Supplementary Table S-1. Up- and down-regulated proteins in CEA10, ISSFT-021 and IF1SW-F4 when normalized to Af293.

Differentially expressed proteins in CEA10

Gene	Protein names	Relative protein abundance*			P-value
		CEA10	ISSFT-021	IF1SW-F4	
AFUA_1G15010	AMP binding domain protein, putative	-4.47	-3.65	-3.15	2.42E-03
AFUA_1G13530	Uncharacterized protein	-4.30	-3.82	-2.75	3.15E-04
AFUA_1G10550	CBF/NF-Y family transcription factor, putative	-4.29	-5.75	-3.37	3.43E-06
AFUA_2G03390	Histone deacetylase (EC 3.5.1.98)	-4.27	-5.76	-3.78	1.15E-03
AFUA_1G01812	MFS transporter, putative	-4.17	-2.93	-2.20	4.25E-03
AFUA_6G02830	Uncharacterized protein	-4.08	-2.59	-1.87	6.97E-04
AFUA_6G12450	Chaperone/heat shock protein Hsp12, putative	-4.05	-5.81	-5.12	5.46E-05
AFUA_1G03710	C2H2 finger domain protein, putative	-4.02	-4.17	-3.69	7.80E-03
AFUA_1G11640	Cytosolic Cu/Zn superoxide dismutase, putative	-3.95	-2.30	-3.07	3.00E-06
AFUA_1G12070	Glycine cleavage system H protein	-3.95	-4.38	-4.79	8.05E-05
AFUA_1G06100	Glutaredoxin Grx1, putative	-3.93	-1.25	-0.60	2.72E-08
AFUA_7G05270	COMPASS complex subunit Sdc1, putative	-3.87	-3.18	-2.60	3.89E-03
AFUA_6G12000	Uncharacterized protein	-3.87	-5.08	-3.22	6.46E-06
AFUA_6G08990	Uncharacterized protein	-3.86	-1.45	-1.56	3.84E-04
AFUA_6G04390	E3 ubiquitin-protein ligase bre1 (EC 2.3.2.27) (RING-type E3 ubiquitin transferase bre1)	-3.76	-4.23	-4.24	8.60E-05
AFUA_5G12180	Ran-specific GTPase-activating protein 1, putative	-3.75	-3.12	-3.01	9.69E-08
AFUA_3G14540	Heat shock protein Hsp30/Hsp42, putative	-3.73	-4.52	-4.20	3.63E-08
AFUA_4G10020	Clathrin light chain	-3.70	-3.30	-2.33	1.95E-06
AFUA_4G08960	GPI anchored cell wall protein, putative	-3.69	-5.18	-5.37	8.40E-05
AFUA_6G13670	Reticulon-like protein	-3.69	-5.29	-2.62	3.96E-08
AFUA_2G10020	Uncharacterized protein	-3.67	-5.69	-3.86	3.03E-07
AFUA_2G10810	Nuclear protein export protein Yrb2, putative	-3.67	-3.85	-2.59	3.31E-02
AFUA_1G06830	60S acidic ribosomal protein P1 (AfP1)	-3.67	-3.62	-1.95	2.73E-05
AFUA_7G04930	Alkaline serine protease (PR1)/allergen F18-like (EC 3.4.21.-)	-3.63	-5.32	-5.53	1.14E-06
AFUA_1G01950	Uncharacterized protein	-3.62	-4.06	-3.24	4.23E-04
AFUA_6G10700	Chaperonin, putative	-3.60	-4.94	-3.42	8.19E-05
AFUA_1G13550	Uncharacterized protein	-3.59	-6.12	-5.23	5.82E-03
AFUA_2G08640	Uncharacterized protein	-3.54	-3.32	-2.18	4.06E-04
AFUA_4G00860	Cell surface protein, putative	-3.54	-5.64	-4.62	1.37E-07
AFUA_6G09120	Uncharacterized protein	-3.52	-4.91	-2.97	1.10E-05
AFUA_2G14330	Uncharacterized protein	-3.51	-5.48	-6.27	2.39E-06
AFUA_5G13100	Uncharacterized protein	-3.50	-5.95	-5.15	9.50E-09
AFUA_4G14205	Uncharacterized protein	-3.49	-6.22	-4.43	9.36E-06
AFUA_2G13040	GrpE protein homolog	-3.48	-4.15	-3.01	2.23E-08
AFUA_7G02340	L-PSP endoribonuclease family protein (Hmf1), putative	-3.47	-2.50	-2.31	2.66E-06
AFUA_7G01200	Aspergillopepsin, putaitve (EC 3.4.23.-)	-3.45	-4.45	-2.66	8.43E-07
AFUA_4G09600	GPI anchored protein, putative	-3.43	-6.26	-5.82	1.33E-07
AFUA_1G08880	Iron/copper transporter Atx1, putative	-3.41	-3.69	-2.06	9.37E-11
AFUA_4G10280	Phosphotransmitter protein Ypd1, putative	-3.40	-3.09	-2.65	1.54E-06
AFUA_4G00730	HHE domain protein	-3.40	-1.32	-0.37	1.99E-09
AFUA_5G12590	Solid-state culture expressed protein (Aos23), putative	-3.38	-2.76	-3.75	2.32E-03
AFUA_4G09750	50S ribosomal protein L12	-3.36	-4.10	-3.30	9.15E-05
AFUA_1G13670	Uncharacterized protein	-3.36	-3.10	-2.85	4.02E-08
AFUA_7G04030	Uncharacterized protein	-3.36	-4.62	-2.54	1.06E-04
AFUA_7G01340	RPEL repeat protein	-3.36	-5.15	-5.55	4.07E-10
AFUA_3G11550	LEA domain protein	-3.34	-2.74	-2.50	2.51E-06
AFUA_3G10610	Uncharacterized protein	-3.33	-3.48	-3.28	7.75E-04
AFUA_3G12790	Conserved glutamic acid-rich protein	-3.32	-3.53	-3.82	1.63E-04
AFUA_7G04520	Uncharacterized protein	-3.31	-5.06	-4.87	1.19E-05
AFUA_4G02805	Asp hemolysin-like protein	-3.31	-4.42	-2.02	7.88E-05
AFUA_6G09740	Thioredoxin reductase gliT (EC 1.8.1.-) (Gliotoxin biosynthesis protein T)	-3.30	-3.75	-4.59	9.90E-08
AFUA_3G10920	Telomere and ribosome associated protein Stm1, putative	-3.30	-4.13	-2.02	1.67E-07
AFUA_2G11840	Transcriptional corepressor Cyc8, putative	-3.28	-3.54	-2.12	4.54E-06

AFUA_8G01980	Uncharacterized protein	-3.27	-4.01	-3.02	3.84E-06
AFUA_3G14260	Mismatched base pair and cruciform DNA recognition protein, putative	-3.27	-5.16	-3.37	2.05E-06
AFUA_4G06820	Protein ecm33	-3.26	-4.32	-3.59	5.49E-10
AFUA_2G10100	60S acidic ribosomal protein P2 (AfP2) (allergen Asp f 8)	-3.24	-2.65	-2.04	1.16E-06
AFUA_1G13560	Uncharacterized protein	-3.23	-5.10	-3.77	1.79E-06
AFUA_5G11390	APSES transcription factor, putative	-3.22	-3.30	-1.63	3.38E-04
AFUA_5G14210	Glucose repressible protein Grg1, putative	-3.21	-7.14	-4.80	1.87E-07
AFUA_6G02260	Uncharacterized protein	-3.21	-3.41	-2.20	1.03E-05
AFUA_6G13500	Uncharacterized protein	-3.21	-5.61	-3.77	7.19E-07
AFUA_2G01540	Uncharacterized protein	-3.19	-3.99	-2.73	1.21E-05
AFUA_1G16840	Translationally-controlled tumor protein homolog (TCTP)	-3.18	-2.43	-1.94	1.32E-06
AFUA_2G03790	Oxysterol binding protein (Osh7), putative	-3.18	-4.47	-2.85	8.13E-03
AFUA_6G05350	Probable aspartic-type endopeptidase opsB (EC 3.4.23.-)	-3.15	-3.64	-1.88	7.65E-06
AFUA_6G08660	M protein repeat protein	-3.12	-3.33	-2.87	4.62E-05
AFUA_4G06670	Allergen Asp f 7 (allergen Asp f 7)	-3.09	-1.97	-1.95	2.08E-03
AFUA_2G03590	40S ribosomal protein S21	-3.07	-3.22	0.19	2.54E-06
AFUA_1G12190	Uncharacterized protein	-3.06	-1.41	-1.50	1.89E-05
AFUA_3G08270	Pyruvate dehydrogenase complex component Pdx1, putative	-3.01	-0.87	0.46	7.81E-03
AFUA_2G10320	SH3 domain protein	-2.98	-2.27	-2.08	2.01E-03
AFUA_3G08230	MRS7 family protein	-2.97	-3.12	-1.63	4.35E-04
AFUA_2G13380	GATA transcription factor (AreB), putative	-2.97	-2.48	-2.78	4.61E-03
AFUA_2G15810	Uncharacterized protein	-2.96	-5.32	-5.18	3.13E-03
AFUA_6G04690	Uncharacterized protein	-2.96	-2.89	-2.57	8.64E-03
AFUA_4G10150	Alpha-glucosidase AgdA, putative (EC 3.2.1.20)	-2.96	-3.13	-3.34	5.33E-05
AFUA_1G17370	Heat shock protein Awh11, putative	-2.95	-5.23	-4.26	4.25E-07
AFUA_4G12450	Conserved lysine-rich protein, putative	-2.94	-2.01	-0.91	1.88E-07
AFUA_3G05570	Spindle poison sensitivity protein Scp3, putative	-2.94	-5.28	-4.83	4.20E-04
AFUA_6G07390	Isocitrate dehydrogenase LysB (EC 1.1.1.41)	-2.92	-1.46	-1.36	9.63E-11
AFUA_7G04210	Tropomyosin, putative	-2.91	-3.60	-2.17	6.38E-06
AFUA_4G11110	C2 domain protein	-2.90	-2.46	-1.53	7.18E-05
AFUA_6G08530	Sister chromatid separation protein (Src1), putative	-2.89	-0.99	-1.07	5.71E-03
AFUA_1G03580	Uncharacterized protein	-2.87	-3.41	-3.86	1.07E-03
AFUA_3G05430	ATP-dependent RNA helicase dhh1 (EC 3.6.4.13)	-2.86	-5.81	-4.16	7.98E-04
AFUA_4G12490	Guanine nucleotide exchange factor Vps9, putative	-2.86	-4.52	-3.77	1.66E-04
AFUA_7G01510	SNARE domain protein	-2.85	-1.22	-1.04	5.25E-05
AFUA_5G10550	ATP synthase subunit beta (EC 3.6.3.14)	-2.85	-3.44	-1.63	9.29E-07
AFUA_2G07950	ATP dependent RNA helicase, putative	-2.84	-2.54	-2.06	4.88E-04
AFUA_3G09030	Regulatory protein SUAPRGA1	-2.83	-3.80	-3.30	3.56E-03
AFUA_3G10410	Conserved serine-rich protein	-2.82	-4.81	-3.94	3.68E-05
AFUA_7G06010	Uncharacterized protein	-2.81	-1.84	-1.57	3.36E-04
AFUA_6G12500	AhpC/TSA family protein	-2.80	-1.50	-0.18	2.31E-08
AFUA_8G00550	Methyltransferase psoC (EC 2.1.1.-) (Pseurotin biosynthesis protein C)	-2.78	-2.15	-2.19	2.53E-08
AFUA_2G05635	Uncharacterized protein	-2.73	-4.18	-4.06	4.08E-03
AFUA_1G09030	Uncharacterized protein	-2.72	-3.81	-1.86	4.70E-07
AFUA_4G09740	T-complex protein 1, theta subunit, putative	-2.71	-4.22	-2.49	2.19E-07
AFUA_5G02420	Splicing factor 3a subunit 3, putative	-2.70	-4.03	-2.28	1.60E-02
AFUA_7G02020	Uncharacterized protein	-2.67	-3.38	-2.69	3.83E-05
AFUA_1G09280	Protein phosphatase 2C, putative (EC 3.1.3.16)	-2.66	-2.78	-1.51	2.23E-03
AFUA_6G06670	Uncharacterized protein	-2.65	-2.85	-2.68	5.35E-05
AFUA_3G13430	Uncharacterized protein	-2.63	-2.56	-3.12	2.45E-02
AFUA_5G11320	Thioredoxin	-2.63	-1.09	-1.17	8.05E-05
AFUA_6G07120	Nuclear movement protein NudC	-2.62	-1.57	-1.32	5.54E-05
AFUA_2G17330	Extracelular serine carboxypeptidase, putative (EC 3.4.-.-)	-2.62	-0.17	-0.75	2.88E-06
AFUA_1G07280	Uncharacterized protein	-2.60	-2.14	-0.97	1.21E-05
AFUA_8G01090	Thioredoxin, putative	-2.59	-0.57	-0.53	3.58E-04
AFUA_2G15070	26S proteasome regulatory subunit S5A	-2.59	-4.07	-3.12	8.53E-06
AFUA_3G09990	Uncharacterized protein	-2.59	-3.39	-2.84	4.40E-04

AFUA_1G12390	G2/M phase checkpoint control protein Sum2, putative	-2.58	-3.14	-1.76	3.72E-05
AFUA_4G01030	Uncharacterized protein	-2.57	-1.27	-2.29	2.17E-05
AFUA_2G15180	Uncharacterized protein	-2.56	-0.07	0.65	5.13E-03
AFUA_8G04310	Uncharacterized protein	-2.55	-3.87	-2.86	2.62E-03
AFUA_4G09280	Uncharacterized protein	-2.55	-2.57	-1.65	1.51E-06
AFUA_2G15290	DUF636 domain protein	-2.54	-2.53	0.18	8.12E-06
AFUA_2G09800	Uncharacterized protein	-2.51	-1.75	-1.43	9.85E-04
AFUA_2G18000	Chanoclavine-I dehydrogenase easD (ChaDH) (EC 1.1.1.332) (Ergot alkaloid synthesis protein A)	-2.51	-0.60	0.40	5.63E-03
AFUA_6G08320	Uncharacterized protein	-2.49	-3.08	-2.11	1.21E-07
AFUA_8G04270	AAA family ATPase, putative	-2.48	-3.22	-2.58	4.41E-04
AFUA_6G12430	Ran-interacting protein Mog1, putative	-2.45	-1.91	-0.83	9.45E-04
AFUA_3G00600	Uncharacterized protein	-2.43	-0.04	-0.17	2.70E-07
AFUA_6G13120	Filament-forming protein (Tpr/p270), putative	-2.42	-2.55	-1.72	5.43E-07
AFUA_6G12680	HIT domain protein	-2.42	0.27	0.12	3.25E-07
AFUA_3G02340	CBF/NF-Y family transcription factor, putative	-2.41	-3.75	-2.28	4.63E-04
AFUA_2G09290	Antigenic mitochondrial protein HSP60, putative	-2.39	-1.04	-0.37	4.15E-11
AFUA_6G10930	Extracellular protein, putative (EC 2.7.7.6)	-2.39	-0.17	-1.71	1.38E-07
AFUA_7G02170	Peptidyl-prolyl cis-trans isomerase-like 4 (PPIase) (EC 5.2.1.8) (Rotamase)	-2.38	-2.47	-1.41	4.54E-02
AFUA_2G15840	HET-C domain protein HetC	-2.38	-1.65	-1.82	8.39E-03
AFUA_4G14490	Oxidoreductase tpcJ (EC 1.-.-.-) (Trypacidin synthesis protein J)	-2.37	0.01	0.16	2.53E-05
AFUA_1G05220	Selenoprotein domain protein	-2.37	-0.79	-0.23	1.50E-04
AFUA_1G16430	Uncharacterized protein	-2.37	-0.51	-0.09	1.67E-03
AFUA_2G12190	Mitochondrial import inner membrane translocase subunit tim13	-2.36	-2.32	-1.49	2.80E-03
AFUA_7G01010	Alcohol dehydrogenase, putative (EC 1.1.1.1)	-2.36	-1.74	-1.73	3.63E-08
AFUA_3G06460	Uncharacterized protein	-2.35	-1.54	0.04	1.35E-05
AFUA_8G05650	Uncharacterized protein	-2.35	-3.36	-3.61	2.53E-03
AFUA_4G03420	L-PSP endoribonuclease family protein, putative	-2.35	-2.93	-1.93	1.30E-03
AFUA_1G12590	RNA-binding La domain protein	-2.34	-2.41	-2.04	2.24E-03
AFUA_7G02570	NIMA-interacting protein TinC	-2.34	-2.21	-1.85	1.13E-03
AFUA_3G10190	Peroxisomal membrane anchor protein (Pex14), putative	-2.34	-2.48	-3.06	2.78E-03
AFUA_1G15050	Hsp70 family chaperone Lhs1/Orp150, putative	-2.32	-0.79	0.27	2.11E-05
AFUA_6G12290	PH domain protein	-2.32	-2.92	-2.73	1.83E-04
AFUA_6G04610	DNA-directed RNA polymerase I and III 14 kDa polypeptide	-2.32	-2.56	-1.91	1.48E-02
AFUA_2G10030	Actin cytoskeleton protein (VIP1), putative	-2.32	-2.87	-1.72	1.19E-09
AFUA_5G14740	Fucose-specific lectin FleA	-2.31	-0.76	-1.64	2.23E-06
AFUA_5G09380	Uncharacterized protein	-2.31	-3.71	-2.68	1.67E-03
AFUA_2G08360	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase) (OMPDCase) (OMPdecase) (Uridine 5'-monophosphate synthase) (UMP synthase)	-2.29	-0.48	-0.23	9.06E-06
AFUA_2G13820	SAP domain protein, putative	-2.28	-1.54	-1.70	9.89E-07
AFUA_7G04950	Lipase, putative (EC 3.1.1.-)	-2.28	-4.33	-0.49	1.12E-06
AFUA_7G04920	Uncharacterized protein	-2.28	-3.48	-3.20	3.66E-02
AFUA_3G13850	LRP16 family protein	-2.27	-4.37	-4.88	1.16E-03
AFUA_2G11740	Lon protease homolog, mitochondrial (EC 3.4.21.53)	-2.25	-3.40	-2.33	9.12E-05
AFUA_3G00240	TPR domain protein	-2.23	1.00	-1.43	2.05E-05
AFUA_8G07060	Hydrophobin, putative	-2.23	-1.93	-2.21	1.08E-07
AFUA_5G04160	NTF2 and RRM domain protein	-2.21	-2.29	-1.29	2.29E-03
AFUA_1G06680	VHS domain protein	-2.21	-1.78	-1.34	5.91E-04
AFUA_8G04570	PWWP domain protein	-2.20	-2.26	-1.89	4.06E-07
AFUA_2G08540	DNA-directed RNA polymerase subunit	-2.19	-2.84	-1.80	1.46E-05
AFUA_2G08150	NEDD8-like protein (RubA), putative	-2.17	-1.48	-1.23	4.94E-06
AFUA_2G14490	Endoglucanase, putative (EC 3.2.1.-)	-2.17	-3.83	-3.33	1.17E-04
AFUA_4G14800	Short chain dehydrogenase 1 (EC 1.1.1.-) (Helvolic acid synthesis protein sdr1)	-2.17	0.72	-0.14	1.77E-03
AFUA_2G05540	Pre-mRNA-splicing factor cef1	-2.16	-3.57	-3.66	5.22E-03
AFUA_8G06970	Beta-glucosidase (EC 3.2.1.21)	-2.14	-2.14	-1.45	1.78E-02
AFUA_5G10240	Uncharacterized protein	-2.14	-2.48	-1.96	4.17E-04

AFUA_2G11860	Uncharacterized protein	-2.13	-2.64	-2.05	1.13E-06
AFUA_6G03210	Conidiation-specific protein (Con-10), putative	-2.13	-4.73	-3.82	3.46E-04
AFUA_4G09580	Major allergen Asp f 2 (Allergen Asp f II) (allergen Asp f 2)	-2.12	-2.88	-2.68	1.20E-03
AFUA_2G10600	NADH-ubiquinone oxidoreductase 299 kDa subunit, putative (EC 1.6.5.3)	-2.11	-2.28	-1.33	2.39E-07
AFUA_1G02420	Uncharacterized protein	-2.11	-1.73	-0.73	7.63E-03
AFUA_8G01530	HHE domain protein	-2.10	-0.30	0.86	2.42E-06
AFUA_1G08840	Guanylate kinase (EC 2.7.4.8)	-2.09	-1.18	-1.17	4.52E-06
AFUA_2G03010	Cytochrome c subunit Vb, putative	-2.09	-3.83	-3.13	8.44E-07
AFUA_4G10540	Transcription regulator BDF1, putative	-2.07	-1.51	-0.99	3.91E-03
AFUA_2G09490	Eukaryotic translation initiation factor subunit eIF-4F, putative	-2.07	-1.60	-1.44	4.05E-05
AFUA_5G02910	NAP family protein	-2.07	0.27	-0.15	4.27E-06
AFUA_3G10700	Actin-related protein 2/3 complex subunit 5	-2.06	-0.39	-0.64	1.23E-04
AFUA_2G02320	Hsp70 chaperone (BiP), putative	-2.06	-3.07	-2.16	3.26E-05
AFUA_8G07130	AhpC/TSA family thioredoxin peroxidase, putative	-2.06	-2.15	0.17	1.13E-05
AFUA_4G10010	Hsp90 co-chaperone Cdc37	-2.06	-1.27	-1.10	4.25E-04
AFUA_3G13820	Glycolipid transfer protein HET-C2, putative	-2.05	-0.16	0.16	2.64E-05
AFUA_5G07040	Ubiquitin conjugating enzyme (UbcA), putative (EC 6.3.2.19)	-2.05	-1.20	0.75	3.16E-02
AFUA_7G00580	Uncharacterized protein	-2.04	-1.96	-2.49	3.96E-07
AFUA_1G09250	CUE domain protein, putative	-2.03	-3.06	-2.38	4.12E-02
AFUA_2G00970	Alcohol dehydrogenase, zinc-containing, putative (EC 1.1.1.1)	-2.01	0.95	1.71	3.73E-04
AFUA_6G03820	Nascent polypeptide-associated complex subunit alpha (NAC-alpha) (Alpha-NAC)	-2.01	-2.13	-0.86	4.66E-06
AFUA_1G17310	MFS lactose permease, putative	-2.01	-1.93	-1.04	3.30E-05
AFUA_6G00160	Ser/Thr protein phosphatase family protein	-2.01	-0.50	0.46	5.58E-04
AFUA_2G07600	SRP receptor beta subunit (Srp102), putative	-2.01	-4.19	-2.72	3.98E-03
AFUA_2G08670	Acetyl-CoA carboxylase	-2.01	-2.80	-1.74	3.47E-02
AFUA_7G05470	Electron transfer flavoprotein alpha subunit, putative	-2.00	-1.96	-2.30	2.77E-03
AFUA_8G04920	LEA domain protein	-2.00	-2.70	-2.54	4.55E-04
AFUA_2G02360	UDP-glucose:glycoprotein glucosyltransferase, putative	-1.99	-1.10	0.04	3.50E-02
AFUA_3G06140	Cytoskeleton assembly control protein Sla2, putative	-1.99	-1.49	-0.90	7.32E-06
AFUA_1G11870	Mitochondrial processing peptidase alpha subunit, putative (EC 3.4.24.64)	-1.96	-2.37	-1.88	1.36E-02
AFUA_1G06170	Proteasome regulatory particle subunit Rpt5, putative	-1.96	-2.16	-0.64	2.13E-03
AFUA_4G08030	MICOS complex subunit mic60 (Mitofilin)	-1.95	-2.68	-1.76	2.21E-02
AFUA_3G01790	Isoflavone reductase family protein (EC 1.3.1.-)	-1.93	-0.08	0.47	1.54E-03
AFUA_3G02220	DUF427 domain protein	-1.93	-0.73	-1.26	2.89E-03
AFUA_6G14540	Endo-1,3(4)-beta-glucanase, putative (EC 3.2.1.6)	-1.93	-0.56	-1.11	1.81E-02
AFUA_1G04470	Mitochondrial import inner membrane translocase subunit tim10	-1.92	-3.78	-2.26	1.15E-03
AFUA_1G09830	Hsc70 cochaperone (SGT), putative (EC 3.1.3.16)	-1.92	-1.61	-1.14	1.16E-04
AFUA_7G01860	Heat shock protein (Sti1), putative	-1.92	-1.21	-0.96	2.63E-07
AFUA_1G10350	Phosphoglycerate kinase (EC 2.7.2.3)	-1.92	-0.46	0.75	1.36E-09
AFUA_2G16020	T-complex protein 1, alpha subunit, putative	-1.91	-3.60	-1.79	1.56E-02
AFUA_2G01250	Serine peptidase, putative (EC 3.4.-.-)	-1.91	-1.15	-1.51	1.13E-04
AFUA_2G13590	Uncharacterized protein	-1.88	-1.80	-2.20	1.78E-07
AFUA_2G11060	Acyl CoA binding protein family	-1.87	-1.01	-1.69	2.34E-07
AFUA_3G09870	Uncharacterized protein	-1.85	-2.52	-2.36	9.93E-03
AFUA_2G03360	Polarized growth protein (Boi2), putative	-1.85	-0.59	-0.52	3.78E-03
AFUA_5G07240	SAP domain protein	-1.84	-2.11	-2.42	1.82E-03
AFUA_5G02750	Cytochrome c oxidase subunit Va, putative	-1.79	-3.20	-2.26	3.37E-07
AFUA_4G03780	Probable rhamnogalacturonate lyase A (EC 4.2.2.23)	-1.78	-2.88	-2.67	2.33E-02
AFUA_7G06610	Isochorismatase family hydrolase, putative	-1.78	-0.51	1.29	2.45E-03
AFUA_5G11100	DUF775 domain protein	-1.78	-0.37	0.49	4.00E-02
AFUA_5G01340	Lysophospholipase 2 (EC 3.1.1.5) (Phospholipase B 2)	-1.77	-1.14	-1.25	2.57E-06
AFUA_5G07080	Beta-glucosidase, putative (EC 3.2.1.21)	-1.76	-1.77	-1.67	3.56E-05
AFUA_1G09330	Eukaryotic translation initiation factor 3 subunit F (eIF3f)	-1.76	-1.75	-0.85	7.35E-03
AFUA_8G02730	Translation machinery-associated protein 22	-1.76	-0.86	-0.69	2.28E-03

AFUA_1G10630	S-adenosylmethionine synthase (EC 2.5.1.6)	-1.74	-1.55	-0.37	1.75E-03
AFUA_3G07870	Extracellular serine-rich protein, putative	-1.73	-2.89	-3.23	1.27E-06
AFUA_4G11390	Ubiquinol-cytochrome c reductase complex 17 kd protein	-1.72	-2.64	-2.94	3.97E-08
AFUA_3G00840	FAD-dependent oxygenase, putative	-1.72	-1.31	-1.95	3.99E-09
AFUA_7G04320	UBX domain protein (Ubx5), putative	-1.71	0.06	-0.06	4.69E-02
AFUA_3G08420	Cystathionine beta-synthase (Beta-thionase), putative	-1.70	0.51	0.93	1.06E-04
AFUA_7G03870	Actin cytoskeleton-regulatory complex protein pan1	-1.70	-1.04	-1.43	2.40E-03
AFUA_1G06660	CBS domain protein	-1.69	-1.60	-0.57	2.84E-02
AFUA_1G15780	3-isopropylmalate dehydrogenase (EC 1.1.1.85)	-1.67	-2.72	-2.26	5.25E-09
AFUA_7G06050	DNA damage-inducible protein 1	-1.67	-1.35	-1.16	7.27E-03
AFUA_3G08750	Uncharacterized protein	-1.66	-0.72	-0.10	1.27E-02
AFUA_4G07340	Ubiquitin fusion degradation protein UfdB, putative	-1.65	-1.55	-1.21	2.91E-02
AFUA_7G06820	Galactose oxidase, putative (EC 1.1.3.9)	-1.63	-0.76	-0.86	7.89E-03
AFUA_6G06370	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	-1.61	-1.44	-0.10	7.68E-05
AFUA_3G14970	Thioredoxin	-1.60	-0.17	0.01	4.41E-04
AFUA_2G05400	Sugar hydrolase, putative	-1.59	-1.70	-1.59	7.69E-05
AFUA_2G14670	Eukaryotic translation initiation factor 3 subunit D (eIF3d)	-1.59	-2.17	-1.62	2.36E-02
AFUA_5G04250	Homocysteine synthase CysD (EC 2.5.1.49)	-1.59	-1.11	-1.34	1.11E-05
AFUA_3G13240	Aldose 1-epimerase, putative (EC 5.1.3.3)	-1.59	-1.36	-2.73	2.77E-06
AFUA_6G08360	Thiamine thiazole synthase (Thiazole biosynthetic enzyme)	-1.59	-0.65	-2.09	9.43E-06
AFUA_4G14510	Methyltransferase tpcH (EC 2.1.1.-) (Trypacidin synthesis protein H)	-1.58	-0.95	0.45	5.38E-04
AFUA_2G12870	Vesicular-fusion protein sec17	-1.52	-1.40	-0.72	1.24E-02
AFUA_3G08880	Uncharacterized protein	-1.51	-1.94	-1.23	4.76E-05
AFUA_3G10940	Peroxisomal membrane protein receptor Pex19, putative	-1.50	-0.96	-1.25	1.21E-03
AFUA_4G04318	Copper resistance protein Crd2, putative	-1.49	-2.35	-2.86	1.30E-07
AFUA_1G09890	Uncharacterized protein	-1.49	-1.80	-1.53	3.17E-03
AFUA_5G07120	RNP domain protein	-1.49	-1.72	-0.65	1.85E-02
AFUA_1G04550	HMG box protein, putative	-1.48	0.00	0.53	4.75E-04
AFUA_7G05610	Glucanase, putative (EC 3.2.1.-)	-1.47	-2.53	-2.26	1.18E-04
AFUA_3G00350	Uncharacterized protein	-1.46	-0.43	-0.95	2.62E-04
AFUA_1G03510	ATP synthase subunit gamma	-1.46	-1.77	0.34	8.67E-06
AFUA_2G06150	Protein disulfide-isomerase (EC 5.3.4.1)	-1.44	-0.37	0.05	2.32E-07
AFUA_5G06240	Alcohol dehydrogenase, putative (EC 1.1.1.1)	-1.44	-1.06	-1.71	1.25E-08
AFUA_8G05570	Transcription factor (Sin3), putative	-1.43	-1.95	-1.13	5.73E-05
AFUA_2G15940	Cofactor for methionyl-and glutamyl-tRNA synthetases, putative	-1.42	-0.57	-0.27	5.33E-04
AFUA_2G17110	Cell division control protein Cdc48 (EC 3.6.1.-)	-1.41	-1.06	0.57	3.26E-05
AFUA_3G11740	RNAPII degradation factor Def1, putative	-1.40	-2.40	-1.63	1.23E-02
AFUA_8G02850	Actin binding protein, putative	-1.40	-0.91	-1.18	4.94E-03
AFUA_2G13290	GYF domain protein	-1.40	-1.66	-1.13	1.99E-02
AFUA_3G00270	Probable glucan endo-1,3-beta-glucosidase eglC (EC 3.2.1.39) (Endo-1,3-beta-glucanase eglC) (Laminarinase eglC)	-1.39	0.35	-1.60	2.49E-06
AFUA_6G04700	Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)	-1.38	-1.09	-0.98	9.00E-03
AFUA_5G10920	DUF221 domain protein, putative	-1.38	-2.08	-0.85	4.09E-02
AFUA_2G04620	Hsp70 chaperone BiP/Kar2, putative	-1.38	-0.70	-0.50	5.03E-04
AFUA_4G04550	Xanthine-guanine phosphoribosyl transferase Xpt1, putative	-1.37	-0.71	-0.55	2.25E-03
AFUA_6G03060	MFS monosaccharide transporter, putative	-1.37	-0.85	-1.28	1.54E-02
AFUA_1G03570	Acid phosphatase (EC 3.1.3.2)	-1.36	-0.63	-0.11	3.19E-03
AFUA_1G02020	SWIB/MDM2 domain protein (EC 5.99.1.2)	-1.34	-0.11	-0.49	2.31E-03
AFUA_6G05210	Malate dehydrogenase, NAD-dependent (EC 1.1.1.37)	-1.33	0.36	0.90	1.18E-07
AFUA_4G03240	Cell wall serine-threonine-rich galactomannoprotein Mp1	-1.32	-1.48	-1.83	8.46E-08
AFUA_1G02540	EF hand domain protein	-1.32	-1.29	-1.02	3.44E-06
AFUA_4G14500	Questin oxidase (EC 1.-.-.-) (Trypacidin synthesis protein K)	-1.31	-0.02	0.79	3.62E-04
AFUA_5G03690	Phosphatidylinositol transfer protein sfh5 (PITP sfh5)	-1.29	-0.48	0.46	2.08E-03

AFUA_5G01260	Ankyrin repeat protein	-1.29	-0.27	-1.38	3.55E-07
AFUA_5G06060	E3 ubiquitin ligase complex SCF subunit sconC (Sulfur controller C) (Sulfur metabolite repression control protein C)	-1.29	-0.68	-0.09	1.29E-04
AFUA_5G12940	Arylsulfatase, putative (EC 3.1.6.1)	-1.29	-0.57	-1.52	5.40E-04
AFUA_5G08970	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit WBP1 (Oligosaccharyl transferase subunit WBP1) (EC 2.4.99.18)	-1.28	-1.44	0.16	9.80E-03
AFUA_8G06550	Carbonic anhydrase (EC 4.2.1.1) (Carbonate dehydratase)	-1.28	-1.24	-1.12	2.66E-04
AFUA_1G04320	40S ribosomal protein S8	-1.27	-1.39	1.48	3.23E-02
AFUA_6G02090	ATP synthase subunit E, putative (EC 3.6.3.14)	-1.26	-1.17	-0.77	5.70E-06
AFUA_7G04760	Gamma-glutamyltranspeptidase (EC 2.3.2.2)	-1.25	-0.80	-0.92	8.11E-03
AFUA_3G01070	Tyrosinase, putative (EC 1.14.18.1)	-1.23	0.24	-0.26	3.73E-05
AFUA_8G01490	Endoglucanase, putative	-1.23	-0.50	-0.42	2.63E-03
AFUA_2G17540	Multicopper oxidase abr1 (EC 1.-.-.-) (Conidial pigment biosynthesis oxidase abr1)	-1.23	-2.30	-1.71	2.97E-04
AFUA_3G07160	Class V chitinase, putative (EC 3.2.1.14)	-1.22	0.27	1.69	2.70E-08
AFUA_3G13750	Uncharacterized protein	-1.21	-0.92	-2.66	1.02E-03
AFUA_8G06870	MFS sugar transporter, putative	-1.21	0.16	0.72	2.87E-03
AFUA_6G07855	Conserved threonine rich protein	-1.21	-0.42	-1.18	1.90E-02
AFUA_7G06840	Class III aminotransferase, putative (EC 2.6.1.-)	-1.19	1.01	-0.22	8.20E-03
AFUA_8G05440	Mitochondrial ATPase subunit ATP4, putative (EC 3.6.3.14)	-1.19	-1.15	0.29	5.86E-06
AFUA_6G03810	ATP synthase D chain, mitochondrial, putative (EC 3.6.3.14)	-1.19	-0.38	0.74	9.43E-03
AFUA_5G13920	Hsp90 binding co-chaperone (Sba1), putative	-1.18	-0.68	-0.47	3.75E-05
AFUA_3G10490	DNA damage response protein (Dap1), putative	-1.18	-1.46	-0.13	3.46E-03
AFUA_2G17180	Sorting nexin mvp1	-1.17	-0.80	-0.57	3.07E-02
AFUA_6G00510	NADP-dependent alcohol dehydrogenase (EC 1.1.1.1)	-1.16	-1.55	-1.36	3.35E-06
AFUA_3G02200	Uncharacterized protein	-1.15	-0.68	-1.72	2.08E-02
AFUA_2G05590	Ubiquitin carboxyl-terminal hydrolase (EC 3.4.19.12)	-1.13	-1.32	-0.62	1.38E-04
AFUA_7G01230	DnaJ domain protein	-1.13	-0.49	-0.95	1.92E-02
AFUA_5G10990	Uncharacterized protein	-1.13	-0.61	-1.79	7.89E-06
AFUA_2G08190	Tubulin-specific chaperone A	-1.13	-0.58	-0.71	5.93E-04
AFUA_2G17550	Heptaketide hydrolyase ayg1 (EC 3.7.1.-) (Conidial pigment biosynthesis protein ayg1)	-1.11	1.18	0.25	5.29E-10
AFUA_2G15760	Poly(A)+ RNA transport protein (UbaA), putative (EC 6.3.2.19)	-1.11	0.63	1.33	2.53E-05
AFUA_5G14830	Glyoxalase family protein (EC 4.4.1.5)	-1.10	-0.19	-0.36	3.12E-04
AFUA_4G00960	ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	-1.10	-0.70	-0.09	1.81E-02
AFUA_1G10110	TIM-barrel enzyme family protein	-1.10	-0.95	-1.16	2.05E-02
AFUA_2G17620	Cellobiose dehydrogenase	-1.08	-1.36	-2.19	1.66E-03
AFUA_2G11250	Aryl-alcohol dehydrogenase Aad14, putative (EC 1.1.1.-)	-1.07	0.70	1.79	4.39E-05
AFUA_7G03860	DNA-directed RNA polymerase II subunit RPB11a, putative	-1.06	-1.71	-0.54	3.88E-03
AFUA_1G05050	Cytosine deaminase, putative (EC 3.5.4.1)	-1.04	0.34	0.71	2.94E-03
AFUA_3G08940	Proteasome regulatory particle subunit (RpnL), putative	-1.03	0.27	1.05	1.13E-02
AFUA_5G08090	Pyridoxine biosynthesis protein	-1.03	-0.90	-1.31	5.36E-06
AFUA_1G14280	C6 finger domain protein, putative	-1.03	-0.91	-2.25	6.39E-03
AFUA_2G17600	Conidial pigment polyketide synthase alb1 (EC 2.3.1.-) (Conidial pigment biosynthesis protein alb1) (Naphthopyrone synthase)	-1.02	-0.04	0.12	3.02E-02
AFUA_3G00880	UPF0619 GPI-anchored membrane protein AFUA_3G00880	-1.02	-1.53	-1.89	6.79E-04
AFUA_4G08580	Mitochondrial peroxiredoxin Prx1, putative (EC 1.11.1.7)	-1.02	0.45	2.05	7.03E-07
AFUA_5G07890	SsDNA binding protein, putative	-1.01	-1.33	-1.91	1.19E-06
AFUA_6G07070	Probable 1,4-beta-D-glucan cellobiohydrolase A (EC 3.2.1.91) (Beta-glucancellobiohydrolase A) (Cellobiohydrolase D) (Exocellobiohydrolase A) (Exoglucanase A)	-1.01	-1.12	0.42	3.99E-02
AFUA_4G07700	Clathrin heavy chain	1.01	1.28	1.93	7.89E-07

