AY196080	
BF_mfxxxx_007205.13m.scf_1	0.52	0.09	0.49	0.08	0.60	0.04	0.46	0.03	2.43	0.00	1.68	0.26	1.88	0.07	2.13	0.01	NA	
MICRO 3971.C1_2941	0.28	0.01	0.38	0.01	0.38	0.01	0.24	0.02	3.84	0.00	2.92	0.01	1.51	0.04	1.90	0.04	AY439028	
SDRN04D20u.scf_291	0.24	0.00	0.39	0.03	0.31	0.02	0.35	0.04	2.62	0.01	2.92	0.00	2.31	0.01	1.97	0.02	NA	
MICRO 1643.C7_559	0.19	0.01	0.33	0.03	0.15	0.02	0.28	0.07	1.99	0.08	2.62	0.00	2.88	0.01	3.11	0.01	NA	
MICRO 2980.C1_1571	0.20	0.01	0.21	0.00	0.36	0.01	0.90	0.02	1.86	0.01	2.18	0.00	2.10	0.01	2.01	0.01	AC117236	
MICRO 26.C1_109	0.04	0.00	0.03	0.00	0.02	0.00	0.12	0.00	2.51	0.00	3.13	0.00	5.15	0.00	13.91	0.00	AB148037	
BF_mfxxxx_0036811.13m.scf_111	0.69	0.03	0.77	0.18	0.88	0.41	0.87	0.37	1.18	0.25	1.37	0.09	1.81	0.00	1.79	0.01	BT012736	
MICRO 7123.C1_894	0.32	0.01	0.32	0.01	0.31	0.01	0.31	0.01	1.37	0.01	1.15	0.22	1.18	0.10	1.15	0.22	hypothetical protein Os1_007448 (Oryza sativa [japonica cultivar-group])	
MICRO 1348.C1_584	0.67	0.03	0.78	0.20	0.77	0.13	0.83	0.30	1.20	0.22	1.20	0.44	1.26	0.13	1.22	0.30	NA	
BF_mfxxxx_0036811.13m.scf_22	0.38	0.02	0.25	0.00	0.44	0.02	0.98	0.87	1.57	0.03	1.00	0.99	1.41	0.28	1.78	0.03	AK224815	
MICRO 958.C1_89	0.11	0.04	0.04	0.01	0.07	0.02	0.72	0.12	7.02	0.00	1.78	0.02	1.12	0.01	1.76	0.01	NA	
BF_mfxxxx_0066403.13m.scf_72	0.53	0.35	0.22	0.04	0.38	0.04	0.54	0.21	2.11	0.01	1.24	0.20	1.75	0.02	1.12	0.70	AF009299	
BF_mfxxxx_0069811.13m.scf_463	0.46	0.00	0.43	0.00	0.60	0.01	0.66	0.02	2.56	0.00	2.32	0.08	2.48	0.01	3.21	0.01	AC122484	
MICRO 2286.C40_64	0.22	0.00	0.26	0.01	0.26	0.01	0.74	0.18	2.62	0.00	2.12	0.00	2.17	0.00	2.01	0.01	NA	
LS7B44N14H_269	0.23	0.00	0.24	0.04	0.33	0.08	0.74	0.50	1.54	0.05	1.59	0.03	1.88	0.01	5.18	0.00	CG350360	
BF_mfxxxx_0083411.17m.scf_306	0.90	0.81	0.52	0.01	0.61	0.01	0.68	0.03	1.58	0.22	1.80	0.07	2.56	0.06	3.78	0.04	NA	
MICRO 8671.C1_703	0.38	0.00	0.38	0.00	0.62	0.03	0.62	0.04	1.62	0.02	1.62	0.02	1.62	0.02	1.34	0.02	NA	
MICRO 5702.C2_644	0.55	0.02	0.63	0.05	0.71	0.05	0.93	0.85	1.38	0.15	1.30	0.16	1.47	0.05	1.81	0.04	AC122164	
LS7B3A57H_247	0.42	0.12	0.39	0.07	0.29	0.05	1.09	0.72	0.66	0.15								

MICRO332.C3_960	0.77	0.21	0.85	0.34	0.61	0.02	0.32	0.39	0.01	2.00	1.43	1.40	1.30	0.09	1.14	0.50	AY498744	40S ribosomal protein S5 (Capsicum annuum)
STMIC247RB_443	0.46	0.15	0.51	0.21	0.42	0.03	0.24	0.01	2.02	0.00	1.42	0.13	1.68	0.01	1.54	0.24	AF496987	BEL1-related homeotic protein 5 (Solanum tuberosum)
MICRO331.C29_82	0.24	0.09	0.36	0.03	0.26	0.02	0.26	0.12	1.58	0.04	1.83	0.05	1.48	0.06	2.13	0.01	AF269684	NA
STMAA87V_62	0.26	0.00	0.35	0.01	0.27	0.01	0.35	0.05	11.42	0.00	9.06	0.00	6.74	0.00	2.05	0.01	NA	NA
MICRO335.C2_1862	0.38	0.00	0.37	0.02	0.37	0.01	0.48	0.04	1.77	0.03	1.46	0.10	1.58	0.02	1.59	0.05	AY182188	ATPDL1-4 - electron transporter / isomerase / thiol-disulfide exchange intermediate [Arabidopsis thaliana]
MICRO1091.C2_442	0.10	0.03	0.19	0.01	0.14	0.00	0.11	0.00	3.08	0.01	3.01	0.01	3.00	0.01	4.31	0.01	NA	NA
MICRO1437B.C1_1085	0.33	0.01	0.42	0.03	0.32	0.02	0.41	0.07	2.15	0.00	1.97	0.01	2.02	0.01	1.51	0.11	AM454415	protein binding [Arabidopsis thaliana]
BF_LB359XXX_0054h03.13m.scf.601	0.87	0.41	0.65	0.14	0.64	0.10	0.57	0.19	2.48	0.00	1.61	0.06	1.51	0.08	1.62	0.03	NA	NA
MICRO2611.C1_1504	0.27	0.02	0.31	0.01	0.20	0.01	0.24	0.04	3.78	0.01	3.71	0.01	3.87	0.01	1.38	0.01	U58957	Adenosine precursor (ATP-diphosphatase) (Adenosine diphosphatase) (ADPase) (ATP-diphosphatase)
MICRO3036.C1_784	0.40	0.00	0.38	0.03	0.61	0.03	1.12	0.74	1.10	0.46	1.24	0.67	1.99	0.00	2.92	0.00	NA	Non-A-like (Medicago truncatula)
MICRO2094.C4_349	0.35	0.01	0.59	0.05	0.79	0.05	1.02	0.90	1.20	0.30	1.15	0.60	1.32	0.54	1.89	0.00	NA	Phytidoyl-S-phosphate-dependent enzyme, beta subunit [Medicago truncatula]
MICRO1268B.C1_446	0.20	0.00	0.28	0.01	0.49	0.01	0.49	0.06	2.15	0.02	2.63	0.04	2.11	0.01	2.87	0.01	NA	NA
SDNBDNF29u.scf.610	0.35	0.00	0.32	0.02	0.50	0.00	0.58	0.05	2.14	0.00	1.70	0.01	1.65	0.01	1.63	0.03	AF119940	NA
SSNDN20A79u.scf.489	0.18	0.01	0.28	0.07	0.14	0.03	0.18	0.14	1.52	0.07	2.68	0.00	1.93	0.01	3.65	0.00	NA	NA
MICRO11487.C1_739	0.37	0.00	0.47	0.01	0.68	0.03	0.88	0.40	1.51	0.02	1.20	0.27	1.52	0.01	1.46	0.08	AM428463	Chloroplast35400 [Chrysa salina (epionica cultivar-group)]
MICRO187.C2_212	0.10	0.00	0.16	0.00	0.34	0.08	1.60	0.07	0.84	0.73	2.59	0.21	6.64	0.00	29.08	0.00	U73733	NA
BF_LB359XXX_0057e08.13m.scf.66	0.42	0.03	0.61	0.03	0.66	0.03	0.57	0.03	2.12	0.02	1.49	0.06	1.77	0.00	1.63	0.03	AK224856	unknown [Arabidopsis thaliana]
BF_LB359XXX_0010h10.13m.scf.147	0.32	0.02	0.44	0.01	0.53	0.01	0.37	0.02	4.98	0.00	3.58	0.01	2.82	0.04	4.81	0.00	DC241945	NA
MICRO2286.C2_189	0.06	0.00	0.14	0.00	0.63	0.00	0.14	0.01	4.10	0.00	3.81	0.00	3.81	0.00	2.54	0.00	NA	NA
MICRO165.C11_970	0.44	0.00	0.47	0.00	0.66	0.03	0.69	0.30	1.83	0.00	1.38	0.05	1.81	0.00	2.47	0.00	U75994	SRE1b [Solanum tuberosum]
MICRO6224.C2_866	0.59	0.01	0.37	0.00	0.59	0.00	0.32	0.01	4.29	0.00	2.31	0.02	2.46	0.00	2.69	0.00	DC274179	Polyprotein, putative [Solanum demissum]
MICRO1018a.C2_511	0.23	0.00	0.23	0.00	0.21	0.00	0.46	0.01	2.27	0.00	2.02	0.01	2.14	0.00	1.70	0.00	NA	NA
LSTB45C12H_1	0.45	0.00	0.59	0.03	0.55	0.01	1.08	0.65	1.30	0.09	1.30	0.10	0.87	0.40	1.56	0.05	NA	NA
BF_LB359XXX_0012a02.17m.scf.610	0.48	0.05	0.51	0.12	0.31	0.00	0.84	0.06	2.47	0.00	2.09	0.01	1.85	0.02	1.86	0.01	AM471678	Actinidin-like [Medicago truncatula]
BF_LB359XXX_0004f09.13m.scf.562	0.35	0.15	0.39	0.08	0.30	0.02	0.63	0.23	1.28	0.16	1.71	0.02	1.82	0.02	2.07	0.01	NA	NA
BF_LB359XXX_0023a09.13m.scf.562	0.34	0.00	0.34	0.01	0.25	0.04	0.26	0.02	2.17	0.00	2.41	0.00	2.54	0.06	4.07	0.00	NA	calcium ion binding [Arabidopsis thaliana]
MICRO752H.C1_769	0.71	0.04	0.80	0.18	0.89	0.38	0.94	0.85	1.38	0.06	1.36	0.05	1.36	0.08	1.95	0.01	NA	NA
LSTB45H700	0.83	0.19	0.44	0.01	0.54	0.15	0.44	0.03	6.60	0.00	2.88	0.01	2.53	0.00	1.04	0.74	NA	BiP/R [Medicago truncatula]
BF_LB359XXX_0057e10.13m.scf.179	0.45	0.00	0.41	0.00	0.41	0.00	0.29	0.00	2.12	0.00	1.97	0.00	1.87	0.00	2.04	0.01	BT014607	NA
MICRO1222.C2_3168	0.68	0.01	0.65	0.02	0.63	0.01	0.53	0.01	1.57	0.01	1.30	0.10	1.39	0.11	1.24	0.20	AK228556	Armadillo-like helical [Medicago truncatula]
MICRO1762.C1_234	0.21	0.01	0.41	0.01	0.18	0.07	0.64	0.07	1.61	0.01	1.78	0.23	1.17	0.11	1.27	0.01	AF009261	NA
LPROH18H_1	0.61	0.01	0.58	0.03	0.72	0.07	0.61	0.02	1.35	0.07	1.59	0.02	1.78	0.01	1.38	0.10	NA	NA
BF_LB359XXX_0065e04.13m.scf.51	0.74	0.22	0.64	0.11	0.81	0.24	0.49	0.06	1.75	0.02	2.13	0.01	1.68	0.02	1.17	0.50	NA	NA
MICRO3024.C5_388	0.35	0.01	0.41	0.01	0.47	0.01	0.47	0.07	1.64	0.01	1.11	0.17	1.87	0.01	1.75	0.01	NA	hypothetical protein Ch1_018903 [Chrysa salina (epionica cultivar-group)]
MICRO1214b.C1_423	0.63	0.02	0.65	0.07	0.74	0.11	0.94	0.75	1.51	0.03	1.26	0.14	1.26	0.17	1.44	0.08	NA	protein kinase [Malus x domestica]
MICRO2298.C91_1360	0.13	0.00	0.19	0.01	0.13	0.01	0.26	0.04	3.45	0.00	2.48	0.00	2.53	0.00	2.51	0.00	NA	NA
MICRO1212.C1_771	0.84	0.04	0.84	0.04	0.88	0.04	0.88	0.01	1.04	0.01	1.04	0.01	1.04	0.01	1.04	0.01	BT013178	Chloroplast31700 [Chrysa salina (epionica cultivar-group)]
MICRO8460.C2_1243	0.53	0.00	0.67	0.03	0.74	0.07	0.81	0.58	1.10	0.48	1.25	0.14	1.37	0.03	1.82	0.01	AM454905	carboxyl ester hydrolase / catalytic hydrolase [Arabidopsis thaliana]
BF_LB359XXX_0062a12.13m.scf.655	0.30	0.01	0.37	0.04	0.58	0.06	0.88	0.64	3.41	0.00	1.30	0.25	2.24	0.00	1.41	0.28	NA	NA
MICRO888H.C1_226	0.42	0.01	0.38	0.01	0.39	0.01	0.41	0.01	2.68	0.00	2.19	0.00	2.19	0.00	2.49	0.00	NA	1-epigallocatechin [Arabidopsis thaliana]
BF_LB359XXX_0017c08.13m.scf.223	0.42	0.01	0.59	0.12	0.39	0.05	0.77	0.41	1.85	0.01	1.74	0.06	1.78	0.04	2.00	0.03	NA	NA
POCBW127V_551	0.68	0.08	0.82	0.17	0.83	0.17	0.81	0.17	1.13	0.33	1.38	0.03	1.06	0.52	1.54	0.04	NM_005273	G protein beta 2 subunit [Rattus norvegicus]
MICRO709.C2_869	0.50	0.01	0.52	0.08	0.48	0.03	0.68	0.29	1.48	0.07	1.40	0.07	1.34	0.03	1.43	0.16	NA	NA
MICRO1115.C2_1798	0.48	0.01	0.48	0.01	0.56	0.01	0.56	0.01	2.27	0.01	2.46	0.00	2.00	0.00	1.24	0.15	AF482891	cystathionine gamma-synthase isoform 1 [Solanum tuberosum]
BF_LB359XXX_0057f12.13m.scf.569	0.20	0.00	0.20	0.00	0.32	0.00	0.25	0.00	2.61	0.01	2.55	0.00	2.73	0.03	1.99	0.01	NA	NA
BF_LB359XXX_0056b06.13m.scf.171	0.46	0.00	0.64	0.02	0.79	0.38	0.88	0.04	1.31	0.40	1.53	0.02	2.23	0.00	2.87	0.00	NA	NA
MICRO876H.C4_1	0.83	0.01	0.83	0.01	0.97	0.01	0.96	0.01	1.26	0.01	1.26	0.01	1.26	0.01	1.26	0.01	AF422548	17.8 kDa class I heat shock protein (Hsp20.0)
MICRO1017.C2_1119	0.72	0.04	0.78	0.14	0.90	0.45	0.81	0.29	1.13	0.43	1.10	0.48	1.12	0.45	1.49	0.08	BA800042	ATPK5, phosphoglycolate phosphatase [Arabidopsis thaliana]
MICRO1839H.C1_690	0.23	0.01	0.29	0.10	0.19	0.02	0.36	0.13	6.34	0.00	3.22	0.00	3.17	0.00	1.71	0.06	NA	NA
MICRO3807.C1_710	0.88	0.01	0.74	0.01	0.76	0.01	1.36	0.12	1.47	0.01	1.56	0.01	1.47	0.01	1.82	0.01	AB192882	iron chain dehydrogenase [Solanum tuberosum]
MICRO1193b.C1_1438	0.39	0.01	0.51	0.02	0.48	0.01	0.69	0.08	1.19	0.16	1.36	0.08	1.45	0.02	1.12	0.46	NA	NA
MICRO1212.C1_64	0.84	0.01	0.44	0.02	0.48	0.01	0.58	0.05	2.20	0.00	2.16	0.00	1.79	0.01	2.12	0.01	AC193778	NA
MICRO7929.C1_557	0.22	0.02	0.22	0.02	0.17	0.01	0.22	0.11	4.43	0.08	1.92	0.12	1.98	0.01	1.98	0.01	NA	NA
