LIST OF GENES DIFFERENTIALLY EXPRESSED IN THE MICROARRAY DATASETS

AD.1 *A. fumigatus* ATCC46645 transcript profile during initiation of murine infection

Locus	T0 vs T4	T0 vs T8	T0 vs T16	Comm_Name
Afu1g00810	1.09	2.08		Asp f7-like allergen, putative
Afu1g01300	0.42	1.9	3.91	GPI anchored protein, putative
Afu1g01310	0.37	1.49	3.42	carboxylesterase, putative
Afu1g01370	1.84	2.53	2.45	glutathione S-transferase, putative
Afu1g01490	2.76	1.92	2.6	NACHT domain protein
Afu1g01530	0.3	2	3.09	GrpB domain protein
Afu1g01540	2.06	4.7	4.91	Endonuclease/Exonuclease/phosphatase family family
Afu1g01550	1.52	3.54	4.09	high affinity zinc ion transporter, putative
Afu1g01640	1.79	2.11	1.44	kinesin family protein
Afu1g01680	3	3.22	3.41	branched-chain amino acid aminotransferase
Afu1g01690	2.38	4.26	4.54	cytochrome P450 alkane hydroxylase, putative
Afu1g01740	2.98	2.36	1.64	t-complex protein 1, beta subunit, putative
Afu1g01790	1.61	2.32	1.98	hypothetical protein
Afu1g01940	1.95	2.07	1.86	hypothetical protein
Afu1g02070	3.29	3.05	2.64	cytochrome c1, heme protein precursor
Afu1g02340	0.53	1.1	2.16	hypothetical protein
Afu1g02540	2.4	3.09	3.38	EF hand domain protein
Afu1g02550	2.56	3.63	2.53	tubulin alpha-1 subunit
Afu1g02860	1.79	1.78	2.81	C2H2 transcription factor, putative
Afu1g02880	3.5	4.33	2.13	Phosphotransferase enzyme family domain protein
Afu1g02890	4.18	4.82	5.29	dUTPase (Dut), putaive
Afu1g02900	2.32	2.36	2.97	pyridoxal kinase, putative
Afu1g02910	2.75	4.56	4.97	hypothetical protein
Afu1g02930	1.24	3.16	2.97	Ca2+ binding protein (calmodulin), putative
Afu1g03060	2.38	3.12	2.2	F-actin capping protein beta subunit
Afu1g03080	1.94	2.43	2.97	carboxylic ester hydrolase (Ppe1), putative
Afu1g03100	1.98	2.71	2.23	ATP synthase delta chain, mitochondrial precursor, putative
Afu1g03120	2.96	3.24	2.92	hypothetical protein
Afu1g03420	1.37	2.16	1.1	adenylate kinase 2

Afu1g03550	4.09	3.94	2.73	mitochondrial dihydroxy acid dehydratase, putative
Afu1g03610	1.9	2.39	4.35	hypothetical protein
Afu1g03630	3.4	5.36	5.91	GPI anchored serine-threonine rich protein
Afu1g03720	2.17	2.94	2.2	UPF0136 domain protein
Afu1g03890	2.92	2.81	3.75	alpha/beta hydrolase, putative
Afu1g04130	3.3	3.61	3.15	FG-GAP repeat protein, putative
Afu1g04150	1.1	0.82	2.24	tartrate dehydrogenase
Afu1g04280	2.36	2.07	2.5	Ribosomal protein S7p/S5e, putative
Afu1g04300	3.99	4.1	5.14	hypothetical protein
Afu1g04310	1.9	2.27	1.99	hypothetical protein
Afu1g04320	2.13	1.91	1.93	ribosomal protein S8.e
Afu1g04340	1.4	1.93	2.24	SH3 and Ded_cyto domain protein, putative
Afu1g04430	1.23	2.06	2.41	conserved hypothetical protein
Afu1g04440	1.99	2.15	2.12	PrnX protein
Afu1g04460	1.98	1.95	2.2	lysyl-tRNA synthetase, putative
Afu1g04540	2.81	3.24	3.21	NADH-cytochrome b5 reductase precursor
Afu1g04550	2.17	2.48	3.12	HMG box protein, putative
Afu1g04560	3.21	3.27	4.08	urease, putative
Afu1g04760	1.55	2.39	1.95	conserved hypothetical protein
Afu1g04900	1.39	2.3	1.51	proliferating cell nuclear antigen (pcna)
Afu1g05080	3.09	2.7	1.14	ribosomal protein P0
Afu1g05100	2	1.89	2.07	GARP complex subunit Vps53, putative
Afu1g05280	3.23	3.66	3.44	conserved hypothetical protein
Afu1g05300	1.9	2.24	2.02	capsular associated protein, putative
Afu1g05320	2.17	2.66	2.03	disulfide isomerase, putative
Afu1g05340	2.07	2.36	2.11	ribosomal protein S19 (s16)
Afu1g05520	3.64	3.62	3.51	mandelate racemase/muconate lactonizing enzyme family protein
Afu1g05580	1.39	2.46	2.11	glycogenin
Afu1g05630	3.31	3.38	3.09	40s ribosomal protein s3
Afu1g05790	2.76	4.87	4.62	GPI anchored serine-rich protein
Afu1g05810	2.09	2.28	3.17	conserved hypothetical protein
Afu1g05820	2.45	2.81	2.97	conserved hypothetical protein
Afu1g05870	2.28	2	2.28	scs3 protein
Afu1g05930	3.11	3.48	3.09	serine/threonine protein kinase, putative
Afu1g05940	4.11	4.32	4.92	conserved hypothetical protein
Afu1g05960	2.89	3.81	4.07	Peptidase family M28 family
Afu1g06110	2.56	2.5	2.49	conserved hypothetical protein

Afu1g06200	2.06	2.9	1.93	Mn2+ homeostasis protein (Per1), putative
Afu1g06240	2.1	2.56	1.71	riboflavin synthase, alpha subunit
Afu1g06250	2.26	2.74	0.93	CAIB/BAIF family enzyme
Afu1g06330	-0.04	2	1.38	conserved hypothetical protein
Afu1g06680	1.9	2.56	2.08	VHS domain protein
Afu1g06790	2.24	1.68	2.3	importin beta-3 subunit, putative
Afu1g06940	2.97	3.33	3.47	chorismate synthase
Afu1g07080	2.21	1.7	2.22	tRNA-specific adenosine-34 deaminase subunit Tad3, putative
Afu1g07130	2.13	2.88	1.51	dienelactone hydrolase family protein
Afu1g07200	2.5	2.72	1.8	mitochondrial cytochrome b2, putative
Afu1g07230	1.9	1.75	2.54	DSBA-like thioredoxin domain protein
Afu1g07320	2.2	2.07	2	chromosome segregation protein (SepB), putative
Afu1g07330	1.71	2.01	-0.38	dihydroxy-acid dehydratase, putative
Afu1g07380	2.05	1.58	1.52	NADH-dependent glutamate synthase (GLT1), putative
Afu1g07400	2	2.09	1.88	hypothetical protein
Afu1g07430	1.87	2.52	2.69	hypothetical protein
Afu1g07440	2.24	2.28	2.35	molecular chaperone Hsp70
Afu1g07520	3.14	3.44	2.25	dimeric dihydrodiol dehydrogenase, putative
Afu1g07560	1.56	1.65	2.4	MYB DNA-binding domain protein
Afu1g07570	2	2.39	2.33	hypothetical protein
Afu1g08850	2.14	2.42	1.9	septin
Afu1g08930	2.33	2.33	2.1	WD repeat protein
Afu1g09010	1.89	2.25	2	methionyl-tRNA synthetase
Afu1g09310	1.62	2.07		DUF6 domain protein, putative
Afu1g09480	1.66	2.31	1.75	vacuolar protein sorting 29, putative
Afu1g09510	2.38		2.21	GPI anchored serine-threonine rich protein
Afu1g09520	1.69	1.76	2.46	hypothetical protein
Afu1g09600	2.19	2.06	2.11	N-acetyltransferase complex ARD1 subunit, putative
Afu1g09660	1.92	1.92	2.19	mitochondrial 2-oxodicarboxylate carrier protein, putative
Afu1g09690	2.41	3.6	4.17	tRNA ligase
Afu1g09760	1.86	2.43	1.75	UPF0171 domain protein
Afu1g09810	2.32	2.92	3.13	PUA RNA binding domain protein, putative
Afu1g09830	2.05	1.75	1.37	Hsc70 cochaperone (SGT), putative
Afu1g09960	2.41	2.46	1.98	conserved hypothetical protein
Afu1g10020	2.32	4.87	3.48	reverse transcriptase, RNaseH
Afu1g10030	1.32	2.35	1.98	hypothetical protein
Afu1g10100	3.11	2.75	2.22	3-oxoacyl-(acyl-carrier-protein) reductase

Afu1g10110	2.19	2.05	1.69	TIM-barrel enzyme family protein
Afu1g10120	1.77	1.74	2.84	ABC transporter permease protein
Afu1g10220	-0.64	0.82	2.58	hypothetical protein
Afu1g10350	2.68	3	2.96	phosphoglycerate kinase PgkA, putative
Afu1g10460	1.05	2.41	2.74	hypothetical protein
Afu1g10520	2.97	3.11	2.97	hypothetical protein
Afu1g10570	2.06	2.33	2.56	glycerol-3-phosphate phosphatase (GppA), putative
Afu1g10580	1.49	2.11	1.69	homeobox transcription factor, putative
Afu1g10590	1.88	2.53	2.9	GPI anchored protein, putative
Afu1g10780	5.18	5.42	5.95	glycine cleavage system T protein
Afu1g10790	1.88	2.07	2.31	alpha-1,2-mannosidase family protein, putative
Afu1g10800	4.09	3.83	3.72	thioesterase family protein
Afu1g10820	2.75	2.7	2.74	adenylylsulfate kinase
Afu1g10840	2.19	2.34	2.42	hypothetical protein
Afu1g10900	2.01	3.13	2.95	conserved hypothetical protein
Afu1g10910	3.36	3.77	2.89	tubulin beta, putative
Afu1g10930	4.51	3.79	2.39	ammonium transporter
Afu1g11010	1.82	3.03	1.81	oxidoreductase, short chain dehydrogenase/reductase family superfamily
Afu1g11040	0.89	3.17		hypothetical protein
Afu1g11250	0.85	2.5	0.24	amidohydrolase, putative
Afu1g11380	1.7	2.19	1.77	integral membrane protein, putative
Afu1g11390	2.29	3.07		cytochrome P450, putative
Afu1g11450	0.9	2.32	1.21	myosin class II heavy chain (MHC), putative
Afu1g11470	2.48	2.88	2.74	endosomal cargo receptor (P24), putative
Afu1g11480	4.97	5.52	5.29	hypothetical protein
Afu1g11530	3.26	3.01	2.18	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase
Afu1g11540	2.17	2.07	1.18	CORD and CS domain protein
Afu1g11790	1.31	2.06	0.83	PUTATIVE NUCLEOSIDE HYDROLASE PROTEIN
Afu1g11800	1.49	2.06	2.6	HLH transcription factor, putative
Afu1g11810	0.78	2.01	0.79	hypothetical protein
Afu1g11820	0.98	2.83		MFS transporter, putative
Afu1g11990	2.09	2.27	2.67	conserved hypothetical protein
Afu1g12050	2.38	2.81	2.42	acetyltransferase, GNAT family family
Afu1g12190	3.32	3.75	3.58	conserved hypothetical protein
Afu1g12270	0.68	0.95	2.03	hypothetical protein
Afu1g12290	3.93	4.46	4.54	possible NADH-ubiquinone oxidoreductase
Afu1g12310	2.75	2.85		GABA permease GabA

Afu1g12510	3.3	4.11	3.57	isoflavone reductase family protein
Afu1g12620	1.71	2.76	3.72	MFS toxin efflux pump (AflT), putative
Afu1g12690	3.51	4.29	4.28	ABC multidrug transporter Mdr4
Afu1g12740	2.35	3.02	3.22	hypothetical protein
Afu1g12860	0.93	1.95	2.08	DUF718 domain protein
Afu1g12920	2.6	2.66	1.38	glycogen phosphorylase 1; possible glycogen phosphorylase
Afu1g13090	1.79	2.13	2.61	anthranilate synthase multifunctional protein
Afu1g13200	1.4	1.43	2.86	conserved hypothetical protein
Afu1g13230	2.14	3.54	4.91	conserved hypothetical protein
Afu1g13240	2.36	2.76	3.82	adenosine deaminase, putative
Afu1g13330	3.47	3.52	2.96	Arp2/3 complex subunit (Arp2), putative
Afu1g13480	1.67	2.04	2.16	ubiquinol-cytochrome C reductase complex subunit UcrQ, putative
Afu1g13490	2.96	2.86	2.91	spermidine synthase
Afu1g13500	3.89	4.14	3.55	transketolase TktA
Afu1g13620	1.72	2.34	3.04	oligopeptide transporter, OPT family, putative
Afu1g13720	2.7	2.96	1.98	intracellular protein transport protein (UsoA), putative
Afu1g13740	3.55	3.45	3.68	pentafunctional polypeptide (AroM), putative
Afu1g13780	1.94	3.89	3.11	histone H4
Afu1g13860	0.51	1.34	2.16	conserved hypothetical protein
Afu1g13930	2.94	3.67	2.87	Leucine carboxyl methyltransferase superfamily
Afu1g13960	2.6	3.26		DUF292 domian protein
Afu1g14200	2.59	2.32	1.91	mitochondrial processing peptidase beta subunit, putative
Afu1g14210	3.09	2.72	1.41	putative nucleoside-diphosphate-sugar epimerase
Afu1g14240	2.31	2.12	2.86	conserved hypothetical protein
Afu1g14260	2.19	2.28	1.67	related to TGF beta receptor associated protein 1
Afu1g14350	3.71	3.54	3.38	2-deoxy-D-gluconate 3-dehydrogenase, putative
Afu1g14380	3.31	3.72	3.46	3-ketoacyl-acyl carrier protein reductase
Afu1g14390	4.9	5.75	5.88	zinc binding dehydrogenase family protein
Afu1g14400	2.1	2.39	1.6	glyoxylate reductase
Afu1g14450	0.36	2.26	1.08	exo-beta-1,3-glucanase Exg0
Afu1g14520	3.12	2.88	4.99	pyridine nucleotide-disulphide oxidoreductase, putative
Afu1g14530	3.58	3.87	2.63	general amidase-B
Afu1g14540	2.83	3.11	1.64	oxidoreductase, short-chain dehydrogenase/reductase family
Afu1g14550	5.98	6.76	6.71	Mn superoxide dismutase MnSOD
Afu1g15040	1.3	2.11	2.24	hypothetical protein

Afu1g15050	2.04	2.64	1.36	Hsp70 chaperone (Orp150), putative
Afu1g15060	2.09	2.15	1.28	hypothetical protein
Afu1g15150	1.71	2.27	1.75	alpha-amylase (amyE)
Afu1g15210	2.88	2.74	2.37	conserved hypothetical protein
Afu1g15220	1.74	2.34	2.6	conserved hypothetical protein
Afu1g15240	2.49	2.69	2.95	prefoldin subunit 4, putative
Afu1g15280	3.55	3.58	4.4	polysaccharide deacetylase family protein
Afu1g15290	2	2.1	1.25	hypothetical protein
Afu1g15330	4.48	4.95	4.94	T10O22.24
Afu1g15550	1.47	2.23	1.87	homeobox and C2H2 transcription factor, putative
Afu1g15680	2.49	3.76	3.14	C6 finger domain protein, putative
Afu1g15690	0.33	2.37	1.86	conserved hypothetical protein
Afu1g15780	2.63	2.1	2.1	3-isopropylmalate dehydrogenase
Afu1g15960	2.15	1.89	1.66	glutathione reductase
Afu1g16190	1.92	2.41	1.91	cell wall glucanase Crf1
Afu1g16200	0.48	2.05	1.67	hypothetical protein
Afu1g16250	5.68	6.62	5.96	alpha-glucosidase B
Afu1g16270	0.79	2.82		xylitol dehydrogenase XdhB, putative
Afu1g16470	2.71	2.88	3.29	metallo-beta-lactamase domain protein, putative
Afu1g16480	4.36	4.16	4.45	acid phosphatase, putative
Afu1g16510	1.51	1.86	2.34	heme/steroid binding domain protein, putative
Afu1g16560	0.43	3.02	3.33	MIF domain protein
Afu1g16640	2.67	4.01	3.72	hypothetical protein
Afu1g16670	1.89	2.38	0.9	hypothetical protein
Afu1g16700	2.49	3.46	4.17	beta galactosidase, putative
Afu1g16760	1.32	3.88	3.86	acetyltransferase, GNAT family family
Afu1g16770	1.46	3.63	3.81	amidase
Afu1g16880	2.01	2.36	2.27	ABC multidrug transporter, putative
Afu1g17030	1.37	1.6	2.34	glycosyl transferase, putative
Afu1g17050	1.6	2.6	1.41	hypothetical protein
Afu1g17140	2.49	4.51	2.22	voltage-gated K+ channel beta subunit (KCNAB), putative
Afu1g17150	1.88	3.39	2	C6 transcription factor, putative
Afu1g17160	1.55	2.9	1.37	transporter, putative
Afu1g17170	4.99	6.79	6.42	alpha-ketoglutarate-dependent taurine dioxygenase
Afu1g17180	6.58	7.25	7.49	pyridine nucleotide-disulphide oxidoreductase, putative
Afu1g17190	4.47	5.67	5.98	long-chain-fatty-acid-CoA ligase, putative
Afu1g17200	4.63	5	5.55	nonribosomal peptide synthase, putative

Afu1g17270	1.48	2.94	3.41	ferric-chelate reductase (Fre2), putative
Afu1g17390	1.11	2.31	1.08	hypothetical protein
Afu1g17470	1.9	2.36	2.22	high affinity nitrate transporter NrtB
Afu1g17480	2.44	3.81	3.77	conserved hypothetical protein
Afu1g17490	1.91	3.35	2.42	glucokinase regulator family protein, putative
Afu1g17530	2.21	3.29	3.05	MFS transporter, putative
Afu1g17590	2.17	4.23	2.6	phosphoesterase superfamily protein
Afu1g17640	2.8	2.74	2.51	melanin biosynthesis transcription factor RegA
Afu1g17650	2.52	2.37	2.04	short chain dehydrogenase, putative
Afu1g17670	1.84	2.06		salicylate hydroxylase, putative
Afu1g17680	2.16	2.41	2.54	MFS transporter, putative
Afu1g17700	2.81	5.13	2.53	short chain dehydrogenase, putative
Afu1g17750	3.38	3.13	3.94	nicotinamide N-methyltransferase, putative
Afu2g00260	1.52	2.42		phenylacetaldoxime dehydratase family protein, putative
Afu2g00320	2.9	4.47	4.44	sterol delta 5,6-desaturase, putative
Afu2g00370	-0.21	1.47	2.05	conserved hypothetical protein
Afu2g00500	-0.05	3.11	2.92	conserved hypothetical protein
Afu2g00540	0.45	1.47	2.44	carboxyphosphonoenolpyruvate phosphonomutase, putative
Afu2g00570	0.61	3.02	3.5	GNAT family acetyltransferase, putative
Afu2g00590	2.43	2.95	2.46	glutathione-S-transferase, putative
Afu2g00640	4.03	5.32	4.43	beta-N-hexosaminidase, putative
Afu2g00710		2.13		alpha-amylase, putative
Afu2g00720	2.52	3.99	4.35	aldehyde dehydrogenase, putative
Afu2g00750	2.35	3.06	2.44	oxidoreductase, 2OG-Fe(II) oxygenase family, putative
Afu2g00760	0.61	3.13	2.33	pectate lyase A
Afu2g00770	4.13	3.87	5.12	salicylate hydroxylase
Afu2g00790	1.78	2.21	3.01	hypothetical protein
Afu2g00820	2.65	3.93	4.21	extracellular GDSL-like lipase/acylhydrolase, putative
Afu2g00870	0.84	2.97		hypothetical protein
Afu2g00880	1.99	3.22	3.49	conserved hypothetical protein
Afu2g00890	1.58	2.37	3.05	hypothetical protein
Afu2g01010	1.83	2	1.25	myo-inositol-phosphate synthase, putative
Afu2g01030	2.3	3.54	3.18	1-aminocyclopropane-1-carboxylate deaminase, putative
Afu2g01040	3.9	4.52	3.84	formaldehyde dehydrogenase
Afu2g01070	3.64	4.14	3.91	GPI-anchor biosynthesis protein (Pig-F), putative
Afu2g01130	1.3	2.09	1.81	ubiquitin conjugating enzyme (UbcJ), putative
Afu2g01240	3.14	1.82	1.33	beta-D-fructofuranoside fructohydrolase