AFUA_2G02810	Alcohol dehydrogenase, zinc-containing, putative	1.02	0.68	0.87	3.08E-02
AFUA_2G11940	Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	1.02	0.94	2.56	1.32E-06
AFUA_1G12340	Carnitine acetyl transferase	1.02	1.01	2.16	3.89E-03
AFUA_6G10830	Serine/threonine-protein phosphatase (EC 3.1.3.16)	1.03	0.77	1.62	3.21E-03
AFUA_3G03000	Phosphatidylethanolamine-binding protein, putative	1.03	1.47	1.62	1.71E-02
AFUA_5G12130	Rab small monomeric GTPase Rab7, putative	1.04	0.50	0.48	4.22E-04
AFUA_6G01790	Uncharacterized protein	1.04	0.89	1.43	2.72E-03
AFUA_2G09210	60S ribosomal protein L10	1.05	0.67	3.59	2.78E-08
AFUA_7G00860	Lipoxygenase, putative (EC 1.13.11.-)	1.05	1.73	2.86	2.58E-04
AFUA_4G09010	mRNA splicing protein (Prp39), putative	1.05	1.27	2.22	2.27E-02
AFUA_8G07190	Uncharacterized protein	1.05	1.18	2.56	8.55E-04
AFUA_8G05040	Dihydrodipicolinate synthetase family protein (EC 4.2.1.-)	1.05	0.77	0.20	4.15E-03
AFUA_4G08240	Zinc-containing alcohol dehydrogenase, putative (EC 1.1.1.1)	1.05	-0.23	-0.58	8.38E-08
AFUA_5G05450	40S ribosomal protein S1	1.05	0.25	2.44	8.15E-08
AFUA_4G11340	Saccharopine dehydrogenase Lys9, putative (EC 1.5.1.7)	1.06	0.52	1.87	2.32E-05
AFUA_1G14170	Probable beta-galactosidase A (EC 3.2.1.23) (Lactase A)	1.06	1.73	1.16	7.03E-03
AFUA_6G10980	UV-damaged DNA binding protein, putative	1.06	1.81	3.04	6.09E-05
AFUA_1G14490	Aminotransferase, putative	1.06	1.40	1.61	1.36E-02
AFUA_2G01220	GTP cyclohydrolase II, putative (EC 3.5.4.25)	1.06	2.20	3.30	5.88E-03
AFUA_4G13460	SNF2 family helicase/ATPase, putative	1.07	-0.26	1.29	1.77E-02
AFUA_1G15720	Importin beta-1 subunit	1.07	1.05	1.43	4.24E-02
AFUA_1G06960	Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	1.08	1.40	2.85	5.87E-08
AFUA_1G05990	Ribosomal protein L16a	1.08	0.75	3.23	1.40E-07
AFUA_2G14470	Oxidoreductase, FAD-binding, putative	1.08	1.94	1.01	1.21E-04
AFUA_2G17430	Oxidoreductase 2-nitropropane dioxygenase family, putative (EC 1.13.11.-)	1.09	1.52	2.01	3.46E-03
AFUA_3G06610	Proteasome regulatory particle subunit (RpnE), putative	1.09	-0.11	1.18	1.97E-04
AFUA_6G14330	5-oxo-L-prolinase, putative (EC 3.5.2.9)	1.09	0.30	1.15	3.96E-02
AFUA_4G07435	60S ribosomal protein L36	1.10	0.82	4.07	2.59E-04
AFUA_3G11900	Oxidoreductase, zinc-binding (EC 1.1.1.2)	1.10	0.76	-0.01	5.14E-04
AFUA_4G03050	Profilin	1.11	0.85	0.86	4.83E-03
AFUA_3G10310	Acetolactate synthase (EC 2.2.1.6)	1.11	2.68	2.31	4.10E-07
AFUA_6G14340	Glucooligosaccharide oxidase, putative (EC 1.5.3.-)	1.11	0.13	-0.37	1.05E-06
AFUA_2G16370	60S ribosomal protein L32	1.11	0.28	3.19	5.74E-07
AFUA_3G01920	Acyl-CoA dehydrogenase, putative	1.11	-0.77	-1.31	7.17E-04
AFUA_1G06770	40S ribosomal protein S26	1.12	0.35	3.21	2.81E-03
AFUA_4G04210	Leucine aminopeptidase 1 (EC 3.4.11.-) (Leucyl aminopeptidase 1) (LAP1)	1.12	-0.05	0.08	1.65E-04
AFUA_2G15660	Aldehyde dehydrogenase	1.13	1.10	1.38	2.25E-04
AFUA_1G13590	Uncharacterized protein	1.13	1.36	0.90	2.35E-02
AFUA_2G03030	Pre-mRNA splicing factor (Prp8), putative	1.14	0.09	0.09	3.31E-02
AFUA_4G08600	Aldehyde dehydrogenase, putative (EC 1.2.1.3)	1.14	2.06	2.52	5.58E-06
AFUA_4G04460	60S ribosomal protein L13	1.14	0.48	3.26	1.59E-08
AFUA_5G07340	DnaJ domain protein Psi, putative	1.14	0.20	-0.32	9.87E-04
AFUA_2G04460	Uncharacterized protein	1.15	-0.16	0.59	3.39E-02
AFUA_4G07845	60S ribosomal protein L38, putative	1.15	1.37	3.10	7.41E-05
AFUA_6G12930	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase) (Homocitrate dehydratase) (EC 4.2.1.-)	1.16	1.88	3.20	6.24E-07
AFUA_2G09850	Oxidoreductase, 2-nitropropane dioxygenase family, putative (EC 1.-.-.-)	1.16	-0.08	0.05	4.17E-02
AFUA_1G15730	40S ribosomal protein S22	1.16	0.42	3.28	6.61E-06
AFUA_4G11220	Xanthine dehydrogenase HxA, putative (EC 1.17.1.4)	1.16	0.78	0.55	3.91E-03
AFUA_1G05340	40S ribosomal protein S19	1.17	0.13	3.23	1.01E-04
AFUA_3G02190	Uncharacterized protein	1.17	-1.23	-0.36	1.20E-02
AFUA_5G11230	RAS small monomeric GTPase RasA	1.17	0.92	1.22	6.77E-03
AFUA_2G03490	Calcium/calmodulin-dependent protein kinase, putative	1.17	0.85	1.38	1.60E-02
AFUA_1G03740	Glutamate carboxypeptidase, putative	1.17	0.43	0.34	1.22E-03

AFUA_7G04380	Alcohol dehydrogenase, putative (EC 1.1.1.1)	1.17	1.16	1.10	4.69E-03
AFUA_7G01430	Opsin, putative	1.17	0.44	1.26	5.24E-04
AFUA_6G14200	Acetyl-CoA-acetyltransferase, putative (EC 2.3.1.9)	1.18	0.33	-0.05	1.89E-05
AFUA_4G07910	Mitochondrial presequence protease (EC 3.4.24.-)	1.18	1.01	1.04	7.78E-06
AFUA_2G11150	Rab GDP dissociation inhibitor	1.18	1.90	2.40	1.79E-04
AFUA_5G07000	NAD binding Rossmann fold oxidoreductase, putative (EC 1.-.-.-)	1.19	2.13	2.22	4.38E-07
AFUA_3G10390	Uncharacterized protein	1.19	0.52	0.28	1.60E-04
AFUA_6G12250	Succinyl-CoA:3-ketoacid-coenzyme A transferase (EC 2.8.3.5)	1.20	1.90	1.74	1.35E-02
AFUA_2G01940	Uncharacterized protein	1.20	0.01	-1.22	2.82E-02
AFUA_1G11770	COPII-coated vesicle protein SurF4/Erv29, putative	1.20	0.65	2.51	2.85E-03
AFUA_2G13530	Translation elongation factor EF-2 subunit, putative	1.20	0.63	1.73	2.42E-07
AFUA_5G11040	Pantoate--beta-alanine ligase (EC 6.3.2.1)	1.20	2.08	2.46	1.10E-04
AFUA_3G05610	Uncharacterized protein	1.20	1.33	0.81	4.71E-05
AFUA_2G04230	Fumarylacetoacetate hydrolase FahA (EC 3.7.1.2)	1.21	0.85	0.25	2.77E-04
AFUA_1G13370	Aflatoxin B1-aldehyde reductase GliO-like, putative (EC 1.1.1.-)	1.21	1.00	1.94	2.87E-03
AFUA_2G07500	Probable Xaa-Pro aminopeptidase pepP (EC 3.4.11.9) (Aminoacylproline aminopeptidase) (Prolidase)	1.22	0.45	0.05	4.75E-08
AFUA_2G10520	Uricase (EC 1.7.3.3) (Urate oxidase)	1.22	1.71	0.55	9.87E-03
AFUA_4G13310	Metallo-beta-lactamase domain protein, putative	1.22	1.02	0.72	1.34E-02
AFUA_3G02257	Uncharacterized protein	1.22	1.29	2.68	3.05E-04
AFUA_8G01100	Melibiase subfamily, putative (EC 3.2.1.22)	1.22	1.62	2.77	4.36E-04
AFUA_2G04940	KH domain RNA binding protein	1.23	0.41	1.74	1.66E-02
AFUA_2G18030	Catalase easC (EC 1.11.-.-) (Ergot alkaloid synthesis protein C)	1.23	1.60	2.07	1.29E-04
AFUA_6G08740	3-dehydroshikimate dehydratase, putative (EC 4.2.1.-)	1.23	1.28	1.52	1.10E-03
AFUA_8G04810	Casein kinase, putative (EC 2.7.11.1)	1.23	1.84	1.89	4.01E-02
AFUA_7G02190	Zinc knuckle nucleic acid binding protein, putative	1.23	-0.28	-0.32	2.60E-03
AFUA_8G04100	N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	1.23	0.94	1.12	2.79E-02
AFUA_1G06580	High expression lethality protein Hel10, putative	1.24	-1.04	-1.37	4.99E-06
AFUA_3G05350	Histone H2B	1.24	1.37	2.21	5.77E-07
AFUA_3G10130	Fructosyl amino acid oxidasesarcosine oxidase, putative	1.24	1.03	1.15	2.40E-02
AFUA_5G12250	Posttranscriptional regulation nuclease (Mkt1), putative	1.24	1.75	2.19	5.16E-05
AFUA_1G11130	60S ribosomal protein L6	1.24	0.67	2.98	4.44E-04
AFUA_1G13140	G-protein complex alpha subunit GpaA/FadA	1.24	0.75	1.69	9.24E-05
AFUA_6G11380	Mitochondrial import receptor subunit (Tom20), putative	1.25	-0.59	-0.38	2.28E-03
AFUA_1G02670	Arp2/3 complex 34 kDa subunit	1.26	1.18	2.31	1.01E-04
AFUA_5G02470	Thiamine biosynthesis protein (Nmt1), putative	1.27	0.44	0.77	8.85E-05
AFUA_1G03070	Transcription initiation factor TFIID subunit, putative	1.27	0.46	1.37	1.73E-02
AFUA_4G11310	Fructose-1,6-bisphosphatase Fbp1, putative (EC 3.1.3.11)	1.27	0.19	1.11	3.52E-03
AFUA_6G08700	Probable beta-glucosidase F (EC 3.2.1.21) (Beta-D-glucoside glucohydrolase F) (Cellobiase F) (Gentiobiase F)	1.28	0.45	-0.30	1.32E-08
AFUA_6G03520	Short-chain dehydrogenase/reductase family protein, putative (EC 1.1.1.47)	1.29	0.51	0.50	5.27E-04
AFUA_4G11730	Glycerol dehydrogenase (GldB), putative (EC 1.1.1.72)	1.29	2.83	3.70	5.34E-07
AFUA_5G04230	Citrate synthase	1.29	2.25	3.43	2.08E-07
AFUA_3G09910	Phosphatidylinositol transporter, putative	1.29	1.59	2.31	5.91E-05
AFUA_1G09810	Translation machinery-associated protein 20	1.30	2.29	1.98	1.31E-04
AFUA_1G10130	Adenosylhomocysteinase (EC 3.3.1.1)	1.30	1.01	2.02	3.28E-05
AFUA_4G04200	Myo-inositol-1(Or 4)-monophosphatase (EC 3.1.3.7)	1.30	1.26	0.92	7.10E-03
AFUA_6G10650	ATP citrate lyase, subunit 1, putative (EC 2.3.3.8)	1.30	2.00	2.76	3.74E-08
AFUA_3G04220	Fatty acid synthase beta subunit, putative	1.30	1.38	2.47	5.78E-09
AFUA_2G15190	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	1.31	1.55	1.37	1.38E-07
AFUA_5G10640	Tyrosine--tRNA ligase (EC 6.1.1.1) (Tyrosyl-tRNA synthetase)	1.31	0.16	2.06	2.72E-02
AFUA_4G04660	Proteasome regulatory particle subunit Rpt6, putative	1.32	0.28	2.21	9.10E-03
AFUA_1G05630	40S ribosomal protein S3, putative	1.32	0.34	2.85	3.90E-08

AFUA_6G04210	Mannosyl-oligosaccharide glucosidase, putative	1.32	2.11	1.78	2.46E-05
AFUA_4G06000	50S ribosomal protein L3	1.32	-0.65	1.08	1.77E-02
AFUA_3G10730	40S ribosomal protein S7	1.32	0.33	3.31	8.79E-05
AFUA_1G08810	Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	1.32	0.84	1.94	5.22E-03
AFUA_5G03480	Methylenetetrahydrofolate reductase (EC 1.5.1.20)	1.32	1.59	2.06	4.56E-02
AFUA_5G06700	Serine/threonine-protein phosphatase (EC 3.1.3.16)	1.32	0.64	1.04	4.23E-02
AFUA_1G06180	Trimethyllysine dioxygenase TmlH, putative	1.32	0.37	0.74	2.71E-02
AFUA_8G05590	Oxidoreductase, short chain dehydrogenase/reductase family	1.33	1.35	1.27	7.36E-05
AFUA_1G05080	60S acidic ribosomal protein P0	1.33	0.33	2.99	1.59E-08
AFUA_6G07080	WD repeat-containing protein jip5	1.33	0.00	-0.47	7.25E-05
AFUA_5G12830	DUF1264 domain protein	1.33	0.98	0.82	3.96E-07
AFUA_3G02430	Uncharacterized protein	1.34	2.01	1.93	8.65E-07
AFUA_1G04820	Probable NAD(P)H-dependent D-xylose reductase xyl1 (XR) (EC 1.1.1.307)	1.34	1.48	1.27	3.13E-08
AFUA_4G11290	Proteasome activator subunit 4, putative	1.35	1.17	1.93	9.16E-04
AFUA_1G14780	BAP31 domain protein, putative	1.35	0.09	1.25	4.36E-05
AFUA_1G08940	Pheromone-processing carboxypeptidase kex1 (EC 3.4.16.6) (Carboxypeptidase D)	1.35	1.13	1.04	3.43E-02
AFUA_2G16070	Urease accessory protein UreD	1.36	1.42	0.67	2.51E-02
AFUA_4G13580	Gamma-glutamyltranspeptidase (EC 2.3.2.2)	1.36	0.72	0.27	1.00E-05
AFUA_5G13180	Agmatinase, putative (EC 3.5.3.11)	1.37	0.07	-1.07	2.51E-03
AFUA_6G12580	Anthranilate synthase component I, putative (EC 4.1.3.27)	1.37	1.63	2.21	2.10E-07
AFUA_4G13510	Isocitrate lyase (ICL) (Isocitrase) (Isocitratase) (EC 4.1.3.1) (Methylisocitrate lyase) (MICA) (EC 4.1.3.30) (Threo-D(S)-isocitrate glyoxylate-lyase)	1.37	2.27	3.61	6.63E-08
AFUA_1G12610	Hsp70 chaperone Hsp88	1.37	1.56	1.54	1.28E-03
AFUA_1G14570	Histidine biosynthesis trifunctional protein [Includes: Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19); Phosphoribosyl-ATP pyrophosphohydrolase (EC 3.6.1.31); Histidinol dehydrogenase (HDH) (EC 1.1.1.23)]	1.38	1.80	1.44	5.84E-08
AFUA_2G09180	Coatomer subunit zeta, putative	1.38	1.53	2.49	2.59E-02
AFUA_4G06950	Integral ER membrane protein Scs2, putative	1.38	-0.35	-0.44	3.27E-04
AFUA_5G01450	NADH-dependent flavin oxidoreductase, putative (EC 1.-.-.-)	1.38	0.75	2.43	2.37E-02
AFUA_2G17560	Hydroxynaphthalene reductase arp2 (EC 1.1.-.-) (Conidial pigment biosynthesis oxidase arp2)	1.38	1.98	2.22	3.81E-07
AFUA_4G08490	Acyl-CoA dehydrogenase, putative (EC 1.3.99.-)	1.38	0.03	-0.33	7.77E-04
AFUA_4G13170	G-protein comlpex beta subunit CpcB	1.39	0.68	0.52	7.53E-06
AFUA_2G01030	1-aminocyclopropane-1-carboxylate deaminase, putative (EC 3.5.99.7)	1.39	1.42	1.51	6.06E-04
AFUA_6G11130	Possible replication factor-a protein	1.40	0.52	0.48	5.89E-03
AFUA_4G10780	Ubiquitin-protein ligase (Tom1), putative	1.40	0.57	1.66	3.15E-02
AFUA_6G00370	Aminotransferase, putative	1.40	1.87	0.59	1.39E-03
AFUA_4G07710	Pyruvate carboxylase (EC 6.4.1.1)	1.40	1.84	2.74	9.52E-08
AFUA_6G12990	Cytosolic large ribosomal subunit protein L7A	1.41	1.13	3.48	6.45E-08
AFUA_3G08840	Coatomer subunit alpha	1.41	0.96	1.73	5.58E-06
AFUA_3G08470	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	1.41	3.06	3.33	8.66E-07
AFUA_6G00260	Phosphatidylserine decarboxylase family protein (EC 4.1.1.-)	1.42	1.79	1.02	3.32E-05
AFUA_6G08830	2-oxoisovalerate dehydrogenase complex alpha subunit, putative (EC 1.2.4.4)	1.42	0.90	0.40	3.48E-03
AFUA_4G08170	Succinate-semialdehyde dehydrogenase Uga2, putative (EC 1.2.1.24)	1.43	2.03	2.87	8.68E-06
AFUA_5G02610	Cytochrome P450, putative (EC 1.14.-.-)	1.43	0.88	0.12	6.54E-03
AFUA_1G13710	Isoleucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.5)	1.43	1.69	2.43	1.72E-06
AFUA_6G04010	Chromosome segregation protein Cse1, putative	1.43	1.60	2.03	7.04E-05
AFUA_1G12940	Mitogen-activated protein kinase hog1 (MAP kinase hog1) (EC 2.7.11.24)	1.43	1.34	2.07	8.26E-03
AFUA_6G08020	ABC transporter, putative	1.44	2.23	2.27	8.59E-04
AFUA_7G01060	Cysteine-rich secreted protein	1.44	-1.60	-0.47	8.24E-07
AFUA_3G01580	GMC oxidoreductase, putative	1.44	1.53	1.48	2.64E-02
AFUA_1G16600	Ribonuclease T2, putative (EC 3.1.27.1)	1.44	-0.63	-0.49	8.65E-03
AFUA_1G02070	Cytochrome C1/Cyt1, putative (EC 1.10.2.2)	1.45	0.49	1.37	2.80E-02

AFUA_3G11710	Saccharopine dehydrogenase [NAD(+), L-lysine-forming] (SDH) (EC 1.5.1.7) (Lysine--2-oxoglutarate reductase)	1.46	1.93	2.62	3.46E-05
AFUA_6G03590	Citrate synthase	1.46	0.88	0.73	7.70E-05
AFUA_3G05740	Aldose 1-epimerase, putative (EC 5.1.3.3)	1.47	1.36	1.46	1.87E-02
AFUA_5G06680	4-aminobutyrate transaminase GatA (EC 2.6.1.19)	1.48	1.64	1.32	1.25E-07
AFUA_8G05020	Beta-hexosaminidase (EC 3.2.1.52)	1.48	0.97	0.10	6.98E-05
AFUA_1G09930	Glycerol dehydrogenase Gcy1, putative (EC 1.1.1.-)	1.48	2.06	2.98	9.11E-09
AFUA_8G00230	Verruculogen synthase (EC 1.14.11.38) (Fumitremorgin biosynthesis protein F)	1.49	2.12	2.00	2.82E-04
AFUA_3G07300	ABC multidrug transporter, putative (EC 3.6.3.-)	1.49	1.40	1.92	1.46E-03
AFUA_3G05360	Histone H2A	1.50	2.69	3.49	3.10E-05
AFUA_4G10800	40S ribosomal protein S6	1.50	0.17	2.43	1.34E-05
AFUA_5G08130	Protein transport protein Sec61 alpha subunit, putative	1.50	0.46	1.79	2.47E-03
AFUA_2G06320	Replication protein A 70 kDa DNA-binding subunit	1.51	0.64	0.54	2.81E-02
AFUA_4G09140	L-ornithine aminotransferase Car2, putative (EC 2.6.1.13)	1.51	1.35	1.05	2.77E-07
AFUA_8G07080	Extracellular metalloproteinase mep (EC 3.4.24.-) (Elastinolytic metalloproteinase mep) (Fungalysin mep)	1.52	0.41	0.16	3.81E-02
AFUA_4G08710	Short chain dehydrogenase, putative (EC 1.-.-.-)	1.52	1.69	1.11	1.14E-08
AFUA_4G11540	Glycerol kinase, putative (EC 2.7.1.30)	1.52	3.18	2.94	5.99E-05
AFUA_1G04620	Alcohol dehydrogenase, zinc-containing, putative (EC 1.1.1.-)	1.52	1.12	2.28	9.14E-03
AFUA_8G01780	Nitrilase, putative	1.52	3.82	-0.30	4.70E-06
AFUA_6G10610	Ribose 5-phosphate isomerase A (EC 5.3.1.6)	1.53	0.80	0.37	1.14E-04
AFUA_1G01970	VeA-like protein	1.53	2.00	3.12	1.12E-03
AFUA_2G04130	40S ribosomal protein S11	1.54	0.29	3.44	1.24E-05
AFUA_4G04410	3-hydroxybutyryl-CoA dehydrogenase, putative (EC 1.1.1.157)	1.54	1.62	1.58	8.61E-05
AFUA_1G04530	60S ribosomal protein L20	1.54	0.72	3.47	2.47E-06
AFUA_5G03760	Endochitinase A1 (EC 3.2.1.14) (Chitinase A1)	1.55	1.10	1.52	1.32E-03
AFUA_4G10770	Psi-producing oxygenase A (Fatty acid oxygenase ppoA) [Includes: Linoleate 8R-lipoxygenase (EC 1.13.11.60); 9,12-octadecadienoate 8-hydroperoxide 8R-isomerase (EC 5.4.4.5)]	1.55	-0.58	-1.21	2.94E-06
AFUA_8G01390	Glycosyl hydrolase, putative	1.55	2.14	2.67	1.14E-04
AFUA_8G01420	Quinone oxidoreductase, putative (EC 1.6.5.5)	1.55	1.38	1.85	5.05E-04
AFUA_4G14520	Monoogygenase tpcG (EC 1.-.-.-) (Trypacidin synthesis protein G)	1.55	1.86	3.24	4.15E-05
AFUA_2G09130	NADH-ubiquinone dehydrogenase 24 kDa subunit, putative (EC 1.6.5.3)	1.56	1.46	1.71	3.08E-05
AFUA_2G13250	Tryptophan synthase (EC 4.2.1.20)	1.57	1.05	2.10	4.86E-03
AFUA_2G09380	Probable cutinase 1 (EC 3.1.1.74) (Cutin hydrolase 1)	1.57	-0.89	-0.41	6.84E-06
AFUA_5G02480	Glycogen [starch] synthase (EC 2.4.1.11)	1.58	1.39	2.40	6.34E-05
AFUA_1G11480	Uncharacterized protein	1.60	1.67	0.73	7.90E-05
AFUA_5G09450	Isoflavone reductase family protein (EC 1.3.1.-)	1.60	1.94	2.92	3.41E-05
AFUA_6G00750	Pyruvate decarboxylase, putative (EC 4.1.1.1)	1.60	1.72	1.26	4.56E-04
AFUA_3G11480	Mitochondrial methylglutaconyl-CoA hydratase (Auh), putative (EC 4.2.1.18)	1.61	2.12	3.01	1.14E-06
AFUA_4G00610	Aryl-alcohol dehydrogenase, putative (EC 1.1.-.-)	1.62	2.71	2.45	1.28E-03
AFUA_4G07650	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) (Rotamase B)	1.62	2.05	2.52	4.36E-03
AFUA_1G14710	Beta-glucosidase, putative	1.63	2.70	3.52	4.34E-05
AFUA_4G14450	Mannitol 2-dehydrogenase (M2DH) (MDH) (EC 1.1.1.67)	1.63	1.31	1.97	1.45E-06
AFUA_1G02030	Eukaryotic translation initiation factor 3 subunit B (eIF3b) (Eukaryotic translation initiation factor 3 90 kDa subunit homolog) (eIF3 p90) (Translation initiation factor eIF3 p90 subunit homolog)	1.64	1.28	1.67	5.02E-03
AFUA_1G08980	UPF0160 domain protein MYG1, putative	1.65	1.77	1.65	1.28E-08
AFUA_8G03880	Alanine--tRNA ligase (EC 6.1.1.7) (Alanyl-tRNA synthetase) (AlaRS)	1.65	0.33	0.70	1.65E-02
AFUA_6G12660	40S ribosomal protein S10b	1.66	0.41	4.49	1.26E-03
AFUA_1G05390	Mitochondrial ADP,ATP carrier protein (Ant), putative	1.66	0.56	1.46	1.52E-03
AFUA_5G03770	Lipase, putative (EC 3.1.1.3)	1.66	1.62	2.66	1.25E-03

AFUA_8G07110	Alanyl-tRNA synthetase, putative (EC 6.1.1.7)	1.67	2.06	2.33	2.91E-02
AFUA_3G06840	40S ribosomal protein S4	1.67	0.34	3.34	1.55E-08
AFUA_1G05120	COPII-coated vesicle membrane protein Erv46, putative	1.67	-0.05	1.37	7.16E-03
AFUA_2G10090	40S ribosomal protein S15, putative	1.67	0.87	2.93	1.64E-04
AFUA_7G01320	Beta-mannosidase B (EC 3.2.1.25) (Mannanase B) (Mannase B)	1.67	2.03	1.98	7.67E-05
AFUA_3G03060	Cell wall protein PhiA	1.68	0.08	1.16	3.16E-04
AFUA_5G07740	DSB repair complex subunit Ku70, putative	1.68	0.98	1.20	2.50E-03
AFUA_6G02630	ATP-dependent RNA helicase sub2 (EC 3.6.4.13)	1.68	0.23	1.98	3.08E-03
AFUA_5G07750	Ferrochelatase (EC 4.99.1.1)	1.68	1.14	1.65	3.04E-02
AFUA_3G07810	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1)	1.68	1.72	1.63	7.09E-11
AFUA_2G04930	Uncharacterized protein	1.69	1.61	1.26	4.59E-03
AFUA_6G12300	RNP domain protein	1.69	0.90	1.09	8.91E-05
AFUA_3G10110	Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)	1.69	0.95	1.96	2.07E-02
AFUA_6G10900	UV-endonuclease UVE-1	1.70	2.63	2.73	1.88E-03
AFUA_5G10370	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (EC 1.3.5.1)	1.70	1.70	1.94	1.61E-03
AFUA_5G10280	Oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor (EC 1.1.1.31)	1.71	1.70	1.26	8.32E-03
AFUA_1G03390	60S ribosomal protein L12	1.71	0.76	3.35	1.44E-04
AFUA_4G11260	Aldo-keto reductase, putative (EC 1.1.1.-)	1.72	2.15	1.57	5.59E-07
AFUA_6G13250	60S ribosomal protein L31e	1.73	2.03	4.41	2.79E-05
AFUA_4G03660	Acid phosphatase, putative (EC 3.1.3.2)	1.73	2.31	2.00	1.27E-04
AFUA_5G09180	Uncharacterized protein	1.73	0.83	0.79	4.15E-03
AFUA_5G09790	Beta-lactamase	1.73	0.38	0.18	2.79E-03
AFUA_1G10970	Coatomer subunit beta (Beta-coat protein)	1.74	0.71	2.18	9.06E-03
AFUA_3G00900	Alpha-amylase, putative	1.74	1.28	0.97	1.10E-05
AFUA_4G12840	Methylthioribulose-1-phosphate dehydratase (MTRu-1-P dehydratase) (EC 4.2.1.109)	1.74	1.75	1.64	1.23E-03
AFUA_2G12630	Allergen Asp f 15 (Allergen Asp f 13) (allergen Asp f 15)	1.74	0.84	1.21	7.76E-04
AFUA_5G14310	Short chain dehydrogenase/reductase family protein	1.74	0.36	2.65	1.11E-02
AFUA_6G13180	CECR1 family adenosine deaminase, putative	1.74	1.99	2.52	3.02E-05
AFUA_2G02490	Uncharacterized protein	1.74	1.54	1.77	3.09E-03
AFUA_4G12010	2-oxo acid dehydrogenases acyltransferase, putative (EC 2.3.1.-)	1.75	0.76	0.37	2.23E-03
AFUA_2G15430	Sorbitol/xylulose reductase Sou1-like, putative (EC 1.-.-.-)	1.75	2.56	2.72	6.09E-04
AFUA_2G08130	60S ribosomal protein L44	1.76	1.02	4.10	2.38E-06
AFUA_4G08480	26S proteasome regulatory subunit Rpn2, putative	1.76	0.03	2.01	1.73E-02
AFUA_2G11020	Triosephosphate isomerase (EC 5.3.1.1)	1.77	2.19	2.49	5.43E-05
AFUA_6G06460	Fumarylacetoacetate hydrolase family protein	1.77	1.86	1.92	9.09E-05
AFUA_2G04710	Cytochrome b5, putative	1.77	-0.14	-0.24	2.88E-03
AFUA_6G02470	Fumarate hydratase, putative (EC 4.2.1.2)	1.78	1.92	2.06	3.59E-06
AFUA_1G09750	Aldehyde reductase (AKR1), putative (EC 1.1.1.2)	1.78	3.04	3.54	1.03E-08
AFUA_1G14410	60S ribosomal protein L17	1.79	1.58	4.32	4.06E-08
AFUA_3G01450	3-methyl-2-oxobutanoate dehydrogenase, putative	1.80	1.21	0.64	2.22E-04
AFUA_8G04710	Xylosidase, putative (EC 3.2.1.37)	1.81	1.72	1.89	6.76E-04
AFUA_4G03120	Mitochondrial cytochrome b2, putative (EC 1.1.2.3)	1.81	1.78	1.94	1.46E-05
AFUA_4G07580	Translation initiation factor EF-2 gamma subunit, putative	1.81	0.08	1.85	2.37E-05
AFUA_1G04540	NADH-cytochrome b5 reductase 2 (EC 1.6.2.2) (Mitochondrial cytochrome b reductase)	1.81	1.61	2.16	3.37E-06
AFUA_5G09920	Peptidase, putative (EC 3.-.-.-)	1.81	2.04	1.63	2.44E-06
AFUA_1G07200	Mitochondrial cytochrome b2, putative (EC 1.1.2.3)	1.82	1.54	1.70	1.56E-06
AFUA_1G05500	40S ribosomal protein S12	1.83	0.32	1.82	4.21E-06
AFUA_4G10330	CaaX farnesyltransferase beta subunit Ram1 (EC 2.5.1.58)	1.83	2.27	2.17	3.61E-04
AFUA_5G10490	Amidase, putative (EC 3.5.1.-)	1.83	-0.86	-1.42	3.08E-05
AFUA_5G11610	Protein arginine N-methyltransferase	1.83	2.28	1.82	2.99E-02
AFUA_6G04920	Formate dehydrogenase (FDH) (EC 1.2.1.2) (NAD-dependent formate dehydrogenase)	1.83	1.45	1.22	2.23E-08
AFUA_3G00640	Uncharacterized protein	1.84	0.70	2.90	2.45E-03

AFUA_2G04520	Fe-containing alcohol dehydrogenase, putative (EC 1.1.1.-)	1.84	2.61	2.46	2.08E-05
AFUA_3G12800	Clathrin-coated vesiclec protein (Bud7), putative	1.84	1.48	0.84	3.28E-02
AFUA_3G14990	Alpha/beta hydrolase, putative (EC 3.-.-.-)	1.85	1.14	1.66	5.44E-05
AFUA_6G08780	Proline utilization protein PrnX, putative (EC 4.3.1.12)	1.85	1.46	1.85	2.55E-03
AFUA_7G02470	mRNA processing protein (Mss51), putative	1.86	2.70	3.53	1.59E-03
AFUA_7G00700	Aldo-keto reductase (AKR13), puatative (EC 1.1.1.-)	1.86	1.56	2.73	2.34E-05
AFUA_5G02530	Ribokinase (EC 2.7.1.15)	1.86	2.75	2.17	6.59E-05
AFUA_6G08250	CwfJ domain protein	1.86	0.20	0.58	1.12E-02
AFUA_4G00280	Uncharacterized protein	1.86	0.50	-0.25	2.24E-04
AFUA_7G05360	FACT complex subunit pob3 (Facilitates chromatin transcription complex subunit pob3)	1.86	1.41	2.07	6.65E-04
AFUA_1G15140	Mitochondrial phosphate carrier protein (Mir1), putative	1.88	0.40	1.45	3.74E-04
AFUA_1G14220	Fibrillarin	1.88	-0.05	1.63	5.00E-07
AFUA_5G05480	Rheb small monomeric GTPase RhbA	1.88	1.54	1.84	1.32E-02
AFUA_6G05110	Mitochondrial import receptor subunit (Tom40), putative	1.88	0.90	1.59	3.67E-04
AFUA_2G05510	Mitochondrial F1F0 ATP synthase subunit F (Atp17), putative (EC 3.6.3.14)	1.89	1.16	2.45	1.23E-04
AFUA_4G09840	Kynureninase 2 (EC 3.7.1.3) (Biosynthesis of nicotinic acid protein 5-2) (L-kynurenine hydrolase 2)	1.89	1.03	1.19	1.40E-06
AFUA_2G00330	Beta-alanine synthase, putative (EC 3.5.1.-)	1.89	1.60	0.59	7.65E-04
AFUA_5G05680	Peptide chain release factor eRF/aRF, subunit 1	1.89	1.57	2.19	8.67E-06
AFUA_8G02780	Vacuolar protein sorting/targeting protein 10 (Carboxypeptidase Y receptor) (CPY receptor) (Sortilin vps10) (Vacuolar carboxypeptidase sorting receptor vps10)	1.89	0.72	1.07	1.69E-03
AFUA_4G10200	Transcription factor RfeF, putative	1.90	1.23	0.40	1.32E-06
AFUA_7G02140	40S ribosomal protein S24	1.90	1.10	3.49	1.13E-02
AFUA_1G04660	Ribosomal protein L15	1.90	0.74	3.30	1.58E-05
AFUA_5G12840	Hydroxyacylglutathione hydrolase, putative (EC 3.1.2.6)	1.91	1.96	1.58	2.01E-09
AFUA_6G02280	Peroxiredoxin Asp f3 (Prx) (EC 1.11.1.15) (Thioredoxin peroxidase) (TPx) (allergen Asp f 3)	1.92	1.22	1.20	9.23E-10
AFUA_6G04570	Translation elongation factor eEF-1 subunit gamma, putative	1.92	1.53	1.72	4.63E-06
AFUA_1G13780	Histone H4	1.92	1.56	2.39	1.19E-03
AFUA_1G09440	40S ribosomal protein S23	1.93	0.27	4.03	1.00E-05
AFUA_1G11535	Glutaredoxin-like protein	1.93	2.19	1.56	1.53E-03
AFUA_4G12850	Calnexin homolog	1.94	2.01	1.68	1.06E-05
AFUA_5G07360	Amine oxidase (EC 1.4.3.-)	1.94	0.47	0.11	3.31E-05
AFUA_4G03900	Peroxisomal multifunctional beta-oxidation protein (MFP), putative	1.94	0.92	0.41	2.85E-04
AFUA_5G08900	D-arabinitol dehydrogenase ArbD, putative (EC 1.1.1.69)	1.95	0.61	-0.15	2.25E-03
AFUA_5G05820	Homoserine kinase (EC 2.7.1.39)	1.95	0.36	1.92	3.41E-03
AFUA_3G11070	Pyruvate decarboxylase (EC 4.1.1.1)	1.95	3.42	3.43	9.50E-08
AFUA_2G16090	Importin subunit alpha	1.96	0.04	1.44	2.65E-02
AFUA_4G08410	Mannose-6-phosphate isomerase, class I (EC 5.3.1.8)	1.96	2.75	1.97	8.29E-06
AFUA_5G09640	Conserved fungal protein	1.96	2.01	1.97	6.03E-04
AFUA_7G02230	mRNA binding post-transcriptional regulator (Csx1), putative	1.96	1.06	1.46	4.21E-02
AFUA_4G11050	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial (EC 1.6.5.3) (EC 1.6.99.3)	1.96	1.85	3.19	1.70E-06
AFUA_4G00740	Uncharacterized protein	1.97	1.06	2.46	2.53E-06
AFUA_2G11560	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.12)	1.97	1.56	1.62	1.77E-04
AFUA_6G00600	Uncharacterized protein	1.97	0.70	0.22	1.47E-05
AFUA_7G05660	Translation elongation factor eEF-3, putative (EC 3.6.3.-)	1.97	0.18	0.60	1.40E-04
AFUA_6G00180	Uncharacterized protein	1.98	0.29	0.05	2.37E-04
AFUA_3G10460	Nuclear transport factor NTF-2, putative	1.98	1.40	1.80	6.04E-05
AFUA_3G11750	Oxysterol binding protein (Osh5), putative	1.98	1.18	2.24	1.90E-04
AFUA_7G05510	RSC complex subunit (RSC8), putative	1.99	0.63	0.59	3.10E-02

AFUA_7G05740	Malate dehydrogenase (EC 1.1.1.37)	1.99	2.20	1.80	2.64E-09
AFUA_2G10440	40S ribosomal protein S11	2.00	0.84	3.26	6.32E-05
AFUA_1G13280	Mannose-6-phosphate isomerase (EC 5.3.1.8) (Phosphohexomutase) (Phosphomannose isomerase) (PMI)	2.00	2.77	2.85	5.16E-06
AFUA_6G06900	Rho GTPase Rho1	2.00	1.49	1.54	6.27E-06
AFUA_7G05160	Fumarylacetoacetate hydrolase family protein	2.01	2.33	1.56	1.16E-02
AFUA_4G07610	Zinc metalloprotease, putative	2.02	1.67	0.28	2.41E-07
AFUA_6G04660	Centromere protein Cse4, putative	2.02	1.28	2.55	1.63E-02
AFUA_4G10610	Stress responsive A/B barrel domain protein	2.02	0.96	0.20	5.96E-05
AFUA_1G09020	Nuclear pore complex protein (SonA), putative	2.02	1.20	1.02	2.25E-04
AFUA_7G01460	Ribosomal protein S5	2.02	0.64	3.32	4.53E-09
AFUA_2G10500	40S ribosomal protein Rps16, putative	2.04	1.54	3.83	3.79E-05
AFUA_1G14850	Acyl-CoA dehydrogenase, putative (EC 1.3.99.-)	2.04	1.69	1.34	2.97E-10
AFUA_4G12600	Phosphoribosyl-aminoimidazole carboxylase (EC 4.1.1.21)	2.05	2.13	2.49	3.52E-06
AFUA_2G04310	Argininosuccinate synthase (EC 6.3.4.5)	2.05	1.20	2.41	2.55E-03
AFUA_6G10600	NEDD8-activating enzyme E1 regulatory subunit	2.06	1.76	2.38	5.36E-04
AFUA_2G12450	Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4)	2.07	1.98	1.96	1.61E-05
AFUA_4G06910	Outer mitochondrial membrane protein porin	2.08	0.22	1.99	5.95E-07
AFUA_3G13010	Zn-dependent hydrolase/oxidoreductase family protein, putative	2.08	-0.14	-1.12	3.42E-03
AFUA_1G16270	Xylitol dehydrogenase XdhB (EC 1.1.1.14)	2.08	2.20	2.82	1.45E-03
AFUA_5G03250	Ubiquitin C-terminal hydrolase (HAUSP), putative (EC 3.1.2.15)	2.08	0.78	0.57	3.17E-05
AFUA_2G09030	Dipeptidyl-peptidase 5 (EC 3.4.14.-) (Dipeptidyl-peptidase V) (DPP V) (DppV)	2.08	3.28	1.89	1.63E-07
AFUA_5G08910	3-methylcrotonyl-CoA carboxylase subunit alpha (MccA), putative (EC 6.4.1.4)	2.09	1.12	1.26	7.48E-06
AFUA_5G06390	Adenosine kinase, putative (EC 2.7.1.20)	2.09	1.25	3.06	2.24E-06
AFUA_3G12690	Uncharacterized protein	2.09	2.55	2.09	4.39E-10
AFUA_4G02840	NmrA-like family protein, putative	2.09	1.42	-0.34	2.28E-04
AFUA_3G13320	40S ribosomal protein S0	2.09	0.99	3.67	3.50E-07
AFUA_3G03020	Phosphoglucomutase, putative	2.09	2.13	1.66	1.24E-04
AFUA_6G08750	Delta-1-pyrroline-5-carboxylate dehydrogenase PrnC (EC 1.2.1.88)	2.10	1.56	1.26	3.94E-08
AFUA_7G02550	Probable D-xylulose reductase A (EC 1.1.1.9) (Xylitol dehydrogenase A)	2.11	3.08	3.00	2.95E-08
AFUA_2G10220	Glycerol dehydrogenase, putative (EC 1.1.1.-)	2.11	1.89	1.74	2.26E-05
AFUA_2G00967	Cupin domain protein	2.11	2.50	0.92	4.17E-03
AFUA_1G05200	Eukaryotic translation initiation factor 3 subunit A (eIF3a) (Eukaryotic translation initiation factor 3 110 kDa subunit homolog) (eIF3 p110) (Translation initiation factor eIF3, p110 subunit homolog)	2.11	0.30	1.59	1.79E-03
AFUA_5G09400	Carbonyl reductase, putative (EC 1.-.-.-)	2.11	2.49	2.20	2.04E-04
AFUA_6G11430	Aldehyde dehydrogenase AldA, putative (EC 1.2.1.3)	2.11	2.91	2.59	4.34E-10
AFUA_4G06860	Uncharacterized protein	2.13	2.09	1.49	1.46E-04
AFUA_1G08930	Probable cytosolic iron-sulfur protein assembly protein 1	2.13	2.22	3.31	2.02E-03
AFUA_7G05290	40S ribosomal protein S13	2.13	1.40	4.21	4.71E-06
AFUA_2G03380	Alkaline serine protease	2.14	1.37	4.85	1.02E-04
AFUA_2G09090	Prohibitin, putative	2.14	0.81	2.15	1.23E-03
AFUA_5G03520	Uncharacterized protein	2.15	2.36	2.43	6.41E-07
AFUA_4G13700	Threonyl-tRNA synthetase, putative (EC 6.1.1.3)	2.15	1.98	2.27	1.50E-05
AFUA_2G17920	Uncharacterized protein	2.15	2.58	2.12	1.62E-06
AFUA_4G13500	Aldehyde dehydrogenase	2.15	1.42	2.54	6.03E-05
AFUA_3G06890	RRM domain protein	2.15	1.66	1.07	3.71E-04
AFUA_5G02410	ATP-dependent RNA helicase fal1 (EC 3.6.4.13)	2.16	0.34	2.42	8.11E-03
AFUA_1G13790	Histone H3	2.16	2.07	2.90	5.44E-05
AFUA_6G02870	Uncharacterized protein	2.16	0.48	0.54	1.18E-03
AFUA_3G13140	Methyltransferase, putative	2.16	2.14	2.09	1.35E-03
AFUA_6G12720	40S ribosomal protein S29, putative	2.17	0.92	5.44	5.97E-06
AFUA_8G04340	Cystathionine gamma-lyase (EC 4.4.1.8)	2.17	1.72	2.46	1.22E-03
AFUA_3G00320	Endo-1,4-beta-xylanase xynf11a (Xylanase xynf11a) (EC 3.2.1.8) (1,4-beta-D-xylan xylanohydrolase xynf11a)	2.17	0.50	0.09	3.80E-05

