

Supplementary Materials

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International Space Station conditions alter genomics, proteomics, and metabolomics in *Aspergillus nidulans*

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Supplemental Methods. Space flight hardware, science preparation and loading, flight operations, and ISS environmental parameters.

Approximately 10 days prior to flight, fungal spores were aseptically spotted on glucose minimal solid media (GMM) in Nunc® OmniTray plates (Sigma-Aldrich). The entire edge of each OmniTray plate was then wrapped with a micropore tape. The samples were kept at 4°C once loaded into the OmniTrays. A total of seven (7) OmniTrays were stacked and then placed inside of BioServe Space Technologies space flight hardware called a Plate Habitat (PHAB). The PHAB is an anodized, aluminum box that provides one level of sealed containment per NASA safety requirements but can easily conduct temperature from a heated or cooled surface and is capable of gas exchange for aerobic samples. The experiment utilized eight (8) PHABs for flight and eight (8) PHABs for the corresponding ground controls. The PHABs were labeled A-H. The final integration of the samples into the flight and ground PHABs occurred approximately 4 days before the SpaceX rocket was set to launch to the ISS. This integration took place in a large cold room set at 4°C in order to maintain sample stasis. Each PHAB contained a datalogger that recorded temperature every 5 minutes during the entire mission duration beginning at the point science was loaded into the PHABs and ending when the science samples were deintegrated from the PHABs after experiment completion.

The flight PHABs were placed in NASA provided cold bags at 4°C approximately 28 hours prior to launch and then loaded onto the rocket and subsequently launched to the International Space Station (ISS) aboard NASA's eighth cargo resupply flight of the Space Exploration Technologies (SpaceX) Dragon spacecraft on April 8th, 2016 at 20:43 (GMT). After a two day journey towards the ISS, the Dragon capsule was captured and berthed to the nadir port of Node 2 using the robotic arm on 4/10/2016 at 11:23 (GMT). Subsequently, the crew-members, 3 Russian and 2 US and 1 EU, unpacked the capsule and transferred all experiments, supplies, and consumable onboard the ISS. The fungal samples were transferred from the cold bags and placed into two separate BioServe Space Automated Bioproduct Lab (SABL) incubators which were set at 4°C. PHABs A-D were placed in SABL1 and E-H were placed in SABL2. Approximately 23 days after launch the SABL1 incubator temperature was changed to 37°C. Within 4 hours of the SABL1 temperature being set at 37°C, one 2.54 cm foam wedge was placed in the SABL1 door. This kept the door open 2.54 cm in order to reduce CO₂ buildup from the samples inside of the SABL incubator. Samples were held at 37°C for 7 days. Approximately 26 days after launch, the SABL2 incubator temperature was changed to 37°C. Within 4 hours of the SABL2 temperature being set at 37°C, a 2.54 cm foam wedge was placed in the SABL2 door. After seven (7) days of incubation for samples A-D and four (4) days of incubation for samples E-H, both SABL1 and 2 incubator temperature were changed to 4°C and the foam wedge removed from the doors and the doors closed. All temperature changes were completed remotely via BioServe's payload operations and command center (POCC). Temperature set points were confirmed via health and status data sent on a continuous basis during acquisition of signal with the ISS from the SABL incubator to BioServe's POCC. SABL temperature set points were monitored on a daily basis throughout the entire mission duration.

Once flight samples were turned over to NASA for launch, the ground controls were carefully packed in Bioshippers with 4°C cold packs and transported back to the PI lab via Fed Ex custom critical temperature control shipping and placed in a ground based SABL research module and

then placed in a 4°C lab refrigerator within the PI's lab. The ground based SABL research module was utilized so that temperature changes within the ground incubator would more closely resemble temperature changes that occurred in the flight SABL incubator given the lack of convection in space. The ground controls were operated on an eight (8) hour delay in order for the science team to match the required temperature changes of the space flight samples once the information from the ISS was received on the ground. The ground controls, with the eight (8) hour delay, followed the same temperature profile as the space flight samples.

ISS-grown samples were packed into 4°C cold bags on 5/9/16 at 18:00 (GMT) prior to being transferred to the dragon capsule. On 5/11/16 at 13:21 (GMT) the capsule was unberthed from the ISS and deorbit ignition occurred at 18:06 (GMT). The Dragon capsule splashed down into the Pacific Ocean few minutes later at 18:49 (GMT). After retrieval of the capsule from the ocean, the samples were handed over on 5/12/16 at 20:00 (GMT) for de-integration and sample processing while maintaining the 4°C temperature. Once at the science team's lab, all flight and ground samples were deintegrated from the PHABs and handed over to the science team for analysis.

Mission Parameters	Launch	Berth	Unberth	De-orbit ignition	Splashdown	Docked Duration
SpX-8	04/08/2016 20:43:00 (GMT)	04/10/2016 11:23:00 (GMT)	05/11/2016 13:21:00 (GMT)	05/11/2016 18:06:00 (GMT)	05/11/2016 18:49:00 (GMT)	31 Days
USOS Crewmembers	Timothy L. Kopra (CDR-47), Timothy Peake, and Jeffrey N. Williams					

ISS Environmental Parameters	SpX-8 Mission
Temperature inside Destiny (US laboratory)	21.1°C
Pressure inside Destiny (US Laboratory)	99.147 kPa
Humidity inside Columbus (EU Laboratory)	46.15%
Partial Pressure of Air Constituents inside Columbus (EU Laboratory)	ppO ₂ : 19.332 kPa ppCO ₂ : 0.3786 kPa
Radiation inside Destiny (US Laboratory)	Total dose: 6.901 mGy Total Dose equivalent: 17.003 mGy

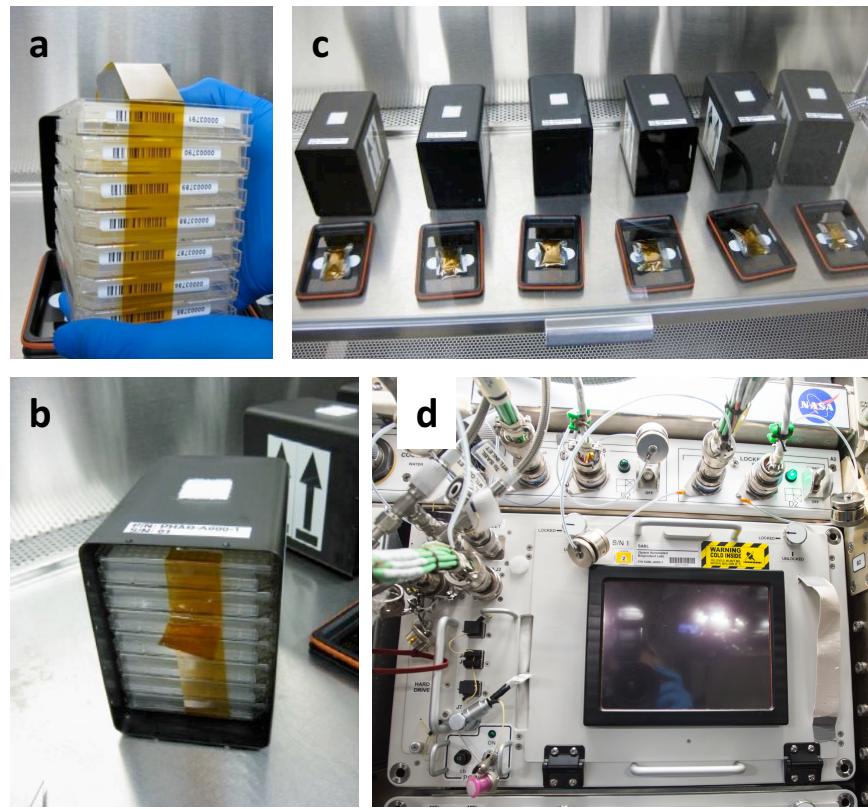


Figure S1. Hardware used in *A. nidulans* ISS flight experiment: **a** Omnitray plates, **b** Omnitrays in Plate Habitat (PHAB) systems, **c** PHAB systems with temperature logger (HOBO), **d** Space Automated Bioproduction Lab (SABL) system.

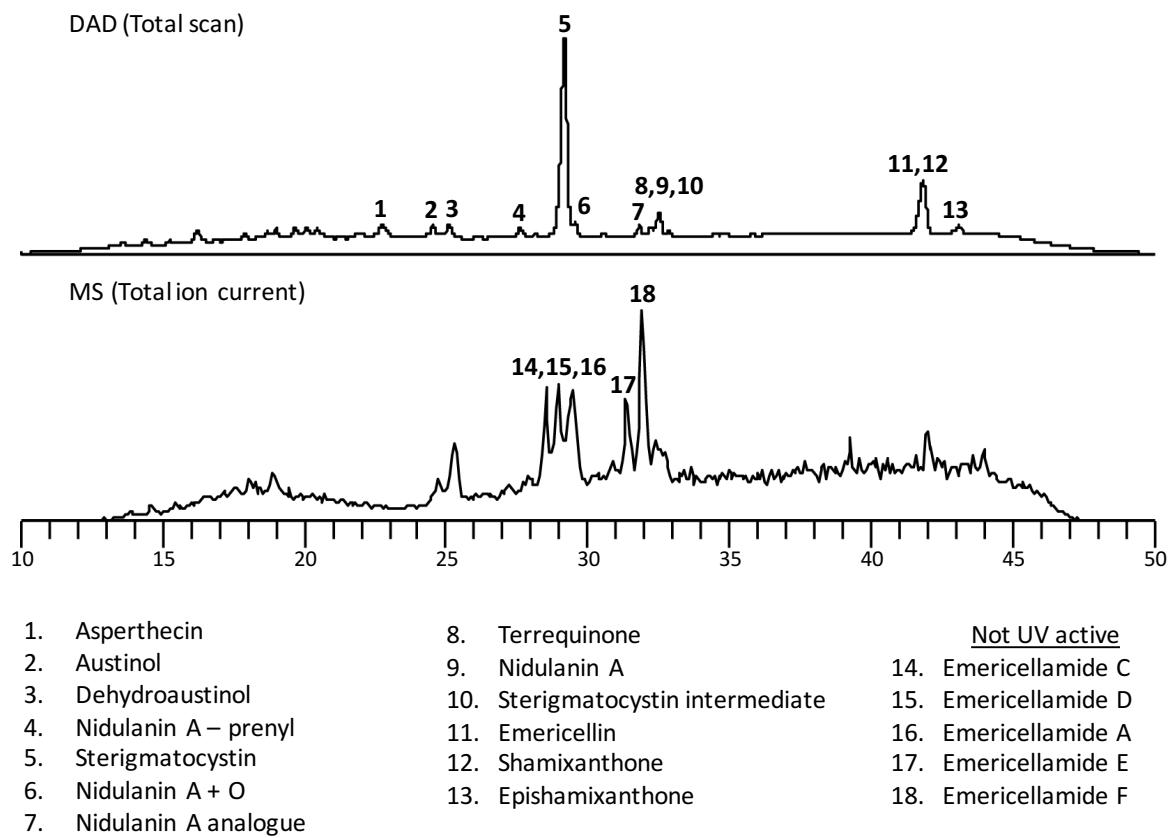


Figure S2. LC-MS profile of SMs identified in *A. nidulans* strains following growth on GMM for 7 days at 37°C, as detected by Diode Array Detector (DAD) total scan and MS total ion current (TIC).

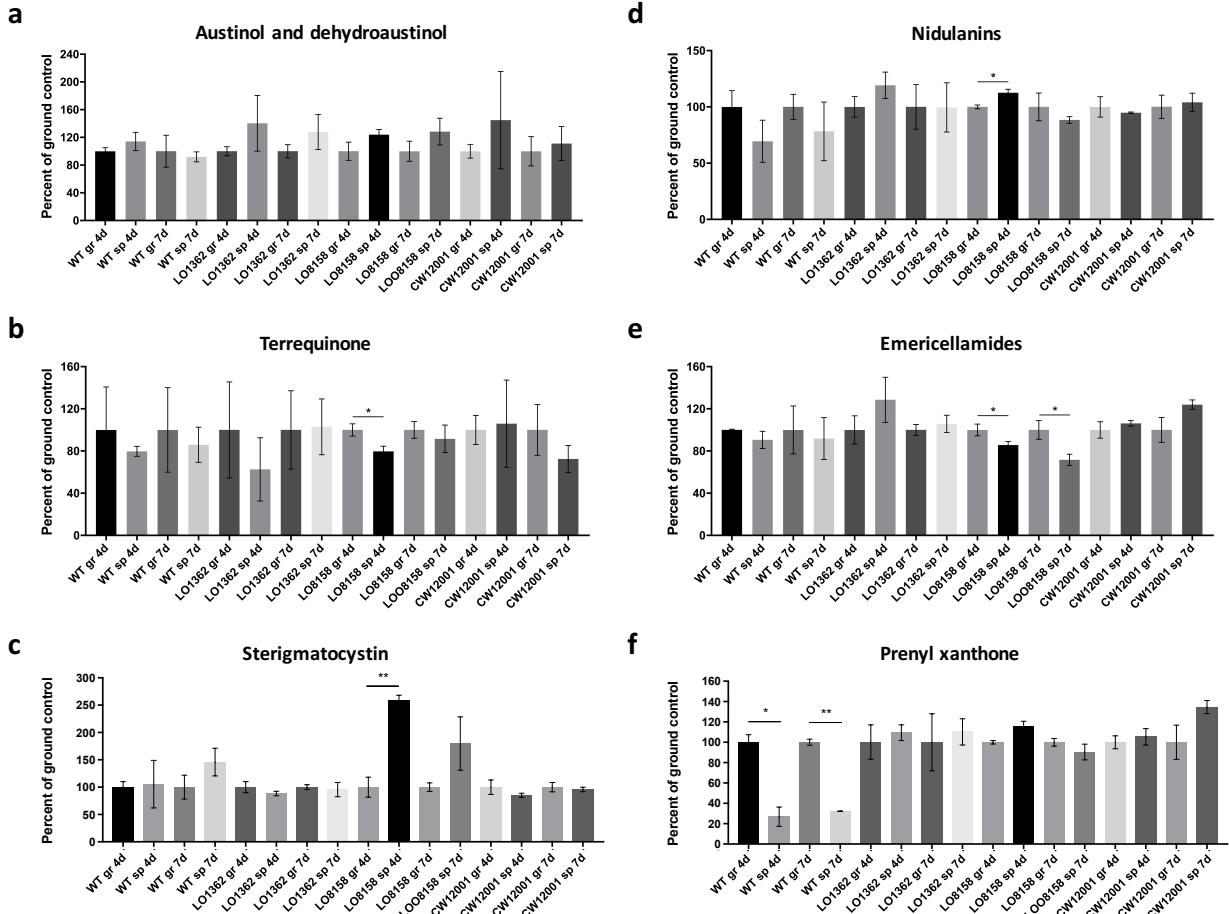


Figure S3. Secondary metabolite quantification showing percent change for ISS-grown samples in relation to Earth-grown counterparts for **a** austinol and dehydroaustinol, **b** terrequinone, **c** sterigmatocystin, **d** nidulanins, **e** emericellamides, and **f** prenyl xanthones. Significance was determined using Welch's t-test.

Table S1. Strains used in this study.

Fungal name	Strain #	Genotype	Significance
WT	FGSC A4	WT	Well-characterized model fungus
nkuA-	LO1362	<i>pyroA4, riboB2, pyrG89, nkuA::argB</i>	Essential gene for NHEJ DNA repair
mcrA- oe:laeA	LO8158 CW12001	<i>pyroA4, riboB2, pyrG89, nkuA::argB (mcrA)::AfpyroA</i> <i>pyroA4, riboB2, pyrG89, nkuA::argB AfpyrG-gpdA(p)laeA</i>	Negative regulator of secondary metabolism Positive regulator of secondary metabolism

Table S2. Primers designed for this study (5' → 3').

AfpyrG_Fw	CAATGCTCTTCACCCTCTCG
AfpyrG_Rev	CTGTCTGAGAGGAGGCAGTG
PgpdA_Fw	CAGTGCCTCCTCTCAGACAGTCGGAGAATATGGAGCTTCA
PgpdA_Rev	TGTGATGTCTGCTCAAGCG
oe:laeA_PgpdA_P1	TCAAGCAAATGAATGGACGA
oe:laeA_PgpdA_P2	GGCGTTGGGGATATATTAA
oe:laeA_PgpdA_P3	CGAAGAGGGTGAAGAGCATTGTTGACGATTGACAGGCTG AG
oe:laeA_PgpdA_P4	CGCTTGAGCAGACATCACAAATGTTGAGATGGGCCCGGT
oe:laeA_PgpdA_P5	CCAGCGATAGACACGACTGA
oe:laeA_PgpdA_P6	CGAGTTGCTGGATTCTCTCC
oe:laeA_PgpdA_P4_ver2	CGATCTTGTACCCTGTTCG

Table S3. SNPs and INDELs identified in ISS-grown FGSC A4

Chromosome	Position	Flanking	Type	Gene/nearest gene	FGSC A4 control	FGSC A4 4d ISS	FGSC A4 7d ISS
I	435907	TTTCTTTCTTTTTTTTT	intergenic	AN6353	C/	CTTTTTTTTTTTTTT/	C/
I	79668	GGGCGTCCTGCCCCCTCC	intergenic	AN6243	G/	GCCCCCCCCCCCCCCCCCCC/	G/
I	1011575	CAAAAAAAACAAAAAAA	intergenic	AN6181	CAAAAAAAAAAAAAAAA/	C/	/
I	2264342	TATAAAGCTTTAGTAA	intergenic	AN10829	C/	C/	T/
I	2265536	ATCTAATTTAAAGTAGTT	intergenic	AN10829	C/	T/	T/
I	2265770	TTATTAAGATAGAGATT	intergenic	AN10829	G/	G/	A/
I	2265992	ATAGCAACTATAACTAGATA	intergenic	AN10829	A/	A/	G/
I	2384542	ACCGGGGTGTTTTTTT	intergenic	AN6528	G/	GT/	G/
I	3181498	TCTTTTTGTTTTTTT	intergenic	AN6790	G/	G/	GT/
I	3302710	AACACATCTGTTTTTTT	intergenic	AN6826	GT/	G/	G/
I	3745558	GTGCTCAGGTAATCAGTC	intergenic	AN6968	G/	A/	G/
I	3745696	TTGCATCCTGTACTAGCT	intergenic	AN6968	CCA/	C/	C/
I	3745698	GCCATCCGTACTAGCTTA	intergenic	AN6968	G/	GTA/	GTA/
I	3745703	CCCTGACTAGCTTACTTAT	intergenic	AN6968	G/	A/	A/
I	3745716	TACTTATATGGCTAACAGC	intergenic	AN6968	A/	G/	G/
I	3745719	TTATATGGCTAACAGCATC	intergenic	AN6968	C/	T/	T/
I	3745745	ACCTCTAAGTATGCTAAAT	intergenic	AN6968	A/	G/	G/
I	3745757	TGCTAAATTCAATGTCATCG	intergenic	AN6968	T/	C/	C/
I	3745762	AATTCTATGTCATGCTACT	intergenic	AN6968	T/	C/	C/
I	3745800	AAAATACCTGTAAGTCTAC	intergenic	AN6968	A/	A/	G/
I	3745815	CTATCTCTATAGCTTCCC	intergenic	AN6968	C/	C/	T/
I	3745907	CTTTCTATTAGCTCTC	intergenic	AN6968	C/	T/	C/
I	3746146	AAAGTAGCTTAAACTGG	intergenic	AN6968	C/	T/	C/
I	3746363	AAAGGGTTGCGGGTATAGA	intergenic	AN6968	G/	A/	G/
I	3746365	GGAGGTTGCGGGTATAGAA	intergenic	AN6968	C/	T/	C/
I	3746377	GTATAGAAAGTAGCTAAAGA	intergenic	AN6968	G/	A/	G/
I	3757760	TAGATGATCGGAGAAATTG	5' UTR premature start	AN6972	G/	A/	/
I	3757872	GGAAATGAGTACAGCAAG	intergenic	AN6972	A/	A/	G/
I	3757902	AAAGAGGAAAAGAAAAGGCC	intergenic	AN6972	G/	A/	A/
I	3758071	CGGCCAGCAAGGTAGGCA	intergenic	AN6972	A/	G/	G/
I	3758273	TGGCTGATTGAACTGCAGAG	intergenic	AN6972	A/	G/	A/
II	410248	TTTTCTTTCTTTTTTTT	intergenic	AN12458	C/	CTTTTTTTTTTTTTT/	C/
II	766232	CTTTCTTTCTTTTTTTT	intergenic	AN8103	C/	CTTTTTTTTTTTTTT/	CTTTTTTTTTTTTTT/
II	1416471	ATATAAAAAGATAAGATA	intergenic	AN8293	AAG/	AAG/	A/
II	1481863	TCTTATAACCCCTAACCA	intergenic	AN9416	G/	A/	G/
II	3848365	GGGTATGAATCACACAC	intergenic	AN3538	T/	T/	TAC/
III	2370871	ATTTTTTTGGGGGGGGGG	intergenic	AN4331	T/	TGGGGG/	T/
III	2458831	TGGCTTATACAGCCAGGG	intergenic	AN4303	C/	C/	T/
III	2459470	CCCTCTCTCAACTCTGTAC	intergenic	AN4303	C/	T/	C/
III	2471080	TGGCTTATACAGCAGGG	intergenic	AN4298	C/	C/	T/
III	2471088	ACAGCCAGGGGATTATAAGT	intergenic	AN4298	G/	A/	A/
III	2471100	TTAATAGTAGGTACTACTA	intergenic	AN4298	G/	A/	A/
III	2665402	GAACTGGGCAAAAAAAA	intergenic	AN8830	CAAAAAAAAAAAAAAAA/	C/	C/
III	3243139	ATGTTAGGCTTAAAGCCCC	intergenic	AN8654	CTAAA/	C/	CTAAA/
III	3356136	CTCAATGCCCTTTTTTTT	intergenic	AN8618	CTTTTTTTT/	C/	C/
IV	328603	GACTCTACACCCCCCCCC	intergenic	AN7316	A/	ACCCCCCCC/	A/
IV	329029	CTTAGGGCGCCCCCCCCCCC	intergenic	AN7316	GCCCCCCC/	G/	G/
IV	772502	ATAAAAATAGAAAAAAA	intergenic	AN7175	GAAAAAAAAAAAAAAAA	G/	GAAAAAAAAAAAAAAAAGAAAAAA
IV	1079345	TTATGATACTAAAAAAA	intergenic	AN7086	T/	T/	AAAAAAA/
IV	1443358	AGCTACTATTATAATATA	intergenic	AN6973	T/	T/	A/
IV	1443417	ATACATACTATACACT	intergenic	AN6973	C/	C/	T/
IV	1444358	GCTGCAAGCCATTTTTC	intergenic	AN6973	C/	C/	CCA/
IV	1444409	TTAACATCTAGCTGCAAGT	intergenic	AN6973	T/	G/	T/
IV	2882599	GCAACCTGTATTTAC	intergenic	AN11577	A/	G/	/
IV	2882617	ATTACTACTATCACAGCAG	intergenic	AN11577	G/	A/	A/
IV	2882620	ATTACTATCACAGCAGCAT	intergenic	AN11577	G/	A/	A/
IV	2882628	CACCGAGCAGCATCAGCAG	intergenic	AN11577	T/	C/	C/
IV	2887172	CAGTCACCTTAATATAT	intergenic	AN7848	C/	T/	T/
IV	2887303	GTCACCAAGCAGCGGG	intergenic	AN7848	G/	G/	A/
V	539952	TAACAACTCTCAAAAAAAA	intergenic	AN8453	CAA/	C/	C/
V	565012	TTTTCTTTCTTTTTTTT	intergenic	AN8461	C/	C/	CT/
V	1147783	TTTATAAAAATAGTATAT	intergenic	AN5098	A/	G/	G/
V	1148404	CTTATTAAGGATACTAA	intergenic	AN5098	A/	G/	/
V	1150151	ATTCCTTAGACTATAGATA	intergenic	AN5098	C/	T/	/
V	1150167	ATTAATAAAAGATAAAC	intergenic	AN5098	A/	G/	/
V	1465303	CACCGTGGGTTTTTTT	intergenic	AN5197	GT/	G/	G/
V	1670698	TATACACTATTATAAATT	intergenic	AN5797	T/	C/	T/
V	1670709	ATAAAATTATAAATTCT	intergenic	AN5797	A/	G/	A/
V	2360704	AGGTGAGGACTTTTTTT	intergenic	AN5575	CTTT/	C/	/
V	2686824	ATAGAAATTATTTTTTT	intergenic	AN5477	ATTTT/	A/	A/
V	3093092	GGGGGGGGGGGGAGAGGA	intergenic	AN5344	G/	C/	G/
V	3367079	TCCGTTATCATTTCTGAAT	intergenic	AN5254	C/	C/	A/
V	3367369	CTCCATGACAAGTGGCG	missense variant	AN5254	A/	G/	A/
V	3367409	GCGGGATGCAAGTACAG	missense variant	AN5254	C/	T/	C/
V	3367410	CCGGGATGCAAGTACAG	synonymous variant	AN5254	A/	G/	A/
V	3367449	GGAAAAGACATTGAGTTCT	synonymous variant	AN5254	T/	T/	C/
V	3367453	AAAGCACATTGAGTTCTGAA	missense variant	AN5254	A/	A/	G/
V	3367916	AATTCCAACGCTTGGCTA	missense variant	AN5254	G/	A/	A/
V	3368023	CCACCTACCCAAAGATTACCA	stop gained	AN5254	T/	T/	C/
V	3368024	CACCTACCCAAAGATTACCA	missense variant	AN5254	G/	G/	A/
V	3368096	TTATGAAATCAACCTGCAAT	missense variant	AN5254	T/	T/	C/
VI	262647	CGATATTGTTAAAAAAA	intergenic	AN1170	T/	TAAAAAAA/	/
VI	570709	AAATAATAATTATATTCTT	intergenic	AN1162	T/	T/	C/

VI	572081	CTTATATAAGCTTATTITA	intergenic	AN9057	A/	G/	A/
VI	572831	TCTAACTTATTCTTACTATA	intergenic	AN9057	C/	/	T/
VI	572847	TATAATTATTATTATTAACT	intergenic	AN9057	C/	./	T/
VI	1119514	TTAGTCGGTAAAGAAAAAAA	intergenic	AN3322	TAAAAAAAAAAAAAAAAAAAAA/	T/	T/
VI	1436309	AAATTTGTTGGGGGGGG	intergenic	AN3217	TGGGGG/	T/	T/
VI	2486002	CCTCGATATGAAAAAAA	intergenic	AN2890	G/	GAAA/	GAAAAAAA/
VI	2700629	GTAAACAGCAGAAAAAAA	intergenic	AN2820	CAAAAAAA/	C/	C/
VI	3403282	GGATTATTATAAATACATA	intergenic	AN10328	C/	C/	T/
VI	3403542	ATAGAGGCTGATACAAAGTA	intergenic	AN10328	G/	A/	A/
VI	3403819	TGCCATAGCACAAGCAAAT	intergenic	AN10328	T/	C/	C/
VI	3403856	GCAAATCATAGCCCTATA	intergenic	AN10328	T/	C/	C/
VI	3403860	ACTATCAGCCTATACAGG	intergenic	AN10328	A/	G/	G/
VI	3403885	GATCAAGCTGAGGCCAGTAC	intergenic	AN10328	A/	G/	A/
VI	3404244	TACAGAGCACGTACACTGCC	intergenic	AN10328	C/	T/	T/
VI	3405078	ACTCTGGCCAATGCCGGG	intergenic	AN10328 - Chr end	C/	T/	T/
VI	3405081	CTCTGCCAATGCCGGG	intergenic	AN10328 - Chr end	T/	C/	C/
VI	3405107	CCAAAGACCCGATAGGTGC	intergenic	AN10328 - Chr end	C/	T/	T/
VI	3405116	CGCATAGTGACAGCCGC	intergenic	AN10328 - Chr end	G/	A/	A/
VI	3405135	CGTCGACCCGGCAGCACT	intergenic	AN10328 - Chr end	C/	A/	A/
VII	663222	ATTAAAGTAGTTAAATTITA	intergenic	AN9419	A/	G/	A/
VII	663234	TAATTTAACTAATAGCTC	intergenic	AN9419	T/	C/	T/
VII	663252	TCTATAAGTCAGTAAATATT	intergenic	AN9419	T/	C/	T/
VII	663370	AGTATAATAGATCTTAGAG	intergenic	AN9419	A/	G/	G/
VII	663464	AGTATTTAATTACTATTIT	intergenic	AN9419	A/	G/	A/
VII	664360	ATTAAATTAAATTACTTACT	intergenic	AN9419	A/	G/	./
VII	664649	TTATAGCTGGAGGTTAAAT	intergenic	AN9419	T/	G/	G/
VII	664695	TTAACTAATAAATAGTTAA	intergenic	AN9419	T/	T/	TA/
VII	664711	TTAAGCTAATAAGGTTAA	intergenic	AN9419	C/	T/	./
VII	664722	AGGGTTAAATTAAATAAT	intergenic	AN9419	C/	T/	T/
VII	664745	ATTAACCTAAATTCTAAA	intergenic	AN9419	G/	A/	A/
VII	664751	TCTAATTTCTAAAGGACAG	intergenic	AN9419	T/	C/	C/
VII	664772	TATTTTACTGCCATTAAAA	intergenic	AN9419	A/	G/	G/
VII	664791	AATATTAGAAAAGAAAATTA	intergenic	AN9419	G/	A/	./
VII	664820	TTTTTAATAGTTAGAGGTTA	intergenic	AN9419	A/	G/	./
VII	664826	ATAGTTAGAGGTTAGCTTAA	intergenic	AN9419	A/	G/	G/
VII	3722669	CCACCACTCCAAAAAA	intergenic	AN2373	CAAAA/	CAAAAAA/	C/
VII	4413781	CAGCGCGGTTTTTTT	intergenic	AN2577	G/	G/	GT TTTTTTT/
VIII	559071	TATTTAATTTTACTAATA	intergenic	AN9410	T/	T/	C/
VIII	559104	ATATTATAATTATATAAT	intergenic	AN9410	T/	T/	C/
VIII	559117	ATATAATAAATTTTAGAA	intergenic	AN9410	A/	A/	G/
VIII	559121	AATAAATTTTAGAAATTA	intergenic	AN9410	T/	T/	C/
VIII	559139	TAGGAAAGCAGGACTACAG	intergenic	AN9410	C/	C/	T/
VIII	1142597	CAGCTGAAGAAAAAAA	intergenic	AN1225	GAAAAA/	GAAAAA/	GAAAAAAA/
VIII	3254743	CTGACTATTAGTGGCTG	intergenic	AN0539	C/	C/	T/
VIII	3254746	ACTACCTATTAGTGGCTG	intergenic	AN0539	C/	C/	T/
VIII	3254776	GTTAGGTCTGACTGCTG	intergenic	AN0539	C/	C/	T/
VIII	3254860	ATGAATACTTGTCTGTT	intergenic	AN0539	T/	C/	T/
VIII	3254885	AGCATGTACAATCCCTGGC	intergenic	AN0539	G/	G/	A/
VIII	3255292	ATTCTCTTGTATTCTACC	intergenic	AN0539	T/	T/	C/
VIII	3255446	CACTTGTAACTGTATATT	intergenic	AN0539	G/	G/	A/
VIII	3255460	TATTTTGTATTCTTCAG	intergenic	AN0539	C/	C/	T/
VIII	3255508	GAATATTCAAAGGTTCA	intergenic	AN0539	G/	G/	A/
VIII	3255658	TATTTCCCTGATCTGGAT	synonymous variant	AN0537	T/	C/	./
VIII	3255781	TGTTACAGTATTGATAGCC	missense variant	AN0537	T/	C/	C/
VIII	3255863	GTATGTCCTACTACAGTAT	intergenic	AN0539	T/	T/	C/
VIII	3255871	CTACTACAGTATTGCTTGC	intergenic	AN0539	T/	T/	C/
VIII	3256876	TCTTATGGTTAGAAGAAC	intergenic	AN0538	T/	C/	T/
VIII	3256935	TCCAGGCACTGTACACAGC	intergenic	AN0538	C/	./	T/
VIII	3256980	TAGTTCTCTGAGGGGA	intergenic	AN0538	T/	C/	C/
VIII	3257135	AGGCTGTATTGAAAGCAIT	intergenic	AN0538	C/	T/	T/
VIII	3257418	TCAAACCTGACTTGTGAT	intergenic	AN0538	T/	C/	T/
VIII	3257429	CTTGTGATATCTAGGAAACA	intergenic	AN0538	A/	G/	A/
VIII	3257692	TGCAATCCAGATTTGTGG	synonymous variant	AN0536	G/	A/	A/
VIII	3257764	TCACTGTCTTGTGATAAAGG	splice region variant	AN0536	C/	T/	T/
VIII	3257806	TGTTAATAGTATTAAAGGG	intergenic	AN0538	T/	T/	C/
VIII	3257886	GCAGCAGGTAAGCTGTC	intergenic	AN0538	G/	A/	./
VIII	3258022	GTACAGCTGATCTGTG	intergenic	AN0538	T/	T/	C/
VIII	3258256	CGTAAGACCTGTAGGCTT	intergenic	AN0538	C/	T/	C/
VIII	3258275	TAGGGTTAGGTGGGTG	intergenic	AN0538	A/	G/	A/
VIII	3258667	AGTCATGTAAGAGCGTTA	intergenic	AN0538	A/	G/	A/
VIII	3258700	GTCCTAGTTAAGTAGCTTA	intergenic	AN0538	G/	G/	A/
VIII	3258735	CCATGACTTGTACAGGGT	intergenic	AN0538	C/	C/	T/
VIII	3258750	GGGTTATTATTCTCGAC	intergenic	AN0538	C/	C/	T/
VIII	3258751	GGTTATTATTCTCGACT	intergenic	AN0538	G/	G/	A/
VIII	3258780	CCTCTTCCATGTTAAC	intergenic	AN0538	C/	C/	T/
VIII	3258838	AGGCAAGAGGTACATTC	intergenic	AN0538	G/	GTCACAT/	GTCACAT/
VIII	3259075	GCTGGCTTGTACGTGCC	intergenic	AN0538	C/	C/	T/
VIII	3259095	GGGTCACTCAGCTAGGGT	intergenic	AN0538	G/	G/	A/
VIII	3259230	ACTCTCTGGTACATGTC	stop gained	AN0535	A/	./	G/
VIII	3259256	ATGCCACCTGTATTCA	missense variant	AN0535	A/	./	G/
VIII	3259257	TGCCACCTGTATTCA	missense variant	AN0535	C/	./	T/
VIII	3259346	AGAGCTTTGTGTCGGTC	missense variant	AN0535	C/	T/	T/

Table S4. SNPs and INDELs identified in ISS-grown LO1362

Chromosome	Position	Flankng	Type	Gene/nearest gene	LO1362 control	LO1362 4d ISS	LO1362 7d ISS
I	105172	CCTGGGTCAAACAAAAAAA	intergenic	AN6460	C/	CAAAAAAAAAAAAAA/	C/
I	435907	TTTCCTTTCTTTTTTTT	intergenic	AN6353	CTTTTTTTTTTTTTT/	C/	C/
I	733281	GGGGGGGGGGCAGAGATG	intergenic	AN6261	G/	GGGGGGGGGGGGGA/	G/
I	779668	GGGCCTCTGCCCTCTCC	intergenic	AN6243	GCCCCCCCCCCCCCCCCC/	GCCCCCCCCCCCCCCCCCCCC/	CCCCCCC/
I	1011575	CAAAAAAAACAAAAAAA	intergenic	AN6181	C/	C/	CAAAAAAAAAAAAAAAA/
I	1104405	AAAAAAAAGGGGGGGGG	intergenic	AN12045	A/	A/	AGGGGGGG/
I	1104418	GGGGGGGGGAGGGGAGGG	intergenic	AN12045	A/	A/	G/
I	1721676	GCTTAACCGCCCCCCCCC	intergenic	AN5943	G/	G/	GCCCCCCCCCCCCCCCC/
I	2265536	ATCTATTTAAAGTAGTT	intergenic	AN10829	C/	C/	T/
I	2265770	TTTTAAAGATAGAGATT	intergenic	AN10829	G/	A/	G/
I	2384542	ACCGGGGTTTTTTTT	intergenic	AN6528	GT/	G/	G/
I	3745510	TAAGCCTTGGCTAGCCCTA	intergenic	AN6968	A/	G/	A/
I	3745512	AGGCTTGGCTAGCCCTATA	intergenic	AN6968	A/	C/	A/
I	3745604	GTCCTGCTGGCTTTATG	intergenic	AN6968	C/	C/	T/
I	3745651	ACCTTGCATCCCTGAGTT	intergenic	AN6968	T/	T/	TCCCTGC/
I	3745673	CCCTGCTATCCCTGAGTTA	intergenic	AN6968	C/	T/	/
I	3745703	CCCTGACTAGCTTACTTAT	intergenic	AN6968	A/	G/	G/
I	3745952	ATAGTCTTCAGATATATCA	intergenic	AN6968	C/	T/	C/
I	3746021	TTCTCCACCACTTACCA	intergenic	AN6968	C/	T/	C/
I	3746183	AAGGCAGTCAAATATAT	intergenic	AN6968	T/	/	C/
I	3746195	ATATATTTGGGATAGTAAG	intergenic	AN6968	A/	/	G/
I	3746222	CTATAGCTGGCAAGGATT	intergenic	AN6968	A/	A/	G/
I	3746251	GTATATAAGAACAGGCA	intergenic	AN6968	C/	T/	T/
I	3746264	GCAGGCAACTAAAGGTTAG	intergenic	AN6968	C/	T/	T/
I	3746274	AAAGGTTATGTATAAGGAGT	intergenic	AN6968	A/	G/	G/
I	3746281	ATGTATAAGGAGTATAAACG	intergenic	AN6968	A/	G/	G/
I	3746312	ATCTAGCTGCAAAGTACT	intergenic	AN6968	T/	T/	C/
I	3746340	TTCTCTTATTATTATTG	intergenic	AN6968	A/	A/	T/
I	3746350	TATTATTGCTAAAGGAGG	intergenic	AN6968	A/	A/	G/
I	3746363	AAGGAGGTGCGGTATAG	intergenic	AN6968	A/	A/	G/
I	3746365	GGAGGTTGTCGGGTATAGA	intergenic	AN6968	T/	T/	C/
I	3746377	GTATAGAAAGTAGCTAAAGA	intergenic	AN6968	A/	A/	G/
I	3746388	AGCTAAGAAGGAGTTGATC	intergenic	AN6968	A/	A/	G/
I	3757717	TTGGAGGGCATGAGCACAG	5' UTR variant	AN6972	C/	T/	C/
I	3757721	AGAGGCCATGAGCACCAA	5' UTR variant	AN6972	C/	T/	C/
I	3757999	CATAGCAACGCCACATCCC	intergenic	AN6972	G/	A/	A/
I	3758010	CCACATCCCAAGCAACAGTA	intergenic	AN6972	C/	T/	T/
II	766232	TCTTTTTCTTTTTTTT	intergenic	AN8103	CTTTTTTTTTTTTT/	CTTTTTTTTTTTTT/	C/
II	902038	TATGGGGTTGGGGGGGG	intergenic	AN8147	TGGGGGGGGGG/	T/	/
II	1321889	CCCCCCACCCCCCTCC	intergenic	AN8264	A/	A/	C/
II	1481817	TACTAGAGATTCTTAAT	intergenic	AN9416	AT/	T/	/
II	1565458	TCTAAAGCTCAAACAAAAA	intergenic	AN4270	CAAAAAAAAAAAA/	C/	C/
II	3223141	GGGATGGCTGGGAATGGA	intergenic	AN3739	T/	G/	T/
III	93930	CGGGGCTCTTTTTTTT	intergenic	AN5069	CT/	C/	C/
III	247175	ATACCAAGTAAAAAAA	3' UTR variant	AN5027	T/	T/	TAAAAAAAAAAAAAAA/
III	1964161	GTTCCTCCGGTTTTTTT	3' UTR variant	AN10557	GTTTTTTTTTTTTTT/	G/	GTTTTTTTTTTTTTT/
III	2458717	TTGGAATGGATATCAGA	intergenic	AN4303	A/	G/	A/
III	2470914	TAAGAGATCTAACAGATAATT	intergenic	AN4298	T/	T/	C/
III	2470966	TTGGAATGGGATATCAGA	intergenic	AN4298	G/	A/	A/
III	2471016	CTTGTCTATGGGCTTAATT	intergenic	AN4298	G/	A/	A/
III	2471064	AATACCAAGGCAAATCTGGC	intergenic	AN4298	C/	T/	T/
III	2471072	GCAAATATGGCTTACAG	intergenic	AN4298	G/	A/	A/
III	2471080	TGGCTTACAGCCAGGGGA	intergenic	AN4298	C/	T/	T/
III	2471088	ACAGCAAGGGGATTATAAGT	intergenic	AN4298	G/	A/	A/
III	2665402	GAACTGGAGCAAAAAAAA	intergenic	AN8830	C/	CAAAAAA/	C/
III	3431574	TGCCCTCGCTAAACAAAAA	intergenic	AN8590	T/	CAAAAAA/	T/
IV	317111	TCTTTTTATTTTTTTT	intergenic	AN7318	ATTTTTTTTTTTTT/	A/	A/
IV	1432912	TGAAACAAGAAAAAAA	intergenic	AN12058	TTT/		
IV	1444358	GCTAGCAAGCCATTATTC	intergenic	AN6973	G/	CAAAAAAAAAAAA/	G/
IV	1444409	TAAATCTAGCTGCAAGTA	intergenic	AN6973	CCA/	C/	C/
IV	1444600	TATATATCAGGTTATGAT	intergenic	AN6973	T/	T/	G/
IV	2887197	CCATAGCACAAGCAACACC	intergenic	AN7848	T/	C/	C/
IV	2887201	AGCACAAAGCAAACCTGCA	intergenic	AN7848	A/	G/	G/
IV	2887303	GTCAACAGCACAGGGGG	intergenic	AN7848	A/	G/	A/
V	332544	CGGCACAGGCAAAAAAAA	frameshift variant	AN8388	CAAAAAAAAAA/	C/	CAAAAAAAA/
V	539952	TAAACTCTCAAACAAAAA	intergenic	AN8453	C/	C/	CA/
V	809317	CTGAGCTGACCAGAGTATT	intergenic	AN8543	G/	A/	G/
V	870796	TTAGTTTGAAACAAAAAA	intergenic	AN8561	GAA/	GAAA/	G/
V	1147639	ACTGCTAAAGTACTGCTAG	intergenic	AN5098	A/	G/	/
V	1148365	TTATTACTCAGAATTCTAT	intergenic	AN5098	C/	C/	T/
V	1148587	GCAAGAGATTAAATTATA	intergenic	AN5098	C/	T/	C/
V	2447240	TGGCTGAGTTTTTTTTT	intergenic	AN5550	GT/	G/	G/
V	2932060	CTCTTAACTCATCTTATGC	intergenic	AN5400	C/	T/	/
V	2932907	AGCAACTTGTATAGGTATA	intergenic	AN5400	A/	G/	/
V	3367409	GCCGGATGCAAGTTACAG	missense variant	AN5254	C/	C/	T/
V	3367410	CGGGATGCAAGTTACAG	synonymous variant	AN5254	A/	A/	G/
V	3367733	AAGGAGCCCCGTATGCCAA	missense variant	AN5254	C/	C/	T/
V	3368312	CTGTGGATCCCCAGAACATA	missense variant	AN5254	T/	C/	C/
V	3379998	GAGACTACTCCAGGAGCCA	intergenic	AN5251	C/	CCAGGAGGCCACACTGCAAGAGGCTGC AACAGGAGACTACTCCAGGAGGCCACCA CTGCAAGAGGCTGCAACAGGAGACT	C/