Afu2g01280	4.15	3.59	4.04	D-mandelate dehydrogenase, putative
Afu2g01300	2.35	3.47	3.47	conserved hypothetical protein
Afu2g01310	1.38	2.69	2.42	EF-hand domain protein
Afu2g01320	4.47	5.26	5.12	P-type ATPase, putative
Afu2g01360	2.52	2.9	2.86	nucleotide-binding GAF domain protein
Afu2g01380	2.07	3.81	5.14	GNAT family acetyltransferase, putative
Afu2g01390	1.45	1.61	2.66	S-adenosylmethionine-dependent methyltransferase, putative
Afu2g01460	1.53	2.09	1.86	ZIP Zinc transporter, putaitve
Afu2g01540	2.47	2.83	2.59	conserved hypothetical protein
Afu2g01690	1.67	2.63	1.37	conserved hypothetical protein
Afu2g01710	-0.43	2.12	1.88	GPI anchored protein, putative
Afu2g01790	1.15	2.12	1.68	conserved serine proline-rich protein
Afu2g02050	2.37	2.58	1.97	peptidyl-prolyl cis-trans isomerase, putative
Afu2g02090	2.3	2.98	2.41	methylated-DNA-protein-cysteine methyltransferase
Afu2g02100	2.4	2.02	1.86	dihydrolipoamide dehydrogenase
Afu2g02140	1.84	1.92	2.56	CUE domain protein, putative
Afu2g02490	1.71	2.5	2.54	hypothetical protein
Afu2g02500	1.27	2.49	2.81	conserved hypothetical protein
Afu2g02590	2.15	2.09	0.78	aspartyl-tRNA synthetase
Afu2g02810	2.57	1.87	1.1	alcohol dehydrogenase, zinc-containing, putative
Afu2g03150	0	0.41	2.63	kinesin family protein
Afu2g03330	2.64	3.28	3.53	phytanoyl-CoA dioxygenase family protein
Afu2g03510	1.3	2.2	1.11	pheromone processing carboxypeptidase (Sxa2), putative
Afu2g03570	2.3	2.41	2.43	transposase
Afu2g03600	1.76	2.1		NUDIX family hydrolase, putative
Afu2g03730	1.89	3.25	1.85	Ctr copper transporter family protein
Afu2g03770	2.01	2.12	1.24	isochorismatase family hydrolase, putative
Afu2g03830	3.3	4.68	4.88	allergen Asp F4
Afu2g03840	3.03	3.33	2.52	mitochondrial import receptor subunit (Tom37), putative
Afu2g03870	2.44	2.91	2.63	FKBP-type peptidyl-prolyl isomerase, putative
Afu2g03880	2.38	2.96	2.82	heme binding protein, putative
Afu2g03990	2.01	2.48	2.39	hypothetical protein
Afu2g04060	2.05	1.88	0.96	NADH:flavin oxidoreductase/NADH oxidase family protein
Afu2g04220	0.34	2.18	0.35	homogentisate 1,2-dioxygenase (HmgA), putative
Afu2g04280	1.86	1.19	2.21	asparaginase, putative
Afu2g04300	3.57	3.76	4.54	lipase/esterase, putative

Afu2g04310	2.2	1.99	2.45	argininosuccinate synthase
Afu2g04370	1.67	2.01	2.51	glutamate carboxypeptidase
Afu2g04390	2.55	2.68	2.34	cytomegalovirus gH-receptor family protein, putative
Afu2g04490	3.49	4.17	4.55	D-3-phosphoglycerate dehydrogenase
Afu2g04520	2.6	2.91	3.16	Fe-containing alcohol dehydrogenase, putative
Afu2g04540	2.39	3.42	2.85	hypothetical protein
Afu2g04560	2.4	1.85	1.22	oxidoreductase, short-chain dehydrogenase/reductase family
Afu2g04570	4.63	4.75	4.86	BNR/Asp-box repeat domain protein
Afu2g04590	3.98	3.64	3.35	alcohol dehydrogenase, putative
Afu2g04600	2.8	3.06	2.39	C6 transcription factor, putative
Afu2g04610	1.82	1.8	2.29	DUF967 domain protein
Afu2g04620	2.3	1.96	2.03	ER Hsp70 chaperone BiP, putative
Afu2g04700	2.16	1.75	1.32	RNA binding effector protein (Scp160), putative
Afu2g04710	2.27	2.75	2.45	cytochrome b5, putative
Afu2g04980	1.63	2.52	2.41	tyrosine decarboxylase, putative
Afu2g05080	2.56	2.86	2.96	hypothetical protein
Afu2g05150	2.81	5.54	6.01	cell wall galactomannoprotein Mp2
Afu2g05180	1.91	1.8	2.98	NF-X1 finger and helicase domain protein, putative
Afu2g05190	1.91	1.49	2.53	monosaccharide transporter
Afu2g05220	1.4	2.41		conserved hypothetical protein
Afu2g05260	1.61	2.11	1.83	salicylate hydroxylase
Afu2g05310	2.28	2.43	2.46	C6 transcription factor, putative
Afu2g05320	2.42	2.18	1.97	ion transporter
Afu2g05340	2.6	2.92	3.15	1,3-beta-glucanosyltransferase, putative
Afu2g05360	3.37	2.23	2.2	C6 transcription factor, putative
Afu2g05400	1.99	3.25	3.32	sugar hydrolase, putative
Afu2g05590	3.39	3.65	3.2	ubiquitin C-terminal hydrolase L3
Afu2g05650	2.25	2.49	2.5	cytoplasmic asparaginyl-tRNA synthetase, putative
Afu2g05720	1.03	1.94	2.24	conserved hypothetical protein
Afu2g05750	1.41	2.66	1.91	agmatinase, putative
Afu2g05800	4.64	5.43	5.23	IdgA domain protein
Afu2g05810	3.43	3.26	3.76	dienelactone hydrolase
Afu2g05820	3.62	3.88	3.72	Riboflavin kinase, putative
Afu2g05860	1.4	1.17	2	calcium/mangenease P-type ATPase, putative
Afu2g05890	1.26	2	1.28	conserved hypothetical protein
Afu2g06150	2.45	2.62	1.44	disulfide isomerase, putative
Afu2g07440	1.59	2.66	2.27	thioesterase family protein

Afu2g07680	4.13	4.69	5.01	L-ornithine N5-oxygenase SidA
Afu2g07750	2.84	3.9	4.69	haloacid dehalogenase, type II
Afu2g07780	3.18	3.52	3.73	acyl-CoA synthetase, putative
Afu2g07810	3.96	4.17	4.41	cytosolic hydroxymethyltransferase, putative
Afu2g07840	1.86	3.57	2.83	competence/damage-inducible protein CinA, putative
Afu2g07910	2.84	3.59	3.82	myo-inositol transporter
Afu2g07940	2.34	3.04	3.27	NADPH-cytochrome P450 reductase (CprA), putative
Afu2g07970	1.95	2.06	2.17	ribosomal protein L19
Afu2g08050	1.51	2.32	1.13	short chain dehydrogenase/reductase family protein
Afu2g08090	0.47	1.78	2.8	hypothetical protein
Afu2g08180	0.49	2.39	1.63	flotillin domain protein
Afu2g08260	1.41	1.98	2.54	FMN binding oxidoreductase, putative
Afu2g08300	3.58	3.34	1.98	DnaJ domain protein, putative
Afu2g08430	1.71	2.35	2.13	acetyltransferase, CysE/LacA/LpxA/NodL family
Afu2g08460	1.94	1.19	2.24	pseudouridylate synthase
Afu2g08470	0.31	2.47	1.23	GTP binding protein (Bud4), putative
Afu2g08550	1.95	2.86	1.93	peptidyl-prolyl cis/trans isomerase
Afu2g08790	1.73	2.15	2.31	zinc carboxypeptidase, putative
Afu2g08800	2.36	3.56	3.13	amino acid permease (Dip5), putative
Afu2g08880	1.66	2.01	1.28	hypothetical protein
Afu2g08890	2.01	1.63	1.38	dihydrofolate reductase
Afu2g09030	2.45	4.64	4.24	secreted dipeptidyl peptidase
Afu2g09060	3.3	4.15	4.27	DNA replication licensing factor Mcm4, putative
Afu2g09070	2.38	3.69	3.86	DUF221 domain protein, putative
Afu2g09290	2.03	1.37	1	antigenic mitochondrial protein HSP60, putative
Afu2g09450	2.56	4.05	3.26	carboxylic acid transport protein
Afu2g09560	2.05	1.91	2.21	Mgm101 protein
Afu2g09620	1.74	2	2.07	phytanoyl-CoA dioxygenase family protein
Afu2g09650	1.67	1.48	2.14	aspartate transaminase, putative
Afu2g09670	3.36	3.69	4.08	SNARE protein (Ufe1), putative
Afu2g09680	1.59	1.84	2.33	PB1 domain protein, putative
Afu2g09780	2.66	2.95	3.22	hypothetical protein
Afu2g09790	2.64	3.04	2.17	glucose-6-phosphate isomerase
Afu2g09810	2.82	2.85	2.35	mandelate racemase/muconate lactonizing enzyme family protein
Afu2g09840	2.82	2.71	2.78	folic acid synthesis protein
Afu2g09850	3.43	4.47	3	oxidoreductase, 2-nitropropane dioxygenase family, putative

Afu2g10140	1.6	2.45	2.46	DNA replication licensing factor Mcm7, putative
Afu2g10150	2.61	3.05	2.64	peroxisome biosynthesis protein (PAS1/Peroxin-1), putative
Afu2g10190	0.94	2.04	1.86	hypothetical protein
Afu2g10220	2.68	3.62	1.48	glycerol dehydrogenase, putative
Afu2g10230	1.05	1.4	2.15	myo-inositol oxygenase
Afu2g10280	1.63	2	0.55	ketoreductase
Afu2g10560	0.95	0.9	2.31	amino acid permease
Afu2g10650	3	3.32	2.79	enoyl-CoA hydratase
Afu2g10660	1.8	2.02	1.28	mannitol-1-phosphate dehydrogenase
Afu2g10730	3.2	4.31	4.22	DNA polymerase alpha catalytic subunit, putative
Afu2g10910	1.59	2.91	2.33	maltose permease
Afu2g10920	1.95	2.86	1.53	enoyl-CoA hydratase/isomerase family protein
Afu2g10950	2.79	3.53	3.84	hypothetical protein
Afu2g11010	3.93	4.22	4.16	dihydroorotate reductase PyrE, putative
Afu2g11060	2.24	3.09	2.4	Acyl CoA binding protein family
Afu2g11490	2.15	2.13	3.28	acetylglutamate synthase
Afu2g11520	3.09	3.01	2.8	MFS monosaccharide transporter, putative
Afu2g11540	2.1	2.23	1.48	ketoreductase, putative
Afu2g11600	2.97	3.71	2.61	oxidoreductase, putative
Afu2g11860	1.18	2.02	2.61	hypothetical protein
Afu2g11970	2.4	2.49	3.52	phospholipase A2 (PlaA), putative
Afu2g11990	1.78	1.28	2.63	phosphoinositide phosphatase Pten/Tep1, putative
Afu2g12020	1.71	2.33	1.9	U6 snRNA-associated Sm-like protein LSM4, putative
Afu2g12080	2.08	2.55	2.06	mitochondrial phosphate transporter, putative
Afu2g12400	2.17	1.93	1.78	ATP synthase oligomycin sensitivity conferral protein, putative
Afu2g12600	0.69	3.27	3.32	hypothetical protein
Afu2g12680	-0.46	3.6	2.7	conserved hypothetical protein
Afu2g12740	1.98	2.35	2.1	methyltransferase, putative
Afu2g12760	2.57	2.91	3.38	conserved hypothetical protein
Afu2g12790	2.84	3.77	3.78	monocarboxylate transporter-like protein
Afu2g12900	2.24	2.19	1.61	Ni ion binding urease accessory protein UreG, putative
Afu2g12940	1.81	1.9	2.23	conserved hypothetical protein
Afu2g12980	2.7	3.17	3.27	protein transport protein (SEC31), putative
Afu2g13010	2.34	2.48	2.68	cytochrome c oxidase polypeptide vib
Afu2g13160	2.03	3.12	4.86	hypothetical protein
Afu2g13170	2.76	3.03	3.35	hypothetical protein

Afu2g13250	2.07	1.46	1.24	bifunctional tryptophan synthase TRPB
Afu2g13270	1.18	3.81	2.88	alcohol dehydrogenase, putative
Afu2g13290	2.69	3.93	3.64	GYF domain protein
Afu2g13450	2.36	3.21	2.52	dynactin, putative
Afu2g13460	0.52	1.22	2.07	alpha-amylase, putative
Afu2g13580	2.09	2.51	2.15	conserved hypothetical protein
Afu2g13620	2.16	1.72	1.69	thiamine pyrophosphate enzyme, putative
Afu2g13650	1.53	2.06		hypothetical protein
Afu2g13740	2.29	2.58	2.21	conserved hypothetical protein
Afu2g13800	2.63	3.04	3.44	malate dehydrogenase
Afu2g13880	1.35	2.01	2.69	SH3 domain protein
Afu2g13890	1.28	1.88	2.03	annexin ANXC3.2
Afu2g13900	0.99	2.13	1.05	multidrug resistance protein MDR
Afu2g14020	0.41	0.41	2.34	ATP transporter, putative
Afu2g14180	2.78	1.82	2.08	conserved hypothetical protein
Afu2g14220	2.54	2.22	2.71	conserved hypothetical protein
Afu2g14230	0.98	2.48		MFS transporter, putative
Afu2g14270	2.61	3.13	2.45	actin-binding protein, putative
Afu2g14390	2.82	4.49	3.7	methyltransferase, putative
Afu2g14420	1.2	3.71	1.89	cutinase, putative
Afu2g14450	1.28	2.18	2.8	hypothetical protein
Afu2g14490	1.51	4.51	4.85	endoglucanase, putative
Afu2g14510	1.89	1.97	2.27	hypothetical protein
Afu2g14600	2.73	2.73	1.53	ab-hydrolase associated lipase family
Afu2g14610	2.02	3.13	2.09	Oxalate decarboxylase
Afu2g14740	0.54	3.32	1.58	DUF821 domain protein
Afu2g14790	2.09	3.07	4.19	hypothetical protein
Afu2g14850	3.22	3.81	4.34	enoyl-CoA hydratase/isomerase family protein
Afu2g14920	3.59	4.59	4.24	protein kinase, putative
Afu2g14930	2.51	2.78	2.06	alanine racemase
Afu2g14970	2.72	2.82	2	Gamma-butyrobetaine hydroxylase subfamily, putative
Afu2g14990	2.1	3.31	2.86	tubulin alpha-2 subunit
Afu2g15490	2.54	3.18	2.96	TPR domain protein
Afu2g15510	2.11	3.09	2.9	conserved hypothetical protein
Afu2g15550	3.02	2.38		molybdenum cofactor biosynthesis protein Gephyrin, putative
Afu2g15840	1.77	2.04	2.3	HET-C domain protein
Afu2g15850	1.69	2.84	2.26	phytanoyl-CoA dioxygenase family protein

Afu2g15930	1.8	2.31	1.82	alcohol dehydrogenase, zinc-containing
Afu2g15950	1.26	3.61		aspartic endopeptidase, putative
Afu2g16060	1.38	2.07		conserved hypothetical protein
Afu2g16170	2.17	2.02	1.72	DNA-directed RNA polymerase III RPC4, putative
Afu2g16200	3.45	3.98	4.08	uracil phosphoribosyltransferase
Afu2g16330	0.94	2.5	1.58	glucokinase, putative
Afu2g16360	3.26	3.05	3.67	DRAP deaminase (Rib2), putative
Afu2g16380	2.19	2.19	2.05	conserved hypothetical protein
Afu2g16490	1.78	2.32	1.69	rhomboid family membrane protein
Afu2g16510	1.97	2.29	3.31	hypothetical protein
Afu2g16520	1.61	3.35	2.43	phospholipase D (PLD), putative
Afu2g16630	1.3	1.46	2.38	acyl-CoA dehydrogenase
Afu2g17010	3.17	3.19	3.01	NA
Afu2g17200	1.87	1.96	2.38	hypothetical protein
Afu2g17280	0.89	2.66	2.32	hypothetical protein
Afu2g17300	1.19	3.88	2.98	glutathione S-transferase
Afu2g17320	3.49	4.93	3.92	conserved hypothetical protein
Afu2g17330	0.95	2.87	1.97	serine peptidase, family S28, putative
Afu2g17400	1.8	2.7	1.92	C-3 sterol dehydrogenase/C-4 decarboxylase
Afu2g17450	0.58	2.63	1.94	3-hydroxyanthranilate 3,4-dioxygenase
Afu2g17460	1.53	2.68	2.17	aldehyde dehydrogenase, putative
Afu2g17600	1.53	2.16		polyketide synthetase PksP
Afu2g17610	1.47	2.44	2.23	sulfatase domain protein
Afu2g17620	0.9	2.58	1.12	cellobiose dehydrogenase
Afu2g17640	0.06	2.11	2.33	hypothetical protein
Afu2g17650	-0.34	2.06	3.08	DUF907 domain protein
Afu2g17660	2.15	3.04	2.22	C4-dicarboxylate transporter/malic acid transport protein, putative
Afu2g18050	0.56	1.47	2.22	FAD binding oxidoreductase, putative
Afu3g00180	0.24	2.9	-0.1	short chain dehydrogenase, putative
Afu3g00320	-0.02	3.75	1.84	endo-1,4-beta-xylanase (XlnA), putative
Afu3g00350	2.22	3.1	2.26	hypothetical protein
Afu3g00380	1.2	0.69	2.6	beta-galactosidase, putative
Afu3g00420	1.15	2.54	2.34	acetyl xylan esterase (Axe1), putative
Afu3g00520	-0.3	2.9	0.97	SIR2 family histone deacetylase, putative
Afu3g00560	-0.4	1.27	2.37	conserved hypothetical protein
Afu3g00650	1.53	3.06		aminopeptidase Y, putative
Afu3g00660	2	2.33		conserved hypothetical protein

Afu3g00680	3.1	3.38	2.18	copper amine oxidase
Afu3g00720	-0.15	1.59	3.1	DUF500 and UBA/TS-N domain protein
Afu3g00730	-0.2	1.86	3.01	conserved hypothetical protein
Afu3g00740	3.03	2.84	3.04	2-dehydropantoate 2-reductase, putative
Afu3g00750	3.19	3.64	3.96	short-chain dehydrogenase/reductase, putative
Afu3g00760	0.98	2.54	2.08	GNAT family N-acetyltransferase, putative
Afu3g00840	1.94	2.23	1.39	FAD-dependent oxygenase, putative
Afu3g00880	1.92	2.79	2.58	extracellular conserved serine-rich protein
Afu3g00900	5.1	5.73	6.07	alpha-amylase AmyA
Afu3g00960	3.77	4.9	4.73	conserved hypothetical protein
Afu3g00990	1.66	2.07		flavin-binding monooxygenase, putative
Afu3g01180	0.44	2.38	2.19	sarcosine oxidase, putative
Afu3g01220	0.81	2.25	2.49	aspartic-type endopeptidase, putative
Afu3g01230	0.95	3.95	2.37	sugar transporter-like protein
Afu3g01240	1.5	2.77	4.53	hypothetical protein
Afu3g01280	1.17	3.91	3.5	alpha/beta hydrolase, putative
Afu3g01320	2.91	3.83	2.92	homocysteine S-methyltransferase, putative
Afu3g01330	1.69	2.58	1.52	class II aldolase/adducin domain protein
Afu3g01340	1.53	2.47	1.7	DUF636 domain protein
Afu3g01370	4.43	5.55	6.08	MFS transporter, putative
Afu3g01410	0.64	2.17	2.08	polyketide synthase, putative
Afu3g01430	1	1.98	2.32	benzodiazepine receptor family protein
Afu3g01480	1.72	2.3	2.54	conserved hypothetical protein
Afu3g01490	1.53	2.45	2.25	alcohol dehydrogenase, putative
Afu3g01500	0.7	3.23	2.29	integral membrane protein
Afu3g01530	2.45	5.53	5.6	phosphatidylglycerol specific phospholipase, putative
Afu3g01580	2.72	3.87	4.7	GMC oxidoreductase, putative
Afu3g01610	2.93	4.46	4.9	hypothetical protein
Afu3g01620	0.81	2.07	1.27	Ankyrin and HET domain protein
Afu3g01660	1.37	3.88	3.44	putative hydrolase
Afu3g01670	1.32	3.77	1.31	MFS hexose transporter, putative
Afu3g01700	0.88	2.52	0.78	maltose permease
Afu3g01810	2.07	2.05	1.08	F-box domain protein
Afu3g01850	2.55	3.06	3.28	porphyromonas-type peptidyl-arginine deiminase superfamily
Afu3g01860	0.33	2	1.91	hypothetical protein
Afu3g02220	1.54	2.46	1.51	DUF427 domain protein
Afu3g02250	1.52	3.66	4.48	conserved hypothetical protein