AFUA_2G12530	Carnitine acetyl transferase	2.17	2.17	2.24	1.23E-05
AFUA_6G10480	Peptidyl-prolyl cis-trans isomerase-like 3 (PPIase) (EC 5.2.1.8) (Rotamase)	2.18	1.64	2.28	4.96E-03
AFUA_1G09230	DUF1000 domain protein	2.18	1.93	2.15	2.28E-04
AFUA_3G08660	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	2.19	1.60	1.11	2.02E-07
AFUA_1G10780	Aminomethyltransferase (EC 2.1.2.10) (Glycine cleavage system T protein)	2.19	3.06	2.90	4.94E-05
AFUA_6G13410	Pre-mRNA-splicing factor rse1	2.20	2.89	2.76	1.49E-09
AFUA_2G16200	Uracil phosphoribosyltransferase (EC 2.4.2.9)	2.20	2.25	2.69	1.16E-02
AFUA_2G00830	Short chain dehydrogenase/reductase (EC 1.1.-.-)	2.20	1.98	1.66	3.87E-03
AFUA_5G13450	Triosephosphate isomerase (EC 5.3.1.1)	2.20	2.15	1.85	1.15E-06
AFUA_1G14090	Histidinol-phosphate aminotransferase (EC 2.6.1.9)	2.20	1.47	2.98	3.93E-06
AFUA_1G13500	Transketolase (EC 2.2.1.1)	2.21	3.24	3.23	5.10E-09
AFUA_5G10610	Ubiquinol-cytochrome c reductase iron-sulfur subunit (EC 1.10.2.2)	2.21	2.19	2.15	3.15E-07
AFUA_2G12180	Lectin family integral membrane protein, putative	2.22	0.92	1.78	3.14E-02
AFUA_3G12370	V-type proton ATPase proteolipid subunit	2.23	0.44	0.62	1.65E-03
AFUA_6G11210	3-oxoacyl-(Acyl-carrier-protein) reductase (EC 1.1.1.100)	2.23	1.76	1.69	1.86E-05
AFUA_5G08640	Integral membrane protein	2.24	1.16	-0.60	2.10E-03
AFUA_3G02240	Aromatic-L-amino-acid decarboxylase, putative (EC 4.1.1.28)	2.24	2.44	1.68	7.17E-05
AFUA_6G11310	Bifunctional pyrimidine biosynthesis protein (PyrABCN), putative (EC 6.3.5.5)	2.24	1.17	1.15	9.53E-06
AFUA_4G06640	Sphingomyelin phosphodiesterase	2.24	0.35	0.26	3.36E-03
AFUA_5G06500	Acyl-CoA dehydrogenase family protein (EC 1.3.99.-)	2.25	1.85	1.96	8.24E-05
AFUA_2G10660	Mannitol-1-phosphate 5-dehydrogenase (M1PDH) (MPD) (MPDH) (EC 1.1.1.17)	2.25	2.46	2.14	2.73E-08
AFUA_1G14680	DNA-directed RNA polymerase subunit (EC 2.7.7.6)	2.25	2.02	3.38	4.43E-05
AFUA_3G00280	Metallo-beta-lactamase domain protein, putative	2.26	3.78	3.75	5.18E-04
AFUA_2G02920	Alpha/beta hydrolase, putative (EC 3.-.-.-)	2.26	2.22	2.18	4.64E-05
AFUA_6G02140	Peptidyl-prolyl cis-trans isomerase-like 1 (PPIase) (EC 5.2.1.8) (Rotamase)	2.26	1.98	2.33	3.51E-03
AFUA_4G04350	DEAD helicases superfamily protein (Aquarius), putative	2.26	1.27	2.48	1.26E-02
AFUA_6G12530	Translation initiation factor eif-2b epsilon subunit, putative (EC 2.7.7.-)	2.26	0.53	2.64	1.72E-04
AFUA_1G11120	Uncharacterized protein	2.27	1.76	2.14	5.04E-03
AFUA_1G10460	Uncharacterized protein	2.27	1.93	1.73	9.81E-03
AFUA_4G13760	Uncharacterized protein	2.28	1.38	1.22	1.74E-02
AFUA_2G05790	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 (EC 2.4.99.18)	2.29	1.70	2.33	1.32E-09
AFUA_6G03830	Ribosomal protein L14	2.30	1.58	4.26	6.50E-08
AFUA_1G11790	Nucleoside hydrolase, putative (EC 3.2.2.-)	2.30	2.29	1.85	3.45E-03
AFUA_1G12920	Alpha-1,4 glucan phosphorylase (EC 2.4.1.1)	2.31	2.77	2.48	3.21E-07
AFUA_1G11730	ADP-ribosylation factor, putative	2.32	0.94	2.02	3.18E-05
AFUA_5G07170	Nucleoside-diphosphate-sugar epimerase, putative	2.32	2.57	2.32	5.15E-03
AFUA_6G14460	Haloalkanoic acid dehalogenase, putative (EC 3.8.1.-)	2.32	2.41	1.77	6.44E-05
AFUA_4G03140	Serine protein kinase Sky1, putative (EC 2.7.1.-)	2.32	0.75	1.26	9.40E-03
AFUA_1G04950	Serine/threonine-protein phosphatase (EC 3.1.3.16)	2.33	1.62	1.22	3.67E-08
AFUA_4G11840	Glyoxylate reductase (EC 1.1.1.95)	2.33	2.28	1.99	1.68E-04
AFUA_7G05930	Metallopeptidase MepB (EC 3.4.24.-)	2.34	2.35	2.22	4.82E-07
AFUA_5G03540	Thioredoxin reductase, putative (EC 1.-.-.-)	2.34	1.20	0.36	2.53E-08
AFUA_3G09320	Serine hydroxymethyltransferase (EC 2.1.2.1)	2.34	3.63	2.46	2.26E-10
AFUA_2G08370	Glutathione S-transferase, putative (EC 2.5.1.-)	2.35	0.51	1.16	5.25E-04
AFUA_5G08930	Isovaleryl-CoA dehydrogenase IvdA, putative (EC 1.3.8.4)	2.35	1.94	1.59	6.38E-07
AFUA_1G01680	Branched-chain amino acid aminotransferase (EC 2.6.1.42)	2.36	1.53	1.12	2.97E-04
AFUA_5G12210	G protein complex beta subunit SfaD	2.36	1.81	2.92	7.28E-07
AFUA_2G03720	Peptidyl-prolyl cis-trans isomerase (PPIase) (EC 5.2.1.8)	2.37	2.56	2.42	3.59E-07
AFUA_7G01920	DNA-directed RNA polymerase subunit beta (EC 2.7.7.6)	2.37	1.88	2.91	1.36E-04
AFUA_2G04220	Homogentisate 1,2-dioxygenase (HmgA), putative (EC 1.13.11.5)	2.37	2.00	1.07	3.81E-02

AFUA_1G09960	Kynurenine formamidase (KFA) (KFase) (EC 3.5.1.9) (Arylformamidase) (N-formylkynurenine formamidase) (FKF)	2.37	1.73	1.14	9.20E-03
AFUA_5G08940	3-methylcrotonyl-CoA carboxylase, beta subunit (MccB), putative (EC 6.4.1.3)	2.37	1.48	1.54	3.45E-03
AFUA_3G08640	Eukaryotic translation initiation factor 3 subunit I (eIF3i) (Eukaryotic translation initiation factor 3 39 kDa subunit homolog) (eIF-3 39 kDa subunit homolog)	2.38	1.42	2.53	2.45E-04
AFUA_1G08760	Delta-aminolevulinic acid dehydratase (EC 4.2.1.24)	2.38	0.77	1.07	2.27E-02
AFUA_5G07020	Ribosome biogenesis ABC transporter Arb1, putative (EC 3.6.3.-)	2.39	0.37	1.64	2.14E-02
AFUA_5G03360	NADH pyrophosphatase, putative (EC 3.6.1.-)	2.39	1.95	2.29	1.45E-02
AFUA_6G11620	Formyltetrahydrofolate deformylase, putative (EC 3.5.1.10)	2.40	2.58	3.40	1.24E-06
AFUA_2G08970	Thiamine biosynthetic bifunctional enzyme, putative	2.41	2.37	2.22	1.51E-05
AFUA_1G01490	NACHT domain protein	2.42	1.20	2.02	5.24E-07
AFUA_4G12870	Methylmalonate-semialdehyde dehydrogenase, putative (EC 1.2.1.27)	2.43	2.51	2.47	1.72E-06
AFUA_6G07760	Proteasome regulatory particle subunit (RpnG), putative	2.46	1.02	2.61	2.81E-05
AFUA_2G01040	S-(hydroxymethyl)glutathione dehydrogenase (EC 1.1.1.284)	2.46	1.49	0.21	1.09E-09
AFUA_3G06760	60S ribosomal protein L37	2.46	2.44	5.25	9.40E-06
AFUA_6G11680	Thiamine pyrophosphate enzyme, putative (EC 4.1.-.-)	2.47	2.28	2.39	5.77E-05
AFUA_1G11710	Ribosomal protein	2.47	0.57	2.72	2.45E-06
AFUA_4G07190	Ornithine carbamoyltransferase (EC 2.1.3.3)	2.47	3.65	3.07	6.27E-08
AFUA_1G11960	Alternative NADH-dehydrogenase (EC 1.6.99.3)	2.48	0.73	1.88	5.93E-06
AFUA_2G02150	40S ribosomal protein S10a	2.48	0.92	3.06	1.80E-05
AFUA_1G02090	Quinone oxidoreductase, putative (EC 1.6.5.5)	2.48	2.22	2.44	7.49E-06
AFUA_4G09250	Uncharacterized protein	2.50	0.81	2.23	2.14E-04
AFUA_3G04020	Conserved mitochondrial protein	2.50	2.02	2.39	6.53E-04
AFUA_2G07350	Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	2.50	2.64	2.93	1.11E-04
AFUA_5G08980	NADH-ubiquinone oxidoreductase 9.5 kDa subunit, putative (EC 1.6.5.3)	2.51	1.33	1.80	5.73E-03
AFUA_4G10790	Phosphoribosyl diphosphate synthase isoform 4	2.51	1.61	3.04	1.23E-04
AFUA_2G03980	Alpha-1,3-glucanase/mutanase, putative (EC 3.2.1.-)	2.51	0.30	-0.40	5.32E-09
AFUA_4G05900	Uncharacterized protein	2.52	0.96	1.98	3.18E-03
AFUA_5G06010	Eukaryotic translation initiation factor 6 (eIF-6)	2.53	1.64	2.91	2.74E-04
AFUA_3G12840	Signal peptidase complex catalytic subunit sec11 (EC 3.4.21.89) (Signal peptidase I)	2.53	1.13	1.83	1.78E-02
AFUA_1G06390	Elongation factor 1-alpha	2.55	0.67	1.62	2.21E-10
AFUA_3G06070	Histone H1	2.55	2.66	3.86	1.66E-05
AFUA_2G13860	Histone H4	2.56	2.36	2.68	1.57E-07
AFUA_3G12100	Trehalose synthase (Ccg-9), putative (EC 2.4.1.-)	2.57	2.42	2.69	2.04E-05
AFUA_1G10310	RNase L inhibitor of the ABC superfamily, putative	2.57	1.26	1.67	3.21E-03
AFUA_6G10880	Acyl-CoA dehydrogenase family protein (EC 1.3.99.-)	2.58	-0.22	-1.17	2.02E-08
AFUA_6G07770	Alanine aminotransferase, putative (EC 2.6.1.-)	2.58	2.69	2.13	3.86E-08
AFUA_2G10300	40S ribosomal protein S17, putative	2.58	0.94	3.54	3.51E-05
AFUA_4G07730	60S ribosomal protein L11	2.60	1.32	4.11	1.78E-06
AFUA_5G01440	Allergen, putative (EC 1.-.-.-)	2.60	2.66	2.59	2.39E-07
AFUA_5G02030	Cleavage and polyadenylation specific factor 5	2.60	2.18	2.07	1.02E-06
AFUA_5G08290	Aldo-keto reductase, putative (EC 1.1.1.-)	2.60	2.88	2.20	4.21E-05
AFUA_5G01290	Zinc-binding oxidoreductase, putative (EC 1.-.-.-)	2.61	2.82	2.74	3.61E-04
AFUA_3G08380	Inorganic diphosphatase, putative (EC 3.6.1.1)	2.61	2.82	2.44	1.92E-10
AFUA_6G02860	Isocitrate lyase (EC 4.1.3.1)	2.62	2.79	2.62	3.59E-07
AFUA_3G10970	Protein-tyrosine phosphatase 2 (EC 3.1.3.48)	2.63	1.09	2.48	3.79E-02
AFUA_1G03400	Protein transport protein sec23	2.63	0.89	2.28	5.12E-05
AFUA_5G02040	Extracellular lipase, putative (EC 3.1.1.3)	2.64	0.62	-0.46	1.14E-06
AFUA_3G07790	Argininosuccinate lyase (EC 4.3.2.1)	2.64	2.47	2.26	6.17E-07
AFUA_2G01920	Glutaminyl-tRNA synthetase (EC 6.1.1.18)	2.64	1.85	0.95	1.34E-05
AFUA_5G11660	Autophagy-related protein 18	2.64	2.18	2.57	1.54E-04
AFUA_3G06960	60S ribosomal protein L21, putative	2.65	0.47	3.65	3.25E-05
AFUA_2G05740	Rho GTPase ModA, putative	2.65	1.95	2.38	1.24E-03

AFUA_6G03730	2-methylcitrate dehydratase, putative (EC 4.2.1.79)	2.67	2.66	3.38	1.01E-06
AFUA_1G04130	FG-GAP repeat protein, putative	2.68	0.75	-0.63	2.94E-06
AFUA_6G13300	GTP-binding nuclear protein	2.70	2.02	2.31	8.90E-06
AFUA_7G00360	UDP-galactose 4-epimerase, putative (EC 5.1.3.-)	2.71	1.81	2.62	5.05E-08
AFUA_4G06140	Dipeptidyl peptidase 3 (EC 3.4.14.4) (Dipeptidyl aminopeptidase III) (Dipeptidyl peptidase III)	2.72	2.86	2.43	1.13E-06
AFUA_4G07050	L-lactate dehydrogenase (EC 1.13.12.4)	2.73	2.66	2.52	2.06E-06
AFUA_3G11280	Class V chitinase, putative (EC 3.2.1.14)	2.73	2.36	1.80	8.28E-08
AFUA_2G02580	HAD superfamily hydrolase, putative	2.74	2.58	2.37	2.41E-05
AFUA_2G02950	Aldehyde reductase, putative (EC 1.1.1.-)	2.75	2.40	1.93	5.49E-06
AFUA_3G06970	40S ribosomal protein S9	2.75	0.77	3.13	2.34E-07
AFUA_1G15860	Coatomer subunit delta, putative	2.76	0.78	2.06	8.40E-04
AFUA_3G02370	Short-chain dehydrogenase/reductase, putative (EC 1.-.-.-)	2.77	2.92	3.87	7.65E-07
AFUA_6G07710	Mitochondrial dicarboxylate carrier protein, putative	2.77	2.44	2.24	4.59E-03
AFUA_5G02300	Peroxidase, putative (EC 1.11.1.-)	2.77	1.19	1.51	2.77E-05
AFUA_3G08310	4-nitrophenylphosphatase (PNPPase) (EC 3.1.3.41)	2.77	2.04	1.39	1.34E-02
AFUA_1G15450	Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	2.78	2.76	2.28	2.20E-10
AFUA_4G10760	Steroid alpha reductase family protein	2.80	0.90	1.55	7.90E-06
AFUA_4G08330	Aspartyl-tRNA synthetase, putative (EC 6.1.1.12)	2.81	2.80	3.60	1.77E-06
AFUA_3G06880	Sorting nexin-3	2.81	2.58	3.46	3.16E-04
AFUA_2G00590	Glutathione S-transferase, putative (EC 2.5.1.18)	2.81	1.86	2.26	1.59E-03
AFUA_6G07720	Phosphoenolpyruvate carboxykinase AcuF (EC 4.1.1.49)	2.81	2.33	2.72	2.44E-07
AFUA_8G04090	Choline oxidase (CodA), putative (EC 1.1.3.17)	2.82	2.36	2.08	1.64E-08
AFUA_3G11350	ATPase get3 (EC 3.6.-.-) (Arsenical pump-driving ATPase) (Arsenite-stimulated ATPase) (Golgi to ER traffic protein 3) (Guided entry of tail-anchored proteins 3)	2.82	1.72	3.08	7.97E-03
AFUA_2G04590	Alcohol dehydrogenase, putative (EC 1.1.1.-)	2.84	1.45	1.67	1.37E-04
AFUA_8G04080	Betaine aldehyde dehydrogenase (BadH), putative (EC 1.2.1.8)	2.84	3.00	2.50	1.85E-06
AFUA_5G09860	S-formylglutathione hydrolase (EC 3.1.2.12)	2.85	2.31	2.46	8.48E-06
AFUA_3G11690	Fructose-bisphosphate aldolase, class II (EC 4.1.2.13)	2.85	2.74	2.40	1.96E-10
AFUA_5G02350	Hydrolase, carbon-nitrogen family, putative	2.87	1.32	2.15	1.12E-02
AFUA_2G04320	NADH-dependent flavin oxidoreductase, putative (EC 1.-.-.-)	2.88	3.06	3.15	6.48E-11
AFUA_2G04490	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	2.90	0.19	0.56	5.40E-03
AFUA_8G01670	Catalase-peroxidase (CP) (EC 1.11.1.21) (Catalase-2) (Peroxidase/catalase)	2.91	2.01	1.41	4.44E-09
AFUA_5G10560	Cytochrome c oxidase subunit V	2.91	1.58	2.70	1.01E-06
AFUA_5G03860	Alkaline phosphatase family protein (EC 3.1.-.-)	2.91	1.43	2.99	2.46E-03
AFUA_7G01000	Aldehyde dehydrogenase, putative (EC 1.2.1.3)	2.92	2.41	2.24	6.42E-09
AFUA_4G10240	Small nuclear ribonucleoprotein SmD3, putative	2.93	0.33	1.86	1.92E-03
AFUA_7G02280	U5 snRNP complex subunit, putative	2.93	2.45	2.59	8.28E-03
AFUA_4G08760	Phospho-2-dehydro-3-deoxyheptonate aldolase (EC 2.5.1.54)	2.94	2.29	3.14	1.80E-05
AFUA_3G12950	FAD binding domain protein (EC 1.5.3.-)	2.95	3.08	1.33	2.34E-02
AFUA_1G06240	Riboflavin synthase, alpha subunit (EC 2.5.1.9)	2.97	2.97	2.47	1.10E-04
AFUA_6G12950	Trehalose-6-phosphate synthase (EC 2.4.1.15) (UDP-glucose-glucosephosphate glucosyltransferase)	3.01	1.98	3.52	7.43E-05
AFUA_3G08430	Mitochondrial phosphate carrier protein, putative	3.04	1.57	2.38	5.50E-03
AFUA_2G13630	Aromatic aminotransferase Aro8, putative (EC 2.6.1.-)	3.08	1.96	1.61	7.87E-04
AFUA_2G06040	Actin cortical patch component, putative	3.11	3.03	2.43	5.46E-09
AFUA_1G07010	Phosphatidate cytidylyltransferase (EC 2.7.7.41)	3.12	0.81	2.44	1.15E-02
AFUA_3G07430	Peptidyl-prolyl cis-trans isomerase (PPIase) (EC 5.2.1.8)	3.12	3.35	2.98	9.92E-09
AFUA_2G13295	Aminotransferase family protein (LolT), putative	3.15	1.64	1.91	1.90E-03
AFUA_5G08270	HAD superfamily hydrolase, putative	3.17	3.28	2.43	1.08E-07
AFUA_4G07590	CaaX prenyl protease Ste24 (EC 3.4.24.84)	3.20	1.22	2.67	7.52E-04
AFUA_7G05015	Glyoxalase family protein	3.23	3.11	3.23	5.16E-06
AFUA_5G04330	Aminopeptidase (EC 3.4.11.-)	3.23	3.14	2.91	1.04E-09
AFUA_6G02370	Actin-related protein 2/3 complex subunit 4	3.24	2.67	3.19	5.22E-06
AFUA_6G10260	Aldehyde reductase (AKR1), putative (EC 1.1.1.2)	3.26	3.25	2.95	3.81E-11

AFUA_1G15610	Oxidoreductase, zinc-binding dehydrogenase family, putative (EC 1.3.1.-)	3.27	3.06	3.36	9.47E-09
AFUA_5G03330	HypA-like protein, putative	3.28	2.78	3.08	2.01E-05
AFUA_3G12510	Vesicular fusion ATPase, putative	3.29	1.34	1.38	5.57E-05
AFUA_2G17070	Defective in cullin neddylation protein	3.34	2.92	2.04	2.08E-03
AFUA_1G02570	Aspartyl-tRNA synthetase, cytoplasmic (EC 6.1.1.12)	3.37	1.41	2.82	2.34E-05
AFUA_4G05870	Oxidoreductase, short-chain dehydrogenase/reductase family	3.37	3.29	2.83	6.10E-06
AFUA_5G13510	Cell cycle control protein (Cwf8), putative	3.40	2.49	2.22	1.58E-06
AFUA_3G00680	Amine oxidase (EC 1.4.3.-)	3.44	1.35	1.88	1.22E-03
AFUA_1G09660	Mitochondrial 2-oxodicarboxylate carrier protein, putative	3.45	1.64	2.72	2.28E-05
AFUA_4G07150	Cytochrome c subunit, putative	3.45	2.41	2.78	1.10E-06
AFUA_2G14850	Enoyl-CoA hydratase/isomerase family protein (EC 4.2.-.-)	3.46	2.02	2.40	1.40E-04
AFUA_7G04180	Amine oxidase (EC 1.4.3.-)	3.46	2.15	1.42	5.87E-08
AFUA_6G14100	Mitochondrial carnitine:acyl carnitine carrier, putative	3.46	2.04	2.78	2.40E-04
AFUA_1G04720	C-8 sterol isomerase (Erg-1), putative	3.48	1.57	1.64	3.80E-04
AFUA_6G13440	Choline sulfatase, putative (EC 3.1.6.6)	3.50	1.09	2.07	9.70E-04
AFUA_2G09790	Glucose-6-phosphate isomerase (EC 5.3.1.9)	3.53	3.67	3.45	1.95E-08
AFUA_8G00620	Dimethylallyl tryptophan synthase, putative (EC 2.5.1.-)	3.57	0.95	0.59	4.77E-03
AFUA_6G00770	Probable arabinan endo-1,5-alpha-L-arabinosidase C (EC 3.2.1.99) (Endo-1,5-alpha-L-arabinanase C) (ABN C)	3.60	3.10	2.44	3.91E-04
AFUA_1G06700	Metacaspase-1A (EC 3.4.22.-)	3.64	2.10	2.07	1.94E-03
AFUA_1G10150	Uncharacterized protein	3.69	2.92	3.83	2.18E-05
AFUA_3G14690	Aminotransferase, putative (EC 2.-.-.-)	3.71	1.68	2.25	1.24E-02
AFUA_4G10920	Uncharacterized protein	3.76	2.69	2.97	4.54E-05
AFUA_1G12250	Mitochondrial hypoxia responsive domain protein	3.82	1.09	1.94	2.25E-02
AFUA_3G14270	Aldo-keto reductase (AKR), putative (EC 1.1.1.-)	3.85	3.37	3.39	1.19E-04
AFUA_5G09680	Succinate dehydrogenase cytochrome b560 subunit (EC 1.3.5.1)	4.04	2.82	3.57	1.28E-05
AFUA_4G13750	Neutral protease 2 homolog AFUA_4G13750 (EC 3.4.24.39) (Deuterolysin AFUA_4G13750)	4.36	2.08	0.81	5.27E-05
AFUA_6G02450	40S ribosomal protein S30	4.38	2.31	6.33	5.94E-10
AFUA_8G00430	Uncharacterized protein	4.49	2.93	1.05	9.95E-07
AFUA_5G02640	O-methyltransferase, putative (EC 2.1.1.-)	4.70	1.45	0.38	1.42E-07
AFUA_6G12870	Iron-sulfur clusters transporter atm1, mitochondrial	4.78	2.84	4.54	4.29E-04

Differentially expressed proteins in ISSFT-021

Gene	Protein names	Relative protein abundance*			P-value
		CEA10	ISSFT-021	IF1SW-F4	
AFUA_5G14210	Glucose repressible protein Grg1, putative	-3.21	-7.14	-4.80	1.87E-07
AFUA_4G09600	GPI anchored protein, putative	-3.43	-6.26	-5.82	1.33E-07
AFUA_4G14205	Uncharacterized protein	-3.49	-6.22	-4.43	9.36E-06
AFUA_1G13550	Uncharacterized protein	-3.59	-6.12	-5.23	5.82E-03
AFUA_5G13100	Uncharacterized protein	-3.50	-5.95	-5.15	9.50E-09
AFUA_6G12450	Chaperone/heat shock protein Hsp12, putative	-4.05	-5.81	-5.12	5.46E-05
AFUA_3G05430	ATP-dependent RNA helicase dhh1 (EC 3.6.4.13)	-2.86	-5.81	-4.16	7.98E-04
AFUA_2G03390	Histone deacetylase (EC 3.5.1.98)	-4.27	-5.76	-3.78	1.15E-03
AFUA_1G10550	CBF/NF-Y family transcription factor, putative	-4.29	-5.75	-3.37	3.43E-06
AFUA_2G10020	Uncharacterized protein	-3.67	-5.69	-3.86	3.03E-07
AFUA_4G00860	Cell surface protein, putative	-3.54	-5.64	-4.62	1.37E-07
AFUA_6G13500	Uncharacterized protein	-3.21	-5.61	-3.77	7.19E-07
AFUA_2G14330	Uncharacterized protein	-3.51	-5.48	-6.27	2.39E-06
AFUA_2G15810	Uncharacterized protein	-2.96	-5.32	-5.18	3.13E-03
AFUA_7G04930	Alkaline serine protease (PR1)/allergen F18-like (EC 3.4.21.-)	-3.63	-5.32	-5.53	1.14E-06
AFUA_6G13670	Reticulon-like protein	-3.69	-5.29	-2.62	3.96E-08
AFUA_3G05570	Spindle poison sensitivity protein Scp3, putative	-2.94	-5.28	-4.83	4.20E-04
AFUA_1G17370	Heat shock protein Awh11, putative	-2.95	-5.23	-4.26	4.25E-07
AFUA_4G08960	GPI anchored cell wall protein, putative	-3.69	-5.18	-5.37	8.40E-05
AFUA_3G14260	Mismatched base pair and cruciform DNA recognition protein, putative	-3.27	-5.16	-3.37	2.05E-06
AFUA_7G01340	RPEL repeat protein	-3.36	-5.15	-5.55	4.07E-10
AFUA_1G13560	Uncharacterized protein	-3.23	-5.10	-3.77	1.79E-06
AFUA_6G12000	Uncharacterized protein	-3.87	-5.08	-3.22	6.46E-06
AFUA_7G04520	Uncharacterized protein	-3.31	-5.06	-4.87	1.19E-05
AFUA_6G10700	Chaperonin, putative	-3.60	-4.94	-3.42	8.19E-05
AFUA_6G09120	Uncharacterized protein	-3.52	-4.91	-2.97	1.10E-05
AFUA_3G10410	Conserved serine-rich protein	-2.82	-4.81	-3.94	3.68E-05
AFUA_6G03210	Conidiation-specific protein (Con-10), putative	-2.13	-4.73	-3.82	3.46E-04
AFUA_7G04030	Uncharacterized protein	-3.36	-4.62	-2.54	1.06E-04
AFUA_3G14540	Heat shock protein Hsp30/Hsp42, putative	-3.73	-4.52	-4.20	3.63E-08
AFUA_4G12490	Guanine nucleotide exchange factor Vps9, putative	-2.86	-4.52	-3.77	1.66E-04
AFUA_2G03790	Oxysterol binding protein (Osh7), putative	-3.18	-4.47	-2.85	8.13E-03
AFUA_7G01200	Aspergillopepsin, putaitve (EC 3.4.23.-)	-3.45	-4.45	-2.66	8.43E-07
AFUA_4G02805	Asp hemolysin-like protein	-3.31	-4.42	-2.02	7.88E-05
AFUA_1G12070	Glycine cleavage system H protein	-3.95	-4.38	-4.79	8.05E-05
AFUA_3G13850	LRP16 family protein	-2.27	-4.37	-4.88	1.16E-03
AFUA_7G04950	Lipase, putative (EC 3.1.1.-)	-2.28	-4.33	-0.49	1.12E-06
AFUA_4G06820	Protein ecm33	-3.26	-4.32	-3.59	5.49E-10
AFUA_6G04390	E3 ubiquitin-protein ligase bre1 (EC 2.3.2.27) (RING-type E3 ubiquitin transferase bre1)	-3.76	-4.23	-4.24	8.60E-05
AFUA_4G09740	T-complex protein 1, theta subunit, putative	-2.71	-4.22	-2.49	2.19E-07
AFUA_2G07600	SRP receptor beta subunit (Srp102), putative	-2.01	-4.19	-2.72	3.98E-03
AFUA_2G05635	Uncharacterized protein	-2.73	-4.18	-4.06	4.08E-03
AFUA_1G03710	C2H2 finger domain protein, putative	-4.02	-4.17	-3.69	7.80E-03
AFUA_2G13040	GrpE protein homolog	-3.48	-4.15	-3.01	2.23E-08
AFUA_3G10920	Telomere and ribosome associated protein Stm1, putative	-3.30	-4.13	-2.02	1.67E-07
AFUA_4G09750	50S ribosomal protein L12	-3.36	-4.10	-3.30	9.15E-05
AFUA_2G15070	26S proteasome regulatory subunit S5A	-2.59	-4.07	-3.12	8.53E-06
AFUA_1G01950	Uncharacterized protein	-3.62	-4.06	-3.24	4.23E-04
AFUA_5G02420	Splicing factor 3a subunit 3, putative	-2.70	-4.03	-2.28	1.60E-02
AFUA_8G01980	Uncharacterized protein	-3.27	-4.01	-3.02	3.84E-06
AFUA_2G01540	Uncharacterized protein	-3.19	-3.99	-2.73	1.21E-05
AFUA_8G04310	Uncharacterized protein	-2.55	-3.87	-2.86	2.62E-03
AFUA_2G10810	Nuclear protein export protein Yrb2, putative	-3.67	-3.85	-2.59	3.31E-02
AFUA_2G03010	Cytochrome c subunit Vb, putative	-2.09	-3.83	-3.13	8.44E-07
AFUA_2G14490	Endoglucanase, putative (EC 3.2.1.-)	-2.17	-3.83	-3.33	1.17E-04
AFUA_1G13530	Uncharacterized protein	-4.30	-3.82	-2.75	3.15E-04
AFUA_1G09030	Uncharacterized protein	-2.72	-3.81	-1.86	4.70E-07

AFUA_3G09030	Regulatory protein SUAPRGA1	-2.83	-3.80	-3.30	3.56E-03
AFUA_1G04470	Mitochondrial import inner membrane translocase subunit tim10	-1.92	-3.78	-2.26	1.15E-03
AFUA_6G09740	Thioredoxin reductase gliT (EC 1.8.1.-) (Gliotoxin biosynthesis protein T)	-3.30	-3.75	-4.59	9.90E-08
AFUA_3G02340	CBF/NF-Y family transcription factor, putative	-2.41	-3.75	-2.28	4.63E-04
AFUA_5G09380	Uncharacterized protein	-2.31	-3.71	-2.68	1.67E-03
AFUA_1G08880	Iron/copper transporter Atx1, putative	-3.41	-3.69	-2.06	9.37E-11
AFUA_1G15010	AMP binding domain protein, putative	-4.47	-3.65	-3.15	2.42E-03
AFUA_6G05350	Probable aspartic-type endopeptidase opsB (EC 3.4.23.-)	-3.15	-3.64	-1.88	7.65E-06
AFUA_1G06830	60S acidic ribosomal protein P1 (AfP1)	-3.67	-3.62	-1.95	2.73E-05
AFUA_2G16020	T-complex protein 1, alpha subunit, putative	-1.91	-3.60	-1.79	1.56E-02
AFUA_7G04210	Tropomyosin, putative	-2.91	-3.60	-2.17	6.38E-06
AFUA_2G05540	Pre-mRNA-splicing factor cef1	-2.16	-3.57	-3.66	5.22E-03
AFUA_2G11840	Transcriptional corepressor Cyc8, putative	-3.28	-3.54	-2.12	4.54E-06
AFUA_3G12790	Conserved glutamic acid-rich protein	-3.32	-3.53	-3.82	1.63E-04
AFUA_3G10610	Uncharacterized protein	-3.33	-3.48	-3.28	7.75E-04
AFUA_7G04920	Uncharacterized protein	-2.28	-3.48	-3.20	3.66E-02
AFUA_5G10550	ATP synthase subunit beta (EC 3.6.3.14)	-2.85	-3.44	-1.63	9.29E-07
AFUA_1G03580	Uncharacterized protein	-2.87	-3.41	-3.86	1.07E-03
AFUA_6G02260	Uncharacterized protein	-3.21	-3.41	-2.20	1.03E-05
AFUA_2G11740	Lon protease homolog, mitochondrial (EC 3.4.21.53)	-2.25	-3.40	-2.33	9.12E-05
AFUA_3G09990	Uncharacterized protein	-2.59	-3.39	-2.84	4.40E-04
AFUA_7G02020	Uncharacterized protein	-2.67	-3.38	-2.69	3.83E-05
AFUA_8G05650	Uncharacterized protein	-2.35	-3.36	-3.61	2.53E-03
AFUA_6G08660	M protein repeat protein	-3.12	-3.33	-2.87	4.62E-05
AFUA_2G08640	Uncharacterized protein	-3.54	-3.32	-2.18	4.06E-04
AFUA_4G10020	Clathrin light chain	-3.70	-3.30	-2.33	1.95E-06
AFUA_5G11390	APSES transcription factor, putative	-3.22	-3.30	-1.63	3.38E-04
AFUA_2G03590	40S ribosomal protein S21	-3.07	-3.22	0.19	2.54E-06
AFUA_8G04270	AAA family ATPase, putative	-2.48	-3.22	-2.58	4.41E-04
AFUA_5G02750	Cytochrome c oxidase subunit Va, putative	-1.79	-3.20	-2.26	3.37E-07
AFUA_7G05270	COMPASS complex subunit Sdc1, putative	-3.87	-3.18	-2.60	3.89E-03
AFUA_1G12390	G2/M phase checkpoint control protein Sum2, putative	-2.58	-3.14	-1.76	3.72E-05
AFUA_4G10150	Alpha-glucosidase AgdA, putative (EC 3.2.1.20)	-2.96	-3.13	-3.34	5.33E-05
AFUA_3G08230	MRS7 family protein	-2.97	-3.12	-1.63	4.35E-04
AFUA_5G12180	Ran-specific GTPase-activating protein 1, putative	-3.75	-3.12	-3.01	9.69E-08
AFUA_1G13670	Uncharacterized protein	-3.36	-3.10	-2.85	4.02E-08
AFUA_4G10280	Phosphotransmitter protein Ypd1, putative	-3.40	-3.09	-2.65	1.54E-06
AFUA_6G08320	Uncharacterized protein	-2.49	-3.08	-2.11	1.21E-07
AFUA_2G02320	Hsp70 chaperone (BiP), putative	-2.06	-3.07	-2.16	3.26E-05
AFUA_1G09250	CUE domain protein, putative	-2.03	-3.06	-2.38	4.12E-02
AFUA_4G03420	L-PSP endoribonuclease family protein, putative	-2.35	-2.93	-1.93	1.30E-03
AFUA_1G01812	MFS transporter, putative	-4.17	-2.93	-2.20	4.25E-03
AFUA_6G12290	PH domain protein	-2.32	-2.92	-2.73	1.83E-04
AFUA_3G07870	Extracellular serine-rich protein, putative	-1.73	-2.89	-3.23	1.27E-06
AFUA_6G04690	Uncharacterized protein	-2.96	-2.89	-2.57	8.64E-03
AFUA_4G09580	Major allergen Asp f 2 (Allergen Asp f II) (allergen Asp f 2)	-2.12	-2.88	-2.68	1.20E-03
AFUA_4G03780	Probable rhamnogalacturonate lyase A (EC 4.2.2.23)	-1.78	-2.88	-2.67	2.33E-02
AFUA_2G10030	Actin cytoskeleton protein (VIP1), putative	-2.32	-2.87	-1.72	1.19E-09
AFUA_6G06670	Uncharacterized protein	-2.65	-2.85	-2.68	5.35E-05
AFUA_2G08540	DNA-directed RNA polymerase subunit	-2.19	-2.84	-1.80	1.46E-05
AFUA_2G08670	Acetyl-CoA carboxylase	-2.01	-2.80	-1.74	3.47E-02
AFUA_1G09280	Protein phosphatase 2C, putative (EC 3.1.3.16)	-2.66	-2.78	-1.51	2.23E-03
AFUA_5G12590	Solid-state culture expressed protein (Aos23), putative	-3.38	-2.76	-3.75	2.32E-03
AFUA_3G11550	LEA domain protein	-3.34	-2.74	-2.50	2.51E-06
AFUA_1G15780	3-isopropylmalate dehydrogenase (EC 1.1.1.85)	-1.67	-2.72	-2.26	5.25E-09
AFUA_8G04920	LEA domain protein	-2.00	-2.70	-2.54	4.55E-04
AFUA_4G08030	MICOS complex subunit mic60 (Mitofilin)	-1.95	-2.68	-1.76	2.21E-02

AFUA_2G10100	60S acidic ribosomal protein P2 (AfP2) (allergen Asp f 8)	-3.24	-2.65	-2.04	1.16E-06
AFUA_2G11860	Uncharacterized protein	-2.13	-2.64	-2.05	1.13E-06
AFUA_4G11390	Ubiquinol-cytochrome c reductase complex 17 kd protein	-1.72	-2.64	-2.94	3.97E-08
AFUA_6G02830	Uncharacterized protein	-4.08	-2.59	-1.87	6.97E-04
AFUA_4G09280	Uncharacterized protein	-2.55	-2.57	-1.65	1.51E-06
AFUA_3G13430	Uncharacterized protein	-2.63	-2.56	-3.12	2.45E-02
AFUA_6G04610	DNA-directed RNA polymerase I and III 14 kDa polypeptide	-2.32	-2.56	-1.91	1.48E-02
AFUA_6G13120	Filament-forming protein (Tpr/p270), putative	-2.42	-2.55	-1.72	5.43E-07
AFUA_2G07950	ATP dependent RNA helicase, putative	-2.84	-2.54	-2.06	4.88E-04
AFUA_2G15290	DUF636 domain protein	-2.54	-2.53	0.18	8.12E-06
AFUA_7G05610	Glucanase, putative (EC 3.2.1.-)	-1.47	-2.53	-2.26	1.18E-04
AFUA_3G09870	Uncharacterized protein	-1.85	-2.52	-2.36	9.93E-03
AFUA_3G10340	Rho GTPase Rho 2, putative	-0.96	-2.51	-2.14	2.12E-03
AFUA_7G02340	L-PSP endoribonuclease family protein (Hmf1), putative	-3.47	-2.50	-2.31	2.66E-06
AFUA_2G13310	RING finger domain protein, putative	0.82	-2.49	-1.61	4.25E-03
AFUA_5G10240	Uncharacterized protein	-2.14	-2.48	-1.96	4.17E-04
AFUA_2G13380	GATA transcription factor (AreB), putative	-2.97	-2.48	-2.78	4.61E-03
AFUA_3G10190	Peroxisomal membrane anchor protein (Pex14), putative	-2.34	-2.48	-3.06	2.78E-03
AFUA_7G02170	Peptidyl-prolyl cis-trans isomerase-like 4 (PPIase) (EC 5.2.1.8) (Rotamase)	-2.38	-2.47	-1.41	4.54E-02
AFUA_4G11110	C2 domain protein	-2.90	-2.46	-1.53	7.18E-05
AFUA_1G16840	Translationally-controlled tumor protein homolog (TCTP)	-3.18	-2.43	-1.94	1.32E-06
AFUA_1G12590	RNA-binding La domain protein	-2.34	-2.41	-2.04	2.24E-03
AFUA_3G11740	RNAPII degradation factor Def1, putative	-1.40	-2.40	-1.63	1.23E-02
AFUA_1G11870	Mitochondrial processing peptidase alpha subunit, putative (EC 3.4.24.64)	-1.96	-2.37	-1.88	1.36E-02
AFUA_4G04318	Copper resistance protein Crd2, putative	-1.49	-2.35	-2.86	1.30E-07
AFUA_2G12190	Mitochondrial import inner membrane translocase subunit tim13	-2.36	-2.32	-1.49	2.80E-03
AFUA_2G17540	Multicopper oxidase abr1 (EC 1.-.-.-) (Conidial pigment biosynthesis oxidase abr1)	-1.23	-2.30	-1.71	2.97E-04
AFUA_1G11640	Cytosolic Cu/Zn superoxide dismutase, putative	-3.95	-2.30	-3.07	3.00E-06
AFUA_5G04160	NTF2 and RRM domain protein	-2.21	-2.29	-1.29	2.29E-03
AFUA_2G10600	NADH-ubiquinone oxidoreductase 299 kDa subunit, putative (EC 1.6.5.3)	-2.11	-2.28	-1.33	2.39E-07
AFUA_4G03322	WW domain protein	-0.34	-2.27	-2.52	5.11E-03
AFUA_2G10320	SH3 domain protein	-2.98	-2.27	-2.08	2.01E-03
AFUA_8G04570	PWWP domain protein	-2.20	-2.26	-1.89	4.06E-07
AFUA_2G17470	L-PSP endoribonuclease family protein, putative	0.01	-2.24	-2.03	2.01E-03
AFUA_7G02570	NIMA-interacting protein TinC	-2.34	-2.21	-1.85	1.13E-03
AFUA_2G14670	Eukaryotic translation initiation factor 3 subunit D (eIF3d)	-1.59	-2.17	-1.62	2.36E-02
AFUA_1G06170	Proteasome regulatory particle subunit Rpt5, putative	-1.96	-2.16	-0.64	2.13E-03
AFUA_8G07130	AhpC/TSA family thioredoxin peroxidase, putative	-2.06	-2.15	0.17	1.13E-05
AFUA_8G00550	Methyltransferase psoC (EC 2.1.1.-) (Pseurotin biosynthesis protein C)	-2.78	-2.15	-2.19	2.53E-08
AFUA_8G06970	Beta-glucosidase (EC 3.2.1.21)	-2.14	-2.14	-1.45	1.78E-02
AFUA_1G07280	Uncharacterized protein	-2.60	-2.14	-0.97	1.21E-05
AFUA_6G03820	Nascent polypeptide-associated complex subunit alpha (NAC-alpha) (Alpha-NAC)	-2.01	-2.13	-0.86	4.66E-06
AFUA_5G07240	SAP domain protein	-1.84	-2.11	-2.42	1.82E-03
AFUA_5G10920	DUF221 domain protein, putative	-1.38	-2.08	-0.85	4.09E-02
AFUA_4G12450	Conserved lysine-rich protein, putative	-2.94	-2.01	-0.91	1.88E-07
AFUA_4G06670	Allergen Asp f 7 (allergen Asp f 7)	-3.09	-1.97	-1.95	2.08E-03
AFUA_7G00580	Uncharacterized protein	-2.04	-1.96	-2.49	3.96E-07
AFUA_7G05470	Electron transfer flavoprotein alpha subunit, putative	-2.00	-1.96	-2.30	2.77E-03
AFUA_8G05570	Transcription factor (Sin3), putative	-1.43	-1.95	-1.13	5.73E-05
AFUA_3G08880	Uncharacterized protein	-1.51	-1.94	-1.23	4.76E-05
AFUA_1G17310	MFS lactose permease, putative	-2.01	-1.93	-1.04	3.30E-05
AFUA_8G07060	Hydrophobin, putative	-2.23	-1.93	-2.21	1.08E-07