MICRO867H.C1_1069	0.80	0.17	0.78	0.32	0.67	0.16	0.68	0.30	3.06	0.01	2.42	0.00	1.71	0.06	1.03	0.93	U93444	inositol monophosphatase 1 (IMPase 1) (IMP 1) (inositol-1-lip-dimorphosphatase 1)
BF_LB359XXX_0024c11.13m.scf.41	0.24	0.01	0.27	0.01	0.25	0.03	0.37	0.03	2.95	0.04	2.10	0.00	2.28	0.00	2.41	0.01	NA	NA
MICRO1181.C2_1223	0.46	0.03	0.64	0.04	0.71	0.05	0.67	0.26	1.68	0.01	1.65	0.01	1.68	0.01	1.88	0.01	AM451749	Chloroplast20100 [Chrysa salina (epionica cultivar-group)]
MICRO1781.C1_1624	0.61	0.02	0.56	0.14	0.53	0.03	0.67	0.39	2.19	0.00	1.64	0.07	1.87	0.01	1.03	0.88	NA	hydrolase [Arabidopsis thaliana]
POAC337P_841	0.22	0.00	0.31	0.04	0.34	0.01	0.52	0.14	1.87	0.01	1.86	0.02	2.05	0.01	1.50	0.19	NA	NA
BF_LB359XXX_0005b13.13m.scf.378	0.12	0.00	0.14	0.00	0.16	0.01	0.16	0.01	6.86	0.00	6.80	0.00	6.80	0.00	6.80	0.00	AF151395	NA
MICRO10267.C1_865	0.29	0.00	0.40	0.02	0.28	0.00	0.50	0.03	2.31	0.00	2.19	0.00	1.79	0.01	1.77	0.02	NA	NA
SDNBDN30H.scf.149	0.73	0.05	0.88	0.41	0.98	0.81	0.98	0.77	1.37	0.07	1.29	0.12	1.16	0.67	1.75	0.02	BT014077	contains similarity to poly(A)-binding protein II [Arabidopsis thaliana]
MICRO1408B.C1_1335	0.53	0.01	0.60	0.01	0.68	0.01	0.68	0.01	1.98	0.15	1.98	0.01	1.98	0.01	1.98	0.01	BT0174807	NA
MICRO1593b.C1_736	0.27	0.02	0.32	0.01	0.42	0.00	0.63	0.06	2.52	0.01	3.24	0.04	3.12	0.00	3.07	0.00	NA	unknown protein [Arabidopsis thaliana]
089H10AF.scf.557	0.40	0.01	0.51	0.08	0.55	0.08	0.73	0.37	1.22	0.31	1.39	0.33	1.41	0.09	1.23	0.62	NA	TR-NBS-LRR disease resistance-like protein [Populus balsamifera]
MICRO5245.C1_796	0.84	0.86	0.85	0.86	0.84	0.87	0.84	0.87	2.78	0.00	3.32							

BF_LBCH0000_00180505_TSM_SCF_217	0.32	0.01	0.30	0.05	0.24	0.02	0.57	0.24	0.37	0.00	2.72	0.02	2.82	0.00	2.01	0.02	NA
MICRO_12590.C3_1123	0.46	0.00	0.55	0.02	0.66	0.04	0.38	0.00	1.78	0.01	2.25	0.00	2.46	0.00	1.88	0.01	AM424577
MICRO_12603.C2_209	0.37	0.01	0.36	0.01	0.43	0.00	1.77	0.24	1.06	0.70	1.23	0.22	1.38	0.02	3.35	0.00	AD49492
MICRO_2286.C4_872	0.28	0.08	0.21	0.00	0.16	0.00	0.34	0.01	2.43	0.01	2.08	0.00	1.99	0.00	1.37	0.01	NA
MICRO_12403.C2_373	0.17	0.00	0.29	0.00	0.36	0.06	0.34	0.01	4.10	0.00	5.20	0.00	4.06	0.04	4.79	0.01	AJ217853
MICRO_12727.C1_371	0.86	0.21	0.61	0.03	0.77	0.01	0.77	0.01	1.53	0.03	1.77	0.01	1.77	0.01	1.77	0.01	AT101311
BF_LBCH0000_001007_TSM_SCF_368	0.21	0.02	0.33	0.00	0.29	0.00	0.38	0.01	2.55	0.01	3.32	0.01	2.89	0.00	2.01	0.01	NA
MICRO_1137.C1_1015	0.84	0.68	0.73	0.50	0.79	0.71	0.63	0.25	1.59	0.06	1.96	0.28	1.67	0.10	1.56	0.23	NA
BF_mvfxxxx_00090103_03m_scf_520	0.32	0.01	0.66	0.12	0.54	0.03	0.44	0.03	1.85	0.03	2.18	0.03	1.78	0.15	1.71	0.00	AY167828
BF_mvfxxxx_005105_03m_scf_42	0.58	0.00	0.43	0.01	0.78	0.08	0.98	0.85	1.44	0.08	0.92	0.56	1.75	0.01	2.40	0.00	NA
BF_TUBSXXXX_0022712_TSM_SCF_338	0.13	0.01	0.16	0.03	0.14	0.02	0.43	0.03	0.65	0.00	2.20	0.02	3.46	0.00	3.12	0.01	NA
EST1_TK147H_763	0.82	0.16	0.45	0.01	0.48	0.12	0.45	0.01	0.94	0.01	1.79	0.01	1.78	0.01	1.83	0.01	NA
MICRO_3554.C1_1072	0.62	0.01	0.42	0.00	0.56	0.00	0.35	0.00	2.20	0.00	1.77	0.01	1.88	0.00	1.93	0.00	BT013178
09H08AF_sml_634	0.58	0.00	0.58	0.01	0.52	0.00	1.09	0.51	1.03	0.82	1.39	0.28	1.61	0.01	6.18	0.00	DC200394
BF_mvfxxxx_001560103m_scf_141	0.15	0.00	0.24	0.00	0.18	0.00	0.28	0.01	1.79	0.01	1.78	0.01	1.83	0.01	2.15	0.00	NA
MICRO_10185.C1_1113	0.13	0.00	0.27	0.08	0.09	0.02	0.28	0.11	2.85	0.07	2.49	0.07	3.38	0.05	2.40	0.01	U71107
MICRO_2286.C24_896	0.26	0.00	0.42	0.02	0.34	0.01	0.29	0.05	8.52	0.00	4.08	0.00	4.42	0.00	2.11	0.02	NA
19E11AF_sml_692	0.21	0.07	0.20	0.16	0.20	0.02	0.42	0.11	2.49	0.01	2.51	0.00	2.17	0.00	1.81	0.04	BT013258
BF_mvfxxxx_00090103_03m_scf_76	0.21	0.00	0.29	0.00	0.46	0.05	0.53	0.16	1.56	0.02	1.74	0.13	2.31	0.01	3.37	0.00	NA
MICRO_6888.C1_1002	0.35	0.01	0.63	0.01	0.31	0.02	0.49	0.11	1.48	0.11	2.25	0.11	1.96	0.03	1.80	0.02	NA
MICRO_12584.C1_397	0.50	0.04	0.52	0.01	0.47	0.01	0.13	0.00	4.00	0.00	2.57	0.02	3.39	0.00	1.87	0.08	AJ133601
BF_mvfxxxx_00090103_03m_scf_409	0.53	0.07	0.49	0.00	0.59	0.08	0.37	0.02	5.15	0.00	4.60	0.01	1.39	0.47	2.17	0.09	NA
MICRO_10720.C2_586	0.80	0.09	0.52	0.01	0.52	0.01	0.57	0.04	3.15	0.01	1.84	0.04	1.68	0.07	1.50	0.04	NA
MICRO_12079.C1_950	0.57	0.01	0.80	0.29	0.73	0.10	0.96	0.80	0.97	0.86	2.02	0.04	1.45	0.07	1.86	0.01	NA
MICRO_2286.C78_1794	0.16	0.01	0.16	0.04	0.05	0.03	0.18	0.14	3.89	0.00	2.95	0.05	3.14	0.01	2.30	0.01	NA
MICRO_6877.C3_114	0.35	0.00	0.42	0.00	0.54	0.00	0.75	0.09	1.55	0.03	1.86	0.05	2.41	0.03	4.04	0.00	MC4399
BF_TUBSXXXX_00060505_TSM_SCF_316	0.18	0.00	0.34	0.01	0.38	0.01	0.42	0.05	1.68	0.02	1.72	0.01	1.69	0.03	2.40	0.00	NA
BF_mvfxxxx_00090103_03m_scf_190	0.39	0.01	0.50	0.08	0.51	0.07	0.74	0.44	2.18	0.01	2.02	0.01	1.28	0.23	2.01	0.02	CU120847
MICRO_1508.C1_581	0.39	0.01	0.42	0.08	0.35	0.04	0.70	0.27	2.40	0.05	3.45	0.00	2.58	0.00	5.66	0.00	NA
STM087V_638	0.84	0.37	0.56	0.03	0.56	0.05	0.50	0.05	1.91	0.02	1.36	0.11	1.60	0.02	1.19	0.44	NA
STM087V_373	0.29	0.03	0.26	0.31	0.23	0.05	0.33	0.05	3.33	0.05	3.27	0.06	16.34	0.20	12.92	0.20	L22922
MICRO_250.C1_1275	0.69	0.05	0.48	0.08	0.68	0.28	0.71	0.05	1.65	0.01	3.31	0.21	1.38	0.03	1.76	0.02	BT013388
MICRO_12760.C1_657	0.35	0.02	0.55	0.13	0.42	0.04	0.73	0.37	1.79	0.02	1.63	0.03	1.84	0.02	1.62	0.16	AM438262
MICRO_2286.C83_837	0.16	0.00	0.22	0.07	0.14	0.02	0.14	0.02	3.58	0.02	3.01	0.02	3.81	0.00	2.03	0.00	NA
ESTAS15TH_219	0.07	0.00	0.09	0.00	0.05	0.00	0.09	0.01	2.57	0.00	2.46	0.00	2.46	0.00	2.53	0.00	DC027848
MICRO_13698.C4_392	0.29	0.04	0.36	0.05	0.29	0.04	0.88	0.79	1.67	0.10	1.74	0.02	2.10	0.05	2.64	0.00	NA
MICRO_13698.C1_1885	0.81	0.81	0.78	0.81	0.81	0.81	0.81	0.81	0.81	0.81	0.81	0.81	0.81	0.81	0.81	0.81	AP0909271
MICRO_432.C7_872	0.93	0.89	0.65	0.06	0.53	0.13	0.43	0.08	6.96	0.00	3.47	0.00	2.58	0.00	1.17	0.35	NA
PPCC527H_663	0.56	0.03	0.81	0.39	0.71	0.20	0.46	0.01	2.38	0.04	2.43	0.08	1.84	0.17	2.79	0.01	NA
MICRO_286.C1_1472	0.17	0.01	0.21	0.02	0.19	0.02	0.43	0.02	0.63	0.00	2.78	0.00	2.78	0.00	2.84	0.00	NA
ESTE1F10H_837	0.63	0.04	0.63	0.15	0.53	0.35	0.48	0.10	2.45	0.04	2.37	0.07	3.08	0.01	1.00	0.99	NA
06F02AF_sml_475	0.80	0.14	0.87	0.50	0.70	0.08	0.80	0.42	1.16	0.32	1.26	0.18	1.21	0.28	1.18	0.47	NM_120741
ACDAB03V70m_sml_21	0.57	0.01	0.71	0.10	0.67	0.02	0.83	0.29	1.07	0.80	1.51	0.04	1.85	0.04	2.81	0.00	NA
MICRO_19425.C2_1257	0.13	0.01	0.32	0.08	0.06	0.00	0.11	0.28	0.01	0.29	0.01	0.29	0.01	2.06	0.00	AY242031	
MICRO_8889.C1_823	0.64	0.19	0.54	0.05	0.51	0.00	0.64	0.07	1.66	0.01	2.55	0.00	1.51	0.01	0.84	0.47	NA
MICRO_12343.C1_703	0.44	0.00	0.07	0.00	0.13	0.01	0.08	0.02	6.62	0.00	3.78	0.03	6.64	0.01	132386	NA	
POCAY84TP_462	0.28	0.01	0.28	0.01	0.28	0.01	0.28	0.01	0.28	0.01	0.28	0.01	0.28	0.01	0.28	0.01	NA
MICRO_6410.C1_710	0.37	0.00	0.47	0.04	0.42	0.01	0.61	0.11	1.29	0.13	1.35	0.13	1.54	0.04	1.92	0.01	AP0909256
MICRO_12343.C1_703	0.55	0.10	0.63	0.04	0.64	0.03	0.48	0.02	2.54	0.00	2.74	0.01	2.68	0.01	1.48	0.12	NA
MICRO_12501.C1_698	0.28	0.01	0.38	0.04	0.38	0.03	0.38	0.03	2.06	0.04	2.45	0.01	2.45	0.01	2.45	0.01	NA
ESTP0327H_784	0.52	0.00	0.77	0.16	0.82	0.11	0.62	0.05	1.98	0.00	1.84	0.06	1.83	0.01	2.10	0.00	AP0909271
MICRO_12694.C2_253	0.74	0.16	0.80	0.20	0.65	0.04	0.90	0.81	1.20	0.27	1.54	0.02	1.06	0.64	2.57	0.00	AY137315
MICRO_8693.C2_1677	0.05	0.00	0.16	0.01	0.17	0.01	0.17	0.01	2.49	0.03	2.85	0.03	2.85	0.03	2.85	0.03	BT014206
ESTB411TH_300	0.30	0.00	0.32	0.02	0.32	0.01	0.65	0.14	0.33	0.14	0.40	0.17	0.28	0.89	0.13	NA	
SDNR01L05u_sml_399	0.22	0.01	0.21	0.03	0.24	0.01	0.48	0.05	1.84	0.01	2.20	0.00	2.22	0.01	2.58	0.00	NA
BF_mvfxxxx_00090103_03m_scf_159	0.65	0.08	0.65	0.08	0.65	0.08	0.65	0.08	0.65	0.08	0.65	0.08	0.65	0.08	0.65	0.08	NA
STB0602G13u_sml_383	0.44	0.01	0.38	0.13	0.38	0.16	0.72	0.18	1.69	0.02	1.62	0.05	1.38	0.07	1.96	0.01	AC149290
MICRO_12265.C1_556	0.27	0.00	0.56	0.07	0.44	0.01	1.00	0.99	1.84	0.21	3.35	0.08	2.82	0.11	4.63	0.01	NA
BF_TUBSXXXX_000309_TSM_SCF_247	0.10	0.01	0.21	0.01	0.08	0.02	0.08	0.02	3.04	0.01	3.04	0.01	3.16	0.00	1.98	0.00	NA
MICRO_10277.C1_412	0.72	0.06	0.62	0.03	0.78	0.07	0.67	0.04	1.29	0.19	1.37	0.07	1.56	0.01	1.50	0.04	NA
MICRO_2347.C2_894	0.74	0.08	0.73	0.07	0.75	0.06	0.87	0.27	1.18	0.27	1.59	0.01	1.84	0.00	1.85	0.01	AM446868
MICRO_2286.C107_376	0.48	0.01	0.54	0.08	0.68	0.08	0.68	0.08	0.34	0.32	0.81	0.01	0.81	0.01	0.81	0.01	NA
BF_mvfxxxx_004502_03m_scf_391	0.57	0.03	0.79	0.42	0.69	0.07	1.08	0.79	1.34	0.14	1.88						

POCCR37P_862	0.08	0.00	0.19	0.02	0.06	0.01	0.20	0.02	2.77	0.08	2.99	0.01	2.11	0.14	1.80	0.02	NA	NA
MICRO1081_C29_887	0.49	0.08	0.74	0.31	0.41	0.01	0.35	0.01	1.81	0.06	2.15	0.02	1.24	0.11	1.28	0.05	AP009271	NA
MICRO895.C1_752	0.55	0.07	0.95	0.18	0.65	0.48	0.62	0.41	2.93	0.01	1.65	0.18	2.77	0.04	2.77	0.02	NA	Heat shock protein DnaJ [Medicago truncatula]
MICRO1623.C1_21	0.37	0.04	0.59	0.24	0.46	0.28	1.04	0.89	1.63	0.18	2.77	0.07	2.52	0.00	3.08	0.00	AN430462	nucleic acid binding [Arabidopsis thaliana]
lf_mfxxxx_000305.03m.scd_342	0.62	0.02	0.74	0.11	0.74	0.07	0.74	0.10	2.06	0.01	1.41	0.08	1.85	0.01	1.26	0.01	AY428286	slight resistance protein T18 [Solanum torajense]
MICRO1593.C1_521	0.01	0.01	0.08	0.01	0.01	0.01	0.05	0.01	2.49	0.01	0.01	0.28	0.01	0.01	0.01	0.01	NA	NA
MICRO432_C6_789	0.68	0.03	0.55	0.02	0.54	0.13	0.43	0.05	5.17	0.00	3.07	0.00	2.18	0.01	1.10	0.47	NA	RD22-like protein [Vitis vinifera]