Afu3g02260	2.36	3.19	3.51	hypothetical protein
Afu3g02270	2.46	3.59	1.33	mycelial catalase Cat1
Afu3g02280	4.6	4.78	4.45	alpha,alpha-trehalose glucohydrolase, putative
Afu3g02360	2.53	3.14	2.03	FAD dependent oxidoreductase superfamily
Afu3g02830	1.01	1.75	2.2	ankyrin repeat protein
Afu3g02940	6.08	6.55	6.01	allergen, putative
Afu3g03000	3.45	4.19	5.3	phosphatidylethanolamine-binding protein, putative
Afu3g03010	5.87	6.67	7.2	phosphate-repressible phosphate permease
Afu3g03020	3.64	3.96	3.66	phosphoglucomutase, putative
Afu3g03140	0.84	2.38	1.1	HET domain protein
Afu3g03280	1.46	2.6	3.86	FAD binding monooxygenase, putative
Afu3g03370	1.7	2.23	2.99	cell surface protein, putative
Afu3g03390	5.37	5.8	5.76	siderophore biosynthesis lipase/esterase, putative
Afu3g03400	4.82	5.95	6.06	siderophore biosynthesis acetylase AceI, putative
Afu3g03410	6.66	7.19	7.13	enoyl-CoA hydratase/isomerase family protein
Afu3g03420	5.71	6.25	7.32	hypothetical protein
Afu3g03430	5.35	5.94	6.67	ABC multidrug transporter SitT, putative
Afu3g03440	6.22	7.18	7.57	MFS family siderophore transporter, putative
Afu3g03450	2.3	3.08	3.39	cytochrome P450 pisatin demethylase, putative
Afu3g03600	1.4	2.57	3.09	carboxyl esterase A
Afu3g03640	2.07	5.53	4.67	siderochrome-iron transporter (MirB), putative
Afu3g03660	1.93	3.65	0.7	esterase superfamily protein
Afu3g03670	2.78	5.24	4.8	ABC multidrug transporter, putative
Afu3g03700	5.29	5.74	5.68	Sugar transporter subfamily
Afu3g03720	0.79	2.5	0.83	hypothetical protein
Afu3g03810	3.18	2.1	2.45	hypothetical protein
Afu3g03820	5.39	4.61	5.29	MFS transporter, putative
Afu3g03830	3.16	2.18	2.26	hypothetical protein
Afu3g03850	2.77	2.85	1.81	hypothetical protein
Afu3g03860	5.65	5.4	4.84	3-hydroxyacyl-CoA dehydrogenase, putative
Afu3g05650	2.21	2.23	2.29	alpha,alpha-trehalose-phosphate synthase subunit TPS2, putative
Afu3g05730	2.2	2.64	1.01	nicotinate-nucleotide pyrophosphorylase
Afu3g05740	2.14	2.55	2.13	aldose 1-epimerase, putative
Afu3g05880	3.89	3.85	4.9	oxysterol binding protein (Osh3), putative
Afu3g06520	2.71	3.15	3.89	hypothetical protein
Afu3g07020	1.53	2.94	3.34	annexin ANXC4
Afu3g07140	4.52	4.71	5.06	developmental regulator FluG

Afu3g07150	4.63	5.49	5.43	succinate-semialdehyde dehydrogenase, putative
Afu3g07220	2.04	1.32	1.78	conserved hypothetical protein
Afu3g07310	3	4.05	4.36	conserved hypothetical protein
Afu3g07610	1.31	2.48	1.61	hypothetical protein
Afu3g07620	2.78	2.8	3.6	ABC1 domain protein
Afu3g07640	2.51	2.07	2.23	plasma membrane H+-ATPase
Afu3g07740	2.84	2.93	3.2	hypothetical protein
Afu3g07790	3.03	2.77	2.79	argininosuccinate lyase
Afu3g07810	2.24	1.85	1.91	succinate dehydrogenase, flavoprotein subunit
Afu3g07850	3.2	3.46	4.41	dipeptidyl aminopeptidase Ste13
Afu3g07860	1.72	1.87	2.01	glycosyl transferase, putative
Afu3g07870	4.61	5.52	5.69	extracellular serine-rich protein
Afu3g07890	3.06	4.58	3.85	endo alpha-1,4 polygalactosaminidase, putative
Afu3g07900	1.1	2.85	2.12	conserved hypothetical protein
Afu3g07910	5.05	6.29	6.15	UDP-glucose 4-epimerase, putative
Afu3g07980	1.86	1.62	2.33	conserved hypothetical protein
Afu3g08070	1.4	1.74	2.85	GMC oxidoreductase, putative
Afu3g08110	0.4	3.91	3.33	cell wall protein, putative
Afu3g08130	1.71	2.99	2.09	hypothetical protein
Afu3g08140	2.43	2.35	1.12	fumarylacetoacetate hydrolase family protein
Afu3g08150	2.94	2.99	3.32	hypothetical protein
Afu3g08200	2.38	2.92	2.42	alpha-mannosidase
Afu3g08270	2.34	2.51	2.17	pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase component, putative
Afu3g08290	2.88	2.91	1.22	aspartyl aminopeptidase
Afu3g08310	2.38	2.56	1.91	4-nitrophenylphosphatase
Afu3g08380	2.09	2.15	1.16	inorganic diphosphatase, putative
Afu3g08490	1.52	2.37	2.79	ThiJ/PfpI family protein
Afu3g08610	2.11	2.85	2.43	DUF124 domain protein
Afu3g08660	2.62	1.79	1.91	isocitrate dehydrogenase, NADP-dependent
Afu3g08780	2.33	2.27	2.54	Msn5 protein, putative
Afu3g08850	1.98	2.17	2.2	FAD dependent sulfhydryl oxidase Erv1, putative
Afu3g08870	2.02	2.58	3.42	conserved hypothetical protein
Afu3g08950	1.7	2	1.97	hypothetical protein
Afu3g08980	2.3	2.24	1.89	threonine synthase
Afu3g09140	2.8	4.17	4.67	endo 1,5-alpha-arabinase
Afu3g09150	2.96	4.48	4.6	oxidoreductase, short chain dehydrogenase/reductase family

Afu3g09220	2.95	3.14	2.66	fatty acid hydroxylase, putative
Afu3g09240	2.26	2.17	1.91	CAIB/BAIF family enzyme
Afu3g09280	2.75	2.86	3.41	eukaryotic translation initiation factor 3 subunit EifCk, putative
Afu3g09560	2.05	2.79	2.33	DNA polymerase epsilon, catalytic subunit A/POL2, putative
Afu3g09630	2.83	2.94	2.9	asparaginyl-tRNA synthetase
Afu3g09680	1.32	2.04		ABC transporter, putative
Afu3g09690	1.96	1.49	2.18	extracellular thaumatin domain protein, putative
Afu3g09700	2.97	2.51	2.88	Sec23/Sec24 family protein
Afu3g09710	1.85	2.38	1.6	amino acid permease
Afu3g09720	1.98	2.21	1.75	cleavage and polyadenylylation specificity factor, putative
Afu3g09740	2.11	2.13	2.17	integral plasma membrane protein, putative
Afu3g09850	2.86	3.55	3.81	DNA mismatch repair protein Msh2, putative
Afu3g09890	1.47	2.11	1.88	hypothetical membrane protein, putative
Afu3g10300	2.65	2.32	1.54	galactokinase
Afu3g10330	2.54	2.54	3.42	hypothetical protein
Afu3g10360	1.59	2.08	1.7	vacuolar sorting protein 35
Afu3g10390	2.91	3.11	3.12	conserved hypothetical protein
Afu3g10680	2.32	3.39	3.71	conserved hypothetical protein
Afu3g10700	2.06	1.96	0.9	Arp2/3 complex subunit Arc16, putative
Afu3g10710	2.08	1.96	2.01	conserved hypothetical protein
Afu3g10720	2.09	2.05	2.46	dynactin Arp1 p62 subunit RO2
Afu3g10830	2.14	2.21	2.11	glutathione S-transferase family protein
Afu3g10850	1.93	1.72	2.27	DUF821 domain protein
Afu3g10890	2.69	2.83	3.65	ATP dependent RNA helicase (Dbp8), putative
Afu3g10910	3.37	3.65	3.71	glutaminase A
Afu3g10920	2.62	2.26	1.57	telomere and ribosome associated protein Stm1, putative
Afu3g10980	1.63	1.74	2.31	VanZ domain protein, putative
Afu3g11280	2.22	2.76	2.05	class V chitinase, putative
Afu3g11480	4.33	4.53	3.91	mitochondrial methylglutaconyl-CoA hydratase (Auh), putative
Afu3g11490	3.19	2.94	2.58	GABA permease, putative
Afu3g11510	2.49	3.29	1.91	O-acetyltransferase, putative
Afu3g11640	4.04	4.3	2.85	homoserine dehydrogenase
Afu3g11650	3	4.38	5.37	hypothetical protein
Afu3g11770	2.68	3.22	2.05	hypothetical protein

Afu3g11780	2.84	3.51	2.89	beta-N-acetylglucosaminidase, putative
Afu3g11820	2.43	2.44	2.81	mitochondrial oligoribonuclease, putative
Afu3g11900	3.09	4.29	3.08	oxidoreductase, zinc-binding
Afu3g11920	1.45	3.06	0.62	dihydrodipicolinate synthetase family protein
Afu3g11930	1.63	2.14	1.91	NAD binding Rossmann fold oxidoreductase, putative
Afu3g11980	1.52	1.22	2.69	oxidoreductase, 2OG-Fe(II) oxygenase family family
Afu3g12070	1.53	1.35	2.04	conserved hypothetical protein
Afu3g12090	1.5	1.92	3.44	hypothetical protein
Afu3g12170	1.19	2.41	1.36	MFS sugar transporter, putative
Afu3g12250	0.91	2.42	0.85	protein-tyrosine phosphatase, putative
Afu3g12460	2.02	2.84	2.3	conserved hypothetical protein
Afu3g12600	0.99	2.91	2.59	beta-glucosidase 1
Afu3g12620	1.19	3.34	3.07	acyl-CoA:6-aminopenicillanic-acid-acyltransferase, putative
Afu3g12740	2.06	2.35	1.58	copper resistance-associated P-type ATPase, putative
Afu3g12770	2.72	2.59	1.91	putative nucleoside-diphosphate-sugar epimerase
Afu3g12790	3.28	4.1	3.74	conserved glutamic acid-rich protein
Afu3g12800	2.09	2.38	1.53	conserved hypothetical protein
Afu3g12840	2.92	3.54	3.07	Signal peptidase I
Afu3g12860	1.93	2.02	1.71	hypothetical protein
Afu3g12900	3.22	2.45	2	monocarboxylate transporter (Mch4), putative
Afu3g13110	0.55	2.44	2.59	extracellular serine-threonine rich protein
Afu3g13120	3.55	3.63	1.74	porphobilinogen deaminase
Afu3g13140	1.82	1.92	2.68	7alpha-cephem-methoxylase P8 chain, putative
Afu3g13320	2.83	2.28	0.77	40S ribosomal protein S0, putative
Afu3g13410	1.89	2.1	0.86	hypothetical protein
Afu3g13660	0.66	2.43		Ctr copper transporter family protein
Afu3g13700	-0.07	2.08	0.21	transferase family protein
Afu3g13980	1.97	2.34	2.11	glucose transporter
Afu3g14030	4.05	4.52	5.11	alkaline phosphatase
Afu3g14170	2.01	3.06	1.91	high-affinity hexose transporter
Afu3g14260	1.6	2.01	3.57	mismatched base pair and cruciform DNA recognition protein, putative
Afu3g14320	2.52	2.35	1.71	Golgi transport protein Sly1, putative
Afu3g14380	1.76	2.64	2.15	endosomal sorting complex protein TSG101, putative
Afu3g14460	2.41	2.29	2.63	Rad51 family DNA repair protein, putative
Afu3g14470	3.2	3.12	3.25	Pyridoxal-phosphate dependent enzyme, putative
Afu3g14500	1.39	2.09	1.78	isochorismatase family protein family

Afu3g14510	1.09	3.02	1.77	rhamnogalacturonan acetylesterase, putative
Afu3g14520	2.2	2.19	0.9	enoyl-CoA hydratase/isomerase family protein
Afu3g14570	2.47	3.94	3.43	histidine acid phosphatase, putative
Afu3g14590	2.16	3.17	2.81	copper amine oxidase
Afu3g14600	2.33	2.86	2.32	fungal specific transcription factor, putative
Afu3g14650	3.08	3.66	3.99	hypothetical protein
Afu3g14660	2.5	3.12	2.5	hypothetical protein
Afu3g14670	1.08	1.48	2.87	MFS transporter, putative
Afu3g14680	2.82	5.89	4.8	lysophospholipase Plb3
Afu3g14920	0.99	3.24	1.64	LaeA-like methyltransferase, putative
Afu3g15210	0.38	4.15	1.6	endo-1,4-beta-xylanase, putative
Afu3g15340	2.09	1.95	3.2	hypothetical protein
Afu4g00150	2.41	2.73	1.83	MFS maltose transporter, putative
Afu4g00370	2.51	2.53	2.4	general amidase, putative
Afu4g00390	1.24	4.5	3.62	glycosyl hydrolase, putative
Afu4g00460	1	2.15	0.52	chlorohydrolase family protein, putative
Afu4g00610	0.93	4.62	4.22	aryl-alcohol dehydrogenase, putative
Afu4g00620	1.93	2.32	0.76	glycosyl hydrolase, putative
Afu4g00660	3.13	3.3	4.54	sensor histidine kinase/response regulator, putative
Afu4g00670	2.71	2.19	2.86	nucleoside-diphosphate-sugar epimerases, putative
Afu4g00700	1.36	2.73	2.04	oxidoreductase, zinc-binding
Afu4g00750	2.31		2.9	hypothetical protein
Afu4g00760	1.15	2.98	2.86	hypothetical protein
Afu4g00800	4.56	4.43	4.96	MFS monosaccharide transporter, putative
Afu4g00830	1.72	1.78	3.37	MFS peptide transporter, putative
Afu4g00930	2.13	2.66	3.14	CorA family metal ion transporter, putative
Afu4g00990	1.48	2.47		MFS quinate transporter, putative
Afu4g01000	1.85	2.28	1.86	MFS transporter, putative
Afu4g01060	2.5	2.83	3.7	hypothetical protein
Afu4g01070	0.61	2.53	1.47	acid phosphatase, putative
Afu4g01140	4.87	4.48	5.4	MFS multidrug transporter, putative
Afu4g01160	0.28	2.85	2.05	von Willebrand domain protein
Afu4g01290	0.63	4.08	2.2	endo-chitosanase, pseudogene
Afu4g01350	0.88	2.79	0.89	hypothetical protein
Afu4g01550	2.41	3.87	3.56	aldehyde dehydrogenase, putative
Afu4g01580	0.74	2.68		ankyrin repeat protein
Afu4g05940	2.13	2.51	2.25	phosphoethanolamine
Afu4g05970	2.07	2.36	2.39	para-hydroxybenzoate-polyprenyltransferase precursor

Afu4g06420	2.59	2.18	3.31	fungal specific transcription factor, putative
Afu4g06460	3.79	4.77	4.61	pentafunctional AROM polypeptide, putative
Afu4g06600	3.25	3.14	3.83	hypothetical protein
Afu4g06620	2.47	1.59	1.37	Glutamate/Leucine/Phenylalanine/Valine dehydrogenase, putative
Afu4g06640	3.15	5.22	5.69	acid sphingomyelinase
Afu4g06670	2.66	3.46	3.21	allergen Asp F7
Afu4g06690	1.89	2.28	2.76	ribonucleotide reductase large subunit (Rnr1), putative
Afu4g06750	1.17	2.07	1.95	protein kinase, putative
Afu4g06800	2.28	2.56	2.47	DNA-3-methyladenine glycosylase, putative
Afu4g06850	1.73	1.48	2.17	coenzyme a synthetase
Afu4g06860	4.09	4.92	5.45	conserved hypothetical protein
Afu4g06910	3.28	3.63	2.78	outer mitochondrial membrane protein porin
Afu4g07130	2.67	2.45	2.3	diphosphomevalonate decarboxylase
Afu4g07150	1.58	2.07	2.2	cytochrome-c oxydase chain VIIc-like protein
Afu4g07310	1.96	2.51	2.46	conserved hypothetical protein
Afu4g07320	1.82	2.16	2.95	conserved hypothetical protein
Afu4g07350	1.64	1.96	2.03	conserved hypothetical protein
Afu4g07710	2.36	2.83	3.6	pyruvate carboxylase, putative
Afu4g07790	1.29	2.16	1.63	hypothetical protein
Afu4g07810	1.23	1.93	2.57	L-serine dehydratase, putative
Afu4g07940	2.49	2.86	2.23	oxidoreductase, 2-nitropropane dioxygenase family, putative
Afu4g08020	2.9	3.17	3.4	hypothetical protein
Afu4g08170	2.63	2.52	2.28	succinate-semialdehyde dehydrogenase, putative
Afu4g08580	2.56	2.96	1.87	antioxidant protein LsfA
Afu4g08600	3.28	3.57	2.76	aldehyde dehydrogenase, putative
Afu4g08610	2.79	3.58	2.57	regucalcin homolog [imported]
Afu4g08630	1.42	1.85	2.77	phytase
Afu4g08680	2.02	2.09	2.68	hypothetical protein
Afu4g08690	2.08	2.12	2.69	dihydrodipicolinate synthetase family protein
Afu4g08710	3.2	4.11	2.55	short chain dehydrogenase, putative
Afu4g08730	0.43	2.28	1.16	conserved hypothetical protein
Afu4g08840	1.3	3.97	2.7	RING finger domain protein, putative
Afu4g08880	1.53	2.47	1.04	possible apospory-associated protein c
Afu4g09130	0.74	1.36	2.13	mannosyltransferase, putative
Afu4g09180	2.17	1.35	1.43	SET domain protein
Afu4g09200	2.05	2.05		hypothetical protein