AFUA_6G12430	Ran-interacting protein Mog1, putative	-2.45	-1.91	-0.83	9.45E-04
AFUA_7G05450	Secreted beta-glucosidase sun1 (EC 3.2.1.-)	-0.61	-1.87	-2.15	4.13E-02
AFUA_7G06010	Uncharacterized protein	-2.81	-1.84	-1.57	3.36E-04
AFUA_2G03500	Sugar transporter, putative	-0.06	-1.81	-0.75	4.20E-02
AFUA_1G09890	Uncharacterized protein	-1.49	-1.80	-1.53	3.17E-03
AFUA_3G07520	Exo-beta-1,3-glucanase, putative (EC 3.2.1.58)	-0.11	-1.80	-0.86	5.26E-06
AFUA_2G13590	Uncharacterized protein	-1.88	-1.80	-2.20	1.78E-07
AFUA_6G02750	Nascent polypeptide-associated complex subunit beta (NAC-beta) (Beta-NAC)	-0.07	-1.80	1.06	1.12E-03
AFUA_1G06680	VHS domain protein	-2.21	-1.78	-1.34	5.91E-04
AFUA_5G07080	Beta-glucosidase, putative (EC 3.2.1.21)	-1.76	-1.77	-1.67	3.56E-05
AFUA_1G03510	ATP synthase subunit gamma	-1.46	-1.77	0.34	8.67E-06
AFUA_2G09800	Uncharacterized protein	-2.51	-1.75	-1.43	9.85E-04
AFUA_1G09330	Eukaryotic translation initiation factor 3 subunit F (eIF3f)	-1.76	-1.75	-0.85	7.35E-03
AFUA_7G01010	Alcohol dehydrogenase, putative (EC 1.1.1.1)	-2.36	-1.74	-1.73	3.63E-08
AFUA_1G02420	Uncharacterized protein	-2.11	-1.73	-0.73	7.63E-03
AFUA_5G07120	RNP domain protein	-1.49	-1.72	-0.65	1.85E-02
AFUA_7G03860	DNA-directed RNA polymerase II subunit RPB11a, putative	-1.06	-1.71	-0.54	3.88E-03
AFUA_2G05400	Sugar hydrolase, putative	-1.59	-1.70	-1.59	7.69E-05
AFUA_2G00820	Extracellular GDSL-like lipase/acylhydrolase, putative	-0.17	-1.68	-1.43	4.80E-05
AFUA_7G04680	Uncharacterized protein	-0.60	-1.67	-0.85	4.65E-04
AFUA_2G13290	GYF domain protein	-1.40	-1.66	-1.13	1.99E-02
AFUA_2G15840	HET-C domain protein HetC	-2.38	-1.65	-1.82	8.39E-03
AFUA_2G12400	ATP synthase oligomycin sensitivity conferral protein, putative (EC 3.6.3.14)	-0.02	-1.64	-0.42	4.96E-06
AFUA_5G11540	37S ribosomal protein S5	-0.68	-1.64	0.74	2.42E-03
AFUA_1G09830	Hsc70 cochaperone (SGT), putative (EC 3.1.3.16)	-1.92	-1.61	-1.14	1.16E-04
AFUA_1G06660	CBS domain protein	-1.69	-1.60	-0.57	2.84E-02
AFUA_2G09490	Eukaryotic translation initiation factor subunit eIF-4F, putative	-2.07	-1.60	-1.44	4.05E-05
AFUA_7G01060	Cysteine-rich secreted protein	1.44	-1.60	-0.47	8.24E-07
AFUA_6G07120	Nuclear movement protein NudC	-2.62	-1.57	-1.32	5.54E-05
AFUA_6G00510	NADP-dependent alcohol dehydrogenase (EC 1.1.1.1)	-1.16	-1.55	-1.36	3.35E-06
AFUA_4G07340	Ubiquitin fusion degradation protein UfdB, putative	-1.65	-1.55	-1.21	2.91E-02
AFUA_1G10630	S-adenosylmethionine synthase (EC 2.5.1.6)	-1.74	-1.55	-0.37	1.75E-03
AFUA_3G06460	Uncharacterized protein	-2.35	-1.54	0.04	1.35E-05
AFUA_5G09600	2-nitropropane dioxygenase family oxidoreductase, putative (EC 1.3.1.9)	0.41	-1.54	-1.66	1.28E-03
AFUA_1G11530	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase (EC 4.1.2.20)	-0.99	-1.54	-1.75	2.49E-05
AFUA_2G13820	SAP domain protein, putative	-2.28	-1.54	-1.70	9.89E-07
AFUA_3G00880	UPF0619 GPI-anchored membrane protein AFUA_3G00880	-1.02	-1.53	-1.89	6.79E-04
AFUA_1G06910	Probable arabinogalactan endo-beta-1,4-galactanase A (EC 3.2.1.89) (Endo-1,4-beta-galactanase A) (Galactanase A)	-0.43	-1.53	-2.04	9.05E-06
AFUA_4G10540	Transcription regulator BDF1, putative	-2.07	-1.51	-0.99	3.91E-03
AFUA_6G12500	AhpC/TSA family protein	-2.80	-1.50	-0.18	2.31E-08
AFUA_3G13480	Translation initiation factor 2 alpha subunit, putative	-0.46	-1.50	0.56	1.65E-02
AFUA_3G06140	Cytoskeleton assembly control protein Sla2, putative	-1.99	-1.49	-0.90	7.32E-06
AFUA_4G03240	Cell wall serine-threonine-rich galactomannoprotein Mp1	-1.32	-1.48	-1.83	8.46E-08
AFUA_2G08150	NEDD8-like protein (RubA), putative	-2.17	-1.48	-1.23	4.94E-06
AFUA_1G10920	Nuclear mRNA splicing factor-associated protein, putative	0.20	-1.46	-0.80	2.62E-02
AFUA_1G12290	NADH-ubiquinone oxidoreductase	0.18	-1.46	-0.75	1.28E-02
AFUA_3G10490	DNA damage response protein (Dap1), putative	-1.18	-1.46	-0.13	3.46E-03
AFUA_6G07390	Isocitrate dehydrogenase LysB (EC 1.1.1.41)	-2.92	-1.46	-1.36	9.63E-11
AFUA_6G08990	Uncharacterized protein	-3.86	-1.45	-1.56	3.84E-04
AFUA_5G08970	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit WBP1 (Oligosaccharyl transferase subunit WBP1) (EC 2.4.99.18)	-1.28	-1.44	0.16	9.80E-03
AFUA_2G15510	DUF866 domain protein	0.98	-1.44	-1.51	7.12E-07

AFUA_6G06370	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	-1.61	-1.44	-0.10	7.68E-05
AFUA_6G14490	Probable beta-glucosidase H (EC 3.2.1.21) (Beta-D-glucoside glucohydrolase H) (Cellobiase H) (Gentiobiase H)	-0.21	-1.41	-1.33	4.68E-05
AFUA_1G12190	Uncharacterized protein	-3.06	-1.41	-1.50	1.89E-05
AFUA_3G10800	Clustered mitochondria protein homolog (Protein TIF31 homolog)	-0.83	-1.41	-0.40	9.27E-03
AFUA_2G12870	Vesicular-fusion protein sec17	-1.52	-1.40	-0.72	1.24E-02
AFUA_3G11390	Proteasome regulatory particle subunit Rpt3, putative	-0.27	-1.39	0.80	3.95E-02
AFUA_7G05650	Glutamine-serine rich protein MS8, putative	-0.10	-1.39	-1.40	2.22E-02
AFUA_1G04320	40S ribosomal protein S8	-1.27	-1.39	1.48	3.23E-02
AFUA_5G12260	Disulfide isomerase (TigA), putative (EC 5.3.4.1)	-0.90	-1.38	-0.25	7.20E-03
AFUA_6G06345	6,7-dimethyl-8-ribityllumazine synthase (DMRL synthase) (EC 2.5.1.78)	-0.63	-1.37	-1.59	2.54E-04
AFUA_3G13240	Aldose 1-epimerase, putative (EC 5.1.3.3)	-1.59	-1.36	-2.73	2.77E-06
AFUA_2G17620	Cellobiose dehydrogenase	-1.08	-1.36	-2.19	1.66E-03
AFUA_7G06050	DNA damage-inducible protein 1	-1.67	-1.35	-1.16	7.27E-03
AFUA_3G01210	ThiJ/PfpI family protein	0.03	-1.35	0.43	3.74E-02
AFUA_5G07890	SsDNA binding protein, putative	-1.01	-1.33	-1.91	1.19E-06
AFUA_4G00730	HHE domain protein	-3.40	-1.32	-0.37	1.99E-09
AFUA_2G05590	Ubiquitin carboxyl-terminal hydrolase (EC 3.4.19.12)	-1.13	-1.32	-0.62	1.38E-04
AFUA_6G02800	Uncharacterized protein AFUA_6G02800	0.12	-1.31	-0.76	3.90E-03
AFUA_3G00840	FAD-dependent oxygenase, putative	-1.72	-1.31	-1.95	3.99E-09
AFUA_1G03140	Glycosyl hydrolase, putative (EC 3.2.1.-)	-0.31	-1.31	-1.44	1.39E-06
AFUA_1G02540	EF hand domain protein	-1.32	-1.29	-1.02	3.44E-06
AFUA_4G01030	Uncharacterized protein	-2.57	-1.27	-2.29	2.17E-05
AFUA_4G10010	Hsp90 co-chaperone Cdc37	-2.06	-1.27	-1.10	4.25E-04
AFUA_3G06110	Proteasome regulatory particle subunit (RpnC), putative	0.06	-1.26	0.98	3.31E-02
AFUA_1G06100	Glutaredoxin Grx1, putative	-3.93	-1.25	-0.60	2.72E-08
AFUA_6G09950	Uncharacterized protein	0.00	-1.24	-1.43	1.03E-04
AFUA_2G02020	Formamidase FmdS (EC 3.5.1.49)	-0.41	-1.24	-1.81	1.36E-07
AFUA_2G12900	Urease accessory protein UreG, putative	-0.61	-1.24	0.06	3.55E-03
AFUA_8G06550	Carbonic anhydrase (EC 4.2.1.1) (Carbonate dehydratase)	-1.28	-1.24	-1.12	2.66E-04
AFUA_3G02190	Uncharacterized protein	1.17	-1.23	-0.36	1.20E-02
AFUA_1G04190	Polyadenylate-binding protein, cytoplasmic and nuclear (PABP) (Poly(A)-binding protein) (Polyadenylate tail-binding protein)	-0.90	-1.23	-0.97	5.13E-03
AFUA_4G06790	Cytochrome b-c1 complex subunit 7	-0.50	-1.22	-0.46	1.01E-02
AFUA_7G01510	SNARE domain protein	-2.85	-1.22	-1.04	5.25E-05
AFUA_4G09900	Cell wall biogenesis protein Ecm15, putative	-0.79	-1.21	-0.63	4.30E-02
AFUA_7G01860	Heat shock protein (Sti1), putative	-1.92	-1.21	-0.96	2.63E-07
AFUA_6G05030	Polysaccharide deacetylase family protein	-0.09	-1.21	-1.23	1.53E-03
AFUA_1G05520	Mandelate racemase/muconate lactonizing enzyme family protein (EC 4.2.1.6)	-0.94	-1.21	-1.50	1.37E-02
AFUA_5G07040	Ubiquitin conjugating enzyme (UbcA), putative (EC 6.3.2.19)	-2.05	-1.20	0.75	3.16E-02
AFUA_1G10810	V-type proton ATPase subunit C	-0.50	-1.20	-0.53	4.82E-02
AFUA_3G14950	Multicopper oxidase, putative (EC 1.7.99.-)	-0.62	-1.20	-0.80	9.80E-03
AFUA_1G08840	Guanylate kinase (EC 2.7.4.8)	-2.09	-1.18	-1.17	4.52E-06
AFUA_6G02090	ATP synthase subunit E, putative (EC 3.6.3.14)	-1.26	-1.17	-0.77	5.70E-06
AFUA_2G01250	Serine peptidase, putative (EC 3.4.-.-)	-1.91	-1.15	-1.51	1.13E-04
AFUA_8G05440	Mitochondrial ATPase subunit ATP4, putative (EC 3.6.3.14)	-1.19	-1.15	0.29	5.86E-06
AFUA_5G01340	Lysophospholipase 2 (EC 3.1.1.5) (Phospholipase B 2)	-1.77	-1.14	-1.25	2.57E-06
AFUA_1G04070	Eukaryotic translation initiation factor eIF-5A	-0.20	-1.14	0.40	7.67E-07
AFUA_2G15770	Cell wall biogenesis protein/glutathione transferase (Gto1), putative	-0.46	-1.14	-1.18	6.34E-05
AFUA_1G15960	Glutathione oxidoreductase Glr1, putative (EC 1.8.1.7)	-0.75	-1.13	-1.66	6.15E-07
AFUA_2G04610	DUF967 domain protein	-0.85	-1.13	-1.27	9.14E-04
AFUA_4G08720	Lysophospholipase 1 (EC 3.1.1.5) (Phospholipase B 1)	-0.56	-1.13	-1.47	7.68E-06
AFUA_3G08620	SH3 domain protein	0.08	-1.12	-0.80	3.26E-02

AFUA_6G07070	Probable 1,4-beta-D-glucan cellobiohydrolase A (EC 3.2.1.91) (Beta-glucancellobiohydrolase A) (Cellobiohydrolase D) (Exocellobiohydrolase A) (Exoglucanase A)	-1.01	-1.12	0.42	3.99E-02
AFUA_5G04250	Homocysteine synthase CysD (EC 2.5.1.49)	-1.59	-1.11	-1.34	1.11E-05
AFUA_8G05580	Acetyl-coA hydrolase Ach1, putative (EC 2.8.3.8)	-0.50	-1.11	-1.35	6.16E-07
AFUA_2G02360	UDP-glucose:glycoprotein glucosyltransferase, putative	-1.99	-1.10	0.04	3.50E-02
AFUA_5G11320	Thioredoxin	-2.63	-1.09	-1.17	8.05E-05
AFUA_6G08720	S-methyl-5'-thioadenosine phosphorylase (EC 2.4.2.28) (5'-methylthioadenosine phosphorylase) (MTA phosphorylase) (MTAP) (MTAPase)	-0.64	-1.09	-1.72	7.37E-06
AFUA_6G04700	Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)	-1.38	-1.09	-0.98	9.00E-03
AFUA_4G11580	Superoxide dismutase (EC 1.15.1.1)	-0.57	-1.08	-1.35	2.30E-02
AFUA_1G10790	Alpha-1,2-mannosidase family protein, putative	0.35	-1.08	-0.14	3.11E-04
AFUA_5G06240	Alcohol dehydrogenase, putative (EC 1.1.1.1)	-1.44	-1.06	-1.71	1.25E-08
AFUA_6G14240	Calcium sensor (NCS-1), putative	0.14	-1.06	-0.67	1.68E-02
AFUA_2G17110	Cell division control protein Cdc48 (EC 3.6.1.-)	-1.41	-1.06	0.57	3.26E-05
AFUA_6G14470	Uncharacterized protein	-0.31	-1.05	-1.98	2.67E-06
AFUA_8G00630	Uncharacterized protein	-0.90	-1.05	-0.99	2.08E-04
AFUA_2G09290	Antigenic mitochondrial protein HSP60, putative	-2.39	-1.04	-0.37	4.15E-11
AFUA_1G06580	High expression lethality protein Hel10, putative	1.24	-1.04	-1.37	4.99E-06
AFUA_7G03870	Actin cytoskeleton-regulatory complex protein pan1	-1.70	-1.04	-1.43	2.40E-03
AFUA_1G16523	40S ribosomal protein S25, putative	-0.68	-1.03	2.30	1.88E-06
AFUA_5G02090	UPF0047 domain protein	-0.84	-1.02	-1.54	3.49E-04
AFUA_2G11060	Acyl CoA binding protein family	-1.87	-1.01	-1.69	2.34E-07
AFUA_2G16830	Endonuclease/exonuclease/phosphatase family protein	-0.58	-1.01	-1.62	2.19E-06
AFUA_4G07910	Mitochondrial presequence protease (EC 3.4.24.-)	1.18	1.01	1.04	7.78E-06
AFUA_2G00680	Glycosyl hydrolase, putative	-0.14	1.01	1.63	1.32E-02
AFUA_2G01330	Exosome complex subunit Rrp46, putative (EC 3.1.13.-)	-0.13	1.01	2.12	2.83E-02
AFUA_7G06840	Class III aminotransferase, putative (EC 2.6.1.-)	-1.19	1.01	-0.22	8.20E-03
AFUA_1G10130	Adenosylhomocysteinase (EC 3.3.1.1)	1.30	1.01	2.02	3.28E-05
AFUA_1G12340	Carnitine acetyl transferase	1.02	1.01	2.16	3.89E-03
AFUA_4G13120	Glutamine synthetase (EC 6.3.1.2)	-0.37	1.01	2.23	6.13E-05
AFUA_6G07760	Proteasome regulatory particle subunit (RpnG), putative	2.46	1.02	2.61	2.81E-05
AFUA_4G09090	Thioredoxin, putative	0.49	1.02	0.95	1.25E-04
AFUA_2G08130	60S ribosomal protein L44	1.76	1.02	4.10	2.38E-06
AFUA_4G13310	Metallo-beta-lactamase domain protein, putative	1.22	1.02	0.72	1.34E-02
AFUA_3G10130	Fructosyl amino acid oxidasesarcosine oxidase, putative	1.24	1.03	1.15	2.40E-02
AFUA_3G07150	Succinate-semialdehyde dehydrogenase, putative (EC 1.2.1.24)	0.96	1.03	1.36	1.42E-05
AFUA_4G09840	Kynureninase 2 (EC 3.7.1.3) (Biosynthesis of nicotinic acid protein 5-2) (L-kynurenine hydrolase 2)	1.89	1.03	1.19	1.40E-06
AFUA_2G13250	Tryptophan synthase (EC 4.2.1.20)	1.57	1.05	2.10	4.86E-03
AFUA_1G15720	Importin beta-1 subunit	1.07	1.05	1.43	4.24E-02
AFUA_5G02720	Phosphoribosylformylglycinamidine synthase (EC 6.3.5.3)	0.47	1.06	1.82	1.42E-02
AFUA_4G00740	Uncharacterized protein	1.97	1.06	2.46	2.53E-06
AFUA_2G09140	Uncharacterized protein	0.84	1.06	0.38	7.03E-04
AFUA_7G02230	mRNA binding post-transcriptional regulator (Csx1), putative	1.96	1.06	1.46	4.21E-02
AFUA_5G06710	DUF89 domain protein	-0.36	1.07	1.81	1.10E-04
AFUA_2G01010	Myo-inositol-phosphate synthase, putative (EC 5.5.1.-)	0.55	1.07	0.19	7.52E-05
AFUA_4G05910	NADH-ubiquinone oxidoreductase 21 kDa subunit, putative (EC 1.6.5.3)	0.38	1.07	2.06	4.78E-02
AFUA_5G14840	Uncharacterized protein	-0.69	1.08	-0.13	1.74E-02
AFUA_3G10970	Protein-tyrosine phosphatase 2 (EC 3.1.3.48)	2.63	1.09	2.48	3.79E-02
AFUA_6G13440	Choline sulfatase, putative (EC 3.1.6.6)	3.50	1.09	2.07	9.70E-04
AFUA_8G04000	Acetyl-CoA acetyltransferase, putative (EC 2.3.1.9)	0.93	1.09	0.78	7.20E-05
AFUA_1G12250	Mitochondrial hypoxia responsive domain protein	3.82	1.09	1.94	2.25E-02

AFUA_4G11650	Alpha-ketoglutarate dehydrogenase complex subunit Kgd1, putative (EC 1.2.4.2)	0.89	1.10	1.82	1.61E-04
AFUA_2G12410	Uncharacterized protein	0.60	1.10	1.47	2.47E-05
AFUA_2G15660	Aldehyde dehydrogenase	1.13	1.10	1.38	2.25E-04
AFUA_7G02140	40S ribosomal protein S24	1.90	1.10	3.49	1.13E-02
AFUA_5G03760	Endochitinase A1 (EC 3.2.1.14) (Chitinase A1)	1.55	1.10	1.52	1.32E-03
AFUA_2G01240	Beta-fructofuranosidase, putative (EC 3.2.1.-)	0.50	1.11	-0.22	3.75E-05
AFUA_1G13330	Arp2/3 complex subunit (Arp2), putative	0.87	1.12	2.22	4.22E-04
AFUA_5G08910	3-methylcrotonyl-CoA carboxylase subunit alpha (MccA), putative (EC 6.4.1.4)	2.09	1.12	1.26	7.48E-06
AFUA_1G04620	Alcohol dehydrogenase, zinc-containing, putative (EC 1.1.1.-)	1.52	1.12	2.28	9.14E-03
AFUA_6G12990	Cytosolic large ribosomal subunit protein L7A	1.41	1.13	3.48	6.45E-08
AFUA_3G12840	Signal peptidase complex catalytic subunit sec11 (EC 3.4.21.89) (Signal peptidase I)	2.53	1.13	1.83	1.78E-02
AFUA_1G08940	Pheromone-processing carboxypeptidase kex1 (EC 3.4.16.6) (Carboxypeptidase D)	1.35	1.13	1.04	3.43E-02
AFUA_4G09110	Cytochrome c peroxidase, mitochondrial (CCP) (EC 1.11.1.5)	0.78	1.14	1.59	1.79E-04
AFUA_5G07750	Ferrochelatase (EC 4.99.1.1)	1.68	1.14	1.65	3.04E-02
AFUA_5G01970	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	0.76	1.14	1.82	2.55E-05
AFUA_3G14990	Alpha/beta hydrolase, putative (EC 3.-.-.-)	1.85	1.14	1.66	5.44E-05
AFUA_1G06820	Uncharacterized protein	-0.98	1.15	1.60	3.42E-04
AFUA_4G03760	Glycine cleavage system P protein (EC 1.4.4.2)	0.84	1.15	0.71	3.35E-04
AFUA_2G11290	Orotate phosphoribosyltransferase (EC 2.4.2.10)	-0.51	1.15	2.21	5.62E-08
AFUA_5G08640	Integral membrane protein	2.24	1.16	-0.60	2.10E-03
AFUA_2G05510	Mitochondrial F1F0 ATP synthase subunit F (Atp17), putative (EC 3.6.3.14)	1.89	1.16	2.45	1.23E-04
AFUA_7G04380	Alcohol dehydrogenase, putative (EC 1.1.1.1)	1.17	1.16	1.10	4.69E-03
AFUA_4G11290	Proteasome activator subunit 4, putative	1.35	1.17	1.93	9.16E-04
AFUA_6G11310	Bifunctional pyrimidine biosynthesis protein (PyrABCN), putative (EC 6.3.5.5)	2.24	1.17	1.15	9.53E-06
AFUA_4G13530	Trehalase (EC 3.2.1.28) (Alpha-trehalose glucohydrolase)	0.41	1.17	1.64	7.73E-03
AFUA_2G17550	Heptaketide hydrolyase ayg1 (EC 3.7.1.-) (Conidial pigment biosynthesis protein ayg1)	-1.11	1.18	0.25	5.29E-10
AFUA_8G07190	Uncharacterized protein	1.05	1.18	2.56	8.55E-04
AFUA_3G10760	Phosphoketolase, putative	0.95	1.18	1.96	3.89E-03
AFUA_3G11750	Oxysterol binding protein (Osh5), putative	1.98	1.18	2.24	1.90E-04
AFUA_1G02670	Arp2/3 complex 34 kDa subunit	1.26	1.18	2.31	1.01E-04
AFUA_5G02300	Peroxidase, putative (EC 1.11.1.-)	2.77	1.19	1.51	2.77E-05
AFUA_5G03540	Thioredoxin reductase, putative (EC 1.-.-.-)	2.34	1.20	0.36	2.53E-08
AFUA_1G01490	NACHT domain protein	2.42	1.20	2.02	5.24E-07
AFUA_1G09020	Nuclear pore complex protein (SonA), putative	2.02	1.20	1.02	2.25E-04
AFUA_2G05910	Phosphotransferase (EC 2.7.1.-)	-0.01	1.20	2.12	8.68E-07
AFUA_2G04310	Argininosuccinate synthase (EC 6.3.4.5)	2.05	1.20	2.41	2.55E-03
AFUA_3G01450	3-methyl-2-oxobutanoate dehydrogenase, putative	1.80	1.21	0.64	2.22E-04
AFUA_1G05850	Erythromycin esterase, putative	-0.16	1.22	2.48	6.61E-03
AFUA_4G07590	CaaX prenyl protease Ste24 (EC 3.4.24.84)	3.20	1.22	2.67	7.52E-04
AFUA_6G02280	Peroxiredoxin Asp f3 (Prx) (EC 1.11.1.15) (Thioredoxin peroxidase) (TPx) (allergen Asp f 3)	1.92	1.22	1.20	9.23E-10
AFUA_4G09660	Secretory component protein shr3, putative	0.78	1.23	2.32	4.55E-02
AFUA_4G14070	Glycosyl transferase, putative (EC 2.-.-.-)	-0.24	1.23	1.60	4.77E-04
AFUA_3G00230	Beta-glucosidase, putative (EC 3.2.1.21)	0.64	1.23	0.35	1.46E-02
AFUA_3G03950	Endoglucanase, putative	0.49	1.23	-0.02	4.45E-03
AFUA_4G10200	Transcription factor RfeF, putative	1.90	1.23	0.40	1.32E-06
AFUA_1G09800	Obg-like ATPase 1	0.49	1.23	1.67	2.22E-05
AFUA_2G15980	3' exoribonuclease family protein	0.02	1.24	2.20	4.73E-03
AFUA_5G06390	Adenosine kinase, putative (EC 2.7.1.20)	2.09	1.25	3.06	2.24E-06
AFUA_1G10310	RNase L inhibitor of the ABC superfamily, putative	2.57	1.26	1.67	3.21E-03
AFUA_4G08070	Glycylpeptide N-tetradecanoyltransferase (EC 2.3.1.97) (Myristoyl-CoA:protein N-myristoyltransferase) (NMT) (Peptide N-myristoyltransferase)	0.76	1.26	2.14	1.19E-02
AFUA_4G04200	Myo-inositol-1(Or 4)-monophosphatase (EC 3.1.3.7)	1.30	1.26	0.92	7.10E-03

AFUA_5G02240	NAD dependent epimerase/dehydratase family protein (EC 1.1.1.133)	0.63	1.26	1.48	1.13E-05
AFUA_4G09010	mRNA splicing protein (Prp39), putative	1.05	1.27	2.22	2.27E-02
AFUA_1G05210	G-protein complex gamma subunit GpgA	0.33	1.27	1.49	1.70E-03
AFUA_4G04350	DEAD helicases superfamily protein (Aquarius), putative	2.26	1.27	2.48	1.26E-02
AFUA_4G11770	Glutathione transferase, putative	0.91	1.27	1.25	1.16E-03
AFUA_1G02030	Eukaryotic translation initiation factor 3 subunit B (eIF3b) (Eukaryotic translation initiation factor 3 90 kDa subunit homolog) (eIF3 p90) (Translation initiation factor eIF3 p90 subunit homolog)	1.64	1.28	1.67	5.02E-03
AFUA_3G00900	Alpha-amylase, putative	1.74	1.28	0.97	1.10E-05
AFUA_6G04660	Centromere protein Cse4, putative	2.02	1.28	2.55	1.63E-02
AFUA_6G08740	3-dehydroshikimate dehydratase, putative (EC 4.2.1.-)	1.23	1.28	1.52	1.10E-03
AFUA_4G07700	Clathrin heavy chain	1.01	1.28	1.93	7.89E-07
AFUA_3G02257	Uncharacterized protein	1.22	1.29	2.68	3.05E-04
AFUA_4G00290	Succinyl-CoA synthetase beta subunit, putative (EC 6.2.1.4)	0.63	1.29	1.82	3.89E-02
AFUA_4G14450	Mannitol 2-dehydrogenase (M2DH) (MDH) (EC 1.1.1.67)	1.63	1.31	1.97	1.45E-06
AFUA_5G02350	Hydrolase, carbon-nitrogen family, putative	2.87	1.32	2.15	1.12E-02
AFUA_4G07730	60S ribosomal protein L11	2.60	1.32	4.11	1.78E-06
AFUA_4G14560	Atrochrysone carboxylic acid synthase (ACAS) (EC 2.3.1.-) (Non-reducing polyketide synthase tpcC) (Trypacidin synthesis protein C)	-0.13	1.32	0.89	4.83E-02
AFUA_3G11610	Non-histone chromosomal protein 6	0.61	1.32	1.38	1.58E-05
AFUA_3G05610	Uncharacterized protein	1.20	1.33	0.81	4.71E-05
AFUA_5G08980	NADH-ubiquinone oxidoreductase 9.5 kDa subunit, putative (EC 1.6.5.3)	2.51	1.33	1.80	5.73E-03
AFUA_4G09320	Probable dipeptidyl peptidase 4 (EC 3.4.14.5) (Dipeptidyl peptidase IV) (DPP IV) (DppIV)	0.99	1.33	0.18	9.60E-07
AFUA_3G12510	Vesicular fusion ATPase, putative	3.29	1.34	1.38	5.57E-05
AFUA_1G12940	Mitogen-activated protein kinase hog1 (MAP kinase hog1) (EC 2.7.11.24)	1.43	1.34	2.07	8.26E-03
AFUA_7G01830	UTP-glucose-1-phosphate uridylyltransferase Ugp1, putative	0.00	1.35	2.11	4.43E-05
AFUA_8G05590	Oxidoreductase, short chain dehydrogenase/reductase family	1.33	1.35	1.27	7.36E-05
AFUA_4G09140	L-ornithine aminotransferase Car2, putative (EC 2.6.1.13)	1.51	1.35	1.05	2.77E-07
AFUA_3G00680	Amine oxidase (EC 1.4.3.-)	3.44	1.35	1.88	1.22E-03
AFUA_4G11720	Phosphatidyl synthase	0.57	1.36	2.06	3.69E-08
AFUA_1G13590	Uncharacterized protein	1.13	1.36	0.90	2.35E-02
AFUA_6G13330	RNA binding protein, putative	0.65	1.36	1.72	1.25E-06
AFUA_3G05740	Aldose 1-epimerase, putative (EC 5.1.3.3)	1.47	1.36	1.46	1.87E-02
AFUA_2G03380	Alkaline serine protease	2.14	1.37	4.85	1.02E-04
AFUA_1G13260	Coatomer subunit epsilon	0.97	1.37	1.31	1.66E-02
AFUA_3G05350	Histone H2B	1.24	1.37	2.21	5.77E-07
AFUA_4G07845	60S ribosomal protein L38, putative	1.15	1.37	3.10	7.41E-05
AFUA_8G01420	Quinone oxidoreductase, putative (EC 1.6.5.5)	1.55	1.38	1.85	5.05E-04
AFUA_3G04220	Fatty acid synthase beta subunit, putative	1.30	1.38	2.47	5.78E-09
AFUA_4G13760	Uncharacterized protein	2.28	1.38	1.22	1.74E-02
AFUA_4G00180	Fatty acid oxygenase, putative (EC 1.-.-.-)	0.87	1.39	2.19	7.54E-03
AFUA_5G02480	Glycogen [starch] synthase (EC 2.4.1.11)	1.58	1.39	2.40	6.34E-05
AFUA_1G06960	Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	1.08	1.40	2.85	5.87E-08
AFUA_7G05290	40S ribosomal protein S13	2.13	1.40	4.21	4.71E-06
AFUA_3G10460	Nuclear transport factor NTF-2, putative	1.98	1.40	1.80	6.04E-05
AFUA_1G14490	Aminotransferase, putative	1.06	1.40	1.61	1.36E-02
AFUA_3G07300	ABC multidrug transporter, putative (EC 3.6.3.-)	1.49	1.40	1.92	1.46E-03
AFUA_1G02570	Aspartyl-tRNA synthetase, cytoplasmic (EC 6.1.1.12)	3.37	1.41	2.82	2.34E-05
AFUA_7G05360	FACT complex subunit pob3 (Facilitates chromatin transcription complex subunit pob3)	1.86	1.41	2.07	6.65E-04
AFUA_4G13500	Aldehyde dehydrogenase	2.15	1.42	2.54	6.03E-05
AFUA_2G16070	Urease accessory protein UreD	1.36	1.42	0.67	2.51E-02

AFUA_3G08640	Eukaryotic translation initiation factor 3 subunit I (eIF3i) (Eukaryotic translation initiation factor 3 39 kDa subunit homolog) (eIF-3 39 kDa subunit homolog)	2.38	1.42	2.53	2.45E-04
AFUA_4G02840	NmrA-like family protein, putative	2.09	1.42	-0.34	2.28E-04
AFUA_2G01030	1-aminocyclopropane-1-carboxylate deaminase, putative (EC 3.5.99.7)	1.39	1.42	1.51	6.06E-04
AFUA_6G06500	Actin-related protein 2/3 complex subunit 1A, putative	0.87	1.42	1.99	2.53E-05
AFUA_5G06130	Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial (EC 6.2.1.5) (Succinyl-CoA synthetase subunit alpha) (SCS-alpha)	-0.10	1.42	2.15	4.63E-07
AFUA_5G03860	Alkaline phosphatase family protein (EC 3.1.-.-)	2.91	1.43	2.99	2.46E-03
AFUA_5G11720	26S proteasome regulatory subunit Mts4, putative	0.63	1.44	2.69	8.14E-05
AFUA_2G04590	Alcohol dehydrogenase, putative (EC 1.1.1.-)	2.84	1.45	1.67	1.37E-04
AFUA_5G02640	O-methyltransferase, putative (EC 2.1.1.-)	4.70	1.45	0.38	1.42E-07
AFUA_3G08650	C1 tetrahydrofolate synthase, putative (EC 6.3.4.3)	0.76	1.45	2.18	3.94E-07
AFUA_6G04920	Formate dehydrogenase (FDH) (EC 1.2.1.2) (NAD-dependent formate dehydrogenase)	1.83	1.45	1.22	2.23E-08
AFUA_6G08780	Proline utilization protein PrnX, putative (EC 4.3.1.12)	1.85	1.46	1.85	2.55E-03
AFUA_2G09130	NADH-ubiquinone dehydrogenase 24 kDa subunit, putative (EC 1.6.5.3)	1.56	1.46	1.71	3.08E-05
AFUA_4G08880	Glucose-6-phosphate 1-epimerase (EC 5.1.3.15)	-0.32	1.46	2.61	7.00E-05
AFUA_1G14090	Histidinol-phosphate aminotransferase (EC 2.6.1.9)	2.20	1.47	2.98	3.93E-06
AFUA_5G11560	Arp2/3 complex subunit (Arp3), putative	1.00	1.47	2.29	2.40E-04
AFUA_3G03000	Phosphatidylethanolamine-binding protein, putative	1.03	1.47	1.62	1.71E-02
AFUA_6G12630	Leucyl-tRNA synthetase (EC 6.1.1.4)	0.81	1.47	2.60	8.15E-04
AFUA_3G12800	Clathrin-coated vesiclec protein (Bud7), putative	1.84	1.48	0.84	3.28E-02
AFUA_5G08940	3-methylcrotonyl-CoA carboxylase, beta subunit (MccB), putative (EC 6.4.1.3)	2.37	1.48	1.54	3.45E-03
AFUA_1G04820	Probable NAD(P)H-dependent D-xylose reductase xyl1 (XR) (EC 1.1.1.307)	1.34	1.48	1.27	3.13E-08
AFUA_4G00370	General amidase, putative	-0.03	1.49	0.19	5.38E-03
AFUA_3G13900	Glutamate-cysteine ligase Gcs1, putative	0.85	1.49	2.61	2.19E-03
AFUA_2G01040	S-(hydroxymethyl)glutathione dehydrogenase (EC 1.1.1.284)	2.46	1.49	0.21	1.09E-09
AFUA_6G06900	Rho GTPase Rho1	2.00	1.49	1.54	6.27E-06
AFUA_3G04170	Pyruvate dehydrogenase E1 beta subunit PdbA, putative (EC 1.2.4.1)	0.96	1.49	2.82	9.42E-09
AFUA_5G03350	Glutamine-dependent NAD(+) synthetase (EC 6.3.5.1) (NAD(+) synthase [glutamine-hydrolyzing])	0.47	1.51	1.84	5.06E-03
AFUA_2G17430	Oxidoreductase 2-nitropropane dioxygenase family, putative (EC 1.13.11.-)	1.09	1.52	2.01	3.46E-03
AFUA_1G01680	Branched-chain amino acid aminotransferase (EC 2.6.1.42)	2.36	1.53	1.12	2.97E-04
AFUA_2G09180	Coatomer subunit zeta, putative	1.38	1.53	2.49	2.59E-02
AFUA_3G01580	GMC oxidoreductase, putative	1.44	1.53	1.48	2.64E-02
AFUA_6G04570	Translation elongation factor eEF-1 subunit gamma, putative	1.92	1.53	1.72	4.63E-06
AFUA_3G06210	Phosphoribosyl-aminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)	-0.11	1.53	2.33	2.96E-06
AFUA_2G10500	40S ribosomal protein Rps16, putative	2.04	1.54	3.83	3.79E-05
AFUA_5G05480	Rheb small monomeric GTPase RhbA	1.88	1.54	1.84	1.32E-02
AFUA_2G02490	Uncharacterized protein	1.74	1.54	1.77	3.09E-03
AFUA_1G07200	Mitochondrial cytochrome b2, putative (EC 1.1.2.3)	1.82	1.54	1.70	1.56E-06
AFUA_2G15190	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	1.31	1.55	1.37	1.38E-07
AFUA_2G11560	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.12)	1.97	1.56	1.62	1.77E-04
AFUA_6G08750	Delta-1-pyrroline-5-carboxylate dehydrogenase PrnC (EC 1.2.1.88)	2.10	1.56	1.26	3.94E-08
AFUA_1G12610	Hsp70 chaperone Hsp88	1.37	1.56	1.54	1.28E-03
AFUA_3G10480	Meiotic sister chromatid recombination protein Ish1/Msc1, putative	0.76	1.56	2.10	3.29E-06
AFUA_7G00700	Aldo-keto reductase (AKR13), puatative (EC 1.1.1.-)	1.86	1.56	2.73	2.34E-05
AFUA_1G13780	Histone H4	1.92	1.56	2.39	1.19E-03
AFUA_5G05680	Peptide chain release factor eRF/aRF, subunit 1	1.89	1.57	2.19	8.67E-06
AFUA_1G04720	C-8 sterol isomerase (Erg-1), putative	3.48	1.57	1.64	3.80E-04