TBSK018FD04.03m.scd_150	0.47	0.00	0.60	0.02	0.60	0.01	1.47	0.03	1.04	0.84	1.37	0.42	1.92	0.00	7.48	0.00	DC020394	NA
MICRO2335.C1_690	0.47	0.02	0.72	0.02	0.68	0.01	0.68	0.10	1.43	0.09	1.55	0.06	1.77	0.01	1.45	0.06	CG372924	unknown protein product [Arabidopsis thaliana]
MICRO12017.C1_741	0.35	0.03	0.43	0.04	0.22	0.00	0.50	0.03	1.58	0.02	1.43	0.06	1.18	0.01	1.62	0.04	AK224807	NA
STMCH07V_168	0.57	0.06	0.64	0.06	0.41	0.01	0.55	0.03	2.27	0.01	1.92	0.01	1.20	0.18	1.79	0.01	NA	NA
POCR307V_419	0.68	0.05	0.78	0.05	0.68	0.04	0.60	0.05	3.98	0.00	2.54	0.00	2.72	0.01	1.45	0.08	NA	NA
lPROIE147H_203	0.49	0.00	0.63	0.04	0.64	0.02	0.44	0.01	2.87	0.00	2.86	0.00	1.75	0.05	3.49	0.04	AP009271	NA
MICRO11861.C1_1015	0.10	0.01	0.18	0.04	0.15	0.01	0.36	0.10	3.07	0.00	2.62	0.03	3.40	0.00	2.46	0.01	NA	NA
STMJ07V_219	0.29	0.00	0.35	0.04	0.40	0.03	0.98	0.93	1.99	0.15	1.20	0.47	1.81	0.01	3.10	0.00	AN488786	Chp70691200 [Oryza sativa (japonica cultivar-group)]
MICRO847.C1_241	0.49	0.08	0.70	0.17	0.58	0.04	0.76	0.22	1.77	0.02	1.85	0.01	1.55	0.17	2.83	0.00	AC149395	NA
MICRO10360.C2_733	0.39	0.12	0.41	0.11	0.25	0.00	0.39	0.00	1.59	0.18	1.83	0.12	1.73	0.01	2.38	0.00	CG329701	CTV22 [Panicum tritiforme]
lf_sapxxxx_000909.03m.scd_630	0.91	0.80	0.94	0.98	0.89	0.80	0.31	0.00	1.63	0.24	1.81	0.05	1.95	0.25	1.34	0.07	NA	hypothetical protein MHR4FT_AC107263b2 [Medicago truncatula]
MICRO12460.C2_1173	0.76	0.30	0.71	0.25	0.54	0.01	0.88	0.05	1.99	0.89	1.68	0.03	1.16	0.26	1.94	0.00	NA	UDP-N-acetylglucosamine-2-glucamate lyase [Physocarpus opulifolius]
STMH91TV_533	0.76	0.10	0.64	0.04	0.74	0.07	0.79	0.13	1.22	0.22	1.26	0.16	1.35	0.05	1.27	0.12	ZS4527	Signal recognition particle 54 kDa protein 2 (SRP54)
MICRO8902.C1_429	1.07	0.71	1.00	0.84	0.91	0.01	0.35	0.02	1.91	0.01	1.46	0.15	1.53	0.05	1.24	0.22	AB032038	chromomethylase-like protein [Nicotiana glauca]
MICRO36.C2_147	0.86	0.21	0.78	0.28	0.62	0.02	0.64	0.02	2.22	0.00	3.17	0.00	1.36	0.02	1.92	0.88	DC028446	unknown [Solanum tuberosum]
lSTB13AH7H_425	0.43	0.00	0.50	0.08	0.45	0.02	0.75	0.24	1.45	0.06	1.66	0.04	1.56	0.03	1.43	0.12	NA	NA
MICRO1206C_C4_1279	0.16	0.01	0.23	0.08	0.12	0.02	0.41	0.13	3.53	0.00	2.05	0.01	2.37	0.00	1.62	0.04	AY940339	calcium-dependent protein kinase 4 [Capsicum annuum]
lf_LBCH00X_000306.TM.SCF_241	0.25	0.02	0.47	0.18	0.31	0.06	1.01	0.97	1.45	0.14	1.54	0.10	1.51	0.15	1.95	0.07	NA	NA
MICRO6656.C2_1014	0.25	0.00	0.29	0.05	0.39	0.08	0.76	0.68	1.13	0.36	1.28	0.25	1.58	0.01	3.71	0.00	AK224646	NA
MICRO8726.C1_403	1.17	0.18	0.82	0.33	0.67	0.02	0.17	0.00	4.17	0.03	5.01	0.00	1.42	0.35	0.42	0.00	AK224774	BT2D-like protein [Beta vulgaris]
MICRO3745.C1_1872	0.65	0.01	0.87	0.34	0.95	0.72	0.61	0.03	1.72	0.01	1.46	0.04	1.28	0.21	1.04	0.63	NA	NA
MICRO14770.C1_919	0.30	0.02	0.29	0.02	0.32	0.02	0.79	0.15	0.61	0.04	2.73	0.06	3.22	0.07	5.83	0.01	NA	unknown protein [Arabidopsis thaliana]
MICRO7411_C2_680	0.13	0.00	0.26	0.02	0.16	0.01	0.34	0.04	1.55	0.02	1.60	0.03	1.63	0.01	1.27	0.19	CG191837	NA
MICRO56.C2_721	0.30	0.01	0.27	0.01	0.27	0.01	0.24	0.03	1.93	0.01	1.07	0.01	1.87	0.01	2.00	0.01	NA	Plant cell wall protein [Medicago truncatula]
lSTA3611H_271	0.65	0.04	0.86	0.58	0.69	0.08	0.68	0.52	2.01	0.00	1.75	0.05	1.67	0.02	1.09	0.76	NA	NA
MICRO11789.C1_360	0.51	0.00	0.75	0.07	0.69	0.03	0.73	0.14	1.54	0.02	1.79	0.01	1.34	0.08	1.61	0.17	AC149291	NA
MICRO3259.C1_841	0.34	0.04	0.34	0.04	0.44	0.08	0.44	0.05	2.63	0.02	2.63	0.02	6.34	0.01	2.35	0.00	AN475461	AT3G09K9 [Arabidopsis thaliana]
STMDF68TV_656	0.15	0.01	0.18	0.02	0.15	0.01	0.47	0.08	1.29	0.17	2.06	0.00	1.78	0.05	3.49	0.00	NA	NA
lSTA2624TH_283	0.34	0.01	0.44	0.05	0.19	0.02	0.60	0.24	1.36	0.23	1.89	0.02	2.09	0.01	3.18	0.00	AM431899	unnamed protein product [Arabidopsis thaliana]
STRB0265a.scd_686	0.38	0.00	0.59	0.01	0.59	0.01	1.05	0.01	1.62	0.01	1.62	0.01	1.62	0.01	1.62	0.01	NA	hypothetical protein [Arabidopsis thaliana]
MICRO2013.C7_858	0.50	0.07	0.85	0.73	0.48	0.00	0.58	0.05	1.25	0.19	1.44	0.25	1.41	0.03	1.85	0.01	AC151801	Plum tree disease resistance protein DCS-1 [Solanum demissum]
lf_LBCH00X_000704.TM.SCF_418	0.50	0.00	0.36	0.00	0.50	0.00	0.27	0.00	1.78	0.00	1.74	0.01	1.83	0.00	1.78	0.00	NA	NA
MICRO15819.C1_628	0.62	0.08	0.62	0.08	0.62	0.08	0.62	0.08	1.24	0.07	1.24	0.07	1.24	0.07	1.24	0.07	NA	hypothetical protein Chl_003594 [Oryza sativa (indica cultivar-group)]
lf_mfxxxx_001363.03m.scd_24	0.21	0.00	0.28	0.02	0.22	0.02	0.54	0.05	1.20	0.26	2.65	0.00	1.48	0.03	3.83	0.00	BT012751	NA
lf_LBCH00X_000508.TM.SCF_601	0.65	0.01	0.71	0.08	0.73	0.09	0.57	0.06	1.71	0.01	1.89	0.03	1.02	0.92	2.11	0.01	NA	NA
MICRO4534.C1_986	0.26	0.01	0.31	0.03	0.23	0.03	0.49	0.16	1.74	0.02	2.43	0.00	2.09	0.01	1.80	0.00	NA	NA
MICRO11734.C1_950	0.71	0.16	0.71	0.16	0.89	0.29	0.39	0.24	1.99	0.24	1.99	0.24	1.99	0.24	1.99	0.01	BT013369	putative protein [Arabidopsis thaliana]
MICRO2545.C2_699	0.44	0.01	0.59	0.07	0.52	0.00	0.51	0.04	1.85	0.09	2.42	0.02	1.73	0.15	2.43	0.05	AF411807	transcription factor [Arabidopsis thaliana]
MICRO1622.C1_397	0.48	0.02	0.52	0.01	0.66	0.04	0.75	0.14	1.11	0.47	1.20	0.18	1.37	0.05	1.50	0.03	NA	NA
MICRO13862.C1_591	0.74	0.02	0.74	0.02	0.61	0.08	0.74	0.02	1.29	0.27	1.29	0.27	1.29	0.27	1.29	0.01	AP009283	RNA binding / transcription factor [Arabidopsis thaliana]
MICRO17986.C1_306	0.51	0.00	0.93	0.66	0.75	0.07	0.73	0.06	1.63	0.01	1.94	0.01	1.10	0.48	2.24	0.00	CG120847	NA
MICRO3156.C1_1188	0.77	0.18	0.74	0.09	0.91	0.37	0.66	0.03	1.59	0.01	1.19	0.26	1.35	0.04	1.29	0.00	NA	putative DNA binding protein-like [Solanum tuberosum]
MICRO1663.C5_221	0.38	0.01	0.38	0.01	0.38	0.01	0.38	0.01	2.31	0.00	2.31	0.00	2.31	0.00	2.31	0.00	NA	hypothetical protein [Arabidopsis thaliana]
lf_aryxxxx_004609.07m.scd_611	0.43	0.11	0.38	0.05	0.28	0.01	0.54	0.10	2.54	0.07	2.68	0.02	1.22	0.23	3.98	0.00	BT013402	unknown protein [Arabidopsis thaliana]
MICRO1189.C6_894	0.38	0.00	0.14	0.01	0.39	0.01	0.18	0.02	2.77	0.00	3.49	0.00	3.18	0.00	8.26	0.00	DC035080	CYP72A56 [Nicotiana glauca]
lSTR219TH_66	0.88	0.01	0.88	0.01	0.88	0.01	0.88	0.01	4.02	0.13	4.02	0.13	4.02	0.13	4.02	0.13	NA	NA
MICRO6029.C4_568	0.75	0.09	0.71	0.08	0.75	0.10	0.48	0.01	1.95	0.00	1.51	0.03	1.82	0.01	1.16	0.04	NA	NA
MICRO2525.C1_381	0.33	0.02	0.23	0.04	0.12	0.03	0.19	0.16	3.21	0.00	3.27	0.04	3.38	0.01	4.90	0.01	NA	NA
MICRO9027.C1_728	0.68	0.01	0.68	0.01	0.68	0.01	0.68	0.01	1.54	0.03	1.54	0.03	1.54	0.03	1.54	0.03	AK224798	Taf5 [Nicotiana tomentosifolia]
lf_aryxxxx_004905.07m.scd_659	0.70	0.03	0.72	0.07	0.66	0.03	0.93	0.58	1.01	0.98	1.62	0.02	1.38	0.04	3.14	0.00	BT013317	NA
MICRO8033.C1_707	0.30	0.00	0.50	0.01	0.46	0.01	0.41	0.01	3.15	0.01	4.11	0.00	2.93	0.07	4.09	0.01	NA	NA
lf_mfxxxx_002211.03m.scd_159	0.25	0.01	0.25	0.01	0.25	0.01	0.25	0.01	0.68	0.02	0.74	0.02	0.74	0.02	0.74	0.02	NA	NA
POCD425TV_238	0.43	0.00	0.71	0.08	0.64	0.02	1.15	0.32	1.10	0.55	1.97	0.06	1.19	0.22	2.48	0.00	NA	NA
lf_TUBS00X_005101H.TM.SCF_307	0.27	0.02	0.22	0.03	0.14	0.02	0.43	0.10	1.74	0.02	1.70	0.02	1.92	0.01	2.63	0.00	NA	NA
MICRO3268.C1_1043	0.78	0.01	0.48	0.01	0.48	0.01	0.48	0.01	0.48	0.01	0.48	0.01	0.48	0.01	0.48	0.01	AK248632	nitric acid oxidizing protein 2 [Nicotiana glauca]
MICRO3258.C2_607	0.53	0.02	0.64	0.04	0.48	0.01	0.62	0.05	2.92	0.00	1.72	0.02	1.88	0.04	1.86	0.03	AM459161	ATMPK9 [Arabidopsis thaliana]
MICRO6747.C5_548	0.42	0.03	0.57	0.01	0.70	0.05	0.42	0.07	1.28	0.00	1.82	0.04	2.04	0.01	1.98	0.00	NA	NA
MICRO1603.C1_307	0.72	0.13	0.71	0.13	0.79	0.55	0.73	0.20	1.93	0.30	1.28	0.28	1.22	0.63	2.04	0.01	BT019620	unknown protein [Arabidopsis thaliana]
MICRO7720.C1_678	0.53	0.07	0.58	0.22	0.43	0.01	0.41	0.07	2.17	0.0								

bf. araxxxx_0083a10.17m.scd_685	0.85	0.21	0.72	0.21	0.67	0.05	0.68	0.18	1.33	0.10	1.31	0.13	1.43	0.05	1.78	0.01	NA
MICRO_10626.C1_1240	0.42	0.04	0.42	0.42	0.27	0.08	0.51	0.19	1.44	0.09	1.58	0.16	1.23	0.38	1.81	0.21	NA
MICRO_2296.C1_246	0.10	0.01	0.10	0.10	0.11	0.01	0.22	0.02	4.92	0.01	4.85	0.01	3.97	0.01	2.01	0.01	NA
Pvotr0506.scd_400	0.09	0.00	0.25	0.00	0.45	0.19	1.53	0.29	1.03	0.79	2.74	0.18	5.05	0.00	29.22	0.01	NA
MICRO_7593.C1_798	0.45	0.11	0.56	0.14	0.59	0.10	0.60	0.20	1.37	0.12	1.37	0.08	1.57	0.04	2.33	0.01	NA
MICRO_339.C1_340	0.10	0.01	0.10	0.10	0.10	0.01	0.20	0.01	1.59	0.01	1.53	0.01	1.32	0.01	4.01	0.01	NA
MICRO_1081.C25_1065	0.32	0.00	0.56	0.01	0.45	0.00	0.30	0.00	1.98	0.00	2.14	0.01	1.66	0.02	2.49	0.01	AF090271
POAB1907F_351	0.18	0.00	0.28	0.00	0.22	0.00	0.55	0.01	1.66	0.02	2.14	0.00	2.80	0.04	9.61	0.01	NA
MICRO_2296.C1_434	0.24	0.01	0.31	0.01	0.26	0.01	0.45	0.01	2.61	0.01	2.87	0.01	2.19	0.01	2.07	0.01	NA
MICRO_416.C13_1087	0.45	0.00	0.62	0.01	0.67	0.03	1.04	0.76	1.30	0.30	1.94	0.11	2.26	0.00	6.62	0.00	DQ200394
MICRO_17603.C1_124	0.62	0.01	0.66	0.04	0.71	0.04	0.56	0.01	1.91	0.01	1.81	0.01	2.01	0.01	1.67	0.00	AF008127
MICRO_1564.C1_484	0.20	0.00	0.21	0.00	0.21	0.00	0.36	0.01	1.85	0.01	2.58	0.00	1.86	0.01	2.84	0.01	NA
MICRO_432.C9_610	0.56	0.08	0.56	0.02	0.30	0.01	0.30	0.01	6.08	0.00	3.47	0.00	1.39	0.10	1.20	0.06	NA
MICRO_12406.C1_533	0.57	0.04	0.48	0.00	0.68	0.21	0.33	0.00	1.56	0.02	1.27	0.19	1.26	0.05	1.43	0.03	NA
bf. mxtxxxx_00310a10.13m.scd_188	0.81	0.11	0.68	0.04	0.80	0.06	1.18	0.27	1.13	0.44	1.50	0.02	1.58	0.02	4.35	0.00	DQ241844