Afu4g09210	2.01	2.64	2.79	phosphate transporter
Afu4g09220	1.72	2.27	1.32	hypothetical protein
Afu4g09300	1.38	4.08	4.04	hypothetical protein
Afu4g09310	0.95	4.24	3.35	hypothetical protein
Afu4g09320	5.2	5.25	6.29	antigenic dipeptidyl-peptidase Dpp4
Afu4g09330	2.62	3.99	3.2	conserved hypothetical protein
Afu4g09340	3.35	4.26	3.86	hypothetical protein
Afu4g09350	2.92	2.78	2.13	hypothetical protein
Afu4g09360	2.98	2.69	2.03	ATP synthase proteolipid P2, putative
Afu4g09440	2.94	3.45	3.41	sodium P-type ATPase, putative
Afu4g09450	2.66	3.53	3.65	hypothetical protein
Afu4g09560	3.35	4.07	4.52	ZIP Zinc transporter, putative
Afu4g09580	4.45	6.36	6.99	major allergen Asp F2
Afu4g09920	1.83	1.8	4.38	conserved hypothetical protein
Afu4g10150	4.7	5.91	4.27	alpha-glucosidase
Afu4g10160	1.71	3.64		C6 transcription factor (AmyR), putative
Afu4g10230	2.62	3.42	3.67	conserved hypothetical protein
Afu4g10370	3	2.92	3.09	3-demethylubiquinone-9 3-methyltransferase
Afu4g10410	2.87	3.19	2.93	aspartate aminotransferase, putative
Afu4g10610	1.62	2.72	2.5	hypothetical protein
Afu4g10950	2.45	2.63	2.37	3-ketoacyl-coA thiolase peroxisomal A precursor
Afu4g11050	2.2	1.63	0.88	NADH-ubiquinone oxidoreductase, subunit F, putative
Afu4g11100	3.46	3.47	3.4	conserved hypothetical protein
Afu4g11160	2.77	2.99	3.29	cell division control protein 31
Afu4g11240	2.26	1.95	2.55	alpha-aminoadipate reductase large subunit, putative
Afu4g11320	0.61	1.92	2.68	hypothetical protein
Afu4g11330	2.22	1.63	2.16	Aha1 domain family
Afu4g11400	4.12	4.29	4.23	cell surface receptor/MFS transporter (FLVCR), putative
Afu4g11470	2.9	3.12	3.61	conserved hypothetical protein
Afu4g11500	2.82	2.59	2.6	3-ketosteroid reductase
Afu4g11550	3.13	2.23	0.89	hypothetical protein
Afu4g11590	2.43	2.44	2.41	hypothetical protein
Afu4g11620	3.65	4.13	3.27	conserved hypothetical protein
Afu4g11680	2.13	2.06	2.19	conserved hypothetical protein
Afu4g11740	1.22	2.25	1.04	hypothetical protein
Afu4g11750	2.6	3.11	2.75	hypothetical protein
Afu4g11800	0.69	3.98	2.41	alkaline serine protease Alp1
Afu4g11910	2.08	1.56	1.27	N-terminal acetyltransferase catalytic subunit (NAT1),

				putative
Afu4g12000	1.96	2.2	1.51	phosphatidylinositol phospholipase C
Afu4g12150	2.97	3.5	3.44	HIT domain protein
Afu4g12210	0.61	2.16	1.35	DNA replication helicase (Dna2), putative
Afu4g12240	1.58	1.84	2.05	putitive nitrilase homolog
Afu4g12320	1.68	2.02		toxin biosynthesis protein, putative
Afu4g12370	1.22	3.46	3.35	hypothetical protein
Afu4g12510	0.71	0.89	2.71	hypothetical protein
Afu4g12540	2.14	2.33	1.9	hypothetical protein
Afu4g12620	1.92	2.22	2.99	copper-transporting ATPase, putative
Afu4g12670	2.25	2.78	2.33	DNA repair protein rad1, putative
Afu4g12740	2.32	2.53	3.12	tRNA (adenine-N(1)-)-methyltransferase
Afu4g12840	2.42	2.83	1.89	class II aldolase/adducin domain protein
Afu4g12850	2.82	2.69	2.71	calnexin
Afu4g12880	2.75	3.55	2.89	hypothetical protein
Afu4g12900	2.81	3.18	2.92	alpha-1,6-mannosyltransferase subunit (Ecm39), putative
Afu4g12920	2	1.15	1.59	histidyl-tRNA synthetase, mitochondrial precursor
Afu4g12930	2.42	2.2	2.1	ubiquinone biosynthesis monooxgenase (Coq6), putative
Afu4g12980	0.95	1.72	2.12	conserved hypothetical protein
Afu4g12990	2.01	1.82	1.62	thioredoxin reductase
Afu4g13000	1.82	2.51	1.71	flavin-containing amine oxidase, putative
Afu4g13090	2.19	3.56	3.38	MFS transporter, putative
Afu4g13110	1.47	1.89	3.02	hypothetical protein
Afu4g13250	2.92	2.96	4.15	Calponin homology (CH) domain protein
Afu4g13260	2.07	3.61	3.79	hypothetical protein
Afu4g13420	2.14	1.71	2.59	hypothetical protein
Afu4g13580	3.11	4.07	3.38	gamma-glutamyltranspeptidase
Afu4g13880	2.72	2.57	1.8	ankyrin repeat protein
Afu4g13900	3.7	3.39	2.54	MFS transporter, putative
Afu4g13950	1.14	3.3	2.31	GNAT family acetyltransferase, putative
Afu4g13990	0	2.33	3.31	hypothetical protein
Afu4g14000	0.56	3.51	0.87	tripeptidyl peptidase A
Afu4g14010	2.27	3.19	3.45	oxidoreductase, short chain dehydrogenase/reductase family superfamily
Afu4g14070	0.5	4.82	5.77	glycosyl transferase, putative
Afu4g14090	1.95	4.19	5.35	UDP-glucose 4-epimerase
Afu4g14110	1.4	2.88	1.55	hypothetical protein
Afu4g14120	1.22	2.89	1.82	cutinase, putative

Afu4g14130	1.41	2.35	0.81	ABC multidrug transporter, putative
Afu4g14180	-0.58	1.43	2.3	hypothetical protein
Afu4g14190	1.34	2.3	2.99	hypothetical protein
Afu4g14230	1.09	2.5	3.26	MFS transporter, putative
Afu4g14240	1.11	1.97	2.25	O-methyltransferase
Afu4g14420	2.91	4.48	4.14	secreted glycosyl hydrolase, putative
Afu4g14670	2.3	1.91		MFS quinate transporter, putative
Afu4g14730	0.44	3.26	4.06	GNAT family acetyltransferase, putative
Afu5g00390	3.07	3.37	2.4	hypothetical protein
Afu5g00480	2.89	3.04	2.9	fructan beta-fructosidase, putative
Afu5g00590	2.02	3.24	2.17	hypothetical protein
Afu5g00640	0.9	2.14	0.36	peroxisomal dehydratase, putative
Afu5g00670	2.18	3.15	3.14	glycosyl hydrolase family 35, putative
Afu5g00680	2.04	2.83	2.58	CRAL/TRIO domain protein
Afu5g00710	0.51	2.74	2	GABA permease, putative
Afu5g00720	0.82	2.77	1.5	acetyltransferase, GNAT family family
Afu5g01030	0.33	4.08	4.96	glyceraldehyde 3-phosphate dehydrogenase (Ccg-7), putative
Afu5g01200	-0.39	2.85	0.55	carboxypeptidase S1, putative
Afu5g01230	0.7	2.6	-0.14	RTA1 domain protein, putative
Afu5g01360	0.95	2.28	1.96	cytochrome P450, putative
Afu5g01370	1.02	2.61	1.18	conserved hypothetical protein
Afu5g01380	2.22	1.31	1.23	conserved hypothetical protein
Afu5g01440	2.31	3.08	3.01	allergen, putative
Afu5g01450	2.8	2.27	1.85	NADH-dependent flavin oxidoreductase, putative
Afu5g01620	-1.15	2.29	2.36	extracellular proline-rich protein
Afu5g01630	2.2	3.15	2.06	major facilitator superfamily
Afu5g01680	1.28	1.99	2.24	MFS transporter, putative
Afu5g01690	1.26	2.3	1.09	conserved hypothetical protein
Afu5g01710	2.86	2.14	3.34	cytochrome P450 phenylacetate 2-hydroxylase, putative
Afu5g01730	2.38	2.59	3.52	MYB DNA-binding domain protein
Afu5g01770	2.43	3.18	2.39	conserved hypothetical protein
Afu5g01820	1.66	2.11	1.85	DUF221 domain protein, putative
Afu5g01880	2.21	2.67	2.63	conserved hypothetical protein
Afu5g01910	2.12	2.58	2.45	aldo-keto reductase (AKR), putative
Afu5g01990	-0.59	2.41	1.73	BYS1 domain protein, putative
Afu5g02000	1.2	2.29	-0.67	co-factor independent proline racemase, putative
Afu5g02020	2.08	4.13		aldehyde reductase (GliO), putative

Afu5g02080	2.45	3.23	2.12	NADH-ubiquinone oxidoreductase
Afu5g02250	1.08	1.19	3	conserved hypothetical protein
Afu5g02310	2.84	2.96	3.03	alpha/beta hydrolase, putative
Afu5g02350	3.88	3.94	3.54	hydrolase, carbon-nitrogen family, putative
Afu5g02460	2.18	2.03	2.32	conserved hypothetical protein
Afu5g02490	2.04	1.64	1.05	zinc-binding oxidoreductase, putative
Afu5g02500	1.14	1.39	2.42	hypothetical protein
Afu5g02550	1.89	2.22	2.54	conserved hypothetical protein
Afu5g02590	1.76	2.34	2.26	20S cyclosome subunit (Cut9/Cdc16), putative
Afu5g02750	2.44	2.99	2.48	cytochrome c oxidase subunit Va, putative
Afu5g02820	1.76	2.46	2.37	hypothetical protein
Afu5g02850	2.49	3.23	2.38	conserved hypothetical protein
Afu5g02930	3.79	3.5	4.22	lysophospholipase, putative
Afu5g02940	4.19	3.14	3.67	choline transport protein Ctr, putative
Afu5g02960	3.07	3.5	3.56	hypothetical protein
Afu5g02990	1.98	1.94	2.13	aromatic amino acid aminotransferase, putative
Afu5g03010	0.86	2.91	2.51	conserved hypothetical protein
Afu5g03020	3.47	2.94	2.03	60s ribosomal protein l2
Afu5g03110	2.58	3.69	2.72	conserved hypothetical protein
Afu5g03380	2.72	2.57	1.42	flavin dependent monooxygenase, putative
Afu5g03490	2.25	2.61	2.01	nucleoside diphosphate kinase
Afu5g03540	1.67	2.32	2.62	pyridine nucleotide-disulphide oxidoreductase, class II, putative
Afu5g03550	1.92	2.37	2.02	plasma membrane H(+)ATPase, putative
Afu5g03750	1.38	3.27	2.94	WW domain protein
Afu5g03760	3.48	4.74	4.36	class III chitinase ChiA1
Afu5g03960	0.75	1.38	2.04	class V chitinase Chi100
Afu5g04210	2.7	1.65	1.37	ubiquinol-cytochrome C reductase complex core protein 2, putative
Afu5g04230	2.57	2.04	1.97	citrate synthase, eukaryotic
Afu5g04250	2.42	2.3	1.5	homocysteine synthase, putative
Afu5g06490		2.07		hypothetical protein
Afu5g06500	2.95	3.32	2.86	acyl-CoA dehydrogenase family protein
Afu5g06550	1.7	2.04	2.22	filamentation protein (Rhf1), putative
Afu5g06560	1.91	2.11	2.31	conserved hypothetical protein
Afu5g06570	1.83	2.06	2.01	hypothetical protein
Afu5g06610	2.07	2.26	2.52	glutathione synthetase
Afu5g06680	0.98	2.68	2.38	4-aminobutyrate aminotransferase

Afu5g06710	2.15	1.8	2.03	DUF89 domain protein
Afu5g06780	2.08	1.64	2.21	carbamoyl-phosphate synthase, small subunit
Afu5g06820	0.68	2.01	2.2	hypothetical protein
Afu5g06910	4.1	5.31	5.58	DUF636 domain protein
Afu5g06960	2.49	2.65	2.45	conserved hypothetical protein
Afu5g06990	1.89	2.26		catecholamine-O-methyltransferase, putative
Afu5g07140	2.17	2.55	2.9	translation elongation factor G2, putative
Afu5g07180	2.53	2.87	3.03	conserved proline-glicine rich protein
Afu5g07190	2.86	4.08	3.73	beta-glucosidase
Afu5g07300	1.69	2.23	1.49	electron transfer flavoprotein, beta subunit [imported]
Afu5g07330	1.97	3.65	1.69	carboxypeptidase S1, putative
Afu5g07360	1.15	1.56	2.39	peroxisomal copper amine oxidase
Afu5g07400	2.12	2.81	1.25	phenylacetyl-CoA ligase PclA, putative
Afu5g07500	2.02	1.73	1.51	beta-lactamase
Afu5g07560	2.29	2.37	1.69	capsular associated protein, putative
Afu5g07580	1.15	2.73		methylmalonyl-CoA decarboxylase, alpha subunit, putative
Afu5g07610	2.34	3.5	3.07	NA
Afu5g07620	4.37	5.06	5.68	DUF1212 domain membrane protein
Afu5g07630	2.49	3.23	2.42	ubiE/COQ5 methyltransferase, putative
Afu5g07640	2.32	3.06	3.55	RNA 3'-terminal phosphate cyclase, putative
Afu5g07660	0.51	2.16	1.02	hypothetical protein
Afu5g07670	1.47	2.94	3.22	SH3 domain signalling protein
Afu5g07690	2.18	3.15	1.4	conserved hypothetical protein
Afu5g07700	1.54	3.28	3.34	NA
Afu5g08120	3.51	4.69	5.59	arginine biosynthesis bifunctional protein ArgJ
Afu5g08250	2.73	2.74		hypothetical protein
Afu5g08620	2.22	2.32	1.85	Ser/Thr protein phosphatase family
Afu5g08630	1.81	2.35	2.05	LCCL domain protein
Afu5g08810	3.23	3.38	4.82	epoxide hydrolase, putative
Afu5g08830	1.17	4.15	4.71	HEX1
Afu5g08860	1.2	1.86	2.26	hypothetical protein
Afu5g08890	2.12	1.82	2.62	homoaconitase LysF
Afu5g08900	1.5	1.81	2.03	D-arabinitol dehydrogenase ArbD, putative
Afu5g08970	2.34	2.35	2.25	oligosaccharyl transferase subunit (beta), putative
Afu5g09070	-0.38	3	0.65	hypothetical protein
Afu5g09130	3.77	3.44	3.6	polysaccharide deacetylase family protein
Afu5g09140	3.97	3.41	3.41	amidase, putative

Afu5g09150	2.49	2.18	1.05	oxidoreductase, short-chain dehydrogenase/reductase family
Afu5g09280	2.03	1.96	1.48	conserved hypothetical protein
Afu5g09290	2.01	2.35	2.04	NAD-dependent 15-hydroxyprostaglandin dehydrogenase
Afu5g09340	2.33	2.21	1.96	Phospholipase/Carboxylesterase superfamily
Afu5g09400	4.16	4.8	3.96	carbonyl reductase, putative
Afu5g09530	1.33	2.5	2.72	conserved hypothetical protein
Afu5g09560	2.35	2.07	2.68	ankyrin repeat protein (Yar1), putative
Afu5g09600	1.99	2.78	1.56	2-nitropropane dioxygenase family oxidoreductase, putative
Afu5g09790	2.93	3.74	2.23	beta-lactamase
Afu5g09800	1.9	3.61	3.4	hypothetical protein
Afu5g09860	2.12	2.47	1.94	esterase, putative
Afu5g09940	1.68	1.4	2.05	MFS transporter of unkown specificity
Afu5g09960	1.52	2.42	2.88	GPI anchored protein, putative
Afu5g09970	1.91	1.74	2.24	67 kDa myosin-cross-reactive antigen family protein
Afu5g09990	1.48	2.31	0.62	C6 transcription factor, putative
Afu5g10010	3.25	4.83	5.01	extracellular serine-threonine rich protein
Afu5g10020	3.82	4.39		sensor histidine kinase/response regulator, putative
Afu5g10230	2.08	2.71	2.38	NA
Afu5g10250	1.78	3.28	4.67	hypothetical protein
Afu5g10280	3.4	3.61	2.14	oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor
Afu5g10290	4.86	4.71	4.04	fructose-bisphosphate aldolase, putative
Afu5g10430	2.55	3.1	2.01	MSF multidrug transporter, putative
Afu5g10510	0.86	2.19	2.1	ABC transporter, putative
Afu5g10520	2.09	2.57	2.44	alpha-1,2-mannosidase family protein
Afu5g10550	2.88	2.28	1.62	ATP synthase F1, beta subunit, putative
Afu5g10560	3.65	3.86	3.7	cytochrome c oxidase subunit V
Afu5g10650	1.77	1.72	2.3	pyridoxamine phosphate oxidase, putative
Afu5g10740	2.59	3.07	3.36	conserved hypothetical protein
Afu5g10890	1.88	2.51	2.75	DNA replication licensing factor Mcm6, putative
Afu5g11210	2.23	2.21	1.95	molybdopterin binding domain protein
Afu5g11240	2.23	1.91	0.63	oxidoreductase, short chain dehydrogenase/reductase family
Afu5g11400	2.92	2.82	2.45	mRNA cleavage factor complex II protein Clp1, putative
Afu5g11430	2.2	2.38	2.52	quinone oxidoreductase, putative
Afu5g11440	1.89	2.11	2.32	hypothetical protein

Afu5g11610	1.92	2.22	1.65	shk1 kinase-binding protein 1
Afu5g11810	1.59	3.28	3.78	cytoplasmic dynein heavy chain
Afu5g11850	4.33	4.45	4.04	mitochondrial carrier protein (Pet8), putative
Afu5g12460	1.59	2.28	0.38	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase, putative
Afu5g12480	3.81	4.37	3.24	short chain dehydrogenase/reductase family
Afu5g12550	2.48	2.89	3.38	N-acetylglucosaminyl-phosphatidylinositol deacetylase, putative
Afu5g12600	1.76	2.64	2.45	DNA excision repair protein (Rad5), putative
Afu5g12610	1.41	1.34	2.27	conserved hypothetical protein
Afu5g12690	3.85	3.66	3.61	dihydroxyacetone kinase (DakA), putative
Afu5g12770	1.68	3.57	2.03	metallo-beta-lactamase family protein
Afu5g12790	3.43	3.2	4.07	mitochondrial 3-hydroxyisobutyryl-CoA hydrolase, putative
Afu5g12940	1.75	3.16	2.95	arylsulfatase, putative
Afu5g13020	1.5	1.8	2.71	DNA polymerase alpha/primase associated subunit
Afu5g13030	1.51	1.92	2.67	Apc13 domain protein
Afu5g13060	2.39	2.3	3.01	DUF1275 domain protein
Afu5g13100	1.26	1.47	2.13	hypothetical protein
Afu5g13170	1.86	2.23	1.48	MATE efflux family protein subfamily, putative
Afu5g13180	3.29	2.37		agmatinase, putative
Afu5g13280	1.22	1.21	2.18	hypothetical protein
Afu5g13300	1.67	3.63		aspartic endopeptidase Pep1
Afu5g13460	1.6	1.96	2.73	mitochondrial protein
Afu5g13640	1.76	2.62	3.51	thioredoxin, putative
Afu5g13800	2.17	2.81	3.3	transcriptional regulator, putative
Afu5g13810	4.14	4.83	4	transulfuration enzyme family protein, putative
Afu5g13920	1.85	2	1.83	p21 protein
Afu5g13940	1.61	2.32	2.31	FAD dependent oxidoreductase superfamily
Afu5g14060	0.19	2.3	0.56	Rho GTPase Rho4, putative
Afu5g14230	0.7	2.31	2.76	C6 transcription factor, putative
Afu5g14240	1.15	3.73	3.74	ThiJ/PfpI family protein
Afu5g14380	1.19	1.58	2.04	alpha-glucuronidase
Afu5g14500	1.42	2.67	2	MFS transporter, putative
Afu5g14510	0.55	2.54		beta-lactamase, putative
Afu5g14530	3.5	4.07	3.83	C6 transcription factor, putative
Afu5g14550	2.78	3.43	2.42	beta-galactosidase, putative
Afu5g14650	0.39	2.69	2.36	RING finger protein