AFUA_3G08430	Mitochondrial phosphate carrier protein, putative	3.04	1.57	2.38	5.50E-03
AFUA_5G08650	Uncharacterized protein	0.60	1.57	1.29	4.77E-02
AFUA_1G14410	60S ribosomal protein L17	1.79	1.58	4.32	4.06E-08
AFUA_6G03830	Ribosomal protein L14	2.30	1.58	4.26	6.50E-08
AFUA_5G10560	Cytochrome c oxidase subunit V	2.91	1.58	2.70	1.01E-06
AFUA_5G03480	Methylenetetrahydrofolate reductase (EC 1.5.1.20)	1.32	1.59	2.06	4.56E-02
AFUA_3G09910	Phosphatidylinositol transporter, putative	1.29	1.59	2.31	5.91E-05
AFUA_6G04010	Chromosome segregation protein Cse1, putative	1.43	1.60	2.03	7.04E-05
AFUA_4G14100	Glutathione S-transferase, putative	0.68	1.60	1.64	2.44E-02
AFUA_3G08660	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	2.19	1.60	1.11	2.02E-07
AFUA_2G18030	Catalase easC (EC 1.11.-.-) (Ergot alkaloid synthesis protein C)	1.23	1.60	2.07	1.29E-04
AFUA_2G00330	Beta-alanine synthase, putative (EC 3.5.1.-)	1.89	1.60	0.59	7.65E-04
AFUA_2G04930	Uncharacterized protein	1.69	1.61	1.26	4.59E-03
AFUA_4G10790	Phosphoribosyl diphosphate synthase isoform 4	2.51	1.61	3.04	1.23E-04
AFUA_1G14400	Hydroxyisocaproate dehydrogenase, putative (EC 1.1.1.95)	0.68	1.61	2.50	7.64E-03
AFUA_1G04540	NADH-cytochrome b5 reductase 2 (EC 1.6.2.2) (Mitochondrial cytochrome b reductase)	1.81	1.61	2.16	3.37E-06
AFUA_1G01750	Peptidyl-prolyl cis-trans isomerase, putative (EC 5.2.1.8)	0.38	1.61	1.81	1.91E-02
AFUA_8G01100	Melibiase subfamily, putative (EC 3.2.1.22)	1.22	1.62	2.77	4.36E-04
AFUA_1G04950	Serine/threonine-protein phosphatase (EC 3.1.3.16)	2.33	1.62	1.22	3.67E-08
AFUA_4G04410	3-hydroxybutyryl-CoA dehydrogenase, putative (EC 1.1.1.157)	1.54	1.62	1.58	8.61E-05
AFUA_5G03770	Lipase, putative (EC 3.1.1.3)	1.66	1.62	2.66	1.25E-03
AFUA_8G04550	Sulfonate biosynthesis enzyme, putative (EC 4.4.1.-)	0.80	1.63	1.86	3.19E-02
AFUA_6G12580	Anthranilate synthase component I, putative (EC 4.1.3.27)	1.37	1.63	2.21	2.10E-07
AFUA_5G06680	4-aminobutyrate transaminase GatA (EC 2.6.1.19)	1.48	1.64	1.32	1.25E-07
AFUA_6G10480	Peptidyl-prolyl cis-trans isomerase-like 3 (PPIase) (EC 5.2.1.8) (Rotamase)	2.18	1.64	2.28	4.96E-03
AFUA_2G13295	Aminotransferase family protein (LolT), putative	3.15	1.64	1.91	1.90E-03
AFUA_1G09660	Mitochondrial 2-oxodicarboxylate carrier protein, putative	3.45	1.64	2.72	2.28E-05
AFUA_5G06010	Eukaryotic translation initiation factor 6 (eIF-6)	2.53	1.64	2.91	2.74E-04
AFUA_4G07690	Phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	0.20	1.65	2.06	7.82E-08
AFUA_3G06890	RRM domain protein	2.15	1.66	1.07	3.71E-04
AFUA_1G11480	Uncharacterized protein	1.60	1.67	0.73	7.90E-05
AFUA_4G07610	Zinc metalloprotease, putative	2.02	1.67	0.28	2.41E-07
AFUA_3G14690	Aminotransferase, putative (EC 2.-.-.-)	3.71	1.68	2.25	1.24E-02
AFUA_1G14850	Acyl-CoA dehydrogenase, putative (EC 1.3.99.-)	2.04	1.69	1.34	2.97E-10
AFUA_1G13710	Isoleucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.5)	1.43	1.69	2.43	1.72E-06
AFUA_3G13450	Oxidoreductase, short chain dehydrogenase/reductase family superfamily (EC 1.1.1.100)	0.99	1.69	2.13	5.97E-03
AFUA_4G08710	Short chain dehydrogenase, putative (EC 1.-.-.-)	1.52	1.69	1.11	1.14E-08
AFUA_5G10370	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (EC 1.3.5.1)	1.70	1.70	1.94	1.61E-03
AFUA_5G10280	Oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor (EC 1.1.1.31)	1.71	1.70	1.26	8.32E-03
AFUA_2G05790	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 (EC 2.4.99.18)	2.29	1.70	2.33	1.32E-09
AFUA_6G11980	Exo-beta-1,3-glucanase, putative (EC 3.2.1.58)	-0.54	1.70	0.80	4.83E-05
AFUA_2G10520	Uricase (EC 1.7.3.3) (Urate oxidase)	1.22	1.71	0.55	9.87E-03
AFUA_8G04340	Cystathionine gamma-lyase (EC 4.4.1.8)	2.17	1.72	2.46	1.22E-03
AFUA_3G07810	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1)	1.68	1.72	1.63	7.09E-11
AFUA_3G11350	ATPase get3 (EC 3.6.-.-) (Arsenical pump-driving ATPase) (Arsenite-stimulated ATPase) (Golgi to ER traffic protein 3) (Guided entry of tail-anchored proteins 3)	2.82	1.72	3.08	7.97E-03
AFUA_8G04710	Xylosidase, putative (EC 3.2.1.37)	1.81	1.72	1.89	6.76E-04
AFUA_6G00750	Pyruvate decarboxylase, putative (EC 4.1.1.1)	1.60	1.72	1.26	4.56E-04
AFUA_7G00860	Lipoxygenase, putative (EC 1.13.11.-)	1.05	1.73	2.86	2.58E-04
AFUA_1G14170	Probable beta-galactosidase A (EC 3.2.1.23) (Lactase A)	1.06	1.73	1.16	7.03E-03

AFUA_2G01100	Pirin domain protein, putative	0.33	1.73	2.73	9.67E-04
AFUA_1G09960	Kynurenine formamidase (KFA) (KFase) (EC 3.5.1.9) (Arylformamidase) (N-formylkynurenine formamidase) (FKF)	2.37	1.73	1.14	9.20E-03
AFUA_4G12840	Methylthioribulose-1-phosphate dehydratase (MTRu-1-P dehydratase) (EC 4.2.1.109)	1.74	1.75	1.64	1.23E-03
AFUA_5G12250	Posttranscriptional regulation nuclease (Mkt1), putative	1.24	1.75	2.19	5.16E-05
AFUA_6G03100	Uncharacterized protein	0.36	1.75	2.23	7.03E-07
AFUA_3G11430	Arginase (EC 3.5.3.1)	0.44	1.75	2.07	7.83E-03
AFUA_6G11210	3-oxoacyl-(Acyl-carrier-protein) reductase (EC 1.1.1.100)	2.23	1.76	1.69	1.86E-05
AFUA_6G10600	NEDD8-activating enzyme E1 regulatory subunit	2.06	1.76	2.38	5.36E-04
AFUA_3G11640	Homoserine dehydrogenase (HDH) (EC 1.1.1.3)	-0.21	1.76	2.09	2.66E-06
AFUA_1G11120	Uncharacterized protein	2.27	1.76	2.14	5.04E-03
AFUA_1G08980	UPF0160 domain protein MYG1, putative	1.65	1.77	1.65	1.28E-08
AFUA_4G03120	Mitochondrial cytochrome b2, putative (EC 1.1.2.3)	1.81	1.78	1.94	1.46E-05
AFUA_6G00260	Phosphatidylserine decarboxylase family protein (EC 4.1.1.-)	1.42	1.79	1.02	3.32E-05
AFUA_2G16880	60S ribosomal protein L37a	0.96	1.79	4.84	7.06E-07
AFUA_1G14570	Histidine biosynthesis trifunctional protein [Includes: Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19); Phosphoribosyl-ATP pyrophosphohydrolase (EC 3.6.1.31); Histidinol dehydrogenase (HDH) (EC 1.1.1.23)]	1.38	1.80	1.44	5.84E-08
AFUA_6G10980	UV-damaged DNA binding protein, putative	1.06	1.81	3.04	6.09E-05
AFUA_7G01880	Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	-0.48	1.81	1.87	8.56E-04
AFUA_7G00360	UDP-galactose 4-epimerase, putative (EC 5.1.3.-)	2.71	1.81	2.62	5.05E-08
AFUA_5G12210	G protein complex beta subunit SfaD	2.36	1.81	2.92	7.28E-07
AFUA_4G04680	FGGY-family carbohydrate kinase, putative	0.81	1.82	2.61	1.73E-05
AFUA_5G09080	Transcription factor (SPT8), putative	0.93	1.83	2.21	1.87E-02
AFUA_4G07710	Pyruvate carboxylase (EC 6.4.1.1)	1.40	1.84	2.74	9.52E-08
AFUA_8G04810	Casein kinase, putative (EC 2.7.11.1)	1.23	1.84	1.89	4.01E-02
AFUA_5G06500	Acyl-CoA dehydrogenase family protein (EC 1.3.99.-)	2.25	1.85	1.96	8.24E-05
AFUA_2G01920	Glutaminyl-tRNA synthetase (EC 6.1.1.18)	2.64	1.85	0.95	1.34E-05
AFUA_4G11050	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial (EC 1.6.5.3) (EC 1.6.99.3)	1.96	1.85	3.19	1.70E-06
AFUA_7G00350	Uncharacterized protein	0.62	1.86	2.15	3.63E-03
AFUA_4G14520	Monoogygenase tpcG (EC 1.-.-.-) (Trypacidin synthesis protein G)	1.55	1.86	3.24	4.15E-05
AFUA_6G06460	Fumarylacetoacetate hydrolase family protein	1.77	1.86	1.92	9.09E-05
AFUA_2G00590	Glutathione S-transferase, putative (EC 2.5.1.18)	2.81	1.86	2.26	1.59E-03
AFUA_6G00370	Aminotransferase, putative	1.40	1.87	0.59	1.39E-03
AFUA_7G01920	DNA-directed RNA polymerase subunit beta (EC 2.7.7.6)	2.37	1.88	2.91	1.36E-04
AFUA_6G12930	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase) (Homocitrate dehydratase) (EC 4.2.1.-)	1.16	1.88	3.20	6.24E-07
AFUA_3G00370	Phosphoketolase, putative (EC 4.1.2.-)	0.51	1.88	2.84	3.50E-05
AFUA_2G10220	Glycerol dehydrogenase, putative (EC 1.1.1.-)	2.11	1.89	1.74	2.26E-05
AFUA_2G11150	Rab GDP dissociation inhibitor	1.18	1.90	2.40	1.79E-04
AFUA_6G12250	Succinyl-CoA:3-ketoacid-coenzyme A transferase (EC 2.8.3.5)	1.20	1.90	1.74	1.35E-02
AFUA_2G14030	Arginyl-tRNA synthetase (EC 6.1.1.19)	0.35	1.91	2.08	2.78E-07
AFUA_6G10660	ATP citrate lyase subunit (Acl), putatibe (EC 6.2.1.5)	0.19	1.91	2.65	1.23E-04
AFUA_6G05090	RNA polymerase II Elongator subunit, putative	-0.19	1.92	2.79	3.47E-03
AFUA_6G02470	Fumarate hydratase, putative (EC 4.2.1.2)	1.78	1.92	2.06	3.59E-06
AFUA_1G09230	DUF1000 domain protein	2.18	1.93	2.15	2.28E-04
AFUA_1G10460	Uncharacterized protein	2.27	1.93	1.73	9.81E-03
AFUA_3G11710	Saccharopine dehydrogenase [NAD(+), L-lysine-forming] (SDH) (EC 1.5.1.7) (Lysine--2-oxoglutarate reductase)	1.46	1.93	2.62	3.46E-05
AFUA_3G12560	Allantoicase Alc, putative (EC 3.5.3.4)	-0.32	1.93	2.50	3.74E-05
AFUA_5G09450	Isoflavone reductase family protein (EC 1.3.1.-)	1.60	1.94	2.92	3.41E-05
AFUA_2G14470	Oxidoreductase, FAD-binding, putative	1.08	1.94	1.01	1.21E-04

AFUA_5G08930	Isovaleryl-CoA dehydrogenase IvdA, putative (EC 1.3.8.4)	2.35	1.94	1.59	6.38E-07
AFUA_2G05740	Rho GTPase ModA, putative	2.65	1.95	2.38	1.24E-03
AFUA_5G03360	NADH pyrophosphatase, putative (EC 3.6.1.-)	2.39	1.95	2.29	1.45E-02
AFUA_5G12840	Hydroxyacylglutathione hydrolase, putative (EC 3.1.2.6)	1.91	1.96	1.58	2.01E-09
AFUA_2G13630	Aromatic aminotransferase Aro8, putative (EC 2.6.1.-)	3.08	1.96	1.61	7.87E-04
AFUA_2G17560	Hydroxynaphthalene reductase arp2 (EC 1.1.-.-) (Conidial pigment biosynthesis oxidase arp2)	1.38	1.98	2.22	3.81E-07
AFUA_2G12450	Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4)	2.07	1.98	1.96	1.61E-05
AFUA_6G12950	Trehalose-6-phosphate synthase (EC 2.4.1.15) (UDP-glucose-glucosephosphate glucosyltransferase)	3.01	1.98	3.52	7.43E-05
AFUA_4G13700	Threonyl-tRNA synthetase, putative (EC 6.1.1.3)	2.15	1.98	2.27	1.50E-05
AFUA_2G00830	Short chain dehydrogenase/reductase (EC 1.1.-.-)	2.20	1.98	1.66	3.87E-03
AFUA_1G02140	Glycogen debranching enzyme Gdb1, putative	0.87	1.98	3.18	1.08E-03
AFUA_6G02140	Peptidyl-prolyl cis-trans isomerase-like 1 (PPIase) (EC 5.2.1.8) (Rotamase)	2.26	1.98	2.33	3.51E-03
AFUA_6G13180	CECR1 family adenosine deaminase, putative	1.74	1.99	2.52	3.02E-05
AFUA_6G10650	ATP citrate lyase, subunit 1, putative (EC 2.3.3.8)	1.30	2.00	2.76	3.74E-08
AFUA_1G01970	VeA-like protein	1.53	2.00	3.12	1.12E-03
AFUA_2G04220	Homogentisate 1,2-dioxygenase (HmgA), putative (EC 1.13.11.5)	2.37	2.00	1.07	3.81E-02
AFUA_8G01670	Catalase-peroxidase (CP) (EC 1.11.1.21) (Catalase-2) (Peroxidase/catalase)	2.91	2.01	1.41	4.44E-09
AFUA_5G09640	Conserved fungal protein	1.96	2.01	1.97	6.03E-04
AFUA_4G12850	Calnexin homolog	1.94	2.01	1.68	1.06E-05
AFUA_3G02430	Uncharacterized protein	1.34	2.01	1.93	8.65E-07
AFUA_3G04020	Conserved mitochondrial protein	2.50	2.02	2.39	6.53E-04
AFUA_1G09480	Vacuolar protein sorting-associated protein 29	0.98	2.02	2.31	3.96E-02
AFUA_1G14680	DNA-directed RNA polymerase subunit (EC 2.7.7.6)	2.25	2.02	3.38	4.43E-05
AFUA_6G13300	GTP-binding nuclear protein	2.70	2.02	2.31	8.90E-06
AFUA_2G14850	Enoyl-CoA hydratase/isomerase family protein (EC 4.2.-.-)	3.46	2.02	2.40	1.40E-04
AFUA_6G13250	60S ribosomal protein L31e	1.73	2.03	4.41	2.79E-05
AFUA_7G01320	Beta-mannosidase B (EC 3.2.1.25) (Mannanase B) (Mannase B)	1.67	2.03	1.98	7.67E-05
AFUA_4G08170	Succinate-semialdehyde dehydrogenase Uga2, putative (EC 1.2.1.24)	1.43	2.03	2.87	8.68E-06
AFUA_3G08310	4-nitrophenylphosphatase (PNPPase) (EC 3.1.3.41)	2.77	2.04	1.39	1.34E-02
AFUA_5G09920	Peptidase, putative (EC 3.-.-.-)	1.81	2.04	1.63	2.44E-06
AFUA_6G14100	Mitochondrial carnitine:acyl carnitine carrier, putative	3.46	2.04	2.78	2.40E-04
AFUA_4G07650	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) (Rotamase B)	1.62	2.05	2.52	4.36E-03
AFUA_8G07110	Alanyl-tRNA synthetase, putative (EC 6.1.1.7)	1.67	2.06	2.33	2.91E-02
AFUA_1G09930	Glycerol dehydrogenase Gcy1, putative (EC 1.1.1.-)	1.48	2.06	2.98	9.11E-09
AFUA_4G08600	Aldehyde dehydrogenase, putative (EC 1.2.1.3)	1.14	2.06	2.52	5.58E-06
AFUA_1G13790	Histone H3	2.16	2.07	2.90	5.44E-05
AFUA_4G13750	Neutral protease 2 homolog AFUA_4G13750 (EC 3.4.24.39) (Deuterolysin AFUA_4G13750)	4.36	2.08	0.81	5.27E-05
AFUA_5G11040	Pantoate--beta-alanine ligase (EC 6.3.2.1)	1.20	2.08	2.46	1.10E-04
AFUA_4G06860	Uncharacterized protein	2.13	2.09	1.49	1.46E-04
AFUA_6G03540	Malate synthase (EC 2.3.3.9)	0.38	2.10	2.16	1.22E-07
AFUA_1G06700	Metacaspase-1A (EC 3.4.22.-)	3.64	2.10	2.07	1.94E-03
AFUA_1G02820	NADH-quinone oxidoreductase Pst2, putative	-0.37	2.10	2.55	9.33E-06
AFUA_6G04210	Mannosyl-oligosaccharide glucosidase, putative	1.32	2.11	1.78	2.46E-05
AFUA_3G11480	Mitochondrial methylglutaconyl-CoA hydratase (Auh), putative (EC 4.2.1.18)	1.61	2.12	3.01	1.14E-06
AFUA_8G00230	Verruculogen synthase (EC 1.14.11.38) (Fumitremorgin biosynthesis protein F)	1.49	2.12	2.00	2.82E-04
AFUA_4G12600	Phosphoribosyl-aminoimidazole carboxylase (EC 4.1.1.21)	2.05	2.13	2.49	3.52E-06
AFUA_3G03020	Phosphoglucomutase, putative	2.09	2.13	1.66	1.24E-04
AFUA_5G07000	NAD binding Rossmann fold oxidoreductase, putative (EC 1.-.-.-)	1.19	2.13	2.22	4.38E-07
AFUA_2G07720	Cytochrome b5, putative	0.33	2.14	2.11	2.06E-02

AFUA_8G01390	Glycosyl hydrolase, putative	1.55	2.14	2.67	1.14E-04
AFUA_3G13140	Methyltransferase, putative	2.16	2.14	2.09	1.35E-03
AFUA_4G06380	Sterol carrier protein, putative	0.71	2.15	2.45	7.99E-07
AFUA_5G13450	Triosephosphate isomerase (EC 5.3.1.1)	2.20	2.15	1.85	1.15E-06
AFUA_7G04180	Amine oxidase (EC 1.4.3.-)	3.46	2.15	1.42	5.87E-08
AFUA_4G11260	Aldo-keto reductase, putative (EC 1.1.1.-)	1.72	2.15	1.57	5.59E-07
AFUA_5G08240	MutT/nudix family protein	0.64	2.17	1.60	9.03E-05
AFUA_2G12530	Carnitine acetyl transferase	2.17	2.17	2.24	1.23E-05
AFUA_5G11660	Autophagy-related protein 18	2.64	2.18	2.57	1.54E-04
AFUA_5G02030	Cleavage and polyadenylation specific factor 5	2.60	2.18	2.07	1.02E-06
AFUA_1G11535	Glutaredoxin-like protein	1.93	2.19	1.56	1.53E-03
AFUA_5G10610	Ubiquinol-cytochrome c reductase iron-sulfur subunit (EC 1.10.2.2)	2.21	2.19	2.15	3.15E-07
AFUA_2G11020	Triosephosphate isomerase (EC 5.3.1.1)	1.77	2.19	2.49	5.43E-05
AFUA_7G05740	Malate dehydrogenase (EC 1.1.1.37)	1.99	2.20	1.80	2.64E-09
AFUA_1G16270	Xylitol dehydrogenase XdhB (EC 1.1.1.14)	2.08	2.20	2.82	1.45E-03
AFUA_3G13620	Cupin domain protein	-0.46	2.20	1.33	1.15E-03
AFUA_2G01220	GTP cyclohydrolase II, putative (EC 3.5.4.25)	1.06	2.20	3.30	5.88E-03
AFUA_3G10090	Dihydroneopterin aldolase domain protein (EC 4.1.2.25)	0.71	2.20	2.58	2.09E-05
AFUA_2G03290	14-3-3 family protein ArtA, putative	0.67	2.21	2.82	1.90E-07
AFUA_2G02920	Alpha/beta hydrolase, putative (EC 3.-.-.-)	2.26	2.22	2.18	4.64E-05
AFUA_1G08930	Probable cytosolic iron-sulfur protein assembly protein 1	2.13	2.22	3.31	2.02E-03
AFUA_1G02090	Quinone oxidoreductase, putative (EC 1.6.5.5)	2.48	2.22	2.44	7.49E-06
AFUA_5G10540	Glycogen branching enzyme GbeA, putative	0.91	2.23	3.06	1.39E-07
AFUA_6G08020	ABC transporter, putative	1.44	2.23	2.27	8.59E-04
AFUA_6G04560	37S ribosomal protein S9	0.95	2.24	3.28	4.88E-04
AFUA_5G04230	Citrate synthase	1.29	2.25	3.43	2.08E-07
AFUA_2G16200	Uracil phosphoribosyltransferase (EC 2.4.2.9)	2.20	2.25	2.69	1.16E-02
AFUA_4G10330	CaaX farnesyltransferase beta subunit Ram1 (EC 2.5.1.58)	1.83	2.27	2.17	3.61E-04
AFUA_4G13510	Isocitrate lyase (ICL) (Isocitrase) (Isocitratase) (EC 4.1.3.1) (Methylisocitrate lyase) (MICA) (EC 4.1.3.30) (Threo-D(S)-isocitrate glyoxylate-lyase)	1.37	2.27	3.61	6.63E-08
AFUA_4G11840	Glyoxylate reductase (EC 1.1.1.95)	2.33	2.28	1.99	1.68E-04
AFUA_5G11610	Protein arginine N-methyltransferase	1.83	2.28	1.82	2.99E-02
AFUA_6G11680	Thiamine pyrophosphate enzyme, putative (EC 4.1.-.-)	2.47	2.28	2.39	5.77E-05
AFUA_4G08760	Phospho-2-dehydro-3-deoxyheptonate aldolase (EC 2.5.1.54)	2.94	2.29	3.14	1.80E-05
AFUA_1G09810	Translation machinery-associated protein 20	1.30	2.29	1.98	1.31E-04
AFUA_1G11790	Nucleoside hydrolase, putative (EC 3.2.2.-)	2.30	2.29	1.85	3.45E-03
AFUA_4G03660	Acid phosphatase, putative (EC 3.1.3.2)	1.73	2.31	2.00	1.27E-04
AFUA_5G09860	S-formylglutathione hydrolase (EC 3.1.2.12)	2.85	2.31	2.46	8.48E-06
AFUA_6G02450	40S ribosomal protein S30	4.38	2.31	6.33	5.94E-10
AFUA_6G06750	14-3-3 family protein	0.77	2.32	2.84	2.93E-06
AFUA_6G07720	Phosphoenolpyruvate carboxykinase AcuF (EC 4.1.1.49)	2.81	2.33	2.72	2.44E-07
AFUA_7G05160	Fumarylacetoacetate hydrolase family protein	2.01	2.33	1.56	1.16E-02
AFUA_8G01210	Enoyl-CoA hydratase/isomerase family protein (EC 4.2.1.17)	-0.38	2.33	2.05	5.72E-03
AFUA_7G05930	Metallopeptidase MepB (EC 3.4.24.-)	2.34	2.35	2.22	4.82E-07
AFUA_3G11280	Class V chitinase, putative (EC 3.2.1.14)	2.73	2.36	1.80	8.28E-08
AFUA_8G04090	Choline oxidase (CodA), putative (EC 1.1.3.17)	2.82	2.36	2.08	1.64E-08
AFUA_2G13860	Histone H4	2.56	2.36	2.68	1.57E-07
AFUA_5G03520	Uncharacterized protein	2.15	2.36	2.43	6.41E-07
AFUA_4G03830	Uncharacterized protein	-0.22	2.36	1.14	2.55E-05
AFUA_2G08970	Thiamine biosynthetic bifunctional enzyme, putative	2.41	2.37	2.22	1.51E-05
AFUA_7G02070	AIF-like mitochondrial oxidoreductase (Nfrl), putative	0.65	2.37	2.52	2.26E-08
AFUA_2G02950	Aldehyde reductase, putative (EC 1.1.1.-)	2.75	2.40	1.93	5.49E-06
AFUA_4G07150	Cytochrome c subunit, putative	3.45	2.41	2.78	1.10E-06
AFUA_6G14460	Haloalkanoic acid dehalogenase, putative (EC 3.8.1.-)	2.32	2.41	1.77	6.44E-05
AFUA_7G01000	Aldehyde dehydrogenase, putative (EC 1.2.1.3)	2.92	2.41	2.24	6.42E-09

AFUA_3G12100	Trehalose synthase (Ccg-9), putative (EC 2.4.1.-)	2.57	2.42	2.69	2.04E-05
AFUA_3G02240	Aromatic-L-amino-acid decarboxylase, putative (EC 4.1.1.28)	2.24	2.44	1.68	7.17E-05
AFUA_6G07710	Mitochondrial dicarboxylate carrier protein, putative	2.77	2.44	2.24	4.59E-03
AFUA_3G06760	60S ribosomal protein L37	2.46	2.44	5.25	9.40E-06
AFUA_7G02280	U5 snRNP complex subunit, putative	2.93	2.45	2.59	8.28E-03
AFUA_2G10660	Mannitol-1-phosphate 5-dehydrogenase (M1PDH) (MPD) (MPDH) (EC 1.1.1.17)	2.25	2.46	2.14	2.73E-08
AFUA_3G07790	Argininosuccinate lyase (EC 4.3.2.1)	2.64	2.47	2.26	6.17E-07
AFUA_5G09400	Carbonyl reductase, putative (EC 1.-.-.-)	2.11	2.49	2.20	2.04E-04
AFUA_5G13510	Cell cycle control protein (Cwf8), putative	3.40	2.49	2.22	1.58E-06
AFUA_2G17580	Scytalone dehydratase arp1 (EC 4.2.1.94) (Conidial pigment biosynthesis oxidase arp1)	0.58	2.49	2.69	2.24E-07
AFUA_2G00967	Cupin domain protein	2.11	2.50	0.92	4.17E-03
AFUA_4G12870	Methylmalonate-semialdehyde dehydrogenase, putative (EC 1.2.1.27)	2.43	2.51	2.47	1.72E-06
AFUA_7G04540	Short chain dehydrogenase/reductase family (EC 1.1.1.69)	0.87	2.53	2.98	2.26E-07
AFUA_5G11430	Quinone oxidoreductase, putative (EC 1.6.5.5)	0.95	2.55	2.51	1.45E-09
AFUA_3G12690	Uncharacterized protein	2.09	2.55	2.09	4.39E-10
AFUA_2G15430	Sorbitol/xylulose reductase Sou1-like, putative (EC 1.-.-.-)	1.75	2.56	2.72	6.09E-04
AFUA_2G03720	Peptidyl-prolyl cis-trans isomerase (PPIase) (EC 5.2.1.8)	2.37	2.56	2.42	3.59E-07
AFUA_5G07170	Nucleoside-diphosphate-sugar epimerase, putative	2.32	2.57	2.32	5.15E-03
AFUA_3G06880	Sorting nexin-3	2.81	2.58	3.46	3.16E-04
AFUA_2G17920	Uncharacterized protein	2.15	2.58	2.12	1.62E-06
AFUA_6G11620	Formyltetrahydrofolate deformylase, putative (EC 3.5.1.10)	2.40	2.58	3.40	1.24E-06
AFUA_2G02580	HAD superfamily hydrolase, putative	2.74	2.58	2.37	2.41E-05
AFUA_4G14470	Probable decarboxylase tpcK (EC 1.-.-.-) (Trypacidin synthesis protein K)	0.27	2.58	2.17	3.04E-03
AFUA_2G04520	Fe-containing alcohol dehydrogenase, putative (EC 1.1.1.-)	1.84	2.61	2.46	2.08E-05
AFUA_6G10900	UV-endonuclease UVE-1	1.70	2.63	2.73	1.88E-03
AFUA_2G07350	Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	2.50	2.64	2.93	1.11E-04
AFUA_6G03730	2-methylcitrate dehydratase, putative (EC 4.2.1.79)	2.67	2.66	3.38	1.01E-06
AFUA_5G01440	Allergen, putative (EC 1.-.-.-)	2.60	2.66	2.59	2.39E-07
AFUA_3G06070	Histone H1	2.55	2.66	3.86	1.66E-05
AFUA_4G07050	L-lactate dehydrogenase (EC 1.13.12.4)	2.73	2.66	2.52	2.06E-06
AFUA_6G02370	Actin-related protein 2/3 complex subunit 4	3.24	2.67	3.19	5.22E-06
AFUA_3G10310	Acetolactate synthase (EC 2.2.1.6)	1.11	2.68	2.31	4.10E-07
AFUA_3G05360	Histone H2A	1.50	2.69	3.49	3.10E-05
AFUA_4G10920	Uncharacterized protein	3.76	2.69	2.97	4.54E-05
AFUA_6G07770	Alanine aminotransferase, putative (EC 2.6.1.-)	2.58	2.69	2.13	3.86E-08
AFUA_1G14710	Beta-glucosidase, putative	1.63	2.70	3.52	4.34E-05
AFUA_7G02470	mRNA processing protein (Mss51), putative	1.86	2.70	3.53	1.59E-03
AFUA_4G00610	Aryl-alcohol dehydrogenase, putative (EC 1.1.-.-)	1.62	2.71	2.45	1.28E-03
AFUA_3G11690	Fructose-bisphosphate aldolase, class II (EC 4.1.2.13)	2.85	2.74	2.40	1.96E-10
AFUA_4G08410	Mannose-6-phosphate isomerase, class I (EC 5.3.1.8)	1.96	2.75	1.97	8.29E-06
AFUA_5G02530	Ribokinase (EC 2.7.1.15)	1.86	2.75	2.17	6.59E-05
AFUA_1G15450	Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	2.78	2.76	2.28	2.20E-10
AFUA_1G13280	Mannose-6-phosphate isomerase (EC 5.3.1.8) (Phosphohexomutase) (Phosphomannose isomerase) (PMI)	2.00	2.77	2.85	5.16E-06
AFUA_1G12920	Alpha-1,4 glucan phosphorylase (EC 2.4.1.1)	2.31	2.77	2.48	3.21E-07
AFUA_5G03330	HypA-like protein, putative	3.28	2.78	3.08	2.01E-05
AFUA_6G02860	Isocitrate lyase (EC 4.1.3.1)	2.62	2.79	2.62	3.59E-07
AFUA_4G08330	Aspartyl-tRNA synthetase, putative (EC 6.1.1.12)	2.81	2.80	3.60	1.77E-06
AFUA_5G01290	Zinc-binding oxidoreductase, putative (EC 1.-.-.-)	2.61	2.82	2.74	3.61E-04
AFUA_5G09680	Succinate dehydrogenase cytochrome b560 subunit (EC 1.3.5.1)	4.04	2.82	3.57	1.28E-05
AFUA_3G08380	Inorganic diphosphatase, putative (EC 3.6.1.1)	2.61	2.82	2.44	1.92E-10
AFUA_4G11730	Glycerol dehydrogenase (GldB), putative (EC 1.1.1.72)	1.29	2.83	3.70	5.34E-07

AFUA_6G12870	Iron-sulfur clusters transporter atm1, mitochondrial	4.78	2.84	4.54	4.29E-04
AFUA_4G04300	Alanine racemase family protein, putative	0.78	2.85	3.24	3.63E-04
AFUA_4G06140	Dipeptidyl peptidase 3 (EC 3.4.14.4) (Dipeptidyl aminopeptidase III) (Dipeptidyl peptidase III)	2.72	2.86	2.43	1.13E-06
AFUA_5G08290	Aldo-keto reductase, putative (EC 1.1.1.-)	2.60	2.88	2.20	4.21E-05
AFUA_6G13410	Pre-mRNA-splicing factor rse1	2.20	2.89	2.76	1.49E-09
AFUA_6G11430	Aldehyde dehydrogenase AldA, putative (EC 1.2.1.3)	2.11	2.91	2.59	4.34E-10
AFUA_2G17070	Defective in cullin neddylation protein	3.34	2.92	2.04	2.08E-03
AFUA_1G10150	Uncharacterized protein	3.69	2.92	3.83	2.18E-05
AFUA_3G02370	Short-chain dehydrogenase/reductase, putative (EC 1.-.-.-)	2.77	2.92	3.87	7.65E-07
AFUA_8G00430	Uncharacterized protein	4.49	2.93	1.05	9.95E-07
AFUA_4G14580	O-methyltransferase tpcA (EC 2.1.1.-) (Trypacidin synthesis protein A)	-0.14	2.95	3.06	6.77E-07
AFUA_1G06240	Riboflavin synthase, alpha subunit (EC 2.5.1.9)	2.97	2.97	2.47	1.10E-04
AFUA_8G04080	Betaine aldehyde dehydrogenase (BadH), putative (EC 1.2.1.8)	2.84	3.00	2.50	1.85E-06
AFUA_3G00590	Asp-hemolysin (Asp-HS)	0.00	3.01	3.24	7.48E-09
AFUA_6G09570	Uncharacterized protein	-0.28	3.02	1.48	3.50E-04
AFUA_4G14530	Glutathione S-transferase-like protein tpcF (EC 2.5.1.-) (Trypacidin synthesis protein E)	0.83	3.02	2.46	2.76E-06
AFUA_2G06040	Actin cortical patch component, putative	3.11	3.03	2.43	5.46E-09
AFUA_1G09750	Aldehyde reductase (AKR1), putative (EC 1.1.1.2)	1.78	3.04	3.54	1.03E-08
AFUA_3G08470	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	1.41	3.06	3.33	8.66E-07
AFUA_2G04320	NADH-dependent flavin oxidoreductase, putative (EC 1.-.-.-)	2.88	3.06	3.15	6.48E-11
AFUA_1G15610	Oxidoreductase, zinc-binding dehydrogenase family, putative (EC 1.3.1.-)	3.27	3.06	3.36	9.47E-09
AFUA_1G10780	Aminomethyltransferase (EC 2.1.2.10) (Glycine cleavage system T protein)	2.19	3.06	2.90	4.94E-05
AFUA_3G12950	FAD binding domain protein (EC 1.5.3.-)	2.95	3.08	1.33	2.34E-02
AFUA_7G02550	Probable D-xylulose reductase A (EC 1.1.1.9) (Xylitol dehydrogenase A)	2.11	3.08	3.00	2.95E-08
AFUA_6G00770	Probable arabinan endo-1,5-alpha-L-arabinosidase C (EC 3.2.1.99) (Endo-1,5-alpha-L-arabinanase C) (ABN C)	3.60	3.10	2.44	3.91E-04
AFUA_7G05015	Glyoxalase family protein	3.23	3.11	3.23	5.16E-06
AFUA_5G04330	Aminopeptidase (EC 3.4.11.-)	3.23	3.14	2.91	1.04E-09
AFUA_4G11540	Glycerol kinase, putative (EC 2.7.1.30)	1.52	3.18	2.94	5.99E-05
AFUA_1G13500	Transketolase (EC 2.2.1.1)	2.21	3.24	3.23	5.10E-09
AFUA_6G10260	Aldehyde reductase (AKR1), putative (EC 1.1.1.2)	3.26	3.25	2.95	3.81E-11
AFUA_5G08270	HAD superfamily hydrolase, putative	3.17	3.28	2.43	1.08E-07
AFUA_2G09030	Dipeptidyl-peptidase 5 (EC 3.4.14.-) (Dipeptidyl-peptidase V) (DPP V) (DppV)	2.08	3.28	1.89	1.63E-07
AFUA_4G05870	Oxidoreductase, short-chain dehydrogenase/reductase family	3.37	3.29	2.83	6.10E-06
AFUA_3G07430	Peptidyl-prolyl cis-trans isomerase (PPIase) (EC 5.2.1.8)	3.12	3.35	2.98	9.92E-09
AFUA_3G14270	Aldo-keto reductase (AKR), putative (EC 1.1.1.-)	3.85	3.37	3.39	1.19E-04
AFUA_3G11070	Pyruvate decarboxylase (EC 4.1.1.1)	1.95	3.42	3.43	9.50E-08
AFUA_3G09320	Serine hydroxymethyltransferase (EC 2.1.2.1)	2.34	3.63	2.46	2.26E-10
AFUA_4G07190	Ornithine carbamoyltransferase (EC 2.1.3.3)	2.47	3.65	3.07	6.27E-08
AFUA_2G09790	Glucose-6-phosphate isomerase (EC 5.3.1.9)	3.53	3.67	3.45	1.95E-08
AFUA_3G00280	Metallo-beta-lactamase domain protein, putative	2.26	3.78	3.75	5.18E-04
AFUA_8G01780	Nitrilase, putative	1.52	3.82	-0.30	4.70E-06
AFUA_5G08290	Aldo-keto reductase, putative (EC 1.1.1.-)	2.60	2.88	2.20	4.21E-05
AFUA_5G01290	Zinc-binding oxidoreductase, putative (EC 1.-.-.-)	2.61	2.82	2.74	3.61E-04
AFUA_3G08380	Inorganic diphosphatase, putative (EC 3.6.1.1)	2.61	2.82	2.44	1.92E-10
AFUA_6G02860	Isocitrate lyase (EC 4.1.3.1)	2.62	2.79	2.62	3.59E-07
AFUA_3G10970	Protein-tyrosine phosphatase 2 (EC 3.1.3.48)	2.63	1.09	2.48	3.79E-02
AFUA_1G03400	Protein transport protein sec23	2.63	0.89	2.28	5.12E-05
AFUA_5G02040	Extracellular lipase, putative (EC 3.1.1.3)	2.64	0.62	-0.46	1.14E-06
AFUA_3G07790	Argininosuccinate lyase (EC 4.3.2.1)	2.64	2.47	2.26	6.17E-07
AFUA_2G01920	Glutaminyl-tRNA synthetase (EC 6.1.1.18)	2.64	1.85	0.95	1.34E-05
AFUA_5G11660	Autophagy-related protein 18	2.64	2.18	2.57	1.54E-04
AFUA_3G06960	60S ribosomal protein L21, putative	2.65	0.47	3.65	3.25E-05

AFUA_2G05740	Rho GTPase ModA, putative	2.65	1.95	2.38	1.24E-03
AFUA_6G03730	2-methylcitrate dehydratase, putative (EC 4.2.1.79)	2.67	2.66	3.38	1.01E-06
AFUA_1G04130	FG-GAP repeat protein, putative	2.68	0.75	-0.63	2.94E-06
AFUA_6G13300	GTP-binding nuclear protein	2.70	2.02	2.31	8.90E-06
AFUA_7G00360	UDP-galactose 4-epimerase, putative (EC 5.1.3.-)	2.71	1.81	2.62	5.05E-08
AFUA_4G06140	Dipeptidyl peptidase 3 (EC 3.4.14.4) (Dipeptidyl aminopeptidase III) (Dipeptidyl peptidase III)	2.72	2.86	2.43	1.13E-06
AFUA_4G07050	L-lactate dehydrogenase (EC 1.13.12.4)	2.73	2.66	2.52	2.06E-06
AFUA_3G11280	Class V chitinase, putative (EC 3.2.1.14)	2.73	2.36	1.80	8.28E-08
AFUA_2G02580	HAD superfamily hydrolase, putative	2.74	2.58	2.37	2.41E-05
AFUA_2G02950	Aldehyde reductase, putative (EC 1.1.1.-)	2.75	2.40	1.93	5.49E-06
AFUA_3G06970	40S ribosomal protein S9	2.75	0.77	3.13	2.34E-07
AFUA_1G15860	Coatomer subunit delta, putative	2.76	0.78	2.06	8.40E-04
AFUA_3G02370	Short-chain dehydrogenase/reductase, putative (EC 1.-.-.-)	2.77	2.92	3.87	7.65E-07
AFUA_6G07710	Mitochondrial dicarboxylate carrier protein, putative	2.77	2.44	2.24	4.59E-03
AFUA_5G02300	Peroxidase, putative (EC 1.11.1.-)	2.77	1.19	1.51	2.77E-05
AFUA_3G08310	4-nitrophenylphosphatase (PNPPase) (EC 3.1.3.41)	2.77	2.04	1.39	1.34E-02
AFUA_1G15450	Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	2.78	2.76	2.28	2.20E-10
AFUA_4G10760	Steroid alpha reductase family protein	2.80	0.90	1.55	7.90E-06
AFUA_4G08330	Aspartyl-tRNA synthetase, putative (EC 6.1.1.12)	2.81	2.80	3.60	1.77E-06
AFUA_3G06880	Sorting nexin-3	2.81	2.58	3.46	3.16E-04
AFUA_2G00590	Glutathione S-transferase, putative (EC 2.5.1.18)	2.81	1.86	2.26	1.59E-03
AFUA_6G07720	Phosphoenolpyruvate carboxykinase AcuF (EC 4.1.1.49)	2.81	2.33	2.72	2.44E-07
AFUA_8G04090	Choline oxidase (CodA), putative (EC 1.1.3.17)	2.82	2.36	2.08	1.64E-08
AFUA_3G11350	ATPase get3 (EC 3.6.-.-) (Arsenical pump-driving ATPase) (Arsenite-stimulated ATPase) (Golgi to ER traffic protein 3) (Guided entry of tail-anchored proteins 3)	2.82	1.72	3.08	7.97E-03
AFUA_2G04590	Alcohol dehydrogenase, putative (EC 1.1.1.-)	2.84	1.45	1.67	1.37E-04
AFUA_8G04080	Betaine aldehyde dehydrogenase (BadH), putative (EC 1.2.1.8)	2.84	3.00	2.50	1.85E-06
AFUA_5G09860	S-formylglutathione hydrolase (EC 3.1.2.12)	2.85	2.31	2.46	8.48E-06
AFUA_3G11690	Fructose-bisphosphate aldolase, class II (EC 4.1.2.13)	2.85	2.74	2.40	1.96E-10
AFUA_5G02350	Hydrolase, carbon-nitrogen family, putative	2.87	1.32	2.15	1.12E-02
AFUA_2G04320	NADH-dependent flavin oxidoreductase, putative (EC 1.-.-.-)	2.88	3.06	3.15	6.48E-11
AFUA_2G04490	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	2.90	0.19	0.56	5.40E-03
AFUA_8G01670	Catalase-peroxidase (CP) (EC 1.11.1.21) (Catalase-2) (Peroxidase/catalase)	2.91	2.01	1.41	4.44E-09
AFUA_5G10560	Cytochrome c oxidase subunit V	2.91	1.58	2.70	1.01E-06
AFUA_5G03860	Alkaline phosphatase family protein (EC 3.1.-.-)	2.91	1.43	2.99	2.46E-03
AFUA_7G01000	Aldehyde dehydrogenase, putative (EC 1.2.1.3)	2.92	2.41	2.24	6.42E-09
AFUA_4G10240	Small nuclear ribonucleoprotein SmD3, putative	2.93	0.33	1.86	1.92E-03
AFUA_7G02280	U5 snRNP complex subunit, putative	2.93	2.45	2.59	8.28E-03
AFUA_4G08760	Phospho-2-dehydro-3-deoxyheptonate aldolase (EC 2.5.1.54)	2.94	2.29	3.14	1.80E-05
AFUA_3G12950	FAD binding domain protein (EC 1.5.3.-)	2.95	3.08	1.33	2.34E-02
AFUA_1G06240	Riboflavin synthase, alpha subunit (EC 2.5.1.9)	2.97	2.97	2.47	1.10E-04
AFUA_6G12950	Trehalose-6-phosphate synthase (EC 2.4.1.15) (UDP-glucose-glucosephosphate glucosyltransferase)	3.01	1.98	3.52	7.43E-05
AFUA_3G08430	Mitochondrial phosphate carrier protein, putative	3.04	1.57	2.38	5.50E-03
AFUA_2G13630	Aromatic aminotransferase Aro8, putative (EC 2.6.1.-)	3.08	1.96	1.61	7.87E-04
AFUA_2G06040	Actin cortical patch component, putative	3.11	3.03	2.43	5.46E-09
AFUA_1G07010	Phosphatidate cytidylyltransferase (EC 2.7.7.41)	3.12	0.81	2.44	1.15E-02
AFUA_3G07430	Peptidyl-prolyl cis-trans isomerase (PPIase) (EC 5.2.1.8)	3.12	3.35	2.98	9.92E-09
AFUA_2G13295	Aminotransferase family protein (LolT), putative	3.15	1.64	1.91	1.90E-03
AFUA_5G08270	HAD superfamily hydrolase, putative	3.17	3.28	2.43	1.08E-07
AFUA_4G07590	CaaX prenyl protease Ste24 (EC 3.4.24.84)	3.20	1.22	2.67	7.52E-04
AFUA_7G05015	Glyoxalase family protein	3.23	3.11	3.23	5.16E-06
AFUA_5G04330	Aminopeptidase (EC 3.4.11.-)	3.23	3.14	2.91	1.04E-09
AFUA_6G02370	Actin-related protein 2/3 complex subunit 4	3.24	2.67	3.19	5.22E-06