ESTC4274_53	0.29	0.03	0.25	0.11	0.30	0.06	0.75	0.46	2.04	0.01	1.51	0.09	2.69	0.00	3.33	0.00	AF060681
STMH471V_755	0.21	0.00	0.29	0.04	0.29	0.00	0.34	0.01	2.80	0.00	2.86	0.00	2.38	0.00	2.18	0.00	NA
MICRO_2296.C1_729	0.52	0.01	0.62	0.02	0.64	0.18	0.44	0.01	1.47	0.03	1.62	0.04	1.86	0.03	1.84	0.03	NA
STMH471V_886	1.11	0.78	0.74	0.10	0.93	0.01	0.47	0.01	0.96	0.78	1.61	0.01	1.90	0.04	1.78	0.01	NA
STMH471V_793	0.49	0.00	0.56	0.06	0.65	0.02	0.66	0.06	1.46	0.04	1.42	0.15	1.14	0.22	1.85	0.00	CU074307
POC38697V_36	0.15	0.04	0.36	0.07	0.36	0.07	0.31	0.07	4.94	0.00	3.46	0.00	3.04	0.00	2.53	0.03	NA
MICRO_5462.C1_786	0.31	0.12	0.22	0.02	0.12	0.00	0.22	0.00	1.95	0.04	1.35	0.32	2.78	0.03	2.12	0.00	NA
MICRO_7598.C2_712	0.62	0.01	0.85	0.44	0.01	0.79	0.11	1.21	0.19	1.57	0.02	1.43	0.02	3.11	0.00	AK224626	
bf. swstxxxx_005501.13m.scd_536	0.23	0.01	0.30	0.08	0.33	0.05	0.42	0.14	4.44	0.00	3.55	0.03	3.71	0.00	3.89	0.00	NA
bf. araxxxx_0017601.17m.scd_536	0.26	0.00	0.64	0.58	0.28	0.01	0.68	0.19	0.87	0.38	2.46	0.01	1.89	0.01	3.32	0.00	NA
MICRO_212.C3_1277	0.81	0.11	0.66	0.04	0.54	0.08	0.64	0.06	1.33	0.14	1.46	0.05	1.05	0.68	1.38	0.05	DQ218276
MICRO_3921.C2_483	0.72	0.29	0.58	0.11	0.72	0.12	0.68	0.19	2.01	0.01	1.30	0.32	1.80	0.01	1.09	0.74	NA
MICRO_1968.C2_230	0.08	0.02	0.22	0.08	0.10	0.03	0.17	0.13	3.15	0.02	2.74	0.01	2.89	0.06	2.21	0.01	AM467842
MICRO_414.C2_1031	0.26	0.07	0.22	0.01	0.18	0.01	0.35	0.07	9.59	0.00	7.19	0.00	5.89	0.00	2.72	0.06	DQ118095
MICRO_1081.C16_798	0.13	0.01	0.30	0.04	0.28	0.20	0.55	0.15	2.83	0.06	2.95	0.13	3.01	0.07	3.56	0.00	NA
MICRO_1643.C1_3	0.43	0.03	0.42	0.03	0.47	0.05	0.63	0.01	1.66	0.25	1.67	0.05	1.32	0.02	1.82	0.00	NA
bf. cswtxxxx_002308.13m.scd_606	0.43	0.00	0.58	0.02	0.67	0.25	0.42	0.00	3.04	0.00	2.90	0.02	1.89	0.00	1.24	0.14	NA
EPRO13177H_483	0.60	0.03	0.72	0.17	0.93	0.08	0.66	0.14	1.46	0.05	1.40	0.14	1.43	0.07	2.00	0.02	BT031353
MICRO_7471.C4_834	0.08	0.01	0.08	0.01	0.08	0.01	0.14	0.01	1.04	0.01	1.04	0.01	1.77	0.01	1.71	0.01	NA
SSBTO204x.scd_609	0.46	0.02	0.55	0.07	0.42	0.02	0.41	0.25	2.00	0.02	1.82	0.02	1.55	0.02	1.85	0.06	NA
MICRO_4828.C1_484	0.54	0.01	0.53	0.16	0.26	0.04	0.50	0.08	2.46	0.07	2.64	0.01	2.25	0.00	2.47	0.00	NA
MICRO_1226.C1_989	0.43	0.00	0.63	0.00	0.63	0.00	0.63	0.00	1.58	0.02	1.58	0.00	1.70	0.00	1.74	0.00	NA
bf. araxxxx_001501.17m.scd_731	0.67	0.05	0.62	0.03	0.90	0.71	0.30	0.26	0.00	2.83	0.01	2.31	0.00	0.98	0.87	NA	
MICRO_1081.C18_1218	0.34	0.04	0.47	0.22	0.54	0.02	0.59	0.06	2.18	0.01	1.58	0.08	1.82	0.01	2.40	0.02	AF090271
MICRO_2296.CM_450	0.13	0.01	0.20	0.01	0.20	0.01	0.20	0.01	0.89	0.01	0.89	0.01	0.84	0.01	1.44	0.01	NA
MICRO_6533.C2_955	0.60	0.02	0.51	0.01	0.69	0.22	0.30	0.30	1.10	0.21	1.69	0.04	1.64	0.03	1.37	0.05	AF060681
MICRO_17607.C1_302	0.71	0.33	0.45	0.05	0.28	0.02	0.44	0.05	1.59	0.14	2.20	0.00	1.59	0.08	1.66	0.03	AJ457052
MICRO_1227.C1_690	0.27	0.02	0.39	0.01	0.49	0.00	0.38	0.01	1.97	0.01	2.80	0.00	2.51	0.00	2.91	0.00	AF269684
MICRO_6211.C1_234	0.35	0.08	0.32	0.18	0.33	0.02	0.35	0.11	1.33	0.11	1.42	0.01	1.54	0.01	5.00	0.00	NA
MICRO_413.C1_1341	0.75	0.16	0.78	0.17	0.77	0.06	0.58	0.04	1.62	0.04	2.13	0.01	1.99	0.00	1.03	0.84	AY748245
MICRO_250.C2_719	0.53	0.01	0.42	0.01	0.99	0.94	0.75	0.10	2.55	0.00	1.81	0.08	2.29	0.00	2.03	0.22	BT031398
MICRO_1092.C1_158	0.22	0.00	0.22	0.00	0.22	0.00	0.22	0.00	0.96	0.02	0.96	0.01	0.96	0.01	1.93	0.01	NA
ESTB48M1H_370	0.35	0.00	0.31	0.03	0.34	0.00	0.51	0.03	1.73	0.13	2.69	0.03	2.65	0.04	4.91	0.00	AC145120
MICRO_2296.C26_796	0.36	0.00	0.18	0.00	0.10	0.00	0.16	0.01	4.29	0.00	3.89	0.00	3.16	0.00	2.04	0.01	NA
MICRO_7625.C1_1438	0.54	0.03	0.66	0.03	0.54	0.03	0.66	0.03	1.62	0.03	1.60	0.01	1.78	0.01	1.80	0.01	NA
bf. swstxxxx_005904.13m.scd_492	0.07	0.01	0.21	0.02	0.08	0.02	0.27	0.04	6.07	0.00	4.31	0.00	3.23	0.01	2.26	0.01	NA
bf. swstxxxx_002807.13m.scd_486	0.25	0.01	0.34	0.10	0.13	0.09	0.19	0.15	6.02	0.01	5.42	0.05	4.72	0.01	3.70	0.00	NA
STMES97V_473	0.48	0.01	0.49	0.01	0.47	0.01	0.47	0.01	2.07	0.01	1.78	0.02	1.49	0.01	1.59	0.01	AC151803
MICRO_3768.C1_703	0.32	0.00	0.34	0.01	0.45	0.06	0.47	0.02	2.91	0.05	1.94	0.11	1.27	0.11	3.62	0.02	DQ228326
STMVC77V_202	0.21	0.01	0.33	0.12	0.12	0.02	0.48	0.14	1.98	0.10	1.48	0.12	2.39	0.00	4.10	0.01	NA
MICRO_598.C5_61	0.30	0.01	0.38	0.01	0.38	0.01	0.51	0.01	1.69	0.03	1.94	0.02	1.58	0.01	3.64	0.00	DQ228326
MICRO_4058.C1_1748	0.41	0.00	0.90	0.60	0.61	0.02	0.90	0.41	1.00	0.98	2.03	0.01	1.57	0.01	3.25	0.00	NA
MICRO_4372.C19_298	0.25	0.00	0.38	0.00	0.38	0.00	0.34	0.05	1.88	0.00	1.84	0.00	2.02	0.00	2.52	0.00	AF090270
MICRO_1973.C1_698	0.20	0.03	0.16	0.02	0.18	0.01	0.42	0.09	1.95	0.01	1.66	0.03	3.16	0.00	2.10	0.01	NA
STMEL27V_1	0.63	0.02	0.87	0.34	0.95	0.69	0.63	0.03	1.07	0.71	1.61	0.02	1.30	0.08	1.46	0.03	NA
bf. mxtxxxx_009607.13m.scd_644	0.15	0.00	0.46	0.13	0.32	0.03	0.63	0.17	1.53	0.06	1.67	0.04	1.85	0.01	1.77	0.06	AF090280
MICRO_1088.C1_689	0.12	0.02	0.36	0.11	0.16	0.03	0.43	0.14	2.31	0.01	5.54	0.00	3.72	0.01	15.03	0.00	NA
bf. araxxxx_008612.17m.scd_1	0.19	0.00	0.11	0.00	0.14	0.00	0.30	0.03	12.27	0.00	5.51	0.02	4.58	0.00	2.30	0.01	NA
MICRO_409.C12_56	0.53	0.01	0.67	0.06	0.80	0.15	0.70	0.06	1.71	0.02	1.80	0.04	1.77	0.00	2.39	0.00	DQ191654
SSBNO1026x.scd_443	0.27	0.00	0.38	0.01	0.51	0.01	0.44	0.36	1.18	0.28	1.40	0.07	1.23	0.14	1.81	0.01	NA
MICRO_11493.C2_700	0.35	0.00	0.49	0.01	0.67	0.17	0.62	0.03	1.48	0.25	1.85	0.00	2.69	0.00	3.33	0.00	AM452493
MICRO_708.C12_635	0.48	0.06	0.21	0.03	0.25	0.03	0.17	0.12	2.39	0.02	1.92	0.01	2.44	0.00	1.43	0.15	DQ224843
MICRO_720.C1_968	0.38	0.00	0.53	0.01	0.60	0.08	0.41	0.01	1.80	0.01	1.78	0.01	1.67	0.00	1.36	0.13	AC151803
MICRO_1564.C1_690	0.38	0.01	0.31	0.00	0.56	0.00	0.43	0.28	1.18	0.23	1.24	0.18	1.66	0.01	2.36	0.00	NA
POC3867P_917	0.49	0.00	0.60	0.19	0.46	0.00	0.62	0.04	2.00	0.02	2.31	0.00	2.11	0.00	1.31	0.19	NA
148B114F.scd_637	0																

Probe ID	Hmgmt 1		Hmgmt 2		Hmgmt 3		Hmgmt 4		Hmgmt 5		GenBank	Description						
	Normalized	Least P-value	Normalized	Least P-value	Normalized	Least P-value	Normalized	Least P-value	Normalized	Least P-value								
TBS02719FD0313m scf 317	0.67	0.01	0.91	0.84	0.83	0.25	1.95	0.01	0.96	0.78	0.93	0.66	1.32	0.17	NA	DNA topoisomerase II. Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphate (Medicago truncatula)		
AC004781029.13m scf 81	0.54	0.00	0.84	0.17	0.43	0.93	1.74	0.00	0.91	0.53	0.81	0.32	0.17	0.04	NA	unannotated protein (Arabidopsis thaliana)		
MCR010231.C2_1543	0.65	0.00	0.75	0.05	0.99	0.94	1.62	0.02	0.71	0.07	0.85	0.15	1.51	0.04	2.42	0.00	AT5G56314	
bl. vsmexoe_000902031m scf 41	0.65	0.01	0.89	0.05	0.99	0.94	1.62	0.02	0.71	0.07	0.85	0.15	1.51	0.04	2.42	0.00	AT5G56314	
bl. vsmexoe_000902031m scf 140	0.68	0.03	0.82	0.19	1.06	0.74	2.25	0.00	0.89	0.38	0.91	0.50	0.96	0.09	1.96	0.00	AT5G56314	
MCR01942.C3_342	0.78	0.07	0.85	0.22	0.98	0.89	2.60	0.00	0.76	0.09	0.77	0.11	1.03	0.86	1.65	0.02	CG225162	
bl. vsmexoe_000903103m scf 614	0.68	0.03	0.83	0.26	0.98	0.71	2.02	0.00	0.82	0.22	0.82	0.30	1.20	0.20	2.14	0.00	NA	
MCR01987.C2_1026	0.70	0.04	0.81	0.44	0.76	0.11	1.06	0.61	0.86	0.36	1.05	0.11	1.41	0.06	1.84	0.01	NM_001049281	
MCR01987.C2_1026	0.67	0.04	0.80	0.44	0.76	0.11	1.06	0.61	0.86	0.36	1.05	0.11	1.41	0.06	1.84	0.01	NM_001049281	
MCR012932.C1_697	0.55	0.01	0.76	0.14	0.93	0.66	3.17	0.00	0.77	0.14	0.96	0.80	1.40	0.07	3.13	0.00	U78394	
bl. vsmexoe_001506070m scf 692	0.45	0.02	0.82	0.42	0.93	0.70	1.85	0.26	0.72	0.25	1.04	0.84	0.89	0.98	1.51	0.32	NA	
MCR02292.C1_1150	0.64	0.05	0.86	0.30	0.94	0.74	2.07	0.00	0.80	0.66	0.63	0.00	0.84	0.72	1.81	0.00	CG242525	
MCR01746.C3_1559	0.76	0.17	0.88	0.67	1.04	0.80	4.39	0.00	0.87	0.05	0.85	0.37	0.94	0.76	2.32	0.00	BT012706	
MCR02984.C2_319	0.97	0.01	0.88	0.36	0.94	0.61	1.88	0.00	0.92	0.05	0.90	0.35	1.07	0.48	1.71	0.01	NA	
1684075643_304	0.81	0.52	0.98	0.87	1.07	0.58	2.92	0.00	0.88	0.08	0.90	0.36	0.97	0.82	1.84	0.01	NA	
MCR01941.C1_663	0.66	0.01	0.81	0.32	0.81	0.66	1.85	0.01	0.81	0.03	0.83	0.48	1.63	0.60	1.07	0.04	NA	
MCR01132.C1_1266	0.92	0.46	1.04	0.81	0.93	0.61	1.48	0.02	0.80	0.15	1.10	0.48	0.92	0.56	1.43	0.03	BT014590	
MCR01761.C2_538	0.92	0.01	0.81	0.32	0.88	0.64	1.85	0.01	0.81	0.47	0.87	0.99	1.36	0.08	2.83	0.00	AA043559	
TBS02719FD0313m scf 11	0.62	0.01	0.86	0.24	1.04	0.88	3.00	0.00	0.45	0.00	0.77	0.11	1.08	0.56	2.01	0.01	CG207880	
AC040994986.73m scf 314	0.78	0.22	0.75	0.05	0.98	0.85	4.87	0.00	0.61	0.91	0.92	0.57	1.30	0.20	3.98	0.00	AK224822	
CS1D1413111_624	0.83	0.68	0.87	0.34	1.03	0.82	2.13	0.00	0.93	0.75	0.91	0.41	1.12	0.31	2.12	0.01	BT010103	
bl. vsmexoe_001041111m scf 450	0.68	0.06	0.80	0.68	1.04	0.77	2.05	0.00	1.05	0.74	1.05	0.81	0.88	0.70	1.78	0.02	NA	
bl. vsmexoe_000816111m scf 195	0.65	0.01	0.82	0.78	0.91	0.29	3.02	0.00	0.54	0.00	0.90	0.50	0.88	0.69	1.88	0.01	CG216122	
MCR01874.C2_26	0.19	0.00	0.57	0.03	0.90	0.79	8.39	0.00	0.86	0.58	0.88	0.33	1.43	0.35	8.11	0.00	AT786773	
bl. vsmexoe_000602070m scf 546	0.63	0.16	0.71	0.24	0.83	0.16	1.78	0.00	0.84	0.64	0.84	0.72	1.06	0.61	2.13	0.00	NM_118347	
MCR01893.C6_418	0.94	0.01	1.03	0.83	1.06	0.68	2.70	0.00	0.99	0.06	0.90	0.26	0.92	0.68	1.94	0.03	AA043066	
bl. vsmexoe_00050711m scf 522	0.17	0.00	0.46	0.00	0.55	0.24	3.58	0.01	0.85	0.20	1.17	0.54	1.44	0.09	6.18	0.00	BT01819	