V	3389480	ACTGTCAGCGCCTGGAGCC	synonymous variant	AN5248	G/	T/	T/
V	3399785	CTGATAATGCACCAACAGCT	intron variant	AN9507	T/	T/	C/
V	3403090	TGTCAAGCACAGCAGCCAGG	intergenic	AN9507	C/	C/	T/
V	3403091	GTCAAGCACAGCAGCCAGG	intergenic	AN9507	A/	A/	G/
VI	158376	ATGCTGTTCAAAAAAA	intergenic	AN12140	CA/	C/	C/
VI	570796	TATCTTAGTTTATATAA	intergenic	AN11162	T/	C/	T/
VI	570880	AGAAATAAAAATTATATAT	intergenic	AN11162	A/	A/	G/
VI	572081	CTTATATAAGCTTAAATTAA	intergenic	AN9057	G/	G/	A/
VI	1436309	AAATTGTTGGGGGGGG	intergenic	AN3217	T/	T/	TGGGGGG/
VI	2486002	CCTCGATATGAAAAAAA	intergenic	AN2890	GAAAAAAAAA/ CAAAAAAAAAAAAAAAA AAAAAAA/	G/	G/
VI	2700629	GTAACAGAGCAAAAAAAA	intergenic	AN2820	CAAAAAAAAAAAAAAAA AAAAAAA/	C/	C/
VI	3403542	ATAGAGGCTGATAACAAAGTA	intergenic	AN10328	G/	A/	A/
VI	3403590	CTGTACAGACTGATTG	intergenic	AN10328	G/	G/	C/
VI	3403766	CAGGCCGGGAAGGGCCAGG	intergenic	AN10328	A/	A/	G/
VI	3403771	CGGGGAAAGGCCAGGTTCA	intergenic	AN10328	G/	G/	GC/
VI	3403819	TGCCCATAGCACAAGCAAAT	intergenic	AN10328	C/	T/	C/
VI	3404244	TACAGAGCACGTACACTGCC	intergenic	AN10328	C/	T/	T/
VI	3405078	ACTCTGGCCAATGCCGGG	intergenic	AN10328-Chr end	T/	/	C/
VI	3407093	TAATTAGACGTTAGGAG	intergenic	AN10328-Chr end	C/	G/	/
VI	3407393	GCAGGTAGTCAGCAAGTTAA	intergenic	AN10328-Chr end	T/	C/	C/
VII	74597	AAGAAAATACCAAAAAAAA	intergenic	AN9036	C/	CAAAAAA/	C/
VII	611427	TCTTATTTCTGTTAAAT	intergenic	AN8871	C/	T/	/
VII	611446	TAAGCTATAATTACAAGAT	intergenic	AN8871	G/	A/	/
VII	611879	AAGATTAAAATCCTTTAA	intergenic	AN8871	G/	A/	/
VII	664722	AGGGTTAATTAAATAAT	intergenic	AN9419	T/	C/	T/
VII	3722669	CCACAGTCACAAAAAAA	intergenic	AN2373	CAAAA/	CAAAA/	CAA/
VII	3751158	ATTAAATTGCTTTGGTG	intergenic	AN2383	A/	G/	G/
VII	4049421	TGTCAAGGCTAGGGAGTGA	frameshift; stop gained	AN10311	TCAGCGAGCAGTAGCAGCGCCCTCCAG CCTCGCTGAGGCCCTGAGCGCCAAGTC CCCAGCGCTCTCGAGGACATGCCCG AGCTCTGCCGAATCACAACGCTATC CAGA/	T/	T/
VII	4413781	CAGGGCGGGTTTTTTTTT	intergenic	AN2577	GTTTTTTTTTTT/	G/	G/
VIII	5014	GTAAAATTCCAGCCCCCTA	intergenic	AN11204	C/	T/	C/
VIII	478365	AGTGTGATGAAAAAAA	intergenic	AN9385	G/	GAAA/	G/
VIII	559017	TAACTAGATTTATATAATT	intergenic	AN9410	T/	T/	C/
VIII	559104	ATATTATAATTATATAAT	intergenic	AN9410	T/	C/	T/
VIII	559117	ATATAATAATTTTAGAA	intergenic	AN9410	A/	G/	A/
VIII	559121	AATAAAATTTTAGAAAATTA	intergenic	AN9410	T/	C/	T/
VIII	638089	TTATTTTTTATTTTTTTT	intergenic	AN1396	A/	A/	T/
VIII	3254138	GTAGGTCCATCCTTCGAG	missense variant	AN0538	A/	A/	C/
VIII	3254236	TCCATGTTGATCGGACAT	missense variant	AN0538	T/	C/	T/
VIII	3254348	CCCTTCCCAGTATCTCCCTC	synonymous variant	AN0538	G/	A/	A/
VIII	3254529	CAAGTTACTATTCTGTAT	intergenic	AN0539	T/	C/	T/
VIII	3254965	TATGCTGATTGCGAGCTAA	intergenic	AN0539	C/	T/	C/
VIII	3255089	TTGTTCTGAGGTCTAGGT	intergenic	AN0539	G/	A/	G/
VIII	3255096	GTAGTTCTAGGTGGGATG	intergenic	AN0539	G/	A/	G/
VIII	3255339	TGGACTGCAAGGGAGCTT	intergenic	AN0539	G/	A/	G/
VIII	3255352	GGAGCTTGTATTATCTGCC	intergenic	AN0539	C/	T/	C/
VIII	3255366	TCTGCCAGTTGACAAGGT	intergenic	AN0539	C/	T/	C/
VIII	3255371	CAGTTGACAAGGTCAACAT	intergenic	AN0539	G/	A/	G/
VIII	3255382	GGTCAACATAAAACTGGG	intergenic	AN0539	G/	A/	G/
VIII	3255429	AGGGCATGTTGCTTCAAA	intergenic	AN0539	G/	A/	G/
VIII	3255460	TATTTTGTATTCTTCAG	intergenic	AN0539	C/	T/	T/
VIII	3255781	TTGTCAGAGTATTGATAGCC	missense variant	AN0537	T/	T/	C/
VIII	3255819	AGCTTGTCTTAATCTCCCTG	splice region; intron variant	AN0537	T/	T/	C/
VIII	3255863	GTATGTTCTACTACAGTAT	intergenic	AN0539	C/	T/	C/
VIII	3255871	CTACTACAGTATTGCTTC	intergenic	AN0539	C/	T/	C/
VIII	3255879	GTATTGCTCTGTGTTGAGC	intergenic	AN0539	C/	T/	C/
VIII	3255892	CTGTAGCCCTGTCGTCG	intergenic	AN0539	C/	T/	C/
VIII	3255907	TCTGGGGATAGAAGGAGTT	intergenic	AN0539	G/	A/	G/
VIII	3255914	ATAGAAGGCAGTTGATAGCA	intergenic	AN0539	G/	A/	G/
VIII	3255927	GATAGCAATTGTTAATCCC	intergenic	AN0539	C/	T/	C/
VIII	3255954	TGGCGAGTCTGTTCTATAC	intergenic	AN0539	T/	T/	C/
VIII	3255967	TCTTACTCTACTAACAAAT	splice region; intron variant	AN0537	T/	T/	C/
VIII	3256068	TGAGAAGTCATTGGGCCAT	missense variant	AN0537	G/	A/	G/
VIII	3256130	TAGAATCTGTACAGGCCAT	intergenic	AN0539	C/	T/	T/
VIII	3256180	GTGTGATATATGCGATGGA	intergenic	AN0539	G/	A/	A/
VIII	3256191	TGCCATGGATGTTCTGGGAT	intergenic	AN0539	C/	T/	T/
VIII	3256242	TCTTCCATATTCTGCTG	intergenic	AN0539	A/	G/	G/
VIII	3256272	TCACAGTTCTGACAAATTG	intergenic	AN0539	T/	C/	C/
VIII	3256281	TGTACAAATTGGCGTATATC	intergenic	AN0539	T/	C/	C/
VIII	3256360	CGGGGTGACTGATTAGGGCG	intergenic	AN0539	T/	C/	C/
VIII	3256387	GGGCTGCTGGATCAGGCTT	intergenic	AN0539	G/	/	T/
VIII	3256454	GAGATTTCTGCGCGTCAA	intergenic	AN0538	C/	C/	T/
VIII	3256619	AGGTAAGATAGTGGCTTTG	intergenic	AN0538	A/	A/	G/
VIII	3256647	ATGTCATTACTCTCCCT	intergenic	AN0538	A/	A/	G/
VIII	3256682	TAACGTGATTGTCATGACT	intergenic	AN0538	T/	T/	C/
VIII	3256687	GCATTTGACATGACTCTAAC	intergenic	AN0538	A/	A/	G/
VIII	3256699	ACTCTAACATCATTATTT	intergenic	AN0538	G/	A/	G/
VIII	3256705	ACCAATCATTATTTCTT	intergenic	AN0538	T/	T/	C/
VIII	3256980	TAGTTACTCTGCGAGGGGA	intergenic	AN0538	C/	C/	T/
VIII	3257020	CACAGGGTAGAGGATTAACCC	intergenic	AN0538	G/	G/	A/
VIII	3257429	CTTGTGATATCTAGGAACA	intergenic	AN0538	A/	G/	A/

VIII	3257503	CACGGCTTCTATTAGTGAAG	intergenic	AN0538	T/	C/	T/
VIII	3257506	GGCTTCTATTAGTGAAGACT	intergenic	AN0538	T/	C/	T/
VIII	3257516	AGTGAAGACTAACGATATCAT	intergenic	AN0538	T/	C/	T/
VIII	3257764	TCAGTGTCTTGATAAGGG	splice region; intron variant	AN0536	T/	C/	T/
VIII	3257787	AGAGGATATTAATCTTCTT	intergenic	AN0538	T/	C/	T/
VIII	3257788	GAGGATATTAACTTTCTTG	intergenic	AN0538	A/	G/	A/
VIII	3257806	TGGTAATAGTATTAAGGGG	intergenic	AN0538	T/	C/	T/
VIII	3258780	CCTCTTCCATGTGTTAAC	intergenic	AN0538	C/	C/	T/
VIII	3258786	TTCCACACAGAGGCCATGTT	intergenic	AN0538	G/	G/	A/
VIII	3259230	ACTTCTCTGGTCAATCATGC	stop gained	AN0535	A/	G/	G/
VIII	3259256	ATGCCACCTGTATTCACTAG	missense variant	AN0535	A/	G/	G/
VIII	3259257	TGCCACCTGTATTCACTAGG	missense variant	AN0535	C/	T/	T/
VIII	3259467	CCTCCAGGCAGTAAAGATG	missense variant	AN0535	G/	C/	G/
VIII	3267230	GCGGGGCCACGTATTCAG	missense variant	AN0532	T/	C/	C/
VIII	3518032	GGCAGCGCTCGGGGGGGGG	intergenic	AN0447	CGGGGGGG/	CGGGGGGG/	C/
VIII	3942004	CTTTCTACCGTTTTTTTT	intergenic	AN0314	G/	G/	GTT/

Table S5. SNPs and INDELS identified in ISS-grown LO8158

Table S6. SNPs and INDELs identified in ISS-grown CW12001

Chromosome	Position	Flanking	Type	Gene/nearest gene	CW12001 control	CW12001 4d ISS	CW12001 7d ISS
I	435907	TTTCTTTCTTTTTTTT	intergenic	AN6353	C/	CTTTTTTTTTTTTTT/	CTTTTTTTTTTTTTT/
I	1529400	CGGGCTTTGTTTTTTT	intergenic	AN6006	G/	GT/	G/
I	1721676	GCCTAACGGCCCCCCCCC	intergenic	AN5943	GCCCCCCCCCC	G/	G/
I	2265536	ATCTAATTAAAGTAGTT	intergenic	AN10829	T/	T/	C/
I	2265588	AAGAAAGTCTTAAAGACT	intergenic	AN10829	T/	T/	C/
I	2265696	AGAAAGATAAAAAAGTAAA	intergenic	AN10829	A/	G/	A/
I	2265770	TTTAAAAAGTATAGGATT	intergenic	AN10829	G/	A/	G/
I	2384215	TTTACGGGGTTTTTTT	intergenic	AN6528	G/	G/	GTT/
I	2384542	ACCGGGGGTTTTTTT	intergenic	AN6528	GTT/	GTTTTT/	G/
I	3745572	CAGTCAGGCACTATAATAG	intergenic	AN6968	T/	C/	C/
I	3745604	GTCCTGCTGCTTATAG	intergenic	AN6968	C/	T/	T/
I	3745762	AATTATGTCATCTGTA	intergenic	AN6968	T/	C/	/
I	3745800	AAAATACTGTAAGTATTC	intergenic	AN6968	A/	/	G/
I	3745815	CTATCTCTATAGCCCTCC	intergenic	AN6968	C/	/	T/
I	3746155	CTTAACTGGATATGCAA	intergenic	AN6968	A/	/	G/
I	3746173	AAGGAATGTGAAAGGCAGTC	intergenic	AN6968	A/	G/	G/
I	3746183	AAGGGCAGTCAAATATAT	intergenic	AN6968	T/	C/	C/
I	3746195	ATATATTTGGGATAGTAA	intergenic	AN6968	A/	/	G/
I	3757717	TTGGAGAGGGCATGGAGCAG	5' UTR variant	AN6972	C/	C/	T/
I	3757721	AGAGGCATGAGCAGCCAA	5' UTR variant	AN6972	C/	C/	T/
I	3757999	CATAGCAACGCCACATCC	intergenic	AN6972	A/	G/	A/
I	3758010	CCACATCCAGAACAGTA	intergenic	AN6972	T/	C/	T/
I	3758071	CGCCCGAGCAAGGATGAGCA	intergenic	AN6972	G/	A/	G/
II	766232	TCTTTTTCTTTTTT	intergenic	AN8103	CTTTTTTTTTTTT/	C/	CTTTTTTTTTTTT/
II	1998747	CATTAAATTGAAAAAA	intergenic	AN4131	GAAAAAAA/	G/	G/
II	3223141	GGGATGGCTGGGAATGGA	intergenic	AN3739	T/	G/	G/
II	3848365	GGGTATGAAACACACAC	intergenic	AN3538	TAC/	T/	T/
III	1964161	GTTCCTCGGTTTTTT	3' UTR variant	AN10557	G/	G/	GTTTTTTTTTTTTT/
III	2458547	ATAAATCTCAACCTTATCT	intergenic	AN4303	C/	T/	C/
III	2458556	CAACCTTCTTAATT	intergenic	AN4303	CTTAACATTAG/	C/	CTTAACATTAG/
III	2458717	GTGAGTATGGGATACTAGA	intergenic	AN4303	A/	G/	A/
III	2459044	TTATTCAGCTATACAGAG	intergenic	AN4303	GCT/	GCT/	G/
III	2470914	TAAGATCTAAGATAATT	intergenic	AN4298	T/	C/	C/
III	2471064	AATAACAGGCAAACATGGC	intergenic	AN4298	T/	C/	T/
III	2471147	CAGTCTATCAACTTATTC	intergenic	AN4298	T/	C/	T/
III	2542200	AAAAATTCTAGAAAAAAG	intergenic	AN11131	C/	T/	C/
III	2542203	ATTATCTAGAAAAAAGGAT	intergenic	AN11131	A/	A/	G/
III	2542224	GTCTTAAGATCTTTCTAG	intergenic	AN11131	G/	A/	A/
III	2542239	CTAGTAAATTAAATTATAT	intergenic	AN11131	G/	A/	A/
III	2665402	GAACTGGCAAAAAAAA	intergenic	AN8830	CAAAAAAAAAAAAAAA/	CAAAAAAAAAAAAAAA/	C/
III	3243144	TGGCTTAAAGCCCCCCC	intergenic	AN8654	GTTTC/	GTTTC/	GTTTC/
IV	328603	GACTCTACCCCCCCC	intergenic	AN7316	ACCCCCCCC/	A/	A/
IV	1443164	CCCTGGCTGAAGCTTTA	intergenic	AN6973	G/	G/	T/
IV	1443342	GTATAAGCTGTCAGGAAGCT	intergenic	AN6973	G/	A/	A/
IV	1443348	GCTGCAAGGAAGCTACTATT	intergenic	AN6973	A/	C/	C/
IV	1443358	AGCTACTATTAAATATATA	intergenic	AN6973	T/	A/	A/
IV	1444358	GCTGCAAGGCCATTATTTC	intergenic	AN6973	C/	C/	CCA/
IV	1444409	TTAACATTAGCTGCAAGTA	intergenic	AN6973	T/	T/	G/
IV	1444604	TATATCAGGGTATAGTAATA	intergenic	AN6973	A/	G/	G/
IV	2092366	GACTTAAATTGGGGGGGG	intergenic	AN7599	T/	T/	TGGG/
IV	2883001	TAAGCTTATACTGCTGTT	intergenic	AN11577	T/	T/	C/
IV	2883011	AACTGCTTACCTGTAG	intergenic	AN11577	T/	T/	C/
IV	2883017	GTTCACCTGTAGTAA	intergenic	AN11577	A/	G/	A/
IV	2883746	CAAGGCATTATACTGATGAC	intergenic	AN11577	G/	A/	A/
IV	2883747	CAGGCATTATACTGATGAC	intergenic	AN11577	C/	T/	T/
IV	2883821	CTGTAACCTGTAGTAA	splice region; intron variant	AN7848	C/	T/	T/
IV	2887121	GCTCACGGCTGCCAGCA	intergenic	AN7848	C/	C/	T/
IV	2887303	GTCACCAAGCACCGCCGG	intergenic	AN7848	G/	A/	A/
IV	2887375	ATTCAGCATTAAAGCCAGAT	intergenic	AN7848	C/	C/	T/
V	539952	TAACAACTCTAA	intergenic	AN8453	C/	C/	CA/
V	809317	CTGACGCTGACCAAGTATT	intergenic	AN8543	G/	A/	G/
V	870796	TTAGTTTGA	intergenic	AN8561	G/	GAA/	GAA/
V	1146289	AGTATAGGAGTATCTACTAT	intergenic	AN5098	A/	G/	G/
V	1148275	CTTTTATACTATCTCCCT	intergenic	AN5098	T/	C/	/
V	2931993	AGCAGTCATGCTGTCAGG	intergenic	AN5400	A/	G/	A/
V	2932907	AGCAACCTTGTATAGTTA	intergenic	AN5400	A/	G/	G/
V	3367079	TCCGTTATCATGTTGTA	intergenic	AN5254	A/	C/	A/
V	3367245	TGAATGTTGCAATACTGCA	synonymous variant	AN5254	T/	C/	C/
V	3368005	ATGCTTATGATATAACC	missense variant	AN5254	C/	T/	T/
V	3368023	CCACCTACCCAAGATTACCA	stop gained	AN5254	C/	T/	T/
V	3368024	CACCTACCCAAGATTACCA	missense variant	AN5254	A/	G/	G/
V	3368096	TTATGAAATCACCTGCAAT	missense variant	AN5254	T/	C/	T/
V	3368312	CTGTGGATCCCCAGAACATA	missense variant	AN5254	C/	T/	C/
VI	570796	TATCTTAGTTTTTAA	intergenic	AN11162	T/	T/	C/
VI	572055	GACTTTAAGATCTTCTAC	intergenic	AN9057	A/	G/	G/
VI	1587777	TCGTTAAAGCTTGNNNNN	intergenic	AN12329	CCATGGCAATGCCAGAGTCTCCGGTGT	CCATGGCAATGCCAGAGTCTCCGGTGT	/
VI	2644609	TGTTGCTCTTTTTT	intergenic	AN2836	CCTATGAGAATGATGCTGTTGCGA	CCTATGAGAATG/	C/
VI	2700629	GTAACAGAGCAAAAAAAA	intergenic	AN2820	AGTTTGTCTGGCCAGACCCAG/	CTTTTTTTTTTTTTT/	CAAAAAAAAAAAAAAAA
VI	3403766	CAGGGGGGGAGGCCAGG	intergenic	AN10328	CCTATGAGAATG/	A/	AAAAAA/
VI							G/

Table S7. Relative abundance ratios for proteins identified in ISS-grown 4-day samples compared to Earth-grown counterparts

Gene name	Description	p-value	FGSC A4 4d ISS-	LO1362 4d ISS-	LO8158 4d ISS-	CW12001 4d ISS-
			grown/control	log2 FC	grown/control	log2 FC
aptA AN6000	polyketide synthase, putative (JCVI)	5.40E-10	-0.02	0.24	-0.25	-0.15
AN4421	L-lactate dehydrogenase	8.13E-10	-0.14	-0.84	0.05	0.20
AN10197	sulfonate biosynthesis enzyme, putative	3.66E-09	0.07	-1.00	0.09	-0.89
xptC AN7998	conserved hypothetical protein	7.25E-09	-0.09	-0.54	-0.69	0.05
AN10631	hypothetical protein ANIA_10631	8.66E-09	-0.38	0.25	0.37	0.12
AN3466	dihydrolipoamide S-succinyltransferase	9.45E-09	-0.01	-0.05	0.34	-0.10
AN9006	conserved hypothetical protein	1.21E-08	0.08	0.08	-0.38	0.04
AN0483	conserved hypothetical protein	1.45E-08	0.34	-0.05	0.47	0.59
AN5325	conserved hypothetical protein	1.48E-08	-0.09	0.10	0.18	-0.12
AN5907	conserved hypothetical protein	1.75E-08	0.08	0.48	0.48	0.19
agdC agdD AN7345	Alpha/beta-glucosidase	1.84E-08	-0.09	-0.38	-1.63	0.49
AN11233	class V chitinase, putative	2.42E-08	0.07	0.08	0.44	0.15
AN0950	hypothetical protein ANIA_00950	2.47E-08	0.01	-0.57	0.34	0.32
acuF AN1918	Phosphoenolpyruvate carboxykinase [ATP]	4.26E-08	-0.22	-0.03	-0.01	0.17
AN0604	endonuclease	5.47E-08	-0.04	0.06	0.12	0.08
AN5194	ABC transporter	5.97E-08	-0.14	-0.44	-0.76	0.03
AN9194	conserved hypothetical protein	6.35E-08	-0.16	0.01	0.35	0.28
AN5421	steroid monooxygenase (CpmA), putative	7.25E-08	0.13	0.64	0.07	-0.21
AN7990	conserved hypothetical protein	8.94E-08	0.05	-0.43	-0.71	0.26
AN5564	hypothetical HAD-superfamily hydrolase	9.39E-08	-0.15	-0.04	0.07	-0.12
AN8339	conserved hypothetical protein	1.02E-07	-0.09	-0.21	-0.84	0.23
ausE AN9246	toxin biosynthesis protein (Fum3), putative	1.15E-07	0.44	-0.11	0.11	0.19
pyroA AN7725	Pyridoxine biosynthesis protein pyroA (Pdx1 homolog)	1.30E-07	-0.21	0.07	-0.35	-0.19
AN1142	isoamyl alcohol oxidase, putative	1.82E-07	-0.15	-0.59	-0.83	-0.24
camA cam AN2047	Calmodulin (CaM)	1.94E-07	-0.26	-0.10	-0.71	-0.08
AN2694	oxidoreductase, short chain dehydrogenase/reductase family	1.99E-07	0.24	-0.16	0.38	0.11
AN4977	electron transfer flavoprotein-ubiquinone oxidoreductase	2.14E-07	0.12	0.14	0.00	-0.11
lacA AN0756	beta-galactosidase	2.20E-07	0.09	-0.16	0.56	-0.15
AN1553	Asp hemolysin-like protein	2.29E-07	-0.20	0.03	0.02	0.07
AN2471	hypothetical protein ANIA_02471	2.34E-07	0.00	-0.29	0.37	0.26
lamA AN0887	Putative urea carboxylase (Urea amidolyase)(Lactam utilization protein lamA)	2.35E-07	-0.07	-0.38	0.38	0.18
AN5348	conserved hypothetical protein	2.41E-07	-0.04	-0.46	-0.46	-0.25
AN6274	short chain dehydrogenase/reductase family	2.91E-07	-0.11	0.08	0.65	-0.17
pkaR AN4987	cAMP-dependent protein kinase regulatory subunit (PKA regulatory subunit)	3.04E-07	0.13	0.33	0.20	-0.08
AN5446	hypothetical protein ANIA_05446	3.09E-07	0.00	-0.26	-0.13	0.26
AN8579	conserved hypothetical protein	3.16E-07	0.24	-0.80	0.72	-0.57
AN1715	mannose-6-phosphate isomerase, class I	3.70E-07	-0.18	-0.52	-0.20	0.26
mdpH AN10022	conserved hypothetical protein	3.92E-07	-0.06	-0.62	-0.84	-0.49
AN3931	primary component of eisosomes	4.40E-07	-0.45	0.25	-0.56	0.04
AN3679	oxidoreductase, short-chain dehydrogenase/reductase family	4.47E-07	0.00	-0.28	0.06	0.48
AN4667	Septin	4.70E-07	-0.23	-0.05	0.11	-0.03
AN6963	conserved hypothetical protein	4.84E-07	-0.01	-0.34	-0.33	-0.07
AN9124	heat shock protein (Sti1), putative	5.56E-07	-0.23	-0.28	-0.51	-0.02
AN11035	conserved hypothetical protein	5.64E-07	0.15	0.46	0.09	-0.32
AN0045	solid-state culture expressed protein (Aos23), putative	5.66E-07	-0.01	-0.12	-0.08	0.52
AN7267	conserved hypothetical protein	5.77E-07	0.24	0.72	-0.15	-0.26
AN5311	tyrosinase, putative	5.93E-07	0.13	-0.15	0.15	-0.16
AN1973	Putative vesicle transport v-SNARE protein vti1	6.03E-07	-0.24	0.01	-0.44	0.11
AN3968	conserved hypothetical protein	6.43E-07	-0.16	0.64	-1.09	0.04
AN6930	conserved hypothetical protein	6.49E-07	0.03	0.28	-0.09	-0.15
AN7102	hypothetical protein ANIA_07102	6.90E-07	-0.26	-0.43	-0.41	0.27
AN6810	ThiJ/PfpI family protein	7.31E-07	-0.11	0.40	-0.22	0.05
AN11161	phosphatidylserine decarboxylase family protein	7.56E-07	-0.31	-0.53	-0.49	0.25
AN2720	conserved hypothetical protein	7.81E-07	-0.22	-0.69	-0.06	0.18
AN9090	Putative RNA binding proteinPutative uncharacterized protein	8.57E-07	0.13	0.07	0.51	-0.19
catA AN8637	Catalase A (Spore-specific catalase)	9.38E-07	-0.21	-0.64	-0.35	0.31
nhp6 AN2885	Non-histone chromosomal protein 6	1.17E-06	0.05	0.13	-0.66	0.59
AN5309	cutinase, putative	1.34E-06	0.02	-0.06	0.47	0.09
AN8032	NAD dependent epimerase/dehydratase family protein	1.37E-06	-0.12	-0.15	-0.03	0.18
AN10421	conserved hypothetical protein	1.39E-06	-0.27	-0.62	-0.49	0.22
AN5440	Putative heme-binding peroxidase	1.62E-06	-0.09	-0.41	0.10	0.08
AN3573	conserved hypothetical protein	1.78E-06	-0.21	0.38	0.23	-0.04
AN7262	hypothetical protein ANIA_07262	1.86E-06	-0.22	0.90	0.07	-0.10
AN5353	conserved hypothetical protein	1.89E-06	-0.03	0.00	-0.46	-0.18
AN7717	conserved hypothetical protein	1.98E-06	-0.11	0.44	-0.49	0.03
rsm10 AN6489	30S ribosomal protein S10, mitochondrial Precursor (Mitochondrial ribosomal small subunit protein 10)	2.09E-06	-0.14	0.16	0.19	0.17
AN4041	conserved hypothetical protein	2.14E-06	-0.43	-0.75	-0.95	-0.31
AN0447	NifU-related protein	2.19E-06	-0.27	0.18	-0.26	0.32
AN5942	Protein copper regulatedPutative uncharacterized protein	2.22E-06	-0.35	-0.35	-1.04	0.05

awh11 AN3725	Chaperone/heat shock protein	2.40E-06	-0.04	-1.27	-0.43	0.22
AN11094	hypothetical oxidoreductase	2.42E-06	0.82	0.03	0.29	0.32
AN3485	conserved hypothetical protein	2.43E-06	-0.10	-0.64	-0.68	0.63
AN2529	enoyl-CoA hydratase/isomerase family protein	2.45E-06	0.37	-0.32	-0.10	-0.19
AN10148	ChpADiploid state maintenance protein chpA;	2.45E-06	-0.13	-0.04	-0.21	0.04
AN10109	conserved hypothetical protein	2.46E-06	0.03	0.07	-0.28	0.11
AN7111	peroxisomal multifunctional beta-oxidation protein (MFP), putative	2.49E-06	-0.06	0.24	0.26	0.13
TRX1 AN0170	Thioredoxin (Trx)	2.71E-06	-0.16	0.75	0.28	-0.14
AN2989	glycine-rich RNA-binding protein, putative	2.79E-06	-0.12	-0.60	-0.16	-0.52
AN2119	conserved hypothetical protein similar to Neimann-Pick sphingolipid transporter	3.15E-06	-0.17	-0.29	-0.78	0.09
AN3703	conserved hypothetical protein	3.18E-06	-0.12	-0.43	-0.58	0.45
AN0940	conserved hypothetical protein	3.25E-06	0.16	-0.14	-0.30	0.11
AN7657	1,3-beta-glucanosyltransferase Gel1	3.43E-06	-0.07	-0.76	-0.50	-0.18
AN9037	periplasmic nitrate reductase, putative	3.47E-06	-0.13	-0.49	-0.56	0.01
AN9002	oxidoreductase, short-chain dehydrogenase/reductase family	3.49E-06	-0.13	-0.81	-0.18	0.21
AN5411	cyanamide hydratase, putative	3.57E-06	-0.19	-0.44	0.17	0.16
AN1734	3-dehydroshikimate hydratase, putative	3.62E-06	-0.12	-0.71	-0.08	0.20
AN6398	UDP-galactose 4-epimerase, putative	3.66E-06	-0.19	-0.63	0.03	0.18
AN1852	Chitin deacetylasePutative uncharacterized protein	3.81E-06	-0.12	-0.53	-0.52	0.23
AN6248	mitochondrial co-chaperone GrpE, putative	3.93E-06	-0.23	-0.12	-0.20	0.18
AN5880	V-type ATPase F subunit, putative	3.96E-06	-0.15	0.83	-0.36	0.21
velB AN0363	VelB	4.04E-06	0.08	0.06	0.39	0.13
AN3512	conserved hypothetical protein	4.30E-06	0.11	-0.68	0.05	0.23
dpp5 AN2572	hypothetical dipeptidyl-peptidase	4.37E-06	0.03	-0.25	0.42	0.30
AN8606	hypothetical polysaccharide deacetylase	4.38E-06	-0.24	-0.54	-0.43	0.28
AN1338	GPI anchored serine-threonine rich protein	4.41E-06	0.22	-0.47	-0.64	0.12
AN10499	NADP(+) coupled glycerol dehydrogenase	4.44E-06	-0.30	-0.63	0.21	0.23
AN8435	hypothetical protein ANIA_08435	4.48E-06	-0.07	0.38	-0.19	-0.10
AN4527	putative Myb-like transcription factor	4.65E-06	0.26	-0.13	-0.33	-0.35
AN0860	conserved hypothetical protein	4.73E-06	0.06	-0.31	0.14	-0.52
AN10626	hypothetical protein similar to ATP synthase alpha chain	4.74E-06	0.13	-0.06	0.53	-0.15
AN8553	catalase	4.85E-06	-0.24	-0.30	0.04	0.00
AN11498	hypothetical protein ANIA_11498	4.93E-06	-0.35	-0.38	-0.51	-0.23
AN5373	conserved hypothetical protein	4.96E-06	0.29	-0.54	-0.11	-0.19
pyrG AN6157	hate decarboxylase (OMP decarboxylase)(OMPDecase)(Uridine 5'-monophosphate synthase)(UMP synt	5.04E-06	-0.11	-0.65	-0.13	0.25
AN0694	conserved hypothetical protein	5.13E-06	-0.18	-0.58	0.41	0.29
AN4498	conserved hypothetical protein	5.21E-06	-0.02	0.37	-0.49	0.23
AN6902	60S acidic ribosomal protein P0, putative	5.36E-06	-0.02	0.54	0.38	0.28
AN10296	FAD dependent oxidoreductase, putative	5.61E-06	-0.12	-0.51	-0.34	0.06
AN2896	mitochondrial methylglutaconyl-CoA hydratase (Auh), putative	5.74E-06	-0.13	-0.29	0.01	0.23
AN4852	exo-beta-1,3-glucanase, putative	5.78E-06	0.28	-0.12	0.74	0.04
AN1809	conserved hypothetical protein	5.79E-06	-0.01	-0.07	0.03	0.17
AN5749	putative acetylornithine deacetylase	5.92E-06	-0.26	-0.47	-0.70	0.13
AN1986	mitochondrial chaperone Frataxin, putative	5.99E-06	-0.31	-0.21	-0.34	0.22
AN7959	DUF1264 domain protein	6.06E-06	-0.21	-0.62	-0.50	0.28
cpxA AN5442.2	CarboxypeptidasePutative uncharacterized protein	6.35E-06	-0.33	-0.40	-0.47	0.08
AN10973	citrate synthase, putative	6.38E-06	-0.11	0.25	0.04	-0.09
AN3334	conserved hypothetical protein	6.55E-06	0.00	-0.32	-0.05	0.23
AN0400	conserved hypothetical protein	6.60E-06	0.05	-0.63	-0.23	0.58
AN7040	conserved hypothetical protein	6.88E-06	-0.06	-0.61	-0.42	-0.13
AN3627	conserved hypothetical protein	6.90E-06	0.16	0.04	-0.40	-0.19
AN1222	hypothetical protein similar to S-adenosylmethionine synthetase	6.91E-06	0.10	0.21	-0.24	-0.15
orsC AN7912	conserved hypothetical protein	6.92E-06	-0.14	-0.48	-0.84	-0.16
AN9181	oxidoreductase CipA-like, putative	7.01E-06	0.08	0.38	-0.41	-0.38
AN6354	ubiquitin C-terminal hydrolase, putative	7.03E-06	-0.16	-0.02	-0.07	0.16
AN0693	conserved hypothetical protein	7.08E-06	0.05	-0.27	0.29	0.07
AN4688	Isovaleryl-coenzyme A dehydrogenase	7.21E-06	0.08	-0.47	-0.76	0.14
AN5217	primary component of eisosomes	7.26E-06	0.30	0.31	0.00	0.05
AN8068	extracellular endoglycanase, putative	7.50E-06	0.32	-0.91	-0.11	-0.05
atnl AN7877	RTA1 domain protein, putative	7.58E-06	0.56	0.39	0.13	-0.42
catB AN9339	Catalase B Precursor	7.62E-06	-0.16	-0.64	-0.76	0.46
AN6005	conserved hypothetical protein	7.67E-06	0.15	-0.11	0.38	0.04
cbhB AN0494	1,4-beta-D-glucan-cellulohydrolyasePutative uncharacterized protein	8.21E-06	0.55	-1.02	-0.52	0.22
AN0562	peroxisomal AMP binding enzyme, putative	8.53E-06	0.19	0.22	0.20	-0.19
AN2829	General amidase-C	8.63E-06	-0.12	-0.54	-0.72	-0.16
AN2450	ubiquitin-like activating enzyme (UbaB), putative	8.72E-06	0.03	0.20	-0.16	0.09
AN4177	NAD dependent epimerase/dehydratase family protein	8.95E-06	-0.12	-0.70	-0.23	0.34
AN6077	NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial [Precursor]	9.22E-06	-0.48	0.19	0.05	-0.03
AN2311	phosphomevalonate kinase	9.39E-06	0.22	-0.05	0.10	0.34
acuD AN5634	Isocitrate lyase (ICL)(Isocitratase)(Isocitratase)	9.42E-06	-0.17	-0.19	0.02	0.30
mndA AN1742	beta-1,4-mannosidase	9.46E-06	0.04	-0.51	-0.52	-0.07
AN7989	phosphatidylserine decarboxylase, putative	9.60E-06	0.23	-0.11	1.05	-0.32
AN1074	hypothetical glycine cleavage H-protein	9.71E-06	-0.13	-0.30	0.53	-0.09
AN4899	microbody (peroxisome) biogenesis protein peroxin 19	9.97E-06	-0.16	0.46	0.02	0.31
AN8466	conserved hypothetical protein	1.01E-05	0.08	-0.50	-0.90	-0.54
AN11085	conserved hypothetical protein	1.02E-05	0.13	-0.42	0.30	0.36
AN9407	Fatty acid synthase, alpha subunit	1.02E-05	0.16	-0.13	0.21	0.09
AN2463	beta-galactosidase	1.06E-05	-0.13	-0.62	0.04	0.38
AN7987	polyhydroxybutyrate depolymerase, putative	1.08E-05	-0.12	-0.55	-0.01	0.08
aspC AN6002.2	FAD-dependent monooxygenase, putative	1.08E-05	-0.01	-0.22	-0.26	-0.04