Afu5g14660	-0.54	2.12	1.77	GABA permease, putative
Afu5g14680	4.6	5.25	6.14	hypothetical protein
Afu5g14690	2.85	2.82	5.53	phosphorylase, putative
Afu5g14770	1.86	2.13	1.39	pyrroline-5-carboxylate reductase
Afu6g00140	2.15	3.34	3.04	hypothetical protein
Afu6g00240	1.96	2.68	2.77	4-hydroxyphenylpyruvate dioxygenase, putative
Afu6g00260	2.74	2.66	1.26	phosphatidylserine decarboxylase family protein
Afu6g00290	2.24	4.88	5.67	aminotransferase, putative
Afu6g00300	2.85	3.86	4.31	serine palmitoyltransferase 1, putative
Afu6g00430	-1.75	2.24	1.05	IgE-binding protein
Afu6g00470	2.41	2.37	2.32	plasma membrane zinc ion transporter, putative
Afu6g00510	2.46	1.72	1.78	NADP-dependent alcohol dehydrogenase
Afu6g00600	1.81	3.33	2	hypothetical protein
Afu6g00620	4.03	4.74	4.29	GPI anchored hypothetical protein
Afu6g00630	3.55	5.13	5.04	MFS transporter, putative
Afu6g00640	2.59	3.51	4.18	integral membrane protein
Afu6g00650	2.34	3.53	2.99	hypothetical protein
Afu6g00710	3.17	3.52	3.64	MFS transporter, putative
Afu6g00740	1.02	2.15	1.12	hypothetical protein
Afu6g00750	2.15	3.97	2.33	pyruvate decarboxylase, putative
Afu6g01820	3.7	4.19	5.02	MFS transporter, putative
Afu6g01830	3.22	3.66	5.03	O-methyltransferase, putative
Afu6g01840	1.26	2.08	1.69	C6 transcription factor, putative
Afu6g01850	3.17	2.64	2.75	hypothetical protein
Afu6g01950	2.47	1.97	1.31	hypothetical protein
Afu6g02030	1.52	2.83	3.06	aminotransferase, putative
Afu6g02090	1.64	2.02	1.22	ATP synthase subunit E, putative
Afu6g02260	4.35	4.79	4.7	hypothetical protein
Afu6g02270	1.13	1.64	2.8	ribonuclease P/MRP complex subunit Pop1, putative
Afu6g02280	1.31	2.09	0.66	allergen Asp F3
Afu6g02470	3.92	3.68	4.21	fumarate hydratase, putative
Afu6g02560	2.03	2.09	1.52	alpha-galactosidase
Afu6g02600	2.24	2.34	1.56	phosphoglycerate mutase family protein
Afu6g02750	2.07	2.23	1.82	nascent polypeptide-associated complex (NAC) subunit, putative
Afu6g02910	2.97	2.31	2.99	acetylglutamate kinase, putative
Afu6g02940	1.89	2.32	2.31	chitin synthase activator (Chs3), putative
Afu6g02960	1.69	2.35	2.81	NADH-ubiquinone oxidoreductase 105 kDa subunit

Afu6g03060	2.72	3.43	2.33	monosaccharide transporter
Afu6g03150	2.7	2.61		hypothetical protein
Afu6g03160	2.25	3.62	3.44	NACHT domain protein
Afu6g03170	5.23	5.37	5.88	NA
Afu6g03180	3.56	3.88	4.97	hypothetical protein
Afu6g03190	4.7	5.36	5.55	hypothetical protein
Afu6g03200	4.16	4.84	5.59	solute symporter family transporter
Afu6g03230	0.88	2.68	2.55	cell wall glucanase, putative
Afu6g03250	0.46	1.49	2.45	protein kinase, putative
Afu6g03320	-0.1	0.72	2.12	MFS drug transporter, putative
Afu6g03340	0.87	2.68	1.63	hypothetical protein
Afu6g03350	0.39	4.32	5.34	acetyltransferase, GNAT family, putative
Afu6g03400	1.2	1.92	2.59	hypothetical protein
Afu6g03420	4.72	3.44	3.32	trehalose synthase, putative
Afu6g03460	1.18	2.78	1.61	hypothetical protein
Afu6g03470	-0.47	2.48	2.08	ABC multidrug transporter, putative
Afu6g03520	2.85	2.88	2.31	short-chain dehydrogenase/reductase family protein, putative
Afu6g03570	3.54	4.27	4.62	beta-glucosidase 3
Afu6g03590	3.33	3.65	3.14	methylcitrate synthase
Afu6g03600	2.3	2.29	3.03	integral membrane protein (Pth11), putative
Afu6g03640	3.48	3.87	3.27	aminotransferase, putative
Afu6g03660	2.24	2.38	2.45	onanonoxo-7-onima-8-eninoihtemlysoneda
Afu6g03680	0.6	3.44	1.13	hypothetical protein
Afu6g03730	2.17	2.23	1.09	prpd protein
Afu6g03770	2.66	2.98	3.2	oxidoreductase (Msc7), putative
Afu6g03800	1.05	1.33	2.78	hypothetical protein
Afu6g03900	2.44	1.81	2.24	F-box domain protein
Afu6g03970	2.82	2.64	2.54	NUV101
Afu6g04020	2.69	2.84	3.33	peptidyl-tRNA hydrolase domain protein
Afu6g04040	1.97	2.81	2.23	peroxisomal D3,D2-enoyl-CoA isomerase
Afu6g04250	3.46	3.62	3.8	Protein required for hyphal anastomosis
Afu6g04290	1.23	1.37	2.29	phosphoethanolamine N-methyltransferase, putative
Afu6g04370	1.77	1.4	2.2	hypothetical protein
Afu6g04700	3.15	3.21	3.23	imidazoleglycerol-phosphate dehydratase
Afu6g04730	2.32	1.95	2.56	Ade1p protein
Afu6g04800	2.06	2.81	2.53	lysine decarboxylase-like protein
Afu6g04890	0.78	2.16	1.98	CaaX prenyl proteinase Rce1

Afu6g04900	2.37	2.66	1.21	sucrose cleavage family protein
Afu6g04920	4	4.66	3.41	NAD-dependent formate dehydrogenase
Afu6g05030	3.52	4.55	3.99	polysaccharide deacetylase family protein
Afu6g05130	2.76	2.58	2.65	snRNA cap binding complex subunit (Gcr3), putative
Afu6g05200	1.82	2.21	1.55	Ribosomal L28e protein family
Afu6g05210	1.87	2.43	1.56	malate dehydrogenase, NAD-dependent
Afu6g06460	2.47	2.56	1.92	fumarylacetoacetate hydrolase family protein
Afu6g06520	2.46	2.65	1.96	WW domain protein
Afu6g06690	2.06	2.77	1.94	CFEM domain protein, putative
Afu6g06770	2.77	2.72	2.51	enolase
Afu6g06870	0.86	1.24	2.07	casein kinase I homolog, putative
Afu6g07120	1.78	2.12	2.11	nuclear movement protein
Afu6g07220	1.95	2.21	2	Aromatic-Rich Protein Family family
Afu6g07260	2.78	2.26	2.69	purine-cytosine permease, putative
Afu6g07340	2.26	2.76	1.4	kynurenine 3-monooxygenase
Afu6g07540	2.54	1.95	1.71	t-complex protein 1, epsilon subunit, putative
Afu6g07560	1.89	2.52	1.96	hypothetical protein
Afu6g07610	1.49	3.02	3.27	hypothetical protein
Afu6g07620	3.13	3.82	3.77	GDP-mannose pyrophosphorylase A
Afu6g07640	2.35	2.23	3.07	lysyl-tRNA synthetase
Afu6g07770	3.09	2.83	2.42	alanine aminotransferase, putative
Afu6g07920	2.06	2.37	2.01	acetyltransferase, GNAT family family
Afu6g07950	1.43	1.67	2.29	fungal specific transcription factor, putative
Afu6g08000	2.6	3.56	3.41	general amidase
Afu6g08050	2.25	2.14	1.11	6-phosphogluconate dehydrogenase, decarboxylating
Afu6g08110	2.37	2.53	2.85	DNA (apurinic or apyrimidinic site) lyase, endon uclease
Afu6g08160	3.02	3.48	4.05	MOSC domain protein
Afu6g08170	2.08	2.39	3.38	DNA polymerase V, putative
Afu6g08370	2.05	1.66	2.52	neutral sphingomyelinase
Afu6g08440	3.57	3.43	3.05	protoporphyrinogen oxidase, putative
Afu6g08460	1.13	2.19	2.68	cytochrome P450 alkane hydroxylase, putative
Afu6g08470	1.73	2.59	2.75	glycerol kinase, putative
Afu6g08490	-0.43	1.66	3.49	inorganic diphosphatase, putative
Afu6g08560	2.11	2.56	3.94	nonribosomal peptide synthase (NRPS), putative
Afu6g08570	0.57	1.15	2	DNA damage repair protein Mus42, putative
Afu6g08620	1.98	2.02	1.42	Golgi reassembly stacking protein, putative
Afu6g08630	3.94	4.62	4.35	hypothetical protein
Afu6g08640	3.92	4	4.12	metallopeptidase Mip1

Afu6g08650	2.24	3.27	3.44	hypothetical protein
Afu6g08660	3.19	3.51	4.02	hypotetical protein
Afu6g08700	2.92	4.55	4.47	beta glucosidase, putative
Afu6g08710	3.35	4.51	4.61	alkaline phosphatase, putative
Afu6g08810	1.51	2.3	1.76	NADH-ubiquinone oxidoreductase 304 kDa subunit precursor
Afu6g08890	1.62	1.68	2.08	thioesterase family protein
Afu6g08900	1.64	1.4	2.02	ATP dependent RNA helicase, putative
Afu6g09050	1.63	2.39	1.65	hypothetical protein
Afu6g09320	1.19	2.62	1.98	LysM domain protein, putative
Afu6g09580	2.04	2.07	2.62	hypothetical protein
Afu6g09590	2.8	2.66	2.33	zinc-containing alcohol dehydrogenase, putative
Afu6g09600	2.14	2.32	2.59	peptidase, putative
Afu6g09640	0.04	2.15	4.14	aminotransferase GliI
Afu6g09650	0.12	2.46	4.45	membrane dipeptidase GliJ
Afu6g09670	0.03	3.34	5.93	cytochrome P450 oxidoreductase GliC
Afu6g09680	0.07	4.87	6.54	O-methyltransferase GliM
Afu6g09690	0.35	3.91	6.38	glutathione S-transferase GliG
Afu6g09700	-0.21	2.18	5.46	gliotoxin biosynthesis protein GliK
Afu6g09710	0.78	5.53	6.82	MFS gliotoxin efflux pump GliA
Afu6g09720	0.07	5.62	6.37	methyltransferase GliN
Afu6g09730	0.81	4.96	6.35	cytochrome P450 oxidoreductase GliF
Afu6g09740	1.66	5.09	6.7	thioredoxin reductase GliT
Afu6g09860	1.61	3.61	2.4	hypothetical protein
Afu6g09910	2.63	3.96	3.58	glutaminase A
Afu6g09970	2.29	3.61	3.52	oxidoreductase, short chain dehydrogenase/reductase family
Afu6g10070	1.69	2.32	2.28	PEX11 domain protein
Afu6g10080	3.9	4.45	4.97	conserved hypothetical protein
Afu6g10090	4.15	4.1	4.11	D-isomer specific 2-hydroxyacid dehydrogenase family protein
Afu6g10100	2.08	2.55	2.94	related to monocarboxylate transporter, putative
Afu6g10210	1.97	2.12	2.18	guanine deaminase, putative
Afu6g10220	2.44	2.49	2.22	small oligopeptide transporter, OPT family
Afu6g10280	1.02	2.03	0.22	conserved hypothetical protein
Afu6g10330	1.74	2.42	1.33	GTP binding protein (SPG1), putative
Afu6g10340	3.55	3.95	3.72	hypothetical protein
Afu6g10450	1.92	2.57	1.8	hypothetical protein

Afu6g10660	2.92	2.64	2.34	ATP-citrat-lyase
Afu6g10690	2.32	2.41	2.44	cleavage and polyadenylylation specificity factor subunit Fip1, putative
Afu6g10760	3.24	3.61	3.21	HAD superfamily hydrolase, putative
Afu6g11020	2.35	2.83	1.66	3-hydroxyisobutyrate dehydrogenase
Afu6g11190	1.91	2.21	2.46	protein kinase (VPS15), putative
Afu6g11210	2.78	3.31	2.84	3-oxoacyl-(acyl-carrier-protein) reductase
Afu6g11330	3.16	4.67	3.83	histidine acid phosphatase, putative
Afu6g11340	1.77		2.43	peroxisomal AMP binding enzyme, putative
Afu6g11390	2.14	2.64	2.74	1,3-beta-glucanosyltransferase Gel2
Afu6g11420	2.61	4.06	2.19	conserved hypothetical protein
Afu6g11440	2.1	3.01	2.94	pyridoxamine phosphate oxidase family protein
Afu6g11490	1.72	2.31	2.51	NUDIX domain protein
Afu6g11500	2.05	2.65	2.42	dipeptidase, putative
Afu6g11560	2.83	2.49	3.32	integral membrane protein, putative
Afu6g11570	3.03	2.89	3.26	alpha/beta hydrolase, putative
Afu6g11620	3.29	3.31	3.3	formyltetrahydrofolate deformylase
Afu6g11680	3.67	4.42	4.72	thiamine pyrophosphate enzyme, putative
Afu6g12120	0.57	2.17		BNR/Asp-box repeat domain protein
Afu6g12150	0.57	1.85	3.55	bZIP transcription factor (Atf7), putative
Afu6g12170	2.15	2.81	2.19	FKBP-type peptidyl-prolyl isomerase, putative
Afu6g12180	3.36	3.11	3.38	conserved hypothetical protein
Afu6g12200	1.13	2.19	2.95	hypothetical protein
Afu6g12230	3.02	3.38	3.84	conserved hypothetical protein
Afu6g12240	4.32	5.32	4.84	Glycerophosphoryl diester phosphodiesterase family family
Afu6g12280	1.87	2.27	1.42	NADH-ubiquinone oxidoreductase 213 kDa subunit
Afu6g12310	1.77	2.12	1.48	conserved hypothetical protein
Afu6g12420	0.2	2.92	2.79	SprT family metallopeptidase, putative
Afu6g12470	1.83	2.22	1.87	Golgi transport complex subunit Cog6, putative
Afu6g12580	3.02	3.07	2.61	anthranilate synthase component I
Afu6g12620	1.64	1.88	2.37	related to ribosomal protein MRP49
Afu6g12660	2.33	2.27	2.01	40s ribosomal protein
Afu6g12670	3.59	4.51	1.97	beta-alanine synthase, putative
Afu6g12760	3.46	4.24	3.5	GPI transamidase component (GAA1), putative
Afu6g12910	1.43	2.77	2.29	dsDNA-dependent ATPase (Rad54), putative
Afu6g12960	2.02	2.1	2.1	hypothetical protein
Afu6g13160	2.38	3.16	2.21	serine/threonine protein kinase, putative

Afu6g13330	1.67	1.79	2.38	conserved hypothetical protein
Afu6g13380	1.22	2.53	3.5	hypothetical protein
Afu6g13400	3.71	4.54	3.55	arsenate reductase (Arc2), putative
Afu6g13450	3.62	3.51	3.15	nitrilase
Afu6g13460	3.11	3.19	3.5	hypothetical protein
Afu6g13520	1.93	2.2	2.62	tryptophan synthase
Afu6g13590	3.37	3.43	1.99	3-isopropylmalate dehydrogenase
Afu6g13660	0.96	2.08	2.17	conserved hypothetical protein
Afu6g13700	0.7	3.05	1.28	hypothetical protein
Afu6g13750	5.26	6.73	6.51	ferric-chelate reductase, putative
Afu6g13760	3.44	4.05	3.8	alpha-1,2-mannosidase, putative subfamily
Afu6g13830	2.38	2.47		oxidoreductase, short chain dehydrogenase/reductase family
Afu6g13840	3.1	3.77	3.77	conserved hypothetical protein
Afu6g13850	3.11	4.05	4.51	GTPase activating protein (Evi5), putative
Afu6g13860	2.08	2.27	1.76	conserved hypothetical protein
Afu6g14060	2.59	4.6	4.67	hypothetical protein
Afu6g14090	1.57	2	1	CFEM domain protein, putative
Afu6g14180	2.09	2.51	1.53	beta-1,4-mannosyltransferase (Alg1), putative
Afu6g14220	1.65	2.01	2.17	kinesin family protein (KinA), putative
Afu6g14300	1.11	1.6	2.05	FAD binding domain protein
Afu6g14310	1.61	2	2.12	5'-nucleotidase, putative
Afu6g14330	4.08	4.5	3.95	5-oxo-L-prolinase, putative
Afu6g14360	1.29	1.26	2.17	cytochrome P450, putative
Afu6g14390	0.47	1.03	2.01	extracelular cellulose binding protein (Cip2), putative
Afu6g14420	1.24	4.24	3.34	disintegrin-like metalloproteinase, putative
Afu6g14460	0.93	2.21	0.91	2-haloalkanoic acid dehalogenase
Afu6g14480	0.78	2.49	3.03	alpha-1,3-mannosyltransferase, putative
Afu6g14490	1.97	4.52	4.02	beta-glucosidase, putative
Afu6g14500	3.58	6.66	6.63	MFS sugar transporter, putative
Afu6g14530	3.08	3.93	4.05	L-cystine transporter, putative
Afu7g00380	1.72	5.01	4.96	GNAT family acetyltransferase, putative
Afu7g00440	1.23	2.37	1.14	GABA permease, putative
Afu7g00580	1.06	3.56	4.37	conserved hypothetical protein
Afu7g00700	4.36	3.99	4.32	aldo-keto reductase (AKR13), puatative
Afu7g00710	2.51	3.54	3.85	oxalate/formate antiporter, putative
Afu7g00720	3.16	2.46	2.4	hypothetical protein
Afu7g00730	2.85	2.49	2.69	high affinity methionine permease

Afu7g00780	2.62	3.3	4.4	MFS monocarboxylate transporter, putative
Afu7g00800	0.95	1.88	2	acid phosphatase, putative
Afu7g00850	2.26	4.01	4.64	acetyltransferase, GNAT family, putative
Afu7g00910	1.34	2.44		peptide transporter MTD1
Afu7g00970	0.87	2.44	3.84	GPI-anchored serine-threonine rich protein
Afu7g01030	1.58	1.72	2.17	Calcium-transporting ATPase 1 (PMC1), putative
Afu7g01040	1.21	3.85	3.44	cytidine deaminase, putative
Afu7g01090	4.57	4.87	5.67	proline permease
Afu7g01240	2.2	4.4	3.74	phytase, putative
Afu7g01300	2.66	3.45	3.49	mannosyltransferase (PIG-M), putative
Afu7g01340	1.08	2.44	1.66	RPEL repeat protein
Afu7g01520	2.82	2.95	3.84	BolA domain protein
Afu7g01540	2.23	1.75	2.21	endo-1,4-beta-glucanase
Afu7g01580	2.14	2.59	2.84	molybdopterin synthase small subunit CnxG
Afu7g01590	3.19	3	3.11	cystathionine gamma-synthase
Afu7g01670	2.13	2.19	3.4	MFS amino acid transporter, putative
Afu7g01680	2.84	3.73	4.05	hypothetical protein
Afu7g01690	1.97	2.7	2.13	acetamidase
Afu7g01740	2.95	3.47	4.74	sugar transporter, putative
Afu7g01840	2.54	2.65	2.97	membrane bound C2 domain protein (vp115), putative
Afu7g01860	3.72	3.8	4.01	heat shock protein (Sti1), putative
Afu7g01980	1.88	1.94	2.11	sinapyl alcohol dehydrogenase
Afu7g01990	0.07	2.08	1.28	conserved hypothetical protein
Afu7g02010	0.5	2.49	2.99	hypothetical protein
Afu7g02070	2	2.16	1.69	AIF-like mitochondrial oxidoreductase (Nfrl), putative
Afu7g02080	2	1.64	2.65	RNA polymerase I subunit Rpa43, putative
Afu7g02340	3.92	4.74	4.97	L-PSP endoribonuclease family protein (Hmf1), putative
Afu7g02470	1.57	2	1.73	mRNA processing protein (Mss51), putative
Afu7g03960	1.82	2.29	2.06	thioesterase family protein
Afu7g03990	2.6	2.35	2.34	uridylate kinase
Afu7g04500	3.37	3.54	3.39	ATP phosphoribosyltransferase
Afu7g04570	1.64	3.65	2.92	Na/K ATPase alpha 1 subunit, putative
Afu7g04580	3.13	3.8	4.49	TBC domain protein, putative
Afu7g04690	2.22	2.52	2.48	FAD dependent sulfhydryl oxidase Erv2, putative
Afu7g04720	2.88	3.44	3.52	alpha-1,2-mannosidase, putative
Afu7g04730	3.92	4.43	4.76	siderochrome-iron transporter, putative
Afu7g04760	3.21	3.38	4.04	gamma-glutamyltranspeptidase
Afu7g04800	1.16	2.24	2.17	hypothetical protein