MCR01892.C2_1171	0.99	0.84	1.00	0.84	0.93	0.20	2.12	0.01	0.92	0.48	0.92	0.72	0.66	0.77	1.88	0.04	AA043662	
MCR01482.C3_144	0.48	0.01	0.77	0.14	0.98	0.87	2.50	0.00	0.89	0.47	0.91	0.48	1.24	0.15	2.31	0.00	NA	
MCR01708.C2_572	0.34	0.00	1.57	0.09	0.69	0.20	3.80	0.00	0.58	0.01	0.95	0.61	0.89	0.57	2.50	0.00	BT014113	
RF. LIRCH00X_000001 TMSLC2_313	0.64	0.02	0.81	0.23	0.80	0.62	0.94	0.00	0.92	0.64	0.90	0.23	0.98	0.33	0.93	0.00	CG216122	
MCR01903.C3_963	0.64	0.01	1.11	0.44	1.23	0.23	2.09	0.00	0.68	0.03	0.75	0.13	0.94	0.56	1.94	0.02	CG204269	
MCR01548.C1_1123	0.78	0.19	0.77	0.28	0.88	0.61	1.77	0.00	0.82	0.77	0.82	0.51	1.28	0.19	2.17	0.00	CG216122	
MCR01206.C1_2829	0.99	0.01	0.80	0.44	0.85	0.23	2.89	0.00	0.82	0.25	1.05	0.67	0.88	0.51	2.09	0.01	AA051290	
bl. vsmexoe_001802070m scf 78	0.59	0.01	0.88	0.39	0.92	0.64	3.10	0.00	0.73	0.09	0.86	0.70	0.97	0.90	2.00	0.01	CG225213	
POK02371_586	0.77	0.07	0.81	1.13	0.82	0.29	1.82	0.01	0.81	0.15	0.89	0.24	1.08	0.28	1.94	0.00	NA	
MCR01898.C2_47	0.96	0.84	1.15	0.87	1.48	0.07	2.28	0.01	0.34	0.05	0.96	0.17	0.89	0.71	1.70	0.14	BB0859	
bl. vsmexoe_00040410m scf 16	0.65	0.01	0.80	0.65	0.95	0.84	2.13	0.00	0.79	0.13	0.99	0.89	1.39	0.00	1.71	0.00	NA	
MCR01895.C1_688	0.60	0.01	0.80	0.65	0.95	0.84	2.13	0.00	0.79	0.13	0.99	0.89	1.39	0.00	1.71	0.00	CG224287	
MCR01741.C1_1310	0.36	0.00	0.63	0.08	0.64	0.01	1.39	0.08	0.88	0.32	1.21	0.28	1.41	0.03	1.63	0.01	BT014287	
bl. vsmexoe_00090410m scf 366	0.38	0.00	0.63	0.09	0.63	0.09	1.39	0.08	0.88	0.32	1.21	0.28	1.41	0.03	1.63	0.01	BT014287	
bl. vsmexoe_00040810m scf 486	0.71	0.10	0.87	0.14	0.74	0.29	3.24	0.00	0.77	0.13	0.80	0.23	1.00	1.98	0.01	CG203332		
bl. vsmexoe_00040810m scf 507	0.79	0.10	0.87	0.14	0.74	0.29	3.24	0.00	0.77	0.13	0.80	0.23	1.00	1.98	0.01	CG203332		
bl. vsmexoe_00050810m scf 688	0.75	0.07	0.86	0.30	0.95	0.71	1.89	0.01	1.06	0.87	1.05	0.72	1.18	0.22	1.77	0.02	AA051917	
CS18303177H_288	1.01	0.92	0.95	0.81	1.16	0.36	1.44	0.04	0.87	0.43	0.91	0.56	0.89	0.91	1.71	0.43	BT013602	
MCR01904.C1_809	0.76	0.01	0.86	0.13	1.04	0.81	3.84	0.00	0.80	0.13	0.80	0.11	1.04	0.84	0.00	0.11	1.04	0.84
MCR01910.C1_1078	1.08	0.64	1.15	0.29	0.87	0.13	1.75	0.04	1.06	0.77	0.84	0.42	1.15	0.46	2.40	0.01	AA050011	
MCR01910.C1_1078	0.81	0.07	0.81	0.29	0.87	0.13	1.75	0.04	1.06	0.77	0.84	0.42	1.15	0.46	2.40	0.01	AA050011	
MCR01712.C1_1579	0.47	0.01	0.58	0.02	0.83	0.45	3.31	0.00	0.82	0.32	0.88	0.40	0.35	1.00	0.00	0.00	AA110551	
MCR01903.C6_538	0.36	0.00	0.80	0.29	1.01	0.88	3.78	0.00	0.49	0.00	1.01	0.97	0.87	0.88	2.44	0.00	CG209287	
MCR01903.C6_538	0.44	0.00	0.71	0.05	0.92	0.72	1.87	0.03	0.82	0.19	0.88	0.37	1.34	0.38	1.92	0.00	CG216122	
MCR01882.C1_692	0.39	0.00	0.23	0.01	0.31	0.01	1.57	0.13	0.20	0.56	1.21	0.31	2.36	0.02	11.80	0.00	NA	
MCR01882.C1_692	0.46	0.01	0.87	0.13	0.85	0.01	1.89	0.44	0.83	0.44	0.83	0.27	1.19	0.13	1.80	0.00	CG216122	
MCR01882.C1_692	0.69	0.01	0.87	0.13	0.85	0.01	1.89	0.44	0.83	0.44	0.83	0.27	1.19	0.13	1.80	0.00	CG216122	
0781054564_319	0.99	0.10	0.73	0.16	0.87	0.42	1.84	0.01	0.93	0.62	0.95	0.78	1.31	0.13	1.63	0.03	BT013534	
POK02371_708	0.99	0.02	0.86	0.30	1.02	0.81	1.88	0.04	0.85	0.50	0.82	0.61	1.48	0.03	1.63	0.00	CG203332	
bl. vsmexoe_00090810m scf 562	0.67	0.00	0.73	0.06	0.85	0.18	0.89	0.00	0.84	0.18	0.89	0.42	0.88	0.24	0.41	0.00	CG216122	
BTM027H_886	0.92	0.53	0.94	0.65	1.05	0.72	2.38	0.01	1.00	1.00	0.73	0.06	1.09	0.66	2.43	0.00	CG203256	
MCR01854.C1_443	0.67	0.01	0.88	0.37	0.98	0.60	1.40	0.00	0.88	0.46	1.04	0.78	1.16	0.24	2.40	0.00	AA043662	
MCR01854.C1_443	0.63	0.02	0.84	0.28	1.14	0.88	1.84	0.00	0.82	0.78	0.82	0.31	1.86	0.31	1.98	0.00	CG216122	
AC040994986.73m scf 11	0.67	0.04	0.84	0.29	1.00	0.89	3.22	0.00	0									

MCRO0605C4_217	0.47	0.00	0.96	0.77	0.91	0.48	2.70	0.00	0.47	0.01	0.88	0.40	0.87	0.44	2.02	0.01	AP006287	glutathione S-transferase GST z3 (Glycine maud)
MCRO1080A10_10m scf_429	0.63	0.02	0.99	0.97	0.85	0.87	0.60	0.00	0.87	0.00	0.84	0.87	0.84	0.87	0.00	0.00	Q222494	Q222494
MCRO1898C2_267	0.79	0.09	0.90	0.85	1.07	0.65	4.07	0.00	0.78	0.13	0.93	0.65	1.06	0.71	1.00	0.00	Q022494	unknown (Solanum tuberosum)
MCRO1383C1_1182	0.63	0.00	1.33	0.07	0.91	0.73	3.28	0.00	0.57	0.03	0.98	0.87	0.78	0.19	1.37	0.00	MA128173	HS-PTS, DNA-binding (Medicago truncatula)
MCRO0906C1_1195	0.77	0.04	1.10	0.64	1.02	0.72	0.64	0.00	0.71	0.03	0.83	0.66	1.07	1.00	0.00	0.00	Q1014031	unknown (Solanum tuberosum)
MCRO0809C1_05m scf_119	0.45	0.00	0.72	0.10	1.09	0.66	2.10	0.00	0.78	0.22	0.76	0.12	1.35	0.07	1.88	0.01	AF125500	unknown (Solanum tuberosum)
MCRO1226C2_196	0.69	0.00	0.95	0.82	0.91	0.84	1.04	0.00	0.69	0.17	0.76	0.21	0.81	0.84	0.00	0.00	Q10119532	unknown (Solanum tuberosum)
MCRO1661C4_361	0.38	0.00	0.81	0.19	0.82	0.22	1.87	0.01	0.85	0.24	0.03	0.73	0.99	0.86	1.98	0.01	NA	unknown (Solanum tuberosum)
MCRO1396C1_1044	0.90	0.33	3.55	0.20	0.36	0.04	13.49	0.00	0.20	0.00	0.23	0.00	0.30	0.00	1.12	0.00	NA	unknown (Solanum tuberosum)
PRO114011_733	0.48	0.00	1.00	0.73	0.93	0.72	0.93	0.00	0.71	0.03	0.84	0.77	0.87	0.23	1.10	0.00	Q10222513	unknown (Solanum tuberosum)
MCRO0309C1_05m scf_138	0.40	0.00	0.95	0.63	1.02	0.95	3.13	0.00	0.59	0.02	0.90	0.39	1.15	0.33	2.93	0.00	Q0223123	unknown (Solanum tuberosum)
MCRO1005C1_05m scf_430	0.67	0.11	0.77	0.11	0.87	0.44	1.99	0.00	0.69	0.00	0.87	0.28	0.63	0.66	1.11	0.00	Q0223232	unknown (Solanum tuberosum)
SDBT011016scf_11	0.86	0.05	0.92	0.64	1.01	0.94	3.21	0.00	0.87	0.25	0.99	0.92	1.01	0.84	2.91	0.00	NA	unknown (Solanum tuberosum)
BF_C50X00X_Q022101_TMSCF_109	0.88	0.25	1.23	0.15	1.17	0.26	2.67	0.00	0.78	0.18	0.92	0.56	0.81	0.45	2.03	0.00	Q02110071	SPCL1, Solanum tuberosum
MCRO1705C1_786	0.70	0.02	0.99	0.97	0.84	1.99	0.00	0.51	0.02	0.70	0.06	1.51	0.68	1.72	0.01	AF133423	cruciform1, Lycopodium obscurum	
MCRO1424C4_529	0.62	0.00	0.99	1.22	0.60	1.39	0.00	0.93	0.87	0.73	0.15	1.66	0.02	2.28	0.01	AP006288	homobiosynthetic aspartic protein (Pimpinella brachycarpa)	
MCRO1908C1_586	0.63	0.00	0.75	0.11	0.97	0.84	1.89	0.00	0.96	0.30	1.00	0.97	1.19	0.21	1.61	0.00	Q1014488	protein kinase M1 (Solanum tuberosum)
MCRO3898C2_241	0.87	0.22	0.85	0.31	1.01	0.92	1.82	0.00	0.81	0.16	0.92	0.84	1.08	0.56	1.58	0.00	AM66298	Os02g071800 (Oryza sativa (japonica cultivar-group))
MCRO1226C1_976	0.74	0.04	1.04	0.82	1.23	0.41	3.00	0.00	0.85	0.24	0.88	0.37	1.13	0.45	2.50	0.00	BT014382	unknown (Solanum tuberosum)
MCRO0306C1_460	0.77	0.07	0.85	0.24	1.06	0.87	2.21	0.00	0.87	0.46	0.60	0.60	1.08	0.78	2.38	0.00	Q0240205	unknown (Solanum tuberosum)
MCRO4931C1_746	0.60	0.04	0.83	0.31	0.83	0.39	2.29	0.00	0.80	0.14	1.21	0.32	1.47	0.24	3.37	0.02	BT014337	Os05g0612800 (Oryza sativa (japonica cultivar-group))
EST18471_202	0.72	0.02	0.92	0.54	1.06	0.87	2.03	0.00	0.80	0.15	0.91	0.56	0.98	0.97	2.00	0.00	BT014336	Protein kinase M1 (Solanum tuberosum)
MCRO3898C2_269	0.58	0.03	0.88	0.03	1.11	0.50	2.08	0.01	0.90	0.43	0.69	0.07	1.23	0.28	1.28	0.00	NA	accessory protein 1B (Populus tremula)
MCRO1841C2_1204	0.20	0.00	0.78	0.19	0.52	0.11	3.12	0.00	0.78	0.27	0.82	0.33	2.85	0.25	3.59	0.00	NA	ZOG-Fer11 oxenolase (Medicago truncatula)
MCRO0483C2_304	0.73	0.03	0.74	0.10	0.87	0.33	1.64	0.04	1.02	0.83	1.03	0.85	1.21	0.15	2.18	0.00	BT013555	unknown (Solanum tuberosum)
MCRO1908C2_1016	0.43	0.00	1.04	0.74	1.14	0.56	3.46	0.00	0.44	0.00	0.78	0.07	0.97	0.74	2.47	0.00	Q0207880	unknown (Solanum tuberosum)
MCRO1846C1_520	0.91	0.42	1.12	0.88	0.31	1.80	0.01	0.59	0.05	0.88	0.30	0.86	1.17	0.98	0.00	NA	WOUND-INDUCED PROTEIN 1	
ACDAD0593D5_73m scf_138	0.65	0.02	1.03	0.81	0.97	0.90	2.10	0.00	0.68	0.05	0.92	0.73	0.61	0.95	1.93	0.01	BT013751	NA
MCRO1087C1_1313	0.64	0.00	1.09	0.51	0.76	0.11	2.08	0.00	0.46	0.06	0.90	0.90	0.92	2.47	0.00	AM44291	unknown protein (Arabidopsis thaliana)	
TBR04168FD04_03m scf_150	0.47	0.00	0.60	0.02	0.60	0.01	1.47	0.03	1.04	0.84	1.97	0.42	1.92	0.00	0.00	Q0203084	NA	
MCRO1087C1_1126	0.63	0.02	0.84	0.30	0.81	0.34	2.01	0.00	0.66	0.33	1.25	0.27	3.07	0.00	AM44292	Os02g072800 (Oryza sativa (japonica cultivar-group))		
MCRO1886C1_699	0.22	0.00	1.75	0.22	0.20	0.01	6.90	0.03	0.78	0.58	0.79	0.69	0.93	0.84	40.83	0.00	NA	Ca/calmodulin-binding protein (Medicago truncatula)
MCRO1746C2_617	0.72	0.06	0.85	0.24	1.12	0.37	3.71	0.00	0.84	0.30	0.78	0.09	1.02	0.91	2.52	0.00	BT013706	Ca/calmodulin-binding protein (Medicago truncatula)
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_274	0.73	0.04	1.03	0.71	0.84	0.62	2.00	0.00	0.89	0.43	0.93	0.99	1.18	2.29	0.00	NA	unknown (Solanum tuberosum)	
MCRO1707C1_27																		

bf_suscep_0014693fm_scf_52	0.78	0.23	1.22	0.19	1.22	0.66	3.18	0.00	0.69	0.06	0.05	0.01	0.68	0.08	2.07	0.00	NA		
bf_suscep_0009003fm_scf_152	0.81	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	NA	transcription factor 1 (Arabidopsis thaliana)	
bf_suscep_0017117fm_scf_873	0.82	0.01	0.83	0.26	0.83	0.64	3.81	0.00	0.76	0.13	0.06	0.04	0.76	0.07	0.91	3.07	0.00	hypothetical protein Gm_017842 (Oryza sativa Japonica cultivar-group)	
MCR02347_C1_569	0.87	0.21	0.83	0.25	0.99	0.91	1.88	0.00	0.78	0.11	0.06	0.74	0.95	0.58	1.75	0.00	NA		
MCR03378_C4_1661	0.87	0.00	0.81	0.43	0.00	0.16	2.81	0.00	0.81	0.00	0.00	0.81	0.00	1.17	0.12	0.89	0.00	RNA-binding protein AKR1-like (Solanum tuberosum)	