AN11143	glucoamylase	1.08E-05	0.22	-0.07	-0.87	-0.03
AN4914	acetate kinase, putative	1.13E-05	-0.12	-0.68	-0.24	0.23
mms18 msds AN0787	Alpha-1,2-mannosidase	1.13E-05	-0.12	-0.69	-0.82	-0.01
cysA AN8565	Putative serine O-Acetyltransferase	1.23E-05	-0.20	-0.10	0.14	0.09
AN8182	Septin Fragment	1.24E-05	0.16	-0.25	0.47	-0.19
AN7307	DUF1237 domain protein	1.24E-05	-0.34	-0.54	-0.63	0.06
AN0221	conserved hypothetical protein	1.25E-05	0.13	-0.60	-0.55	-0.08
AN10298	Phosphoserine aminotransferase	1.25E-05	0.06	0.08	0.14	0.09
AN6314	short-chain dehydrogenase/reductase family protein, putative	1.29E-05	-0.25	0.62	-0.34	-0.06
AN3873	zinc-containing alcohol dehydrogenase, putative	1.31E-05	-0.18	-0.83	-0.24	0.10
AN7999	conserved hypothetical protein	1.33E-05	-0.04	-0.54	-0.37	0.00
AN8536	conserved hypothetical protein	1.35E-05	0.09	0.26	-0.05	-0.22
AN8638	HHE domain protein	1.44E-05	-0.41	0.08	-0.23	-0.07
AN7960	conserved hypothetical protein	1.47E-05	0.17	-0.12	-0.01	0.48
AN6699	electron transfer flavoprotein alpha subunit, putative	1.50E-05	0.17	0.17	0.20	0.04
AN3022	tubulin-specific chaperone c, putative	1.52E-05	-0.37	-0.18	-0.14	0.13
AN2939	MRS7 family protein	1.55E-05	-0.03	-0.03	-0.38	0.08
AN1088	conserved hypothetical protein	1.56E-05	-0.15	-0.15	-0.15	0.02
AN2702	hypothetical protein ANIA_02702	1.57E-05	-0.27	-0.74	-0.14	-0.28
AN4646	hypothetical protein ANIA_04646	1.59E-05	-0.08	0.22	-0.61	0.34
AN10702	protein kinase C substrate, putative	1.62E-05	0.04	0.20	-0.53	0.24
AN2814	MFS lactose permease, putative	1.63E-05	0.02	-0.10	0.44	-0.15
AN8770	acetylglutamate kinase	1.67E-05	-0.26	-0.43	-0.25	0.04
AN3305	short chain dehydrogenase/reductase family protein	1.67E-05	0.56	0.96	0.21	0.02
bgfA bgf1 AN4102	beta-glucosidase	1.68E-05	0.17	-0.64	-0.43	0.09
AN0050	iso-oxorotate decarboxylase	1.71E-05	-0.04	-0.65	-0.67	0.02
AN7008	3-hydroxybutyryl-CoA dehydrogenase, putative	1.72E-05	-0.25	-0.31	-0.05	0.14
AN8975	conserved hypothetical protein	1.73E-05	0.05	0.79	-0.38	0.41
AN1837	hypothetical protein ANIA_01837	1.73E-05	0.00	-1.08	-0.36	-0.18
aguA AN9286	alpha-glucuronidase	1.74E-05	0.17	-0.27	0.24	-0.22
AN2315	ATP synthase beta chain, mitochondrial	1.79E-05	0.05	0.32	0.01	0.22
AN7269	conserved hypothetical protein	1.81E-05	0.10	-0.61	-0.50	-0.01
AN5524	metallo-beta-lactamase domain protein, putative	1.82E-05	0.06	-0.61	-0.49	0.08
AN1954	37S ribosomal protein Rsm24, putative	1.87E-05	-0.04	-0.16	0.80	0.15
AN8432	conserved hypothetical protein	1.89E-05	0.25	-0.90	-0.57	0.24
AN1003	hypothetical protein similar to isocitrate dehydrogenase	1.90E-05	-0.02	0.10	0.50	-0.01
aspnd1 AN1832	Antigen 1 Precursor (ASPD1)	1.92E-05	-0.09	-0.98	-0.36	1.42
AN6796	ThiJ/Pfl1 family protein	1.94E-05	-0.30	-0.66	-0.08	0.28
AN9011	conserved hypothetical protein	1.95E-05	-0.04	-0.71	-0.43	0.24
AN5422	beta-lactamase family protein	1.95E-05	-0.16	-0.71	-0.49	0.11
dewA AN8006	Spore-wall fungal hydrophobin dewA Precursor	1.95E-05	-0.09	-0.55	-0.51	0.30
AN10352	pre-rRNA processing nucleolar protein Sik1, putative	1.96E-05	0.27	0.36	-0.09	-0.17
exgA exg1 AN4052	beta-1,3-exoglucosidase	2.01E-05	-0.25	-0.60	-0.16	0.28
AN4653	conserved hypothetical protein	2.12E-05	0.04	-0.41	-0.20	0.10
benA rhiA AN1182	Tubulin beta-1 chain (Beta-1-tubulin)	2.13E-05	-0.05	0.54	0.41	-0.26
AN6287	ATP synthase oligomycin sensitivity conferral protein, putative	2.15E-05	-0.08	-0.13	-0.61	0.23
AN4577	FormamidasePutative uncharacterized protein	2.18E-05	0.38	-0.63	-0.19	0.03
AN0967	Rnt2 Fragment	2.19E-05	-0.16	-0.65	-0.64	-0.02
glnA AN4159	Glutamine synthetase (GS)(Glutamate--ammonia ligase)	2.19E-05	0.72	0.52	0.68	-1.49
AN2236	DUF500 domain protein	2.23E-05	-0.12	-0.26	-0.28	-0.18
AN8392	alpha-1,4-galactosidase	2.28E-05	-0.14	-0.25	0.04	-0.03
AN3246	conserved hypothetical protein	2.31E-05	0.12	-1.00	-1.20	0.15
AN5916	enoyl-CoA hydratase	2.33E-05	-0.19	-0.34	-0.45	0.12
AN3906	M protein repeat protein	2.45E-05	-0.36	0.58	0.07	-0.15
AN3558	DUF636 domain protein	2.46E-05	0.06	0.07	0.85	-0.03
AN9348	conserved hypothetical protein	2.54E-05	-0.26	-0.65	-0.46	-0.21
AN8335	conserved hypothetical protein	2.65E-05	-0.15	-0.45	-0.08	0.16
AN2903	vacuolar aspartyl protease (protease A)	2.66E-05	-0.09	-0.51	-0.52	-0.04
AN7558	conserved hypothetical protein	2.68E-05	-0.55	-0.24	-0.20	0.35
acoB AN3894	aconitate hydratase, mitochondrial, putative	2.69E-05	-0.05	0.25	0.19	0.08
AN9171	conidial pigment biosynthesis protein Ayg1	2.73E-05	-0.21	-0.43	-0.22	0.34
AN4714	ThiF domain protein, putative	2.80E-05	-0.03	0.01	0.12	-0.35
AN8641	conserved hypothetical protein	2.80E-05	-0.02	0.20	-0.10	0.06
AN4843	Putative alpha-glucosidasePutative uncharacterized protein	2.81E-05	0.06	0.22	0.41	-0.02
AN3565	metallo-beta-lactamase domain protein, putative	2.82E-05	-0.10	-0.46	0.26	0.08
AN6422	cellulose-binding GDSL lipase/acylhdroxylase, putative	2.91E-05	0.04	-0.82	-0.01	-0.34
AN2858	NAD binding Rossmann fold oxidoreductase, putative	2.95E-05	0.08	-0.31	0.80	-0.15
AN6933	conserved hypothetical protein similar to yeast mitochondrial NAD-dependent malic enzyme	2.97E-05	-0.06	-0.34	-0.06	0.17
AN1769	3'(2'),5'-bisphosphate nucleotidase (3'(2'),5'-bisphosphonucleoside 3'(2')-phosphohydrolase)(DPNase)	3.01E-05	0.22	-0.20	0.10	0.36
AN5451	ubiquitin-like protein DskB, putative	3.03E-05	-0.37	0.00	-0.68	0.02
AN2012	RfeF	3.04E-05	-0.06	0.41	-0.27	0.14
npc2 AN5879	Phosphatidylglycerol/phosphatidylinositol transfer protein Precursor (PG/PI-TP)	3.16E-05	-0.07	-0.28	-0.52	-0.05
mic60 AN3843	conserved hypothetical protein	3.28E-05	0.07	-0.01	-0.53	0.07
AN6428	conserved hypothetical protein	3.34E-05	0.64	-0.91	0.19	-0.49
AN10864	conserved hypothetical protein	3.40E-05	0.51	0.72	-0.11	-0.21
hse1 AN2066	Class E vacuolar protein-sorting machinery protein hse1	3.40E-05	-0.02	0.61	0.09	0.06
AN7401	beta-1,4-endoxylanase	3.43E-05	0.12	-1.10	-0.36	-0.11
cipB AN7895	Zinc-binding alcohol dehydrogenase domain-containing protein cipB (Concanamycin-induced protein B)	3.45E-05	-0.02	-0.65	0.25	-0.39
AN0895	hypothetical oxidoreductase	3.49E-05	-0.04	-0.61	-0.39	0.11
AN1364	DUF1000 domain protein	3.50E-05	-0.17	-0.52	-0.39	0.02

AN6301	conserved hypothetical protein	3.65E-05	0.11	-0.14	-0.52	0.68
AN10646	fructosamine-3-kinase, putative	3.65E-05	0.19	0.64	0.15	-0.01
AN7752	mitochondrial ferrochelatase, putative	3.74E-05	-0.01	0.35	0.00	0.32
AN1140	hypothetical protein similar to dehydroshikimate dehydratase	3.78E-05	0.00	-0.57	-0.05	0.21
AN8303	conserved hypothetical protein	3.97E-05	-0.19	-0.48	-0.65	-0.17
arp4 AN7441	Actin-related protein 4 (Actin-like protein arp4)(Actin-like protein 4)	4.04E-05	-0.20	0.34	0.24	-0.21
AN1433	triacylglycerol lipase, putative	4.11E-05	-0.19	-0.72	0.03	0.24
bgII AN2227	Putative beta-glucosidase	4.14E-05	-0.09	-0.82	-0.12	-0.16
AN6518	polysaccharide deacetylase family protein	4.32E-05	-0.16	-0.54	-0.64	0.21
pkiA pki AN5210	Pyruvate kinase (PK)	4.40E-05	-0.32	-0.43	-0.22	-0.06
AN3687	thioredoxin peroxidase/alkyl hydroperoxide reductase	4.45E-05	-0.15	0.57	-0.08	0.21
AN6807	conserved hypothetical protein	4.50E-05	-0.34	-0.28	0.69	-0.03
AN1547	Acyl-CoA carboxylate CoA-transferasePutative uncharacterized protein	4.66E-05	-0.03	-0.26	-0.41	0.28
alcB AN3741	Alcohol dehydrogenase 2 (Alcohol dehydrogenase II)(ADH II)	4.66E-05	0.29	-0.27	0.50	0.21
AN0559	mitochondrial import receptor subunit (Tom20), putative	4.68E-05	-0.34	-0.13	-0.20	0.00
AN2470	alcohol dehydrogenase, putative	4.81E-05	-0.04	0.72	0.42	-0.24
AN5571	oxoglutarate dehydrogenase (succinyl-transferring)	4.86E-05	0.12	0.16	0.44	0.35
ivoB AN0231	conserved hypothetical protein: N-acetyl-6-hydroxytryptophan oxidase	4.90E-05	-0.10	-0.74	-0.63	0.22
AN2978	conserved hypothetical protein	4.92E-05	0.16	0.46	-0.09	-0.14
AN7496	conserved hypothetical protein	5.22E-05	-0.54	0.53	-0.18	-0.01
AN6051	phytanoyl-CoA dioxygenase family protein	5.23E-05	0.01	-0.73	-0.44	0.04
AN5021	trehalose synthase (Ccg-9), putative	5.26E-05	-0.21	-0.63	0.15	0.15
AN3869	mevalonate kinase	5.30E-05	-0.19	-0.36	-0.33	-0.08
AN1282	glutamine-rich cytoplasmic protein	5.34E-05	-0.01	0.16	-0.03	0.11
AN2332	iron-sulfur protein subunit of succinate dehydrogenase Sdh2, putative	5.34E-05	-0.15	-0.69	0.09	0.22
AN5782	fumarylacetoacetate hydrolase family protein	5.37E-05	0.24	-0.11	0.56	-0.01
AN3829	succinate-semialdehyde dehydrogenase	5.46E-05	0.16	0.45	0.46	-0.12
mdpK AN10044	toxin biosynthesis protein, putative	5.47E-05	-0.40	0.75	0.02	-0.56
AN1269	mitochondrial carrier protein, putative	5.48E-05	0.16	-0.31	-0.62	-0.14
AN6688	Septin B	5.57E-05	-0.25	0.19	0.04	-0.18
AN8640	conidiation protein Con-6, putative	5.61E-05	0.17	-0.48	-0.25	0.29
AN7214	NADPH-dependent FMN reductase Lot6, putative	5.64E-05	0.20	-0.20	0.36	0.15
ccp1 AN10220	Cytochrome c peroxidase, mitochondrial Precursor (CCP)	5.65E-05	0.36	-0.26	0.51	0.11
AN6639	2-methylcitrate dehydratase	5.78E-05	-0.11	0.01	0.01	0.14
nptA AN11080	DMATS type aromatic prenyltransferase, putative (JCVI)	5.82E-05	-0.28	-0.64	-0.54	-0.04
AN2404	DUF1295 domain protein	5.98E-05	0.13	0.16	0.24	-0.06
AN1362	CUE domain protein, putative	6.13E-05	-0.18	0.22	-0.34	0.24
AN7497	NADH-ubiquinone oxidoreductase 18 kDa subunit, putative	6.21E-05	0.16	0.30	0.02	0.18
AN6487	aspartic-type endopeptidase (OpsB), putative	6.32E-05	0.04	-0.32	-0.19	0.12
AN0262	60S ribosomal protein L12	6.38E-05	0.45	0.42	0.35	-0.13
AN9285	glucose repressible protein Grg1, putative	6.39E-05	0.43	-0.67	0.14	-0.01
AN10444	gamma-glutamyltranspeptidase	6.40E-05	0.32	-0.60	-0.49	0.24
AN6856	conserved hypothetical protein	6.42E-05	-0.04	-0.17	-0.28	0.61
sfh5 AN8233	Phosphatidylinositol transfer protein sfh5 (PTP sfh5)	6.67E-05	0.09	0.38	0.18	-0.35
AN3402	Alpha-amylasePutative uncharacterized protein	6.78E-05	0.18	-0.25	-0.85	-0.08
AN9358	putative CCAAT-box-binding transcription factor	6.95E-05	-0.33	-0.32	-0.66	0.16
AN6337	conserved hypothetical protein	7.13E-05	-0.23	-0.08	-0.77	-0.05
AN2103	Acetate non-utilizing protein 9, mitochondrial Precursor	7.16E-05	-0.16	0.59	0.23	-0.07
aciA AN6525	Probable formate dehydrogenase (NAD-dependent formate dehydrogenase)(FDH)	7.23E-05	-0.24	-0.69	-0.35	0.18
AN9162	conserved hypothetical protein	7.32E-05	-0.04	-0.60	-0.31	0.06
AN1273	cellobiohydrolase (nonreducing end)	7.34E-05	-0.26	-0.62	0.02	-0.18
prnC AN1733	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial Precursor (P5C dehydrogenase)	7.37E-05	0.06	-0.62	-0.66	0.21
AN7177	WW domain protein	7.43E-05	-0.02	0.20	-0.17	0.23
AN9009	conserved hypothetical protein	7.61E-05	-0.10	-0.64	0.09	0.10
AN3057	prenylcysteine lyase, putative	7.69E-05	0.02	0.11	-0.30	0.07
AN2432	chaperonin, putative	7.77E-05	-0.30	-0.27	-0.19	-0.07
amds AN8777	Acetamidase	7.83E-05	-0.06	-0.69	-0.40	0.10
AN4531	alpha/beta hydrolase, putative	7.87E-05	-0.18	-0.56	-0.26	0.22
AN0783	general amidase, putative	7.90E-05	-0.21	-0.43	0.07	0.42
AN3874	raffinose synthase protein Sip1, putative	7.97E-05	0.26	-0.69	-0.35	0.09
acoA AN5525	Aconitase Fragment	8.04E-05	0.06	-0.13	0.36	0.21
AN2557	conserved hypothetical protein	8.10E-05	0.00	0.86	-0.30	-0.46
AN10260	conserved hypothetical protein	8.23E-05	-0.12	-0.49	0.68	0.34
orsB AN7911	conserved hypothetical protein	8.40E-05	-0.24	-0.66	-1.01	0.03
AN9380	Putative uncharacterized protein	8.43E-05	0.38	-0.60	-0.40	-0.02
AN8406	Alcohol dehydrogenase	8.73E-05	-0.08	0.04	0.17	0.05
AN2866	NAD binding Rossmann fold oxidoreductase, putative	8.74E-05	-0.24	-0.44	-0.32	0.26
AN4585	CCR4-NOT transcription complex, subunit 3	8.76E-05	-0.12	0.10	-0.43	0.00
lys4 lysF AN6521	Homoaconitase, mitochondrial Precursor (Homoaconitate hydratase)	8.89E-05	-0.01	0.18	-0.14	0.06
AN4940	meiotic sister chromatid recombination protein Ish1/Msc1, putative	9.06E-05	0.11	0.26	-0.51	-0.22
AN2835	conserved hypothetical protein	9.08E-05	-0.16	-0.32	-0.44	-0.10
mdpG AN0150	hypothetical protein similar to polyketide synthase	9.19E-05	-0.67	0.31	0.21	-0.46
AN7484	Uncharacterized protein AN7484	9.26E-05	-0.43	-0.59	-0.33	-0.43
AN4929	conserved hypothetical protein	9.67E-05	-0.33	0.43	-0.12	0.13
egID AN1602	Putative endo-beta-1,4-glucanasePutative uncharacterized protein	9.99E-05	0.23	-0.21	-0.98	-0.51
AN8619	conserved hypothetical protein	9.99E-05	-0.10	-0.53	-0.56	-0.22
AN5556	conserved hypothetical protein	0.000100275	0.28	-0.47	-0.17	0.29
AN1523	ATP synthase alpha chain, mitochondrial precursor	0.000102038	-0.02	-0.19	0.11	0.03
AN1387	meiotic recombination protein Ski8/Rec14, putative	0.000102499	0.17	-0.18	0.33	0.15
sodA AN0241	Superoxide dismutase [Cu-Zn]	0.000102652	-0.17	-0.67	-0.68	0.24

AN2237	carboxypeptidase S1, putative	0.000103695	-0.10	-0.63	-0.11	0.07
AN2859	dihydrodipicolinate synthetase family protein	0.000103827	-0.11	-0.79	-0.52	0.29
AN5563	NADP(+) -dependent glycerol dehydrogenasePutative uncharacterized protein	0.00010387	-0.17	-0.72	0.28	0.13
AN2217	beta-1,4-xylanidase	0.000104419	-0.05	-0.63	-0.36	-0.01
axha-2 AN7908	arabinoxylan arabinofuranohydrolase	0.00010455	-0.21	-0.61	-0.43	-0.38
AN5710	VHS domain protein	0.000106435	-0.26	0.05	-0.05	-0.34
slp1 alk1 alp prtA AN5558	Alkaline proteasePutative uncharacterized protein	0.000106951	0.00	-0.65	-0.70	0.11
AN10025	conserved hypothetical protein	0.000108334	0.22	0.13	-0.40	0.30
AN0567	hypothetical protein ANIA_00567	0.000108498	0.08	-0.51	-0.24	0.41
pgmB AN2867	Phosphoglucomutase (PGM)(Glucose phosphomutase)	0.000109503	-0.17	-0.13	-0.09	0.00
AN5480	RNA binding protein, putative	0.000109509	-0.18	1.22	-0.25	0.39
cym1 AN3853	Mitochondrial presequence protease Precursor	0.000109992	-0.17	-0.48	-0.05	0.22
AN7477	conserved hypothetical protein	0.00011035	-0.19	-0.85	-0.74	-0.06
AN6033	ARF GTPase activator (Glo3), putative	0.000110873	0.18	0.02	-0.40	-0.27
ubx1 AN11055	UBX domain-containing protein 1	0.000112857	-0.31	-0.37	-0.64	-0.09
AN0691	conserved hypothetical protein	0.000112885	-0.04	-0.41	0.00	0.64
lamB AN0886	Lactam utilization protein lamB	0.000113179	-0.12	-0.66	0.48	0.18
AN5206	LysBPutative uncharacterized protein	0.00011572	-0.10	0.20	-0.12	-0.01
biA AN6644	Coable bifunctional dethiobiotin synthetase/adenosylmethionine-8-amino-7-oxononanoate aminotransferase	0.000117903	-0.01	-0.31	-0.30	0.23
AN1699	acyl-CoA dehydrogenase, putative	0.000118208	-0.04	-0.47	-0.12	0.08
AN6862	conserved hypothetical protein	0.000121129	-0.07	-0.17	-0.15	1.03
AN1754	conserved hypothetical protein	0.000124812	0.13	-0.16	0.08	0.11
AN7836	cysteine-rich secreted protein	0.000126936	-0.61	-0.57	-0.91	0.45
AN11076	DUF427 domain protein	0.000127413	0.24	-0.27	0.11	-0.10
AN0317	EF hand domain protein	0.000133942	-0.06	-0.13	-0.21	0.16
AN10198	oligopeptidase family protein	0.000135081	0.13	-0.09	0.29	-0.29
AN9130	cholinesterase, putative	0.000137097	-0.20	-0.56	-0.27	0.06
AN3860	conserved hypothetical protein	0.000138827	-0.26	-0.77	-0.19	-0.61
AN7992	conserved hypothetical protein	0.000139987	0.36	0.21	-0.34	0.71
AN3972	5-oxo-L-prolinase, putative	0.000140819	0.12	-0.03	0.20	0.16
mdpj AN10038	hypothetical protein ANIA_10038	0.000141019	0.23	0.89	-0.19	-1.06
AN8953	Alpha-glucosidase BPutative uncharacterized protein Precursor;	0.000141455	-0.09	-0.57	-0.39	0.04
nudC AN5181	Nuclear movement protein nudC (Nuclear distribution protein C)	0.000146096	0.02	0.71	-0.02	0.19
AN9042	putative alpha 1,3 glucanase, GH71 family	0.00014644	-0.17	-0.15	-0.95	-0.03
AN2801	aldo-keto reductase (AKR), putative	0.000147319	-0.10	-0.53	0.28	-0.03
AN1428	N-acetylglucosamine-6-phosphate deacetylase (NagA), putative	0.000147628	-0.14	-0.59	0.06	0.26
AN1822	oxidoreductase, short chain dehydrogenase/reductase family protein, putative	0.000147977	0.16	-0.56	0.47	-0.03
AN4979	dihydropneopterin aldolase domain protein	0.000148057	0.09	0.10	0.80	0.25
AN5577	Superoxide dismutase	0.000150134	-0.16	-0.81	-0.40	0.10
AN5354	quinone oxidoreductase, putative	0.000150333	0.54	-0.07	-0.03	-0.12
AN2894	LEA domain protein	0.000150871	-0.15	-0.58	-0.76	0.36
AN4772	deoxyribose-phosphate aldolase, putative	0.000153372	-0.22	-0.62	-0.48	0.11
pab1 fabM AN4000	Polyadenylate-binding protein, cytoplasmic and nuclear (Poly(A)-binding protein)	0.00015468	-0.08	-0.20	-0.31	0.05
AN5604	Fructose-1,6-bisphosphatasePutative uncharacterized protein	0.000155366	-0.09	-0.48	0.08	0.29
AN3137	conserved hypothetical protein	0.000157287	0.25	-0.86	-0.33	0.12
AN8370	conserved hypothetical protein	0.000157491	0.02	0.64	0.13	0.00
AN3867	hypothetical protein similar to CaaX farnesyltransferase alpha subunit	0.000158477	-0.07	-0.36	0.47	0.10
AN10040	hypothetical protein ANIA_10040	0.000161422	-0.06	-0.22	0.67	0.22
AN6447	O-methyltransferase, putative	0.000163036	-0.05	0.36	0.09	0.12
AN4911	conserved hypothetical protein	0.000163392	0.38	0.64	0.63	-0.33
AN8363	phytase, putative	0.000163507	-0.22	0.26	-0.09	-0.18
AN2231	SAP domain protein	0.000164273	-0.03	-0.27	-0.09	0.26
AN8218	thioredoxin reductase, putative	0.000166983	-0.16	-0.47	-0.44	0.12
AN1799	secretory lipase, putative	0.000169129	-0.16	0.11	0.07	-0.50
AN5015	conidiation-specific protein 10	0.000174214	-0.60	0.47	-0.48	0.56
AN3481	conserved hypothetical protein	0.000177505	-0.05	-0.49	0.14	-0.18
AN0052	short chain dehydrogenase/reductase family	0.000179123	0.21	-0.71	0.62	-0.16
AN2051	essential Hsp90p co-chaperone	0.000179636	-0.31	0.48	-0.04	0.04
AN4010	conserved hypothetical protein	0.000179761	0.03	-0.71	-0.71	0.22
AN6697	SUN domain protein	0.000181889	-0.24	-0.25	-0.16	-0.03
AN5028	Fatty acid oxygenasePutative uncharacterized protein	0.000182839	0.07	0.15	0.34	-0.08
AN1105	mitochondrial import receptor subunit tom22	0.000182846	-0.14	0.53	-0.14	0.28
AN1396	glycerol-3-phosphate dehydrogenase, mitochondrial	0.000183258	0.24	0.31	0.15	-0.06
AN5019	Methionine synthase, vitamin-B12 independent, putative	0.000187579	0.55	0.24	0.56	0.35
AN7669	hypothetical arginase family protein	0.000187756	-0.01	-0.55	-0.40	-0.09
AN5953	iron-sulfur cluster assembly accessory protein Isa2, putative	0.000188311	-0.09	0.11	0.09	0.47
AN0224	membrane dipeptidase Glj	0.000188511	0.02	-0.31	-0.13	0.00
AN0089	Small GTPase AvaA	0.000190095	0.33	0.24	0.04	-0.10
AN3649	50S ribosomal protein L2	0.000191411	0.40	0.28	0.07	0.50
AN6010	Heat shock 70 kDa protein Precursor	0.000194726	-0.05	0.11	-0.32	0.37
AN3592	calnexin, putative	0.000196488	-0.22	-0.22	-0.53	0.00
fes1 AN6543	Hsp70 nucleotide exchange factor fes1	0.000199192	-0.19	-0.06	-0.07	-0.27
AN4901	glutaminase, putative	0.000202235	0.08	-0.66	-0.32	0.01
AN7907	conserved hypothetical protein	0.000202985	-0.22	-0.78	-0.41	0.20
AN4913	phosphoketolase, putative	0.000203037	0.18	0.42	-0.36	0.08
rasA AN0182	Ras-like protein Precursor	0.000203749	0.16	0.21	0.24	-0.09
AN9425	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase	0.000205627	-0.03	-0.57	-0.35	0.23
AN10754	nuclear protein export protein Yrb2, putative	0.000207012	-0.19	0.28	0.33	0.27
AN3976	isoflavone reductase family protein	0.000207264	0.37	0.19	0.44	-0.28
eglC AN7950	Beta-1,3-endoglucanasePutative uncharacterized protein	0.000207686	-0.02	-0.80	-0.75	-0.01

AN6993	xanthine-guanine phosphoribosyl transferase Xpt1, putative	0.000208626	0.07	0.05	0.52	0.04
AN2508	cysteine desulfurase, alanine biosynthesis, putative	0.000209049	0.13	0.41	0.21	-0.20
AN4825	conserved hypothetical protein	0.000210501	0.07	-0.38	-0.28	-0.04
AN0687	SPEE_NEUCR Spermidine synthase (Putrescine aminopropyltransferase) (SPDSY)Spermidine synthase;	0.000212117	-0.19	-0.58	-0.30	0.14
AN6442	amino acid transporter	0.000212783	-0.25	-0.54	-0.68	-0.30
end3 sagA AN1023	in cytoskeleton-regulatory complex protein end3 (Endocytosis protein 3)(Cytoskeletal adapter protein sagA)	0.000213111	-0.30	-0.52	-0.53	-0.31
AN2260	NADH-ubiquinone oxidoreductase subunit B17.2, putative	0.000214689	0.13	0.14	0.53	0.14
AN8628	NADP-dependent alcohol dehydrogenase	0.000216034	0.25	-0.11	0.59	0.06
AN0443	alcohol dehydrogenase, zinc-containing, putative	0.000217	0.00	-0.39	0.40	-0.06
dapB ste13 AN2946	Dipeptidyl aminopeptidase	0.000217569	0.16	0.23	0.25	-0.34
bgIL AN2828	beta-1,4-glucosidase	0.00021822	-0.07	-0.82	-0.61	-0.06
AN2936	Alpha-mannosidase	0.00022315	-0.18	-0.61	-0.54	0.04
AN0006	conserved hypothetical protein	0.000226919	0.21	-0.25	-0.35	0.17
rodA AN8803	Rodlet protein Precursor	0.000229252	-0.10	-0.95	0.12	0.08
AN1131	cytosolic Cu/Zn superoxide dismutase, putative	0.000235997	0.34	-0.46	-0.23	-0.05
AN10719	U6 snRNA-associated Sm-like protein LSm6, putative	0.000236409	0.27	-0.29	-0.37	0.16
AN3150	glutamate-cysteine ligase, catalytic subunit	0.000239175	0.49	0.44	0.27	0.06
AN0391	NACHT domain protein	0.0002399	0.17	0.35	0.16	-0.33
AN3877	conserved hypothetical protein	0.000242545	0.14	-0.26	0.74	-0.16
AN5831	glutathione S-transferase	0.000247183	0.05	-0.49	-0.25	0.17
citA AN8275	Citrate synthase, mitochondrial Precursor	0.000248418	-0.29	-0.64	0.21	0.10
AN10494	conserved hypothetical protein	0.00025001	0.29	0.94	0.09	-0.07
AN2999	Mitochondrial NADP-dependent isocitrate dehydrogenase	0.000250933	0.18	-0.10	0.21	0.11
cbhC AN5282	Beta-1,4-glucan-cellulohydrolase	0.000253827	0.43	-0.79	-0.43	0.18
AN10219	conserved hypothetical protein	0.000255929	0.10	0.20	0.42	0.43
AN9180	conserved hypothetical protein	0.0002559203	0.36	0.24	0.41	0.32
AN3223	6-phosphofructo-1-kinase (phosphofructokinase)	0.000260015	-0.11	-0.13	0.07	0.05
AN3955	conserved hypothetical protein	0.000260252	-0.30	-0.19	0.89	0.19
AN2954	extracellular serine-rich protein, putative	0.000262854	0.08	-0.53	-0.67	0.31
AN1827	GPI anchored protein, putative	0.000263876	0.20	-0.37	-0.42	0.19
AN7701	37S ribosomal protein S16	0.00026525	-0.22	-0.37	0.79	0.29
AN8004	cytochrome P450, putative	0.000265644	0.16	0.39	0.09	0.00
AN8496	class II aldolase/adducin domain protein	0.000269002	-0.01	-0.62	-0.25	0.24
AN11238	hypothetical protein ANIA_11238	0.000269079	-0.25	0.52	-0.26	-0.05
AN1278	conserved hypothetical protein	0.000270018	-0.07	-0.36	-0.66	-0.04
sec31 AN6257	Protein transport protein sec31	0.000274217	-0.05	0.27	-0.10	-0.13
AN3349	cytochrome P450, putative	0.00027657	0.19	0.47	-0.01	-0.19
AN2526	acetohydroxacid reductoisomerase	0.000279001	-0.03	0.31	-0.03	0.08
AN4822	tartrate dehydrogenase, putative	0.000279487	0.24	-0.44	0.06	0.04
fahA fah AN1896	Fumarylacetoacetate (FAA)(Fumarylacetoacetate hydrolase)(Beta-diketonase)	0.000285423	-0.21	-0.59	-0.60	0.18
AN2576	xenobiotic compound monooxygenase, DszA family	0.000287669	0.31	-0.37	-0.17	0.06
aroM AroA aroM AN0701	Pentafunctional AROM polypeptide [Includes 3-dehydroquinate synthase(DHQS) synthase](EPSPS)	0.000289877	0.09	0.22	0.26	-0.12
AN1184	conserved hypothetical protein	0.000290904	0.08	-0.41	-0.49	0.19
AN8867	seryl-tRNA synthetase	0.000291927	0.21	0.60	0.13	-0.11
AN7011	copper resistance protein Crd2, putative	0.000293448	0.01	-0.75	-0.48	0.34
AN4058	hypothetical dihydroxyacid dehydratase	0.000293989	-0.12	-0.55	-0.47	0.27
AN8106	conserved hypothetical protein	0.000296105	-0.10	0.58	0.29	-0.21
AN2414	hypothetical protein similar to NADH-ubiquinone oxidoreductase 49 kDa subunit, mitochondrial precursor	0.000297335	0.27	0.34	0.34	0.10
AN6048	aspartate transaminase	0.000300872	-0.34	0.38	-0.09	-0.15
AN4236	hypothetical protein similar to TAT-binding protein 1	0.000308787	-0.20	0.80	-0.45	-0.03
xlnD xylA AN2359	Beta-xyllosidase	0.000309065	0.15	-0.42	0.35	-0.09
AN10469	oxidoreductase, short-chain dehydrogenase/reductase family	0.000309258	0.02	-0.66	-0.11	0.31
AN0393	putative endo mannanase, GH76 family	0.000311615	-0.06	-0.46	-0.36	-0.09
rny1 AN4874	Ribonuclease T2-like Precursor (RNase T2-like)	0.000316478	0.04	-0.43	-0.40	0.04
AN5884	orotate phosphoribosyltransferase	0.000317379	0.02	0.59	0.17	0.19
AN5698	3-ketoacyl-CoA thiolase (POT1), putative	0.000323758	-0.08	-0.39	-0.01	0.29
AN5499	Nuclear pore complex protein An-Mlp1	0.000324241	-0.17	0.17	-0.45	0.12
AN7894	conserved hypothetical protein	0.000325722	0.04	-0.17	0.14	0.05
p2ox AN5281	conserved hypothetical protein	0.000327045	0.43	-0.77	-0.73	0.45
AN0705	isoleucyl-tRNA synthetase, cytoplasmic	0.000328266	0.13	0.58	0.06	0.01
AN7231	hypothetical serine carboxypeptidase	0.000328592	0.12	-0.38	-0.20	0.11
AN10952	FAD monooxygenase, putative	0.00032868	0.18	-0.26	0.07	0.29
gatA AN2248	4-aminobutyrate aminotransferase (Gamma-amino-N-butyrate transaminase)(GABA transaminase)	0.000333377	-0.05	-0.47	-0.33	0.31
AN7568	Gamma-butyrobetaine hydroxylase subfamily, putative	0.000334089	-0.11	-0.29	0.27	0.04
AN8863	Putative nucleosome assembly protein	0.000341682	0.06	-0.07	-0.37	-0.17
stcU verA AN7806	Veriscolorin reductase	0.000345442	-0.12	-0.72	0.06	0.21
AN6535	conserved hypothetical protein	0.000346257	0.00	-0.80	-0.86	-0.02
AN3312	oxidoreductase, short chain dehydrogenase/reductase family	0.000348308	-0.10	-0.81	-0.06	-0.12
AN2144	urease accessory protein UreD	0.000348836	-0.05	-0.41	0.13	0.21
AN5589	conserved hypothetical protein: glycerol kinase	0.000350476	0.21	-0.46	0.03	0.32
AN8086	conserved hypothetical protein	0.000357763	-0.31	-0.69	-0.76	0.22
AN3712	dienelactone hydrolase family protein	0.000359729	-0.11	-0.70	-0.37	0.02
AN4256	lipase, putative	0.000362911	0.10	0.59	-0.77	0.35
AN6365	conserved hypothetical protein	0.000369745	0.21	0.89	-0.47	-0.36
AN0747	Mitochondrial-processing peptidase subunit beta, mitochondrial [Precursor]	0.000369957	0.21	0.84	-0.34	-0.09
AN2924	NRPS-like enzyme, putative (JCVI)	0.000371877	-0.22	0.54	-0.03	-0.17
AN1197	alpha-1,2-mannosidase family protein, putative	0.000376203	0.03	-0.39	-0.81	0.12
AN1688	calcium homeostasis protein Regulcin, putative	0.000381221	0.09	0.25	0.34	0.10
AN7864	conserved hypothetical protein	0.000384116	0.20	-0.20	0.45	0.26
AN8707	fumarate hydratase, putative	0.000384812	0.08	-0.36	0.25	0.27