Afu7g04960	0.68	2.47	2.26	N-acetyltransferase, GNAT family, putative
Afu7g04970	0.83	4.11	2.31	metalloreductase, putative
Afu7g04980	0.72	2.45	0.81	3-ketoacyl-acyl carrier protein reductase
Afu7g04990	2.26	4.32		dUTP diphosphatase Dut, putative
Afu7g05010	3.05	3.07	2.34	glyoxalase family protein
Afu7g05070	4.56	4.14	4.38	FAD dependent oxidoreductase, putative
Afu7g05080	3.01	3.41	2.38	C6 transcription factor, putative
Afu7g05090	3.42	3.99	2.43	glucuronyl hydrolase, putative
Afu7g05100	3.92	3.82	3.22	hexose transporter protein
Afu7g05150	3.34	5.32		hypothetical protein
Afu7g05160	1.35	2.53	1.09	fumarylacetoacetate hydrolase family protein
Afu7g05300	2.28	3.16	3.52	hypothetical protein
Afu7g05450	6.18	7.17	7.06	SUN domain protein (Uth1), putative
Afu7g05470	1.26	2.12	0.78	electron transfer flavoprotein alpha subunit, putative
Afu7g05610	3.68	4.68	5.11	glucanase, putative
Afu7g05720	2.64	2.15	2.32	pyruvate dehydrogenase complex, dihydrolipoamide acetyltransferase component, putative
Afu7g05840	1.67	2.74	2	amidohydrolase family protein
Afu7g05950	0.9	2.21	1.75	EF-hand protein
Afu7g06080	4.5	4.79	4.69	ubiE/COQ5 methyltransferase, putative
Afu7g06090	2.26	3.13	1.77	palmitoyl-CoA oxidase 1
Afu7g06120	1.84	2	2.34	transmembrane transporter, putative
Afu7g06140	2.38	6.43	5.33	beta-D-glucoside glucohydrolase
Afu7g06160	3.16	5.06	5.53	hypothetical protein
Afu7g06360	2.19	2.82	3.5	hypothetical protein
Afu7g06380	5.75	6.06	5.58	maltase
Afu7g06390	4.25	4.69	4.29	maltose permease
Afu7g06490	2.58	2.91	2.43	deoxyribose-phosphate aldolase
Afu7g06540	0.14	2.65	2.14	threonine aldolase, putative
Afu7g06680	0.95	2.22	1.87	AAA family ATPase, putative
Afu7g06750	2.56	4.38	3.96	phosphoglycerate mutase family protein, putative
Afu7g06760	2.72	2.69	2.54	CRAL/TRIO domain protein
Afu7g06800	0.57	2.66	2.3	glutamyl-tRNA(Gln) amidotransferase, subunit A
Afu7g06810	2.69	5.68	6.23	L-amino acid oxidase LaoA, putative
Afu8g00110	2.15	2.26	1.23	oxidoreductase, 2OG-Fe(II) oxygenase family, putative
Afu8g00540	1.29	2.67	1.25	hybrid polyketide synthase/nonribosomal peptide synthase, putative
Afu8g00610	0.42	4.71	2.35	cell surface protein Mas1, putative

Afu8g00730	2.39	2.67	2.93	transcription regulator (RTG2), putative
Afu8g00760	1.28	1.88	2.05	cytochrome P450, putative
Afu8g00770	2.5	3.87	3.91	sugar transporter family protein
Afu8g00790	3.79	5.16	4.88	hypothetical protein
Afu8g00830	0.83	2.78	2.78	conserved hypothetical protein
Afu8g00840	4.27	4.42	4.6	amino acid permease, putative
Afu8g00850	4.86	5.36	5.49	dihydroorotase, homodimeric type
Afu8g00890	1.49	2.47	1.33	glucose transporter
Afu8g00910	0.71	2.55		conserved hypothetical protein
Afu8g00980	1.97	3.59	4.03	hypothetical protein
Afu8g01030	2.16	4.13	3.11	hypothetical protein
Afu8g01070	1.61	2.32	2.42	Lathosterol oxidase, putative
Afu8g01080	0.92	2.21	1.95	hypothetical protein
Afu8g01110	2.41	2.24	2.02	integral membrane protein, putative
Afu8g01120	3.33	3.91	3.69	hypothetical protein
Afu8g01130	1.46	2.1		alpha-galactosidase C
Afu8g01160	2.33	4.3	2.09	tartrate dehydrogenase, putative
Afu8g01250	2.23	2.42	2.78	acetyltransferase, GNAT family family
Afu8g01310	1.74	2.82		metalloreductase, putative
Afu8g01470	0.86	2.03		flavin containing amine oxidase, putative
Afu8g01580	2.96	3.47	3.9	aminotransferase, classes I and II family
Afu8g01670	3.36	3.5	3.87	bifunctional catalase-peroxidase Cat2
Afu8g01710	5.44	5.63	6.64	antigenic thaumatin domain protein, putative
Afu8g01730	1.12	1.34	2.1	Glycosyl transferase family 8 domain containing protein
Afu8g01780	0.49	2.19	0.97	nitrilase, putative
Afu8g01800	1.97	2.31	1.6	Thiosulfate sulfurtransferase
Afu8g01810	1.98	2.44	1.85	conserved hypothetical protein
Afu8g01840	3.4	2.98	4.36	hypothetical protein
Afu8g01850	4.6	4.08	5.24	phosphate-repressible phosphate permease
Afu8g01920	1.93	3.8	3.09	hypothetical protein
Afu8g02010	2.53	1.49	1.71	MFS sugar transporter, putative
Afu8g02030	3.2	4.01	4.14	conserved hypothetical protein
Afu8g02090	0.75	2.16	0.49	nucleotide-sugar transporter family protein
Afu8g02130	0.85	2.04	1.46	1,3-beta-glucanosyltransferase, putative
Afu8g02200	3.47	4.47	4.44	proline permease
Afu8g02440	4.36	5.98	6.61	C-4 methyl sterol oxidase, putative
Afu8g02450	4.6	5.06	5.84	hypothetical protein
Afu8g02470	0.78	2.01	1.73	trihydroxytoluene oxygenase

Afu8g02530	1.89	2.96	1.53	extracellular lipase, putative
Afu8g02550	0.36	2.49	2.19	Ptr2-like MFS peptide transporter, putative
Afu8g02560	1.8	3.78	4.63	glyceraldehyde-3-phosphate dehydrogenase, putative
Afu8g02610	0.9	1.74	2.76	cytochrome P450 monooxygenase, putative
Afu8g02620	0.75	1.67	2.61	CobW domain protein
Afu8g02670	1.59	1.86	3.1	conserved hypothetical protein
Afu8g04000	2.17	2.03	2	acetyl-coa acetyltransferase
Afu8g04200	1.92	2.37	2.25	G-patch domain protein, putative
Afu8g04380	3.15	3.61	3.91	conserved hypothetical protein
Afu8g04610	1.56	2.04	2.3	DnaJ domain protein
Afu8g04650	1.51	2.15	1.76	3-hydroxyanthranilate 3,4-dioxygenase
Afu8g04670	2.06	1.86	1.92	serine/threonine protein kinase, putative
Afu8g04700	3.49	5.42	5.34	conserved hypothetical protein
Afu8g04710	3.31	5.15	5.22	xylosidase
Afu8g04760	2.37	2.58	2.07	ureidoglycolate hydrolase
Afu8g05040	3.64	4.64	4.13	dihydrodipicolinate synthetase family protein
Afu8g05220	1.93	2.23	2.72	acetamidase-A
Afu8g05280	2.69	3.59	3.2	QDE2 protein
Afu8g05310	0.86	2.18	1.27	DUF962 domain protein
Afu8g05320	2.96	2.58	1.83	mitochondrial F1 ATPase subunit alpha, putative
Afu8g05440	3.07	2.96	2.43	mitochondrial ATPase subunit ATP4, putative
Afu8g05500	2.41	2.1	0.99	COP9 signalosome subunit 4 (CsnD), putative
Afu8g05530	2.16	1.78	0.94	soluble fumarate reductase (Osm1), putative
Afu8g05590	1.77	2.03	2.66	oxidoreductase, short chain dehydrogenase/reductase family
Afu8g05600	2.88	4	4.69	hypothetical protein
Afu8g05610	4.78	5.88	6.1	cell wall glucanase (Scw11), putative
Afu8g05630	1.32	1.99	2.27	chitin synthase F
Afu8g05650	2.34	2.88	2.64	hypothetical protein
Afu8g05680	1.58	3.82	3.16	serine/threonine protein kinase, putative
Afu8g05690	3.02	3.45	3.39	acetyltransferase, GNAT family family
Afu8g05800	1.29	3.67	3.61	C6 finger domain protein, putative
Afu8g05850	3.35	3.83	3.97	FAD dependent oxidoreductase superfamily
Afu8g05860	2.82	3.11	3.33	aromatic amino acid and leucine permease
Afu8g05970	1.86	2.74	2.05	TRI7, putative
Afu8g06130	2.73	2.84	2.63	FluG family protein
Afu8g06440	2.7	3.68	2.89	fructosyl amino acid oxidase, putative
Afu8g06450	1.06	2.87	2.85	Rieske 2Fe-2S family protein, putative

Afu8g06460	2	3.56	3.92	C6 transcription factor, putative
Afu8g06470	4.34	5.86	6.03	N,N-dimethylglycine oxidase
Afu8g06560	1.72	3.52	3.4	DUF895 domain membrane protein
Afu8g06700	2.39	3.41	2.67	annexin ANXC3.1
Afu8g06760	1.26	1.72	2.63	integral membrane protein
Afu8g06770	3.16	3.65	2.73	conserved hypothetical protein
Afu8g06830	1	2.69	0.98	endoglucanase, putative
Afu8g06850	0.49	2.23	2.5	conserved hypothetical protein
Afu8g06880	1.94	3.59	3.09	pectin methylesterase, putative
Afu8g06920	1.83	2.4	2.78	K+/H+ antiporter, putative
Afu8g06960	2.33	5	4.06	hypothetical protein
Afu8g07030	1.4	2.36	1.34	endo-1,4-beta-mannosidase, putative
Afu8g07080	2.09	6.39	6.34	elastinolytic metalloproteinase Mep
Afu8g07090	5.16	5.81	6.98	extracellular proline-serine rich protein
Afu8g07130	2.33	2.42	1.81	AhpC/TSA family thioredoxin peroxidase, putative
Afu8g07180	2.41	2.48	3.14	C6 transcription factor, putative
Afu8g07190	1.4	1.36	2.47	hypothetical protein
Afu8g07240	2.64	2.53	2.98	MFS maltose permease, putative
Afu8g07320	0.34	2.1		hypothetical protein
Afu8g07340	1.37	2.26	1.95	HET domain protein

Table AD.1.1: List of up-regulated genes in the ATCC46645 time course. Genes significantly up-regulated were included if showing a fold change of +2 on a $\log_2$ scale at least in one of the time point datasets. T0 vs T4 = 4 hrs, T0 vs T8 hrs = 8 hrs, T0 vs T16 = 16 hrs.

ORFs	T4 vs T0	T8 vs T0	T16 vs T0	Description	Annotation
Afu2g01240	3.14	1.82	1.33	beta-D-fructofuranoside fructohydrolase	extracellular region///cytoplasm///beta-fructofuranosidase activity///sucrose catabolic process
Afu5g04210	2.7	1.65	1.37	ubiquinol-cytochrome C reductase complex core protein 2, putative	aerobic respiration///mitochondrial respiratory chain complex III///mitochondrion///ubiquinol-cytochrome-c reductase activity///"mitochondrial electron transport, ubiquinol to cytochrome c"
Afu3g08660	2.62	1.79	1.91	isocitrate dehydrogenase, NADP-dependent	mitochondrion///glutamate biosynthetic process///isocitrate metabolic process///isocitrate dehydrogenase (NADP+) activity

Afu2g02810	2.57	1.87	1.1	alcohol dehydrogenase, zinc-containing, putative	oxidoreductase activity///cellular component unknown///zinc ion binding///metabolic process///"oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor"
Afu6g07540	2.54	1.95	1.71	t-complex protein 1, epsilon subunit, putative	chaperone activity///cytoplasm///protein folding///cytoskeleton organization///cytoskeleton
Afu8g02010	2.53	1.49	1.71	MFS sugar transporter, putative	membrane///transporter activity///transport
Afu4g06620	2.47	1.59	1.37	Glutamate/Leucine/Phenylalanine/Valine dehydrogenase, putative	cytoplasm///nucleus///glutamate biosynthetic process///glutamate dehydrogenase (NADP+) activity
Afu6g01950	2.47	1.97	1.31	hypothetical protein	
Afu6g00510	2.46	1.72	1.78	NADP-dependent alcohol dehydrogenase	alcohol metabolic process///soluble fraction///alcohol dehydrogenase (NADP+) activity
Afu2g04560	2.4	1.85	1.22	oxidoreductase, short-chain dehydrogenase/reductase family	oxidoreductase activity///lipid particle///biological process unknown
Afu4g14670	2.3	1.91		MFS quinate transporter, putative	mannose transmembrane transporter activity///hexose transport///fructose transmembrane transporter activity///plasma membrane///glucose transmembrane transporter activity
Afu3g07810	2.24	1.85	1.91	succinate dehydrogenase, flavoprotein subunit	tricarboxylic acid cycle///mitochondrial respiratory chain complex II///succinate dehydrogenase (ubiquinone) activity///"mitochondrial electron transport, succinate to ubiquinone"
Afu5g11240	2.23	1.91	0.63	oxidoreductase, short chain dehydrogenase/reductase family	L-serine metabolic process///cytoplasm///nucleus///"oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor"
Afu5g01380	2.22	1.31	1.23	conserved hypothetical protein	
Afu4g11050	2.2	1.63	0.88	NADH-ubiquinone oxidoreductase, subunit F, putative	
Afu2g12400	2.17	1.93	1.78	ATP synthase oligomycin sensitivity conferral protein, putative	structural molecule activity///ATP synthesis coupled proton transport///"mitochondrial proton-transporting ATP synthase, stator stalk"///"hydrogen ion transporting ATP synthase activity, rotational mechanism"
Afu4g09180	2.17	1.35	1.43	SET domain protein	
Afu8g05530	2.16	1.78	0.94	soluble fumarate reductase (Osm1), putative	cytoplasm///metabolic process///fumarate reductase (NADH) activity
Afu2g04700	2.16	1.75	1.32	RNA binding effector protein (Scp160), putative	nuclear envelope-endoplasmic reticulum network///polysome///chromosome

					segregation///intracellular mRNA localization///RNA binding///endoplasmic reticulum membrane
Afu2g13620	2.16	1.72	1.69	thiamine pyrophosphate enzyme, putative	
Afu1g15960	2.15	1.89	1.66	glutathione reductase	glutathione-disulfide reductase activity///response to oxidative stress///cytoplasm///nucleus///mitochondrion
Afu1g04320	2.13	1.91	1.93	ribosomal protein S8.e	structural constituent of ribosome///translation///cytosolic small ribosomal subunit (sensu Eukaryota)
Afu4g11910	2.08	1.56	1.27	N-terminal acetyltransferase catalytic subunit (NAT1), putative	intracellular///peptide alpha-N-acetyltransferase activity///cytoplasm///protein amino acid acetylation///protein binding
Afu2g13250	2.07	1.46	1.24	bifunctional tryptophan synthase TRPB	cytoplasm///tryptophan synthase activity///nucleus///tryptophan biosynthetic process
Afu8g04670	2.06	1.86	1.92	serine/threonine protein kinase, putative	biological process unknown///protein kinase activity
Afu3g10700	2.06	1.96	0.9	Arp2/3 complex subunit Arc16, putative	Arp2/3 protein complex///structural molecule activity///mitochondrial envelope///actin binding///actin cortical patch assembly
Afu1g09830	2.05	1.75	1.37	Hsc70 cochaperone (SGT), putative	protein binding///Hsc70 protein regulator activity
Afu2g04060	2.05	1.88	0.96	NADH:flavin oxidoreductase/NADH oxidase family protein	oxidoreductase activity///NADPH dehydrogenase activity///metabolic process///coenzyme binding
Afu1g07380	2.05	1.58	1.52	NADH-dependent glutamate synthase (GLT1), putative	glutamate synthase (NADH) activity///cell///glutamate biosynthetic process
Afu5g02490	2.04	1.64	1.05	zinc-binding oxidoreductase, putative	oxidoreductase activity///zinc ion binding///metabolic process

Table AD.1.2: 30 ORFs with the highest $\log_2$ values between the up-regulated genes unique to the 4 hrs time point of the ATCC46645 time course.

ORFs	T4 vs T0	T8 vs T0	T16 vs T0	Description	Annotation
Afu3g15210	0.38	4.15	1.6	endo-1,4-beta-xylanase, putative	hydrolase activity, acting on glycosyl bonds///polysaccharide catabolic process
Afu3g01670	1.32	3.77	1.31	MFS hexose transporter, putative	mannose transmembrane transporter activity///hexose transport///fructose transmembrane transporter activity///plasma membrane///glucose transmembrane transporter activity///galactose transmembrane transporter activity
Afu3g00320	-0.02	3.75	1.84	endo-1,4-beta-xylanase (XlnA), putative	xylan metabolic process
Afu2g14420	1.2	3.71	1.89	cutinase, putative	

Afu5g07330	1.97	3.65	1.69	carboxypeptidase S1, putative	carboxypeptidase C activity
Afu3g03660	1.93	3.65	0.7	esterase superfamily protein	hydrolase activity, acting on ester bonds
Afu4g10160	1.71	3.64		C6 transcription factor (AmyR), putative	carbohydrate metabolic process///"regulation of transcription, DNA-dependent"///transcription factor activity///nucleus
Afu5g13300	1.67	3.63		aspartic endopeptidase Pep1	protein catabolic process///aspartic-type endopeptidase activity///extracellular region///pathogenesis
Afu2g15950	1.26	3.61		aspartic endopeptidase, putative	protein catabolic process///aspartic-type endopeptidase activity///extracellular region
Afu4g14000	0.56	3.51	0.87	tripeptidyl peptidase A	protein catabolic process///serine-type endopeptidase activity
Afu6g03680	0.6	3.44	1.13	hypothetical protein	
Afu2g14740	0.54	3.32	1.58	DUF821 domain protein	
Afu2g03730	1.89	3.25	1.85	Ctr copper transporter family protein	copper uptake transmembrane transporter activity///copper ion import///integral to plasma membrane
Afu3g14920	0.99	3.24	1.64	LaeA-like methyltransferase, putative	
Afu1g11040	0.89	3.17		hypothetical protein	
Afu3g11920	1.45	3.06	0.62	dihydrodipicolinate synthetase family protein	catalytic activity///metabolic process
Afu3g00650	1.53	3.06		aminopeptidase Y, putative	proteolysis///aminopeptidase activity
Afu6g13700	0.7	3.05	1.28	hypothetical protein	
Afu1g11010	1.82	3.03	1.81	oxidoreductase, short chain dehydrogenase/reductase family superfamily	cytoplasm///nucleus///"oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor"
Afu3g14510	1.09	3.02	1.77	rhamnogalacturonan acetylesterase, putative	lipase activity
Afu5g09070	-0.38	3	0.65	hypothetical protein	
Afu2g00870	0.84	2.97		hypothetical protein	
Afu8g02530	1.89	2.96	1.53	extracellular lipase, putative	
Afu1g17160	1.55	2.9	1.37	transporter, putative	membrane///transporter activity///transport
Afu3g00520	-0.3	2.9	0.97	SIR2 family histone deacetylase, putative	chromatin silencing at telomere///cytoplasm///NAD-dependent histone deacetylase activity
Afu3g00180	0.24	2.9	-0.1	short chain dehydrogenase, putative	oxidoreductase activity///cytoplasm///metabolic process
Afu4g14120	1.22	2.89	1.82	cutinase, putative	
Afu4g14110	1.4	2.88	1.55	hypothetical protein	
Afu2g17330	0.95	2.87	1.97	serine peptidase, family S28, putative	
Afu2g10920	1.95	2.86	1.53	enoyl-CoA hydratase/isomerase	endocytosis///3-hydroxyisobutyryl-CoA hydrolase

				family protein	activity///mitochondrion///fatty acid beta-oxidation

Table AD.1.3: 30 ORFs with the highest $\log_2$ values between the up-regulated genes unique to the 8 hrs time point of the ATCC46645 time course.