MCR02824_C1_372	0.87	0.01	0.87	0.13	0.81	0.32	1.86	0.01	0.74	0.07	0.12	0.53	0.25	0.11	2.89	0.00	MM_105845	antipeptide transport/transceptor (Arabidopsis thaliana)	
FR020211fm_scf_481	0.87	0.29	0.81	0.27	0.81	0.27	0.81	0.00	0.81	0.00	0.00	0.81	0.00	1.18	0.00	0.00	0.00	transcription factor 1 (Arabidopsis thaliana)	
MCR016375_C1_1254	0.88	0.13	0.86	0.80	1.20	0.29	2.05	0.00	0.77	0.11	0.00	0.50	0.86	0.31	1.57	0.02	CU041360	Zinc finger, GATA-type, ZIM C-CT (Medicago truncatula)	
MCR02046_C1_1254	0.88	0.27	1.14	0.41	1.21	0.19	1.76	0.01	0.69	0.06	0.07	0.29	1.02	0.90	1.43	0.08	NA	hypothetical protein Gm_031408 (Oryza sativa indica cultivar-group)	
ACM0459920_3fm_scf_598	0.89	0.00	1.00	0.13	1.14	0.62	2.05	0.00	0.86	0.04	0.08	0.04	0.88	0.47	1.89	0.00	CU011732	Zinc finger, CCHC-type, Zinc finger, RPD3-like (Medicago truncatula)	
SSR0201N1_scaf_187	0.94	0.02	0.48	0.00	0.93	0.00	2.97	0.00	0.76	0.12	0.14	0.30	1.17	0.23	2.52	0.00	AF070967	NA	
CU015201N_444	0.95	0.14	0.91	0.27	0.93	0.00	1.66	0.00	0.72	0.06	0.00	0.64	0.81	0.00	1.00	0.00	NA	unknown protein (Arabidopsis thaliana)	
MCR014625_C2_1084	0.91	0.05	0.98	0.93	0.99	0.88	6.88	0.00	0.80	0.51	0.02	0.20	1.00	0.99	2.74	0.01	CU047090	unknown protein (Arabidopsis thaliana)	
bf_suscep_0009113fm_scf_11	0.93	0.00	0.76	0.99	0.87	0.53	2.47	0.00	0.85	0.20	1.01	0.94	1.01	0.85	2.57	0.00	AF070967	Sho1-like protein 3 (Petraea inflata)	
P0967006_scf_400	0.99	0.00	0.25	0.00	0.00	0.19	1.53	0.00	0.61	0.03	0.73	0.16	0.05	0.00	0.92	0.24	NA	NA	
MCR02527_C2_400	0.97	0.01	0.91	0.92	0.73	0.96	1.31	0.09	0.60	0.93	0.10	0.44	1.09	0.64	2.26	0.00	AMM7737	CeD110559200 (Oryza sativa Japonica cultivar-group)	
MCR03658_C2_621	0.98	0.17	0.99	0.96	0.94	0.34	4.10	0.00	0.66	0.05	0.82	0.41	1.01	0.97	1.87	0.00	NA	transcription factor zinc ion binding (Arabidopsis thaliana)	
MCR01458_C2_685	0.94	0.00	0.81	0.21	1.08	0.52	1.27	0.11	0.64	0.05	0.82	0.40	0.86	0.00	1.96	0.01	AP06730	unknown protein (Arabidopsis thaliana)	
TBSK01588F02_3fm_scf_108	0.98	0.01	1.06	0.64	0.96	0.60	2.46	0.00	0.78	0.14	0.88	0.86	0.94	0.56	2.03	0.00	NA	transcription factor zinc ion binding (Arabidopsis thaliana)	
MCR02973_C3_413	0.97	0.00	1.10	0.93	0.90	0.12	1.84	0.01	0.53	0.01	0.85	0.33	0.22	0.48	2.03	0.00	CU010385	transcription factor zinc ion binding (Arabidopsis thaliana)	
ACM046897E01_3fm_scf_308	0.44	0.00	0.99	0.92	0.93	0.76	1.92	0.01	0.67	0.02	0.79	0.12	1.11	0.59	1.91	0.01	CU0204268	CeD170028100 (Oryza sativa Japonica cultivar-group)	
MCR01847_C3_108	0.45	0.00	0.67	0.93	1.04	0.76	1.90	0.30	0.54	0.11	0.84	0.11	0.26	0.00	6.83	0.00	CU0204268	unknown (Solanum tuberosum)	
ACM04081C09_3fm_scf_340	0.17	0.00	0.50	0.01	0.73	0.38	8.86	0.00	0.58	0.02	0.69	0.97	0.01	0.02	8.18	0.00	AK224822	NA	
MCR010838_C1_337	0.74	0.05	0.98	0.91	0.97	0.74	1.66	0.03	0.72	0.08	0.99	0.96	0.97	0.80	1.54	0.03	NA	NHLB ubiquitin-protein ligase of zinc ion binding (Arabidopsis thaliana)	
MCR018122_1173	0.68	0.01	0.86	0.41	1.09	0.39	2.14	0.00	0.82	0.19	0.86	0.78	1.08	0.60	1.80	0.01	NA	CU003043500 (Oryza sativa Japonica cultivar-group)	
MCR04429_C1_680	0.64	0.01	0.68	0.03	0.88	0.30	1.64	0.02	0.77	0.18	0.04	0.86	1.13	0.30	1.76	0.08	AMM79511	Dual specificity protein phosphatase (Medicago truncatula)	
MCR01768_C1_277	0.95	0.90	1.62	0.93	0.88	0.49	2.91	0.00	0.60	0.04	1.14	0.40	1.44	0.30	3.03	0.00	AF027957	Epimastix-like MDS3-like protein 8L (Medicago truncatula)	
MCR02073_C5_773	0.94	0.02	0.05	0.65	1.04	0.83	3.84	0.00	0.66	0.11	0.78	0.26	1.05	0.88	3.03	0.01	NA	isochlorogenic acid/caffeoyl-CoA ligase (Medicago truncatula)	
MCR013483_C1_1094	0.73	0.06	0.99	0.92	0.96	0.88	1.66	0.03	0.62	0.15	1.05	0.77	0.98	0.97	1.61	0.05	NA	F-box family protein-like (Oryza sativa Japonica cultivar-group)	
MCR017813_C1_417	0.90	0.00	0.77	0.49	1.06	0.63	8.91	0.00	0.62	0.01	0.79	0.78	1.46	0.56	12.18	0.00	NA	C-methyltransferase (Pisum sativum)	
MCR01416_C17_1426	0.89	0.22	1.30	0.13	1.18	0.22	2.79	0.00	0.62	0.03	0.71	0.19	0.92	0.55	1.50	0.04	CU0203384	unknown protein (Arabidopsis thaliana)	
MCR01053_C2_277	0.41	0.00	0.84	0.21	1.04	0.89	4.24	0.00	0.76	0.04	1.02	0.99	0.07	0.78	4.18	0.00	CU012478	Arabidopsis-unique protein (UC-7) (Solanum tuberosum crystallinum)	
MCR017420_C1_1206	0.77	0.05	0.85	0.29	0.69	0.69	1.61	0.02	0.61	0.21	0.92	0.55	1.08	0.49	1.61	0.02	AF029738	UBIAX1 (Medicago truncatula)	
bf_suscep_0001403fm_scf_634	0.93	0.01	1.07	0.77	1.07	0.77	1.07	0.00	0.81	0.12	0.87	0.81	1.15	0.13	0.77	0.00	AF272345	putative serine/threonine (SR) protein kinase protein (Solanum tuberosum)	
ACM04206402_3fm_scf_59	0.41	0.00	0.93	0.61	1.06	0.79	2.31	0.00	0.69	0.09	0.83	0.42	1.10	0.61	2.46	0.00	CU0204268	NA	
MCR01038_C1_853	0.64	0.00	0.81	0.13	0.84	0.00	0.81	0.00	0.63	0.01	0.87	0.47	0.60	0.00	1.00	0.00	NA	unknown protein (Arabidopsis thaliana)	
MCR00946_C1_648	0.80	0.37	0.93	0.66	1.10	0.43	1.71	0.01	0.79	0.15	0.89	0.49	0.97	0.80	1.33	0.00	AMM5794	S-adenosylmethionine-dependent methyltransferase/catalytic (Arabidopsis thaliana)	
IST442071_252	0.63	0.01	0.71	0.05	0.84	0.15	1.45	0.03	0.97	0.80	1.05	0.42	0.89	0.49	1.65	0.01	NA	putative ATP-dependent RNA helicase (Arabidopsis thaliana)	
ST1867TV_003	0.97	0.03	0.64	0.04	0.84	0.01	2.25	0.00	0.84	0.01	0.83	0.29	1.01	0.83	1.69	0.00	NA	NA	
MCR013884_C2_157	0.47	0.01	0.68	0.66	0.77	0.30	2.17	0.00	0.79	0.28	1.16	0.47	1.13	0.36	2.31	0.00	CU0203393	putative flavonol synthase-like protein (Euphorbia esula)	
ACM046897E01_3fm_scf_308	0.45	0.00	0.67	0.93	1.04	0.76	1.90	0.30	0.54	0.11	0.84	0.11	0.26	0.00	6.83	0.00	CU0204268	unknown (Solanum tuberosum)	
MCR03403_C4_21	0.75	0.15	0.98	0.19	1.44	0.00	1.65	0.02	1.01	0.97	0.88	0.38	0.39	0.18	3.23	0.00	AV497477	zeolobion endonucleonuclease-histone-like XTH5 (Solanum esculentum)	
bf_suscep_0028902fm_scf_495	0.78	0.13	0.93	0.85	1.24	0.12	2.39	0.00	0.82	0.27	0.79	0.97	0.89	0.50	1.43	0.07	NA	unknown protein (Arabidopsis thaliana)	
MCR011894_C4_170	0.14	0.00	0.81	0.00	0.81	0.00	1.89	0.01	0.63	0.00	0.81	0.00	1.00	0.00	1.30	0.00	NA	unknown protein (Arabidopsis thaliana)	
DF5F04F_scf_562	0.93	0.00	0.88	0.69	0.82	0.66	2.88	0.00	0.62	0.00	0.94	0.70	0.90	0.69	2.53	0.00	NA	unknown protein (Arabidopsis thaliana)	
MCR01741_C1_632	0.97	0.17	0.97	0.89	0.82	0.66	2.88	0.00	0.62	0.00	0.94	0.70	0.90	0.69	2.53	0.00	NA	unknown protein (Arabidopsis thaliana)	
MCR02096_C2_1999	0.98	0.03	0.83	0.20	1.02	0.87	1.84	0.00	0.78	0.07	0.92	0.49	0.84	0.82	1.98	0.00	AF136300	35S ribosomal protein L23 precursor (Solanum tuberosum)	
MCR03396_C3_525	0.88	0.02	0.71	0.06	1.24	0.05	2.35	0.00	0.86	0.78	0.73	0.19	1.16	0.39	2.49	0.00	CU0203256	zinc finger protein 2 (Solanum esculentum)	
T09C09F_scf_53	0.98	0.00	0.83	0.06	0.77	0.07	1.77	0.02	0.83	0.23	1.24	0.30	1.24	0.24	0.00	0.00	NA	NA	
MCR013300_C1_462	0.99	0.01	0.75	0.20	0.86	0.32	1.58	0.03	1.00	1.00	1.05	0.74	1.11	0.52	2.00	0.01	NA	unknown protein (Arabidopsis thaliana)	
MCR01762_C1_747	0.61	0.00	0.81	0.28	0.88	0.00	0.81	0.00	0.61	0.00	0.81	0.00	0.81	0.00	0.81	0.00	NA	transcription factor zinc ion binding (Arabidopsis thaliana)	
MCR01043_C1_804	0.97	0.01	0.72	0.09	1.06	0.67	1.89	0.03	0.82	0.18	0.97	0.37	0.38	0.02	2.42	0.00	NA	unknown protein (Arabidopsis thaliana)	
IST3191017M_001	0.88	0.54	0.86	0.28	1.08	0.44	3.88	0.00	0.92	0.44	0.86	0.26	0.87	0.43	3.36	0.00	CU0102803	CeD1a0281000 (Oryza sativa Japonica cultivar-group)	
MCR02096_C3_525	0.99	0.01	1.00	1.00	1.00	0.71	2.96	0.00	0.81	0.17	0.91	0.60	1.05	0.60	2.92	0.02	AF223305	unknown protein (Oryza sativa indica cultivar-group)	
MCR00807_C4_444	0.10	0.00	0.26	0.00	0.26	0.01	0.61	0.02	0.74	0.39	1.57	0.12	1.63	0.23	3.56	0.00	AMM02042	NA	
MCR012588_C2_1424	0.81	0.01	0.79	0.13	0.81	0.00	0.81	0.00	0.61	0.00	0.81	0.00	0.81	0.00	0.81	0.00	NA	unknown protein (Arabidopsis thaliana)	
MCR0458_C3_1317	0.99	0.01	1.02	0.87	0.74	0.13	1.97	0.02	0.81	0.04	1.05	0.72	2.21	0.52	2.42	0.00	CU0102721	EM11075_cytochrome P450 (Arabidopsis thaliana)	
MCR02782_C2_348	0.89	0.02	0.86	0.37	0.89	0.44	1.47	0.04	0.85	0.73	0.97	0.83	1.27	0.17	1.60	0.02	AC187540	Quinonotriene alcohol dehydrogenase-like (Medicago truncatula)	
bf_suscep_0013063fm_scf_432	0.88	0.31	0.88	0.31	0.88	0.31	0.88	0.00	0.88	0.31	0.88	0.31	0.88	0.31	0.88	0.31	0.88	0.31	CU0203250 (Oryza sativa Japonica cultivar-group)
P09C0727V_386	0.66	0.00	0.81	0.29	0.91	0.44	2.69	0.01	0.81	0.30	1.07	0.60	1.01	0.95	1.80	0.01	AMM74727	fiber protein Ft12 (Solanum tuberosum)	
MCR00844_C1_391	0.47	0.06	0.85	0.85	0.91	0.14	2.54	0.00	0.83	0.05	0.82	0.47	1.20	0.46	1.98	0.00	AMM44544	unknown protein (Arabidopsis thaliana)	
MCR01894602_3fm_scf_466	0.53	0.00	0.66	0.00	0.66	0.00	0.66	0.00	0.66	0.00	0.66	0.00	0.66	0.00	0.66	0.00	NA	NA	
MCR03847_C2_1	0.60	0.01	1.12	0.50	0.93	0.63	1.93	0.00	0.81	0.21	0.97	0.74	0.07	0.81	1.69	0.01	AC149290	hypothetical protein STM_2700015 (Solanum demissum)	
MCR03396_C1_646	0.74	0.10	0.91	0.37	1.00	0.60													

MCR0288.C1.1388	2.36	0.02	0.62	0.60	0.89	0.54	0.44	0.00	1.88	0.02	1.12	0.31	0.03	0.80	0.22	0.00	BT012930	PED1 (PEROXISOME DEFECTIVE 1) (Arabidopsis thaliana)	
CS1587H.127	1.66	0.10	0.95	0.93	1.84	0.54	0.44	0.00	1.84	0.02	1.12	0.31	0.03	0.80	0.22	0.00	AT5G5641	sucrose synthase 2 (Solanum tuberosum)	