AFUA_6G10260	Aldehyde reductase (AKR1), putative (EC 1.1.1.2)	3.26	3.25	2.95	3.81E-11
AFUA_1G15610	Oxidoreductase, zinc-binding dehydrogenase family, putative (EC 1.3.1.-)	3.27	3.06	3.36	9.47E-09
AFUA_5G03330	HypA-like protein, putative	3.28	2.78	3.08	2.01E-05
AFUA_3G12510	Vesicular fusion ATPase, putative	3.29	1.34	1.38	5.57E-05
AFUA_2G17070	Defective in cullin neddylation protein	3.34	2.92	2.04	2.08E-03
AFUA_1G02570	Aspartyl-tRNA synthetase, cytoplasmic (EC 6.1.1.12)	3.37	1.41	2.82	2.34E-05
AFUA_4G05870	Oxidoreductase, short-chain dehydrogenase/reductase family	3.37	3.29	2.83	6.10E-06
AFUA_5G13510	Cell cycle control protein (Cwf8), putative	3.40	2.49	2.22	1.58E-06
AFUA_3G00680	Amine oxidase (EC 1.4.3.-)	3.44	1.35	1.88	1.22E-03
AFUA_1G09660	Mitochondrial 2-oxodicarboxylate carrier protein, putative	3.45	1.64	2.72	2.28E-05
AFUA_4G07150	Cytochrome c subunit, putative	3.45	2.41	2.78	1.10E-06
AFUA_2G14850	Enoyl-CoA hydratase/isomerase family protein (EC 4.2.-.-)	3.46	2.02	2.40	1.40E-04
AFUA_7G04180	Amine oxidase (EC 1.4.3.-)	3.46	2.15	1.42	5.87E-08
AFUA_6G14100	Mitochondrial carnitine:acyl carnitine carrier, putative	3.46	2.04	2.78	2.40E-04
AFUA_1G04720	C-8 sterol isomerase (Erg-1), putative	3.48	1.57	1.64	3.80E-04
AFUA_6G13440	Choline sulfatase, putative (EC 3.1.6.6)	3.50	1.09	2.07	9.70E-04
AFUA_2G09790	Glucose-6-phosphate isomerase (EC 5.3.1.9)	3.53	3.67	3.45	1.95E-08
AFUA_8G00620	Dimethylallyl tryptophan synthase, putative (EC 2.5.1.-)	3.57	0.95	0.59	4.77E-03
AFUA_6G00770	Probable arabinan endo-1,5-alpha-L-arabinosidase C (EC 3.2.1.99) (Endo-1,5-alpha-L-arabinanase C) (ABN C)	3.60	3.10	2.44	3.91E-04
AFUA_1G06700	Metacaspase-1A (EC 3.4.22.-)	3.64	2.10	2.07	1.94E-03
AFUA_1G10150	Uncharacterized protein	3.69	2.92	3.83	2.18E-05
AFUA_3G14690	Aminotransferase, putative (EC 2.-.-.-)	3.71	1.68	2.25	1.24E-02
AFUA_4G10920	Uncharacterized protein	3.76	2.69	2.97	4.54E-05
AFUA_1G12250	Mitochondrial hypoxia responsive domain protein	3.82	1.09	1.94	2.25E-02
AFUA_3G14270	Aldo-keto reductase (AKR), putative (EC 1.1.1.-)	3.85	3.37	3.39	1.19E-04
AFUA_5G09680	Succinate dehydrogenase cytochrome b560 subunit (EC 1.3.5.1)	4.04	2.82	3.57	1.28E-05
AFUA_4G13750	Neutral protease 2 homolog AFUA_4G13750 (EC 3.4.24.39) (Deuterolysin AFUA_4G13750)	4.36	2.08	0.81	5.27E-05
AFUA_6G02450	40S ribosomal protein S30	4.38	2.31	6.33	5.94E-10
AFUA_8G00430	Uncharacterized protein	4.49	2.93	1.05	9.95E-07
AFUA_5G02640	O-methyltransferase, putative (EC 2.1.1.-)	4.70	1.45	0.38	1.42E-07
AFUA_6G12870	Iron-sulfur clusters transporter atm1, mitochondrial	4.78	2.84	4.54	4.29E-04

Differentially expressed proteins in IF1SW-F4

Gene	Protein names	Relative protein abundance*			P-value
		CEA10	ISSFT-021	IF1SW-F4	
AFUA_2G14330	Uncharacterized protein	-3.51	-5.48	-6.27	2.39E-06
AFUA_4G09600	GPI anchored protein, putative	-3.43	-6.26	-5.82	1.33E-07
AFUA_7G01340	RPEL repeat protein	-3.36	-5.15	-5.55	4.07E-10
AFUA_7G04930	Alkaline serine protease (PR1)/allergen F18-like (EC 3.4.21.-)	-3.63	-5.32	-5.53	1.14E-06
AFUA_4G08960	GPI anchored cell wall protein, putative	-3.69	-5.18	-5.37	8.40E-05
AFUA_1G13550	Uncharacterized protein	-3.59	-6.12	-5.23	5.82E-03
AFUA_2G15810	Uncharacterized protein	-2.96	-5.32	-5.18	3.13E-03
AFUA_5G13100	Uncharacterized protein	-3.50	-5.95	-5.15	9.50E-09
AFUA_6G12450	Chaperone/heat shock protein Hsp12, putative	-4.05	-5.81	-5.12	5.46E-05
AFUA_3G13850	LRP16 family protein	-2.27	-4.37	-4.88	1.16E-03
AFUA_7G04520	Uncharacterized protein	-3.31	-5.06	-4.87	1.19E-05
AFUA_3G05570	Spindle poison sensitivity protein Scp3, putative	-2.94	-5.28	-4.83	4.20E-04
AFUA_5G14210	Glucose repressible protein Grg1, putative	-3.21	-7.14	-4.80	1.87E-07
AFUA_1G12070	Glycine cleavage system H protein	-3.95	-4.38	-4.79	8.05E-05
AFUA_4G00860	Cell surface protein, putative	-3.54	-5.64	-4.62	1.37E-07
AFUA_6G09740	Thioredoxin reductase gliT (EC 1.8.1.-) (Gliotoxin biosynthesis protein T)	-3.30	-3.75	-4.59	9.90E-08
AFUA_4G14205	Uncharacterized protein	-3.49	-6.22	-4.43	9.36E-06
AFUA_1G17370	Heat shock protein Awh11, putative	-2.95	-5.23	-4.26	4.25E-07
AFUA_6G04390	E3 ubiquitin-protein ligase bre1 (EC 2.3.2.27) (RING-type E3 ubiquitin transferase bre1)	-3.76	-4.23	-4.24	8.60E-05
AFUA_3G14540	Heat shock protein Hsp30/Hsp42, putative	-3.73	-4.52	-4.20	3.63E-08
AFUA_3G05430	ATP-dependent RNA helicase dhh1 (EC 3.6.4.13)	-2.86	-5.81	-4.16	7.98E-04
AFUA_2G05635	Uncharacterized protein	-2.73	-4.18	-4.06	4.08E-03
AFUA_3G10410	Conserved serine-rich protein	-2.82	-4.81	-3.94	3.68E-05
AFUA_1G03580	Uncharacterized protein	-2.87	-3.41	-3.86	1.07E-03
AFUA_2G10020	Uncharacterized protein	-3.67	-5.69	-3.86	3.03E-07
AFUA_6G03210	Conidiation-specific protein (Con-10), putative	-2.13	-4.73	-3.82	3.46E-04
AFUA_3G12790	Conserved glutamic acid-rich protein	-3.32	-3.53	-3.82	1.63E-04
AFUA_2G03390	Histone deacetylase (EC 3.5.1.98)	-4.27	-5.76	-3.78	1.15E-03
AFUA_6G13500	Uncharacterized protein	-3.21	-5.61	-3.77	7.19E-07
AFUA_1G13560	Uncharacterized protein	-3.23	-5.10	-3.77	1.79E-06
AFUA_4G12490	Guanine nucleotide exchange factor Vps9, putative	-2.86	-4.52	-3.77	1.66E-04
AFUA_5G12590	Solid-state culture expressed protein (Aos23), putative	-3.38	-2.76	-3.75	2.32E-03
AFUA_1G03710	C2H2 finger domain protein, putative	-4.02	-4.17	-3.69	7.80E-03
AFUA_2G05540	Pre-mRNA-splicing factor cef1	-2.16	-3.57	-3.66	5.22E-03
AFUA_8G05650	Uncharacterized protein	-2.35	-3.36	-3.61	2.53E-03
AFUA_4G06820	Protein ecm33	-3.26	-4.32	-3.59	5.49E-10
AFUA_6G10700	Chaperonin, putative	-3.60	-4.94	-3.42	8.19E-05
AFUA_3G14260	Mismatched base pair and cruciform DNA recognition protein, putative	-3.27	-5.16	-3.37	2.05E-06
AFUA_1G10550	CBF/NF-Y family transcription factor, putative	-4.29	-5.75	-3.37	3.43E-06
AFUA_4G10150	Alpha-glucosidase AgdA, putative (EC 3.2.1.20)	-2.96	-3.13	-3.34	5.33E-05
AFUA_2G14490	Endoglucanase, putative (EC 3.2.1.-)	-2.17	-3.83	-3.33	1.17E-04
AFUA_4G09750	50S ribosomal protein L12	-3.36	-4.10	-3.30	9.15E-05
AFUA_3G09030	Regulatory protein SUAPRGA1	-2.83	-3.80	-3.30	3.56E-03
AFUA_3G10610	Uncharacterized protein	-3.33	-3.48	-3.28	7.75E-04
AFUA_1G01950	Uncharacterized protein	-3.62	-4.06	-3.24	4.23E-04
AFUA_3G07870	Extracellular serine-rich protein, putative	-1.73	-2.89	-3.23	1.27E-06
AFUA_6G12000	Uncharacterized protein	-3.87	-5.08	-3.22	6.46E-06
AFUA_7G04920	Uncharacterized protein	-2.28	-3.48	-3.20	3.66E-02
AFUA_1G15010	AMP binding domain protein, putative	-4.47	-3.65	-3.15	2.42E-03
AFUA_2G03010	Cytochrome c subunit Vb, putative	-2.09	-3.83	-3.13	8.44E-07
AFUA_3G13430	Uncharacterized protein	-2.63	-2.56	-3.12	2.45E-02
AFUA_2G15070	26S proteasome regulatory subunit S5A	-2.59	-4.07	-3.12	8.53E-06
AFUA_1G11640	Cytosolic Cu/Zn superoxide dismutase, putative	-3.95	-2.30	-3.07	3.00E-06
AFUA_3G10190	Peroxisomal membrane anchor protein (Pex14), putative	-2.34	-2.48	-3.06	2.78E-03
AFUA_8G01980	Uncharacterized protein	-3.27	-4.01	-3.02	3.84E-06

AFUA_5G12180	Ran-specific GTPase-activating protein 1, putative	-3.75	-3.12	-3.01	9.69E-08
AFUA_2G13040	GrpE protein homolog	-3.48	-4.15	-3.01	2.23E-08
AFUA_6G09120	Uncharacterized protein	-3.52	-4.91	-2.97	1.10E-05
AFUA_4G11390	Ubiquinol-cytochrome c reductase complex 17 kd protein	-1.72	-2.64	-2.94	3.97E-08
AFUA_6G08660	M protein repeat protein	-3.12	-3.33	-2.87	4.62E-05
AFUA_8G04310	Uncharacterized protein	-2.55	-3.87	-2.86	2.62E-03
AFUA_4G04318	Copper resistance protein Crd2, putative	-1.49	-2.35	-2.86	1.30E-07
AFUA_2G03790	Oxysterol binding protein (Osh7), putative	-3.18	-4.47	-2.85	8.13E-03
AFUA_1G13670	Uncharacterized protein	-3.36	-3.10	-2.85	4.02E-08
AFUA_3G09990	Uncharacterized protein	-2.59	-3.39	-2.84	4.40E-04
AFUA_2G13380	GATA transcription factor (AreB), putative	-2.97	-2.48	-2.78	4.61E-03
AFUA_1G13530	Uncharacterized protein	-4.30	-3.82	-2.75	3.15E-04
AFUA_6G12290	PH domain protein	-2.32	-2.92	-2.73	1.83E-04
AFUA_2G01540	Uncharacterized protein	-3.19	-3.99	-2.73	1.21E-05
AFUA_3G13240	Aldose 1-epimerase, putative (EC 5.1.3.3)	-1.59	-1.36	-2.73	2.77E-06
AFUA_2G07600	SRP receptor beta subunit (Srp102), putative	-2.01	-4.19	-2.72	3.98E-03
AFUA_7G02020	Uncharacterized protein	-2.67	-3.38	-2.69	3.83E-05
AFUA_5G09380	Uncharacterized protein	-2.31	-3.71	-2.68	1.67E-03
AFUA_6G06670	Uncharacterized protein	-2.65	-2.85	-2.68	5.35E-05
AFUA_4G09580	Major allergen Asp f 2 (Allergen Asp f II) (allergen Asp f 2)	-2.12	-2.88	-2.68	1.20E-03
AFUA_4G03780	Probable rhamnogalacturonate lyase A (EC 4.2.2.23)	-1.78	-2.88	-2.67	2.33E-02
AFUA_3G13750	Uncharacterized protein	-1.21	-0.92	-2.66	1.02E-03
AFUA_7G01200	Aspergillopepsin, putaitve (EC 3.4.23.-)	-3.45	-4.45	-2.66	8.43E-07
AFUA_4G10280	Phosphotransmitter protein Ypd1, putative	-3.40	-3.09	-2.65	1.54E-06
AFUA_6G13670	Reticulon-like protein	-3.69	-5.29	-2.62	3.96E-08
AFUA_7G05270	COMPASS complex subunit Sdc1, putative	-3.87	-3.18	-2.60	3.89E-03
AFUA_2G10810	Nuclear protein export protein Yrb2, putative	-3.67	-3.85	-2.59	3.31E-02
AFUA_8G04270	AAA family ATPase, putative	-2.48	-3.22	-2.58	4.41E-04
AFUA_6G04690	Uncharacterized protein	-2.96	-2.89	-2.57	8.64E-03
AFUA_8G04920	LEA domain protein	-2.00	-2.70	-2.54	4.55E-04
AFUA_7G04030	Uncharacterized protein	-3.36	-4.62	-2.54	1.06E-04
AFUA_4G03322	WW domain protein	-0.34	-2.27	-2.52	5.11E-03
AFUA_3G11550	LEA domain protein	-3.34	-2.74	-2.50	2.51E-06
AFUA_4G09740	T-complex protein 1, theta subunit, putative	-2.71	-4.22	-2.49	2.19E-07
AFUA_7G00580	Uncharacterized protein	-2.04	-1.96	-2.49	3.96E-07
AFUA_5G07240	SAP domain protein	-1.84	-2.11	-2.42	1.82E-03
AFUA_1G09250	CUE domain protein, putative	-2.03	-3.06	-2.38	4.12E-02
AFUA_3G09870	Uncharacterized protein	-1.85	-2.52	-2.36	9.93E-03
AFUA_2G11740	Lon protease homolog, mitochondrial (EC 3.4.21.53)	-2.25	-3.40	-2.33	9.12E-05
AFUA_4G10020	Clathrin light chain	-3.70	-3.30	-2.33	1.95E-06
AFUA_7G02340	L-PSP endoribonuclease family protein (Hmf1), putative	-3.47	-2.50	-2.31	2.66E-06
AFUA_7G05470	Electron transfer flavoprotein alpha subunit, putative	-2.00	-1.96	-2.30	2.77E-03
AFUA_4G01030	Uncharacterized protein	-2.57	-1.27	-2.29	2.17E-05
AFUA_3G02340	CBF/NF-Y family transcription factor, putative	-2.41	-3.75	-2.28	4.63E-04
AFUA_5G02420	Splicing factor 3a subunit 3, putative	-2.70	-4.03	-2.28	1.60E-02
AFUA_7G05610	Glucanase, putative (EC 3.2.1.-)	-1.47	-2.53	-2.26	1.18E-04
AFUA_1G04470	Mitochondrial import inner membrane translocase subunit tim10	-1.92	-3.78	-2.26	1.15E-03
AFUA_5G02750	Cytochrome c oxidase subunit Va, putative	-1.79	-3.20	-2.26	3.37E-07
AFUA_1G15780	3-isopropylmalate dehydrogenase (EC 1.1.1.85)	-1.67	-2.72	-2.26	5.25E-09
AFUA_1G14280	C6 finger domain protein, putative	-1.03	-0.91	-2.25	6.39E-03
AFUA_8G07060	Hydrophobin, putative	-2.23	-1.93	-2.21	1.08E-07
AFUA_6G02260	Uncharacterized protein	-3.21	-3.41	-2.20	1.03E-05
AFUA_2G13590	Uncharacterized protein	-1.88	-1.80	-2.20	1.78E-07
AFUA_1G01812	MFS transporter, putative	-4.17	-2.93	-2.20	4.25E-03
AFUA_8G00550	Methyltransferase psoC (EC 2.1.1.-) (Pseurotin biosynthesis protein C)	-2.78	-2.15	-2.19	2.53E-08
AFUA_2G17620	Cellobiose dehydrogenase	-1.08	-1.36	-2.19	1.66E-03
AFUA_2G08640	Uncharacterized protein	-3.54	-3.32	-2.18	4.06E-04
AFUA_5G03780	L-PSP endoribonuclease family protein Brt1, putative	-0.80	-0.81	-2.17	1.59E-02
AFUA_7G04210	Tropomyosin, putative	-2.91	-3.60	-2.17	6.38E-06

AFUA_2G02320	Hsp70 chaperone (BiP), putative	-2.06	-3.07	-2.16	3.26E-05
AFUA_7G05450	Secreted beta-glucosidase sun1 (EC 3.2.1.-)	-0.61	-1.87	-2.15	4.13E-02
AFUA_3G10340	Rho GTPase Rho 2, putative	-0.96	-2.51	-2.14	2.12E-03
AFUA_2G11840	Transcriptional corepressor Cyc8, putative	-3.28	-3.54	-2.12	4.54E-06
AFUA_6G08320	Uncharacterized protein	-2.49	-3.08	-2.11	1.21E-07
AFUA_6G08360	Thiamine thiazole synthase (Thiazole biosynthetic enzyme)	-1.59	-0.65	-2.09	9.43E-06
AFUA_2G10320	SH3 domain protein	-2.98	-2.27	-2.08	2.01E-03
AFUA_1G08880	Iron/copper transporter Atx1, putative	-3.41	-3.69	-2.06	9.37E-11
AFUA_2G07950	ATP dependent RNA helicase, putative	-2.84	-2.54	-2.06	4.88E-04
AFUA_2G11860	Uncharacterized protein	-2.13	-2.64	-2.05	1.13E-06
AFUA_1G06910	Probable arabinogalactan endo-beta-1,4-galactanase A (EC 3.2.1.89) (Endo-1,4-beta-galactanase A) (Galactanase A)	-0.43	-1.53	-2.04	9.05E-06
AFUA_2G10100	60S acidic ribosomal protein P2 (AfP2) (allergen Asp f 8)	-3.24	-2.65	-2.04	1.16E-06
AFUA_1G12590	RNA-binding La domain protein	-2.34	-2.41	-2.04	2.24E-03
AFUA_4G06960	UBX domain protein, putative	0.16	-0.99	-2.03	8.96E-03
AFUA_2G17470	L-PSP endoribonuclease family protein, putative	0.01	-2.24	-2.03	2.01E-03
AFUA_3G10920	Telomere and ribosome associated protein Stm1, putative	-3.30	-4.13	-2.02	1.67E-07
AFUA_4G02805	Asp hemolysin-like protein	-3.31	-4.42	-2.02	7.88E-05
AFUA_6G14470	Uncharacterized protein	-0.31	-1.05	-1.98	2.67E-06
AFUA_5G10240	Uncharacterized protein	-2.14	-2.48	-1.96	4.17E-04
AFUA_3G00840	FAD-dependent oxygenase, putative	-1.72	-1.31	-1.95	3.99E-09
AFUA_1G06830	60S acidic ribosomal protein P1 (AfP1)	-3.67	-3.62	-1.95	2.73E-05
AFUA_4G06670	Allergen Asp f 7 (allergen Asp f 7)	-3.09	-1.97	-1.95	2.08E-03
AFUA_1G16840	Translationally-controlled tumor protein homolog (TCTP)	-3.18	-2.43	-1.94	1.32E-06
AFUA_4G03420	L-PSP endoribonuclease family protein, putative	-2.35	-2.93	-1.93	1.30E-03
AFUA_6G04610	DNA-directed RNA polymerase I and III 14 kDa polypeptide	-2.32	-2.56	-1.91	1.48E-02
AFUA_5G07890	SsDNA binding protein, putative	-1.01	-1.33	-1.91	1.19E-06
AFUA_3G00880	UPF0619 GPI-anchored membrane protein AFUA_3G00880	-1.02	-1.53	-1.89	6.79E-04
AFUA_8G04570	PWWP domain protein	-2.20	-2.26	-1.89	4.06E-07
AFUA_6G05350	Probable aspartic-type endopeptidase opsB (EC 3.4.23.-)	-3.15	-3.64	-1.88	7.65E-06
AFUA_1G11870	Mitochondrial processing peptidase alpha subunit, putative (EC 3.4.24.64)	-1.96	-2.37	-1.88	1.36E-02
AFUA_6G02830	Uncharacterized protein	-4.08	-2.59	-1.87	6.97E-04
AFUA_1G09030	Uncharacterized protein	-2.72	-3.81	-1.86	4.70E-07
AFUA_7G02570	NIMA-interacting protein TinC	-2.34	-2.21	-1.85	1.13E-03
AFUA_4G03240	Cell wall serine-threonine-rich galactomannoprotein Mp1	-1.32	-1.48	-1.83	8.46E-08
AFUA_2G15840	HET-C domain protein HetC	-2.38	-1.65	-1.82	8.39E-03
AFUA_2G02020	Formamidase FmdS (EC 3.5.1.49)	-0.41	-1.24	-1.81	1.36E-07
AFUA_2G08540	DNA-directed RNA polymerase subunit	-2.19	-2.84	-1.80	1.46E-05
AFUA_5G10990	Uncharacterized protein	-1.13	-0.61	-1.79	7.89E-06
AFUA_2G16020	T-complex protein 1, alpha subunit, putative	-1.91	-3.60	-1.79	1.56E-02
AFUA_4G08030	MICOS complex subunit mic60 (Mitofilin)	-1.95	-2.68	-1.76	2.21E-02
AFUA_1G12390	G2/M phase checkpoint control protein Sum2, putative	-2.58	-3.14	-1.76	3.72E-05
AFUA_5G00870	Uncharacterized protein	-0.50	-0.63	-1.75	4.24E-03
AFUA_1G11530	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase (EC 4.1.2.20)	-0.99	-1.54	-1.75	2.49E-05
AFUA_2G08670	Acetyl-CoA carboxylase	-2.01	-2.80	-1.74	3.47E-02
AFUA_7G01010	Alcohol dehydrogenase, putative (EC 1.1.1.1)	-2.36	-1.74	-1.73	3.63E-08
AFUA_6G13120	Filament-forming protein (Tpr/p270), putative	-2.42	-2.55	-1.72	5.43E-07
AFUA_3G02200	Uncharacterized protein	-1.15	-0.68	-1.72	2.08E-02
AFUA_6G08720	S-methyl-5'-thioadenosine phosphorylase (EC 2.4.2.28) (5'-methylthioadenosine phosphorylase) (MTA phosphorylase) (MTAP) (MTAPase)	-0.64	-1.09	-1.72	7.37E-06
AFUA_2G10030	Actin cytoskeleton protein (VIP1), putative	-2.32	-2.87	-1.72	1.19E-09
AFUA_7G03970	Uncharacterized protein	-0.01	-0.79	-1.72	9.41E-06
AFUA_6G10930	Extracellular protein, putative (EC 2.7.7.6)	-2.39	-0.17	-1.71	1.38E-07

AFUA_5G06240	Alcohol dehydrogenase, putative (EC 1.1.1.1)	-1.44	-1.06	-1.71	1.25E-08
AFUA_2G17540	Multicopper oxidase abr1 (EC 1.-.-.-) (Conidial pigment biosynthesis oxidase abr1)	-1.23	-2.30	-1.71	2.97E-04
AFUA_2G13820	SAP domain protein, putative	-2.28	-1.54	-1.70	9.89E-07
AFUA_2G11060	Acyl CoA binding protein family	-1.87	-1.01	-1.69	2.34E-07
AFUA_5G07080	Beta-glucosidase, putative (EC 3.2.1.21)	-1.76	-1.77	-1.67	3.56E-05
AFUA_2G05340	1,3-beta-glucanosyltransferase gel4 (EC 2.4.1.-) (Glucan elongating glucanosyltransferase 4)	-0.60	-0.83	-1.66	2.02E-04
AFUA_1G15960	Glutathione oxidoreductase Glr1, putative (EC 1.8.1.7)	-0.75	-1.13	-1.66	6.15E-07
AFUA_5G09600	2-nitropropane dioxygenase family oxidoreductase, putative (EC 1.3.1.9)	0.41	-1.54	-1.66	1.28E-03
AFUA_4G09280	Uncharacterized protein	-2.55	-2.57	-1.65	1.51E-06
AFUA_5G14740	Fucose-specific lectin FleA	-2.31	-0.76	-1.64	2.23E-06
AFUA_4G03595	Uncharacterized protein	-0.08	-0.25	-1.63	4.12E-03
AFUA_3G08230	MRS7 family protein	-2.97	-3.12	-1.63	4.35E-04
AFUA_5G10550	ATP synthase subunit beta (EC 3.6.3.14)	-2.85	-3.44	-1.63	9.29E-07
AFUA_2G09650	Aspartate transaminase, putative (EC 2.6.1.1)	-0.71	-0.75	-1.63	5.97E-05
AFUA_5G11390	APSES transcription factor, putative	-3.22	-3.30	-1.63	3.38E-04
AFUA_3G14170	MFS glucose transporter, putative	-0.94	-0.68	-1.63	1.90E-02
AFUA_3G11740	RNAPII degradation factor Def1, putative	-1.40	-2.40	-1.63	1.23E-02
AFUA_3G01130	Cell wall protein, putative	0.30	-0.77	-1.62	6.00E-06
AFUA_2G14670	Eukaryotic translation initiation factor 3 subunit D (eIF3d)	-1.59	-2.17	-1.62	2.36E-02
AFUA_2G16830	Endonuclease/exonuclease/phosphatase family protein	-0.58	-1.01	-1.62	2.19E-06
AFUA_2G13310	RING finger domain protein, putative	0.82	-2.49	-1.61	4.25E-03
AFUA_3G00270	Probable glucan endo-1,3-beta-glucosidase eglC (EC 3.2.1.39) (Endo-1,3-beta-glucanase eglC) (Laminarinase eglC)	-1.39	0.35	-1.60	2.49E-06
AFUA_6G06345	6,7-dimethyl-8-ribityllumazine synthase (DMRL synthase) (EC 2.5.1.78)	-0.63	-1.37	-1.59	2.54E-04
AFUA_2G05400	Sugar hydrolase, putative	-1.59	-1.70	-1.59	7.69E-05
AFUA_7G06010	Uncharacterized protein	-2.81	-1.84	-1.57	3.36E-04
AFUA_1G05770	Probable beta-glucosidase A (EC 3.2.1.21) (Beta-D-glucoside glucohydrolase A) (Cellobiase A) (Gentiobiase A)	0.01	-0.87	-1.57	1.29E-06
AFUA_6G08990	Uncharacterized protein	-3.86	-1.45	-1.56	3.84E-04
AFUA_5G02090	UPF0047 domain protein	-0.84	-1.02	-1.54	3.49E-04
AFUA_4G11110	C2 domain protein	-2.90	-2.46	-1.53	7.18E-05
AFUA_1G09890	Uncharacterized protein	-1.49	-1.80	-1.53	3.17E-03
AFUA_5G12940	Arylsulfatase, putative (EC 3.1.6.1)	-1.29	-0.57	-1.52	5.40E-04
AFUA_2G15510	DUF866 domain protein	0.98	-1.44	-1.51	7.12E-07
AFUA_1G09280	Protein phosphatase 2C, putative (EC 3.1.3.16)	-2.66	-2.78	-1.51	2.23E-03
AFUA_2G01250	Serine peptidase, putative (EC 3.4.-.-)	-1.91	-1.15	-1.51	1.13E-04
AFUA_1G12190	Uncharacterized protein	-3.06	-1.41	-1.50	1.89E-05
AFUA_2G15710	Uncharacterized protein	-0.59	-0.78	-1.50	5.38E-06
AFUA_1G05520	Mandelate racemase/muconate lactonizing enzyme family protein (EC 4.2.1.6)	-0.94	-1.21	-1.50	1.37E-02
AFUA_1G16250	Probable alpha/beta-glucosidase agdC (EC 3.2.1.20) (EC 3.2.1.21)	-0.82	-0.89	-1.50	4.86E-05
AFUA_2G12190	Mitochondrial import inner membrane translocase subunit tim13	-2.36	-2.32	-1.49	2.80E-03
AFUA_4G08720	Lysophospholipase 1 (EC 3.1.1.5) (Phospholipase B 1)	-0.56	-1.13	-1.47	7.68E-06
AFUA_2G11340	Phosphatidylglycerol/phosphatidylinositol transfer protein (PG/PI-TP)	-0.10	-0.64	-1.47	1.83E-05
AFUA_2G04280	Asparaginase, putative (EC 3.5.1.1)	-0.97	-0.60	-1.46	4.14E-03
AFUA_8G06970	Beta-glucosidase (EC 3.2.1.21)	-2.14	-2.14	-1.45	1.78E-02
AFUA_1G03140	Glycosyl hydrolase, putative (EC 3.2.1.-)	-0.31	-1.31	-1.44	1.39E-06
AFUA_2G09490	Eukaryotic translation initiation factor subunit eIF-4F, putative	-2.07	-1.60	-1.44	4.05E-05
AFUA_7G03870	Actin cytoskeleton-regulatory complex protein pan1	-1.70	-1.04	-1.43	2.40E-03
AFUA_1G03600	Probable glucan 1,3-beta-glucosidase A (EC 3.2.1.58) (Exo-1,3-beta-glucanase 1) (Exo-1,3-beta-glucanase A)	-0.80	-0.45	-1.43	3.12E-05
AFUA_6G09950	Uncharacterized protein	0.00	-1.24	-1.43	1.03E-04

AFUA_2G00820	Extracellular GDSL-like lipase/acylhydrolase, putative	-0.17	-1.68	-1.43	4.80E-05
AFUA_3G01330	Class II aldolase/adducin domain protein	-0.67	-0.73	-1.43	1.39E-02
AFUA_2G09800	Uncharacterized protein	-2.51	-1.75	-1.43	9.85E-04
AFUA_5G02330	Ribonuclease mitogillin (EC 3.1.27.-) (Allergen Asp f I) (Allergen I/a) (IgE-binding ribotoxin) (Major allergen Asp f 1) (allergen Asp f 1)	0.03	-0.30	-1.43	9.59E-03
AFUA_3G00240	TPR domain protein	-2.23	1.00	-1.43	2.05E-05
AFUA_5G10490	Amidase, putative (EC 3.5.1.-)	1.83	-0.86	-1.42	3.08E-05
AFUA_3G02253	YjgH family protein	0.11	-0.91	-1.41	3.41E-03
AFUA_7G02170	Peptidyl-prolyl cis-trans isomerase-like 4 (PPIase) (EC 5.2.1.8) (Rotamase)	-2.38	-2.47	-1.41	4.54E-02
AFUA_7G05650	Glutamine-serine rich protein MS8, putative	-0.10	-1.39	-1.40	2.22E-02
AFUA_3G11920	Dihydrodipicolinate synthetase family protein (EC 4.2.1.-)	0.45	-0.73	-1.40	1.01E-04
AFUA_6G13420	Ubiquitin-like protein DskB, putative	-0.51	-0.72	-1.38	9.07E-03
AFUA_5G01260	Ankyrin repeat protein	-1.29	-0.27	-1.38	3.55E-07
AFUA_3G02270	Catalase B (EC 1.11.1.6) (Antigenic catalase) (Slow catalase)	-0.82	-0.13	-1.37	1.14E-06
AFUA_6G11390	1,3-beta-glucanosyltransferase gel2 (EC 2.4.1.-) (Glucan elongating glucanosyltransferase 2)	0.73	-0.39	-1.37	2.14E-05
AFUA_1G06580	High expression lethality protein Hel10, putative	1.24	-1.04	-1.37	4.99E-06
AFUA_6G07390	Isocitrate dehydrogenase LysB (EC 1.1.1.41)	-2.92	-1.46	-1.36	9.63E-11
AFUA_6G00510	NADP-dependent alcohol dehydrogenase (EC 1.1.1.1)	-1.16	-1.55	-1.36	3.35E-06
AFUA_4G11580	Superoxide dismutase (EC 1.15.1.1)	-0.57	-1.08	-1.35	2.30E-02
AFUA_8G05580	Acetyl-coA hydrolase Ach1, putative (EC 2.8.3.8)	-0.50	-1.11	-1.35	6.16E-07
AFUA_5G04250	Homocysteine synthase CysD (EC 2.5.1.49)	-1.59	-1.11	-1.34	1.11E-05
AFUA_1G06680	VHS domain protein	-2.21	-1.78	-1.34	5.91E-04
AFUA_6G14490	Probable beta-glucosidase H (EC 3.2.1.21) (Beta-D-glucoside glucohydrolase H) (Cellobiase H) (Gentiobiase H)	-0.21	-1.41	-1.33	4.68E-05
AFUA_2G01170	1,3-beta-glucanosyltransferase gel1 (EC 2.4.1.-) (Glucan elongating glucanosyltransferase 1)	-0.21	-0.27	-1.33	3.43E-06
AFUA_2G10600	NADH-ubiquinone oxidoreductase 299 kDa subunit, putative (EC 1.6.5.3)	-2.11	-2.28	-1.33	2.39E-07
AFUA_6G07280	ABC transporter (Adp1), putative	0.25	-0.30	-1.32	5.09E-05
AFUA_6G07120	Nuclear movement protein NudC	-2.62	-1.57	-1.32	5.54E-05
AFUA_1G16190	Probable glycosidase crf1 (EC 3.2.-.-) (Crh-like protein 1) (allergen Asp f 9)	0.97	-0.67	-1.32	5.97E-07
AFUA_3G01920	Acyl-CoA dehydrogenase, putative	1.11	-0.77	-1.31	7.17E-04
AFUA_5G08090	Pyridoxine biosynthesis protein	-1.03	-0.90	-1.31	5.36E-06
AFUA_2G11650	Uncharacterized protein	-0.63	-0.97	-1.30	2.51E-04
AFUA_2G08750	Mitochondrial inner membrane nuclease Nuc1, putative (EC 3.1.30.-)	0.48	-0.74	-1.30	4.24E-04
AFUA_5G04160	NTF2 and RRM domain protein	-2.21	-2.29	-1.29	2.29E-03
AFUA_4G04030	Histidinol-phosphatase	-0.15	-0.74	-1.29	2.69E-04
AFUA_6G03060	MFS monosaccharide transporter, putative	-1.37	-0.85	-1.28	1.54E-02
AFUA_2G00760	Probable pectate lyase A (EC 4.2.2.2)	-0.92	0.03	-1.28	6.43E-04
AFUA_2G04610	DUF967 domain protein	-0.85	-1.13	-1.27	9.14E-04
AFUA_2G05750	Agmatinase, putative (EC 3.5.3.11)	0.26	-0.34	-1.26	3.37E-02
AFUA_3G02220	DUF427 domain protein	-1.93	-0.73	-1.26	2.89E-03
AFUA_6G07940	Lactoylglutathione lyase (EC 4.4.1.5) (Glyoxalase I)	-0.74	-0.88	-1.25	1.00E-05
AFUA_5G01340	Lysophospholipase 2 (EC 3.1.1.5) (Phospholipase B 2)	-1.77	-1.14	-1.25	2.57E-06
AFUA_3G10940	Peroxisomal membrane protein receptor Pex19, putative	-1.50	-0.96	-1.25	1.21E-03
AFUA_1G05040	Protein mitochondrial targeting protein (Mas1), putative	-0.26	-0.97	-1.24	1.51E-05
AFUA_3G06830	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	-0.54	-0.73	-1.24	2.91E-04
AFUA_4G08690	Dihydrodipicolinate synthetase family protein (EC 4.2.1.-)	-0.44	-0.64	-1.23	1.13E-02
AFUA_2G08150	NEDD8-like protein (RubA), putative	-2.17	-1.48	-1.23	4.94E-06
AFUA_6G05030	Polysaccharide deacetylase family protein	-0.09	-1.21	-1.23	1.53E-03
AFUA_2G05720	Uncharacterized protein	-0.77	-0.63	-1.23	4.28E-03
AFUA_3G08880	Uncharacterized protein	-1.51	-1.94	-1.23	4.76E-05
AFUA_2G01940	Uncharacterized protein	1.20	0.01	-1.22	2.82E-02