ORFs	T4 vs T0	T8 vs T0	T16 vs T0	Description	Annotation
Afu4g09920	1.83	1.8	4.38	conserved hypothetical protein	
Afu1g01300	0.42	1.9	3.91	GPI anchored protein, putative	
Afu6g12150	0.57	1.85	3.55	bZIP transcription factor (Atf7), putative	transcription///transcription factor activity///nucleus
Afu6g08490	-0.43	1.66	3.49	inorganic diphosphatase, putative	phosphate metabolic process///inorganic diphosphatase activity///cytosol
Afu3g12090	1.5	1.92	3.44	hypothetical protein	
Afu1g01310	0.37	1.49	3.42	carboxylesterase, putative	
Afu4g00830	1.72	1.78	3.37	MFS peptide transporter, putative	peptide transporter activity///plasma membrane///peptide transport
Afu3g00720	-0.15	1.59	3.1	DUF500 and UBA/TS-N domain protein	cellular component unknown///biological process unknown///molecular function unknown
Afu8g02670	1.59	1.86	3.1	conserved hypothetical protein	
Afu4g13110	1.47	1.89	3.02	hypothetical protein	
Afu3g00730	-0.2	1.86	3.01	conserved hypothetical protein	
Afu5g02250	1.08	1.19	3	conserved hypothetical protein	
Afu2g05180	1.91	1.8	2.98	NF-X1 finger and helicase domain protein, putative	DNA binding///DNA helicase activity///nucleus///zinc ion binding///RNA helicase activity
Afu3g14670	1.08	1.48	2.87	MFS transporter, putative	nicotinamide mononucleotide transport///nicotinamide mononucleotide permease activity///integral to plasma membrane
Afu1g13200	1.4	1.43	2.86	conserved hypothetical protein	
Afu3g08070	1.4	1.74	2.85	GMC oxidoreductase, putative	
Afu1g10120	1.77	1.74	2.84	ABC transporter permease protein	
Afu1g02860	1.79	1.78	2.81	C2H2 transcription factor, putative	regulation of transcription, DNA-dependent///transcription factor activity///nucleus///zinc ion binding
Afu6g02270	1.13	1.64	2.8	ribonuclease P/MRP complex subunit Pop1, putative	rRNA processing///nucleolar ribonuclease P complex///ribonuclease MRP activity///tRNA processing///ribonuclease P activity///ribonuclease MRP

					complex
Afu2g08090	0.47	1.78	2.8	hypothetical protein	
Afu6g03800	1.05	1.33	2.78	hypothetical protein	
Afu4g08630	1.42	1.85	2.77	phytase	acid phosphatase activity///polyphosphate catabolic process///cell wall-bounded periplasmic space
Afu8g02610	0.9	1.74	2.76	cytochrome P450 monooxygenase, putative	oxidoreductase activity///metabolic process
Afu5g13460	1.6	1.96	2.73	mitochondrial protein	mitochondrial genome maintenance///mitochondrion inheritance///mitochondrion organization///mitochondrial outer membrane///molecular function unknown
Afu5g13020	1.5	1.8	2.71	DNA polymerase alpha/primase associated subunit	DNA replication initiation///lagging strand elongation///"DNA replication, synthesis of RNA primer"///alpha DNA polymerase:primase complex///alpha DNA polymerase activity
Afu4g12510	0.71	0.89	2.71	hypothetical protein	
Afu3g11980	1.52	1.22	2.69	oxidoreductase, 2OG-Fe(II) oxygenase family family	
Afu4g11320	0.61	1.92	2.68	hypothetical protein	
Afu3g13140	1.82	1.92	2.68	7alpha-cephem-methoxylase P8 chain, putative	
Afu5g13030	1.51	1.92	2.67	Apc13 domain protein	

Table AD.1.4: 30 ORFs with the highest $\log_2$ values between the up-regulated genes unique to the 16 hrs time point of the ATCC46645 time course.

Locus	T0 vs T4	T0 vs T8	T0 vs T16	Common Name
Afu1g00410	-1.86	-3.75	-2.5	C6 transcription factor, putative
Afu1g00480	-2.57	-2.7	-3.23	glucosamine-6-phosphate deaminase, putative
Afu1g00540	-0.99	-1.46	-2.09	beta-N-acetylglucosaminidase, putative
Afu1g00590	-1.08	-1.7	-2.12	CPSF subunit A, putative
Afu1g00910	-3.45	-4.16	-2.98	conserved hypothetical protein
Afu1g01210	-1.59	-2.27	-1.19	hypothetical protein
Afu1g01410	-1.26	-2.12	-1.58	hypothetical protein
Afu1g01760	-1.64	-2.04	-1.41	integral membrane protein
Afu1g01850	-2.41	-2.66	-2.99	hypothetical protein
Afu1g01950	-1.96	-2.41	-2.58	hypothetical protein
Afu1g01970	-2.56	-3.48	-3.65	mutant VeA1 protein
Afu1g02020	-1.9	-2.39	-2.97	SWIB/MDM2 domain protein

Afu1g02120	-2.96	-2.79	-3.17	F-box domain protein
Afu1g02130	-2.74	-3.72	-3.1	DUF221 domain protein, putative
Afu1g02200	-2.51	-1.95		F-box domain protein
Afu1g02210	-2.22	-2.77	-2.17	60S ribosome biogenesis protein Brx1, putative
Afu1g02280	-2.75	-2.15	-1.57	conserved hypothetical protein
Afu1g02350	-1.98	-3.77	-2.78	MFS transporter, putative
Afu1g02410	-1.56	-1.94	-2.88	AAA family ATPase Reptin, putative
Afu1g02460	-1.49	-2.14	-1.78	DNA-directed RNA polymerase III 130 kd polypeptide
Afu1g02590	-2.45	-3.06	-2.94	RNA polymerase I specific transcription initiation factor RRN3 superfamily
Afu1g02600	-2.75	-3.35	-3.24	hypothetical protein
Afu1g02640	-2.76	-3.43	-2.99	conserved hypothetical protein
Afu1g02700	-1.44	-1.89	-2.26	zinc metallopeptidase, putative
Afu1g02760	-1.89	-2.32	-2.22	cell cycle inhibitor Nif1, putative
Afu1g02770	-1.61	-1.1	-2.45	hypothetical protein
Afu1g02830	-1	-2.25	-2.37	npl4 protein
Afu1g02940	-1.51	-1.55	-2.05	mitotic check point protein (Bub2), putative
Afu1g03010	-1.36	-2.05	-1.97	cell cycle control protein (Cwf22), putative
Afu1g03030	-3.08	-3.89	-3.21	hypothetical protein
Afu1g03110	-2.11	-2.26	-1.63	60S ribosomal protein L29, putative
Afu1g03210	-1.37	-2.36	-1.96	MYB family conidiophore development protein FlbD, putative
Afu1g03380	-2.43	-1.3	-1.6	UDP-N-acetylglucosaminyltransferase
Afu1g03500	-2.24	-2.69	-2.83	topoisomerase I
Afu1g03540	-2.55	-2.51	-2.4	hypothetical protein
Afu1g03650	-2.58	-2.43	-2.26	hypothetical protein
Afu1g03710	-1.3	-2.03	-1.46	C2H2 finger domain protein, putative
Afu1g03790	-2.11	-2.77	-1.91	mannosylphosphorylation protein (Mnn4), putative
Afu1g03830	-2.51	-1.94	-2.5	prefoldin subunit 2, putative
Afu1g03840	-1.94	-2.48	-2.43	CCAAT-binding factor complex subunit HapC
Afu1g03970	-1.72	-2.43	-2.63	mitochondrial translation initiation factor IF-2, putative
Afu1g04010	-0.85	-1.01	-2.01	TBC domain protein, putative
Afu1g04100	-2.77	-2.3	-1.57	hypothetical protein
Afu1g04160	-2.71	-1.57	-3.28	aspartate aminotransferase, putative
Afu1g04230	-3.22	-2.75	-2.55	mitoribosomal protein YmL27
Afu1g04240	-1.48	-2.05	-1.8	small nucleolar ribonucleoprotein complex subunit Utp14, putatrive

Afu1g04410	-2.08	-2.91	-3.26	conserved hypothetical protein
Afu1g04500	-1.55	-1.86	-2.76	hypothetical protein
Afu1g04670	-1.9	-2.52	-2.25	related to suppressor protein PSP1
Afu1g04680	-1.94	-2.48	-1.98	NifU-related protein
Afu1g04710	-1.7	-2.32	-2.33	PP-loop ATPase superfamily protein, putative
Afu1g04720	-2.15	-2.95	-2.89	C-8 sterol isomerase (Erg-1), putative
Afu1g04730	-2.14	-3.09	-2.67	endoglucanase, putative
Afu1g04750	-1.15	-2.45	-1.21	cyclin
Afu1g04800	-2.26	-2.73	-1.85	protein phosphatases pp1 regulatory subunit sds22
Afu1g04830	-1.15	-2.45	-1.56	abaA protein
Afu1g04850	-1.91	-2.07	-1.96	8 kDa cytoplasmic dynein light chain
Afu1g04880	-2.67	-3.17	-2.93	conserved hypothetical protein
Afu1g04930	-2.31	-2.52	-1.93	hypothetical protein
Afu1g04950	-1.98	-2.89	-3.06	serine/threonine protein phosphatase pp1
Afu1g04970	-1.95	-2.47	-2.65	Patatin-like serine hydrolase, putative
Afu1g05040	-2.44	-3.17	-2.29	protein mitochondrial targeting protein (Mas1), putative
Afu1g05360	-2.31	-3.01	-2.45	CAIB/BAIF family enzyme
Afu1g05370	-2.57	-2.48	-1.89	conserved hypothetical protein
Afu1g05460	-1.91	-1.79	-2.6	hypothetical protein
Afu1g05470	-1.17	-0.98	-2.04	3-oxo-5-alpha-steroid 4-dehydrogenase, putative
Afu1g05540	-1.75	-2.31	-2.13	PXA domain protein
Afu1g05560	-1.71	-3.3	-3.34	GTP binding protein, putative
Afu1g05660	-1.73	-2.27	-1.77	hypothetical protein
Afu1g05680	-2.28	-2.99	-2.19	hypothetical protein
Afu1g05740	-1.37	-2.25	-1.39	C6 transcription factor, putative
Afu1g05760	-2.08	-2.83	-2.02	arsenite efflux transporter (ArsB), puative
Afu1g05800	-1.76	-2.05	-2.25	MAP kinase kinase (Mkk2), putative
Afu1g05850	-1.52	-2.84	-2.47	erythromycin esterase family protein
Afu1g05890	-1.15	-2.61		hypothetical protein
Afu1g06190	-4.2	-5.69	-4.59	hnrnp arginine n-methyltransferase
Afu1g06280	-2.94	-3.13	-3.25	short-chain dehydrogenase/reductase family protein, putative
Afu1g06290	-2.34	-2.31	-2.17	small nucleolar ribonucleoprotein complex subunit (SOF1), putative
Afu1g06350	-4.21	-4.85	-3.52	virulence related protein (Cap20), putative
Afu1g06380	-1.99	-2.26	-1.41	RNA polymerase III subunit CII
Afu1g06400	-2.01	-3.08	-1.93	cAMP-dependent protein kinase-like, putative

Afu1g06650	-1.36	-2.07	-1.73	conserved hypothetical protein
Afu1g06690	-2.1	-2.83	-2.58	RLI and DUF367 domain protein
Afu1g06720	-2.03	-2.48	-2.93	histone acetyltransferase Spt10, putative
Afu1g06840	-1.82	-2.54	-2.35	vacuolar membrane PQ loop repeat protein
Afu1g06900	-1.01	-1.64	-2.15	C2H2 transcription factor (Crz1), putative
Afu1g06980	-1.57	-3.02	-2.54	mitochondrial small ribosomal subunit protein S4, putative
Afu1g07010	-2.16	-3.19	-2.62	phosphatidate cytidylyltransferase
Afu1g07190	-1.1	-1.55	-2.08	NA
Afu1g07350	-1.99	-2.15	-2.61	RNA12 protein, putative
Afu1g07420	-2.65	-2.89	-3.07	ER-Golgi SNARE complex subunit (Bet1), putative
Afu1g07460	-1.5	-2.58	-2.76	mitochondrial carrier protein
Afu1g07470	-2.55	-2.6	-2.47	autophagic death protein IDI-7, putative
Afu1g07610	-0.6	-0.68	-2.02	peroxisomal membrane protein pex16 (peroxin-16)
Afu1g07630	-2.15	-2.62	-2.8	zinc knuckle domain protein (Byr3), putative
Afu1g07730	-2.22	-2.4	-2.45	metalloprotease MEP1
Afu1g07740	-1.78	-1.98	-2.24	LEM3/CDC50 family protein
Afu1g07750	-2.19	-2.39	-1.51	FUN19 protein
Afu1g08770	-1.84	-2.39	-2.83	C6 finger domain protein, putative
Afu1g08790	-1.57	-1.5	-2.76	exportin KapK
Afu1g08800	-0.42	-2.23	-0.97	cytochrome P450 phenylacetate hydroxylase, putative
Afu1g08870	-2.4	-3.11	-2.72	hypothetical protein
Afu1g08900	-1.77	-2.09	-2.38	CHY and RING finger domain protein, putative
Afu1g09000	-1.53	-1.37	-2.23	conserved hypothetical protein
Afu1g09020	-1.46	-1.84	-2.39	nuclear pore complex protein (SonA), putative
Afu1g09050	-1.73	-1.75	-2.24	phospholipid methyltransferase
Afu1g09140	-2.64	-4.16	-3.49	hypothetical protein
Afu1g09160	-1.75	-1.48	-2.09	hypothetical protein
Afu1g09240	-1.96	-2.2	-1.54	ATP dependent RNA helicase, putative
Afu1g09280	-1.41	-2.59	-2.79	protein phosphatase 2C, putative
Afu1g09400	-1.61	-2.04	-1.51	R3H domain protein, putative
Afu1g09430	-2.03	-2.21		conserved hypothetical protein
Afu1g09490	-1.01	-1.27	-2.14	RNP domain protein
Afu1g09500	-2.6	-2.98	-3.34	ubiquitin-protein ligase (Rsp5), putative
Afu1g09570	-1.61	-2.14	-1.39	hypothetical protein
Afu1g09630	-1.45	-2.42	-3.08	PAB1 binding protein (Pbp1), putative
Afu1g09670	-2.84	-3.45	-3.12	HLH transcription factor (GlcD gamma), putative
Afu1g09680	-1.61	-2.33	-2	sft2 protein

Afu1g09770	-2.37	-4.02	-2.25	La domain family
Afu1g09780	-1.36	-2.46	-3.01	stomatin family protein
Afu1g09940	-2.71	-2.9	-3.03	protein required for survival at high temperature during stationary phase, putative
Afu1g09950	-1.49	-1.91	-2.6	casein kinase II beta subunit CKB2
Afu1g10040	-2.46	-3.02	-3.07	HMG box protein, putative
Afu1g10240	-0.62	-2.6	-1.24	hypothetical protein
Afu1g10290	-2.54		-2.73	chromodomain helicase (Chd1), putative
Afu1g10310	-2.43	-3.53	-3.22	RNase L inhibitor of the ABC superfamily, putative
Afu1g10470	-2.32	-2.7	-2.61	conserved hypothetical protein
Afu1g10540	-1.5	-2.09	-2.71	SIR2 family histone deacetylase (Hst4), putative
Afu1g10610	-2.07	-3.04	-1.93	hypothetical protein
Afu1g10630	-1.76	-2.6	-2.52	S-adenosylmethionine synthetase
Afu1g10710	-0.91	-1.27	-2.04	mRNA splicing protein (Prp5), putative
Afu1g10770	-2.15	-2.3	-2.02	neutral amino acid permease, putative
Afu1g10920	-1.04	-1.51	-2.27	nuclear mRNA splicing factor, putative
Afu1g10950	-4.56	-5.45	-4.78	conserved hypothetical protein
Afu1g10960	-2.18	-1.7	-1.9	Mago nashi domain protein
Afu1g11210	-2.44	-2.64	-2.02	hypothetical protein
Afu1g11240	-2.28	-3.56	-2.09	hypothetical protein
Afu1g11460	-2.04	-2.5	-1.9	1,3-beta-glucanosyltransferase Bgt1
Afu1g11490	-2.23	-2.21		vacuolar endopolyphosphatase, putative
Afu1g11580	-0.89	-1.46	-2.07	MFS quinate transporter, putative
Afu1g11720	-3.36	-3.83	-3.61	conserved hypothetical protein
Afu1g11760	-1.59	-2.28	-2.64	hypothetical protein
Afu1g11860	-2.43	-3.33	-3	mitochondrial import receptor subunit tom22
Afu1g11930	-3.36	-3.81	-3.13	protein kinase, putative
Afu1g11950	-2.52	-2.48	-2.37	mucin, putative
Afu1g12160	-1.35	-1.31	-2.19	possible translation initiation factor
Afu1g12340	-2.62	-3.4	-2.29	carnitine acetyl transferase
Afu1g12410	-2.44	-2.4	-3.27	salicylate hydroxylase
Afu1g12420	-0.96	-2.04	-1.25	hypothetical protein
Afu1g12570	-1.57	-1.54	-2.32	hepatocellular carcinoma-associated antigen 56; HCA56, putative
Afu1g12660	-2.01	-2.96	-3	hypothetical protein
Afu1g12770	-2.49	-2.92	-2.87	conserved hypothetical protein
Afu1g12810	-1.3	-2.47	-1.98	hypothetical protein
Afu1g12870	-1.66	-2.6	-2.97	conserved hypothetical protein

Afu1g12900	-3.26	-3.67	-3.98	Leucine Rich Repeat domain protein
Afu1g12930	-1.63	-2.09	-2.02	G protein complex alpha subunit GpaB
Afu1g12960	-1.74	-2.18	-2.45	SCF ubiquitin ligase complex subunit CulA, putative
Afu1g12980	-2.21	-2.37	-2.87	conserved hypothetical protein
Afu1g13050	-2.87	-4.31	-3.86	C2H2 transcription factor, putative
Afu1g13060	-2.33	-3.35	-3.47	regulator of nonsense transcripts, putative
Afu1g13070	-1.95	-1.96	-2.03	U3 small nucleolar ribonucleoprotein protein IMP4, putative
Afu1g13120	-2	-1.8	-1.7	hypothetical protein
Afu1g13140	-2.07	-2.45	-2.77	G protein complex alpha subunit GpaA
Afu1g13160	-1.59	-2.14	-1.43	geranylgeranyl diphosphate synthase
Afu1g13250	-2.26	-2.74	-2.73	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase 1, putative
Afu1g13350	-3.1	-3.65	-3.13	transporter, putative
Afu1g13400	-2.58	-2.19	-2.42	conserved hypothetical protein
Afu1g13420	-1.3	-0.84	-2	phosphotyrosyl phosphatase activator
Afu1g13520	-0.38	-1.48	-2.16	SET domain protein
Afu1g13660	-0.93	-2.44	-3.33	phenol 2-monooxygenase, putative
Afu1g13700	-2.04	-1.3	-1.05	conserved hypothetical protein
Afu1g13800	-1.33	-2.17	-2.6	mfs-multidrug-resistance transporter
Afu1g13880	-2.6	-3.71	-3.22	NAF1 domain family
Afu1g13910	-2.41	-2.37	-2.53	TFIIH complex helicase (RAD3), putative
Afu1g14010	-2.21	-2.17	-2.39	AP-2 adaptor complex subunit sigma, putative
Afu1g14050	-3.06	-3.7	-3.31	F-box domain protein
Afu1g14060	-2.01	-2.5	-2.6	C2H2 finger domain protein, putative
Afu1g14110	-2.1	-2.94	-2.76	RNA polymerase subunit
Afu1g14310	-1.99	-2.11	-2.72	poly(A)-binding protein-dependent poly(A) ribonuclease, putative
Afu1g14330	-2.72	-2.9	-2.51	ABC transporter, putative
Afu1g14620	-2.02	-2.17	-2.09	Fibronectin type III domain protein
Afu1g14630	-1.36	-1.76	-2.24	tRNAHis guanylyltransferase, putative
Afu1g14660	-3	-4.07	-3.46	regulator of secondary metabolism LaeA
Afu1g14680	-1.43	-2.01	-1.83	DNA-dependent RNA polymerase II largest subunit, putative
Afu1g14740	-3.11	-4.03	-4.52	TFIIA alpha/beta
Afu1g14750	-3.24	-4.27	-3.89	C2H2 transcription factor (Sfp1), putative
Afu1g14770	-2.26	-2.77	-3.03	tRNA dihydrouridine synthase, putative
Afu1g14800	-2.74	-0.86	0.13	hypothetical protein