MCR0186.C5.699	1.89	0.10	0.95	0.93	1.84	0.54	0.44	0.00	1.84	0.02	1.12	0.31	0.03	0.80	0.22	0.00	AT5G5684	sucrose synthase 2 (Solanum tuberosum)	
bt_susceptor_002080015m_scf_311	0.91	0.57	1.07	0.85	0.98	0.50	0.39	0.00	1.55	0.02	1.11	0.43	1.11	0.61	0.43	0.00	AT5G5682	unassigned protein product (Arabidopsis thaliana)	
MCR011705.C1.666	2.68	0.02	1.17	1.18	0.21	0.26	0.44	0.00	0.21	0.33	0.18	0.38	0.87	0.67	0.00	0.00	NA	MAM1662	unassigned protein product (Arabidopsis thaliana)
MCR016638.C1.536	2.95	0.00	1.90	1.83	0.17	0.35	0.00	0.08	0.95	0.81	0.15	0.79	0.48	0.21	0.00	0.00	AMM4370	Phosphatidylserine 3- and 4-kinase catalytic (Ubiquitin Medicago truncatula)	
MCR013121.C1.104	3.92	0.00	1.91	1.84	0.17	0.35	0.00	0.08	0.95	0.81	0.15	0.79	0.48	0.21	0.00	0.00	AT5G1168	unassigned protein product (Arabidopsis thaliana)	
MCR015345.C1.957	4.98	0.00	1.19	1.40	0.24	0.61	0.20	0.00	2.37	0.17	0.06	0.81	0.71	0.60	0.14	0.00	NA	unassigned protein product (Arabidopsis thaliana)	
MCR02262.C1.1024	0.94	0.60	0.98	0.90	0.30	0.73	0.19	0.00	1.30	0.15	1.50	0.33	1.13	0.43	0.21	0.00	BT012541	RAM11B (Locus accession)	
CS181311H.113	1.42	0.17	1.21	1.27	0.21	0.13	0.21	0.00	1.10	0.23	0.43	0.24	0.28	0.29	0.00	0.00	AMM4443	cytochrome P450 (cytochrome P450 subunit, 85G Medicago truncatula)	
MCR014329.451	6.15	0.00	2.20	2.00	1.56	0.14	0.27	0.00	1.81	0.24	0.94	0.67	0.49	0.19	0.23	0.00	AT272748	unassigned protein product (Arabidopsis thaliana)	
MCR010351.C1.328	1.48	0.13	1.30	1.31	0.19	0.02	0.27	0.00	1.60	0.09	0.71	0.18	0.22	0.00	0.00	0.00	AT272748	unassigned protein product (Arabidopsis thaliana)	
MCR012722.C2.22	1.49	0.02	1.16	1.30	1.11	0.44	0.09	0.03	1.15	0.25	0.08	0.84	0.76	0.07	0.54	0.01	AMM51762	unassigned protein product (Arabidopsis thaliana)	
MCR01847.C1.1109	1.48	0.02	1.11	1.20	1.06	0.65	0.55	0.25	1.16	0.40	0.93	0.62	1.03	0.86	0.53	0.00	AMM6502	unassigned protein product (Arabidopsis thaliana)	
MCR013045.C1.691	1.92	0.01	1.22	1.29	0.92	0.65	0.16	1.14	0.48	0.77	0.21	1.08	0.70	0.47	0.10	0.00	NA	unassigned protein product (Arabidopsis thaliana)	
MCR019913.C1.1247	1.86	0.00	1.15	1.34	1.42	0.08	0.05	0.29	1.41	0.04	0.65	0.65	0.91	0.61	0.53	0.00	AMM2781	ATP binding/kinase protein serine/threonine kinase (Arabidopsis thaliana)	
MCR013684.C1.1549	1.47	0.04	0.76	0.77	1.09	0.80	0.86	0.00	2.09	0.65	0.84	0.64	1.14	0.24	0.48	0.00	AT014358	12-cis-hydroxytetradenoate reductase 3.172-oxo-phytylreductase-10.11-reductase 3.1 (QPOA-reductase 3) (Lycopersicon)	
MCR06037.C1.813	1.73	0.01	2.00	2.25	1.25	0.45	0.63	0.05	1.65	0.01	0.90	0.50	0.45	0.26	0.56	0.06	NA	unassigned protein product (Arabidopsis thaliana)	
MCR05162.C1.1715	2.73	0.00	1.39	1.11	1.56	0.21	0.40	0.02	1.54	0.14	0.96	0.75	1.15	0.45	0.38	0.00	BT012722	phosphatidylcholine N-methyltransferase II (cytochrome P450 reductase)	
MCR018131.C1.1430	1.73	0.00	1.66	1.60	1.10	0.51	0.33	0.00	1.39	0.23	1.09	0.56	0.63	0.01	0.24	0.00	AT413501	Aspartate aminotransferase, cytosolic (Transaminase A)	
MCR04345.C1.116	4.07	0.01	1.47	1.04	1.23	0.19	0.59	0.10	0.39	0.00	1.11	0.47	0.96	0.84	0.33	0.00	U118986	unassigned protein product (Arabidopsis thaliana)	
MCR04427.C2.1917	0.98	0.32	0.66	0.53	0.93	0.38	0.39	0.00	1.69	0.22	0.61	0.51	0.42	0.32	0.22	0.00	AT5G3958	unassigned protein product (Arabidopsis thaliana)	
BF_LBCHXXX_004502_TMSMCF_411	1.11	0.40	0.87	0.97	0.65	0.07	0.43	0.00	2.21	0.00	1.44	0.04	0.78	0.01	0.63	0.01	NA	unassigned protein product (Arabidopsis thaliana)	
MCR08922.C1.440	1.42	0.05	0.90	0.91	0.91	0.84	0.30	0.00	2.58	0.01	1.53	0.10	0.82	0.14	0.27	0.00	NA	unassigned protein product (Arabidopsis thaliana)	
MCR013195.C1.815	2.63	0.00	1.90	1.91	1.61	0.04	0.05	0.04	0.88	0.40	0.83	0.28	0.90	0.61	0.41	0.00	AT5G1823	alpha-glucosidase II (cytochrome P450 reductase)	
SSRTO611xsf_413	0.82	0.27	0.89	0.57	0.83	0.46	0.25	0.01	1.24	0.16	1.38	0.20	1.22	0.16	0.23	0.00	AMM6886	RAB11B (Locus accession)	
MCR015831.C1.487	1.63	0.21	1.72	1.56	0.88	0.88	0.85	0.00	3.19	0.00	1.92	0.96	0.62	0.20	0.10	0.00	AT777542	Arp2/3-3 rapidly elicited protein 181 (Nicotiana glauca)	
MCR02001.C1.1205	2.02	0.07	1.28	1.16	0.75	0.15	0.19	0.00	2.12	0.09	1.33	0.26	0.65	0.30	0.15	0.01	BT013838	cytochrome P450-like protein (CYP2A5 human)	
SSRTO516xsf_528	1.74	0.01	1.00	1.00	1.24	0.55	0.22	0.00	1.16	0.11	1.11	0.56	0.84	0.52	0.14	0.00	AMM7530	Os202751800 (Ornithine 5-lyase (ornithine decarboxylase))	
MCR01096.C1.05	1.08	0.56	1.08	0.54	1.18	0.18	0.38	0.00	1.16	0.30	1.04	0.70	0.93	0.19	0.36	0.00	AT272902	non-phosphotransferase (Lycopersicon)	
MCR07018.C1.1121	1.70	0.01	0.70	0.68	1.56	0.43	0.63	0.02	1.84	0.04	0.90	0.61	1.66	0.44	0.59	0.00	AT272992	transcription factor CavPRK1 (Capsicum annuum)	
MCR014951.C1.1199	3.68	0.00	1.77	1.71	0.21	0.78	0.01	0.44	0.61	0.46	0.25	0.89	0.54	0.66	0.11	0.38	0.01	AT166549	unassigned protein product (Arabidopsis thaliana)
MCR0886.C1.369	1.48	0.08	1.19	1.38	1.18	0.22	0.25	0.00	1.37	0.06	1.01	0.96	0.77	0.04	0.27	0.00	MM_112234	unassigned protein product (Arabidopsis thaliana)	
MCR02259.C2.1563	1.66	0.01	1.35	1.41	1.38	0.31	0.43	0.01	2.33	0.00	1.14	0.48	0.72	0.16	0.20	0.00	AT202078	glucose acyltransferase (Solanum tuberosum)	
MCR012305.C1.021	2.13	0.11	0.23	0.13	0.23	0.44	0.05	0.03	1.49	0.01	0.39	0.09	1.20	0.23	0.00	0.00	AMM4121	Ornithine lyase (Ornithine decarboxylase)	
MCR019641.C2.896	3.07	0.00	1.16	0.52	1.06	0.86	0.51	0.01	1.47	0.03	0.97	0.83	0.76	0.11	0.59	0.05	NA	unassigned protein product (Arabidopsis thaliana)	
bt_susceptor_00104010m_scf_369	3.86	0.00	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.00	AT262479	unassigned protein product (Arabidopsis thaliana)	
MCR017593.C1.323	1.26	0.10	0.82	0.44	0.80	0.38	0.44	0.01	3.43	0.00	0.26	0.14	0.95	0.85	0.31	0.00	NA	unassigned protein product (Arabidopsis thaliana)	
MCR02883.C1.891	1.54	0.01	1.02	0.91	0.93	0.78	0.44	0.00	1.87	0.01	1.28	0.11	0.90	0.41	0.38	0.00	BT012930	PED1 (PEROXISOME DEFECTIVE 1) (Arabidopsis thaliana)	
MCR018035.C1.471	1.73	0.00	1.99	1.99	1.80	0.23	0.23	0.00	1.80	0.23	0.23	0.20	0.20	0.20	0.20	0.00	AT262936	carbonate dehydratase/zinc-finger binding (Arabidopsis thaliana)	
MCR012126.C1.685	2.65	0.05	2.26	2.03	1.72	0.08	0.19	0.01	0.72	0.28	1.05	0.75	0.40	0.00	0.13	0.00	BT014571	ACR4: amino acid binding (Arabidopsis thaliana)	
MCR012342.C1.628	2.08	0.00	1.28	1.28	1.28	1.28	1.28	1.28	1.28	1.28	1.28	1.28	1.28	1.28	1.28	0.00	AT262936	carbonate dehydratase/zinc-finger binding (Arabidopsis thaliana)	
MCR010101.C1.842	1.75	0.02	1.14	0.95	1.27	0.17	0.28	0.01	1.29	0.13	0.97	0.86	0.92	0.73	0.18	0.00	AMM43480	unassigned protein product (Arabidopsis thaliana)	
MCR019101.C1.676	1.08	0.60	1.39	0.77	1.07	0.67	0.54	0.01	1.48	0.05	1.23	0.19	0.13	0.83	0.41	0.00	NA	unassigned protein product (Arabidopsis thaliana)	
MCR012626.C1.1446	2.13	0.00	1.49	1.49	1.67	0.63	0.83	0.16	1.41	0.39	0.77	0.26	0.77	0.26	0.41	0.00	AMM16204	cytochrome oxidase zinc-finger binding (Arabidopsis thaliana)	
MCR04693.C1.1269	2.04	0.01	1.39	1.12	1.52	0.02	0.64	0.07	1.70	0.10	0.85	0.35	0.79	0.21	0.35	0.00	NA	unassigned protein product (Arabidopsis thaliana)	
SSRTO2020m_264	1.47	0.00	1.47	1.47	1.47	1.47	1.47	1.47	1.47	1.47	1.47	1.47	1.47	1.47	1.47	0.00	NA	unassigned protein product (Arabidopsis thaliana)	
MCR05336.C1.563	2.30	0.00	1.15	0.56	1.32	0.24	0.36	0.00	1.34	0.06	0.93	0.54	1.18	0.38	0.82	0.25	BT014526	phosphatidylcholine N-methyltransferase II (cytochrome P450 reductase)	
MCR01388.C12.575	1.43	0.02	0.66	0.60	0.93	0.64	0.60	0.01	2.67	0.00	1.32	0.17	1.42	0.17	0.88	0.67	AMM49816	isopentenyl diphosphate isomerase 2 (Nicotiana glauca)	
MCR012626.C1.1446	2.13	0.00	1.49	1.49	1.67	0.63	0.83	0.16	1.41	0.39	0.77	0.26	0.77	0.26	0.41	0.00	AMM16204	cytochrome oxidase zinc-finger binding (Arabidopsis thaliana)	
MCR04693.C1.1269	2.04	0.01	1.39	1.12	1.52	0.02	0.64	0.07	1.70	0.10	0.85	0.35	0.79	0.21	0.35	0.00	NA	unassigned protein product (Arabidopsis thaliana)	
SSRTO2020m_264	1.47	0.00	1.47	1.47	1.47	1.47	1.47	1.47	1.47	1.47	1.47	1.47	1.47	1.47	1.47	0.00	NA	unassigned protein product (Arabidopsis thaliana)	
MCR05336.C1.563	2.30	0.00	1.15	0.56	1.32	0.24	0.36	0.00	1.34	0.06	0.93	0.54	1.18	0.38	0.82	0.25	BT014526	phosphatidylcholine N-methyltransferase II (cytochrome P450 reductase)	
MCR01388.C12.575	1.43	0.02	0.66	0.60	0.93	0.64	0.60	0.01	2.67	0.00	1.32	0.17	1.42	0.17	0.88	0.67	AMM49816	isopentenyl diphosphate isomerase 2 (Nicotiana glauca)	
MCR012626.C1.1446	2.13	0.00	1.49	1.49	1.67	0.63	0.83	0.16	1.41	0.39	0.77	0.26	0.77	0.26	0.41	0.00	AMM16204	cytochrome oxidase zinc-finger binding (Arabidopsis thaliana)	
MCR04693.C1.1269	2.04	0.01	1.39	1.12	1.52	0.02	0.64	0.07	1.70	0.10	0.85	0.35	0.79	0.21	0.35	0.00	NA	unassigned protein product (Arabidopsis thaliana)	
SSRTO2020m_264	1.47	0.00	1.47	1.47															

MCRO4874.C1_626	1.92	0.10	1.08	0.52	0.91	0.92	0.54	0.01	1.71	0.01	0.96	0.73	0.99	0.90	0.54	0.01	AJ077739	w-3 dehydratase (Solanium tuberosum)
MCRO3624.C1_1138	1.98	0.02	0.88	0.89	1.95	0.57	0.65	0.04	1.83	0.01	1.01	0.83	0.94	0.84	0.69	0.19	NA	acid deacetylase (Citrus sinensis)
MCRO2851.C1_604	1.71	0.01	1.27	0.93	0.72	0.48	0.10	1.24	0.21	0.91	0.63	0.88	0.58	0.36	0.10	NA	Glucan-3-phosphate dehydrogenase (NAD+)	
MCRO361.C1_1451	1.73	0.02	0.86	0.88	0.43	0.03	0.03	0.03	0.07	0.03	0.47	0.11	0.97	0.89	0.27	0.11	NA	phosphatase (CORYLIUS COCCUS)