AN3807	oxysterol binding protein (Osh7), putative	0.000387704	-0.06	0.61	0.12	0.25
eglA AN1285	Endo-beta-1,4-glucanasePutative uncharacterized protein	0.00038833	-0.18	-0.62	-0.19	-0.43
AN9408	Fatty acid synthase, beta subunit	0.000388696	0.08	-0.09	0.19	0.11
AN10841	peroxisomal D3,D2-enoyl-CoA isomerase	0.000388849	0.48	0.39	0.06	-0.05
AN5448	hypothetical protein ANIA_05448	0.000390161	0.26	0.42	-0.12	-0.12
AN6847	arylsulfatase, putative	0.00039058	0.26	-0.57	-0.17	0.06
AN10358	conserved hypothetical protein	0.000391627	0.58	-0.53	0.96	-0.01
AN4784	ubiquitin thiolesterase (OtuB1), putative	0.000400108	0.35	0.71	0.13	-0.42
mcr1 AN0432	NADH-cytochrome b5 reductase 2 (Mitochondrial cytochrome b reductase)	0.000405368	0.15	-0.30	0.02	0.69
acuE AN6653	Malate synthase, glyoxysomal	0.000406554	0.29	-0.10	0.29	0.39
AN2824	glycosyl hydrolase, putative	0.000406943	-0.43	-0.72	-0.41	-0.14
AN0271	dUTPase (Dut), putative	0.00040884	0.01	-0.27	-0.17	0.16
AN10290	pyridoxamine phosphate oxidase, putative	0.000408928	-0.09	-0.49	0.19	0.04
AN1543	hypothetical fumarate reductase	0.00041355	-0.06	-0.48	-0.06	0.06
AN1405	conserved hypothetical protein	0.000415777	-0.07	0.07	0.25	0.05
AN1947	metallo-beta-lactamase family protein	0.000418506	-0.18	-0.54	-0.31	0.07
AN3184	aldose 1-epimerase, putative	0.000421302	0.04	0.04	0.96	0.06
AN6564	37S ribosomal protein S9	0.000430582	0.06	-0.17	0.29	0.25
AN6450	oxidoreductase, short-chain dehydrogenase/reductase family, putative	0.000437238	0.27	0.06	0.37	0.09
AN1600	conserved hypothetical protein	0.000438762	0.09	0.58	0.32	-0.35
AN6228	GVF domain protein	0.000441056	-0.37	-0.02	-0.20	0.07
AN3191	lipase/esterase, putative	0.00044492	-0.24	0.70	-0.37	-0.08
AN9401	mitochondrial enoyl reductase, putative	0.000445109	-0.11	-0.56	0.00	0.48
AN3918	aminopeptidase, putative	0.000447057	-0.18	-0.69	-0.59	0.04
AN4281	GTP-binding protein ypt1	0.000449561	0.15	0.32	-0.05	-0.10
AN8162	amine oxidase, flavin-containing superfamily	0.000458246	-0.29	-0.44	-0.14	0.36
AN10563	alkaline phosphatase Pho8	0.000458279	-0.03	-0.57	-0.56	0.07
AN7059	conserved hypothetical protein	0.000461194	-0.14	-0.65	-0.77	-0.03
AN0832	peptidase D, putative	0.000470879	0.08	0.86	0.04	-0.26
AN10918	sorting nexin Mvp1	0.000471537	0.10	-0.01	-0.62	-0.26
AN3020	tripeptidyl peptidase SED3	0.000472676	0.07	-0.27	-0.07	0.01
AN8714	hypothetical protein ANIA_08714	0.000479913	0.08	0.04	-0.56	0.07
AN7691	phosphoesterase superfamily protein	0.000480871	-0.14	-0.36	-0.10	0.16
AN0870	mitochondrial phosphate carrier protein (Mir1), putative	0.000481786	0.24	0.17	-0.23	0.03
AN0470	30S ribosomal protein S7, putative	0.000483561	0.00	0.00	-0.17	0.05
AN4300	NADH-ubiquinone oxidoreductase 21 kDa subunit, putative	0.000485059	0.31	0.30	-0.23	0.15
AN2440	ribose 5-phosphate isomerase A	0.000495549	-0.18	-0.70	-0.33	0.17
AN4889	THUMP domain protein	0.000508912	0.04	-0.75	-0.26	0.16
AN8284	conserved hypothetical protein	0.000518364	0.00	-0.32	0.56	0.37
AN10614	telomere and ribosome associated protein Stm1, putative	0.0005224	-0.18	0.40	-0.17	-0.09
AN7812	conserved hypothetical protein	0.000525178	-0.05	-0.69	0.19	-0.18
AN11077	sugar O-acetyltransferase, putative	0.000531625	-0.09	-0.54	0.71	-0.45
AN8099	oxalate decarboxylase, putative	0.000534323	-0.40	1.78	0.21	0.46
AN6203	conserved hypothetical protein	0.000535708	-0.12	-0.03	-0.71	0.00
AN1163	oligomeric mitochondrial matrix chaperone	0.000544027	-0.19	0.44	-0.20	0.19
AN2659	hypothetical protein ANIA_02659	0.00054578	-0.20	-0.46	-1.08	0.07
AN4781	Lipoyletransferase, putative	0.000549145	-0.23	0.22	-0.18	-0.35
pyrABCN AN0565	Protein pyrABCN [Includes Glutamine-dependent carbamoyl-phosphate;Aspartate carbamoyltransferase]	0.000549216	0.02	0.32	0.04	-0.12
cysD AN8277	ethylhomoserine (thiol)-lyase (O-acetylhomoserine sulfhydrylase)(OAH sulfhydrylase)(Homocysteine synthase)	0.000550419	-0.03	-0.74	-0.54	0.16
AN1591	conserved hypothetical protein	0.000554776	0.10	1.02	0.01	-0.66
manC AN6427	Endo-beta-1,4-mannanasePutative uncharacterized protein	0.000559046	0.28	-0.56	-0.24	-0.58
AN9085	U5 snRNP complex subunit, putative	0.000559883	-0.09	-0.07	0.15	0.20
AN5977	ketoreductase	0.000565966	0.26	-0.33	-0.02	0.14
AN10351	aspartyl aminopeptidase	0.000566552	-0.10	-0.48	-0.70	0.16
AN6708	hypothetical protein similar to dihydrolipoamide acyltransferase, pyruvate dehydrogenase E2 component	0.000567319	-0.09	0.77	0.37	-0.10
AN5061	xyloglucanase	0.00056815	0.22	-1.12	-0.07	-0.03
AN0558	putative 1,3-beta-transglucosylase, GH72 family	0.000569205	-0.05	0.14	0.19	0.22
AN1502	N-acetylglucosaminidasePutative uncharacterized protein	0.000569584	-0.30	-0.66	-0.70	0.29
AN6668	conserved hypothetical protein	0.000571065	-0.03	0.83	1.53	1.03
AN3132	Zn-dependent hydrolase/oxidoreductase family protein, putative	0.000579015	0.30	0.12	-0.28	-0.50
AN7349	Alpha-1,3-glucanaseMutanasePutative uncharacterized protein;	0.000580501	-0.28	-0.50	-1.26	0.43
AN7423	subunit of heterotrimeric Replication Factor	0.00058194	-0.05	-0.30	-0.01	0.11
AN6108	DHFR, dihydrofolate reductase, cytosolic form	0.000583132	-0.24	-0.92	-0.09	0.14
gu1 AN5566	GMP synthase [glutamine-hydrolyzing] (Glutamine amidotransferase)(GMP synthetase)	0.000585635	0.25	0.12	0.16	-0.11
AN3299	glutathione S-transferase, putative	0.00058773	-0.12	-0.83	-0.35	-0.18
AN6338	hypothetical amino acid aminotransferase	0.00059143	0.06	-0.32	0.23	0.13
AN5280	conserved hypothetical protein	0.000599371	0.37	-0.47	-0.31	0.04
spt16 AN5102	FACT complex subunit spt16 (Facilitates chromatin transcription complex subunit spt16)	0.000602299	0.17	0.00	0.25	0.02
AN8009	thiamine biosynthesis protein	0.000603377	-0.14	-0.38	0.09	0.04
AN8225	mitochondrial large ribosomal subunit protein L1, putative	0.000607703	0.33	0.55	0.27	0.18
AN2493	extracellular phytase, putative	0.000608653	-0.36	-0.51	-0.58	-0.25
AN8872	AMP deaminase Amd1, putative , partial	0.000612041	-0.20	-0.23	-0.47	0.09
AN1426	hypothetical serine carboxypeptidase	0.000620899	0.13	0.08	0.77	0.15
AN2747	DNA-directed RNA polymerase I, II, and III subunit Rpb6	0.000626889	-0.23	0.54	-0.27	0.17
AN0205	conserved hypothetical protein: pantethenate synthetase	0.000628132	0.08	0.02	-0.21	0.41
AN10472	thiamine biosynthetic bifunctional enzyme, putative	0.000629085	-0.03	-0.33	0.46	0.19
AN6145	Peptidyl-prolyl cis/trans isomerase	0.000631678	-0.38	0.57	0.01	0.33
AN5938	conserved hypothetical protein	0.000632563	-0.01	-0.48	-0.18	0.21
xk1a AN8790	D-xylulose kinase	0.000634301	0.14	0.13	0.17	0.07
AN3790	putative alpha 1,3 glucanase, GH71 family	0.000639864	0.08	-0.43	-0.79	0.31

AN0767	small nuclear ribonucleoprotein (LSM7), putative	0.0006486	-0.27	-0.15	-0.35	-0.02
AN1493	hypothetical protein ANIA_01493	0.000652969	0.06	-0.48	-0.73	-0.48
cyn1	cyanate hydratase, putative	0.00065562	-0.24	-0.73	-0.55	0.08
AN5704	acyl carrier protein, putative (JCVI)	0.00066162	-0.41	-0.11	-0.92	0.08
AN6253	Phenylalanyl-tRNA synthetase alpha subunit-like protein Fragment	0.000665036	0.39	0.26	0.54	0.15
AN6875	kinesin class 4 (Chromokinesin/Kif4 group)	0.000669888	-0.16	-0.09	-0.58	-0.08
AN5764	conserved hypothetical protein	0.000672191	-0.13	0.30	-0.28	0.09
AN0141	tRNA methyltransferase	0.000677927	-0.10	-0.14	-0.11	0.24
AN1544	conserved hypothetical protein	0.000678179	0.01	0.39	0.09	0.04
AN5672	mandelate racemase/muconate lactonizing enzyme family protein	0.000679823	0.00	-0.65	-0.38	-0.18
tpiA	AN6900 Triosephosphate isomerase (TIM)(Triose-phosphate isomerase)	0.0006832	0.33	-0.56	0.15	0.26
AN10745	serine hydroxymethyltransferase	0.00068576	-0.20	-0.53	-0.73	0.12
AN0184	GMF family protein	0.000689783	0.20	0.48	-0.08	-0.08
AN2776	conserved hypothetical protein	0.000693902	0.26	-0.44	0.71	0.28
AN1863	Bys1 family protein	0.000702359	-0.57	-0.66	-1.36	-0.91
AN2017	Alpha-glucosidase AgdAPutative uncharacterized protein	0.000710251	-0.12	-0.52	-0.77	0.06
AN5619	ADAM family of metalloprotease ADM-B	0.000714326	0.06	-0.31	-0.49	0.16
AN8434	ankyrin repeat protein	0.000714392	-0.12	1.20	-0.27	-0.09
AN4039	Rhodanese domain protein	0.000715728	-0.46	-0.26	0.36	-0.53
AN0229	DUF221 domain protein, putative	0.000717456	0.17	0.43	0.17	-0.28
AN4187	TBP associated factor (Mot1), putative	0.000726572	0.03	0.35	-0.30	-0.33
agaA	AN2901 Arginase	0.000735441	-0.18	-0.64	0.12	0.33
AN7159	hypothetical tripeptidyl-peptidase	0.000737719	-0.15	1.77	0.14	0.04
AN7699	conserved hypothetical protein	0.000752228	-0.03	-0.48	0.70	0.45
AN5686	tropomyosin TpmA	0.000753459	0.18	0.70	0.15	0.35
cp2	AN4467 Peptidyl-prolyl cis-trans isomerase B Precursor (PPIase B)(Rotamase B)	0.000757408	-0.08	-0.47	-0.21	0.00
AN1150	acetylornithine aminotransferase, ornithine transaminase	0.000758263	0.32	-0.53	0.11	0.42
AN4145	conserved hypothetical protein	0.000759783	0.23	0.18	0.14	0.04
chiB	AN4871 ChitinasePutative uncharacterized protein	0.000768729	-0.52	-0.65	-0.90	0.08
AN6853	CRAL/TRIO domain protein	0.000777081	0.51	0.32	0.19	-0.39
AN2898	conserved hypothetical protein	0.000792797	0.10	-0.26	0.46	0.00
hsp60	AN6089 Heat shock protein 60 Precursor (60 kDa chaperonin)(Protein Cpn60)	0.000793808	0.05	0.57	-0.10	-0.17
AN3674	hypothetical PH domain protein	0.00079483	0.00	0.12	0.29	-0.22
AN2704	conserved hypothetical protein	0.000797341	0.54	-0.43	-0.35	-0.04
AN1667	conserved hypothetical protein	0.000800502	-0.04	-0.34	0.14	0.26
AN1765	conserved hypothetical protein	0.000802732	0.10	0.27	1.02	-0.12
AN10641	DSBA-like thioredoxin domain protein	0.000807791	-0.11	-0.03	-0.24	0.22
AN9120	DNA-directed RNA polymerase Fragment	0.000809867	0.17	0.37	0.07	-0.20
AN0757	methyltransferase (Ncl1), putative	0.000809874	0.01	0.30	-0.07	-0.11
AN4549	HAD superfamily hydrolase, putative	0.000819393	0.12	-0.08	0.05	0.31
AN2658	kelch repeat protein	0.000834866	0.40	0.06	0.23	-0.15
AN10229	NADH-ubiquinone oxidoreductase 30.4 kDa subunit, mitochondrial [Precursor]	0.000845735	0.27	0.40	0.31	0.02
AN10146	conserved hypothetical protein	0.000855611	-0.33	-0.64	-0.52	0.17
AN6844	mitochondrial 3-hydroxyisobutyryl-CoA hydrolase, putative	0.000869317	-0.03	0.05	0.17	0.26
AN0999	adenylyl cyclase-associated protein (cap)	0.000870028	0.13	0.29	0.00	-0.23
cbp4	AN8766 Assembly factor cbp4 (Cytochrome b mRNA-processing protein 4)	0.000870362	0.00	-0.13	-0.10	-0.10
AN2731	protein mitochondrial targeting protein (Mas1), putative	0.000872754	-0.36	-0.09	-0.27	-0.26
AN6279	hypothetical protein similar to carnitine acetyl transferase	0.000887136	-0.21	-0.68	0.06	0.39
AN5203	40S ribosomal protein S8	0.000887623	-0.05	-0.35	0.89	0.13
IbsA	AN8049 Lactobacillus shifted protein	0.000889168	0.36	0.20	-0.45	0.17
AN2185	endo-deoxyribonuclease	0.0008896768	-0.24	-0.39	-0.66	-0.14
AN5522	conserved hypothetical protein	0.000903826	-0.06	-0.14	0.16	0.22
rgIa	AN7135 RHGB ASPAC Rhamnogalacturonase B (Rhamnogalacturonan lyase) (RGase B) (RHG B)	0.000910007	0.33	-0.68	0.32	-0.06
AN6346	hypothetical dihydroxy-acid dehydratase	0.000913802	-0.18	-0.58	-0.51	0.33
AN5164	30S ribosomal subunit S4, putative	0.000915312	-0.08	-0.19	0.62	0.20
AN11154	conserved hypothetical protein	0.000915971	-0.27	-0.36	-0.09	0.19
panB	AN1778 3-methyl-2-oxobutanoate hydroxymethyltransferase (Ketopantoate hydroxymethyltransferase)	0.000916501	-0.20	-0.64	-0.66	0.31
atrJ	AN7876 branched-chain amino-acid transaminase, putative	0.000920561	0.32	-0.04	-0.08	0.12
AN0602	extracellular protein, putative	0.000924174	0.05	-0.09	0.06	-0.06
AN3351	conserved hypothetical protein	0.000942408	0.05	-0.53	-0.43	0.25
AN7799	Uncharacterized oxidoreductase AN7799	0.000945816	0.08	0.53	0.12	-0.26
AN0952	acid phosphatase, putative	0.000963891	-0.28	-0.60	-0.38	0.08
AN2213	proteasome regulatory particle subunit Rpt2, putative	0.000976771	0.07	0.48	0.04	-0.22
vps10 vpsT	AN8880 vacuolar protein sorting protein, putative	0.00097717	-0.18	0.14	-0.01	-0.04
AN2916	hypothetical protein similar to succinate dehydrogenase flavoprotein subunit A	0.000978836	-0.09	-0.62	0.13	0.34
AN4297	NADH-ubiquinone oxidoreductase subunit B, putative	0.00098012	0.16	0.00	0.11	-0.04
fkbB	AN8343 FK506-binding protein 2 Precursor (Peptidyl-prolyl cis-trans isomerase)(PPIase)(Rotamase)	0.000987896	0.01	0.03	-0.13	-0.16
AN2014	signal recognition particle protein, putative	0.000993464	0.44	0.28	-0.66	0.21
AN0484	glycerophosphoryl diester phosphodiesterase family protein	0.001009605	0.13	-0.20	-0.16	-0.12
AN0582	possible replication factor-a protein	0.001010057	-0.03	-0.41	-0.18	0.14
AN3173	ribosomal protein S15, putative	0.001026809	-0.22	-0.38	0.18	0.27
chz1	AN5128 Histone H2A.Z-specific chaperone chz1	0.001027492	-0.09	0.20	-0.59	0.37
AN3778	Gephyrin-like proteinPutative uncharacterized protein	0.001034484	0.17	-0.36	0.16	0.03
AN6681	splicing factor u2af large subunit	0.001058413	0.36	0.29	-0.32	0.14
AN11052	exonuclease II	0.001084239	0.01	0.22	0.16	-0.18
AN2756	SlaB	0.001097767	-0.30	0.27	-0.42	-0.11
AN6476	conserved hypothetical protein	0.001097846	-0.39	-0.47	-0.01	0.20
mdpC	AN0146 oxidoreductase, putative	0.00111803	-0.16	-0.19	0.12	-0.09
AN5629	NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial precursor	0.00111877	0.24	0.36	0.18	-0.09
AN5324	conserved hypothetical protein	0.001123404	-0.29	-0.33	-0.14	0.36

AN6317	Chitin synthase	0.001126081	0.29	0.35	0.07	-0.30
AN8750	conserved hypothetical protein	0.001144773	-0.18	0.20	-0.67	0.34
AN7334	phospholipase D (PLD), putative	0.001159324	-0.02	0.53	0.30	-0.36
AN3024	conserved hypothetical protein	0.001167921	-0.06	0.54	0.14	0.04
AN1860	conserved hypothetical protein	0.001170834	0.33	0.62	-0.11	-0.13
AN7287	Mitochondrial succinate-fumarate antiporter	0.001179893	0.06	0.21	-0.34	-0.01
aim24 AN10466	mitochondrial protein Fmp26, putative	0.001185053	0.27	0.25	0.14	-0.07
lia1 AN7498	Deoxyhypusine hydroxylase (DOHH)(Deoxyhypusine monooxygenase)	0.001188247	0.30	1.00	-0.29	0.00
AN0158	quinone oxidoreductase, putative	0.001224949	0.00	-0.43	0.01	0.15
xlnC AN1818	Endo-1,4-beta-xylanase C Precursor (Xylanase C)(1,4-beta-D-xylan xylanohydrolase C)(34 kDa xylanase)	0.001226239	-0.11	-0.85	-0.08	-0.32
AN6399	conserved hypothetical protein	0.001226646	-0.03	-0.35	-0.19	-0.02
AN3840	FPGS, folypolyglutamate synthase	0.001235838	0.09	0.76	0.21	-0.16
AN6985	FGGY-family carbohydrate kinase, putative	0.001237415	0.03	-0.14	0.46	0.14
AN6976	NADH-ubiquinone oxidoreductase 21 kDa subunit, putative	0.001249361	0.14	0.46	-0.09	0.05
AN3375	DnaJ domain protein	0.001249672	-0.24	0.11	-0.26	-0.01
AN10440	NADH-ubiquinone oxidoreductase 39 kDa subunit, putative	0.001251476	0.29	0.29	-0.05	0.15
AN6058	DUF833 domain protein	0.001258972	-0.04	0.22	0.00	-0.30
AN0977	putative microbody (peroxisome) biogenesis protein peroxin 22-like	0.0012604	-0.06	0.36	-0.09	-0.11
AN8121	phosphoribosylformylglycinamide synthase	0.001274027	0.33	0.14	0.33	0.44
AN5074	3-oxoacyl-(acyl-carrier-protein) reductase	0.001310002	0.10	0.28	0.18	0.04
AN1390	iron/copper transporter Atx1, putative	0.001314195	0.13	-0.59	0.10	0.45
AN8977	AkePPutative uncharacterized protein	0.001319076	-0.16	-0.73	-0.49	0.19
AN5833	propionate-CoA ligase	0.001323983	0.12	0.08	0.26	0.32
AN8908	conserved hypothetical protein	0.001330212	0.14	-0.34	-0.15	0.20
AN3636	phosphatidylinositol phospholipase C	0.001331394	0.10	1.02	0.09	-0.42
AN3739	RNP domain protein	0.001356717	0.26	0.03	-0.01	0.27
AN8145	DUF985 domain protein	0.001368035	0.49	-0.45	0.20	0.14
AN5591	aminotransferase, classes I and II, putative	0.001378808	-0.14	0.20	-0.24	0.10
AN1759	hypothetical protein ANIA_01759	0.001405478	-0.49	0.24	-0.44	0.05
AN4453	cytoskeleton organisation protein (Dec1), putative	0.001420732	0.15	0.47	0.37	-0.01
AN0596	damaged DNA binding protein	0.001432113	0.04	0.12	0.15	0.07
AN8224	glutamyl-tRNA synthetase	0.001436575	0.27	0.20	0.09	-0.02
AN0248	PDI related protein A	0.001440284	0.13	-0.17	-0.18	0.20
AN6726	proteasome component Pre8, putative	0.001447586	-0.27	-0.65	-0.51	0.00
AN1050	3-ketoacyl-CoA ketothiolase (Kat1), putative	0.00145928	0.04	0.03	0.27	0.19
AN7511	putative 1,3-beta-transglucosylase, GH72 family	0.001459568	-0.18	-0.71	-0.24	-0.15
isn1 AN3222	IMP-specific 5'-nucleotidase 1	0.001505823	-0.23	-0.34	0.21	-0.51
AN1103	acetoacetyl-CoA synthase	0.001512069	0.06	-0.37	-0.04	-0.19
treB AN5635	Neutral trehalase (Alpha,alpha-trehalase)(Alpha,alpha-trehalose glucohydrolase)	0.001520343	0.07	0.20	-0.28	0.11
AN2878	conserved hypothetical protein	0.001530552	-0.18	-0.41	-0.30	0.12
AN2147	rRNA biogenesis protein RRP5, putative	0.001531644	0.13	0.36	0.24	0.36
AN4164	TPR repeat protein	0.001568825	-0.72	0.64	-0.40	0.07
AN3083	FAD binding domain protein	0.001574997	-0.04	-1.15	-0.45	-0.26
AN7817	conserved hypothetical protein	0.001584555	0.43	0.32	1.24	0.22
AN2092	Putative prolyl aminopeptidase Fragment	0.001600579	-0.24	-0.61	-0.56	0.15
AN10562	peptide methionine sulfoxide reductase	0.0016005918	0.07	0.01	0.21	0.22
AN5607	proteasome activator subunit 4, putative	0.001608586	0.17	-0.20	0.07	-0.16
jip5 AN5177	WD repeat-containing protein jip5	0.00161702	-0.18	-0.46	0.46	0.14
AN4105	erythromycin esterase, putative	0.001620444	0.11	0.09	-1.08	0.30
cysB cysE AN8057	Cysteine synthase (Csase)(O-acetylserine sulfhydrylase)(O-acetylserine (thiol)-lyase)(OAS-TL)	0.001624483	-0.23	-0.81	-0.24	0.24
AN8010	glycogen synthase	0.001628423	-0.23	-0.25	0.50	-0.22
AN4608	NmrA family transcriptional regulator, putative	0.001646441	0.29	0.28	0.30	0.32
AN6267	vesicular-fusion protein sec17	0.001646506	0.11	0.31	-0.22	-0.03
AN5666	MAP protein kinase MPKA	0.001680851	0.19	0.48	0.55	-0.24
AN9509	SAP domain protein, putative	0.00168889	-0.15	-0.38	-0.29	-0.36
AN5671	PH domain protein	0.001698423	0.02	0.26	-0.21	-0.19
AN0579	Isopentenyl diphosphate isomerasePutative uncharacterized protein	0.001704416	-0.25	-0.41	-0.32	-0.08
AN10771	translation initiation protein Sua5	0.00171149	-0.01	0.82	0.50	0.22
AN7299	curved DNA-binding protein (42 kDa protein)	0.001721553	-0.09	-0.40	0.24	0.17
AN4897	cell wall protein, putative	0.001739942	0.34	0.39	0.32	-0.03
nopA AN3361	putative bacteriorhodopsin /opsin, nopA	0.001739965	0.33	0.29	-0.25	-0.29
AN8274	mitochondrial DNA replication protein (Yhm2), putative	0.001747738	0.29	0.36	0.14	0.01
AN10700	DlpA domain protein	0.001760289	-0.25	-0.57	0.11	0.31
AN1263	S-adenosyl-L-homocysteine hydrolase	0.001769065	-0.01	-0.33	0.43	0.20
AN4458	snRNP assembly factor, putative	0.001772523	0.27	-0.07	0.11	0.56
AN3060	prefoldin subunit 6, putative	0.001773572	-0.55	-0.29	0.02	0.01
AN8764	aromatic ring-opening dioxygenase LigB subunit, putative	0.00178463	-0.19	0.03	0.19	0.21
AN6563	elongation factor 1-gamma, putative	0.001791416	0.04	0.40	0.49	-0.36
AN1149	conserved hypothetical protein	0.001800226	-0.17	0.30	0.08	0.37
AN10230	5'-methylthioadenosine phosphorylase (Meu1), putative	0.001809818	-0.06	-0.70	-0.47	0.06
AN6923	High-affinity hexose transporterPutative uncharacterized protein	0.001818194	0.16	0.39	-0.23	-0.10
bgfH AN3903	beta-1,4-glucosidase	0.001821672	0.04	-0.72	0.23	0.09
apdG AN8415	Acyl-CoA dehydrogenase	0.001824759	-0.06	0.13	0.07	-0.03
AN8273	Ubiquinol-cytochrome c reductase complex core protein 2	0.001827639	0.32	0.38	-0.06	0.06
AN8528	beta-lactamase	0.001829388	0.20	-0.27	0.36	-0.18
AN10844	hypothetical protein similar to fructose-2,6-bisphosphatase	0.001837542	0.36	0.23	-0.02	-0.11
AN1320	conserved hypothetical protein	0.001839092	0.17	-0.51	-0.04	0.05
AN9103	apoptosis-inducing factor	0.001866784	0.27	0.09	-0.03	0.27
dpp4 AN6438	hypothetical dipeptidyl aminopeptidase	0.001866815	-0.27	-0.71	-0.54	0.12
AN8203	glutamine dependent NAD synthetase	0.00187971	0.38	0.65	0.27	-0.17

AN4820	succinate semialdehyde dehydrogenase	0.001887899	0.14	0.46	0.50	-0.11
AN10233	6-phosphogluconate dehydrogenase	0.001896716	0.10	0.77	-0.09	-0.22
AN8566	catechol dioxygenase, putative	0.001978421	-0.13	0.91	-0.89	0.40
AN2068	RNA binding effector protein Scp160, putative	0.001987463	-0.03	0.41	-0.55	-0.01
AN4758	dsDNA-binding protein PDCD5, putative	0.002001496	-0.18	-0.07	-0.51	0.22
AN7278	glutamate decarboxylase	0.002010921	0.01	-0.60	-0.56	0.02
AN6775	acyl-CoA:6-aminopenicillanic-acid-acyltransferase, putative	0.00202161	-0.19	-0.47	0.44	-0.11
AN3726	conserved hypothetical protein	0.002078975	0.28	0.78	0.72	0.15
AN0495	formyltetrahydrofolate deformylase, putative	0.002097415	-0.19	-0.28	0.34	0.08
AN10552	acyl-CoA thioester hydrolase, putative	0.002104518	0.06	-0.43	-0.50	-0.14
AN10124	beta-glucosidase, putative	0.002127857	0.37	-0.71	1.14	0.15
AN10533	large subunit of trehalose 6-phosphate synthase	0.002137224	-0.19	0.27	-0.31	-0.19
AN3961	conserved hypothetical protein	0.002138913	-0.21	0.15	-0.28	0.41
AN2875	hypothetical protein similar to fructose 1,6-biphosphate aldolase	0.002140518	-0.13	-0.89	0.61	0.23
hxA AN5613	Xanthine dehydrogenase (Purine hydroxylase I)	0.002153488	-0.06	-0.47	-0.26	0.16
AN7085	beta-lactamase	0.002173497	0.08	0.63	-0.25	-0.19
AN4809	Glutaminase A	0.002176966	-0.27	-0.46	-0.20	0.08
AN2577	peroxisomal dehydratase, putative	0.002189251	0.18	0.32	-0.16	0.39
AN2455	essential protein with two zinc fingers	0.002192421	-0.12	0.44	-0.14	0.14
AN11187	conserved hypothetical protein	0.002236695	-0.17	-0.51	-0.31	0.10
AN5132	mitochondrial GTP/GDP transporter Ggc1, putative	0.002243567	0.31	0.40	0.19	0.07
AN4252	high expression lethality protein Hel10, putative	0.00224447	0.23	0.98	0.02	0.34
AN1923	alanine transaminase	0.002260713	-0.12	-0.31	0.43	0.15
AN1677	short chain dehydrogenase, putative	0.002266787	0.25	-0.35	0.40	0.66
AN1158	cell wall biogenesis protein phosphatase Ssd1, putative	0.002271141	0.05	0.34	-0.05	-0.26
AN4018	glutamate carboxypeptidase, putative	0.002276608	-0.01	-0.01	-0.29	-0.19
AN6677	COMPASS complex subunit Sdc1, putative	0.002303621	0.04	0.14	0.23	0.25
AN3916	glycerol kinase, putative	0.002328788	0.15	0.83	0.09	-0.64
AN11533	conserved hypothetical protein	0.002333355	0.25	-0.24	-0.49	0.86
AN10163	NADH-ubiquinone oxidoreductase 14 kDa subunit, putative	0.002335056	0.09	-0.20	-0.02	-0.14
pfs2 AN6160	Polyadenylation factor subunit 2	0.002379576	0.05	-0.46	0.70	-0.01
AN2116	NAD dependent epimerase/dehydratase, putative	0.002384944	0.13	0.36	0.05	-0.45
AN4865	nucleolin protein Nsr1, putative	0.002389077	0.86	-0.05	-0.72	0.50
pgkA pgk AN1246	Phosphoglycerate kinase	0.002395286	0.17	-0.12	0.43	0.28
AN7632	formaldehyde dehydrogenase	0.00245295	0.20	-0.70	-0.24	0.22
AN7819	conserved hypothetical protein	0.002466465	0.02	0.33	0.53	-0.68
AN3744	mitochondrial ribosomal protein DAP3, putative	0.002471487	-0.06	0.22	0.08	0.09
AN3733	Class I alpha-mannosidase 1A	0.002476646	-0.06	0.44	0.31	-0.16
AN10273	glutathione S-transferase	0.002481264	-0.28	-0.65	-0.61	0.03
AN5404	conserved hypothetical protein	0.002549991	-0.08	-0.17	0.23	-0.25
metG AN7051	Cystathione beta-lyase	0.002553703	-0.11	-0.11	0.13	0.19
AN6031	oxidoreductase, 2-nitropropane dioxygenase family, putative	0.002562595	0.15	0.54	0.22	0.12
clu1 tif31 AN4908	eukaryotic translation initiation factor 3 subunit CLU1/TIF31, putative	0.002612052	0.05	0.63	-0.07	-0.14
AN5618	Spindle pole body protein An-Cdc31	0.002612251	-0.06	0.29	-0.17	0.06
mclA AN8755	Methylisocitrate lyase Precursor	0.002616979	-0.20	-0.60	0.41	0.12
AN1851	t-complex protein 1, theta subunit, putative	0.002643271	0.01	-0.02	-0.33	0.06
AN11072	diacylglycerol acyltransferase type 2A	0.002652319	-0.08	-0.08	0.07	0.15
AN8072	conserved hypothetical protein	0.00265601	-0.05	0.52	-0.13	0.08
AN5447	hypothetical glutamic acid decarboxylase	0.002656921	-0.17	-0.29	0.17	-0.03
AN3937	Cwf1 domain protein	0.002665574	0.41	0.26	0.05	0.12
AN1917	hypothetical protein similar to mitochondrial dicarboxylate/tricarboxylate transporter	0.002678629	0.13	0.29	0.01	-0.03
AN5939	conserved hypothetical protein	0.00268221	-0.07	-0.52	-0.17	0.01
casA AN5712	Metacaspase-1 Precursor	0.002683527	-0.22	0.58	0.28	-0.19
AN4557	mitochondrial inner membrane AAA protease Yta12, putative	0.00269771	-0.01	0.19	-0.47	-0.20
AN2393	short chain oxidoreductase/dehydrogenase, putative	0.002723633	-0.13	-0.75	0.20	0.14
AN2337	hypothetical protein ANIA_02337	0.00275086	-0.11	0.28	0.08	-0.13
gpgA AN2742	G protein gamma subunit	0.002761179	0.24	0.31	0.28	-0.42
AN9359	chromatin remodeling complex subunit (Arp9), putative	0.002763727	0.08	0.23	0.17	-0.23
AN2777	conserved hypothetical protein	0.002786044	-0.04	-0.72	-0.07	0.12
AN11046	conserved hypothetical protein	0.00278676	-0.42	-0.69	-0.35	-0.22
AN7687	mitochondrial outer membrane translocase receptor (TOM70), putative	0.002794636	0.15	0.26	0.02	-0.43
AN5784	putative proteasome core component, beta 6 subunit	0.002846447	-0.07	-0.67	-0.61	0.00
AN0941	alpha-1,4-glucosidase	0.002857414	0.00	-0.53	-0.42	0.17
pkaA AN6305	CAMP-dependent protein kinase PKAC catalytic subunitPutative uncharacterized protein	0.002956056	0.26	0.33	-0.02	-0.31
AN3013	glycosyl hydrolase, putative	0.002967263	-0.09	-0.35	-0.16	-0.01
AN5529	COTA	0.002975095	-0.12	0.48	-0.38	-0.15
AN4288	NADH-ubiquinone oxidoreductase, subunit G, putative	0.002981143	-0.02	0.05	-0.06	0.13
AN6906	cell cycle control protein (Cwf8), putative	0.002981432	-0.02	-0.21	-0.25	0.00
aglcC AN8138	AGLC ASPNG Alpha-galactosidase C (Melibiose)Alpha-galactosidase;	0.002991529	-0.24	-0.32	0.74	-0.09
AN1616	conserved hypothetical protein	0.003012615	0.22	-0.44	0.18	0.36
AN10202	Heat shock protein 70	0.003024501	-0.19	0.92	-0.24	0.37
AN3121	conserved glutamic acid-rich protein	0.003054441	0.32	0.26	0.19	0.27
AN2425	protein phosphatase regulatory subunit Gac1, putative	0.003117819	-0.08	0.37	0.48	-0.07
AN6700	elongation factor 3	0.003131151	0.13	0.50	0.23	-0.14
AN4457	20S proteasome beta-type subunit	0.003152861	-0.20	-0.69	-0.55	0.06
AN7594	DUF636 domain protein	0.003173778	0.10	0.68	0.48	0.16
AN5144	hypothetical protein similar to 6-phosphofructo-2-kinase	0.003180692	0.49	0.60	0.03	-0.02
AN8720	phosphoglycerate mutase family protein	0.003183989	-0.09	-0.07	-0.02	-0.04
nmrA AN8168	Nitrogen metabolite repression regulator NmrA	0.003193289	0.47	0.42	0.03	0.06
AN8223	conserved hypothetical protein	0.003210896	-0.24	-0.18	0.03	-0.06

bgf AN10482	beta-1,4-glucosidase	0.003222709	0.09	-0.29	0.10	-0.03
AN5719	60S acidic ribosomal protein P1	0.003233275	-0.11	0.43	0.59	0.41
AN0635	conserved hypothetical protein	0.003252882	-0.10	-0.03	0.42	0.41
AN11070	vacuolar aspartyl aminopeptidase Lap4, putative	0.003279675	-0.02	-0.58	-0.48	-0.04
AN7181	conserved hypothetical protein	0.003289303	-0.25	-0.55	-0.32	0.19
AN4462	pyruvate carboxylase	0.003295788	-0.03	0.20	-0.09	-0.20
AN3626	phosphoribosyl-aminonimidazole carboxylase	0.003313367	-0.12	-0.21	0.15	-0.01
AN3590	conserved hypothetical protein	0.003331809	-0.16	-0.52	-0.60	-0.03
AN6558	DNA-directed RNA polymerase I and III 14 KDa polypeptide	0.003352567	0.04	-0.13	0.29	-0.03
AN2334	hypothetical protein similar to fructose/tagatose bisphosphate aldolase	0.003371154	-0.05	-0.01	-0.05	0.11
mndB AN3368	Beta-mannosidase	0.003387269	0.13	-0.74	1.00	-0.44
AN2306	Ubiquinol-cytochrome c reductase	0.00340696	0.20	0.47	-0.27	0.05
AN0142	37S ribosomal protein S5	0.003438576	-0.02	-0.08	-0.05	0.31
AN10032	ATP synthase delta chain, mitochondrial precursor, putative	0.003455688	-0.30	-0.07	0.29	0.46
AN2762	glutaryl-CoA dehydrogenase, putative	0.003469845	-0.28	-0.34	0.15	0.07
AN1763	oxidoreductase, short-chain dehydrogenase/reductase family	0.003501892	0.07	-0.59	-0.23	0.16
AN9503	glycosyltransferase, putative	0.003510658	-0.01	-0.42	-0.31	0.10
AN6792	glycerol-3-phosphate dehydrogenase	0.003526436	0.03	0.46	0.26	-0.07
dd1 AN6741	DNA damage-inducible protein 1	0.003538347	-0.06	0.21	-0.38	0.01
AN0330	indoleamine 2,3-dioxygenase pyrrole 2,3-dioxygenase)	0.003555843	-0.11	-0.48	-0.25	0.03
AN4443	Cobalamin-independent methionine synthase	0.003571834	-0.03	-0.60	-0.18	0.03
AN3577	citrate lyase beta subunit, putative	0.003574809	0.20	0.30	-0.51	0.15
AN1462	cytoskeleton assembly control protein Sla1, putative	0.00357805	-0.32	-0.12	0.01	-0.07
AN5971	NADH-ubiquinone oxidoreductase 299 kDa subunit, putative	0.003590119	-0.16	0.15	-0.50	0.16
AN5658	gamma-glutamyltranspeptidase	0.003627903	-0.19	-0.68	-0.40	0.14
AN1418	glucosamine-6-phosphate deaminase, putative	0.00362798	-0.05	-0.45	0.25	0.04
AN3707	beta-alanine synthase, putative	0.003633574	-0.05	-0.50	-0.02	0.04
AN10379	glutathione S-transferase	0.003641267	-0.02	-0.63	-0.25	-0.07
AN2993	DUF124 domain protein	0.003679542	0.11	0.10	0.24	-0.12
AN4615	actin cortical patch protein Sur7, putative	0.003706584	0.12	0.49	-0.17	-0.44
AN3895	CAIB/BAIF family enzyme	0.003732178	0.08	-0.45	-0.11	0.09
AN2532	copper amine oxidase 1	0.003750955	-0.10	-0.78	-0.02	-0.15
AN2815	Mannitol 2-dehydrogenase (M2DH)(MDH)	0.003765549	0.60	0.17	0.07	0.34
AN6179	hypothetical protein similar to SPBC24C6.01c	0.003804907	-0.17	0.55	-0.33	0.36
AN10901	hypothetical glycine cleavage system P protein	0.003813755	0.00	-0.29	-0.03	0.18
AN0075	protein disulfide-isomerase	0.003826586	0.03	0.74	0.01	-0.33
AN1868	Fe-containing alcohol dehydrogenase, putative	0.003835022	-0.03	-0.51	-0.10	0.28
AN11045	actin interacting protein 2	0.003852586	-0.21	-0.71	-0.39	0.22
AN4127	hypothetical protein ANIA_04127	0.003860671	0.32	0.12	-0.14	0.11
AN10311	Cell wall mannoprotein MnpA [Source:UniProtKB/TREMBL;Acc:Q8TG08], partial	0.003880033	0.08	0.33	-1.27	-0.14
AN2479	acetyltransferase, GNAT family, putative	0.003923108	-0.07	0.08	0.48	0.29
AN4230	CAIB/BAIF family enzyme	0.003980795	-0.30	-0.44	-0.04	0.31
AN0365	conserved hypothetical protein	0.003990374	-0.28	0.52	0.55	0.50
AN4474	conserved hypothetical protein	0.003990754	0.51	0.54	0.04	0.02
AN9403	pyruvate dehydrogenase E1 component, beta subunit	0.004003018	0.22	-0.60	0.25	0.23
AN8815	hypothetical oxidoreductase	0.004006017	0.32	1.25	-0.12	-0.21
AN10584	iron-sulfur cluster biosynthesis protein Isd11, putative	0.004008602	-0.04	0.17	-0.57	-0.37
AN3090	G protein alpha subunit homolog GanAp	0.004013683	0.03	0.38	0.03	-0.08
stcl AN7816	Putative sterigmatocystin biosynthesis lipase/esterase stcl	0.004025519	0.03	0.47	0.95	-0.07
AN5007	class II aldolase/adducin domain protein	0.004095953	-0.11	-0.48	-0.20	-0.34
AN10257	KH domain RNA binding protein	0.004096093	0.14	0.16	0.20	-0.34
AN9049	transesterase (LovD), putative	0.004101727	-0.06	-0.71	0.17	0.16
AN4449	proteasome component Pup3, putative	0.004107057	-0.33	-0.95	-0.49	0.18
AN10276	RNP domain protein , partial	0.004143916	-0.03	-0.23	-0.41	0.06
AN1394	Putative uncharacterized proteinSeptin;	0.004146394	-0.16	0.68	0.61	-0.19
AN1882	NADH-dependent flavin oxidoreductase, putative	0.004161503	-0.11	-0.56	-0.40	0.19
AN7491	ubiquitin C-terminal hydrolase L3	0.004188885	-0.19	0.43	-0.81	-0.12
egd2 AN6630	Nascent polypeptide-associated complex subunit alpha (NAC-alpha)(Alpha-NAC)	0.004199565	0.09	0.50	-0.35	0.23
lap1 AN7035	aminopeptidase, putative	0.00420344	-0.22	-0.05	0.12	-0.23
AN8234	hypothetical protein ANIA_08234	0.004237766	0.49	0.27	-0.35	0.23
AN10559	3-oxo-5-alpha-steroi d 4-dehydrogenase family protein	0.004275997	0.30	0.68	0.02	-0.25
AN2415	DNA-directed RNA polymerase I and III subunit Rpc40, putative	0.004276945	-0.15	-0.27	0.32	-0.01
AN3830	hypothetical threonine dehydratase	0.004307478	0.17	0.61	0.50	-0.13
AN7353	oxidoreductase family, NAD-binding Rossmann fold protein	0.004309354	0.15	0.99	0.22	-0.24
AN11102	ubiquitin C-terminal hydrolase, putative	0.004349073	0.07	0.62	0.13	0.10
AN8163	oxidoreductase, short-chain dehydrogenase/reductase family	0.004384345	0.02	-0.70	0.36	0.33
AN8074	MATH and UCH domain protein, putative	0.004406934	0.21	-0.14	0.29	-0.18
AN0753	nuclear segregation protein (Bfr1), putative	0.004411706	-0.06	0.25	-0.25	0.39
AN2325	alpha-1,2-mannosidase family protein	0.004413845	0.15	-0.44	-0.66	0.05
AN8829	conserved hypothetical protein	0.004424588	0.37	-0.35	-1.29	1.03
AN0806	WD repeat protein	0.004450682	0.15	-0.40	-0.22	0.35
AN4390	GPI-anchored cell wall organization protein Ecm33	0.004470284	0.13	-0.38	0.30	-0.02
AN3034	Putative uncharacterized proteinSUAPRGAl;	0.004474966	0.19	0.53	-0.35	0.33
AN1710	Aspartyl-tRNA synthetase, hypothetical mitochondrial protein	0.00451938	0.32	0.45	-0.55	0.02
AN6526	leucyl-tRNA synthetase	0.00453099	0.07	0.36	-0.07	-0.11
AN2230	FAD dependent oxidoreductase superfamily	0.004537325	0.03	-0.34	0.42	0.45
AN8664	dienelactone hydrolase family protein	0.004543631	-0.28	-0.59	-0.44	0.27
AN10030	hypothetical serine protease	0.004573338	-0.07	-0.64	-0.54	0.01
ecm14 AN6119	zinc carboxypeptidase, putative	0.004653382	-0.04	-0.54	-0.51	0.11
AN5662	threonyl-tRNA synthetase, putative	0.004670351	0.19	0.28	0.42	0.28