AFUA_4G10770	Psi-producing oxygenase A (Fatty acid oxygenase ppoA) [Includes: Linoleate 8R-lipoxygenase (EC 1.13.11.60); 9,12-octadecadienoate 8-hydroperoxide 8R-isomerase (EC 5.4.4.5)]	1.55	-0.58	-1.21	2.94E-06
AFUA_4G07340	Ubiquitin fusion degradation protein UfdB, putative	-1.65	-1.55	-1.21	2.91E-02
AFUA_5G03990	Vacuolar aspartyl aminopeptidase Lap4, putative	0.66	-0.49	-1.20	1.16E-06
AFUA_3G10750	Probable acetate kinase (EC 2.7.2.1) (Acetokinase)	-0.67	-0.77	-1.20	2.23E-04
AFUA_5G08050	Probable Xaa-Pro aminopeptidase P (AMPP) (Aminopeptidase P) (EC 3.4.11.9) (Aminoacylproline aminopeptidase) (Prolidase)	-0.43	-0.75	-1.19	1.04E-04
AFUA_6G07855	Conserved threonine rich protein	-1.21	-0.42	-1.18	1.90E-02
AFUA_2G05240	Uncharacterized protein	0.05	-0.38	-1.18	5.24E-03
AFUA_2G15770	Cell wall biogenesis protein/glutathione transferase (Gto1), putative	-0.46	-1.14	-1.18	6.34E-05
AFUA_8G02850	Actin binding protein, putative	-1.40	-0.91	-1.18	4.94E-03
AFUA_5G11320	Thioredoxin	-2.63	-1.09	-1.17	8.05E-05
AFUA_1G08840	Guanylate kinase (EC 2.7.4.8)	-2.09	-1.18	-1.17	4.52E-06
AFUA_6G10880	Acyl-CoA dehydrogenase family protein (EC 1.3.99.-)	2.58	-0.22	-1.17	2.02E-08
AFUA_6G12480	NGG1 interacting factor Nif3, putative	-0.91	-0.72	-1.17	3.23E-04
AFUA_5G07500	Beta-lactamase family protein	-0.19	-0.58	-1.16	1.28E-05
AFUA_1G10110	TIM-barrel enzyme family protein	-1.10	-0.95	-1.16	2.05E-02
AFUA_7G06050	DNA damage-inducible protein 1	-1.67	-1.35	-1.16	7.27E-03
AFUA_3G10830	Glutathione S-transferase GstA (EC 2.5.1.18)	-0.94	-0.99	-1.15	5.01E-05
AFUA_4G03722	Uncharacterized protein	-0.62	-0.51	-1.15	4.07E-03
AFUA_1G03550	Mitochondrial dihydroxy acid dehydratase, putative (EC 4.2.1.-)	-0.26	-0.63	-1.14	8.65E-07
AFUA_1G09830	Hsc70 cochaperone (SGT), putative (EC 3.1.3.16)	-1.92	-1.61	-1.14	1.16E-04
AFUA_7G01070	Endo-1,4-beta-mannosidase	0.19	-0.86	-1.14	1.90E-06
AFUA_2G13290	GYF domain protein	-1.40	-1.66	-1.13	1.99E-02
AFUA_8G05570	Transcription factor (Sin3), putative	-1.43	-1.95	-1.13	5.73E-05
AFUA_5G04290	WW domain protein, putative	-0.47	-0.88	-1.13	6.13E-03
AFUA_3G13010	Zn-dependent hydrolase/oxidoreductase family protein, putative	2.08	-0.14	-1.12	3.42E-03
AFUA_8G06550	Carbonic anhydrase (EC 4.2.1.1) (Carbonate dehydratase)	-1.28	-1.24	-1.12	2.66E-04
AFUA_6G14540	Endo-1,3(4)-beta-glucanase, putative (EC 3.2.1.6)	-1.93	-0.56	-1.11	1.81E-02
AFUA_7G05840	Amidohydrolase family protein	0.09	-0.82	-1.10	1.56E-02
AFUA_6G08960	Proteasome subunit alpha type (EC 3.4.25.1)	-0.57	-0.77	-1.10	2.52E-05
AFUA_4G10010	Hsp90 co-chaperone Cdc37	-2.06	-1.27	-1.10	4.25E-04
AFUA_1G17250	Conidial hydrophobin RodB	0.59	-0.40	-1.09	1.14E-07
AFUA_6G07430	Pyruvate kinase (EC 2.7.1.40)	-0.96	-0.78	-1.09	1.34E-07
AFUA_3G11400	Vacuolar protease A (EC 3.4.23.25) (Aspartic endopeptidase pep2) (Aspartic protease pep2)	-0.37	-0.91	-1.09	4.03E-07
AFUA_8G04890	Uncharacterized protein	0.33	-0.55	-1.09	5.73E-03
AFUA_2G04920	Nuclear pore complex subunit Nup159, putative	0.54	-0.20	-1.08	2.21E-02
AFUA_2G00690	Glucoamylase (EC 3.2.1.3) (1,4-alpha-D-glucan glucohydrolase) (Glucan 1,4-alpha-glucosidase)	0.01	0.02	-1.08	1.56E-04
AFUA_6G09170	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)	-0.71	-0.99	-1.08	9.24E-03
AFUA_2G14520	Hydrolase, putative (EC 3.-.-.-)	-0.06	-0.45	-1.07	2.94E-06
AFUA_4G11920	Caffeine-induced death protein Cid2, putative	-0.06	-0.23	-1.07	9.82E-03
AFUA_1G07500	Uncharacterized protein	-0.84	-0.84	-1.07	6.76E-05
AFUA_6G06350	Proteasome endopeptidase complex (EC 3.4.25.1)	-0.35	-0.58	-1.07	1.11E-03
AFUA_5G13180	Agmatinase, putative (EC 3.5.3.11)	1.37	0.07	-1.07	2.51E-03
AFUA_6G08530	Sister chromatid separation protein (Src1), putative	-2.89	-0.99	-1.07	5.71E-03
AFUA_4G10050	Calmodulin	-0.90	-0.62	-1.06	7.68E-05
AFUA_5G08370	Polyubiquitin binding protein (Doa1/Ufd3), putative	-0.10	-0.62	-1.06	8.08E-03
AFUA_6G09980	Patched sphingolipid transporter (Ncr1), putative	0.13	-0.36	-1.06	9.10E-04
AFUA_2G16530	Cyanate hydratase (Cyanase) (EC 4.2.1.104) (Cyanate hydrolase) (Cyanate lyase)	-0.58	-0.98	-1.05	7.36E-06
AFUA_7G01510	SNARE domain protein	-2.85	-1.22	-1.04	5.25E-05
AFUA_1G17310	MFS lactose permease, putative	-2.01	-1.93	-1.04	3.30E-05
AFUA_2G02100	Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	-0.20	-0.51	-1.04	2.22E-07
AFUA_2G16720	DUF1237 domain protein	0.03	-0.46	-1.03	4.55E-03
AFUA_5G09130	Polysaccharide deacetylase family protein	0.57	-0.33	-1.02	7.43E-04

AFUA_1G02540	EF hand domain protein	-1.32	-1.29	-1.02	3.44E-06
AFUA_8G02770	Cytidine deaminase (EC 3.5.4.5) (Cytidine aminohydrolase)	-0.28	-0.78	-1.01	2.97E-02
AFUA_8G02510	Glycosyl hydrolase family 43 protein	0.97	-0.19	-1.00	1.44E-03
AFUA_3G14490	Ketol-acid reductoisomerase (EC 1.1.1.86)	0.66	0.35	1.01	2.80E-04
AFUA_2G14470	Oxidoreductase, FAD-binding, putative	1.08	1.94	1.01	1.21E-04
AFUA_1G09020	Nuclear pore complex protein (SonA), putative	2.02	1.20	1.02	2.25E-04
AFUA_6G00260	Phosphatidylserine decarboxylase family protein (EC 4.1.1.-)	1.42	1.79	1.02	3.32E-05
AFUA_4G07910	Mitochondrial presequence protease (EC 3.4.24.-)	1.18	1.01	1.04	7.78E-06
AFUA_1G08940	Pheromone-processing carboxypeptidase kex1 (EC 3.4.16.6) (Carboxypeptidase D)	1.35	1.13	1.04	3.43E-02
AFUA_5G06700	Serine/threonine-protein phosphatase (EC 3.1.3.16)	1.32	0.64	1.04	4.23E-02
AFUA_4G09140	L-ornithine aminotransferase Car2, putative (EC 2.6.1.13)	1.51	1.35	1.05	2.77E-07
AFUA_8G00430	Uncharacterized protein	4.49	2.93	1.05	9.95E-07
AFUA_3G08940	Proteasome regulatory particle subunit (RpnL), putative	-1.03	0.27	1.05	1.13E-02
AFUA_6G02750	Nascent polypeptide-associated complex subunit beta (NAC-beta) (Beta-NAC)	-0.07	-1.80	1.06	1.12E-03
AFUA_7G03940	Alpha,alpha-trehalose phosphate synthase subunit TPS3, putative (EC 2.4.1.15)	0.64	-0.30	1.07	2.67E-02
AFUA_2G04220	Homogentisate 1,2-dioxygenase (HmgA), putative (EC 1.13.11.5)	2.37	2.00	1.07	3.81E-02
AFUA_1G08760	Delta-aminolevulinic acid dehydratase (EC 4.2.1.24)	2.38	0.77	1.07	2.27E-02
AFUA_3G06890	RRM domain protein	2.15	1.66	1.07	3.71E-04
AFUA_8G02780	Vacuolar protein sorting/targeting protein 10 (Carboxypeptidase Y receptor) (CPY receptor) (Sortilin vps10) (Vacuolar carboxypeptidase sorting receptor vps10)	1.89	0.72	1.07	1.69E-03
AFUA_4G06000	50S ribosomal protein L3	1.32	-0.65	1.08	1.77E-02
AFUA_3G13030	T-complex protein 1 subunit gamma	0.30	-0.34	1.09	4.20E-02
AFUA_6G12300	RNP domain protein	1.69	0.90	1.09	8.91E-05
AFUA_7G04380	Alcohol dehydrogenase, putative (EC 1.1.1.1)	1.17	1.16	1.10	4.69E-03
AFUA_3G08660	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)	2.19	1.60	1.11	2.02E-07
AFUA_4G08710	Short chain dehydrogenase, putative (EC 1.-.-.-)	1.52	1.69	1.11	1.14E-08
AFUA_5G09930	Uncharacterized protein	0.27	0.28	1.11	3.94E-03
AFUA_4G11310	Fructose-1,6-bisphosphatase Fbp1, putative (EC 3.1.3.11)	1.27	0.19	1.11	3.52E-03
AFUA_8G04100	N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	1.23	0.94	1.12	2.79E-02
AFUA_1G13090	Multifunctional tryptophan biosynthesis protein	-0.34	-0.01	1.12	3.94E-02
AFUA_1G01680	Branched-chain amino acid aminotransferase (EC 2.6.1.42)	2.36	1.53	1.12	2.97E-04
AFUA_6G09070	3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7)	0.39	0.89	1.13	3.12E-04
AFUA_4G06930	Methionine aminopeptidase 2-3 (MAP 2-3) (MetAP 2-3) (EC 3.4.11.18) (Peptidase M)	-0.66	0.37	1.13	1.96E-02
AFUA_2G07620	Cystathionine beta-synthase (EC 4.2.1.22)	0.94	0.66	1.14	2.67E-03
AFUA_1G09960	Kynurenine formamidase (KFA) (KFase) (EC 3.5.1.9) (Arylformamidase) (N-formylkynurenine formamidase) (FKF)	2.37	1.73	1.14	9.20E-03
AFUA_4G03830	Uncharacterized protein	-0.22	2.36	1.14	2.55E-05
AFUA_6G14330	5-oxo-L-prolinase, putative (EC 3.5.2.9)	1.09	0.30	1.15	3.96E-02
AFUA_6G11310	Bifunctional pyrimidine biosynthesis protein (PyrABCN), putative (EC 6.3.5.5)	2.24	1.17	1.15	9.53E-06
AFUA_3G10130	Fructosyl amino acid oxidasesarcosine oxidase, putative	1.24	1.03	1.15	2.40E-02
AFUA_5G04170	Heat shock protein 90 (65 kDa IgE-binding protein) (Heat shock protein hsp1) (allergen Asp f 12)	-0.54	0.21	1.15	2.15E-04
AFUA_3G03060	Cell wall protein PhiA	1.68	0.08	1.16	3.16E-04
AFUA_1G14170	Probable beta-galactosidase A (EC 3.2.1.23) (Lactase A)	1.06	1.73	1.16	7.03E-03
AFUA_2G08370	Glutathione S-transferase, putative (EC 2.5.1.-)	2.35	0.51	1.16	5.25E-04
AFUA_7G05720	Acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	-0.94	-0.53	1.16	9.08E-03
AFUA_5G02370	Vacuolar ATP synthase catalytic subunit A, putative (EC 3.6.3.14)	0.14	0.54	1.17	1.85E-04
AFUA_3G06610	Proteasome regulatory particle subunit (RpnE), putative	1.09	-0.11	1.18	1.97E-04

AFUA_4G11080	Acetyl-coenzyme A synthetase (EC 6.2.1.1)	0.56	0.29	1.19	7.07E-03
AFUA_3G08160	ATP-dependent RNA helicase eIF4A (EC 3.6.4.13) (Eukaryotic initiation factor 4A) (eIF-4A) (Translation initiation factor 1)	0.71	-0.30	1.19	2.88E-04
AFUA_4G11500	3-ketosteroid reductase	0.87	-0.07	1.19	4.89E-02
AFUA_4G09840	Kynureninase 2 (EC 3.7.1.3) (Biosynthesis of nicotinic acid protein 5-2) (L-kynurenine hydrolase 2)	1.89	1.03	1.19	1.40E-06
AFUA_2G10170	Uncharacterized protein	-0.56	0.20	1.19	1.01E-04
AFUA_5G07740	DSB repair complex subunit Ku70, putative	1.68	0.98	1.20	2.50E-03
AFUA_6G02280	Peroxiredoxin Asp f3 (Prx) (EC 1.11.1.15) (Thioredoxin peroxidase) (TPx) (allergen Asp f 3)	1.92	1.22	1.20	9.23E-10
AFUA_2G12630	Allergen Asp f 15 (Allergen Asp f 13) (allergen Asp f 15)	1.74	0.84	1.21	7.76E-04
AFUA_6G04740	Actin Act1	0.85	-0.22	1.21	3.55E-03
AFUA_6G04920	Formate dehydrogenase (FDH) (EC 1.2.1.2) (NAD-dependent formate dehydrogenase)	1.83	1.45	1.22	2.23E-08
AFUA_4G13760	Uncharacterized protein	2.28	1.38	1.22	1.74E-02
AFUA_5G11230	RAS small monomeric GTPase RasA	1.17	0.92	1.22	6.77E-03
AFUA_1G04950	Serine/threonine-protein phosphatase (EC 3.1.3.16)	2.33	1.62	1.22	3.67E-08
AFUA_1G14780	BAP31 domain protein, putative	1.35	0.09	1.25	4.36E-05
AFUA_4G11770	Glutathione transferase, putative	0.91	1.27	1.25	1.16E-03
AFUA_2G04930	Uncharacterized protein	1.69	1.61	1.26	4.59E-03
AFUA_5G08910	3-methylcrotonyl-CoA carboxylase subunit alpha (MccA), putative (EC 6.4.1.4)	2.09	1.12	1.26	7.48E-06
AFUA_6G00750	Pyruvate decarboxylase, putative (EC 4.1.1.1)	1.60	1.72	1.26	4.56E-04
AFUA_6G08750	Delta-1-pyrroline-5-carboxylate dehydrogenase PrnC (EC 1.2.1.88)	2.10	1.56	1.26	3.94E-08
AFUA_7G01430	Opsin, putative	1.17	0.44	1.26	5.24E-04
AFUA_4G03140	Serine protein kinase Sky1, putative (EC 2.7.1.-)	2.32	0.75	1.26	9.40E-03
AFUA_5G10280	Oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor (EC 1.1.1.31)	1.71	1.70	1.26	8.32E-03
AFUA_2G07610	Short chain dehydrogenase/reductase, putative	0.74	0.79	1.27	1.62E-03
AFUA_8G05590	Oxidoreductase, short chain dehydrogenase/reductase family	1.33	1.35	1.27	7.36E-05
AFUA_1G04820	Probable NAD(P)H-dependent D-xylose reductase xyl1 (XR) (EC 1.1.1.307)	1.34	1.48	1.27	3.13E-08
AFUA_7G06770	Uncharacterized protein	-0.05	-0.47	1.28	1.92E-05
AFUA_5G08650	Uncharacterized protein	0.60	1.57	1.29	4.77E-02
AFUA_4G13460	SNF2 family helicase/ATPase, putative	1.07	-0.26	1.29	1.77E-02
AFUA_7G06610	Isochorismatase family hydrolase, putative	-1.78	-0.51	1.29	2.45E-03
AFUA_8G04320	NADH-ubiquinone oxidoreductase 178 kDa subunit, putative	0.90	-0.21	1.29	2.19E-02
AFUA_3G10000	cAMP-dependent protein kinase regulatory subunit (PKA regulatory subunit)	-0.91	0.66	1.31	3.53E-06
AFUA_1G13260	Coatomer subunit epsilon	0.97	1.37	1.31	1.66E-02
AFUA_4G10510	Mitochondrial chaperone Frataxin, putative	-0.26	0.88	1.31	2.10E-05
AFUA_5G06680	4-aminobutyrate transaminase GatA (EC 2.6.1.19)	1.48	1.64	1.32	1.25E-07
AFUA_3G13620	Cupin domain protein	-0.46	2.20	1.33	1.15E-03
AFUA_2G15760	Poly(A)+ RNA transport protein (UbaA), putative (EC 6.3.2.19)	-1.11	0.63	1.33	2.53E-05
AFUA_3G12950	FAD binding domain protein (EC 1.5.3.-)	2.95	3.08	1.33	2.34E-02
AFUA_7G04070	Phospho-2-dehydro-3-deoxyheptonate aldolase (EC 2.5.1.54) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase) (DAHP synthase) (Phospho-2-keto-3-deoxyheptonate aldolase)	-0.08	0.48	1.34	5.46E-03
AFUA_1G14850	Acyl-CoA dehydrogenase, putative (EC 1.3.99.-)	2.04	1.69	1.34	2.97E-10
AFUA_5G14790	Phosphoenolpyruvate synthase, putative (EC 2.7.9.2)	-0.36	0.69	1.34	1.68E-02
AFUA_3G07150	Succinate-semialdehyde dehydrogenase, putative (EC 1.2.1.24)	0.96	1.03	1.36	1.42E-05
AFUA_6G04970	Phosphoserine aminotransferase (EC 2.6.1.52)	0.12	0.82	1.36	1.83E-07
AFUA_1G02070	Cytochrome C1/Cyt1, putative (EC 1.10.2.2)	1.45	0.49	1.37	2.80E-02
AFUA_1G03070	Transcription initiation factor TFIID subunit, putative	1.27	0.46	1.37	1.73E-02
AFUA_1G02980	6-phosphogluconolactonase, putative (EC 3.1.1.31)	0.18	0.77	1.37	2.00E-05
AFUA_2G15190	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	1.31	1.55	1.37	1.38E-07
AFUA_1G05120	COPII-coated vesicle membrane protein Erv46, putative	1.67	-0.05	1.37	7.16E-03

AFUA_2G14960	Thioredoxin, putative	0.82	0.34	1.37	2.49E-02
AFUA_2G15660	Aldehyde dehydrogenase	1.13	1.10	1.38	2.25E-04
AFUA_3G12510	Vesicular fusion ATPase, putative	3.29	1.34	1.38	5.57E-05
AFUA_2G03490	Calcium/calmodulin-dependent protein kinase, putative	1.17	0.85	1.38	1.60E-02
AFUA_3G11610	Non-histone chromosomal protein 6	0.61	1.32	1.38	1.58E-05
AFUA_3G08310	4-nitrophenylphosphatase (PNPPase) (EC 3.1.3.41)	2.77	2.04	1.39	1.34E-02
AFUA_5G03550	Plasma membrane ATPase (EC 3.6.3.6)	0.72	0.56	1.40	2.42E-04
AFUA_8G01670	Catalase-peroxidase (CP) (EC 1.11.1.21) (Catalase-2) (Peroxidase/catalase)	2.91	2.01	1.41	4.44E-09
AFUA_7G04180	Amine oxidase (EC 1.4.3.-)	3.46	2.15	1.42	5.87E-08
AFUA_1G15720	Importin beta-1 subunit	1.07	1.05	1.43	4.24E-02
AFUA_6G08050	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	-0.47	-0.74	1.43	1.45E-07
AFUA_6G01790	Uncharacterized protein	1.04	0.89	1.43	2.72E-03
AFUA_5G03930	Alcohol dehydrogenase, putative (EC 1.-.-.-)	-0.88	-0.97	1.44	5.10E-06
AFUA_1G14570	Histidine biosynthesis trifunctional protein [Includes: Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19); Phosphoribosyl-ATP pyrophosphohydrolase (EC 3.6.1.31); Histidinol dehydrogenase (HDH) (EC 1.1.1.23)]	1.38	1.80	1.44	5.84E-08
AFUA_2G16090	Importin subunit alpha	1.96	0.04	1.44	2.65E-02
AFUA_2G12470	Acetylornithine aminotransferase (EC 2.6.1.1)	0.53	0.72	1.44	1.04E-03
AFUA_1G15140	Mitochondrial phosphate carrier protein (Mir1), putative	1.88	0.40	1.45	3.74E-04
AFUA_7G02230	mRNA binding post-transcriptional regulator (Csx1), putative	1.96	1.06	1.46	4.21E-02
AFUA_1G05390	Mitochondrial ADP,ATP carrier protein (Ant), putative	1.66	0.56	1.46	1.52E-03
AFUA_3G05740	Aldose 1-epimerase, putative (EC 5.1.3.3)	1.47	1.36	1.46	1.87E-02
AFUA_2G12410	Uncharacterized protein	0.60	1.10	1.47	2.47E-05
AFUA_1G04320	40S ribosomal protein S8	-1.27	-1.39	1.48	3.23E-02
AFUA_5G02240	NAD dependent epimerase/dehydratase family protein (EC 1.1.1.133)	0.63	1.26	1.48	1.13E-05
AFUA_3G01580	GMC oxidoreductase, putative	1.44	1.53	1.48	2.64E-02
AFUA_6G09570	Uncharacterized protein	-0.28	3.02	1.48	3.50E-04
AFUA_1G05210	G-protein complex gamma subunit GpgA	0.33	1.27	1.49	1.70E-03
AFUA_4G06860	Uncharacterized protein	2.13	2.09	1.49	1.46E-04
AFUA_2G01660	Mitochondrial outer membrane translocase receptor (TOM70), putative	0.29	-0.25	1.50	1.86E-02
AFUA_5G12790	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial (EC 3.1.2.4) (3-hydroxyisobutyryl-coenzyme A hydrolase)	-0.79	0.49	1.51	3.15E-03
AFUA_3G05370	Dihydrolipoamide succinyltransferase, putative (EC 2.3.1.61)	0.03	0.27	1.51	3.67E-04
AFUA_5G02300	Peroxidase, putative (EC 1.11.1.-)	2.77	1.19	1.51	2.77E-05
AFUA_5G05500	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	-0.44	0.99	1.51	1.70E-04
AFUA_2G01030	1-aminocyclopropane-1-carboxylate deaminase, putative (EC 3.5.99.7)	1.39	1.42	1.51	6.06E-04
AFUA_2G16010	Prolyl-tRNA synthetase (EC 6.1.1.15)	0.30	-0.75	1.52	5.29E-07
AFUA_6G07520	Cell wall integrity signaling protein Lsp1/Pil1, putative	-0.04	-0.03	1.52	3.93E-04
AFUA_5G03760	Endochitinase A1 (EC 3.2.1.14) (Chitinase A1)	1.55	1.10	1.52	1.32E-03
AFUA_6G08740	3-dehydroshikimate dehydratase, putative (EC 4.2.1.-)	1.23	1.28	1.52	1.10E-03
AFUA_1G07380	Glutamate synthase Glt1, putative (EC 1.4.1.13)	0.10	0.72	1.53	1.87E-05
AFUA_6G11020	3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31)	0.21	0.96	1.54	4.47E-02
AFUA_4G11240	Alpha-aminoadipate reductase large subunit, putative (EC 1.2.1.31)	-0.12	0.91	1.54	3.55E-05
AFUA_1G12610	Hsp70 chaperone Hsp88	1.37	1.56	1.54	1.28E-03
AFUA_6G06900	Rho GTPase Rho1	2.00	1.49	1.54	6.27E-06
AFUA_5G08940	3-methylcrotonyl-CoA carboxylase, beta subunit (MccB), putative (EC 6.4.1.3)	2.37	1.48	1.54	3.45E-03
AFUA_4G10760	Steroid alpha reductase family protein	2.80	0.90	1.55	7.90E-06
AFUA_1G11535	Glutaredoxin-like protein	1.93	2.19	1.56	1.53E-03
AFUA_7G05160	Fumarylacetoacetate hydrolase family protein	2.01	2.33	1.56	1.16E-02
AFUA_6G08930	Protein fmp52, mitochondrial	0.43	0.69	1.57	5.36E-03

AFUA_4G11260	Aldo-keto reductase, putative (EC 1.1.1.-)	1.72	2.15	1.57	5.59E-07
AFUA_4G04410	3-hydroxybutyryl-CoA dehydrogenase, putative (EC 1.1.1.157)	1.54	1.62	1.58	8.61E-05
AFUA_5G12840	Hydroxyacylglutathione hydrolase, putative (EC 3.1.2.6)	1.91	1.96	1.58	2.01E-09
AFUA_6G02230	Phosphotransferase (EC 2.7.1.-)	0.59	0.98	1.58	9.15E-07
AFUA_2G06000	NAD-specific glutamate dehydrogenase (EC 1.4.1.2)	0.33	0.54	1.58	8.08E-03
AFUA_6G05110	Mitochondrial import receptor subunit (Tom40), putative	1.88	0.90	1.59	3.67E-04
AFUA_4G09110	Cytochrome c peroxidase, mitochondrial (CCP) (EC 1.11.1.5)	0.78	1.14	1.59	1.79E-04
AFUA_6G04220	Uncharacterized protein	0.27	0.16	1.59	3.47E-03
AFUA_5G08930	Isovaleryl-CoA dehydrogenase IvdA, putative (EC 1.3.8.4)	2.35	1.94	1.59	6.38E-07
AFUA_1G05200	Eukaryotic translation initiation factor 3 subunit A (eIF3a) (Eukaryotic translation initiation factor 3 110 kDa subunit homolog) (eIF3 p110) (Translation initiation factor eIF3, p110 subunit homolog)	2.11	0.30	1.59	1.79E-03
AFUA_4G14070	Glycosyl transferase, putative (EC 2.-.-.-)	-0.24	1.23	1.60	4.77E-04
AFUA_1G06820	Uncharacterized protein	-0.98	1.15	1.60	3.42E-04
AFUA_5G08240	MutT/nudix family protein	0.64	2.17	1.60	9.03E-05
AFUA_2G13630	Aromatic aminotransferase Aro8, putative (EC 2.6.1.-)	3.08	1.96	1.61	7.87E-04
AFUA_1G14490	Aminotransferase, putative	1.06	1.40	1.61	1.36E-02
AFUA_3G03000	Phosphatidylethanolamine-binding protein, putative	1.03	1.47	1.62	1.71E-02
AFUA_1G06390	Elongation factor 1-alpha	2.55	0.67	1.62	2.21E-10
AFUA_6G10830	Serine/threonine-protein phosphatase (EC 3.1.3.16)	1.03	0.77	1.62	3.21E-03
AFUA_4G04520	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial (EC 6.2.1.5) (Succinyl-CoA synthetase beta chain) (SCS-beta)	0.64	0.96	1.62	2.26E-05
AFUA_2G11560	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.12)	1.97	1.56	1.62	1.77E-04
AFUA_5G09920	Peptidase, putative (EC 3.-.-.-)	1.81	2.04	1.63	2.44E-06
AFUA_1G13195	MICOS complex subunit MIC10	0.97	0.50	1.63	1.91E-04
AFUA_1G14220	Fibrillarin	1.88	-0.05	1.63	5.00E-07
AFUA_3G07810	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1)	1.68	1.72	1.63	7.09E-11
AFUA_2G00680	Glycosyl hydrolase, putative	-0.14	1.01	1.63	1.32E-02
AFUA_4G13530	Trehalase (EC 3.2.1.28) (Alpha-trehalose glucohydrolase)	0.41	1.17	1.64	7.73E-03
AFUA_1G04720	C-8 sterol isomerase (Erg-1), putative	3.48	1.57	1.64	3.80E-04
AFUA_5G07020	Ribosome biogenesis ABC transporter Arb1, putative (EC 3.6.3.-)	2.39	0.37	1.64	2.14E-02
AFUA_4G12840	Methylthioribulose-1-phosphate dehydratase (MTRu-1-P dehydratase) (EC 4.2.1.109)	1.74	1.75	1.64	1.23E-03
AFUA_4G14100	Glutathione S-transferase, putative	0.68	1.60	1.64	2.44E-02
AFUA_5G07750	Ferrochelatase (EC 4.99.1.1)	1.68	1.14	1.65	3.04E-02
AFUA_1G08980	UPF0160 domain protein MYG1, putative	1.65	1.77	1.65	1.28E-08
AFUA_3G03020	Phosphoglucomutase, putative	2.09	2.13	1.66	1.24E-04
AFUA_3G14990	Alpha/beta hydrolase, putative (EC 3.-.-.-)	1.85	1.14	1.66	5.44E-05
AFUA_2G00830	Short chain dehydrogenase/reductase (EC 1.1.-.-)	2.20	1.98	1.66	3.87E-03
AFUA_4G10780	Ubiquitin-protein ligase (Tom1), putative	1.40	0.57	1.66	3.15E-02
AFUA_1G10310	RNase L inhibitor of the ABC superfamily, putative	2.57	1.26	1.67	3.21E-03
AFUA_2G04590	Alcohol dehydrogenase, putative (EC 1.1.1.-)	2.84	1.45	1.67	1.37E-04
AFUA_1G09800	Obg-like ATPase 1	0.49	1.23	1.67	2.22E-05
AFUA_1G02030	Eukaryotic translation initiation factor 3 subunit B (eIF3b) (Eukaryotic translation initiation factor 3 90 kDa subunit homolog) (eIF3 p90) (Translation initiation factor eIF3 p90 subunit homolog)	1.64	1.28	1.67	5.02E-03
AFUA_3G02240	Aromatic-L-amino-acid decarboxylase, putative (EC 4.1.1.28)	2.24	2.44	1.68	7.17E-05
AFUA_4G12850	Calnexin homolog	1.94	2.01	1.68	1.06E-05
AFUA_1G10960	Mago nashi domain protein	0.69	0.68	1.68	2.11E-02
AFUA_1G13140	G-protein complex alpha subunit GpaA/FadA	1.24	0.75	1.69	9.24E-05
AFUA_3G07160	Class V chitinase, putative (EC 3.2.1.14)	-1.22	0.27	1.69	2.70E-08
AFUA_6G11210	3-oxoacyl-(Acyl-carrier-protein) reductase (EC 1.1.1.100)	2.23	1.76	1.69	1.86E-05

AFUA_1G07200	Mitochondrial cytochrome b2, putative (EC 1.1.2.3)	1.82	1.54	1.70	1.56E-06
AFUA_2G09130	NADH-ubiquinone dehydrogenase 24 kDa subunit, putative (EC 1.6.5.3)	1.56	1.46	1.71	3.08E-05
AFUA_2G00970	Alcohol dehydrogenase, zinc-containing, putative (EC 1.1.1.1)	-2.01	0.95	1.71	3.73E-04
AFUA_6G13330	RNA binding protein, putative	0.65	1.36	1.72	1.25E-06
AFUA_6G04570	Translation elongation factor eEF-1 subunit gamma, putative	1.92	1.53	1.72	4.63E-06
AFUA_2G13530	Translation elongation factor EF-2 subunit, putative	1.20	0.63	1.73	2.42E-07
AFUA_1G07520	Dimeric dihydrodiol dehydrogenase, putative (EC 1.-.-.-)	-0.11	0.53	1.73	8.87E-03
AFUA_1G10460	Uncharacterized protein	2.27	1.93	1.73	9.81E-03
AFUA_5G10780	UDP-glucose 4-epimerase (EC 5.1.3.2)	-0.33	0.59	1.73	1.81E-04
AFUA_3G08840	Coatomer subunit alpha	1.41	0.96	1.73	5.58E-06
AFUA_1G12800	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	0.88	0.43	1.73	1.07E-03
AFUA_6G12250	Succinyl-CoA:3-ketoacid-coenzyme A transferase (EC 2.8.3.5)	1.20	1.90	1.74	1.35E-02
AFUA_2G10220	Glycerol dehydrogenase, putative (EC 1.1.1.-)	2.11	1.89	1.74	2.26E-05
AFUA_2G04940	KH domain RNA binding protein	1.23	0.41	1.74	1.66E-02
AFUA_2G01590	Non-classical export protein Nce102, putative	0.79	0.01	1.77	1.22E-03
AFUA_6G14460	Haloalkanoic acid dehalogenase, putative (EC 3.8.1.-)	2.32	2.41	1.77	6.44E-05
AFUA_2G02490	Uncharacterized protein	1.74	1.54	1.77	3.09E-03
AFUA_2G12180	Lectin family integral membrane protein, putative	2.22	0.92	1.78	3.14E-02
AFUA_6G04210	Mannosyl-oligosaccharide glucosidase, putative	1.32	2.11	1.78	2.46E-05
AFUA_2G11250	Aryl-alcohol dehydrogenase Aad14, putative (EC 1.1.1.-)	-1.07	0.70	1.79	4.39E-05
AFUA_5G08130	Protein transport protein Sec61 alpha subunit, putative	1.50	0.46	1.79	2.47E-03
AFUA_7G05740	Malate dehydrogenase (EC 1.1.1.37)	1.99	2.20	1.80	2.64E-09
AFUA_3G11280	Class V chitinase, putative (EC 3.2.1.14)	2.73	2.36	1.80	8.28E-08
AFUA_5G08980	NADH-ubiquinone oxidoreductase 9.5 kDa subunit, putative (EC 1.6.5.3)	2.51	1.33	1.80	5.73E-03
AFUA_2G10855	Phosphoribosylglycinamide formyltransferase, putative (EC 2.1.2.2)	-0.79	0.80	1.80	8.32E-07
AFUA_3G10460	Nuclear transport factor NTF-2, putative	1.98	1.40	1.80	6.04E-05
AFUA_1G01750	Peptidyl-prolyl cis-trans isomerase, putative (EC 5.2.1.8)	0.38	1.61	1.81	1.91E-02
AFUA_5G06710	DUF89 domain protein	-0.36	1.07	1.81	1.10E-04
AFUA_5G01970	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	0.76	1.14	1.82	2.55E-05
AFUA_4G11650	Alpha-ketoglutarate dehydrogenase complex subunit Kgd1, putative (EC 1.2.4.2)	0.89	1.10	1.82	1.61E-04
AFUA_1G06610	NADH-quinone oxidoreductase, 23 kDa subunit, putative (EC 1.6.5.3)	-0.16	0.09	1.82	1.68E-02
AFUA_4G00290	Succinyl-CoA synthetase beta subunit, putative (EC 6.2.1.4)	0.63	1.29	1.82	3.89E-02
AFUA_1G05500	40S ribosomal protein S12	1.83	0.32	1.82	4.21E-06
AFUA_5G02720	Phosphoribosylformylglycinamidine synthase (EC 6.3.5.3)	0.47	1.06	1.82	1.42E-02
AFUA_7G02180	UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23)	0.56	0.87	1.82	6.32E-05
AFUA_5G11610	Protein arginine N-methyltransferase	1.83	2.28	1.82	2.99E-02
AFUA_3G12840	Signal peptidase complex catalytic subunit sec11 (EC 3.4.21.89) (Signal peptidase I)	2.53	1.13	1.83	1.78E-02
AFUA_5G03350	Glutamine-dependent NAD(+) synthetase (EC 6.3.5.1) (NAD(+) synthase [glutamine-hydrolyzing])	0.47	1.51	1.84	5.06E-03
AFUA_5G05480	Rheb small monomeric GTPase RhbA	1.88	1.54	1.84	1.32E-02
AFUA_6G08780	Proline utilization protein PrnX, putative (EC 4.3.1.12)	1.85	1.46	1.85	2.55E-03
AFUA_5G13450	Triosephosphate isomerase (EC 5.3.1.1)	2.20	2.15	1.85	1.15E-06
AFUA_1G11790	Nucleoside hydrolase, putative (EC 3.2.2.-)	2.30	2.29	1.85	3.45E-03
AFUA_4G07580	Translation initiation factor EF-2 gamma subunit, putative	1.81	0.08	1.85	2.37E-05
AFUA_8G01420	Quinone oxidoreductase, putative (EC 1.6.5.5)	1.55	1.38	1.85	5.05E-04
AFUA_2G11260	3-isopropylmalate dehydratase (EC 4.2.1.33) (Alpha-IPM isomerase) (Isopropylmalate isomerase)	0.96	0.72	1.85	3.27E-03
AFUA_8G04550	Sulfonate biosynthesis enzyme, putative (EC 4.4.1.-)	0.80	1.63	1.86	3.19E-02

AFUA_4G10240	Small nuclear ribonucleoprotein SmD3, putative	2.93	0.33	1.86	1.92E-03
AFUA_7G01880	Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	-0.48	1.81	1.87	8.56E-04
AFUA_4G11340	Saccharopine dehydrogenase Lys9, putative (EC 1.5.1.7)	1.06	0.52	1.87	2.32E-05
AFUA_1G11960	Alternative NADH-dehydrogenase (EC 1.6.99.3)	2.48	0.73	1.88	5.93E-06
AFUA_5G05460	Cytosine deaminase-uracil phosphoribosyltransferase fusion protein (EC 2.4.2.9)	0.80	-0.36	1.88	3.92E-03
AFUA_3G00680	Amine oxidase (EC 1.4.3.-)	3.44	1.35	1.88	1.22E-03
AFUA_2G09030	Dipeptidyl-peptidase 5 (EC 3.4.14.-) (Dipeptidyl-peptidase V) (DPP V) (DppV)	2.08	3.28	1.89	1.63E-07
AFUA_8G04710	Xylosidase, putative (EC 3.2.1.37)	1.81	1.72	1.89	6.76E-04
AFUA_8G04810	Casein kinase, putative (EC 2.7.11.1)	1.23	1.84	1.89	4.01E-02
AFUA_2G13295	Aminotransferase family protein (LolT), putative	3.15	1.64	1.91	1.90E-03
AFUA_1G02410	RuvB-like helicase 2 (EC 3.6.4.12)	0.59	-0.36	1.91	8.45E-06
AFUA_4G08550	Pantetheine-phosphate adenylyltransferase family protein	0.33	0.97	1.92	7.70E-03
AFUA_5G05820	Homoserine kinase (EC 2.7.1.39)	1.95	0.36	1.92	3.41E-03
AFUA_3G07300	ABC multidrug transporter, putative (EC 3.6.3.-)	1.49	1.40	1.92	1.46E-03
AFUA_6G06460	Fumarylacetoacetate hydrolase family protein	1.77	1.86	1.92	9.09E-05
AFUA_4G10730	RuvB-like helicase 1 (EC 3.6.4.12)	0.44	-0.28	1.92	4.88E-03
AFUA_3G02430	Uncharacterized protein	1.34	2.01	1.93	8.65E-07
AFUA_2G02950	Aldehyde reductase, putative (EC 1.1.1.-)	2.75	2.40	1.93	5.49E-06
AFUA_4G11290	Proteasome activator subunit 4, putative	1.35	1.17	1.93	9.16E-04
AFUA_4G07700	Clathrin heavy chain	1.01	1.28	1.93	7.89E-07
AFUA_4G03120	Mitochondrial cytochrome b2, putative (EC 1.1.2.3)	1.81	1.78	1.94	1.46E-05
AFUA_8G04730	Oligopeptidase family protein	0.64	0.95	1.94	3.87E-06
AFUA_1G13370	Aflatoxin B1-aldehyde reductase GliO-like, putative (EC 1.1.1.-)	1.21	1.00	1.94	2.87E-03
AFUA_1G08810	Glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)	1.32	0.84	1.94	5.22E-03
AFUA_5G10370	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (EC 1.3.5.1)	1.70	1.70	1.94	1.61E-03
AFUA_1G12250	Mitochondrial hypoxia responsive domain protein	3.82	1.09	1.94	2.25E-02
AFUA_5G06500	Acyl-CoA dehydrogenase family protein (EC 1.3.99.-)	2.25	1.85	1.96	8.24E-05
AFUA_3G10760	Phosphoketolase, putative	0.95	1.18	1.96	3.89E-03
AFUA_3G10110	Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)	1.69	0.95	1.96	2.07E-02
AFUA_2G12450	Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4)	2.07	1.98	1.96	1.61E-05
AFUA_4G14450	Mannitol 2-dehydrogenase (M2DH) (MDH) (EC 1.1.1.67)	1.63	1.31	1.97	1.45E-06
AFUA_4G08410	Mannose-6-phosphate isomerase, class I (EC 5.3.1.8)	1.96	2.75	1.97	8.29E-06
AFUA_5G09640	Conserved fungal protein	1.96	2.01	1.97	6.03E-04
AFUA_1G09810	Translation machinery-associated protein 20	1.30	2.29	1.98	1.31E-04
AFUA_6G02630	ATP-dependent RNA helicase sub2 (EC 3.6.4.13)	1.68	0.23	1.98	3.08E-03
AFUA_4G05900	Uncharacterized protein	2.52	0.96	1.98	3.18E-03
AFUA_7G01320	Beta-mannosidase B (EC 3.2.1.25) (Mannanase B) (Mannase B)	1.67	2.03	1.98	7.67E-05
AFUA_4G06910	Outer mitochondrial membrane protein porin	2.08	0.22	1.99	5.95E-07
AFUA_4G11840	Glyoxylate reductase (EC 1.1.1.95)	2.33	2.28	1.99	1.68E-04
AFUA_6G06500	Actin-related protein 2/3 complex subunit 1A, putative	0.87	1.42	1.99	2.53E-05
AFUA_1G12370	DUF255 domain protein	0.65	0.88	1.99	1.59E-02
AFUA_5G02690	C6 transcription factor, putative	0.58	-0.16	1.99	1.07E-02
AFUA_8G00230	Verruculogen synthase (EC 1.14.11.38) (Fumitremorgin biosynthesis protein F)	1.49	2.12	2.00	2.82E-04
AFUA_4G03660	Acid phosphatase, putative (EC 3.1.3.2)	1.73	2.31	2.00	1.27E-04
AFUA_4G08480	26S proteasome regulatory subunit Rpn2, putative	1.76	0.03	2.01	1.73E-02
AFUA_2G17430	Oxidoreductase 2-nitropropane dioxygenase family, putative (EC 1.13.11.-)	1.09	1.52	2.01	3.46E-03
AFUA_1G10130	Adenosylhomocysteinase (EC 3.3.1.1)	1.30	1.01	2.02	3.28E-05
AFUA_1G11730	ADP-ribosylation factor, putative	2.32	0.94	2.02	3.18E-05
AFUA_1G01490	NACHT domain protein	2.42	1.20	2.02	5.24E-07
AFUA_2G07970	60S ribosomal protein L19	0.73	0.74	2.02	3.21E-03
AFUA_6G04010	Chromosome segregation protein Cse1, putative	1.43	1.60	2.03	7.04E-05
AFUA_2G17070	Defective in cullin neddylation protein	3.34	2.92	2.04	2.08E-03