MCRO7102.C1_583	2.36	0.01	1.13	0.81	1.33	0.57	0.18	0.00	3.04	0.02	1.06	0.63	0.80	0.11	0.14	0.00	NA	unknown (Arabidopsis thaliana)
MCRO3908.C1_1208	1.80	0.09	0.64	0.85	0.89	0.50	0.00	0.00	0.02	0.00	0.60	0.80	0.80	0.80	0.80	0.80	NA	Ornithine O-methyltransferase (Nicotiana glauca)
MCRO12466.C1_775	1.96	0.00	1.41	0.99	1.06	0.69	0.60	0.00	1.88	0.00	1.10	0.52	0.63	0.04	0.51	0.04	AM45767	hydroxylase protein MdDRAFT_AC146757.00 Medicago truncatula
MCRO2996.C2_1443	1.62	0.01	1.16	0.41	1.19	0.27	0.22	0.00	1.29	0.16	1.03	0.82	0.65	0.06	0.17	0.00	AK229933	nucleic acid binding transcription factor zinc ion binding (Arabidopsis thaliana)
MCRO1105.C2_14	1.99	0.12	0.91	0.12	0.98	0.42	0.14	0.01	0.88	0.42	0.71	0.24	0.15	0.14	0.43	0.00	AK081243	hydroxylase protein Arabidopsis thaliana Nucleosuccinyl transferase TH13 (Lycopersicon esculentum)
MCRO13509.C1_686	2.03	0.00	1.17	0.20	1.35	0.56	0.10	0.00	1.27	0.17	0.85	0.48	0.47	0.12	0.00	0.00	AF147775	TK1-like deoxyribonucleic acid kinase 4 (Lycopersicon esculentum)
U31247111_534	0.89	0.00	0.95	0.56	0.58	0.20	0.00	0.27	0.01	0.11	0.00	0.00	0.00	0.00	0.00	0.00	AM441073	unknown (Arabidopsis thaliana)
MCRO4755.C1_544	1.31	0.05	1.15	0.25	1.08	0.57	0.66	0.01	2.07	0.00	0.00	0.98	1.11	0.37	0.68	0.00	AJ007739	Ornithine-3-lyase-like dehydratase, chloroplast precursor, cytosolic, expressed (Opuntia stricta (cactus/cactaceae))
MCRO1547.C1_1038	1.18	0.34	0.84	0.46	1.06	0.45	0.32	0.00	1.56	0.44	1.33	0.10	1.13	0.39	0.43	0.00	NA	DNA binding /transcription factor (Arabidopsis thaliana)
MCRO3672.C1_663	1.91	0.02	1.01	0.61	1.00	0.30	0.21	0.00	1.64	0.22	1.05	0.56	0.67	0.09	0.04	0.00	NA	Ornithine-3-lyase-like dehydratase, chloroplast precursor, cytosolic, expressed (Opuntia stricta (cactus/cactaceae))
U31247111_534	1.29	0.10	1.46	0.08	1.18	0.43	0.37	0.01	1.38	0.03	0.91	0.72	0.60	0.01	0.25	0.00	AF177655	erythrose-binding protein (Lycopersicon esculentum)
U31247111_534	1.56	0.05	0.91	0.68	0.99	0.31	0.56	0.00	1.96	0.00	1.64	0.01	0.66	0.48	0.03	0.00	U22922	phenolase oxidase 8, chloroplast precursor (Populus alba (cottonwood))
MCRO646.C3_150	3.72	0.03	0.97	0.18	1.14	0.38	0.26	0.00	1.24	0.36	1.14	0.31	0.74	0.14	0.28	0.00	U22922	phenolase oxidase 8, chloroplast precursor (Populus alba (cottonwood))
MCRO3774.C1_930	2.92	0.00	1.37	0.14	0.54	0.38	0.14	0.00	2.10	0.00	1.63	0.02	0.22	0.01	0.20	0.02	NA	Flavin-8-oxidase (Arabidopsis thaliana)
MCRO4278.C1_708	1.90	0.01	0.63	0.68	0.30	0.32	0.00	1.20	0.22	1.60	0.03	0.66	0.81	0.66	0.38	0.00	AK06008	Ornithine-3-lyase
MCRO6622.C1_1146	1.66	0.05	1.13	0.42	1.09	0.52	0.36	0.02	1.68	0.17	1.04	0.77	0.82	0.30	0.32	0.03	BT013054	aldose 1-epimerase (Arabidopsis thaliana)
U31247111_534	1.18	0.15	1.06	0.63	1.28	0.87	0.44	0.01	1.33	0.06	0.99	0.97	0.72	0.03	0.41	0.00	AF181034	ATPase (Arabidopsis thaliana)
MCRO1889.C3_1473	1.04	0.74	0.97	0.85	1.30	0.10	0.44	0.00	1.27	0.33	0.64	0.67	1.08	0.58	0.28	0.00	AK0606	1,4-alpha-glucan branching enzyme (Solanium tuberosum)
MCRO2815.C1_603	2.86	0.00	0.93	0.69	0.69	0.36	0.34	0.01	1.97	0.07	1.37	0.10	0.84	0.66	0.37	0.02	U2460179	acid phosphatase (Arabidopsis thaliana)
MCRO13463.C1_820	2.00	0.03	1.21	0.28	1.31	0.69	0.42	0.00	1.12	0.56	0.93	0.81	0.66	0.68	0.26	0.00	NA	unknown (Arabidopsis thaliana)
MCRO1889.C4_21	1.00	0.76	1.01	0.92	1.26	0.56	0.43	0.01	1.37	0.21	0.98	0.85	0.86	0.82	0.31	0.00	AK078786	1,4-alpha-glucan branching enzyme (Solanium tuberosum)
U31247111_534	1.79	0.02	1.23	0.20	1.60	0.01	0.63	0.01	1.42	0.22	0.80	0.38	0.44	0.24	0.43	0.01	AK051079	protein (Arabidopsis thaliana)
U31247111_534	1.75	0.03	0.84	0.67	1.41	0.09	0.08	0.00	1.70	0.24	1.02	0.92	1.18	0.81	0.11	0.00	AF154655	peroxidase
MCRO1889.C3_1473	1.18	0.15	1.06	0.63	1.28	0.87	0.44	0.01	1.33	0.06	0.99	0.97	0.72	0.03	0.41	0.00	AF181034	ATPase (Arabidopsis thaliana)
MCRO2815.C1_603	2.86	0.00	0.93	0.69	0.69	0.36	0.34	0.01	1.97	0.07	1.37	0.10	0.84	0.66	0.37	0.02	U2460179	acid phosphatase (Arabidopsis thaliana)
MCRO13463.C1_820	2.00	0.03	1.21	0.28	1.31	0.69	0.42	0.00	1.12	0.56	0.93	0.81	0.66	0.68	0.26	0.00	NA	unknown (Arabidopsis thaliana)
MCRO1889.C4_21	1.00	0.76	1.01	0.92	1.26	0.56	0.43	0.01	1.37	0.21	0.98	0.85	0.86	0.82	0.31	0.00	AK078786	1,4-alpha-glucan branching enzyme (Solanium tuberosum)
U31247111_534	1.79	0.02	1.23	0.20	1.60	0.01	0.63	0.01	1.42	0.22	0.80	0.38	0.44	0.24	0.43	0.01	AK051079	protein (Arabidopsis thaliana)
MCRO499.C1_1039	1.75	0.03	0.84	0.67	1.41	0.09	0.08	0.00	1.70	0.24	1.02	0.92	1.18	0.81	0.11	0.00	AF154655	peroxidase
MCRO3923.C1_702	1.18	0.15	1.06	0.63	1.28	0.87	0.44	0.01	1.33	0.06	0.99	0.97	0.72	0.03	0.41	0.00	AF181034	ATPase (Arabidopsis thaliana)
MCRO4490.C1_1107	1.63	0.04	1.19	0.36	1.36	0.44	0.51	0.03	1.61	0.02	0.70	0.09	0.95	0.68	0.48	0.00	AM44185	ATP-binding /kinase protein kinase/protein-tyrosine kinase/structural constituent of cell wall (Arabidopsis thaliana)
U31247111_534	1.00	0.76	1.01	0.92	1.26	0.56	0.43	0.01	1.37	0.21	0.98	0.85	0.86	0.82	0.31	0.00	AK078786	1,4-alpha-glucan branching enzyme (Solanium tuberosum)
MCRO2815.C1_603	2.86	0.00	0.93	0.69	0.69	0.36	0.34	0.01	1.97	0.07	1.37	0.10	0.84	0.66	0.37	0.02	U2460179	acid phosphatase (Arabidopsis thaliana)
MCRO13463.C1_820	2.00	0.03	1.21	0.28	1.31	0.69	0.42	0.00	1.12	0.56	0.93	0.81	0.66	0.68	0.26	0.00	NA	unknown (Arabidopsis thaliana)
MCRO1889.C4_21	1.00	0.76	1.01	0.92	1.26	0.56	0.43	0.01	1.37	0.21	0.98	0.85	0.86	0.82	0.31	0.00	AK078786	1,4-alpha-glucan branching enzyme (Solanium tuberosum)
U31247111_534	1.79	0.02	1.23	0.20	1.60	0.01	0.63	0.01	1.42	0.22	0.80	0.38	0.44	0.24	0.43	0.01	AK051079	protein (Arabidopsis thaliana)
MCRO2815.C1_603	2.86	0.00	0.93	0.69	0.69	0.36	0.34	0.01	1.97	0.07	1.37	0.10	0.84	0.66	0.37	0.02	U2460179	acid phosphatase (Arabidopsis thaliana)
MCRO13463.C1_820	2.00	0.03	1.21	0.28	1.31	0.69	0.42	0.00	1.12	0.56	0.93	0.81	0.66	0.68	0.26	0.00	NA	unknown (Arabidopsis thaliana)
MCRO1889.C4_21	1.00	0.76	1.01	0.92	1.26	0.56	0.43	0.01	1.37	0.21	0.98	0.85	0.86	0.82	0.31	0.00	AK078786	1,4-alpha-glucan branching enzyme (Solanium tuberosum)
U31247111_534	1.79	0.02	1.23	0.20	1.60	0.01	0.63	0.01	1.42	0.22	0.80	0.38	0.44	0.24	0.43	0.01	AK051079	protein (Arabidopsis thaliana)
MCRO499.C1_1039	1.75	0.03	0.84	0.67	1.41	0.09	0.08	0.00	1.70	0.24	1.02	0.92	1.18	0.81	0.11	0.00	AF154655	peroxidase
MCRO3923.C1_702	1.18	0.15	1.06	0.63	1.28	0.87	0.44	0.01	1.33	0.06	0.99	0.97	0.72	0.03	0.41	0.00	AF181034	ATPase (Arabidopsis thaliana)
MCRO4490.C1_1107	1.63	0.04	1.19	0.36	1.36	0.44	0.51	0.03	1.61	0.02	0.70	0.09	0.95	0.68	0.48	0.00	AM44185	ATP-binding /kinase protein kinase/protein-tyrosine kinase/structural constituent of cell wall (Arabidopsis thaliana)
U31247111_534	1.00	0.76	1.01	0.92	1.26	0.56	0.43	0.01	1.37	0.21	0.98	0.85	0.86	0.82	0.31	0.00	AK078786	1,4-alpha-glucan branching enzyme (Solanium tuberosum)
MCRO2815.C1_603	2.86	0.00	0.93	0.69	0.69	0.36	0.34	0.01	1.97	0.07	1.37	0.10	0.84	0.66	0.37	0.02	U2460179	acid phosphatase (Arabidopsis thaliana)
MCRO13463.C1_820	2.00	0.03	1.21	0.28	1.31	0.69	0.42	0.00	1.12	0.56	0.93	0.81	0.66	0.68	0.26	0.00	NA	unknown (Arabidopsis thaliana)
MCRO1889.C4_21	1.00	0.76	1.01	0.92	1.26	0.56	0.43	0.01	1.37	0.21	0.98	0.85	0.86	0.82	0.31	0.00	AK078786	1,4-alpha-glucan branching enzyme (Solanium tuberosum)
U31247111_534	1.79	0.02	1.23	0.20	1.60	0.01	0.63	0.01	1.42	0.22	0.80	0.38	0.44	0.24	0.43	0.01	AK051079	protein (Arabidopsis thaliana)
MCRO499.C1_1039	1.75	0.03	0.84	0.67	1.41	0.09	0.08	0.00	1.70	0.24	1.02	0.92	1.18	0.81	0.11	0.00	AF154655	peroxidase
MCRO3923.C1_702	1.18	0.15	1.06	0.63	1.28	0.87	0.44	0.01	1.33	0.06	0.99	0.97	0.72	0.03	0.41	0.00	AF181034	ATPase (Arabidopsis thaliana)
MCRO4490.C1_1107	1.63	0.04	1.19	0.36	1.36	0.44	0.51	0.03	1.61	0.02	0.70	0.09	0.95	0.68	0.48	0.00	AM44185	ATP-binding /kinase protein kinase/protein-tyrosine kinase/structural constituent of cell wall (Arabidopsis thaliana)
U31247111_534	1.00	0.76	1.01	0.92	1.26	0.56	0.43	0.01	1.37	0.21	0.98	0.85	0.86	0.82	0.31	0.00	AK078786	1,4-alpha-glucan branching enzyme (Solanium tuberosum)
MCRO2815.C1_603	2.86	0.00	0.93	0.69	0.69	0.36	0.34	0.01	1.97	0.07	1.37	0.10	0.84	0.66	0.37	0.02	U2460179	acid phosphatase (Arabidopsis thaliana)</

MCR0384.G2_677	1.01	0.96	1.10	0.86	0.76	0.37	0.20	0.01	2.10	0.00	3.24	0.00	1.93	0.06	0.42	0.02	BT019342	unknown protein (Arabidopsis thaliana)
bl_mw000_00391062fm.scd_1	0.91	0.49	1.09	0.01	1.69	0.21	0.74	0.06	1.92	0.50	1.11	0.48	0.08	0.08	0.23	0.01	NA	hypothetical protein (Sal. typhimuriana) (salicin catabolism group)
MCR0322.C1_884	1.31	0.05	0.87	0.60	1.02	0.87	0.55	0.00	0.99	0.96	1.48	0.03	1.33	0.20	0.47	0.06	AJ237988	cellulose repeat-unit-binding protein (Musa sapientum)
bl_mw000_001260219m.scd_192	4.42	0.00	2.20	0.93	1.32	0.34	0.43	0.00	1.08	0.84	1.49	0.08	0.60	0.00	0.44	0.00	D3622994	proteinase inhibitor isoflavan (Solanum elaeagnifolium)
bl_mw000_006700717m.scd_435	1.03	0.75	1.36	0.22	0.91	0.33	0.40	0.00	0.90	0.93	1.54	0.02	1.00	0.56	0.76	0.24	NA	polygalacturonase-inhibiting protein (Panicum americanum)
bl_mw000_004490918m.scd_243	0.93	0.55	0.96	0.73	0.67	0.01	0.48	0.00	3.38	0.02	5.55	0.00	2.00	0.01	0.80	0.38	AK224774	B12D-like protein (Beta vulgaris)