pela AN2331	Pectin lyase	0.004689196	-0.50	-0.54	-0.36	0.08
AN10863	FAD dependent oxidoreductase superfamily	0.004705647	0.10	-0.49	-0.21	0.07
cnaA AN8820	Serine/threonine-protein phosphatase 2B catalytic subunit (Calmodulin-dependent calcineurin A subunit)	0.004774815	-0.26	0.52	0.21	-0.11
AN2930	fumarylacetoacetate hydrolase family protein	0.004816952	-0.29	-0.74	-0.20	0.18
AN0131	secretory pathway protein Ssp120, putative	0.004832111	-0.65	-0.67	-0.61	-0.19
AN6804	conserved hypothetical protein	0.004914285	0.18	0.44	0.16	-0.20
AN5994	YjeF domain protein	0.004925494	-0.03	-0.39	0.09	0.19
AN7000	succinyl-CoA synthetase beta subunit, putative	0.004984124	0.19	0.53	0.11	-0.26
AN7268	short chain dehydrogenase/reductase, putative	0.00498533	0.19	1.10	0.13	-0.45
AN5715	40S ribosomal protein S26E	0.005072138	0.31	0.48	-0.02	-0.07
AN7711	MutT/nudix family protein	0.005079782	-0.11	-0.40	-0.06	0.07
AN4064	ADP,ATP carrier protein	0.00509465	0.29	0.41	0.12	-0.01
AN8024	hydrolase, carbon-nitrogen family, putative	0.005098692	-0.19	-0.59	-0.33	0.12
cprA AN0595	NADPH-cytochrome P450 reductase	0.005128788	0.25	0.17	0.28	0.15
AN8118	cytochrome c oxidase subunit Va, putative	0.005152552	-0.06	0.57	-0.62	0.07
AN7044	histidinol phosphatase	0.005165277	-0.10	-0.62	-0.49	-0.03
AN1545	hypothetical protein similar to protein phosphatase 2A regulatory B subunit	0.00516677	0.10	0.01	0.00	-0.10
AN10743	BAR domain protein	0.005174549	-0.43	0.16	-0.37	0.01
AN2921	conserved hypothetical protein	0.005211676	0.22	-0.48	0.20	0.24
pan1 AN4270	Actin cytoskeleton-regulatory complex protein pan1	0.005224297	-0.32	0.43	-0.42	0.04
AN4575	hypothetical protein ANIA_04575	0.005291089	-0.10	0.02	-0.29	-0.34
AN6185	conserved hypothetical protein	0.005310317	0.23	-0.33	-0.06	0.30
AN5637	short chain dehydrogenase/reductase family	0.005340504	-0.09	-0.28	-0.04	0.57
AN0875	homoserine acetyltransferase family protein	0.005349606	0.17	-0.55	0.53	0.17
hat1 AN6214	Histone acetyltransferase type B catalytic subunit	0.005361015	0.19	0.67	0.12	-0.11
AN6547	proteasome component Pre5, putative	0.005414395	-0.15	-0.70	-0.48	0.00
AN0951	putative b-zip transcription factor	0.005419265	-0.03	0.07	-0.12	0.12
AN6232	Vacuolar ATP synthase subunit B Fragment	0.005452967	0.26	0.57	-0.04	0.19
AN1639	thioredoxin, putative	0.005457038	-0.13	-0.29	0.55	0.14
AN1469	DnaJ domain protein	0.005464069	0.16	0.11	0.05	0.13
AN1965	phosphoribosyl diphosphate synthase isoform 4	0.005486228	-0.05	0.29	0.18	-0.29
AN8639	synthase subunit of trehalose-6-phosphate synthase/phosphatase complex	0.00549627	0.17	0.41	-0.10	-0.20
pacC AN2855	pH-response transcription factor pacC/RIM101 Precursor	0.005497602	-0.03	0.15	0.26	0.31
AN6723	amidohydrolase family protein	0.00553432	-0.09	-0.60	-0.66	0.29
AN5999	carbamoyl-phosphate synthetase, arginine-specific large chain	0.005539247	0.19	0.55	-0.06	0.36
fal1 AN8016	ATP-dependent RNA helicase fal1	0.005595672	0.21	0.07	0.10	-0.26
AN9067	TINC	0.005618719	0.23	0.63	0.22	-0.26
AN10278	electron transfer flavoprotein, beta subunit, putative	0.005621547	-0.11	0.15	-0.29	0.02
tubA AN0316	Tubulin alpha-1 chain	0.005647633	0.12	0.60	0.23	-0.39
AN1084	hypothetical protein similar to elongation factor EF-Tu	0.005657532	-0.14	0.45	-0.11	-0.09
AN5731	chorismate synthase	0.005728865	0.19	-0.26	-0.07	0.22
AN0779	exo-beta-1,3-glucanase, putative	0.005834802	0.06	-0.63	-0.66	-0.04
AN5110	YdiU domain protein	0.005852286	0.10	0.37	0.18	0.35
AN0280	glycosyl hydrolase, putative	0.0058787398	0.24	-0.62	-0.02	-0.24
AN10194	pre-mRNA splicing helicase, putative	0.005893443	-0.21	-0.13	-0.55	-0.10
AN11278	DUF543 domain protein	0.005899425	0.02	0.12	-0.47	-0.35
AN0764	catechol dioxygenase, putative	0.005997058	0.11	-0.07	0.00	0.02
AN4655	iron-sulfur cofactor synthesis protein (Isu1), putative	0.006002715	-0.15	0.46	-0.14	0.06
AN8756	phenol monooxygenase, putative	0.006008986	0.17	0.05	0.70	0.15
AN2085	proteasome component Pup1, putative	0.006044785	-0.13	-0.67	-0.57	0.14
AN6876	oxidoreductase, FAD-binding, putative	0.006164952	0.11	-0.24	-0.05	0.15
npl4 AN0295	Nuclear protein localization protein 4	0.006217246	-0.01	-0.22	-0.46	0.18
hcr1 AN5745	Eukaryotic translation initiation factor 3 subunit J (eIF3j)	0.00621795	-0.19	0.02	-0.61	0.53
AN2469	short chain dehydrogenase, putative	0.006224475	0.01	-0.62	-0.08	-0.01
tim50 AN4490	Mitochondrial import inner membrane translocase subunit tim50 Precursor	0.006239888	-0.06	-0.08	-0.49	0.21
AN4997	putative phosphatidylinositol transporter	0.006279116	-0.10	0.04	0.04	-0.20
AN0351	Glycerol 3-phosphate dehydrogenase (NAD+)-Putative uncharacterized protein	0.006293354	-0.22	0.12	0.20	0.19
AN8662	conserved hypothetical protein	0.006325362	-0.30	-0.39	0.20	-0.17
AN6505	transcriptional corepressor	0.006356435	0.30	0.31	-0.21	0.04
hog1 hog4 sakA AN1017	Mitogen-activated protein kinase hog1 (MAP kinase hog1)	0.006357676	0.09	0.67	0.18	-0.20
AN5134	Glutamate synthase Fragment	0.006359806	0.26	0.18	0.19	-0.31
AN10399	short-chain dehydrogenase/reductase, putative	0.006395359	0.12	0.46	0.25	-0.18
AN1059	Carnitine acetyl transferase FacC	0.006431938	0.24	0.15	0.38	-0.10
AN10392	conserved hypothetical protein	0.006462568	-0.12	-0.53	-0.13	0.06
AN0034	dihydroxyacetone kinase	0.006488375	0.28	0.55	-0.02	-0.05
AN6066	isochorismatase family hydrolase, putative	0.00649277	-0.16	-0.79	-0.34	0.19
AN2565	conserved hypothetical protein	0.006495805	-0.24	-0.58	-0.66	-0.22
AN7350	translation initiation factor 4B	0.006495852	-0.09	0.20	-0.65	0.08
AN7579	26S proteasome regulatory subunit SSA	0.006505232	0.04	-0.03	0.03	0.17
AN2238	DnaJ domain protein Psi, putative	0.006583552	0.08	0.18	-0.61	0.15
AN3740	conserved hypothetical protein	0.006606983	0.18	-0.78	-0.28	-0.11
AN8015	splicing factor 3a subunit 3, putative	0.006667379	-0.02	0.00	-0.28	0.07
AN0297	NADH-quinone oxidoreductase Pst2, putative	0.0067227	-0.22	-0.59	-0.37	0.20
AN10437	NGG1 interacting factor Nif3, putative	0.006788821	-0.25	-0.50	-0.46	0.18
AN10762	thiamin biosynthesis protein (Thi-4), putative	0.006815503	0.17	0.23	-0.69	0.13
AN5737	short chain dehydrogenase, putative	0.006823977	-0.07	-0.79	-0.41	0.02
AN4024	conserved hypothetical protein	0.006858559	0.13	0.42	-0.16	-0.02
AN2316	hypothetical protein similar to cytochrome c oxidase polypeptide V, mitochondrial precursor	0.006883844	0.23	0.47	0.18	0.06
AN9322	Nmra-like family protein	0.006946642	0.04	-0.66	0.40	0.11
AN7680	hypothetical protein ANIA_07680	0.007059399	-0.28	0.44	-0.07	0.29

AN7600	SE, putative sulfite reductase beta subunit-hemoprotein,ferredoxin oxidoreductase	0.007073208	-0.14	-0.46	-0.14	0.03
AN3748	conserved hypothetical protein:ATP-phosphoribosyltransferase	0.007082006	-0.10	-0.54	-0.38	0.02
AN1409	acetyl-CoA acetyltransferase, putative	0.007097504	-0.21	-0.49	0.15	0.19
yA AN6635	ccase-1 Precursor (Laccase I)(Benzenediol:oxygen oxidoreductase 1)(Urishiol oxidase 1)(Diphenol oxidase 1)	0.007119641	0.15	-0.33	-0.39	0.30
AN1503	Dihydrodipicolinate synthase-like protein AN1503 (DHDPS-like protein)	0.007183291	-0.09	-0.54	-0.42	0.46
AN8054	proteasome component Pre6, putative	0.007194651	-0.11	-0.78	-0.70	0.04
AN0912	hypothetical 3-isopropylmalate dehydrogenase	0.007201905	0.20	-0.03	-0.16	-0.02
orLA AN3441	Trehalose-6-phosphate phosphatase	0.007203827	0.16	0.36	0.30	-0.19
AN4086	phenylalanyl-tRNA synthetase, beta subunit	0.00721468	-0.16	-0.12	0.35	-0.13
AN4532	catechol dioxygenase, putative	0.007261731	0.24	-0.23	0.53	0.40
AN11543	conserved hypothetical protein	0.007265884	-0.14	1.03	0.94	0.09
alcC adh3 AN2286	Alcohol dehydrogenase 3 (Alcohol dehydrogenase III)(ADH III)	0.007292997	0.13	-0.01	0.00	0.29
AN4807	hypothetical protein AN1A_04807	0.007395563	0.88	-0.35	1.11	-0.35
AN0390	conserved hypothetical protein	0.007492657	0.19	0.34	-0.21	-0.12
AN9513	conserved hypothetical protein	0.007530141	0.06	0.00	-0.06	0.08
AN1063	hypothetical protein similar to possible NADH-ubiquinone oxidoreductase	0.00756016	0.23	0.44	0.12	0.13
AN5610	aminoacidate reductase large subunit	0.007575412	0.10	-0.17	0.24	0.23
AN4905	Putative uncharacterized proteinTheta class glutathione S-transferase;	0.007580282	-0.25	-0.66	0.00	-0.21
cbhA celD AN5176	Putative beta-1,4-glucan-cellulohydrolyasePutative uncharacterized protein	0.007634041	0.45	-0.44	-0.12	-0.35
AN2870	beta-N-acetylglucosaminidase, putative	0.007639674	-0.10	-0.49	0.59	0.06
AN4965	Ccr4-Not transcription complex subunit (NOT1), putative	0.007709189	-0.02	0.25	0.18	-0.15
AN5356	Carnitine/acyl carnitine carrierPutative uncharacterized protein	0.007722178	0.18	0.05	-0.09	-0.01
AN5981	SH3 domain protein	0.007739288	-0.35	0.10	-0.43	-0.07
AN4496	polarized growth protein (BoI2), putative	0.007792779	-0.19	0.53	0.04	-0.29
AN1841	NmrA-like family protein, putative	0.007798106	0.11	-0.46	0.03	0.09
AN5872	alpha subunit of the 20S proteasome	0.007869697	-0.08	-0.59	-0.46	0.01
AN10103	HMG box protein, putative	0.007892046	-0.20	0.06	-0.44	0.58
AN0861	autophagy-related protein Atg27	0.007909119	-0.21	0.27	-0.27	-0.22
fpr4 AN10489	FK506-binding protein 4 (Peptidyl-prolyl cis-trans isomerase)(PPIase)(Rotamase)	0.007912628	-0.27	-0.20	-0.37	0.20
AN4402	outer mitochondrial membrane protein porin	0.007956918	0.16	0.52	0.26	0.02
AN3923	ubiquitin-protein ligase E3 component (UBR1), putative	0.00797441	0.10	0.40	0.24	-0.22
AN4803	hypothetical protein similar to 40S ribosomal protein S9	0.007977307	0.16	0.16	0.41	-0.10
AN5454	class V chitinase ChiB1	0.007987915	-0.21	-0.20	-0.38	-0.23
AN2343	nitroreductase family protein, putative	0.008002398	0.00	-0.52	-0.26	0.16
abnC AN8007	Endo-alpha-1,5-arabinanasePutative uncharacterized protein	0.008044397	0.13	-0.94	-0.79	0.16
hex1 AN4695	Woronin body major protein	0.0080949	-0.16	-0.35	-0.76	-0.33
AN4956	hypothetical acetolactate synthase, large subunit, biosynthetic	0.008099766	0.15	0.56	0.17	-0.04
AN3954	hypothetical protein similar to 6-phosphogluconate dehydrogenase	0.008142467	0.06	0.35	0.33	0.20
AN8071	conserved hypothetical protein similar to striatin	0.008174179	-0.18	0.27	-0.44	-0.38
AN10839	conserved hypothetical protein	0.008221763	-0.01	0.07	0.20	0.20
AN4174	glyoxalase	0.008269023	-0.19	-0.67	-0.77	-0.01
AN5068	conserved hypothetical protein	0.008271163	-0.07	-0.61	-0.13	0.08
AN4081	cysteine dioxygenase Cdo1, putative	0.00835452	-0.18	-0.21	-0.32	-0.18
AN5109	ketoreductase, putative	0.008355824	-0.15	-0.54	-0.61	0.24
AN8861	nucleoside triphosphatase	0.008366097	0.02	0.37	0.12	-0.33
AN9394	coenzyme A transferase, putative	0.008523548	0.00	-0.42	-0.39	0.00
AN1104	mitochondrial processing peptidase alpha subunit, putative	0.008608041	0.24	0.55	-0.50	-0.19
abfc AN1277	Alpha-arabinofuranosidasePutative uncharacterized protein	0.008677497	-0.20	-0.76	-0.22	0.05
AN1204	conserved hypothetical protein	0.008677539	-0.23	-0.30	-0.29	-0.29
AN3382	Putative uncharacterized proteinSalicylate 1-monooxygenase;	0.008685531	-0.29	0.25	-0.11	-0.19
hxN5 AN91782	conserved hypothetical protein	0.008697411	0.06	-0.47	-0.20	0.15
AN5162	pyruvate dehydrogenase E1 component, alpha subunit	0.008707211	0.28	-0.64	0.26	0.32
ipnA ips AN2622	Isopenicillin N synthetase (Isopenicillin N synthase)(IPNS)	0.008723818	-0.36	-0.55	0.62	0.15
AN7230	cellobiose dehydrogenase	0.008732937	-0.21	-0.82	-0.24	0.29
AN4613	37S ribosomal protein Rsm22	0.008783077	-0.26	0.38	-0.46	0.35
AN3605	conserved hypothetical protein	0.008855026	0.10	-0.34	0.08	0.29
AN10896	conserved hypothetical protein	0.008871657	0.35	0.34	0.42	-0.25
AN6919	RNA annealing protein YraJ, putative	0.008907157	0.15	0.44	-0.44	0.73
AN4245	neutral/alkaline nonlysosomal ceramidase, putative	0.008946851	0.07	-0.49	-0.05	-0.07
AN1216	Glycerol-3-phosphate phosphatasePutative uncharacterized protein	0.008959455	0.02	1.07	0.15	-0.33
AN0797	hypothetical histidine biosynthesis trifunctional protein	0.008959562	-0.24	-0.56	0.25	0.13
AN8808	hypothetical protein ANIA_08808	0.009000421	0.11	-0.37	-0.08	0.06
nip1 AN7105	Eukaryotic translation initiation factor 3 subunit C (eIF3c)	0.009039277	0.00	0.15	-0.35	0.04
AN8853	ERF1 PODAN Eukaryotic peptide chain release factor subunit 1 (ERF1) (Eukaryotic release factor 1)	0.009070585	-0.21	0.17	-0.32	-0.26
AN5996	60S acidic ribosomal protein P2/allergen Asp F 8	0.009078085	-0.13	0.21	-0.55	-0.01
AN0252	ATP synthase gamma chain, mitochondrial precursor, putative	0.009194945	0.02	0.47	0.06	0.24
AN0809	DNA-directed RNA polymerase Fragment	0.009219141	0.33	0.34	-0.07	-0.09
axeA aceA AN6093	Acetylxylan esterase	0.009287298	0.08	-0.73	0.13	-0.15
AN6382	conserved hypothetical protein	0.009346175	0.04	-0.50	0.48	0.02
AN3601	conserved hypothetical protein	0.009377408	-0.03	-0.46	0.08	-0.19
AN0788	epoxide hydrolase, putative	0.009394739	0.01	-0.33	0.32	0.01
AN7708	aldo-keto reductase, putative	0.009423338	0.31	-0.40	0.60	0.30
AN0504	Serine/threonine protein phosphatase	0.009498168	-0.18	-0.03	0.12	0.10
AN10495	coenzyme A transferase, putative	0.009547707	0.48	-0.13	-0.41	0.60
tpsA AN5523	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] (Trehalose-6-phosphate synthase)	0.009565912	0.05	0.71	0.18	-0.39
AN9093	zinc knuckle nucleic acid binding protein, putative	0.009609102	0.17	-0.39	-0.28	0.35
AN9138	acetamidase	0.009628494	0.26	0.67	0.20	-0.07
AN4525	cytochrome c subunit Vb, putative	0.009630117	-0.08	0.29	-0.60	-0.02
AN5762	CFEM domain protein, putative	0.00967142	-0.07	-0.08	-0.27	-0.12
AN10930	FAD-dependent oxygenase, putative	0.009782186	-0.05	-0.55	-0.89	0.22

AN1015	hypothetical protein similar to glycogen phosphorylase 1	0.009808772	0.21	0.08	0.22	-0.03
AN10476	inosine-5'-monophosphate dehydrogenase	0.009850402	0.06	0.10	0.46	0.26
AN3017	epoxide hydrolase, putative	0.01001819	0.02	-0.70	0.31	0.20
xlnA AN3613	Endo-1,4-beta-xylanase A Precursor (Xylanase A)(1,4-beta-D-xylan xylanohydrolase A)	0.01004576	0.15	-0.48	-0.05	-0.26
bgIM AN7396	beta-glucosidase	0.01010688	0.19	-0.72	0.29	0.21
AN10079	urease, urea amidohydrolase alpha subunit	0.01017724	-0.07	-0.34	0.14	-0.17
AN6512	ABC transporter	0.01021714	-0.26	-0.45	0.25	0.27
AN6394	acyl-CoA dehydrogenase family protein	0.01026138	0.05	-0.13	0.26	-0.13
AN10981	GTP cyclohydrolase II, putative	0.01026226	0.04	0.62	-0.15	-0.10
AN6060	eukaryotic translation initiation factor subunit eIF-4F, putative	0.0102898	-0.26	0.20	-0.48	-0.02
AN3785	component of the chromatin assembly complex	0.01028995	0.00	0.41	0.76	-0.14
AN8547	glucose-methanol-choline oxidoreductase	0.01030665	0.23	-0.44	0.48	0.30
AN6256	peptidyl prolyl cis-trans isomerase Cyclophilin, putative	0.01036783	0.00	-0.24	-0.53	0.02
AN3595	50S ribosomal protein L36, putative	0.01039537	0.20	1.12	0.22	0.34
AN8797	conserved fungal protein	0.01042285	0.15	-0.37	0.37	0.08
AN1638	hypothetical protein similar to aminopeptidase	0.01049627	-0.20	-0.70	-0.62	0.10
hsp70 AN5129	Heat shock 70 kDa protein (HSP70)	0.01052294	0.26	0.53	-0.18	0.48
AN11053	conserved hypothetical protein	0.01056394	-0.10	-0.39	0.17	0.02
AN6918	conserved hypothetical protein	0.01060602	0.12	-0.72	0.35	0.45
AN0285	6-phosphogluconolactonase, putative	0.01061726	-0.14	-0.42	-0.10	0.33
AN5305	DUF1680 domain protein	0.01064209	-0.16	-0.50	-0.03	-0.24
AN4547	Coatomer subunit gamma, putative	0.01064246	0.03	1.00	0.60	-0.14
AN5793	proteasome subunit alpha type 3, putative	0.01074768	-0.12	-0.70	-0.50	-0.01
AN1480	ureidoglycolate hydrolase, putative	0.01078994	-0.44	-0.36	0.43	0.26
AN9080	L-PSP endoribonuclease family protein (Hmf1), putative	0.01079397	-0.23	-0.63	-0.54	-0.02
AN1427	DUF895 domain membrane protein	0.01079578	-0.02	0.66	-0.13	0.46
AN2769	transcription initiation factor TFIID subunit 12, putative	0.01082118	-0.18	0.80	0.11	0.05
AN8430	Kelch repeat protein	0.01085894	0.21	0.40	-0.17	-0.09
AN6341	putative coronin homolog	0.01086635	0.23	0.97	0.41	0.22
AN2967	tRNA dihydrouridine synthase (Smm1), putative	0.01086697	-0.10	-0.04	-0.28	-0.16
AN5918	Catalase	0.01091855	0.36	0.24	0.61	0.17
AN0866	Hsp70 family protein	0.01104479	0.27	0.32	-0.07	-0.30
phpA AN6391	Serine/threonine-protein phosphatase PP2A catalytic subunit (Protein phosphatase 2a)	0.01109713	-0.13	-0.07	0.11	0.16
AN10150	Putative beta-transglucosidase. Family GH17. A fumigatus Bgt1-like	0.01114708	0.26	0.11	0.19	0.09
AN1188	nuclear mRNA splicing factor-associated protein, putative	0.01115142	0.14	0.13	-0.27	0.42
AN7590	hypothetical protein similar to NADP-dependent mannitol dehydrogenase	0.01119051	0.27	-0.66	0.37	0.29
AN4250	mitochondrial carrier protein (Ymc1), putative	0.01131567	0.19	0.79	0.44	0.03
tdIB AN8514	Putative uncharacterized protein TdIB;	0.0113378	-0.02	-0.90	0.60	-0.29
AN0775	hydroxyisocaproate dehydrogenase, putative	0.0113397	0.01	-0.58	0.69	0.14
AN2914	arginosuccinate lyase	0.01154698	-0.16	-0.51	0.25	0.14
easD AN2549	conserved hypothetical protein	0.01165248	0.42	0.20	0.20	0.22
AN6812	conserved hypothetical protein	0.01165878	0.37	-0.10	0.11	0.18
AN11097	conserved hypothetical protein	0.01167258	-0.24	-0.19	0.43	-0.25
AN7630	60S ribosome biogenesis protein Sqt1, putative	0.01184054	0.45	0.39	0.70	0.43
AN8868	hypothetical protein similar to small GTPase RAS2	0.01192205	0.03	0.33	0.25	-0.26
rps0 AN3172	40S ribosomal protein S0	0.01192896	0.21	0.49	0.38	-0.03
AN10096	NUDIX domain protein	0.0120542	0.07	0.06	-0.11	-0.13
AN4988	conserved hypothetical protein	0.01207128	0.30	-0.29	-0.09	0.29
AN7962	penicillolysin/deuterolysin metalloprotease, putative	0.01212065	-0.01	-0.61	0.40	-0.03
AN4220	ankyrin repeat protein	0.01214408	0.07	0.68	-0.33	0.24
AN6234	siderophore biosynthesis acetylase Ace1, putative	0.01221327	0.03	-0.64	0.19	-0.63
AN5970	disulfide isomerase, putative	0.01233442	0.03	0.28	-0.06	-0.26
AN10520	alpha/beta hydrolase, putative	0.01240007	0.17	0.34	0.20	0.21
AN9522	isopenicillin N-CoA epimerase, putative	0.01242666	0.24	-0.42	0.40	0.25
AN7641	peroxisomal copper amine oxidase	0.01244116	-0.12	-0.69	-0.09	0.28
ypdA AN2005	histidine-containing phosphotransfer protein	0.01254334	-0.20	0.10	-0.26	0.38
AN7389	conserved hypothetical protein	0.0125623	0.15	-0.78	-0.45	0.08
AN1883	arginosuccinate synthetase	0.01264019	0.28	0.57	0.39	0.34
AN5675	UBX domain protein (Ubx5), putative	0.01268055	0.33	0.30	-0.22	0.14
AN1913	lysyl-tRNA synthetase, hypothetical	0.0127364	0.20	0.62	0.28	0.61
AN2383	hypothetical protein ANIA_02383	0.01274809	0.10	-0.54	-0.15	-0.20
AN1167	conserved hypothetical protein	0.01277667	0.09	0.16	-0.01	-0.34
AN7742	ssDNA binding protein, putative	0.01281518	-0.08	-0.49	-0.26	0.19
AN3255	glutathione transferase 1	0.01284316	0.08	-0.28	0.49	0.35
AN5387	DUF453 domain protein	0.01285577	0.30	0.04	0.14	0.21
AN0065	WD repeat protein	0.01286033	-0.15	-0.33	0.58	0.05
AN3201	beta-galactosidase	0.01297005	-0.13	-0.54	0.49	-0.19
AN5597	ubiquinol-cytochrome c reductase complex 17 kd protein	0.01297212	-0.10	-0.57	-1.11	0.52
AN9304	translation elongation factor eEF-1B gamma subunit, putative	0.01306265	-0.14	-0.20	0.20	0.39
AN1274	conserved aldo-keto oxidoreductase, NADPH-dependent	0.013173	-0.11	-0.53	0.15	0.07
AN4397	coenzyme A synthetase, putative	0.01326506	0.13	0.35	0.21	0.64
AN10721	adoMet-dependent tRNA methyltransferase (MTase) complex subunit Trm112, putative	0.01340117	0.07	0.22	-0.58	0.21
AN0445	60S ribosomal protein L15	0.01341238	0.25	-0.50	0.83	0.22
AN2278	catalytic subunit of the SWI/SNF chromatin remodeling complex	0.01342216	0.34	-0.08	-0.60	0.16
AN7298	endonuclease/exonuclease/phosphatase family protein	0.01343955	0.35	-0.56	0.12	-0.04
AN0070	conserved hypothetical protein	0.01345886	-0.19	0.46	-0.01	0.11
AN6035	mandelate racemase/muconate lactonizing enzyme family protein	0.01351891	0.00	-0.72	0.55	0.17
AN4830	phosphopantetheate-cysteine ligase, putative	0.01353531	0.24	0.41	-0.23	-0.33
AN11121	conserved hypothetical protein	0.01358191	-0.40	-0.57	-0.20	0.11
AN1849	conserved hypothetical protein	0.01364125	-0.12	-0.58	-0.41	0.04

AN10182	eukaryotic translation initiation factor 3 subunit EifCf, putative	0.01385104	0.18	0.95	-0.59	-0.04
AN10718	DMRL synthase family protein	0.01386653	-0.01	-0.40	-0.17	-0.01
AN5602	co-chaperone	0.01386992	-0.08	0.26	-0.32	-0.05
tubC AN6838	Tubulin beta-2 chain (Beta-2-tubulin)	0.01388839	0.35	0.50	0.31	-0.07
AN5790	isocitrate dehydrogenase subunit 1, mitochondrial precursor	0.01398915	0.14	0.50	-0.06	-0.06
rps1 AN8870	40S ribosomal protein S3Ae	0.01415089	0.24	0.36	0.09	-0.17
AN2992	translational initiation factor 2 beta	0.01429444	-0.17	0.31	-0.61	-0.17
AN11487	conserved hypothetical protein	0.01445277	0.08	0.55	-0.22	-0.11
AN0686	prohibitin complex subunit Phb1, putative	0.01449674	0.03	0.63	-0.32	0.13
AN7786	conserved hypothetical protein	0.01456106	0.02	-0.20	0.25	0.02
AN1066	mitochondrial hypoxia responsive domain protein	0.01460151	0.34	0.27	-0.22	0.09
sconC skpA AN3202	SconCp	0.01476103	0.07	0.07	-0.61	0.19
AN1249	formin binding protein (FNB3), putative	0.01497767	-0.36	-0.01	-0.71	-0.23
AN1151	carboxy-cis,cis-muconate cyclase, putative	0.01499789	-0.10	-0.29	0.27	0.26
AN9063	oxysterol binding protein (Osh1), putative	0.01500367	-0.22	0.06	-0.50	-0.03
AN9402	Ser/Thr protein phosphatase family	0.01503178	-0.14	-0.53	-0.14	-0.24
AN0839	hypothetical protein ANIA_00839	0.01512191	0.10	-0.43	-0.64	0.08
AN2436	ATP citrate lyase, subunit 1, putative	0.01517403	0.24	0.58	0.24	-0.35
AN2062	hypothetical protein similar to bipA	0.01518904	-0.02	0.63	-0.28	0.34
AN5757	casein kinase I homolog, putative	0.01528335	-0.13	0.12	0.20	-0.30
AN10586	2-dehydropanoate 2-reductase, putative	0.01531295	0.32	0.06	0.32	0.18
AN10284	glutathione synthetase, putative, partial	0.0153388	-0.32	-0.59	-0.15	0.07
AN4464	hypothetical bifunctional AICARFT/IMPCHase bienzyme	0.01536387	0.33	0.97	0.04	-0.19
AN1380	methionyl-tRNA synthetase	0.01548737	0.35	0.54	-0.14	0.27
AN0824	acyl-CoA dehydrogenase, putative	0.01565109	-0.25	-0.67	-0.74	0.18
AN6168	Malic enzyme	0.01571229	0.18	0.69	0.07	-0.22
AN2588	conserved hypothetical protein	0.01572726	0.05	-0.19	0.34	-0.16
xyI1 AN0423	NAD(P)H-dependent D-xylose reductase	0.01573329	0.29	0.61	0.62	-0.17
AN6073	putative prohibitin	0.01574721	0.27	0.27	-0.15	-0.04
AN10318	conserved hypothetical protein	0.01575911	0.05	-0.14	-0.30	-0.24
AN5997	40S ribosomal protein S15	0.0157835	0.00	0.95	0.06	0.00
AN10214	2-hydroxyphytanoyl-CoA lyase, putative	0.0158287	0.23	-0.33	0.55	0.79
AN0240	transaldolase	0.01590235	0.01	-0.22	-0.24	0.12
AN2395	hydrolase, putative	0.0159127	-0.27	-0.59	-0.87	0.25
AN6815	guanine deaminase, putative	0.01592755	0.19	-0.42	0.18	-0.02
AN0842	AMP-binding enzyme, putative (JCVI)	0.0159678	-0.06	0.17	-0.17	-0.17
AN3897	conserved hypothetical protein	0.01598174	-0.27	-0.46	-0.28	0.14
rna14 AN4892	mRNA 3'-end-processing protein rna14	0.01603908	0.20	0.38	0.36	-0.47
AN1534	ATP synthase subunit 4, mitochondrial precursor	0.01610761	0.12	0.39	-0.28	0.00
agdD axIA AN7505	Alpha-xilosidasePutative uncharacterized protein	0.0161848	-0.03	-0.67	0.75	0.08
AN1486	ribonuclease P complex subunit Pop2, putative	0.01620151	0.07	-0.64	0.27	0.03
AN2906	mitochondrial large ribosomal subunit L49, putative	0.01621044	0.25	1.01	-0.30	0.87
AN5747	hypothetical protein similar to PSMC6 subunit	0.01622805	-0.16	0.57	-0.07	-0.25
AN1870	xylosidase/arabinosidase, putative	0.01630299	0.42	-0.16	0.21	-0.36
facA acuA AN5626	Acetyl-coenzyme A synthetase (Acetate--CoA ligase)(Acyl-activating enzyme)	0.01639278	0.19	0.60	0.27	-0.20
AN6842	mitochondrial large ribosomal subunit Yml35, putative	0.01648112	0.07	0.99	-0.21	0.05
AN0943	mitochondrial F1FO-ATP synthase g subunit, putative	0.01655098	0.21	0.27	-0.32	-0.11
AN3702	leucyl-tRNA synthetase	0.01656271	-0.03	0.53	0.02	0.04
AN7451	NAD dependent glutamate dehydrogenase	0.0165781	-0.11	0.46	-0.32	-0.22
AN7367	nitrilase	0.0165964	-0.11	-0.45	0.09	0.11
AN7194	quinone oxidoreductase, putative	0.01671124	-0.05	-0.74	-0.26	0.18
AN6640	amido hydrolase, putative	0.0167144	0.15	-0.39	-0.50	0.18
AN6705	component of the RSC chromatin remodeling complex	0.01691236	0.25	0.11	-0.08	0.08
AN10873	mitochondrial outer membrane protein (Sam50), putative	0.01698087	0.17	0.27	-0.03	0.04
AN10795	conserved hypothetical protein	0.01702323	-0.03	-0.44	-0.03	0.16
xdhA AN9064	hypothetical protein similar to xylitol dehydrogenase	0.0171483	0.33	-0.55	0.78	0.31
AN2964	probable mitochondrial E3-binding protein of the pyruvate dehydrogenase complex	0.01719436	-0.28	0.70	-0.34	-0.01
AN4430	acetolactate synthase, regulatory subunit, hypothetical protein	0.01719916	0.26	0.60	-0.03	-0.38
AN0768	Fasciclin domain family protein	0.01725946	-0.19	-0.40	-0.46	0.06
AN7128	conserved hypothetical protein	0.01728279	-0.50	-0.33	0.52	0.16
AN6176	tubulin-specific chaperone Rbl2, putative	0.01734467	-0.31	-0.49	-0.14	0.10
AN2150	prolyl-tRNA synthetase	0.01745537	0.23	0.83	0.24	-0.27
AN8403	conserved hypothetical protein	0.01750084	0.48	-0.38	0.48	0.36
gdhA AN4376	NADP-specific glutamate dehydrogenase (NADP-GDH)(NADP-dependent glutamate dehydrogenase)	0.01760654	0.02	-0.64	-0.18	-0.43
AN6620	endo-1,3(4)-beta-glucanase, putative	0.01764731	-0.18	-0.18	-0.77	0.28
AN3983	conserved hypothetical protein	0.01782227	-0.18	-0.73	0.16	-0.12
AN6642	sodium ion P-type ATPase	0.01788844	0.04	0.34	0.08	-0.21
AN7567	hydroperoxide and superoxide-radical responsive glutathione-dependent oxidoreductase	0.01797521	-0.01	0.02	-0.14	-0.20
AN4939	DNA damage response protein (Dap1), putative	0.01818076	0.03	0.00	-0.70	-0.10
snx4 atg24 AN3584	Sorting nexin-4 (Autophagy-related protein 24)	0.0182863	-0.03	0.32	-0.51	-0.24
AN7704	polyubiquitin binding protein (Doa1/Ufd3), putative	0.01838461	-0.16	-0.11	-0.22	0.00
AN11146	cytidine deaminase, putative	0.01846384	0.11	-0.41	-0.08	0.34
AN6286	conserved hypothetical protein	0.01847017	-0.05	0.47	0.27	-0.25
bimG AN0410	Serine/threonine-protein phosphatase PP1	0.0184941	-0.07	-0.14	0.26	0.16
AN4794	40S ribosomal protein S4, putative	0.01852622	0.32	0.38	0.60	-0.02
AN10174	conserved hypothetical protein	0.0185503	0.28	0.61	-0.05	0.09
AN5601	saccharopine dehydrogenase (NADP+, L-glutamate-forming)	0.0185769	0.17	0.21	-0.06	0.17
AN2026	conserved hypothetical protein	0.01870213	0.22	-0.13	0.40	0.13
AN8531	conserved hypothetical protein	0.01882138	-0.13	-0.40	0.49	-0.25
AN7598	conserved hypothetical protein	0.01887567	-0.25	-0.62	0.33	-0.14