AFUA_4G08580	Mitochondrial peroxiredoxin Prx1, putative (EC 1.11.1.7)	-1.02	0.45	2.05	7.03E-07
AFUA_8G01210	Enoyl-CoA hydratase/isomerase family protein (EC 4.2.1.17)	-0.38	2.33	2.05	5.72E-03
AFUA_6G02470	Fumarate hydratase, putative (EC 4.2.1.2)	1.78	1.92	2.06	3.59E-06
AFUA_4G07690	Phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	0.20	1.65	2.06	7.82E-08
AFUA_4G05910	NADH-ubiquinone oxidoreductase 21 kDa subunit, putative (EC 1.6.5.3)	0.38	1.07	2.06	4.78E-02
AFUA_5G03480	Methylenetetrahydrofolate reductase (EC 1.5.1.20)	1.32	1.59	2.06	4.56E-02
AFUA_5G10640	Tyrosine--tRNA ligase (EC 6.1.1.1) (Tyrosyl-tRNA synthetase)	1.31	0.16	2.06	2.72E-02
AFUA_4G11720	Phosphatidyl synthase	0.57	1.36	2.06	3.69E-08
AFUA_1G15860	Coatomer subunit delta, putative	2.76	0.78	2.06	8.40E-04
AFUA_5G02030	Cleavage and polyadenylation specific factor 5	2.60	2.18	2.07	1.02E-06
AFUA_1G12940	Mitogen-activated protein kinase hog1 (MAP kinase hog1) (EC 2.7.11.24)	1.43	1.34	2.07	8.26E-03
AFUA_7G05360	FACT complex subunit pob3 (Facilitates chromatin transcription complex subunit pob3)	1.86	1.41	2.07	6.65E-04
AFUA_3G11430	Arginase (EC 3.5.3.1)	0.44	1.75	2.07	7.83E-03
AFUA_1G06700	Metacaspase-1A (EC 3.4.22.-)	3.64	2.10	2.07	1.94E-03
AFUA_6G13440	Choline sulfatase, putative (EC 3.1.6.6)	3.50	1.09	2.07	9.70E-04
AFUA_2G18030	Catalase easC (EC 1.11.-.-) (Ergot alkaloid synthesis protein C)	1.23	1.60	2.07	1.29E-04
AFUA_2G14030	Arginyl-tRNA synthetase (EC 6.1.1.19)	0.35	1.91	2.08	2.78E-07
AFUA_8G04090	Choline oxidase (CodA), putative (EC 1.1.3.17)	2.82	2.36	2.08	1.64E-08
AFUA_3G11640	Homoserine dehydrogenase (HDH) (EC 1.1.1.3)	-0.21	1.76	2.09	2.66E-06
AFUA_6G08630	MICOS complex subunit	0.53	0.88	2.09	3.78E-02
AFUA_3G12690	Uncharacterized protein	2.09	2.55	2.09	4.39E-10
AFUA_3G13140	Methyltransferase, putative	2.16	2.14	2.09	1.35E-03
AFUA_3G10480	Meiotic sister chromatid recombination protein Ish1/Msc1, putative	0.76	1.56	2.10	3.29E-06
AFUA_2G13250	Tryptophan synthase (EC 4.2.1.20)	1.57	1.05	2.10	4.86E-03
AFUA_2G07720	Cytochrome b5, putative	0.33	2.14	2.11	2.06E-02
AFUA_7G01830	UTP-glucose-1-phosphate uridylyltransferase Ugp1, putative	0.00	1.35	2.11	4.43E-05
AFUA_2G17920	Uncharacterized protein	2.15	2.58	2.12	1.62E-06
AFUA_2G01330	Exosome complex subunit Rrp46, putative (EC 3.1.13.-)	-0.13	1.01	2.12	2.83E-02
AFUA_2G05910	Phosphotransferase (EC 2.7.1.-)	-0.01	1.20	2.12	8.68E-07
AFUA_6G07770	Alanine aminotransferase, putative (EC 2.6.1.-)	2.58	2.69	2.13	3.86E-08
AFUA_3G13450	Oxidoreductase, short chain dehydrogenase/reductase family superfamily (EC 1.1.1.100)	0.99	1.69	2.13	5.97E-03
AFUA_2G10660	Mannitol-1-phosphate 5-dehydrogenase (M1PDH) (MPD) (MPDH) (EC 1.1.1.17)	2.25	2.46	2.14	2.73E-08
AFUA_4G08070	Glycylpeptide N-tetradecanoyltransferase (EC 2.3.1.97) (Myristoyl-CoA:protein N-myristoyltransferase) (NMT) (Peptide N-myristoyltransferase)	0.76	1.26	2.14	1.19E-02
AFUA_1G11120	Uncharacterized protein	2.27	1.76	2.14	5.04E-03
AFUA_1G09230	DUF1000 domain protein	2.18	1.93	2.15	2.28E-04
AFUA_5G06130	Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial (EC 6.2.1.5) (Succinyl-CoA synthetase subunit alpha) (SCS-alpha)	-0.10	1.42	2.15	4.63E-07
AFUA_5G02350	Hydrolase, carbon-nitrogen family, putative	2.87	1.32	2.15	1.12E-02
AFUA_2G09090	Prohibitin, putative	2.14	0.81	2.15	1.23E-03
AFUA_5G10610	Ubiquinol-cytochrome c reductase iron-sulfur subunit (EC 1.10.2.2)	2.21	2.19	2.15	3.15E-07
AFUA_7G00350	Uncharacterized protein	0.62	1.86	2.15	3.63E-03
AFUA_1G15020	40S ribosomal protein S5, putative	0.51	-0.18	2.15	9.30E-07
AFUA_1G12340	Carnitine acetyl transferase	1.02	1.01	2.16	3.89E-03
AFUA_1G04540	NADH-cytochrome b5 reductase 2 (EC 1.6.2.2) (Mitochondrial cytochrome b reductase)	1.81	1.61	2.16	3.37E-06
AFUA_6G03540	Malate synthase (EC 2.3.3.9)	0.38	2.10	2.16	1.22E-07
AFUA_2G14810	Oxidoreductase, putative	-0.70	0.11	2.16	6.56E-04
AFUA_4G10330	CaaX farnesyltransferase beta subunit Ram1 (EC 2.5.1.58)	1.83	2.27	2.17	3.61E-04
AFUA_5G02530	Ribokinase (EC 2.7.1.15)	1.86	2.75	2.17	6.59E-05

AFUA_4G14470	Probable decarboxylase tpcK (EC 1.-.-.-) (Trypacidin synthesis protein K)	0.27	2.58	2.17	3.04E-03
AFUA_1G10870	Urea hydro-lyase/cyanamide hydratase, putative (EC 4.2.1.-)	0.63	0.64	2.18	4.23E-02
AFUA_2G02920	Alpha/beta hydrolase, putative (EC 3.-.-.-)	2.26	2.22	2.18	4.64E-05
AFUA_3G08650	C1 tetrahydrofolate synthase, putative (EC 6.3.4.3)	0.76	1.45	2.18	3.94E-07
AFUA_1G10970	Coatomer subunit beta (Beta-coat protein)	1.74	0.71	2.18	9.06E-03
AFUA_4G00180	Fatty acid oxygenase, putative (EC 1.-.-.-)	0.87	1.39	2.19	7.54E-03
AFUA_5G05680	Peptide chain release factor eRF/aRF, subunit 1	1.89	1.57	2.19	8.67E-06
AFUA_5G12250	Posttranscriptional regulation nuclease (Mkt1), putative	1.24	1.75	2.19	5.16E-05
AFUA_2G15980	3' exoribonuclease family protein	0.02	1.24	2.20	4.73E-03
AFUA_5G08290	Aldo-keto reductase, putative (EC 1.1.1.-)	2.60	2.88	2.20	4.21E-05
AFUA_5G09400	Carbonyl reductase, putative (EC 1.-.-.-)	2.11	2.49	2.20	2.04E-04
AFUA_3G05350	Histone H2B	1.24	1.37	2.21	5.77E-07
AFUA_4G04660	Proteasome regulatory particle subunit Rpt6, putative	1.32	0.28	2.21	9.10E-03
AFUA_5G09080	Transcription factor (SPT8), putative	0.93	1.83	2.21	1.87E-02
AFUA_6G12580	Anthranilate synthase component I, putative (EC 4.1.3.27)	1.37	1.63	2.21	2.10E-07
AFUA_2G11290	Orotate phosphoribosyltransferase (EC 2.4.2.10)	-0.51	1.15	2.21	5.62E-08
AFUA_7G05930	Metallopeptidase MepB (EC 3.4.24.-)	2.34	2.35	2.22	4.82E-07
AFUA_4G03450	NmrA-like family protein	-0.34	0.85	2.22	3.64E-05
AFUA_5G13510	Cell cycle control protein (Cwf8), putative	3.40	2.49	2.22	1.58E-06
AFUA_5G07000	NAD binding Rossmann fold oxidoreductase, putative (EC 1.-.-.-)	1.19	2.13	2.22	4.38E-07
AFUA_2G17560	Hydroxynaphthalene reductase arp2 (EC 1.1.-.-) (Conidial pigment biosynthesis oxidase arp2)	1.38	1.98	2.22	3.81E-07
AFUA_4G09010	mRNA splicing protein (Prp39), putative	1.05	1.27	2.22	2.27E-02
AFUA_2G08970	Thiamine biosynthetic bifunctional enzyme, putative	2.41	2.37	2.22	1.51E-05
AFUA_1G13330	Arp2/3 complex subunit (Arp2), putative	0.87	1.12	2.22	4.22E-04
AFUA_4G09250	Uncharacterized protein	2.50	0.81	2.23	2.14E-04
AFUA_4G13120	Glutamine synthetase (EC 6.3.1.2)	-0.37	1.01	2.23	6.13E-05
AFUA_6G03100	Uncharacterized protein	0.36	1.75	2.23	7.03E-07
AFUA_3G11750	Oxysterol binding protein (Osh5), putative	1.98	1.18	2.24	1.90E-04
AFUA_6G07710	Mitochondrial dicarboxylate carrier protein, putative	2.77	2.44	2.24	4.59E-03
AFUA_2G12530	Carnitine acetyl transferase	2.17	2.17	2.24	1.23E-05
AFUA_7G01000	Aldehyde dehydrogenase, putative (EC 1.2.1.3)	2.92	2.41	2.24	6.42E-09
AFUA_3G14690	Aminotransferase, putative (EC 2.-.-.-)	3.71	1.68	2.25	1.24E-02
AFUA_3G07790	Argininosuccinate lyase (EC 4.3.2.1)	2.64	2.47	2.26	6.17E-07
AFUA_2G00590	Glutathione S-transferase, putative (EC 2.5.1.18)	2.81	1.86	2.26	1.59E-03
AFUA_6G08020	ABC transporter, putative	1.44	2.23	2.27	8.59E-04
AFUA_6G08840	Beta-mannosidase A (EC 3.2.1.25) (Mannanase A) (Mannase A)	0.14	0.75	2.27	5.60E-03
AFUA_4G13700	Threonyl-tRNA synthetase, putative (EC 6.1.1.3)	2.15	1.98	2.27	1.50E-05
AFUA_6G10480	Peptidyl-prolyl cis-trans isomerase-like 3 (PPIase) (EC 5.2.1.8) (Rotamase)	2.18	1.64	2.28	4.96E-03
AFUA_1G04620	Alcohol dehydrogenase, zinc-containing, putative (EC 1.1.1.-)	1.52	1.12	2.28	9.14E-03
AFUA_1G15450	Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	2.78	2.76	2.28	2.20E-10
AFUA_1G03400	Protein transport protein sec23	2.63	0.89	2.28	5.12E-05
AFUA_5G11560	Arp2/3 complex subunit (Arp3), putative	1.00	1.47	2.29	2.40E-04
AFUA_5G03360	NADH pyrophosphatase, putative (EC 3.6.1.-)	2.39	1.95	2.29	1.45E-02
AFUA_1G16523	40S ribosomal protein S25, putative	-0.68	-1.03	2.30	1.88E-06
AFUA_1G09480	Vacuolar protein sorting-associated protein 29	0.98	2.02	2.31	3.96E-02
AFUA_6G13300	GTP-binding nuclear protein	2.70	2.02	2.31	8.90E-06
AFUA_3G09910	Phosphatidylinositol transporter, putative	1.29	1.59	2.31	5.91E-05
AFUA_1G02670	Arp2/3 complex 34 kDa subunit	1.26	1.18	2.31	1.01E-04
AFUA_3G10310	Acetolactate synthase (EC 2.2.1.6)	1.11	2.68	2.31	4.10E-07
AFUA_5G07170	Nucleoside-diphosphate-sugar epimerase, putative	2.32	2.57	2.32	5.15E-03
AFUA_4G09660	Secretory component protein shr3, putative	0.78	1.23	2.32	4.55E-02
AFUA_2G05790	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 (EC 2.4.99.18)	2.29	1.70	2.33	1.32E-09
AFUA_6G02140	Peptidyl-prolyl cis-trans isomerase-like 1 (PPIase) (EC 5.2.1.8) (Rotamase)	2.26	1.98	2.33	3.51E-03

AFUA_3G06210	Phosphoribosyl-aminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)	-0.11	1.53	2.33	2.96E-06
AFUA_8G07110	Alanyl-tRNA synthetase, putative (EC 6.1.1.7)	1.67	2.06	2.33	2.91E-02
AFUA_2G02580	HAD superfamily hydrolase, putative	2.74	2.58	2.37	2.41E-05
AFUA_3G08430	Mitochondrial phosphate carrier protein, putative	3.04	1.57	2.38	5.50E-03
AFUA_2G05740	Rho GTPase ModA, putative	2.65	1.95	2.38	1.24E-03
AFUA_6G10600	NEDD8-activating enzyme E1 regulatory subunit	2.06	1.76	2.38	5.36E-04
AFUA_3G04020	Conserved mitochondrial protein	2.50	2.02	2.39	6.53E-04
AFUA_6G11680	Thiamine pyrophosphate enzyme, putative (EC 4.1.-.-)	2.47	2.28	2.39	5.77E-05
AFUA_1G13780	Histone H4	1.92	1.56	2.39	1.19E-03
AFUA_3G11690	Fructose-bisphosphate aldolase, class II (EC 4.1.2.13)	2.85	2.74	2.40	1.96E-10
AFUA_5G02480	Glycogen [starch] synthase (EC 2.4.1.11)	1.58	1.39	2.40	6.34E-05
AFUA_2G14850	Enoyl-CoA hydratase/isomerase family protein (EC 4.2.-.-)	3.46	2.02	2.40	1.40E-04
AFUA_2G11150	Rab GDP dissociation inhibitor	1.18	1.90	2.40	1.79E-04
AFUA_2G11850	60S ribosomal protein L3 (allergen Asp f 23)	-0.85	-0.17	2.41	3.44E-06
AFUA_2G04310	Argininosuccinate synthase (EC 6.3.4.5)	2.05	1.20	2.41	2.55E-03
AFUA_2G03720	Peptidyl-prolyl cis-trans isomerase (PPIase) (EC 5.2.1.8)	2.37	2.56	2.42	3.59E-07
AFUA_5G02410	ATP-dependent RNA helicase fal1 (EC 3.6.4.13)	2.16	0.34	2.42	8.11E-03
AFUA_5G01450	NADH-dependent flavin oxidoreductase, putative (EC 1.-.-.-)	1.38	0.75	2.43	2.37E-02
AFUA_4G06140	Dipeptidyl peptidase 3 (EC 3.4.14.4) (Dipeptidyl aminopeptidase III) (Dipeptidyl peptidase III)	2.72	2.86	2.43	1.13E-06
AFUA_1G13710	Isoleucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.5)	1.43	1.69	2.43	1.72E-06
AFUA_6G11260	Ribosomal protein L26	-0.95	-0.57	2.43	2.45E-02
AFUA_5G08270	HAD superfamily hydrolase, putative	3.17	3.28	2.43	1.08E-07
AFUA_5G03520	Uncharacterized protein	2.15	2.36	2.43	6.41E-07
AFUA_2G06040	Actin cortical patch component, putative	3.11	3.03	2.43	5.46E-09
AFUA_4G10800	40S ribosomal protein S6	1.50	0.17	2.43	1.34E-05
AFUA_3G08380	Inorganic diphosphatase, putative (EC 3.6.1.1)	2.61	2.82	2.44	1.92E-10
AFUA_1G02090	Quinone oxidoreductase, putative (EC 1.6.5.5)	2.48	2.22	2.44	7.49E-06
AFUA_5G05450	40S ribosomal protein S1	1.05	0.25	2.44	8.15E-08
AFUA_1G07010	Phosphatidate cytidylyltransferase (EC 2.7.7.41)	3.12	0.81	2.44	1.15E-02
AFUA_6G00770	Probable arabinan endo-1,5-alpha-L-arabinosidase C (EC 3.2.1.99) (Endo-1,5-alpha-L-arabinanase C) (ABN C)	3.60	3.10	2.44	3.91E-04
AFUA_4G06380	Sterol carrier protein, putative	0.71	2.15	2.45	7.99E-07
AFUA_2G05510	Mitochondrial F1F0 ATP synthase subunit F (Atp17), putative (EC 3.6.3.14)	1.89	1.16	2.45	1.23E-04
AFUA_4G00610	Aryl-alcohol dehydrogenase, putative (EC 1.1.-.-)	1.62	2.71	2.45	1.28E-03
AFUA_5G11040	Pantoate--beta-alanine ligase (EC 6.3.2.1)	1.20	2.08	2.46	1.10E-04
AFUA_2G04520	Fe-containing alcohol dehydrogenase, putative (EC 1.1.1.-)	1.84	2.61	2.46	2.08E-05
AFUA_5G09860	S-formylglutathione hydrolase (EC 3.1.2.12)	2.85	2.31	2.46	8.48E-06
AFUA_4G00740	Uncharacterized protein	1.97	1.06	2.46	2.53E-06
AFUA_8G04340	Cystathionine gamma-lyase (EC 4.4.1.8)	2.17	1.72	2.46	1.22E-03
AFUA_3G09320	Serine hydroxymethyltransferase (EC 2.1.2.1)	2.34	3.63	2.46	2.26E-10
AFUA_4G14530	Glutathione S-transferase-like protein tpcF (EC 2.5.1.-) (Trypacidin synthesis protein E)	0.83	3.02	2.46	2.76E-06
AFUA_3G04210	Fatty acid synthase alpha subunit FasA	0.72	0.76	2.47	5.17E-05
AFUA_4G12870	Methylmalonate-semialdehyde dehydrogenase, putative (EC 1.2.1.27)	2.43	2.51	2.47	1.72E-06
AFUA_1G06240	Riboflavin synthase, alpha subunit (EC 2.5.1.9)	2.97	2.97	2.47	1.10E-04
AFUA_3G04220	Fatty acid synthase beta subunit, putative	1.30	1.38	2.47	5.78E-09
AFUA_3G10970	Protein-tyrosine phosphatase 2 (EC 3.1.3.48)	2.63	1.09	2.48	3.79E-02
AFUA_1G05850	Erythromycin esterase, putative	-0.16	1.22	2.48	6.61E-03
AFUA_1G12920	Alpha-1,4 glucan phosphorylase (EC 2.4.1.1)	2.31	2.77	2.48	3.21E-07
AFUA_4G04350	DEAD helicases superfamily protein (Aquarius), putative	2.26	1.27	2.48	1.26E-02
AFUA_2G11020	Triosephosphate isomerase (EC 5.3.1.1)	1.77	2.19	2.49	5.43E-05
AFUA_4G12600	Phosphoribosyl-aminoimidazole carboxylase (EC 4.1.1.21)	2.05	2.13	2.49	3.52E-06
AFUA_2G09180	Coatomer subunit zeta, putative	1.38	1.53	2.49	2.59E-02

AFUA_8G04080	Betaine aldehyde dehydrogenase (BadH), putative (EC 1.2.1.8)	2.84	3.00	2.50	1.85E-06
AFUA_3G12560	Allantoicase Alc, putative (EC 3.5.3.4)	-0.32	1.93	2.50	3.74E-05
AFUA_1G14400	Hydroxyisocaproate dehydrogenase, putative (EC 1.1.1.95)	0.68	1.61	2.50	7.64E-03
AFUA_5G11430	Quinone oxidoreductase, putative (EC 1.6.5.5)	0.95	2.55	2.51	1.45E-09
AFUA_1G11770	COPII-coated vesicle protein SurF4/Erv29, putative	1.20	0.65	2.51	2.85E-03
AFUA_6G13180	CECR1 family adenosine deaminase, putative	1.74	1.99	2.52	3.02E-05
AFUA_4G07650	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) (Rotamase B)	1.62	2.05	2.52	4.36E-03
AFUA_7G02070	AIF-like mitochondrial oxidoreductase (Nfrl), putative	0.65	2.37	2.52	2.26E-08
AFUA_4G08600	Aldehyde dehydrogenase, putative (EC 1.2.1.3)	1.14	2.06	2.52	5.58E-06
AFUA_4G07050	L-lactate dehydrogenase (EC 1.13.12.4)	2.73	2.66	2.52	2.06E-06
AFUA_3G08640	Eukaryotic translation initiation factor 3 subunit I (eIF3i) (Eukaryotic translation initiation factor 3 39 kDa subunit homolog) (eIF-3 39 kDa subunit homolog)	2.38	1.42	2.53	2.45E-04
AFUA_4G13500	Aldehyde dehydrogenase	2.15	1.42	2.54	6.03E-05
AFUA_6G04660	Centromere protein Cse4, putative	2.02	1.28	2.55	1.63E-02
AFUA_1G02820	NADH-quinone oxidoreductase Pst2, putative	-0.37	2.10	2.55	9.33E-06
AFUA_8G07190	Uncharacterized protein	1.05	1.18	2.56	8.55E-04
AFUA_2G11940	Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	1.02	0.94	2.56	1.32E-06
AFUA_5G11660	Autophagy-related protein 18	2.64	2.18	2.57	1.54E-04
AFUA_3G10090	Dihydroneopterin aldolase domain protein (EC 4.1.2.25)	0.71	2.20	2.58	2.09E-05
AFUA_7G02280	U5 snRNP complex subunit, putative	2.93	2.45	2.59	8.28E-03
AFUA_5G01440	Allergen, putative (EC 1.-.-.-)	2.60	2.66	2.59	2.39E-07
AFUA_6G11430	Aldehyde dehydrogenase AldA, putative (EC 1.2.1.3)	2.11	2.91	2.59	4.34E-10
AFUA_6G12630	Leucyl-tRNA synthetase (EC 6.1.1.4)	0.81	1.47	2.60	8.15E-04
AFUA_4G08880	Glucose-6-phosphate 1-epimerase (EC 5.1.3.15)	-0.32	1.46	2.61	7.00E-05
AFUA_3G13900	Glutamate-cysteine ligase Gcs1, putative	0.85	1.49	2.61	2.19E-03
AFUA_6G07760	Proteasome regulatory particle subunit (RpnG), putative	2.46	1.02	2.61	2.81E-05
AFUA_4G04680	FGGY-family carbohydrate kinase, putative	0.81	1.82	2.61	1.73E-05
AFUA_6G02860	Isocitrate lyase (EC 4.1.3.1)	2.62	2.79	2.62	3.59E-07
AFUA_3G11710	Saccharopine dehydrogenase [NAD(+), L-lysine-forming] (SDH) (EC 1.5.1.7) (Lysine--2-oxoglutarate reductase)	1.46	1.93	2.62	3.46E-05
AFUA_7G00360	UDP-galactose 4-epimerase, putative (EC 5.1.3.-)	2.71	1.81	2.62	5.05E-08
AFUA_1G12890	60S ribosomal protein L5, putative	0.76	0.02	2.64	4.72E-09
AFUA_6G13550	Ribosomal protein S13p/S18e	0.35	0.31	2.64	7.41E-05
AFUA_6G12530	Translation initiation factor eif-2b epsilon subunit, putative (EC 2.7.7.-)	2.26	0.53	2.64	1.72E-04
AFUA_5G14310	Short chain dehydrogenase/reductase family protein	1.74	0.36	2.65	1.11E-02
AFUA_6G10660	ATP citrate lyase subunit (Acl), putatibe (EC 6.2.1.5)	0.19	1.91	2.65	1.23E-04
AFUA_5G03770	Lipase, putative (EC 3.1.1.3)	1.66	1.62	2.66	1.25E-03
AFUA_2G13710	NADH-ubiquinone oxidoreductase 49 kDa subunit, putative (EC 1.6.5.3)	0.42	0.93	2.66	2.07E-02
AFUA_4G07590	CaaX prenyl protease Ste24 (EC 3.4.24.84)	3.20	1.22	2.67	7.52E-04
AFUA_8G01390	Glycosyl hydrolase, putative	1.55	2.14	2.67	1.14E-04
AFUA_2G13860	Histone H4	2.56	2.36	2.68	1.57E-07
AFUA_3G02257	Uncharacterized protein	1.22	1.29	2.68	3.05E-04
AFUA_5G11720	26S proteasome regulatory subunit Mts4, putative	0.63	1.44	2.69	8.14E-05
AFUA_3G12100	Trehalose synthase (Ccg-9), putative (EC 2.4.1.-)	2.57	2.42	2.69	2.04E-05
AFUA_2G16200	Uracil phosphoribosyltransferase (EC 2.4.2.9)	2.20	2.25	2.69	1.16E-02
AFUA_2G17580	Scytalone dehydratase arp1 (EC 4.2.1.94) (Conidial pigment biosynthesis oxidase arp1)	0.58	2.49	2.69	2.24E-07
AFUA_5G10560	Cytochrome c oxidase subunit V	2.91	1.58	2.70	1.01E-06
AFUA_1G09660	Mitochondrial 2-oxodicarboxylate carrier protein, putative	3.45	1.64	2.72	2.28E-05
AFUA_6G07720	Phosphoenolpyruvate carboxykinase AcuF (EC 4.1.1.49)	2.81	2.33	2.72	2.44E-07
AFUA_2G15430	Sorbitol/xylulose reductase Sou1-like, putative (EC 1.-.-.-)	1.75	2.56	2.72	6.09E-04
AFUA_1G11710	Ribosomal protein	2.47	0.57	2.72	2.45E-06

AFUA_7G00700	Aldo-keto reductase (AKR13), puatative (EC 1.1.1.-)	1.86	1.56	2.73	2.34E-05
AFUA_2G01100	Pirin domain protein, putative	0.33	1.73	2.73	9.67E-04
AFUA_6G10900	UV-endonuclease UVE-1	1.70	2.63	2.73	1.88E-03
AFUA_5G01290	Zinc-binding oxidoreductase, putative (EC 1.-.-.-)	2.61	2.82	2.74	3.61E-04
AFUA_4G07710	Pyruvate carboxylase (EC 6.4.1.1)	1.40	1.84	2.74	9.52E-08
AFUA_6G13410	Pre-mRNA-splicing factor rse1	2.20	2.89	2.76	1.49E-09
AFUA_6G10650	ATP citrate lyase, subunit 1, putative (EC 2.3.3.8)	1.30	2.00	2.76	3.74E-08
AFUA_8G01100	Melibiase subfamily, putative (EC 3.2.1.22)	1.22	1.62	2.77	4.36E-04
AFUA_6G02440	60S ribosomal protein L24a	0.27	0.41	2.77	1.05E-03
AFUA_6G14100	Mitochondrial carnitine:acyl carnitine carrier, putative	3.46	2.04	2.78	2.40E-04
AFUA_4G07150	Cytochrome c subunit, putative	3.45	2.41	2.78	1.10E-06
AFUA_6G05090	RNA polymerase II Elongator subunit, putative	-0.19	1.92	2.79	3.47E-03
AFUA_1G09100	60S ribosomal protein L9, putative	0.09	-0.26	2.81	1.62E-06
AFUA_1G16270	Xylitol dehydrogenase XdhB (EC 1.1.1.14)	2.08	2.20	2.82	1.45E-03
AFUA_2G03290	14-3-3 family protein ArtA, putative	0.67	2.21	2.82	1.90E-07
AFUA_1G02570	Aspartyl-tRNA synthetase, cytoplasmic (EC 6.1.1.12)	3.37	1.41	2.82	2.34E-05
AFUA_3G04170	Pyruvate dehydrogenase E1 beta subunit PdbA, putative (EC 1.2.4.1)	0.96	1.49	2.82	9.42E-09
AFUA_4G05870	Oxidoreductase, short-chain dehydrogenase/reductase family	3.37	3.29	2.83	6.10E-06
AFUA_6G06750	14-3-3 family protein	0.77	2.32	2.84	2.93E-06
AFUA_3G00370	Phosphoketolase, putative (EC 4.1.2.-)	0.51	1.88	2.84	3.50E-05
AFUA_2G07380	60S ribosomal protein L18	0.87	0.05	2.85	7.06E-04
AFUA_1G13280	Mannose-6-phosphate isomerase (EC 5.3.1.8) (Phosphohexomutase) (Phosphomannose isomerase) (PMI)	2.00	2.77	2.85	5.16E-06
AFUA_1G06960	Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	1.08	1.40	2.85	5.87E-08
AFUA_1G05630	40S ribosomal protein S3, putative	1.32	0.34	2.85	3.90E-08
AFUA_7G00860	Lipoxygenase, putative (EC 1.13.11.-)	1.05	1.73	2.86	2.58E-04
AFUA_4G08170	Succinate-semialdehyde dehydrogenase Uga2, putative (EC 1.2.1.24)	1.43	2.03	2.87	8.68E-06
AFUA_3G00640	Uncharacterized protein	1.84	0.70	2.90	2.45E-03
AFUA_1G13790	Histone H3	2.16	2.07	2.90	5.44E-05
AFUA_1G10780	Aminomethyltransferase (EC 2.1.2.10) (Glycine cleavage system T protein)	2.19	3.06	2.90	4.94E-05
AFUA_5G06010	Eukaryotic translation initiation factor 6 (eIF-6)	2.53	1.64	2.91	2.74E-04
AFUA_5G04330	Aminopeptidase (EC 3.4.11.-)	3.23	3.14	2.91	1.04E-09
AFUA_7G01920	DNA-directed RNA polymerase subunit beta (EC 2.7.7.6)	2.37	1.88	2.91	1.36E-04
AFUA_5G12210	G protein complex beta subunit SfaD	2.36	1.81	2.92	7.28E-07
AFUA_5G09450	Isoflavone reductase family protein (EC 1.3.1.-)	1.60	1.94	2.92	3.41E-05
AFUA_2G10090	40S ribosomal protein S15, putative	1.67	0.87	2.93	1.64E-04
AFUA_2G07350	Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	2.50	2.64	2.93	1.11E-04
AFUA_4G11540	Glycerol kinase, putative (EC 2.7.1.30)	1.52	3.18	2.94	5.99E-05
AFUA_6G10260	Aldehyde reductase (AKR1), putative (EC 1.1.1.2)	3.26	3.25	2.95	3.81E-11
AFUA_4G10920	Uncharacterized protein	3.76	2.69	2.97	4.54E-05
AFUA_1G14090	Histidinol-phosphate aminotransferase (EC 2.6.1.9)	2.20	1.47	2.98	3.93E-06
AFUA_3G07430	Peptidyl-prolyl cis-trans isomerase (PPIase) (EC 5.2.1.8)	3.12	3.35	2.98	9.92E-09
AFUA_1G09930	Glycerol dehydrogenase Gcy1, putative (EC 1.1.1.-)	1.48	2.06	2.98	9.11E-09
AFUA_1G11130	60S ribosomal protein L6	1.24	0.67	2.98	4.44E-04
AFUA_7G04540	Short chain dehydrogenase/reductase family (EC 1.1.1.69)	0.87	2.53	2.98	2.26E-07
AFUA_1G05080	60S acidic ribosomal protein P0	1.33	0.33	2.99	1.59E-08
AFUA_5G03860	Alkaline phosphatase family protein (EC 3.1.-.-)	2.91	1.43	2.99	2.46E-03
AFUA_7G02550	Probable D-xylulose reductase A (EC 1.1.1.9) (Xylitol dehydrogenase A)	2.11	3.08	3.00	2.95E-08
AFUA_3G11480	Mitochondrial methylglutaconyl-CoA hydratase (Auh), putative (EC 4.2.1.18)	1.61	2.12	3.01	1.14E-06
AFUA_4G10790	Phosphoribosyl diphosphate synthase isoform 4	2.51	1.61	3.04	1.23E-04
AFUA_6G10980	UV-damaged DNA binding protein, putative	1.06	1.81	3.04	6.09E-05
AFUA_4G14580	O-methyltransferase tpcA (EC 2.1.1.-) (Trypacidin synthesis protein A)	-0.14	2.95	3.06	6.77E-07
AFUA_5G06390	Adenosine kinase, putative (EC 2.7.1.20)	2.09	1.25	3.06	2.24E-06

AFUA_2G02150	40S ribosomal protein S10a	2.48	0.92	3.06	1.80E-05
AFUA_5G10540	Glycogen branching enzyme GbeA, putative	0.91	2.23	3.06	1.39E-07
AFUA_4G07190	Ornithine carbamoyltransferase (EC 2.1.3.3)	2.47	3.65	3.07	6.27E-08
AFUA_5G03330	HypA-like protein, putative	3.28	2.78	3.08	2.01E-05
AFUA_3G11350	ATPase get3 (EC 3.6.-.-) (Arsenical pump-driving ATPase) (Arsenite-stimulated ATPase) (Golgi to ER traffic protein 3) (Guided entry of tail-anchored proteins 3)	2.82	1.72	3.08	7.97E-03
AFUA_3G08460	60S ribosomal protein L35Ae	0.98	0.77	3.10	9.03E-03
AFUA_4G07845	60S ribosomal protein L38, putative	1.15	1.37	3.10	7.41E-05
AFUA_1G01970	VeA-like protein	1.53	2.00	3.12	1.12E-03
AFUA_3G06970	40S ribosomal protein S9	2.75	0.77	3.13	2.34E-07
AFUA_4G08760	Phospho-2-dehydro-3-deoxyheptonate aldolase (EC 2.5.1.54)	2.94	2.29	3.14	1.80E-05
AFUA_2G04320	NADH-dependent flavin oxidoreductase, putative (EC 1.-.-.-)	2.88	3.06	3.15	6.48E-11
AFUA_1G02140	Glycogen debranching enzyme Gdb1, putative	0.87	1.98	3.18	1.08E-03
AFUA_4G11050	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial (EC 1.6.5.3) (EC 1.6.99.3)	1.96	1.85	3.19	1.70E-06
AFUA_2G16370	60S ribosomal protein L32	1.11	0.28	3.19	5.74E-07
AFUA_6G02370	Actin-related protein 2/3 complex subunit 4	3.24	2.67	3.19	5.22E-06
AFUA_6G12930	Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.3) (Citrate hydro-lyase) (Homocitrate dehydratase) (EC 4.2.1.-)	1.16	1.88	3.20	6.24E-07
AFUA_1G06770	40S ribosomal protein S26	1.12	0.35	3.21	2.81E-03
AFUA_1G05340	40S ribosomal protein S19	1.17	0.13	3.23	1.01E-04
AFUA_1G13500	Transketolase (EC 2.2.1.1)	2.21	3.24	3.23	5.10E-09
AFUA_7G05015	Glyoxalase family protein	3.23	3.11	3.23	5.16E-06
AFUA_1G05990	Ribosomal protein L16a	1.08	0.75	3.23	1.40E-07
AFUA_5G08350	37S ribosomal protein S16	0.79	0.27	3.23	3.46E-08
AFUA_3G00590	Asp-hemolysin (Asp-HS)	0.00	3.01	3.24	7.48E-09
AFUA_4G14520	Monoogygenase tpcG (EC 1.-.-.-) (Trypacidin synthesis protein G)	1.55	1.86	3.24	4.15E-05
AFUA_4G04300	Alanine racemase family protein, putative	0.78	2.85	3.24	3.63E-04
AFUA_1G06340	60S ribosomal protein L27	0.97	0.79	3.25	8.93E-06
AFUA_4G04460	60S ribosomal protein L13	1.14	0.48	3.26	1.59E-08
AFUA_2G10440	40S ribosomal protein S11	2.00	0.84	3.26	6.32E-05
AFUA_6G04560	37S ribosomal protein S9	0.95	2.24	3.28	4.88E-04
AFUA_1G15730	40S ribosomal protein S22	1.16	0.42	3.28	6.61E-06
AFUA_3G12300	60S ribosomal protein L22, putative	0.20	-0.02	3.29	1.33E-04
AFUA_2G01220	GTP cyclohydrolase II, putative (EC 3.5.4.25)	1.06	2.20	3.30	5.88E-03
AFUA_4G03880	60S ribosomal protein L7	0.03	0.25	3.30	1.24E-07
AFUA_1G04660	Ribosomal protein L15	1.90	0.74	3.30	1.58E-05
AFUA_3G10730	40S ribosomal protein S7	1.32	0.33	3.31	8.79E-05
AFUA_1G08930	Probable cytosolic iron-sulfur protein assembly protein 1	2.13	2.22	3.31	2.02E-03
AFUA_7G01460	Ribosomal protein S5	2.02	0.64	3.32	4.53E-09
AFUA_3G08470	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	1.41	3.06	3.33	8.66E-07
AFUA_3G06840	40S ribosomal protein S4	1.67	0.34	3.34	1.55E-08
AFUA_1G03390	60S ribosomal protein L12	1.71	0.76	3.35	1.44E-04
AFUA_2G09200	60S ribosomal protein L30, putative	0.99	0.46	3.36	2.88E-07
AFUA_1G15610	Oxidoreductase, zinc-binding dehydrogenase family, putative (EC 1.3.1.-)	3.27	3.06	3.36	9.47E-09
AFUA_6G03730	2-methylcitrate dehydratase, putative (EC 4.2.1.79)	2.67	2.66	3.38	1.01E-06
AFUA_1G14680	DNA-directed RNA polymerase subunit (EC 2.7.7.6)	2.25	2.02	3.38	4.43E-05
AFUA_3G14270	Aldo-keto reductase (AKR), putative (EC 1.1.1.-)	3.85	3.37	3.39	1.19E-04
AFUA_6G11620	Formyltetrahydrofolate deformylase, putative (EC 3.5.1.10)	2.40	2.58	3.40	1.24E-06
AFUA_3G11070	Pyruvate decarboxylase (EC 4.1.1.1)	1.95	3.42	3.43	9.50E-08
AFUA_5G04230	Citrate synthase	1.29	2.25	3.43	2.08E-07
AFUA_2G04130	40S ribosomal protein S11	1.54	0.29	3.44	1.24E-05
AFUA_2G09790	Glucose-6-phosphate isomerase (EC 5.3.1.9)	3.53	3.67	3.45	1.95E-08
AFUA_3G06880	Sorting nexin-3	2.81	2.58	3.46	3.16E-04
AFUA_1G04530	60S ribosomal protein L20	1.54	0.72	3.47	2.47E-06
AFUA_6G12990	Cytosolic large ribosomal subunit protein L7A	1.41	1.13	3.48	6.45E-08

AFUA_7G02140	40S ribosomal protein S24	1.90	1.10	3.49	1.13E-02
AFUA_3G05360	Histone H2A	1.50	2.69	3.49	3.10E-05
AFUA_1G14710	Beta-glucosidase, putative	1.63	2.70	3.52	4.34E-05
AFUA_6G12950	Trehalose-6-phosphate synthase (EC 2.4.1.15) (UDP-glucose-glucosephosphate glucosyltransferase)	3.01	1.98	3.52	7.43E-05
AFUA_2G03040	Ribosomal protein L34 protein, putative	0.10	0.60	3.53	1.60E-08
AFUA_7G02470	mRNA processing protein (Mss51), putative	1.86	2.70	3.53	1.59E-03
AFUA_1G09750	Aldehyde reductase (AKR1), putative (EC 1.1.1.2)	1.78	3.04	3.54	1.03E-08
AFUA_2G10300	40S ribosomal protein S17, putative	2.58	0.94	3.54	3.51E-05
AFUA_5G03020	60S ribosomal protein L4, putative	0.77	0.80	3.56	1.23E-08
AFUA_6G05200	60S ribosomal protein L28	0.62	-0.07	3.56	1.05E-04
AFUA_5G09680	Succinate dehydrogenase cytochrome b560 subunit (EC 1.3.5.1)	4.04	2.82	3.57	1.28E-05
AFUA_2G09210	60S ribosomal protein L10	1.05	0.67	3.59	2.78E-08
AFUA_4G08330	Aspartyl-tRNA synthetase, putative (EC 6.1.1.12)	2.81	2.80	3.60	1.77E-06
AFUA_4G13510	Isocitrate lyase (ICL) (Isocitrase) (Isocitratase) (EC 4.1.3.1) (Methylisocitrate lyase) (MICA) (EC 4.1.3.30) (Threo-D(S)-isocitrate glyoxylate-lyase)	1.37	2.27	3.61	6.63E-08
AFUA_3G06960	60S ribosomal protein L21, putative	2.65	0.47	3.65	3.25E-05
AFUA_3G13320	40S ribosomal protein S0	2.09	0.99	3.67	3.50E-07
AFUA_4G11730	Glycerol dehydrogenase (GldB), putative (EC 1.1.1.72)	1.29	2.83	3.70	5.34E-07
AFUA_5G06360	60S ribosomal protein L8, putative	0.78	0.65	3.74	6.35E-08
AFUA_2G16820	Curved DNA-binding protein (42 kDa protein) (EC 3.4.11.18)	0.20	0.97	3.74	3.30E-08
AFUA_3G00280	Metallo-beta-lactamase domain protein, putative	2.26	3.78	3.75	5.18E-04
AFUA_1G10150	Uncharacterized protein	3.69	2.92	3.83	2.18E-05
AFUA_5G05630	60S ribosomal protein L23	0.55	0.44	3.83	1.16E-04
AFUA_2G10500	40S ribosomal protein Rps16, putative	2.04	1.54	3.83	3.79E-05
AFUA_3G06070	Histone H1	2.55	2.66	3.86	1.66E-05
AFUA_3G02370	Short-chain dehydrogenase/reductase, putative (EC 1.-.-.-)	2.77	2.92	3.87	7.65E-07
AFUA_1G09440	40S ribosomal protein S23	1.93	0.27	4.03	1.00E-05
AFUA_4G07435	60S ribosomal protein L36	1.10	0.82	4.07	2.59E-04
AFUA_2G08130	60S ribosomal protein L44	1.76	1.02	4.10	2.38E-06
AFUA_4G07730	60S ribosomal protein L11	2.60	1.32	4.11	1.78E-06
AFUA_3G05600	60S ribosomal protein L27a, putative	0.74	0.90	4.14	8.86E-09
AFUA_7G05290	40S ribosomal protein S13	2.13	1.40	4.21	4.71E-06
AFUA_6G03830	Ribosomal protein L14	2.30	1.58	4.26	6.50E-08
AFUA_1G14410	60S ribosomal protein L17	1.79	1.58	4.32	4.06E-08
AFUA_6G13250	60S ribosomal protein L31e	1.73	2.03	4.41	2.79E-05
AFUA_6G12660	40S ribosomal protein S10b	1.66	0.41	4.49	1.26E-03
AFUA_6G12870	Iron-sulfur clusters transporter atm1, mitochondrial	4.78	2.84	4.54	4.29E-04
AFUA_2G16880	60S ribosomal protein L37a	0.96	1.79	4.84	7.06E-07
AFUA_2G03380	Alkaline serine protease	2.14	1.37	4.85	1.02E-04
AFUA_3G06760	60S ribosomal protein L37	2.46	2.44	5.25	9.40E-06
AFUA_6G12720	40S ribosomal protein S29, putative	2.17	0.92	5.44	5.97E-06
AFUA_6G02450	40S ribosomal protein S30	4.38	2.31	6.33	5.94E-10

* Log2 fold change of CEA10, ISSFT-021, and IF1SW-F4 compared to Af293 ($P < 0.05$)