AN2212	ubiquitin conjugating enzyme (UbcA), putative	0.01894521	0.03	0.28	-0.11	-0.25
AN10012	aminomethyl transferase, putative	0.01901922	0.23	0.16	0.51	-0.29
AN10169	3-oxoacyl-(acyl-carrier-protein) reductase	0.01915116	0.46	-0.35	0.58	0.29
AN0162	putative APSES transcription factor	0.01917636	0.03	-0.13	-0.32	0.10
AN4523	MRNA splicing protein PRP8	0.01931609	0.17	0.52	-0.29	-0.28
hisHF AN7430	Imidazole glycerol phosphate synthase hisHF (ImGP synthase)(IGP synthase)(IGPS)	0.01933073	0.00	0.23	-0.04	0.34
AN9116	nicotinate phosphoribosyltransferase	0.01956456	0.28	-0.47	0.40	0.27
AN8050	UPF0047 domain protein	0.01957175	-0.27	-0.82	-0.42	0.04
cpr6 AN4583	Peptidyl-prolyl cis-trans isomerase D (PPIase D)(Rotamase D)	0.01970528	-0.11	0.29	-0.07	0.17
AN5718	hypothetical protein ANIA_05718	0.01981131	0.11	0.53	-0.04	-0.16
manF AN9276	beta-1,4-endomannanase	0.01996713	0.19	-0.91	-0.80	-0.32
AN7014	DEAD helicases superfamily protein (Aquarius), putative	0.02008327	0.44	0.70	0.51	-0.44
treA AN9340	Acid trehalase Precursor (Alpha, alpha-trehalase)(Alpha,alpha-trehalose glucohydrolase)	0.02016515	-0.17	-0.54	0.22	0.09
AN11069	alkaline phosphatase family protein	0.02029565	0.07	0.72	-0.29	-0.12
AN4329	progesterone binding protein, putative	0.02033059	0.21	0.27	0.01	-0.18
AN3657	putative TeaA receptor TeaR	0.0205277	0.05	0.00	-0.14	0.16
AN4967	acid phosphatase, putative	0.02057884	0.23	0.47	0.15	0.14
AN4957	galactokinase	0.02064503	0.05	-0.13	0.11	0.30
AN3417	AMP-binding enzyme, putative	0.02074552	0.06	-0.14	-0.38	0.33
AN4388	ubiquinol-cytochrome c reductase complex 14 kDa protein	0.02076735	0.10	0.60	-0.18	-0.08
AN4416	conserved hypothetical protein, Syntaxin-like	0.02078929	-0.16	-0.01	-0.41	0.03
AN0858	heat shock protein	0.02105326	-0.05	0.36	-0.15	-0.22
AN5004	hypothetical protein ANIA_05004	0.02106338	-0.71	0.03	-0.82	0.05
AN10708	hypothetical proteasome beta 7 subunit	0.02117885	0.06	-0.89	-0.58	0.00
AN11049	conserved hypothetical protein	0.02121972	-0.21	-0.65	0.10	-0.15
cft1 AN1413	Protein cft1 (Cleavage factor two protein 1)	0.02133437	0.03	-0.24	0.36	-0.02
alcA AN8979	Alcohol dehydrogenase 1 (Alcohol dehydrogenase I)(ADH I)	0.02142167	0.19	0.18	0.14	0.85
tim10 AN0429	Mitochondrial import inner membrane translocase subunit tim10	0.0215254	-0.23	0.22	-0.56	0.07
AN6473	conserved hypothetical protein	0.02154842	0.02	-0.66	-0.23	0.12
AN2050	clathrin light chain	0.02155815	0.20	-0.36	-1.08	0.15
AN10188	hypothetical protein similar to guanylate kinase	0.02158786	0.18	0.57	-0.41	0.21
tdiC AN8515	Putative uncharacterized protein TdiC;	0.0217546	0.12	0.32	0.05	-0.43
AN1287	stomatin family protein	0.02178003	-0.13	0.29	-0.28	0.01
trpC AN0648	Anthrani late synthase component 2 (Anthrani late synthase component II)	0.02179807	0.09	0.28	0.34	0.10
AN4890	Putative SNARE-dependent exocytosis protein Sro7	0.02180897	0.04	-0.30	0.37	-0.26
AN5909	Dihydroorotate dehydrogenasePutative uncharacterized protein	0.02215937	0.23	0.43	0.03	0.03
celB eglB eglC AN3418	Endo-1,4-beta-glucanase	0.0222234	-0.31	-0.25	-0.07	-0.16
AN0377	conserved hypothetical protein	0.02231865	0.66	0.15	1.03	-0.93
AN8917	DUF636 domain protein	0.02234553	0.40	0.55	0.39	0.27
AN11039	hypothetical protein ANIA_11039	0.02244061	0.43	-0.40	0.10	0.66
AN3058	glycine hydroxymethyltransferase	0.02250539	-0.15	-0.62	0.05	0.07
AN0328	conserved hypothetical protein	0.02253305	-0.03	0.03	-0.21	0.19
AN2976	cystathione beta-synthase (beta-thionase), putative	0.02255021	-0.13	0.53	-0.14	0.34
AN1777	PHD finger domain protein, putative	0.02263786	0.18	0.06	-0.29	0.36
AN1805	Carbonic anhydrase (Carbonate dehydratase)	0.02270793	-0.35	-0.60	-0.45	0.05
mri1 AN4290	translation initiation factor, putative	0.02276716	-0.17	0.38	-0.45	0.08
AN2846	phospholipid hydroperoxide glutathione peroxidase	0.02279436	0.05	0.56	-0.02	0.01
AN6541	phosphoribosylamine-glycine ligase	0.02285488	0.25	0.31	0.31	-0.12
AN3413	ribosomal protein S5	0.02287657	0.25	0.37	0.35	-0.07
AN4446	endosomal cargo receptor (Erp5), putative	0.02292026	0.15	1.21	0.20	-0.04
AN0083	transcription factor TFIIH complex subunit	0.02301574	-0.11	0.24	0.40	0.20
AN1430	betaine aldehyde dehydrogenase (BadH), putative	0.02302086	-0.23	-0.78	0.18	0.14
AN10510	hypothetical protein ANIA_10510	0.02304146	0.63	0.68	0.44	0.48
AN7734	PENR2 protein	0.02316626	0.00	-0.12	-0.09	0.02
AN10175	PUA RNA binding domain protein, putative	0.02319999	0.19	0.02	0.88	0.52
AN4602	prefoldin subunit 3, putative	0.02363189	-0.09	0.58	0.16	0.17
AN4869	proteasome core alpha 1 component	0.02385644	-0.16	-0.62	-0.53	0.07
AN7564	threonine aldolase or alanine racemase, putative	0.02390019	-0.09	-0.62	-0.17	0.25
chsB AN2523	Chitin synthase B (Chitin-UDP acetyl-glucosaminyl transferase B)(Class-III chitin synthase B)	0.02405204	0.07	0.61	0.40	-0.14
AN7488	putative agmatinase	0.02406477	-0.07	-0.22	-0.46	0.11
AN8533	conserved hypothetical protein	0.02413071	0.00	0.44	0.67	0.15
AN2105	small nuclear ribonucleoprotein SmD1, putative	0.02413109	-0.06	0.33	0.49	0.16
AN3200	conserved hypothetical protein	0.02418229	0.26	0.06	0.19	0.23
enoA AN5746	Enolase (2-phosphoglycerate hydratase)(2-phospho-D-glycerate hydro-lyase)	0.02420194	-0.18	-0.55	-0.36	0.14
AN10946	conserved hypothetical protein	0.02436926	-0.04	0.39	0.10	-0.27
gpdA AN8041	Glyceraldehyde 3-phosphate dehydrogenase (GAPDH)	0.02440448	0.33	0.25	0.11	0.12
AN0338	cytochrome P450, putative	0.02443871	0.22	0.53	0.04	-0.39
kapC AN10378	Putative transcription factor kapC	0.02446968	0.24	-0.13	0.06	0.31
agIG AN9035	Putative alpha-galactosidasePutative uncharacterized protein	0.02459886	0.30	0.78	0.41	-0.04
AN0472	putative endo beta 1,3 glucanase, GH81 family	0.02486742	-0.19	-0.43	-0.69	-0.30
AN6083	hypothetical protein similar to ribosomal L10 protein	0.0250726	0.09	-0.33	0.84	0.14
AN5580	hypothetical protein ANIA_05580	0.02510197	0.30	0.60	0.10	0.19
AN5338	flavin-binding monooxygenase-like protein	0.02534005	0.11	0.47	0.17	-0.55
AN8866	3-phosphoglycerate dehydrogenase, hypothetical	0.02534055	0.45	0.66	-0.07	0.09
AN5812	Leukotriene A-4 hydrolase (Leukotriene A(4) hydrolase)(LTA-4 hydrolase)	0.02535339	-0.14	-0.64	-0.26	0.16
AN0847	molecular chaperone	0.02542025	-0.04	-0.06	0.27	0.06
pepP AN5810	ProlidasePutative uncharacterized protein	0.02549691	-0.23	-0.55	-0.18	0.24
AN5111	zinc knuckle domain protein (Byr3), putative	0.02554888	0.35	-0.62	-0.38	0.26
AN2871	RNAII degradation factor Def1, putative	0.02560346	-0.19	-0.09	-0.20	0.14
AN4623	UDP-glucose-glycoprotein glucosyltransferase	0.02574434	0.05	0.24	0.05	-0.41

AN2860	oxidoreductase, zinc-binding	0.02599431	0.15	-0.36	0.58	0.18
AN3554	conserved hypothetical protein	0.02602872	0.23	0.88	0.35	-0.39
AN3499	UPF0075 domain protein	0.02604543	-0.10	-0.58	0.00	-0.08
AN9097	37S ribosomal protein S24	0.02642082	0.34	0.65	0.39	0.00
AN10507	heat shock protein Hsp20/Hsp26, putative	0.02654868	0.60	1.03	-0.48	0.99
AN10475	tryptophanyl-tRNA synthetase	0.02673447	0.11	0.61	0.05	-0.36
AN6276	pterin-4-alpha-carbinolamine dehydratase family protein	0.02702685	-0.21	-1.11	-0.04	0.03
AN3156	translation initiation factor eIF2 alpha subunit	0.0270882	-0.06	0.74	0.14	0.00
AN3206	conserved hypothetical protein	0.02712049	0.04	-0.58	0.12	-0.07
AN5716	CBS and PB1 domain protein	0.02712786	-0.09	-0.25	-0.28	0.04
AN3591	methylmalonate-semialdehyde dehydrogenase, putative	0.02740686	0.02	-0.74	-0.09	0.25
AN10965	DUF866 domain protein	0.02748454	0.22	-0.61	0.14	0.20
cmkA AN2412	Calcium/calmodulin-dependent protein kinase (CMPK)	0.02755627	-0.09	0.37	0.26	-0.36
AN0212	conserved hypothetical protein	0.02775436	-0.09	-0.65	-0.50	0.03
spt5 AN1698	transcription initiation protein spt5	0.02776356	-0.38	0.02	-0.43	-0.22
AN6209	adenylosuccinate lyase	0.02778877	0.04	0.07	-0.20	-0.21
AN4711	conserved hypothetical protein	0.02780938	0.30	0.25	0.19	-0.20
AN1333	dynein light chain	0.02781699	0.20	0.78	-0.31	-0.05
AN1379	Putative uncharacterized protein SONA;	0.02785834	-0.28	-0.34	0.11	0.02
AN1984	protein involved in transcription initiation at TATA-containing promoters	0.02792707	0.28	-0.26	-0.66	0.30
AN6654	glutamine synthetase, putative	0.02798489	-0.44	-0.46	-0.35	0.04
fprA AN3598	06-binding protein 1A (FKBP)(FkbA)(Peptidyl-prolyl cis-trans isomerase)(PPase)(Rapamycin-binding protein)	0.02800407	0.36	0.63	0.41	-0.03
AN4504	putative endo mannanase, GH76 family	0.02805798	0.00	0.14	0.02	-0.04
AN4777	40S ribosomal protein S27	0.02821592	0.41	0.25	0.80	0.09
ampp AN11005	aminopeptidase P, putative	0.02835987	-0.18	-0.60	-0.34	0.04
AN2917	hypothetical protein similar to 26S proteasome regulatory subunit	0.02844724	-0.18	-0.19	-0.25	-0.15
AN4304	glutaredoxin	0.02845769	0.19	0.10	-0.35	0.43
AN8036	aldo-keto reductase (AKR), putative	0.02846708	-0.08	-0.31	0.26	-0.12
AN3059	hypothetical protein similar to cofactor-independent phosphoglycerate mutase	0.02846958	-0.23	-0.69	-0.25	0.07
AN5830	haloacid dehalogenase, type II	0.02857533	0.02	-0.41	0.17	0.02
AN0072	pseudouridine synthase	0.02859782	-0.18	-0.05	-0.11	-0.01
AN4862	Ran specific GTPase activating protein An-RanGAP	0.02863325	-0.10	-0.32	0.33	0.08
AN4934	3'-oxoacyl-(acyl-carrier-protein) reductase, putative	0.02866156	0.24	0.46	0.28	0.39
AN2351	zinc-containing alcohol dehydrogenase, putative	0.02878738	0.02	-0.57	0.41	-0.14
ccr4 AN3602	glucose-repressible alcohol dehydrogenase transcriptional effector (Carbon catabolite repressor protein 4)	0.02880322	0.04	0.30	-0.15	-0.22
AN7222	NACHT domain protein	0.02883165	-0.05	0.80	-0.09	-0.23
AN11477	hypothetical protein ANIA_11477	0.02884997	-0.04	0.68	0.49	0.21
AN4591	phosphoglucomutase, putative	0.02885855	-0.20	-0.41	-0.06	0.18
tubB AN7570	Tubulin alpha-2 chain	0.0288909	0.18	0.50	0.15	-0.34
AN7635	Putative uncharacterized protein Putative uncharacterized protein binA;	0.02893872	0.09	-0.15	0.35	-0.17
AN8942	conserved hypothetical protein	0.02894482	0.07	0.88	0.15	-0.06
AN6004	actin cytoskeleton protein (VIP1), putative	0.02906652	0.02	-0.20	-0.25	-0.12
AN10266	E1 ubiquitin activating enzyme	0.02916508	0.09	0.99	0.17	-0.08
AN0932	hypothetical glutathione reductase	0.02921278	-0.23	-0.61	-0.60	0.28
AN0745	hypothetical protein similar to fibrillarin, nucleolar protein	0.02926364	0.01	0.24	0.01	-0.03
AN9148	UDP-glucos pyrophosphorylase	0.02926367	0.03	-0.24	0.50	0.15
AN10020	26S proteasome regulatory subunit Mts4, putative	0.02929903	0.16	0.69	0.09	-0.36
uaZ AN9470	Uricase (Urate oxidase)	0.02930426	-0.06	-0.56	-0.17	0.24
katG cpeA AN7388	Catalase-peroxidase (CP)(Peroxidase/catalase)	0.0294173	-0.06	-0.65	0.59	0.06
AN4055	acid phosphatase PHOa	0.02944937	-0.12	-0.46	-0.39	-0.05
mpdA AN5975	Mannitol-1-phosphate 5-dehydrogenase (M1PDH)(MPDH)(MPD)	0.02997379	0.11	0.75	-0.07	-0.31
AN3706	40S ribosomal protein S10b	0.02997532	0.39	0.42	-0.21	-0.17
AN5222	40S ribosomal protein S11	0.03029396	0.28	0.38	0.42	-0.02
AN4470	hypothetical protein similar to translation initiation factor 2 gamma subunit	0.03064356	0.22	0.47	0.17	-0.22
AN5904	Acyl CoA binding protein family	0.03067108	-0.36	0.41	-0.38	0.05
AN8982	hypothetical fructosyl amine:oxygen oxidoreductase	0.03109385	0.16	-0.40	0.10	0.20
AN2304	UV excision repair protein (RadW), putative	0.03109422	-0.27	0.02	-0.29	0.19
AN2149	t-complex protein 1, alpha subunit, putative	0.03114688	-0.04	0.40	0.00	-0.13
rsm25 AN4434	37S ribosomal protein S25, mitochondrial	0.03126035	0.11	-0.32	0.84	0.33
AN6903	U1 small nuclear ribonucleoprotein 70 kDa	0.03128028	-0.15	0.35	-0.04	-0.39
AN4207	AP-1 adaptor complex subunit gamma, putative	0.03173431	0.26	0.29	0.14	0.11
AN7517	HypA-like protein, putative	0.03174698	-0.34	-0.63	-0.35	0.27
AN1209	proteasome regulatory particle subunit (Nas6), putative	0.03262337	0.42	1.42	-0.78	0.45
AN10712	snoRNP protein (gar1), putative	0.03268904	0.32	-0.42	0.39	0.24
AN2918	t-complex protein 1, delta subunit, putative	0.03275613	0.04	0.42	0.09	-0.31
AN4303	phosphoethanolamine	0.03284981	0.27	0.42	0.14	0.09
AN6402	conserved hypothetical protein	0.03303549	0.08	0.30	-0.06	0.12
AN3919	nuclear polyadenylated RNA-binding protein Nab2, putative	0.03315958	-0.43	-0.49	-0.72	0.24
AN0357	Ubiquinol-cytochrome c reductase	0.0332585	0.09	0.58	-0.30	0.26
AN2970	4-nitrophenylphosphatase	0.03360411	-0.09	-0.28	0.40	0.35
sfaD AN0081	G-protein beta subunit	0.03372962	0.28	0.27	0.43	-0.19
AN7961	conserved hypothetical protein	0.03380171	-0.57	-0.67	-0.11	-0.11
AN1252	conserved hypothetical protein	0.03417866	-0.10	-0.55	0.09	0.22
AN5631	Sit4-associated protein (Sap185), putative	0.03418339	-0.01	0.11	-0.94	0.01
AN4268	oxidoreductase, 2-nitropropane dioxygenase family, putative	0.03438074	0.28	0.15	0.92	0.22
AN4745	hypothetical protein similar to Rho GTPase activating protein	0.03497635	-0.05	0.33	-0.06	-0.08
AN3737	WD repeat-containing protein AN3737	0.0349952	-0.18	-1.01	0.44	0.01
csnG acbB csn7 AN3623	COP9 signalosome complex subunit 7 (CSN complex subunit 7)	0.03513092	0.03	0.76	0.31	-0.31
AN5979	40S ribosomal protein S17, putative	0.03518551	0.19	0.65	0.45	-0.02
AN6006	nonsense-mediated mRNA decay protein (Nmd5), putative	0.03548989	-0.04	0.52	-0.62	-0.10

AN10418	conserved hypothetical protein	0.035519	0.01	-0.39	-0.17	0.15
AN2775	eukaryotic translation initiation factor subunit eIF2A, putative	0.03558043	-0.23	-0.10	-0.35	0.20
AN8210	SH3 domain protein (Cyk3), putative	0.03591788	-0.21	-0.31	0.14	0.26
AN3467	conserved hypothetical protein	0.03599213	0.00	0.65	-0.07	-0.02
AN11054	alpha glucosidase II, alpha subunit, putative	0.0360682	0.07	0.05	0.49	-0.18
AN8170	NapBPutative uncharacterized protein	0.03614034	0.07	0.67	-0.31	0.09
AN5669	succinyl-CoA:3-ketoacid-coenzyme A transferase (ScoT), putative	0.03637739	0.02	-0.34	0.16	0.23
AN8044	a-pheromone processing metallopeptidase Ste23	0.03697521	-0.14	-0.54	-0.10	0.02
AN8330	alcohol dehydrogenase, zinc-containing, putative	0.03716869	-0.11	-0.74	0.26	0.11
AN1198	hypothetical glycine cleavage system T protein	0.0378037	0.18	-0.51	0.25	0.33
AN6732	Myosin light chain, putative	0.03788073	-0.26	0.00	-0.09	-0.31
AN1904	t-complex protein 1, epsilon subunit, putative	0.03866023	-0.02	0.41	-0.65	0.03
AN1429	choline oxidase (Coda), putative	0.03876179	-0.26	-0.60	-0.29	0.15
AN3082	cleavage and polyadenylation specificity factor, putative	0.03937835	0.04	0.57	0.17	-0.25
AN4647	phytanoyl-CoA dioxygenase family protein	0.03949667	-0.05	0.01	0.28	-0.17
xptA AN6784	DMATS type aromatic prenyltransferase, putative (JCVI)	0.03957973	-0.27	0.98	0.12	-0.54
AN2366	serine protease similarity, trypsin family	0.03970686	0.22	-0.62	-0.37	0.04
nudG AN0420	Dynein light chain, cytoplasmic (8 kDa cytoplasmic dynein light chain)	0.03981516	-0.17	-0.08	0.37	0.12
AN1662	DUF757 domain protein	0.03986297	-0.07	0.51	-0.13	-0.09
AN10028	cytochrome P450, putative	0.04002	0.06	0.61	-0.44	-0.17
AN6024	hypothetical protein ANIA_06024	0.04017516	-0.04	-0.81	0.11	-0.19
AN4652	conserved hypothetical protein	0.04023852	0.02	0.07	0.71	0.20
AN4259	Eukaryotic translation initiation factor 3 subunit M (eIF3m)	0.04044374	0.13	0.38	-0.28	-0.08
AN3104	allantocase, expressed, purine use	0.04050296	0.02	-0.51	0.30	0.11
mpg1 AN5586	Mannose-1-phosphate guanylyltransferase (GTP-mannose-1-phosphate guanylyltransferase)	0.04074235	0.18	0.47	0.24	-0.22
AN0232	urease accessory protein UreG, putative	0.04120393	0.22	0.49	-0.03	0.05
AN3628	N-terminal acetyltransferase catalytic subunit (NAT1), putative	0.04151785	0.14	0.79	-0.29	-0.17
argB AN4409	Ornithine carbamoyltransferase, mitochondrial Precursor (Ornithine transcarbamylase)(OTCase)	0.04162699	-0.19	-0.60	-0.27	0.14
AN7712	NUDIX family hydrolase, putative	0.04169329	0.29	0.03	0.69	0.56
AN10459	translation initiation factor eif-2b epsilon subunit, putative	0.04214601	0.12	0.48	-0.19	0.13
AN8874	dynamin-like GTPase Dnm1, putative	0.04230978	-0.13	0.22	-0.42	-0.20
AN8932	TIM-barrel enzyme family protein	0.04236589	-0.22	0.59	0.26	-0.04
tif35 AN10765	aryotic translation initiation factor 3 subunit G (eIF3g)(Translation initiation factor eIF3 p33 subunit homolog)	0.04237349	0.18	0.66	-0.21	-0.03
AN2120	importin subunit beta-4, putative (JCVI)	0.04256482	-0.12	0.25	-0.05	-0.17
AN4178	UPF0160 domain protein MYG1, putative	0.04275959	-0.07	-0.72	-0.50	0.09
AN4171	PH domain protein	0.04311749	0.37	0.31	0.14	0.01
AN2295	succinyl-CoA synthetase alpha subunit, putative	0.04346128	0.33	1.02	0.34	-0.20
AN4087	hypothetical protein similar to 40S ribosomal protein s3	0.04378557	0.21	0.50	0.43	-0.04
AN8599	conserved hypothetical protein	0.0439146	-0.02	0.46	0.34	-0.18
AN6082	60S ribosomal protein L30, putative	0.0440866	0.02	-0.39	0.98	0.26
AN2226	THO complex component (Rr1), putative	0.0441863	0.03	0.36	0.43	0.01
AN0123	mitochondrial ribosomal protein L23, putative	0.04455193	0.01	0.60	-0.07	-0.02
stcL cyp60B AN11013	Probable sterigmatocystin biosynthesis P450 monooxygenase stcL (Cytochrome P450 60B)	0.04458108	0.05	-0.21	0.44	-0.20
AN5800	60S ribosomal protein L18	0.0449341	0.20	-0.53	0.90	0.21
AN10546	beta regulatory subunit of casein kinase 2	0.04511009	-0.09	0.25	0.19	-0.04
AN8445	aminopeptidase Y, putative	0.04527945	-0.27	0.02	0.02	-0.05
AN6510	mitochondrial import receptor subunit (tom40), putative	0.04538065	0.11	0.28	0.06	0.12
AN6507	snRNA cap binding complex subunit (Gcr3), putative	0.04585076	0.21	0.28	0.09	0.10
hhoA AN2765	Histone H1	0.04589651	0.59	0.19	-0.61	0.99
AN1675	lysophospholipase Plb1	0.04591412	-0.14	-0.17	0.07	0.03
tdiA AN8513	TdiA	0.0459287	-0.17	0.22	0.27	-0.38
AN7258	hypothetical protein similar to 25D9-6	0.04598356	0.08	0.55	-0.34	0.15
AN4727	UDP-glucose 4-epimerase	0.04601528	0.30	0.85	0.02	0.26
AN8546	phosphatidylglycerol specific phospholipase, putative	0.04630851	-0.01	-0.38	-0.35	-0.22
AN4916	40S ribosomal protein S7	0.04730603	0.29	0.81	0.28	-0.21
AN10281	serine/threonine protein phosphatase PPT1	0.04747795	-0.38	-0.31	0.04	-0.17
AN1116	hypothetical protein ANIA_01116	0.04756153	0.23	0.89	0.39	0.07
AN1177	Coatomer subunit beta, putative	0.04768344	0.20	0.32	0.14	-0.27
AN7944	conserved hypothetical protein	0.0486866	0.26	0.45	0.01	-0.22
AN3197	dihydrofolate reductase family protein	0.04912567	0.52	-0.31	0.02	0.18
AN1345	40S ribosomal protein S23	0.04912656	0.10	0.29	0.02	0.24
AN6717	malate dehydrogenase	0.04928771	-0.14	-0.70	0.00	0.25
AN7121	conserved hypothetical protein	0.04976642	-0.42	-0.32	-0.10	0.25
AN5520	cytosolic large ribosomal subunit protein L7A	0.04987983	0.19	-0.66	0.85	0.27
AN5484	lipid transfer protein, putative	0.0499425	-0.23	0.23	0.09	0.06

Table S8. Relative abundance ratios for proteins identified in ISS-grown 7-day samples compared to Earth-grown counterparts

Gene name	Description	p-value	FGSC A4 7d ISS	LO1362 7d ISS	LO8158 7d ISS	CW12001 7d ISS
			grown/control log2 FC	grown/control log2 FC	grown/control log2 FC	grown/control log2 FC
AN4421	L-lactate dehydrogenase	2.60E-08	-0.22	-0.55	-1.08	0.71
AN8579	conserved hypothetical protein	4.24E-08	0.32	-1.08	1.23	-0.42
AN0483	conserved hypothetical protein	8.95E-08	-0.21	-0.21	-0.84	0.94
AN2704	conserved hypothetical protein	1.00E-07	1.02	-0.69	0.75	-0.07
AN4646	hypothetical protein ANIA_04646	2.00E-07	-0.17	-0.35	-0.46	0.38
AN6447	O-methyltransferase, putative	3.23E-07	0.14	-0.24	-0.12	0.24
AN1050	3-ketoacyl-CoA ketothiolase (Kat1), putative	3.46E-07	-0.03	-0.11	0.03	0.10
AN0950	hypothetical protein ANIA_00950	4.32E-07	0.01	-0.68	-0.86	1.01
AN6963	conserved hypothetical protein	5.77E-07	-0.10	-0.17	-1.08	0.86
AN10197	sulfonate biosynthesis enzyme, putative	9.58E-07	-0.22	-0.88	-0.25	0.58
AN6862	conserved hypothetical protein	1.44E-06	0.18	-0.22	-0.89	1.32
AN2315	ATP synthase beta chain, mitochondrial	1.49E-06	0.07	-0.05	-0.10	0.13
AN6668	conserved hypothetical protein	1.73E-06	-0.47	0.73	-0.74	0.38
AN8074	MATH and UCH domain protein, putative	2.01E-06	-0.05	-0.10	0.11	-0.16
AN1699	acyl-CoA dehydrogenase, putative	2.13E-06	0.42	-0.42	-0.22	0.18
AN11035	conserved hypothetical protein	2.63E-06	0.63	-0.36	0.20	1.26
AN5348	conserved hypothetical protein	3.12E-06	0.36	-0.76	0.07	0.43
AN6487	aspartic-type endopeptidase (OpsB), putative	3.76E-06	-0.11	-0.75	-0.50	0.30
awh11 AN3725	Chaperone/heat shock protein	5.18E-06	-0.16	-0.68	-1.07	-0.02
AN7990	conserved hypothetical protein	7.17E-06	-0.19	0.10	-1.37	0.83
AN0400	conserved hypothetical protein	1.12E-05	-0.05	0.04	-1.08	0.93
AN9037	periplasmic nitrate reductase, putative	1.21E-05	-0.20	-0.47	-0.74	0.38
alp1 alk1 alp prtA AN5558	Alkaline protease/Putative uncharacterized protein;	1.43E-05	0.56	-0.37	0.19	-0.22
tif35 AN10765	Eukaryotic translation initiation factor 3 subunit G (elf3 ^g ng subunit)(elf-3 RNA-binding subunit)	1.48E-05	-0.19	0.75	-0.46	0.43
AN0083	transcription factor TFIIF complex subunit	1.58E-05	-0.12	0.04	-0.24	0.16
bgfH AN3903	beta-1,4-glucosidase	1.90E-05	-0.13	-0.86	0.23	-0.24
AN8829	conserved hypothetical protein	1.98E-05	0.09	-0.07	-0.60	1.24
AN0694	conserved hypothetical protein	2.03E-05	-0.28	-0.73	-1.39	0.75
AN7159	hypothetical tripeptidyl-peptidase	2.05E-05	0.38	1.01	-0.11	-0.25
AN5591	aminotransferase, classes I and II, putative	2.55E-05	0.26	-0.33	-0.36	0.04
AN11477	hypothetical protein ANIA_11477	2.56E-05	-0.41	-0.12	-1.50	0.78
IbsA AN8049	Lactobacillus shifted protein	2.72E-05	0.04	0.60	-0.39	0.16
AN7960	conserved hypothetical protein	3.03E-05	-0.17	-0.40	-0.78	0.85
AN9358	putative CCAAT-box-binding transcription factor	3.08E-05	-0.20	0.07	0.00	-0.03
AN0045	solid-state culture expressed protein (Aos23), putative	3.13E-05	-0.28	-0.26	-0.78	0.85
AN8640	conidiation protein Con-6, putative	3.19E-05	-0.05	-0.68	-1.21	1.47
AN9285	glucose repressible protein Grg1, putative	3.79E-05	0.00	-1.25	-1.37	0.43
pyrG AN6157	Orotidine 5'-phosphate decarboxylase (OMP decarboxylase)(OMPdecase)(OMPDecase)	4.11E-05	-0.14	-0.40	-0.54	0.51
AN3558	DUF636 domain protein	4.31E-05	0.21	0.03	-0.89	1.37
AN2260	NADH-ubiquinone oxidoreductase subunit B17.2, putative	4.41E-05	0.38	0.01	-0.41	0.20
AN3512	conserved hypothetical protein	4.44E-05	-0.11	-0.62	-1.55	0.92
p2ox AN5281	conserved hypothetical protein	4.69E-05	0.39	-0.05	-0.08	0.25
AN10952	FAD monooxygenase, putative	4.77E-05	0.30	-0.73	0.15	-0.03
AN1544	conserved hypothetical protein	5.42E-05	-0.09	0.66	-0.12	-0.38
AN5916	enoyl-CoA hydratase	5.53E-05	-0.21	-0.35	-0.03	-0.25
AN3034	Putative uncharacterized proteinSUAPRGA1;	5.69E-05	0.02	0.12	-0.30	0.20
AN6203	conserved hypothetical protein	5.71E-05	-0.31	-0.07	-0.16	-0.21
AN0693	conserved hypothetical protein	6.33E-05	0.03	-0.45	-1.06	0.91
AN3931	primary component of eisosomes	6.46E-05	-0.31	0.20	-0.77	0.26
AN3022	tubulin-specific chaperone c, putative	6.91E-05	-0.17	0.19	-0.64	0.67
AN4585	CCR4-NOT transcription complex, subunit 3	7.20E-05	-0.21	0.44	-0.48	-0.02
AN8162	amine oxidase, flavin-containing superfamily	7.31E-05	0.27	-0.24	0.64	-0.64
AN4957	galactokinase	7.98E-05	0.08	0.02	-0.47	0.38
AN5028	Fatty acid oxygenase/Putative uncharacterized protein;	8.02E-05	0.21	0.07	-0.04	-0.09
sec31 AN6257	Protein transport protein sec31	9.03E-05	-0.03	-0.10	-0.19	-0.21
AN2471	hypothetical protein ANIA_02471	9.64E-05	-0.12	-0.99	-1.89	1.06
AN8714	hypothetical protein ANIA_08714	9.85E-05	-0.26	-0.16	-0.38	0.37
AN7121	conserved hypothetical protein	9.88E-05	-0.31	-0.76	0.11	-0.13
AN0447	NifU-related protein	0.00010	-0.06	-0.12	-0.54	0.48
AN0691	conserved hypothetical protein	0.000108	-0.16	-0.27	-0.86	0.84
AN2896	mitochondrial methylglutaconyl-CoA hydratase (Auh), putative	0.000111	-0.10	-0.25	-0.22	0.24
AN8553	catalase	0.000114	-0.36	0.03	-1.53	0.68
AN5206	LysB/Putative uncharacterized protein;	0.000121	0.01	0.02	-0.27	0.14
AN2432	chaperonin, putative	0.000123	-0.36	-0.08	-0.03	0.18
aptA AN6000.2	polyketide synthase, putative (JCVI)	0.000127	0.90	-0.42	-0.61	1.06
AN2720	conserved hypothetical protein	0.000127	-0.29	-0.46	-0.31	0.44
agdC agdD AN7345	Alpha/beta-glucosidase	0.000127	0.13	-0.52	-0.14	0.10
AN11161	phosphatidylserine decarboxylase family protein	0.000130	-0.33	-0.41	-1.31	0.72
AN5698	3-ketoacyl-CoA thiolase (POT1), putative	0.000132	0.21	-0.66	-0.07	0.12

AN2898	conserved hypothetical protein	0.000137	-0.13	-0.44	-0.20	-0.17
faeC AN5267	feruloyl esterase	0.000137	-0.06	-0.38	0.72	-0.30
AN10421	conserved hypothetical protein	0.000142	-0.25	-0.39	-1.31	1.09
AN2147	rRNA biogenesis protein RRP5, putative	0.000148	0.30	-0.04	0.14	0.24
AN8004	cytochrome P450, putative	0.000149	0.20	0.09	-0.06	-0.34
ypdA AN2005	histidine-containing phosphotransfer protein	0.000151	-0.31	0.10	-0.28	0.14
AN1715	mannose-6-phosphate isomerase, class I	0.000154	-0.16	-0.39	-1.49	0.92
AN6005	conserved hypothetical protein	0.000154	-0.26	-0.33	-1.30	0.93
AN1547	Acyl-CoA carboxylate CoA-transferasePutative uncharacterized protein;	0.000167	-0.17	-0.30	-0.57	0.60
AN9171	conidial pigment biosynthesis protein Agy1	0.000169	0.05	-0.28	-1.33	0.77
AN7894	conserved hypothetical protein	0.000179	-0.32	-1.03	0.40	-0.36
pim1 AN6193	mitochondrial serine protease Pim1, putative	0.000197	-0.24	0.26	-0.81	0.14
AN5637	short chain dehydrogenase/reductase family	0.000198	0.06	-0.27	0.02	-0.02
acuF AN1918	Phosphoenolpyruvate carboxykinase [ATP]	0.000207	-0.26	-0.16	-1.38	0.90
AN11533	conserved hypothetical protein	0.000209	0.04	-0.04	-1.14	1.00
AN2846	phospholipid hydroperoxide glutathione peroxidase	0.000213	-0.07	0.21	-0.06	-0.39
AN5646	3-ketoacyl-CoA thiolase peroxisomal A precursor	0.000227	0.05	-0.32	-0.32	0.32
AN7959	DUF1264 domain protein	0.000228	-0.37	-0.46	-0.71	0.63
AN0354	Phe-inhibited DAHP synthase	0.000232	-0.22	0.87	-0.74	0.30
AN6933	conserved hypothetical protein similar to yeast mitochondrial NAD-dependent malic enzyme	0.000233	-0.07	-0.42	-0.57	0.56
AN9002	oxidoreductase, short-chain dehydrogenase/reductase family	0.000243	-0.20	-0.58	-1.03	0.71
mdpG AN0150	hypothetical protein similar to polyketide synthase	0.000247	-0.09	-0.16	-0.33	-0.06
biA AN6644	double bifunctional dethiobiotin synthetase/adenosylmethionine-8-amino-7-oxononanoate aminotransferase	0.000249	-0.01	0.24	-0.26	0.14
panB AN1778	3-methyl-2-oxobutanoate hydroxymethyltransferase (Ketopantoate hydroxymethyltransferase)	0.000249	-0.14	-0.59	0.13	-0.22
AN10096	NUDIX domain protein	0.000250	-0.14	-0.11	0.17	-0.05
pab1 fabM AN4000	Polyadenylate-binding protein, cytoplasmic and nuclear (Poly(A)-binding protein)(PABP)	0.000251	0.10	-0.02	-0.45	0.07
AN3679	oxidoreductase, short-chain dehydrogenase/reductase family	0.000255	-0.15	-0.43	-1.36	0.90
chz1 AN5128	Histone H2A.Z-specific chaperone chz1	0.000270	-0.04	0.26	-0.58	-0.20
AN3968	conserved hypothetical protein	0.000279	-0.04	-0.11	-0.65	0.17
AN2332	iron-sulfur protein subunit of succinate dehydrogenase Sdh2, putative	0.000297	0.00	-0.40	-0.06	0.38
AN7786	conserved hypothetical protein	0.000308	0.01	-0.66	0.48	-0.39
isn1 AN3222	IMP-specific 5'-nucleotidase 1	0.000308	-0.19	-0.14	-0.17	0.06
AN4177	NAD dependent epimerase/dehydratase family protein	0.000327	-0.24	-0.49	-1.16	0.87
AN5556	conserved hypothetical protein	0.000336	0.08	-0.59	-0.13	0.59
AN11094	hypothetical oxidoreductase	0.000357	0.69	0.26	-1.64	1.37
catA AN8637	Catalase A (Spore-specific catalase)	0.000367	-0.24	-0.41	-1.65	0.90
AN4914	acetate kinase, putative	0.000371	-0.18	-0.41	-0.61	0.79
AN9093	zinc knuckle nucleic acid binding protein, putative	0.000372	0.07	-0.11	-0.49	0.42
AN4531	alpha/beta hydrolase, putative	0.000389	-0.26	-0.26	-0.48	0.48
AN10499	NADP(+) coupled glycerol dehydrogenase	0.000396	-0.20	-0.38	-1.89	1.10
AN5111	zinc knuckle domain protein (Byr3), putative	0.000399	0.11	-0.41	-0.13	0.06
AN2393	short chain oxidoreductase/dehydrogenase, putative	0.000415	-0.01	-0.54	0.04	0.20
AN7907	conserved hypothetical protein	0.000422	-0.20	-0.07	-0.70	0.61
AN5833	propionate-CoA ligase	0.000426	0.25	-0.31	0.29	0.40
AN7287	Mitochondrial succinate-fumarate antiporter	0.000427	-0.06	0.28	-0.64	0.36
AN9401	mitochondrial enoyl reductase, putative	0.000445	0.05	-0.36	-0.84	0.75
AN6699	electron transfer flavoprotein alpha subunit, putative	0.000463	-0.09	0.31	-0.44	-0.02
AN1163	oligomeric mitochondrial matrix chaperone	0.000464	0.13	-0.16	-0.31	0.14
AN8975	conserved hypothetical protein	0.000479	-0.07	0.91	-2.00	1.34
vps10 vpsT AN8880	vacuolar protein sorting protein, putative	0.000487	-0.02	-0.16	0.09	-0.11
AN2916	hypothetical protein similar to succinate dehydrogenase flavoprotein subunit A	0.000491	-0.10	-0.55	-0.10	0.24
AN4402	outer mitochondrial membrane protein porin	0.000497	-0.01	0.56	-0.31	0.15
AN1809	conserved hypothetical protein	0.000498	0.35	-0.45	-0.13	0.55
AN6010	Heat shock 70 kDa protein Precursor	0.000502	0.00	0.02	-0.61	0.57
AN9394	coenzyme A transferase, putative	0.000505	0.04	-0.24	0.12	-0.10
AN7102	hypothetical protein ANIA_07102	0.000509	-0.33	-0.23	-1.36	0.37
AN6248	mitochondrial co-chaperone GrpE, putative	0.000511	-0.18	-0.35	-0.26	0.32
AN10276	RNP domain protein , partial	0.000519	-0.24	-0.28	1.08	-0.55
AN11102	ubiquitin C-terminal hydrolase, putative	0.000548	0.11	0.39	0.18	-0.12
AN10229	NADH-ubiquinone oxidoreductase 30.4 kDa subunit, mitochondrial [Precursor]	0.000550	0.16	0.31	-0.29	0.33
AN3783	hypothetical protein ANIA_03783	0.000559	-0.18	0.15	-1.01	0.79
dpp5 AN2572	hypothetical dipeptidyl-peptidase	0.000577	0.04	-0.36	0.57	-0.20
rasA AN0182	Ras-like protein Precursor	0.000584	0.05	0.17	-0.02	-0.07
AN5356	Carnitine/acyl carnitine carrierPutative uncharacterized protein;	0.000597	-0.02	0.24	-0.22	0.22
AN5604	Fructose-1,6-bisphosphatasePutative uncharacterized protein ;	0.000602	-0.21	-0.67	-0.32	0.53
IamA AN0887	Putative urea carboxylase (Urea amidolyase)(Lactam utilization protein IamA)	0.000606	-0.04	-0.50	-0.82	0.47
AN7999	conserved hypothetical protein	0.000615	0.85	-0.77	-0.03	-0.12
AN6450	oxidoreductase, short-chain dehydrogenase/reductase family, putative	0.000622	0.38	-0.36	0.37	-0.05
AN6558	DNA-directed RNA polymerase I and III 14 KDa polypeptide	0.000623	0.40	-0.39	-0.07	-0.07
AN10700	DlpA domain protein	0.000625	-0.24	-0.60	-0.08	0.43
cym1 AN3853	Mitochondrial presequence protease Precursor	0.000638	-0.20	-0.38	-0.45	0.47
AN5447	hypothetical glutamic acid decarboxylase	0.000641	-0.50	-0.24	0.52	-0.04
mdpD AN0147	conserved hypothetical protein	0.000648	-0.11	1.24	-0.04	0.37
AN2747	DNA-directed RNA polymerase I, II, and III subunit Rpb6	0.000651	-0.20	0.14	-0.50	0.11
AN4667	Septin	0.000652	0.29	-0.24	-0.12	-0.04
stcl AN7816	Putative sterigmatocystin biosynthesis lipase/esterase stcl	0.000694	0.20	0.36	-0.28	0.50
treB AN5635	Neutral trehalase (Alpha,alpha-trehalase)(Alpha,alpha-trehalose glucohydrolase)	0.000697	-0.16	0.46	-0.70	0.44
dewA AN8006	Spore-wall fungal hydrophobin dewA Precursor	0.000705	0.15	0.34	0.98	0.63
AN11487	conserved hypothetical protein	0.000708	0.03	0.55	-0.41	0.55
AN10198	oligopeptidase family protein	0.000720	0.23	-0.14	0.15	-0.31

AN6796	ThiJ/Pfpl family protein	0.000728	-0.25	-0.43	-1.37	0.94
AN5938	conserved hypothetical protein	0.000752	-0.29	-0.33	-0.95	0.58
AN3873	zinc-containing alcohol dehydrogenase, putative	0.000768	-0.21	-0.60	-1.57	0.80
AN2939	MRS7 family protein	0.000771	-0.27	0.68	-0.41	-0.21
AN8874	dynamin-like GTPase Dnm1, putative	0.000791	-0.14	0.02	-0.58	0.46
AN4843	Putative alpha-glucosidasePutative uncharacterized protein;	0.000794	0.09	-0.02	-0.20	0.42
AN3778	Gephyrin-like proteinPutative uncharacterized protein;	0.000796	0.37	-0.49	-0.13	0.48
AN5907	conserved hypothetical protein	0.000801	-0.03	-0.11	0.31	-0.43
sey1 AN1085	Protein sey1	0.000834	0.06	0.13	-0.59	0.34
AN6048	aspartate transaminase	0.000834	-0.12	0.17	-0.05	0.01
AN9194	conserved hypothetical protein	0.000863	-0.10	0.12	-2.03	1.06
AN7989	phosphatidylserine decarboxylase, putative	0.000880	0.20	-0.02	-0.64	0.53
AN8638	HHE domain protein	0.000884	-0.42	0.69	-2.21	0.91
AN7278	glutamate decarboxylase	0.000889	-0.25	-0.46	-0.07	0.10
AN4820	succinate semialdehyde dehydrogenase	0.000902	0.05	0.19	-0.23	0.42
AN2062	hypothetical protein similar to bipA	0.000909	0.05	0.21	-0.07	0.34
AN8106	conserved hypothetical protein	0.000912	-0.02	0.18	0.03	0.03
AN9522	isopenicillin N-CoA epimerase, putative	0.000929	0.37	-0.65	1.15	0.20
AN9363	conserved hypothetical protein	0.000930	0.51	-0.14	0.18	0.36
lamB AN0886	Lactam utilization protein lamB	0.000930	-0.07	-0.66	0.12	0.43
AN6775	acyl-CoA:6-aminopenicillanic-acid-acyltransferase, putative	0.000940	-0.41	-0.52	0.22	-0.08
AN5217	primary component of eisosomes	0.000946	0.01	0.41	-1.04	0.75
AN1986	mitochondrial chaperone Frataxin, putative	0.000961	-0.14	-0.29	-0.55	0.50
AN1074	hypothetical glycine cleavage H-protein	0.000964	-0.40	-0.38	-0.29	0.12
AN10602	aldehyde dehydrogenase family protein, putative	0.000968	0.09	-0.04	0.19	-0.05
AN5109	ketoreductase, putative	0.001016	0.09	-0.29	0.11	0.22
AN1553	Asp hemolysin-like protein	0.001022	-0.18	-0.12	-1.32	0.98
AN0574	3-oxoacyl-(acyl-carrier-protein) reductase	0.001039	0.26	0.02	-0.02	0.06
AN8478	conserved hypothetical protein	0.001051	0.64	0.25	-0.23	0.12
AN5411	cyanamide hydratase, putative	0.001053	-0.25	-0.31	-1.55	0.94
AN5446	hypothetical protein ANIA_05446	0.001101	-0.14	0.07	-0.88	0.54
AN7074	oxidoreductase, short chain dehydrogenase/reductase family, putative	0.001116	0.31	-0.53	0.45	0.07
AN1734	3-dehydroshikimate dehydratase, putative	0.001118	-0.21	-0.31	-1.73	0.78
AN11085	conserved hypothetical protein	0.001195	0.21	-0.64	0.38	0.10
AN3554	conserved hypothetical protein	0.001205	-0.30	0.74	-0.48	0.00
AN4256	lipase, putative	0.001220	-0.26	-0.25	-0.39	0.63
AN3674	hypothetical PH domain protein	0.001221	0.12	-0.20	0.31	-1.06
bglM AN7396	beta-glucosidase	0.001224	0.04	-0.56	1.33	-0.46
AN11139	actin binding protein	0.001231	-0.24	-0.16	0.00	-0.61
AN1003	hypothetical protein similar to isocitrate dehydrogenase	0.001235	-0.15	0.24	-0.61	0.31
AN5831	glutathione S-transferase	0.001238	0.24	-0.82	0.62	-0.31
AN1222	hypothetical protein similar to S-adenosylmethionine synthetase	0.001240	0.09	-0.01	0.14	-0.29
AN7008	3-hydroxybutyryl-CoA dehydrogenase, putative	0.001241	-0.04	-0.37	-0.41	0.25
AN4889	THUMP domain protein	0.001244	0.06	-0.73	0.11	0.23
AN2894	LEA domain protein	0.001282	-0.21	0.26	-1.55	0.90
AN8764	aromatic ring-opening dioxygenase LigB subunit, putative	0.001303	0.04	-0.86	0.43	-0.12
AN5713	t-complex protein 1, eta subunit, putative	0.001312	0.04	0.24	-0.32	-0.01
AN7181	conserved hypothetical protein	0.001318	0.24	-0.36	0.43	-0.43
AN3703	conserved hypothetical protein	0.001343	-0.13	-0.23	-1.31	1.04
AN9103	apoptosis-inducing factor	0.001358	0.30	-0.04	-0.52	0.28
AN1882	NADH-dependent flavin oxidoreductase, putative	0.001364	-0.20	-0.43	-0.22	0.19
AN5719	60S acidic ribosomal protein P1	0.001373	0.01	0.31	0.04	0.26
AN6287	ATP synthase oligomycin sensitivity conferral protein, putative	0.001378	0.00	-0.13	-0.50	-0.12
acuD AN5634	Isocitrate lyase (ICL)(Isocitratase)(Isocitrase)	0.001379	-0.03	0.09	-1.57	0.91
AN1396	glycerol-3-phosphate dehydrogenase, mitochondrial	0.001392	0.04	0.22	-0.43	0.38
AN5280	conserved hypothetical protein	0.001411	0.17	-0.02	-0.77	0.81
AN6812	conserved hypothetical protein	0.001412	0.14	-0.56	0.29	0.01
AN0385	branched-chain amino-acid transaminase, putative	0.001452	0.20	-0.70	0.41	-0.08
AN1754	conserved hypothetical protein	0.001455	-0.12	-0.06	-1.04	0.50
AN11121	conserved hypothetical protein	0.001463	-0.53	-0.46	0.09	-0.03
velB AN0363	VelB	0.001495	0.07	0.01	-0.41	0.25
AN10469	oxidoreductase, short-chain dehydrogenase/reductase family	0.001496	0.32	-0.58	0.20	0.17
AN7349	Alpha-1,3-glucanaseMutanasePutative uncharacterized protein;;	0.001508	0.16	-0.13	-0.51	0.22
AN11498	hypothetical protein ANIA_11498	0.001526	-0.37	-0.78	0.70	-0.74
AN8434	ankyrin repeat protein	0.001534	-0.17	0.83	-0.18	-0.05
AN6398	UDP-galactose 4-epimerase, putative	0.001548	-0.26	-0.36	-1.77	0.87
AN3687	thioredoxin peroxidase/alkyl hydroperoxide reductase	0.001553	-0.11	0.19	-0.42	0.17
AN10150	Putative beta-transglucosylase. Family GH17. A fumigatus Bgt1-like	0.001575	0.45	-0.05	-0.17	0.08
cnaA AN8820	Serine/threonine-protein phosphatase 2B catalytic subunit (Calmodulin-dependent calcineurin A subunit)	0.001585	-0.09	0.22	-0.08	-0.29
AN10631	hypothetical protein ANIA_10631	0.001594	-0.38	-0.61	-1.07	0.75
AN5535	cell cycle control protein (Cwf19), putative	0.001606	-0.27	0.00	-0.02	-0.12
AN10032	ATP synthase delta chain, mitochondrial precursor, putative	0.001640	0.13	-0.78	-0.08	-0.21
AN0952	acid phosphatase, putative	0.001644	-0.10	-0.37	0.12	-0.01
AN4055	acid phosphatase PHOa	0.001651	-0.25	-0.34	0.15	-0.19
AN10754	nuclear protein export protein Yrb2, putative	0.001738	-0.15	-0.26	-0.13	-0.36
AN4300	NADH-ubiquinone oxidoreductase 21 kDa subunit, putative	0.001742	0.22	0.35	-0.09	0.14
AN2231	SAP domain protein	0.001787	-0.12	-0.20	-0.30	-0.10
AN4977	electron transfer flavoprotein-ubiquinone oxidoreductase	0.001802	-0.14	0.15	-0.59	0.20
AN1105	mitochondrial import receptor subunit tom22	0.001837	0.09	0.16	-0.21	0.11
AN2069	cytochrome b5, putative	0.001913	0.14	-0.63	0.65	-0.63

AN6856	conserved hypothetical protein	0.001921	0.05	-0.29	-1.29	0.84	
AN7817	conserved hypothetical protein	0.001923	-0.37	0.32	0.07	0.33	
sfh5 AN8233	Phosphatidylinositol transfer protein sfh5 (PITP_sfh5)	0.001935	0.15	-0.01	0.06	-0.35	
stcT AN7807	Putative sterigmatocystin biosynthesis protein stcT	0.002000	0.12	0.92	-0.46	0.22	
AN10219	conserved hypothetical protein	0.002009	-0.15	-0.28	-0.11	-0.47	
AN4297	NADH-ubiquinone oxidoreductase subunit B, putative	0.002012	0.07	0.38	-0.14	0.40	
AN3223	6-phosphofructo-1-kinase (phosphofructokinase)	0.002023	-0.07	-0.24	-0.35	0.24	
AN6185	conserved hypothetical protein	0.002038	0.17	-0.18	0.27	0.09	
AN0567	hypothetical protein ANIA_00567	0.002046	0.23	-0.62	1.37	-0.65	
AN5970	disulfide isomerase, putative	0.002057	-0.03	0.20	-0.08	-0.01	
AN5563	NADP(+)-dependent glycerol dehydrogenasePutative uncharacterized protein ;	0.002073	-0.15	-0.50	-0.46	0.64	
AN1523	ATP synthase alpha chain, mitochondrial precursor	0.002079	0.03	-0.02	-0.44	0.44	
mcr1 AN0432	NADH-cytochrome b5 reductase 2 (Mitochondrial cytochrome b reductase)	0.002084	0.25	-0.10	-0.47	0.87	
AN5994	yjeF domain protein	0.002127	0.08	-0.28	-0.23	0.40	
mic60 AN3843	conserved hypothetical protein	0.002173	0.01	0.04	0.13	-0.32	
citA AN8275	Citrate synthase, mitochondrial Precursor	0.002197	-0.08	-0.38	-0.93	0.75	
AN4039	Rhodanese domain protein	0.002209	0.17	-0.61	-0.46	0.09	
AN8867	seryl-tRNA synthetase	0.002217	-0.01	0.68	-0.32	0.26	
AN8641	conserved hypothetical protein	0.002243	-0.17	0.16	-1.69	0.52	
AN1094	NADH dehydrogenase	0.002286	-0.09	0.67	-0.10	-0.10	
AN11072	diacylglycerol acyltransferase type 2A	0.002293	-0.03	-0.16	-0.16	-0.01	
AN5577	Superoxide dismutase	0.002297	-0.31	-0.37	-0.87	0.58	
AN4825	conserved hypothetical protein	0.002297	-0.10	-0.60	0.21	-0.33	
AN4474	conserved hypothetical protein	0.002314	0.25	0.59	-0.37	0.75	
mndB AN3368	Beta-mannosidase	0.002320	0.55	-0.82	0.38	-0.07	
AN3739	RNP domain protein	0.002329	0.41	0.05	0.18	-0.09	
aspC AN6002.2	FAD-dependent monooxygenase, putative	0.002341	0.53	-0.24	-0.70	0.96	
AN3197	dihydrofolate reductase family protein	0.002345	-0.09	-0.49	-0.12	-0.10	
AN10495	coenzyme A transferase, putative	0.002405	0.41	-0.43	-0.16	0.80	
AN1426	hypothetical serine carboxypeptidase	0.002426	0.22	-0.22	0.91	-0.46	
AN2311	phosphomevalonate kinase	0.002446	0.15	0.12	0.02	0.47	
AN3351	conserved hypothetical protein	0.002483	-0.18	-0.67	0.56	-0.41	
AN8370	conserved hypothetical protein	0.002522	0.16	0.37	-0.19	0.01	
AN10533	large subunit of trehalose 6-phosphate synthase	0.002568	-0.10	0.35	-0.53	0.12	
AN1140	hypothetical protein similar to dehydroshikimate dehydratase	0.002594	1.12	-0.55	0.18	-0.23	
AN6346	hypothetical dihydroxy-acid dehydratase	0.002596	-0.28	-0.47	0.14	0.07	
AN1059	Carnitine acetyl transferase FacC	0.002634	0.02	0.14	-0.60	0.44	
AN2588	conserved hypothetical protein	0.002643	0.04	-0.23	0.43	-0.05	
AN7367	nitrilase	0.002691	0.10	-0.69	0.61	-0.47	
AN5953	iron-sulfur cluster assembly accessory protein Isa2, putative	0.002714	-0.09	0.30	-0.45	0.49	
AN5021	trehalose synthase (Ccg-9), putative	0.002726	-0.16	-0.44	-1.12	0.87	
AN10358	conserved hypothetical protein	0.002740	0.17	-0.35	0.52	-0.21	
AN2439	Spindle assembly checkpoint protein SLDB	0.002757	0.26	-0.55	0.24	0.06	
AN7558	conserved hypothetical protein	0.002771	-0.26	-0.13	-0.43	0.07	
AN1342	hypothetical alanine-glyoxylate aminotransferase	0.002781	-0.14	-0.96	0.42	-0.06	
AN7600	SE, putative sulfite reductase beta subunit hemoprotein,ferredoxin oxidoreductase	0.002783	-0.21	-0.45	0.23	-0.04	
AN2776	conserved hypothetical protein	0.002856	-0.03	-0.11	-0.05	0.27	
tdiB AN8514	Putative uncharacterized protein TdiB;	0.002886	0.09	-0.97	0.59	-0.73	
AN4064	ADP,ATP carrier protein	0.002901	0.07	0.34	-0.21	0.28	
AN5803	hypothetical protein similar to fimbrin	0.002920	-0.05	0.34	-0.06	0.18	
AN0747	Mitochondrial-processing peptidase subunit beta, mitochondrial [Precursor]	0.002969	0.13	0.46	-0.34	0.17	
AN3466	dihydrolipamide S-succinyltransferase	0.002984	-0.08	0.25	-1.06	0.57	
AN3867	hypothetical protein similar to CaaX farnesyltransferase alpha subunit	0.002992	-0.09	-0.60	-0.04	-0.09	
AN2977	mitochondrial phosphate carrier protein, putative	0.002999	-0.04	0.17	-0.15	0.26	
AN10440	NADH-ubiquinone oxidoreductase 39 kDa subunit, putative	0.003078	0.09	0.27	-0.34	0.11	
AN0943	mitochondrial F1F0-ATP synthase g subunit, putative	0.003090	0.29	0.36	-0.24	-0.01	
AN10472	thiamine biosynthetic bifunctional enzyme, putative	0.003139	-0.11	-0.36	-0.45	0.61	
AN6677	COMPASS complex subunit Sdc1, putative	0.003166	-0.04	0.31	-0.33	0.16	
AN5325	conserved hypothetical protein	0.003177	-0.09	0.55	-1.09	0.67	
cbhB AN0494	1,4-beta-D-glucan-cellulohydrolyasePutative uncharacterized protein ;	0.003308	-0.07	-1.13	0.43	-1.25	
AN1841	NmrA-like family protein, putative	0.003320	0.24	-0.69	0.50	-0.14	
AN1269	mitochondrial carrier protein, putative	0.003335	-0.14	0.43	-1.33	0.41	
AN2236	DUF500 domain protein	0.003339	-0.15	0.44	-0.65	0.25	
AN10973	citrate synthase, putative	0.003347	0.51	-0.28	-0.07	0.58	
AN6807	conserved hypothetical protein	0.003369	0.01	-0.53	0.89	-0.94	
AN10712	snoRNP protein (gar1), putative	0.003386	0.76	-0.04	0.55	0.28	
rse1 AN5452	Pre-mRNA-splicing factor rse1	0.003402	-0.12	-0.59	0.03	-0.04	
AN6639	2-methylcitrate dehydratase	0.003421	0.04	-0.29	-0.29	0.58	
AN0052	short chain dehydrogenase/reductase family	0.003457	0.51	-0.66	0.58	0.10	
AN3431	nicotinate-nucleotide diphosphorylase	0.003486	-0.31	-0.72	0.33	0.22	
AN2470	alcohol dehydrogenase, putative	0.003531	0.01	0.51	-1.56	0.82	
AN5629	NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial precursor	0.003534	0.02	0.29	-0.67	0.56	
AN4250	mitochondrial carrier protein (Ymc1), putative	0.003600	0.15	0.63	0.06	0.10	
AN2762	glutaryl-CoA dehydrogenase, putative	0.003600	-0.17	-0.71	0.15	0.07	
AN5132	mitochondrial GTP/GDP transporter Ggc1, putative	0.003654	0.12	0.37	-0.19	0.19	
AN2415	DNA-directed RNA polymerase I and III subunit Rpc40, putative	0.003661	0.15	-0.23	-0.03	0.23	
AN0558	putative 1,3-beta-transglycosylase, GH72 family	0.003688	-0.04	0.22	0.98	-0.43	
AN0861	autophagy-related protein Atg27	0.003704	-0.14	0.05	-0.25	-0.23	
AN1154	endosomal cargo receptor (P24), putative	0.003728	0.28	0.51	0.19	0.63	
AN0034	dihydroxyacetone kinase	0.003735	0.09	0.16	-0.28	0.37	

AN8274	mitochondrial DNA replication protein (Yhm2), putative	0.003748	-0.06	0.31	-0.19	-0.02
AN1480	ureidoglycolate hydrolase, putative	0.003753	-0.06	-0.79	0.12	0.09
AN4127	hypothetical protein ANIA_04127	0.003773	0.42	-0.24	-0.31	0.82
AN0075	protein disulfide-isomerase	0.003798	-0.06	0.49	-0.19	-0.30
AN10901	hypothetical glycine cleavage system P protein	0.003842	0.07	-0.43	-0.14	0.25
AN3842	RAB GTPase Ypt5, putative	0.003850	0.00	0.02	-0.41	-0.09
AN6354	ubiquitin C-terminal hydrolase, putative	0.003912	-0.17	0.07	-0.51	0.27
AN6717	malate dehydrogenase	0.003951	-0.06	-0.58	0.04	0.20
AN4230	CAIB/BAIF family enzyme	0.004006	0.24	-0.40	-0.58	0.69
AN0858	heat shock protein	0.004041	0.00	0.60	-0.47	0.06
AN6279	hypothetical protein similar to carnitine acetyl transferase	0.004047	0.04	-0.49	-0.51	0.64
AN10552	acyl-CoA thioester hydrolase, putative	0.004115	0.01	-0.27	-0.88	0.99
cysA AN8565	Putative serine O-acetyltransferase	0.004126	-0.19	-0.13	-0.73	0.66
AN3573	conserved hypothetical protein	0.004139	0.32	-0.07	0.22	-0.52
AN6394	acyl-CoA dehydrogenase family protein	0.004194	0.25	-0.29	0.05	0.16
AN7497	NADH-ubiquinone oxidoreductase 18 kDa subunit, putative	0.004278	0.23	0.42	-0.33	0.33
AN5589	conserved hypothetical protein: glycerol kinase	0.004356	0.22	-0.31	-0.72	0.77
AN3793	Serine/threonine protein phosphatase	0.004365	-0.06	-0.16	-0.14	0.30
AN10365	ubiquitin conjugating enzyme (UbcB), putative	0.004380	-0.08	0.35	-0.12	0.04
AN11187	conserved hypothetical protein	0.004419	0.06	-0.42	0.67	-0.39
AN10012	aminomethyl transferase, putative	0.004545	0.39	0.53	-0.42	0.91
AN10709	Glutamine-fructose-6-phosphate transaminase	0.004636	-0.07	0.44	-0.46	0.08
AN6176	tubulin-specific chaperone Rbl2, putative	0.004645	-0.12	-0.26	0.35	-0.25
AN9090	Putative RNA binding proteinPutative uncharacterized protein;	0.004667	0.39	-0.24	-0.40	0.47
AN5387	DUF453 domain protein	0.004710	0.30	-0.19	0.03	0.32
aspnd1 AN1832	Antigen 1 Precursor (ASPND1)	0.004773	0.16	-1.17	-0.47	0.21
AN1394	Putative uncharacterized proteinSeptin;	0.004836	0.29	0.39	-0.18	0.14
AN0559	mitochondrial import receptor subunit (Tom20), putative	0.004839	-0.24	0.39	-0.70	-0.02
AN1270	Eukaryotic translation initiation factor 3 subunit H (eIF3h)	0.004883	-0.14	1.16	-0.29	-0.10
cipB AN7895	Zinc-binding alcohol dehydrogenase domain-containing protein cipB (Concanamycin-induced protein B)	0.004927	0.09	-1.21	0.72	-0.53
sec23 AN0261	Protein transport protein sec23	0.004977	0.25	0.24	-0.23	0.32
AN7770	oxidoreductase, short-chain dehydrogenase/reductase family	0.005009	0.38	-0.26	0.88	-0.12
AN2479	acetyltransferase, GNAT family, putative	0.005018	0.18	-0.01	-1.22	1.36
AN3790	putative alpha 1,3 glucanase, GH71 family	0.005036	0.85	-0.15	0.27	-0.43
AN10626	hypothetical protein similar to ATP synthase alpha chain	0.005044	0.14	0.36	-1.22	1.10
AN1252	conserved hypothetical protein	0.005086	-0.18	-0.17	0.19	-0.05
AN8182	Septin Fragment	0.005094	0.20	-0.34	0.01	0.03
AN0338	cytochrome P450, putative	0.005111	0.00	0.25	0.46	-0.35
AN1591	conserved hypothetical protein	0.005114	0.33	0.72	-0.27	-0.05
AN6274	short chain dehydrogenase/reductase family	0.005150	0.02	0.21	-1.65	0.90
AN1433	triacylglycerol lipase, putative	0.005157	0.11	-0.21	0.94	-0.82
AN4009	conserved hypothetical protein	0.005174	0.60	-0.41	0.29	-0.22
AN8872	AMP deaminase Amd1, putative , partial	0.005183	-0.03	-0.24	-0.51	0.36
AN3140	hypothetical protein ANIA_03140	0.005189	-0.16	0.96	-0.32	-0.06
AN4281	GTP-binding protein ypt1	0.005230	0.06	0.10	0.08	-0.18
AN7011	copper resistance protein Crd2, putative	0.005257	-0.03	-0.01	-1.27	0.62
AN2875	hypothetical protein similar to fructose 1,6-biphosphate aldolase	0.005270	-0.10	-0.59	-0.05	0.43
AN10202	Heat shock protein 70	0.005414	-0.11	0.51	-0.31	0.34
AN2264	Sad1/UNC domain protein	0.005451	0.15	-0.11	0.55	-0.23
AN7657	1,3-beta-glucanosyltransferase Gel1	0.005518	-0.07	-0.76	0.54	-0.81
AN2404	DUF1295 domain protein	0.005581	-0.09	0.54	-1.03	0.79
AN0390	conserved hypothetical protein	0.005623	0.29	0.38	-0.27	0.21
cpyA AN5442.2	CarboxypeptidasePutative uncharacterized protein;	0.005629	-0.07	-0.31	0.34	-0.43
casA AN5712	Metacaspase-1 Precursor	0.005644	0.11	0.39	0.13	-0.24
AN6642	sodium ion P-type ATPase	0.005668	-0.04	0.39	-0.24	-0.08
AN1769	3'(2'),5'-bisphosphate nucleotidase (3'(2'),5'-bisphosphonucleoside 3'(2')-phosphohydrolase)(DPNPase)	0.005732	0.24	-0.06	0.17	0.45
AN2116	NAD dependent epimerase/dehydratase, putative	0.005792	0.43	0.40	-0.51	0.23
chiB AN4871	ChitinasePutative uncharacterized protein;	0.005832	-0.20	-0.93	-0.23	-0.45
AN2237	carboxypeptidase S1, putative	0.005923	-0.17	-0.70	0.70	-0.41
AN10753	phosphoribosylglycinamide formyltransferase	0.005951	0.16	1.04	-0.81	0.71
lys4 lysF AN6521	Homoaconitase, mitochondrial Precursor (Homoaconitate hydratase)	0.005974	-0.15	0.04	-0.40	0.37
AN4965	Ccr4-Not transcription complex subunit (NOT1), putative	0.005994	-0.49	0.06	-0.04	-0.20
AN4390	GPI-anchored cell wall organization protein Ecm33	0.006000	0.24	-0.17	1.23	-0.72
AN0297	NADH-quinone oxidoreductase Pst2, putative	0.006041	-0.19	-0.51	0.38	-0.19
AN10771	translation initiation protein Sua5	0.006104	0.00	0.62	-0.58	0.42
AN8050	UPF0047 domain protein	0.006119	-0.43	-0.48	0.25	-0.30
AN10459	translation initiation factor eif-2b epsilon subunit, putative	0.006345	-0.02	0.56	-0.21	0.08
AN6301	conserved hypothetical protein	0.006473	-0.05	0.16	-0.62	0.83
AN4613	37S ribosomal protein Rsm22	0.006483	-0.31	0.25	-0.24	0.19
AN4809	Glutaminase A	0.006554	-0.10	-0.52	0.87	-0.86
AN5015	condidiation-specific protein 10	0.006554	-0.18	-0.14	-1.57	0.90
AN6640	amidohydrolase, putative	0.006589	-0.09	-0.38	-0.54	0.34
AN5830	haloacid dehalogenase, type II	0.006635	0.01	-0.45	-0.23	0.36
AN4739	hypothetical protein similar to N-succinyl-5-aminoimidazole-4-carboxamide ribotide synthetase	0.006669	0.08	0.65	-0.65	0.58
AN0443	alcohol dehydrogenase, zinc-containing, putative	0.006685	-0.01	-0.36	0.00	-0.01
AN6423	conserved hypothetical protein	0.006755	-0.02	-0.74	0.61	-0.40
stcL cyp60B AN11013	Probable sterigmatocystin biosynthesis P450 monooxygenase stcL (Cytochrome P450 60B)	0.006846	-0.13	0.72	0.56	-0.41
AN3121	conserved glutamic acid-rich protein	0.006908	-0.03	0.21	-0.27	-0.14
AN1780	metallopeptidase family M24, putative	0.006997	0.00	-0.48	-0.34	0.20
rsm10 AN6489	30S ribosomal protein S10, mitochondrial Precursor (Mitochondrial ribosomal small subunit protein 10)	0.007060	0.14	0.15	-0.46	0.38

AN4967	acid phosphatase, putative	0.007092	0.17	-0.17	-0.22	0.16
AN8808	hypothetical protein ANIA_08808	0.007147	-0.15	-0.54	0.80	-0.65
AN4021	C2H2 finger domain protein, putative	0.007161	0.23	-0.31	0.01	-0.19
AN1150	acetylornithine aminotransferase, ornithine transaminase	0.007178	0.31	-0.37	-0.05	0.46
AN6705	component of the RSC chromatin remodeling complex	0.007190	0.00	0.13	-0.50	0.10
AN5977	ketoreductase	0.007289	0.40	-0.28	-0.23	0.42
AN10864	conserved hypothetical protein	0.007295	0.35	0.43	-0.08	-0.46
AN10981	GTP cyclohydrolase II, putative	0.007326	0.17	0.47	-0.19	-0.05
ecm14 AN6119	zinc carboxypeptidase, putative	0.007348	0.11	-0.32	0.57	-0.52
AN1063	hypothetical protein similar to possible NADH-ubiquinone oxidoreductase	0.007399	-0.06	0.66	-0.48	0.24
acoB AN3894	aconitase hydratase, mitochondrial, putative	0.007418	0.08	-0.01	-0.33	0.38
AN11097	conserved hypothetical protein	0.007421	0.58	-0.34	0.73	-0.85
AN5454	class V chitinase ChiB1	0.007475	-0.13	-0.16	0.87	-0.43
AN3601	conserved hypothetical protein	0.007496	0.37	-0.54	1.01	-0.83
AN7111	peroxisomal multifunctional beta-oxidation protein (MFP), putative	0.007498	0.30	0.17	-0.18	0.17
AN1149	conserved hypothetical protein	0.007548	-0.19	0.40	-0.34	-0.07
AN0562	peroxisomal AMP binding enzyme, putative	0.007568	0.22	0.16	-0.39	0.44
glnA AN4159	Glutamine synthetase (GS)(Glutamate--ammonia ligase)	0.007580	0.35	0.57	-0.33	0.18
AN10584	iron-sulfur cluster biosynthesis protein Isd11, putative	0.007588	0.09	0.35	-0.62	0.24
AN2835	conserved hypothetical protein	0.007646	0.00	-0.35	0.12	-0.96
AN0686	prohibitin complex subunit Phb1, putative	0.007685	0.06	0.38	-0.59	0.21
AN3627	conserved hypothetical protein	0.007724	0.00	0.22	-1.30	0.37
fal1 AN8016	ATP-dependent RNA helicase fal1	0.007839	0.09	0.77	-0.44	-0.09
AN0065	WD repeat protein	0.007945	-0.14	-0.25	0.50	-0.02
AN0646	hypothetical protein similar to possible regulator of nonsense transcripts	0.008036	0.02	0.34	-0.63	0.78
AN6505	transcriptional corepressor	0.008083	0.45	0.23	-0.34	0.18
AN10661	5'-nucleotidase, putative	0.008134	0.81	0.42	-0.03	0.36
AN6286	conserved hypothetical protein	0.008143	-0.04	0.56	-0.49	0.45
AN1428	N-acetylglucosamine-6-phosphate deacetylase (NagA), putative	0.008213	-0.02	-0.54	-0.12	0.50
AN0183	molybdopterin binding domain protein	0.008219	-0.01	0.68	-0.32	0.49
AN6231	Bifunctional tryptophan synthase TRPB	0.008239	-0.06	0.08	-0.34	-0.11
AN10965	DUF866 domain protein	0.008524	0.14	-0.78	0.86	-0.48
AN3807	oxysterol binding protein (Osh7), putative	0.008555	-0.08	-0.04	0.01	-0.53
aim24 AN10466	mitochondrial protein Fmp26, putative	0.008642	-0.11	0.09	-0.65	0.24
rhoA AN5740	GTP-binding protein rhoA Precursor (Rho1 protein homolog)	0.008667	0.23	0.46	-0.23	-0.19
AN7864	conserved hypothetical protein	0.008685	0.52	-0.46	0.14	0.42
AN2061	alcohol dehydrogenase, putative	0.008695	-0.24	-0.16	0.13	0.00
AN8335	conserved hypothetical protein	0.008706	-0.13	-0.55	-0.98	0.88
AN5790	isocitrate dehydrogenase subunit 1, mitochondrial precursor	0.008795	-0.03	0.44	-0.57	0.20
AN5880	V-type ATPase F subunit, putative	0.008873	0.07	-0.06	0.19	-0.31
AN8068	extracellular endogluconase, putative	0.008883	-0.25	-0.79	1.53	-1.03
AN6232	Vacuolar ATP synthase subunit B Fragment	0.008949	0.15	0.41	-0.02	-0.03
AN5068	conserved hypothetical protein	0.008968	-0.05	-0.79	0.66	-0.45
AN1364	DUF1000 domain protein	0.009113	-0.03	-0.99	1.12	-0.35
AN0870	mitochondrial phosphate carrier protein (Mir1), putative	0.009129	0.06	0.27	-0.99	0.49
AN2316	hypothetical protein similar to cytochrome c oxidase polypeptide V, mitochondrial precursor	0.009153	-0.03	0.39	-0.19	0.37
AN4915	RAB GTPase Vps21/Ypt51, putative	0.009220	0.16	0.38	-0.21	-0.31
AN0472	putative endo beta 1,3 glucanase, GH81 family	0.009246	-0.28	-0.54	-0.70	-0.12
AN8866	3-phosphoglycerate dehydrogenase, hypothetical	0.009288	0.16	0.58	-0.64	1.00
apdG AN8415	Acyl-CoA dehydrogenase	0.009305	-0.02	0.13	0.43	-0.47
AN6031	oxidoreductase, 2-nitropropane dioxygenase family, putative	0.009347	0.11	0.49	0.02	-0.03
AN8330	alcohol dehydrogenase, zinc-containing, putative	0.009400	-0.12	-0.59	0.37	-0.14
AN3082	cleavage and polyadenylation specificity factor, putative	0.009440	0.42	0.35	-0.82	0.13
AN6906	cell cycle control protein (Cwf8), putative	0.009507	-0.12	0.20	0.14	-0.13
AN5671	PH domain protein	0.009679	0.03	0.17	-0.08	0.02
AN3334	conserved hypothetical protein	0.009707	0.04	-0.16	-1.41	0.84
AN2866	NAD binding Rossmann fold oxidoreductase, putative	0.009829	-0.02	-0.54	0.46	-0.30
AN7554	oxidoreductase, putative	0.009871	0.01	-0.45	0.17	0.09
AN1158	cell wall biogenesis protein phosphatase Ssd1, putative	0.009904	0.02	0.33	-0.50	0.28
AN2144	urease accessory protein UreD	0.009915	-0.18	-0.65	0.74	-0.80
mpdA AN5975	Mannitol-1-phosphate 5-dehydrogenase (M1PDH)(MPDH)(MPD)	0.010013	0.21	0.29	-0.31	0.17
AN3695	anthranilate synthetase	0.010022	0.05	0.42	-0.38	0.62
AN3019	proteasome regulatory particle subunit (RpnL), putative	0.010374	0.03	0.18	-0.47	0.11
AN1444	NADH-ubiquinone oxidoreductase 178 kDa subunit, putative	0.010400	-0.19	0.07	-0.11	0.13
AN6066	isochorismatase family hydrolase, putative	0.010472	-0.29	-0.55	0.79	-0.53
AN0470	30S ribosomal protein S7, putative	0.010549	0.12	0.04	-0.33	0.36
AN5909	Dihydroorotate dehydrogenasePutative uncharacterized protein ;	0.010569	0.13	0.27	-0.52	0.02
AN6557	NADH-ubiquinone oxidoreductase B14 subunit, putative	0.010714	0.22	0.11	-0.29	0.14
AN0745	hypothetical protein similar to fibrillarin, nucleolar protein	0.010742	-0.03	0.31	-0.57	0.31
AN0895	hypothetical oxidoreductase	0.010866	0.18	-0.52	-1.33	0.88
AN4018	glutamate carboxypeptidase, putative	0.010998	0.00	-0.20	-0.14	0.17
AN8435	hypothetical protein ANIA_08435	0.011020	0.04	0.18	-0.12	-0.41
AN3163	stomatin family protein	0.011140	0.16	0.24	0.51	-0.38
AN6810	ThiI/Pfpl family protein	0.011242	-0.22	0.40	-1.29	0.75
AN0797	hypothetical histidine biosynthesis trifunctional protein	0.011269	-0.16	-0.58	0.03	0.23
AN4145	conserved hypothetical protein	0.011283	-0.05	0.18	0.11	0.03
AN7568	Gamma-butyrobetaine hydroxylase subfamily, putative	0.011386	0.08	-0.41	-0.78	0.67
AN2930	fumarylacetate hydrolase family protein	0.011414	-0.08	0.68	0.08	-0.03
AN3070	t-complex protein 1, zeta subunit, putative	0.011429	-0.07	0.51	-0.56	-0.20
alcC adh3 AN2286	Alcohol dehydrogenase 3 (Alcohol dehydrogenase III)(ADH III)	0.011431	0.35	-0.50	0.26	-0.47

AN5747	hypothetical protein similar to PSMC6 subunit	0.011468	0.08	0.19	-0.18	0.02
AN10257	KH domain RNA binding protein	0.011599	-0.08	0.24	-0.46	-0.11
AN0941	alpha-1,4-glucosidase	0.011604	-0.11	-0.44	0.23	-0.33
AN7194	quinone oxidoreductase, putative	0.011658	-0.02	-0.54	0.05	0.05
AN9085	U5 snRNP complex subunit, putative	0.011718	-0.07	-0.15	0.19	-0.09
be1 AN2314	1,4-alpha-glucan-branched enzyme (Glycogen-branched enzyme)	0.011835	0.15	0.29	-0.38	0.20
AN5004	hypothetical protein ANIA_05004	0.011897	-0.32	0.27	-0.54	-0.04
AN0051	conserved hypothetical protein: thymine dioxygenase	0.011920	-0.05	0.65	-0.27	0.16
AN4714	ThiF domain protein, putative	0.012001	0.16	0.03	-0.63	0.40
AN2105	small nuclear ribonucleoprotein SmD1, putative	0.012017	0.10	0.07	0.21	0.33
AN4655	iron-sulfur cofactor synthesis protein (Isu1), putative	0.012025	-0.10	0.55	-0.60	0.16
AN7992	conserved hypothetical protein	0.012075	0.12	-0.01	-1.43	1.83
cysB cysE AN8057	Cysteine synthase (CSase)(O-acetylserine sulfhydrylase)(O-acetylserine (thiol)-lyase)(OAS-TL)	0.012176	-0.23	-0.59	0.53	-0.11
AN2999	Mitochondrial NADP-dependent isocitrate dehydrogenase	0.012271	0.20	-0.13	-0.31	0.65
aguA AN9286	alpha-glucuronidase	0.012299	0.30	-0.33	0.76	-0.54
AN5908	conserved hypothetical protein similar to triosephosphate isomerase	0.012303	0.02	-0.54	0.64	-0.34
AN4483	calcium/calmodulin-dependent protein kinase, putative	0.012368	0.05	0.71	-0.91	0.03
AN2230	FAD dependent oxidoreductase superfamily	0.012379	-0.02	-0.67	0.39	0.17
AN1639	thioredoxin, putative	0.012389	0.15	-0.24	-0.22	0.14
mcsA AN6650	2-methylcitrate synthase, mitochondrial Precursor (Methylcitrate synthase)(Citrate synthase 2)	0.012401	-0.16	-0.58	0.45	-0.02
AN6014	fatty acid activator Faa4, putative	0.012413	-0.24	0.54	-0.42	-0.05
AN2577	peroxisomal dehydratase, putative	0.012457	0.00	-0.52	0.47	-0.13
AN4653	conserved hypothetical protein	0.012465	0.03	-0.81	1.26	-0.72
AN8044	a-pheromone processing metallopeptidase Ste23	0.012584	-0.16	-0.37	-0.06	0.28
AN2435	citrate lyase subunit	0.012602	0.25	0.59	-0.90	0.60
AN4784	ubiquitin thiolesterase (Otub1), putative	0.012605	0.54	0.73	-0.36	-0.34
mde1 AN3593	class II aldolase/adducin domain protein	0.012643	-0.15	-0.61	0.17	0.16
AN8639	synthase subunit of trehalose-6-phosphate synthase/phosphatase complex	0.012750	-0.08	0.46	-0.69	0.41
tdiC AN8515	Putative uncharacterized protein TdiC;	0.012773	0.16	-0.04	-0.29	-0.06
AN6876	oxidoreductase, FAD-binding, putative	0.012776	-0.03	-0.59	0.88	-0.56
AN1763	oxidoreductase, short-chain dehydrogenase/reductase family	0.012937	0.18	-0.62	0.77	-0.66
AN10281	serine/threonine protein phosphatase PPT1	0.013039	-0.22	-0.29	0.21	-0.26
AN4911	conserved hypothetical protein	0.013050	-0.05	0.46	-0.66	0.17
AN8406	Alcohol dehydrogenase	0.013317	0.21	-0.24	0.14	-0.12
AN4830	phosphopantetheoyl-cysteine ligase, putative	0.013327	0.22	0.69	-0.83	0.59
AN10131	ORF Fragment	0.013341	-0.23	-0.57	0.56	-0.19
AN3485	conserved hypothetical protein	0.013368	-0.08	-0.40	-1.16	0.87
AN8606	hypothetical polysaccharide deacetylase	0.013397	0.09	-0.48	0.61	-0.59
AN7944	conserved hypothetical protein	0.013439	-0.13	0.20	-0.30	-0.01
maiA AN1895	Maleylacetooctate isomerase (MAAI)	0.013601	0.46	0.30	-0.09	-0.33
AN0205	conserved hypothetical protein: pantethoyl synthetase	0.013653	0.26	-0.03	-0.77	0.86
cbp4 AN8766	Assembly factor cbp4 (Cytochrome b mRNA-processing protein 4)	0.014016	0.17	0.62	-0.43	0.02
AN6227	aminotransferase family protein (LoiT), putative	0.014030	0.10	-0.16	-0.32	0.33
hmgA AN1897	Homogentisate 1,2-dioxogenase (Homogentisic acid oxidase)	0.014073	0.27	-0.73	0.54	0.06
AN3565	metallo-beta-lactamase domain protein, putative	0.014084	-0.08	-0.75	1.06	-0.92
AN10040	hypothetical protein ANIA_10040	0.014085	-0.02	-0.06	-1.15	1.19
AN4458	snRNP assembly factor, putative	0.014228	0.09	0.35	0.11	0.30
AN0141	tRNA methyltransferase	0.014259	-0.31	-0.07	0.03	0.40
AN8392	alpha-1,4-galactosidase	0.014314	-0.03	-0.56	0.78	-0.68
AN1683	oligosaccharyltransferase subunit ribophorin II, putative	0.014335	-0.15	0.53	0.06	0.03
AN3937	Cwf1 domain protein	0.014385	0.35	-0.03	-0.47	0.80
AN7290	conserved hypothetical protein	0.014408	-0.12	-0.46	-0.78	0.41
AN2306	Ubiquinol-cytochrome c reductase	0.014538	-0.02	0.12	-0.11	-0.04
AN8339	conserved hypothetical protein	0.014582	0.03	0.01	-1.08	0.35
AN8547	glucose-methanol-choline oxidoreductase	0.014586	0.53	-0.42	0.58	0.51
AN1486	ribonuclease P complex subunit Pop2, putative	0.014714	-0.20	-0.62	0.57	-0.65
AN7590	hypothetical protein similar to NADP-dependent mannitol dehydrogenase	0.014775	0.39	-0.36	-0.34	0.58
AN6697	SUN domain protein	0.014821	0.53	-0.20	0.19	-0.49
AN9157	Glutaminyl-tRNA synthetase	0.015286	0.19	-0.21	-0.14	0.25
pkiA pki AN5210	Pyruvate kinase (PK)	0.015295	-0.27	-0.57	0.66	-0.59
AN11039	hypothetical protein ANIA_11039	0.015437	0.44	-0.15	-1.04	0.92
AN2450	ubiquitin-like activating enzyme (UbaB), putative	0.015475	0.34	0.26	-0.36	0.63
chsB AN2523	Chitin synthase B (Chitin-UDP acetyl-glucosaminyl transferase B)(Class-III chitin synthase B)	0.015662	0.09	0.03	0.13	0.11
AN10399	short-chain dehydrogenase/reductase, putative	0.015725	-0.01	0.06	-0.09	-0.05
AN6526	Ieucyl-tRNA synthetase	0.015730	0.19	0.53	-0.58	0.45
AN1759	hypothetical protein ANIA_01759	0.015801	-0.05	0.30	0.53	0.02
AN10507	heat shock protein Hsp20/Hsp26, putative	0.015862	0.69	0.99	-1.38	2.20
AN0142	37S ribosomal protein S5	0.015963	0.13	-0.37	-0.09	0.44
AN8445	aminopeptidase Y, putative	0.016135	0.10	-0.42	0.22	-0.22
easD AN2549	conserved hypothetical protein	0.016187	0.57	0.22	-0.09	0.58
AN1677	short chain dehydrogenase, putative	0.016292	0.24	-0.54	0.29	0.25
AN1015	hypothetical protein similar to glycogen phosphorylase 1	0.016364	0.15	0.03	0.48	-0.54
fes1 AN6543	Hsp70 nucleotide exchange factor fes1	0.016492	-0.08	0.31	-0.40	0.12
AN9138	acetamidase	0.016596	0.14	0.21	0.26	-0.39
AN0380	peptidyl-prolyl cis-trans isomerase, putative	0.016720	0.28	-0.47	-0.18	0.23
AN3955	conserved hypothetical protein	0.016743	-0.07	0.52	-0.19	-0.53
AN4015	eukaryotic translation initiation factor 5A-2	0.016816	-0.08	0.15	-0.08	-0.42
afsf1 AN4891	Histone chaperone asf1 (Anti-silencing function protein 1)	0.016999	0.42	1.05	-0.33	0.22
AN8218	thioredoxin reductase, putative	0.017063	-0.05	-0.46	0.48	-0.58
AN10298	Phosphoserine aminotransferase	0.017072	0.10	0.05	-0.33	0.53

AN2334	hypothetical protein similar to fructose/tagatose bisphosphate aldolase	0.017151	0.08	-0.49	1.13	-0.69
AN2694	oxidoreductase, short chain dehydrogenase/reductase family	0.017240	0.31	-0.24	0.45	-0.41
AN9513	conserved hypothetical protein	0.017261	0.18	-0.28	0.36	-0.64
AN2993	DUF124 domain protein	0.017272	0.00	0.08	0.28	-0.28
candA-C AN2458	cullin binding protein CanA, putative	0.017485	-0.03	0.47	-0.63	0.19
AN2469	short chain dehydrogenase, putative	0.017983	0.60	-0.85	0.41	-0.09
AN4245	neutral/alkaline nonlysosomal ceramidase, putative	0.018172	0.10	-0.66	0.35	-0.61
AN5522	conserved hypothetical protein	0.018246	0.21	-0.46	-0.54	0.47
AN9180	conserved hypothetical protein	0.018297	0.45	0.34	-0.51	0.78
AN1543	hypothetical fumarate reductase	0.018324	0.13	-0.83	0.65	-0.33
AN3020	tripeptidyl peptidase SED3	0.018363	-0.36	0.22	-0.13	0.23
AN5602	co-chaperone	0.018364	-0.15	0.04	-0.10	-0.31
AN1409	acetyl-CoA acetyltransferase, putative	0.018383	0.12	-0.42	0.44	-0.11
AN5354	quinone oxidoreductase, putative	0.018421	0.36	-0.27	-1.22	0.97
AN5564	hypothetical HAD-superfamily hydrolase	0.018431	0.08	0.14	-1.49	0.75
axeA aceA AN6093	Acetylxylose esterase	0.018500	0.17	-0.60	0.76	-0.91
xyI AN0423	NAD(P)H-dependent D-xylene reductase	0.018546	0.25	0.34	0.02	0.28
cprA AN0595	NADPH-cytochrome P450 reductase	0.018661	0.18	-0.04	0.16	0.19
AN10512	acetyl-CoA-acetyltransferase, putative	0.018735	0.07	-0.43	0.23	-0.01
AN1430	betaine aldehyde dehydrogenase (BadH), putative	0.018934	0.01	-0.92	0.55	-0.04
AN11278	DUF543 domain protein	0.018956	0.07	0.20	-0.30	-0.27
AN1405	conserved hypothetical protein	0.018980	0.15	-0.11	-0.48	0.51
AN10174	conserved hypothetical protein	0.018994	-0.12	0.68	-0.24	0.48
AN8862	Aspergillus nidulans myosin V homolog	0.019015	-0.21	0.02	-0.01	-0.34
AN6341	putative coronin homolog	0.019024	0.19	0.56	0.18	0.06
AN5959	prephenate dehydrogenase	0.019115	-0.29	1.20	-0.55	-0.11
xlnD xylA AN2359	Beta-xylosidase	0.019286	0.11	-0.43	0.86	-0.31
AN8710	chitin biosynthesis protein (Chs5), putative	0.019365	0.09	0.21	-0.41	0.05
AN0922	Coatomer subunit delta, putative	0.019412	-0.12	0.53	-0.32	0.23
AN1765	conserved hypothetical protein	0.019536	-0.21	0.33	0.23	-1.20
AN3897	conserved hypothetical protein	0.019874	-0.22	-0.80	-0.33	-0.10
AN2091	tyrosine decarboxylase, putative	0.019995	0.07	-0.42	0.81	-0.22
AN3382	Putative uncharacterized proteinSalicylate 1-monoxygenase;	0.020056	0.02	0.20	0.13	0.49
AN4163	GBLP_NEUCR Guanine nucleotide-binding protein beta subunit-like protein	0.020190	-0.07	-0.37	0.34	-0.22
AN8032	NAD dependent epimerase/dehydratase family protein	0.020234	0.09	-0.10	-0.87	0.79
AN2414	hypothetical protein similar to NADH-ubiquinone oxidoreductase 49 kDa subunit, mitochondrial precursor	0.020251	0.20	-0.03	-0.26	0.22
AN11146	cytidine deaminase, putative	0.020340	0.14	-0.74	0.80	-0.51
AN7230	cellobiose dehydrogenase	0.020341	0.30	-0.63	0.14	-0.11
AN11543	conserved hypothetical protein	0.020470	-0.31	1.06	-0.15	0.08
AN0174	D-amino acid oxidase	0.020631	-0.11	-0.33	0.35	-0.50
nopS8 AN3167	Nucleolar protein 58	0.020729	0.56	0.42	-0.16	0.13
rodA AN8803	Rodlet protein Precursor	0.020898	-0.36	-0.14	-2.36	0.72
AN4897	cell wall protein, putative	0.020944	0.15	0.36	0.53	-0.88
AN0832	peptidase D, putative	0.021016	0.41	0.37	-0.41	0.24
AN0753	nuclear segregation protein (bfr1), putative	0.021115	-0.03	0.28	-0.21	-0.28
AN5440	Putative heme-binding peroxidase	0.021184	-0.06	-0.28	-0.77	0.31
agaA AN2901	Arginase	0.021339	0.00	-0.28	-0.78	0.69
AN4187	TBP associated factor (Mot1), putative	0.021346	-0.05	0.49	-0.21	-0.11
AN3059	hypothetical protein similar to cofactor-independent phosphoglycerate mutase	0.021420	-0.25	-0.50	0.45	-0.19
AN4901	glutaminase, putative	0.021554	0.15	-0.62	0.74	-0.79
AN6476	conserved hypothetical protein	0.021578	0.11	-0.24	-0.42	0.20
AN4899	microbody (peroxisome) biogenesis protein peroxin 19	0.021707	-0.45	-0.09	0.32	-0.74
AN11052	exonuclease II	0.021782	0.03	0.27	-0.83	0.42
AN1667	conserved hypothetical protein	0.021861	0.34	-0.24	-0.55	0.59
AN9130	cholinesterase, putative	0.021871	-0.22	-0.66	0.53	-0.60
AN3191	lipase/esterase, putative	0.021964	0.12	0.04	0.09	-0.11
aldA aspA AN0554	Aldehyde dehydrogenase (ALDH)(ALDH)	0.022045	-0.05	-0.63	0.63	-0.27
AN4948	conserved hypothetical protein	0.022062	0.02	-0.41	0.30	-0.23
nudG AN0420	Dynein light chain, cytoplasmic (8 kDa cytoplasmic dynein light chain)	0.022147	0.04	-0.27	0.54	-0.57
AN8009	thiamine biosynthesis protein	0.022261	0.19	-0.47	0.04	-0.06
AN10243	cell wall biogenesis protein Ecm15, putative	0.022303	-0.26	-0.27	-0.23	0.35
AN7598	conserved hypothetical protein	0.022423	0.23	-0.73	0.80	-0.98
AN5782	fumarylacetate hydrolase family protein	0.022472	0.30	-0.04	-0.06	0.26
AN5764	conserved hypothetical protein	0.022638	-0.09	0.45	-1.07	0.56
AN8932	TIM-barrel enzyme family protein	0.022678	-0.22	0.00	0.28	-0.17
AN4859	Plasma membrane H(+)-ATPasePutative uncharacterized protein;	0.022754	-0.10	0.45	0.14	-0.26
acuE AN6653	Malate synthase, glyoxysomal	0.022800	0.35	0.11	-0.65	0.93
AN0089	Small GTPase AvaA	0.022847	0.34	0.00	0.22	-0.53
AN8628	NADP-dependent alcohol dehydrogenase	0.022847	0.41	-0.03	-1.14	0.80
AN5580	hypothetical protein ANIA_05580	0.022994	-0.06	0.60	-0.52	0.60
AN2508	cysteine desulfurase, alanine biosynthesis, putative	0.023052	-0.03	0.16	-0.51	0.67
AN2878	conserved hypothetical protein	0.023198	-0.09	-0.57	0.40	-0.10
AN9074	conserved glycine-rich protein	0.023438	-0.37	-0.45	-0.51	-0.22
alcB AN3741	Alcohol dehydrogenase 2 (Alcohol dehydrogenase II)(ADH II)	0.023508	0.18	-0.24	0.50	-0.15
AN10637	SPX domain protein	0.023777	0.09	0.66	-0.61	0.22
tim50 AN4490	Mitochondrial import inner membrane translocase subunit tim50 Precursor	0.023833	-0.14	0.17	-0.45	0.40
alcA AN8979	Alcohol dehydrogenase 1 (Alcohol dehydrogenase I)(ADH I)	0.023853	0.39	-0.09	0.45	-0.38
AN1954	37S ribosomal protein Rsm24, putative	0.023941	0.18	-0.17	-0.66	0.66
AN10593	Phosphoserine phosphatase, hypothetical	0.024101	-0.21	0.90	-0.68	0.71
pacC AN2855	pH-response transcription factor pacC/RIM101 Precursor	0.024187	-0.12	-0.14	-0.11	-0.19

AN7691	phosphoesterase superfamily protein	0.024281	-0.06	-0.40	1.23	-0.93
AN2208	conserved expressed oxidoreductase	0.024304	0.01	-0.53	0.03	0.27
AN8145	DUF985 domain protein	0.024362	0.39	-0.29	1.35	-0.79
AN4822	tartrate dehydrogenase, putative	0.024418	0.34	-0.74	0.71	-0.85
AN4216	alpha-L-rhamnosidase B, putative	0.024540	-0.17	0.46	-0.54	0.15
AN1923	alanine transaminase	0.024579	0.05	-0.42	-0.20	0.40
cbf5 swoc AN8851	tromere/microtubule-binding protein CBF5 (Centromere-binding factor 5)(Small nucleolar RNP protein CBF5)	0.024619	0.62	-0.03	0.23	0.37
AN8763	NADH-ubiquinone oxidoreductase 105 kDa subunit	0.024845	-0.14	0.04	-0.35	-0.08
AN4504	putative endo mannanase, GH76 family	0.024886	-0.07	-0.47	0.08	-0.05
AN3168	vacuolar ATP synthase subunit d, putative	0.024986	0.03	0.54	-0.01	-0.18
AN2801	aldo-keto reductase (AKR), putative	0.025250	-0.15	-0.06	-0.22	0.41
AN6792	glycerol-3-phosphate dehydrogenase	0.025265	-0.02	0.21	-1.35	1.03
AN2914	arginosuccinate lyase	0.025345	-0.03	-0.39	-0.13	0.55
hisHF AN7430	imidazole glycerol phosphate synthase hisHF (ImGP synthase)(IGP synthase)(IGPS)	0.025479	0.17	0.51	-0.35	0.44
AN4591	phosphoglucomutase, putative	0.025487	-0.09	-0.63	0.71	-0.41
htxA hta1 AN3468	Histone H2A	0.025527	-0.02	0.58	-0.30	0.18
abfC AN1277	Alpha-arabinofuranosidasePutative uncharacterized protein;	0.025578	-0.04	-0.72	1.09	-0.71
AN2149	t-complex protein 1, alpha subunit, putative	0.025578	-0.02	0.49	-0.53	0.07
celB egIB egIC AN3418	Endo-1,4-beta-glucanase	0.025589	0.09	-0.28	0.57	-0.51
AN7699	conserved hypothetical protein	0.025597	0.33	-0.47	-0.17	0.63
AN0788	epoxide hydrolase, putative	0.025665	0.04	-0.32	0.62	-0.49
AN3877	conserved hypothetical protein	0.025859	0.25	-0.83	1.19	-1.58
mrn1 AN4290	translation initiation factor, putative	0.025899	-0.03	0.16	-0.21	-0.25
tif34 AN2997	Eukaryotic translation initiation factor 3 subunit I (eIF3i)	0.025976	0.09	0.73	-0.52	0.52
ironA aroA aroM AN0703	Pentafunctional AROM polypeptide [Includes 3-dehydroquinate synthase(DHQS)	0.025981	0.14	0.14	-0.38	0.51
csnG acoB csn7 AN3623	COP9 signalosome complex subunit 7 (CSN complex subunit 7)	0.026046	-0.07	-0.26	-0.52	0.36
AN1616	conserved hypothetical protein	0.026142	0.47	-0.40	-1.05	0.63
AN8977	AkePPutative uncharacterized protein;	0.026144	-0.07	-0.65	0.82	-0.21
AN7387	Pyrrole-5-carboxylate reductase	0.026301	0.01	0.14	-0.81	0.39
AN9514	D-isomer specific 2-hydroxyacid dehydrogenase family protein	0.026370	-0.09	-0.59	0.20	0.05
AN2343	nitroreductase family protein, putative	0.026479	0.23	-1.09	0.31	-0.03
AN1197	alpha-1,2-mannosidase family protein, putative	0.026550	-0.04	-0.38	-0.03	-0.08
AN2529	enoyl-CoA hydratase/isomerase family protein	0.026617	0.07	-0.15	-0.09	-0.05
AN10795	conserved hypothetical protein	0.026866	0.18	-0.63	0.60	-0.77
AN5404	conserved hypothetical protein	0.027000	-0.41	0.17	-0.26	-0.45
hse1 AN2066	Class E vacuolar protein-sorting machinery protein hse1	0.027158	-0.10	-0.12	0.32	-0.45
AN9466	conserved hypothetical protein	0.027294	0.25	0.34	0.10	-0.44
AN6382	conserved hypothetical protein	0.027420	0.15	-0.45	0.29	-0.27
adb oxpA AN0893	Adenylosuccinate synthetase	0.027433	-0.10	-0.51	-0.01	-0.04
AN0163	rho-gdp dissociation inhibitor	0.027481	-0.13	-0.07	-0.27	0.47
AN8599	conserved hypothetical protein	0.027610	0.26	0.13	-0.54	0.53
AN0285	6-phosphogluconolactonase, putative	0.027904	0.00	-0.33	-0.59	0.60
nudC AN5181	Nuclear movement protein nudC (Nuclear distribution protein C)	0.027926	-0.09	0.19	0.04	-0.38
AN1822	oxidoreductase, short chain dehydrogenase/reductase family protein, putative	0.028012	0.12	-0.70	1.24	-0.88
AN3184	aldose 1-epimerase, putative	0.028105	0.28	-0.26	0.31	0.13
AN1216	Glycerol-3-phosphate phosphatasePutative uncharacterized protein;	0.028152	0.11	0.33	-0.69	0.38
AN4048	Cut9 interacting protein Scn1, putative	0.028245	0.38	-0.23	0.20	0.67
ornA orn4 AN7722	glutamate N-acetyltransferase	0.028248	-0.03	-0.78	0.51	-0.20
AN6077	NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial [Precursor]	0.028491	-0.40	-0.08	-0.07	-0.10
AN6422	cellulose-binding GDSL lipase/acylhodrase, putative	0.028512	0.17	-0.62	0.92	-1.02
AN5448	hypothetical protein ANIA_05448	0.028590	0.05	0.53	0.10	-0.74
spt16 AN5102	FACT complex subunit spt16 (Facilitates chromatin transcription complex subunit spt16)	0.028709	-0.15	0.28	-0.14	0.47
catB AN9339	Catalase B Precursor	0.028721	-0.09	-0.76	0.37	-0.56
AN6004	actin cytoskeleton protein (VIP1), putative	0.029076	0.07	-0.23	0.37	-0.56
AN11227	heat shock 70 kDa protein	0.029105	-0.06	0.91	-0.60	1.04
AN5012	exoinulinase InuD	0.029188	-0.33	-0.68	0.58	-0.23
AN7710	HAD-superfamily hydrolase	0.029450	0.10	-0.48	0.51	-0.36
fmp52 AN1753	Protein fmp52, mitochondrial Precursor	0.029465	0.11	0.51	-0.75	0.23
AN10392	conserved hypothetical protein	0.029788	0.00	-0.34	0.38	-0.49
AN10278	electron transfer flavoprotein, beta subunit, putative	0.029956	-0.23	0.04	-0.12	-0.26
AN8531	conserved hypothetical protein	0.030087	-0.22	-0.36	0.98	-0.48
AN0757	methyltransferase (Ncl1), putative	0.030406	0.01	0.16	-0.82	0.70
AN7809	conserved hypothetical protein	0.030462	0.11	-0.07	0.87	-0.24
AN6598	conserved hypothetical protein	0.030518	0.01	0.14	-0.57	0.35
AN7479	cytoplasmic asparaginyl-tRNA synthetase, putative	0.030838	0.11	0.36	-0.31	0.50
facA acuA AN5626	Acetyl-coenzyme A synthetase (Acetate-CoA ligase)(Acyl-activating enzyme)	0.030945	0.09	0.58	-0.27	0.13
AN4304	glutaredoxin	0.031066	-0.12	0.02	-0.44	0.25
AN5606	vacuolar ATPase 98 kDa subunit, putative	0.031109	-0.02	0.48	-0.15	-0.04
mcIa AN8755	Methylisocitrate lyase Precursor	0.031211	-0.11	-0.22	-0.17	0.51
AN10519	proteasome regulatory particle subunit (RpnF), putative	0.031339	0.04	0.27	-0.47	-0.10
AN11046	conserved hypothetical protein	0.031759	0.59	-0.32	0.50	-0.74
acoA AN5525	Aconitase Fragment	0.031850	0.34	-0.20	-0.78	0.76
nhp6 AN2885	Non-histone chromosomal protein 6	0.031856	0.11	0.01	0.47	-0.82
cyp10 AN2453	Peptidyl-prolyl cis-trans isomerase-like 3 (PPlase)(Rotamase)	0.031894	0.45	-0.34	0.55	0.18
AN8163	oxidoreductase, short-chain dehydrogenase/reductase family	0.031910	0.28	-0.66	1.23	-0.30
AN10946	conserved hypothetical protein	0.031915	0.06	0.34	0.38	-0.33
AN1084	hypothetical protein similar to elongation factor EF-Tu	0.032123	-0.21	0.10	-0.33	-0.04
AN10260	conserved hypothetical protein	0.032607	0.12	-0.13	-0.65	0.69
AN8536	conserved hypothetical protein	0.032756	0.15	0.38	0.42	-0.89
AN8707	fumarate hydratase, putative	0.032761	0.17	-0.35	-0.66	0.54

gdhA AN4376	NADP-specific glutamate dehydrogenase (NADP-GDH)(NADP-dependent glutamate dehydrogenase)	0.032949	-0.10	-1.13	0.70	-0.41
AN7299	curved DNA-binding protein (42 kDa protein)	0.032968	0.16	-0.31	0.19	0.48
rglA AN7135	RHGB_ASPAC Rhamnogalacturonase B (Rhamnogalacturonan lyase) (RGase B) (RHG B)	0.033038	0.35	-0.60	1.48	-1.08
AN6732	Myosin light chain, putative	0.033285	0.00	-0.31	0.30	-0.50
stcU verA AN7806	Versicolorin reductase	0.033306	-0.21	-0.67	0.90	-0.98
AN4105	erythromycin esterase, putative	0.033426	-0.10	0.10	-0.52	0.49
AN8770	acetylglutamate kinase	0.033465	-0.09	-0.34	-0.31	0.31
AN0977	putative microbody (peroxisome) biogenesis protein peroxin 22-like	0.033586	-0.54	0.24	-0.01	-0.79
AN10170	GTP-binding protein YchF	0.033601	0.03	1.07	-0.62	0.83
AN6362	arsenate reductase (Arc2), putative	0.033668	0.43	-0.30	0.89	-0.56
AN4288	NADH-ubiquinone oxidoreductase, subunit G, putative	0.033703	-0.20	-0.15	0.14	-0.31
AN8273	Ubiquinol-cytochrome c reductase complex core protein 2	0.033785	0.11	0.53	-0.27	-0.04
AN3649	50S ribosomal protein L2	0.033812	0.36	0.90	-0.94	0.79
AN8363	phytase, putative	0.033828	0.04	-0.15	0.39	-0.77
AN5162	pyruvate dehydrogenase E1 component, alpha subunit	0.033883	0.36	-0.55	-0.12	0.56
AN5918	Catalase	0.033886	0.14	-0.18	0.92	-0.46
AN3367	translin-associated factor TraX, putative	0.033887	0.03	-0.23	0.33	-0.17
AN10214	2-hydroxyphytanoyl-CoA lyase, putative	0.033925	0.08	-0.33	0.51	0.32
AN9359	chromatin remodeling complex subunit (Arp9), putative	0.033973	-0.01	0.27	-0.64	0.43
AN0229	DUF221 domain protein, putative	0.034020	-0.26	0.27	0.30	-0.54
AN5688	cyclopropane-fatty-acyl-phospholipid synthase, putative	0.034037	0.10	0.43	-0.69	0.35
AN6145	Peptidyl-prolyl cis/trans isomerase	0.034107	0.13	-0.19	0.49	-0.28
AN5164	30S ribosomal subunit S4, putative	0.034117	0.17	-0.04	-0.31	0.51
AN10169	3-oxoacyl-(acyl-carrier-protein) reductase	0.034131	0.39	-0.45	-0.09	0.03
AN5353	conserved hypothetical protein	0.034340	-0.10	0.01	0.84	-1.16
AN10233	6-phosphogluconate dehydrogenase	0.034403	-0.06	0.67	-1.17	0.61
AN3961	conserved hypothetical protein	0.034586	0.08	0.33	-0.11	-0.20
AN2921	conserved hypothetical protein	0.034638	0.29	-0.55	1.48	-1.00
AN5571	oxoglutarate dehydrogenase (succinyl-transferring)	0.034673	0.24	0.18	-0.67	0.92
AN4615	actin cortical patch protein Sur7, putative	0.034883	-0.56	0.48	-1.34	0.37
AN10124	beta-glucosidase, putative	0.034983	0.44	-0.72	0.32	0.13
AN10194	pre-mRNA splicing helicase, putative	0.034992	-0.16	0.01	-0.28	-0.18
ipnA ips AN2622	Isopenicillin N synthetase (Isopenicillin N synthase)(IPNS)	0.035019	0.06	-0.86	0.60	-0.24
AN8756	phenol monooxygenase, putative	0.035453	0.40	-0.30	0.56	-0.20
AN3972	5-oxo-L-prolinase, putative	0.035754	0.29	-0.04	-0.50	0.39
AN7712	NUDIX family hydrolase, putative	0.035764	0.50	-0.45	0.31	-0.37
ivoB AN0231	conserved hypothetical protein: N-acetyl-6-hydroxytryptophan oxidase	0.035796	-0.29	-0.92	0.34	-0.43
AN7635	Putative uncharacterized proteinPutative uncharacterized protein binA;	0.035922	-0.05	-0.46	0.61	0.26
AN0391	NACHT domain protein	0.036012	-0.06	0.47	-1.40	0.58
AN4683	oligosaccharyl transferase subunit (beta), putative	0.036051	0.04	0.24	0.02	-0.23
AN0484	glycerophosphoryl diester phosphodiesterase family protein	0.036082	0.03	-0.37	0.15	-0.32
AN8528	beta-lactamase	0.036154	0.02	-0.67	-0.31	0.30
AN5996	60S acidic ribosomal protein P2/allergen Asp F 8	0.036225	-0.15	0.52	-0.04	-0.38
AN0271	dUTPase (Dut), putative	0.036326	0.09	-0.31	0.19	-0.18
AN1358	type 2C protein phosphatase	0.036337	-0.08	0.17	-0.34	-0.06
AN7517	HypA-like protein, putative	0.036400	-0.09	-0.58	0.32	-0.12
AN2425	protein phosphatase regulatory subunit Gac1, putative	0.036432	-0.12	0.11	0.35	-0.90
AN4557	mitochondrial inner membrane AAA protease Yta12, putative	0.036867	-0.02	0.01	-0.19	-0.04
AN10255	conserved hypothetical protein	0.037050	0.27	0.50	0.15	0.09
xlnC AN1818	Endo-1,4-beta-xylanase C Precursor (Xylanase C)	0.037314	0.11	-0.82	1.01	-0.88
AN1917	hypothetical protein similar to mitochondrial dicarboxylate/tricarboxylate transporter	0.037368	0.04	0.63	0.44	-0.46
AN3764	conserved hypothetical protein	0.037472	0.28	-0.57	0.43	-0.01
AN5607	proteasome activator subunit 4, putative	0.037852	-0.07	-0.01	-0.66	0.38
AN0240	transaldolase	0.037956	0.09	-0.30	0.16	0.13
AN9011	conserved hypothetical protein	0.038019	-0.08	-0.68	1.41	-1.14
AN3349	cytochrome P450, putative	0.038261	-0.01	-0.08	0.33	-0.31
AN2140	translocon-associated protein, alpha subunit, putative	0.038340	-0.02	0.37	-0.25	0.23
AN1611	flavin-binding monooxygenase-like protein	0.038368	0.07	0.56	-0.18	-0.03
AN1849	conserved hypothetical protein	0.038404	0.13	-0.31	0.76	-0.75
hsp60 AN6089	Heat shock protein 60 Precursor (60 kDa chaperonin)(Protein Cpn60)	0.038515	-0.02	0.80	-0.82	0.39
AN2210	ABC transporter	0.038569	-0.11	0.40	-0.68	0.13
AN9162	conserved hypothetical protein	0.038599	-0.10	-0.35	0.98	-0.94
AN8664	dienelactone hydrolase family protein	0.038662	-0.17	-0.58	0.37	-0.11
AN2924	NRPS-like enzyme, putative (JCVI)	0.038852	-0.31	0.30	-0.18	-0.22
AN0347	Ras GTPase similar to RAB11B	0.038861	0.01	0.08	0.14	0.08
AN3058	glycine hydroxymethyltransferase	0.038957	-0.04	-0.51	-0.22	0.26
AN5894	Pol II transcription elongation factor subunit Cdc73, putative	0.038978	-0.22	-0.39	-0.08	0.05
AN3855	oxidoreductase, 2-nitropropane dioxygenase family, putative	0.039475	0.62	0.71	0.01	0.15
AN6252	RNA polymerase II subunit 3	0.039584	0.11	0.34	-0.40	0.26
AN4572	conserved hypothetical protein	0.040002	0.14	0.73	-0.26	0.83
AN3702	leucyl-tRNA synthetase	0.040031	-0.08	0.24	-0.59	0.12
AN3987	TPR domain protein	0.040056	-0.04	-0.29	0.67	-0.17
pkar AN4987	cAMP-dependent protein kinase regulatory subunit (PKA regulatory subunit)	0.040090	0.13	0.33	-0.35	0.40
AN4008	hypothetical O-methyltransferase	0.040118	-0.04	-0.50	0.31	0.28
tif1 tif41 AN2932	ATP-dependent RNA helicase eIF4A (Eukaryotic initiation factor 4A)(eIF-4A)(Translation initiation factor 1)	0.040203	-0.03	0.38	-0.53	0.07
AN3895	CAIB/BAIF family enzyme	0.040525	0.20	-0.54	0.81	-0.62
AN9443	conserved hypothetical protein	0.040537	0.55	-0.32	1.14	-0.58
AN2455	essential protein with two zinc fingers	0.040822	0.12	0.10	-0.19	-0.01
AN5670	NADH-ubiquinone oxidoreductase 213 kDa subunit	0.040884	0.15	0.31	-0.32	0.16
AN6564	37S ribosomal protein S9	0.040898	0.31	0.03	-0.37	0.60

AN5990	phenylacetyl-CoA ligase, putative	0.041402	-0.55	-0.07	0.02	-0.20
AN1870	xylosidase/arabinosidase, putative	0.041483	0.07	0.00	0.10	-0.28
AN1913	lysyl-tRNA synthetase, hypothetical	0.041496	0.13	0.83	-0.30	0.85
AN6035	mandelate racemase/muconate lactonizing enzyme family protein	0.041502	-0.20	-0.68	1.58	-0.85
AN2383	hypothetical protein ANIA_02383	0.041888	0.22	-0.30	0.51	-0.52
AN6024	hypothetical protein ANIA_06024	0.041911	0.10	-0.75	1.26	-0.85
AN8223	conserved hypothetical protein	0.042177	0.40	-0.32	0.31	-0.39
AN5686	tropomyosin TpmA	0.042196	0.17	0.32	0.62	-0.65
AN0860	conserved hypothetical protein	0.042210	0.47	-0.15	-0.32	0.16
AN3060	prefoldin subunit 6, putative	0.042425	0.08	-0.64	0.89	-0.79
metG AN7051	Cystathionine beta-lyase	0.042528	-0.09	-0.22	-0.22	0.19
nopA AN3361	putative bacteriorhodopsin /opsin, nopA	0.042834	-0.17	0.70	-0.84	-0.10
AN7511	putative 1,3-beta-transglucosylase, GH72 family	0.043086	-0.27	-0.51	-0.28	-0.30
AN1115	nucleoside hydrolase, putative	0.043105	-0.18	-0.41	0.24	-0.50
AN6182	galactose-1-phosphate uridylyltransferase	0.043416	0.01	-0.30	-0.15	0.22
AN3312	oxidoreductase, short chain dehydrogenase/reductase family	0.043701	0.00	-0.53	1.16	-1.10
AN7632	formaldehyde dehydrogenase	0.043702	0.32	-0.65	0.59	-0.63
lap1 AN7035	aminopeptidase, putative	0.043705	-0.09	-0.26	0.25	-0.26
AN7268	short chain dehydrogenase/reductase, putative	0.043765	-0.12	0.87	0.08	-0.63
hog1 hogA sakA AN1017	Mitogen-activated protein kinase hog1 (MAP kinase hog1)	0.044021	-0.01	0.35	-0.66	0.07
AN6307	lectin family integral membrane protein, putative	0.044042	0.01	0.29	-0.03	0.13
AN3080	vesicle coat complex COPII, subunit Sec24 family protein, putative	0.044119	0.17	0.35	-0.46	0.12
AN3150	glutamate-cysteine ligase, catalytic subunit	0.044199	0.29	0.43	-0.43	0.24
AN2862	EB1 homolog	0.044222	-0.06	0.42	0.07	-0.24
AN0365	conserved hypothetical protein	0.044488	0.00	-0.09	0.64	-0.70
AN4492	proteasome regulatory particle subunit (RpnK), putative	0.044610	-0.07	0.52	-0.49	0.08
prnC AN1733	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial Precursor (P5C dehydrogenase)	0.044674	0.13	-0.58	0.93	-0.64
AN0504	Serine/threonine protein phosphatase	0.044702	-0.16	-0.08	0.23	-0.12
argB AN4409	Ornithine carbamoyltransferase, mitochondrial Precursor (Ornithine transcarbamylase)(OTCase)	0.044795	-0.28	-0.42	0.26	-0.10
AN2775	eukaryotic translation initiation factor subunit elf2A, putative	0.044978	0.07	-0.14	0.09	-0.37
AN4252	high expression lethality protein Hel10, putative	0.044987	-0.05	0.53	0.17	-0.64
AN0999	adenylyl cyclase-associated protein (cap)	0.045217	0.12	0.09	-0.19	-0.36
AN5911	nuclear actin-related protein	0.045245	-0.25	0.50	-0.76	0.67
AN0579	Isopentenyl diphosphate isomerasePutative uncharacterized protein;	0.045408	0.02	-0.33	0.81	-0.80
AN6676	transformer-SR ribonucleoprotein, putative	0.045540	0.26	0.49	-0.26	0.24
AN3906	M protein repeat protein	0.045620	-0.04	0.13	0.56	-0.93
lacA AN0756	beta-galactosidase	0.045976	0.31	-0.30	1.09	-1.05
AN3017	epoxide hydrolase, putative	0.046116	-0.19	-0.91	1.14	-0.67
AN6253	Phenylalanyl-tRNA synthetase alpha subunit-like protein Fragment	0.046204	0.15	0.27	-0.50	0.67
AN4742	translation initiation factor SUI1, putative	0.046209	-0.05	0.19	0.00	-0.16
AN7812	conserved hypothetical protein	0.046650	0.07	-0.74	0.96	-1.15
AN4727	UDP-glucose 4-epimerase	0.046904	0.34	0.56	0.34	0.09
AN2853	transcription regulator PAB1642, putative	0.047055	0.08	-0.28	-0.01	0.15
npta AN11080	DMATS type aromatic prenyltransferase, putative (JCVI)	0.047064	0.12	-0.64	0.67	-0.73
TRX1 AN0170	Thioredoxin (Trx)	0.047265	0.19	0.40	-0.99	0.30
AN3829	succinate-semialdehyde dehydrogenase	0.047869	0.23	0.44	-0.74	0.81
AN5731	chorismate synthase	0.048001	0.28	-0.22	-0.71	0.73
AN5926	Yip1 domain protein	0.048094	-0.15	0.45	-0.38	0.16
AN4164	TPR repeat protein	0.048332	-0.30	-0.12	-1.01	0.68
AN1546	transcription factor (Sin3), putative	0.048706	0.09	0.05	-0.40	0.03
egd2 AN6630	Nascent polypeptide-associated complex subunit alpha (NAC-alpha)(Alpha-NAC)	0.048988	0.00	0.15	0.16	-0.39
AN0158	quinone oxidoreductase, putative	0.049184	0.02	-0.59	0.70	-0.33
AN5666	MAP protein kinase MPKA	0.049266	-0.11	-0.09	-0.12	-0.33
AN7962	penicillolysin/deuterolysin metalloprotease, putative	0.049626	0.06	-0.55	0.21	-1.06
orsB AN7911	conserved hypothetical protein	0.049641	0.01	-0.72	0.39	-0.61
AN1282	glutamine-rich cytoplasmic protein	0.049866	0.08	0.03	0.66	-0.66
AN10368	DUF636 domain protein	0.049927	0.14	-0.12	0.63	0.11
bgfA bgf1 AN4102	beta-glucosidase	0.049935	0.15	-0.55	0.99	-0.65