Afu1g14930	-1.78	-2.01	-2.17	hypothetical protein
Afu1g15340	-3.16	-4.3	-4.02	polymerase
Afu1g15390	-1.95	-2.15	-2.79	DUF1014 domain protein
Afu1g15410	-3.04	-4.87	-3.43	CUE domain protein, putative
Afu1g15500	-2.32	-3	-2.77	GTP-binding protein Obg
Afu1g15530	-2.21	-1.28	-1.83	lactam utilization protein LamB, putative
Afu1g15570	-1.7	-2.45	-1.95	ubiquitin-conjugating enzyme, putative
Afu1g15620	-2.84	-4.4	-3.17	DEAD box RNA helicase HelA, putative
Afu1g15720	-1.11	-2.68	-1.83	importin beta-1 subunit
Afu1g15790	-2.61	-3.57	-2.63	ecylglycaid-PDC
Afu1g15810	-1.97	-3.09	-3.21	RNA splicing factor (Pad-1), putative
Afu1g15820	-2.68	-4.28	-3.51	fatty acid hydroxylase, putative
Afu1g15840	-2.54	-2.87	-2.48	hypothetical protein
Afu1g15850	-1.77	-3.75	-2.8	C6 transcription factor, putative
Afu1g15870	-2.24	-3.55	-2.98	DNA topoisomerase IV subunit A, putative
Afu1g15880	-2.64	-2.94	-3.42	DUF803 domain membrane protein
Afu1g15890	-2.3	-3.11	-2.9	SacI domain protein
Afu1g15900	-2.07	-2.16	-2.35	importin beta-2 subunit, putative
Afu1g15940	-2.22	-3.15	-3.17	Auxin Efflux Carrier superfamily
Afu1g16170	-1.13	-1.4	-2.06	hypothetical protein
Afu1g16380	-1.58	-2.03	-1.42	molybdopterin cofactor biosynthetic protein
Afu1g16430	-1.42	-2.95	-1.81	hypothetical protein
Afu1g16450	-3.35	-4.15	-2.92	hypothetical protein
Afu1g16490	-1.3	-1.66	-2.14	short chain dehydrogenase/reductase, putative
Afu1g16520	-2.19	-2.42	-1.46	hypothetical protein
Afu1g16530	-2.23	-3.19	-2.52	NA
Afu1g16550	-1.77	-2.16	-2.38	dihydrouridine synthase family protein, putative
Afu1g16570	-3.39	-3.59	-3.38	G4P04 protein
Afu1g16580	-1.02	-2.54	-1.27	conserved hypothetical protein
Afu1g16610	-2.04	-2.86	-2.98	Swr1p complex component (Swc5), putative
Afu1g16710	-2.14	-3.03	-2.4	fatty acid elongase (Gig30), putative
Afu1g16780	-1.99	-2.57	-1.92	protein kinase (Lkh1), putative
Afu1g16790	-2.67	-3.12	-3.21	related to tpa inducible protein, putative
Afu1g16850	-2.41	-2.96	-2.18	sur2 protein
Afu1g16870	-2.75	-3.07	-2.8	hypothetical protein
Afu1g16930	-2.04	-3.04	-2.15	phosphatidylserine decarboxylase, putative
Afu1g16940	-2.39	-2.67	-2.68	DEAD/DEAH box helicase, putative
Afu1g16960	-1.61	-2.49	-2.4	hypothetical protein

Afu1g16990	-2.06	-2.57	-2.1	mRNA splicing factor (Prp18), putative
Afu1g17060	-2.91	-4.26	-3.36	HLH DNA binding domain protein, putative
Afu1g17340	-1.55	-2.28		beta,beta-carotene 9',10'-dioxygenase, putative
Afu1g17350	-1.68	-2	-1.69	CP2 transcription factor, putative
Afu1g17360	-3.29	-4.38	-3.26	bZIP transcription factor (BACH2), putative
Afu1g17370	-1.53	-2.42	-1.75	chaperone/heat shock protein Hsp9, putative
Afu1g17380	-1.77	-2.75	-2.15	3-oxoacyl-(acyl-carrier-protein) reductase, putative
Afu1g17440	-2.06	-1.44		ABC drug exporter AbcA
Afu2g00160	-1.1	-2.02	-0.45	hypothetical protein
Afu2g00170	-1.58	-2.55	-1.39	glutathione-dependent formaldehyde dehydrogenase
Afu2g00200	-4.35	-6.14	-4.73	catalase, putative
Afu2g00210	-1.67	-2	-2.24	hypothetical protein
Afu2g00940	-2.1	-2.82	-1.77	hypothetical protein
Afu2g01050	-2.38	-2.25	-1.94	mitochondrial intermembrane space translocase subunit Tim9, putative
Afu2g01060	-2.14	-2.86	-1.82	Rho GTPase activator (Sac7), putative
Afu2g01110	-1.11	-1.35	-3.34	hypothetical protein
Afu2g01120	-2.53	-1.9	-1.67	DNA repair protein, putative
Afu2g01150	-2.57	-2.67	-2.59	conserved hypothetical protein
Afu2g01160	-2.62	-2.86	-3.54	C-4 methyl sterol oxidase, putative
Afu2g01550	-2.09	-2.64	-2.71	maf1 protein
Afu2g01590	-1.86	-2.26	-2.37	non-classical export protein (Nce2), putative
Afu2g01630	-2.73	-2.83	-2.96	MSF1 domain protein
Afu2g01670	-2.06	-2.81	-2.41	hypothetical protein
Afu2g01900	-1.89	-2.2	-2.75	Rtf1p, putative
Afu2g02000	-1.81	-2.46	-2.27	hypothetical protein
Afu2g02010	-1.73	-2.18	-1.86	transmembrane protein UsgS
Afu2g02020	-2.19	-1.96	-2.22	formamidase
Afu2g02030	-1.88	-3.14	-3.38	fructosyl amine:oxygen oxidoreductase
Afu2g02060	-2.08	-2.49	-2.41	D-tyrosyl-tRNA(Tyr) deacylase
Afu2g02180	-1.98	-2.44	-2.01	hypothetical protein
Afu2g02290	-2.68	-3.24	-2.87	hypothetical protein
Afu2g02310	-1.55	-2.17	-2.76	sur7 protein, putative
Afu2g02390	-3.46	-3.89	-3.51	hypothetical protein
Afu2g02400	-1.46	-2.28	-1.91	hypothetical protein
Afu2g02410	-1.77	-2.28	-2.33	hypothetical protein
Afu2g02420	-2.44	-3.34	-2.7	FHA domain protein
Afu2g02570	-2.59	-3.03	-3.6	F-box domain protein

Afu2g02600	-1.5	-1.84	-2.68	hypothetical protein
Afu2g02670	-1.91	-2.48	-2.47	DUF1295 domain protein
Afu2g02690	-2.31	-3.27	-2.64	fungal specific transcription factor, putative
Afu2g02760	-2.78	-3.6	-2.99	protein-tyrosine phosphatase, putative
Afu2g02850	-3.18	-3.85	-3.81	serine/threonine protein kinase, putative
Afu2g03030	-1.51	-2.6	-2.38	pre-mRNA splicing factor (PRP8), putative
Afu2g03070	-2.02	-2.93	-2.46	hypothetical protein
Afu2g03090	-2.68	-3.76	-3.13	vacuolar ABC heavy metal transporter (Hmt1), putative
Afu2g03130	-0.86	-2.42		hypothetical protein
Afu2g03160	-2.14	-3.61	-2.1	hypothetical protein
Afu2g03170	-1.79	-2.31	-1.64	cyclic nucleotide-binding domain protein
Afu2g03220	-0.93	-1.75	-2.17	Bax Inhibitor family protein
Afu2g03280	-1.14	-2.54	-2.34	hypothetical protein
Afu2g03340	-2.43	-2.48	-3.11	DUF652 domain protein
Afu2g03460	-1.77	-2.15	-2.6	C6 transcription factor (Leu3), putative
Afu2g03520	-2.68	-2.52	-2.07	monocarboxylate transporter, putative
Afu2g03560	-1.38	-2.13	-2.93	two-component osmosensing histidine kinase (Bos1), putative
Afu2g03680	-2.53	-2.75	-2.35	SH3 domain protein
Afu2g03790	-1.76	-2.14	-1.94	oxysterol binding protein (Osh7), putative
Afu2g03850	-1.92	-2.15	-1.25	hypothetical protein
Afu2g03950	-4.02	-5.31	-4.66	serine/threonine protein phosphatase, putative
Afu2g04000	-3.03	-4.35	-3.17	Png1p
Afu2g04040	-2.04	-2.27	-2.11	hypothetical protein
Afu2g04050	-1.67	-2	-1.29	hypothetical protein
Afu2g04080	-2.52	-3.63	-3.76	GPR/FUN34 family protein
Afu2g04100	-2.3	-3.45	-3.34	hypothetical protein
Afu2g04170	-2.42	-3.18	-2.59	conserved hypothetical protein
Afu2g04190	-2.36	-2.3	-2.07	conserved hypothetical protein
Afu2g04210	-2.67	-1.37	-1.55	conserved hypothetical protein
Afu2g04250	-1.12	-1.01	-2.62	C6 finger domain protein, putative
Afu2g04630	-0.37	-0.95	-2.01	translation elongation factor EF-1 subunit, putative
Afu2g04720	-1.95	-2.2	-2.01	ubiquitin C-terminal hydrolase, putative
Afu2g04730	-1.35	-3.12	-1.09	NA
Afu2g04740	-2.5	-2.83	-2.96	vacuolar sorting-associated protein (Vps27), putative
Afu2g04750	-2.15	-2.65	-2.1	hypothetical protein
Afu2g04780	-1.63	-2.37	-2.01	WD repeat protein

Afu2g04870	-1.03	-2.04	-1.76	dehydrogenase complex alpha subunit, putative
Afu2g05010	-1.84	-2.82	-3.12	conserved hypothetical protein
Afu2g05120	-2.34	-2.34	-1.18	hypothetical protein
Afu2g05250	-3.27	-4.4	-3.49	RfeD
Afu2g05420	-1.59	-2.5	-2.24	hypothetical protein
Afu2g05440	-2.31	-2.24	-2.55	Hypothetical protein
Afu2g05530	-2.43	-3.36	-2.89	histone acetyltransferase (Esa1), putative
Afu2g05550	-1.84	-2.53	-2.24	conserved hypothetical protein
Afu2g05570	-0.96	-0.84	-2.06	hypothetical protein
Afu2g05620	-1.83	-1.84	-2.06	conserved hypothetical protein
Afu2g05630	-2.43	-2.6	-1.73	hypothetical protein
Afu2g05730	-2.95	-3.97	-3.57	siderochrome-iron transporter (MirC), putative
Afu2g05770	-1.56	-2.1	-2.08	conserved hypothetical protein
Afu2g05840	-0.5	-2.08	-1.56	multidrug transporter, putative
Afu2g05940	-2.47	-2.73	-2.6	conserved hypothetical protein
Afu2g05970	-2.46	-2.97	-2.71	PHD finger and JmjC domain protein, putative
Afu2g05980	-1.85	-2.77		conserved hypothetical protein
Afu2g06050	-2.03	-2.22	-1.91	conserved hypothetical protein
Afu2g06060	-2.01	-2.49	-2.46	transcriptional co-activator (Hfi1/Ada1), putative
Afu2g06070	-2.84	-3.77	-3.97	NA
Afu2g06080	-1.76	-3.12	-2.99	GTPase activating protein (Gyp1), putative
Afu2g06120	-1.97	-2.93	-2.93	hypothetical protein
Afu2g06160	-1.67	-2.33		mutanase
Afu2g06170	-1.79	-2.25	-2.39	autophagy protein Atg22, putative
Afu2g06220	-2.58	-2.75	-2.96	zinc knuckle domain protein
Afu2g06280	-1.58	-1.87	-2.41	oligosaccharyl transferase subunit (gamma), putative
Afu2g06290	-4.21	-4.35	-3.95	nuclear division rft1 protein
Afu2g06300	-1.75	-1.97	-2.09	nuclear division rft1 protein
Afu2g06310	-1.47	-2.11	-2.28	ATP-dependent RNA helicase, putative
Afu2g06320	-2.06	-2.3	-3.25	replication protein A 70 kDa DNA-binding subunit
Afu2g07390	-1.5	-2.01	-3.04	hypothetical protein
Afu2g07460	-2.08	-1.93	-2.05	RNA polymerase II transcriptional coactivator, putative
Afu2g07610	-1.13	-1.85	-2.03	alcohol dehydrogenase PAN2
Afu2g07620	-2.74	-3.75	-3.66	cystathionine beta-synthase, putative
Afu2g07710	-0.33	-1.4	-2.01	mRNA splicing factor RNA helicase (Cdc28), putative
Afu2g08080	-2.84	-3.53	-2.99	conserved hypothetical protein
Afu2g08150	-2.14	-1.89	-2.41	NEDD8-like protein (RubA), putative

Afu2g08170	-2.04	-2.16	-2.45	hypothetical protein
Afu2g08440	-2.02	-2.26	-3.49	ubiquitin C-terminal hydrolase, putative
Afu2g08620	-1.58	-1.87	-2.56	20S cyclosome subunit (BimA/Nuc2/Cdc27), putative
Afu2g08660	-1.41	-2.12	-1.49	conserved hypothetical protein
Afu2g08680	-1.68	-2.9	-1.46	hypothetical protein
Afu2g08730	-0.91	-2.48		hypothetical protein
Afu2g08990	-1.86	-2.08	-2.06	eukaryotic translation initiation factor 5
Afu2g09190	-2.14	-2.75	-2.78	hypothetical protein
Afu2g09460	-1.95	-2.68		potassium transporter
Afu2g09500	-1.76	-2.13	-2.18	universal stress protein family domain protein
Afu2g09510	-3.54	-4.35	-3.82	hypothetical protein
Afu2g09530	-2.71	-2.66	-3.52	PUTATIVE SIGNAL PEPTIDE PROTEIN
Afu2g09630	-2.97	-3.99	-3.18	hypothetical protein
Afu2g09640	-2.42	-2.97	-2.85	RING finger domain protein, putative
Afu2g09820	-2.63	-3.75	-4.02	conserved hypothetical protein
Afu2g09860	-1.29	-2.46	-2.44	purine-cytosine permease
Afu2g09880	-1.57	-2.02	-1.42	hypothetical protein
Afu2g09890	-2.59	-4.23	-3.34	conserved hypothetical protein
Afu2g09990	-2.77	-3.08	-2.6	hypothetical protein
Afu2g10030	-2.94	-2.45	-1.94	vip1 protein
Afu2g10050	-2.12	-2.47	-3.57	hypothetical protein
Afu2g10110	-2.58	-3.46	-3.46	hypothetical protein
Afu2g10120	-2.61	-3.06	-3.56	YjeF domain protein
Afu2g10130	-3.18	-4.94	-3.86	phase-specific adhesin, putative
Afu2g10310	-2.39	-3.18	-3.04	DUF408 domain protein
Afu2g10330	-2.28	-2.91	-2.87	conserved hypothetical protein
Afu2g10400	-3.16	-3.9	-3.32	C6 transcription factor, putative
Afu2g10480	-1.41	-1.91	-2.29	conserved hypothetical protein
Afu2g10540	-2.11	-1.91	-1.28	hypothetical protein
Afu2g10550	-3.23	-4.15	-3.19	C2H2 transcription factor (RfeC), putative
Afu2g10750	-1.63	-3.54	-2.8	RNA helicase (Dbp), putative
Afu2g10770	-2.4	-2.47	-2.32	C2H2 transcription factor (Con7), putative
Afu2g10790	-1.05	-2.17	-1.74	pentatricopeptide repeat protein
Afu2g10850	-1.92	-2.06	-2.54	C6 finger domain protein, putative
Afu2g10870	-1.96	-1.67	-2.12	hypothetical protein
Afu2g10890	-2.04	-2.09	-2.06	VPS9 domain protein, putative
Afu2g10900	-2.17	-2.28	-2.37	autophagy related lipase (Atg15), putative
Afu2g10980	-3.3	-3.57	-3.68	ADP-ribosylation factor, putative

Afu2g11100	-2.83	-3.24	-3	AMFR protein, putative
Afu2g11180	-3.22	-3.74	-3.94	developmental regulator FlbA
Afu2g11210	-2.01	-2.79	-2	PHD finger and SET domain protein, putative
Afu2g11250	-1.78	-2.43	-2.48	aryl-alcohol dehydrogenase (AAD), putative
Afu2g11300	-1.46	-2.35		G2882
Afu2g11390	-2.05	-3.01	-2.2	hypothetical protein
Afu2g11500	-2.55	-2.81	-2.81	acetyltransferase, GNAT family family
Afu2g11570	-1.77	-2.28	-2.1	F-box domain protein
Afu2g11740	-1.17	-1.7	-2.82	LON domain serine protease, putative
Afu2g11770	-1.33	-2	-1.8	hypothetical protein
Afu2g11800	-2.05	-3.02	-2.95	small nuclear ribonucleoprotein (LSM1), putative
Afu2g11900	-2.84	-3.56	-2.27	pyruvate dehydrogenase kinase
Afu2g11920	-1.28	-2.02	-2.53	hypothetical protein
Afu2g12060	-1.53	-2.28	-2.35	F-box and WD repeat-containing protein
Afu2g12120	-1.74	-2.23	-1.61	hypothetical protein
Afu2g12200	-1.74	-2.15	-2.4	cAMP-dependent protein kinase catalytic subunit PkaC1
Afu2g12220	-2.53	-3	-2.76	DNA replication factor C subunit Rfc1, putative
Afu2g12250	-1.21	-1.56	-2.06	DNA replication factor C subunit Rfc5, putative
Afu2g12260	-1.93	-2.56	-2.55	cytochrome c oxidase assembly protein cox11
Afu2g12290	-2.01	-2.08	-2.02	NA
Afu2g12310	-3.11	-4.13	-3.39	HLH transcription factor, putative
Afu2g12330	-2.02	-3	-2.93	conserved hypothetical protein
Afu2g12360	-1.04	-1.71	-2.02	WD repeat protein
Afu2g12440	-2.06	-2.37	-2.36	Dph2l1 protein
Afu2g12510	-1.51	-2.21	-2.07	hypothetical protein
Afu2g12620	-1.77	-2.27		NA
Afu2g12630	-2.71	0.24	-1.18	allergen Asp F13
Afu2g13040	-2.35	-3.44	-2.84	mitochondrial co-chaperone GrpE, putative
Afu2g13230	-1.25	-2.03	-2.25	universal stress protein family domain protein
Afu2g13360	-2.09	-2.32	-2.53	SNF2 family helicase/ATPase, putative
Afu2g13380	-1.66	-2.32	-1.93	GATA transcription factor (AreB), putative
Afu2g13390	-2.36	-3.49	-2.93	MFS transporter, putative
Afu2g13400	-2.53	-2.55	-2.09	TDE domain protein, putative
Afu2g13440	-2.83	-3.65	-3.71	chitin synthase E
Afu2g13490	-1.74	-2.2	-2.07	KH domain protein
Afu2g13510	-1.88	-2.33	-2.06	DUF300 domain protein, putative
Afu2g13720	-2.15	-2.06	-1.12	RNA-polymerase I

Afu2g13760	-1.52	-1.54	-2	plasma membrane SNARE protein (Sec9), putative
Afu2g13830	-2.22	-3.22	-2.33	conserved hypothetical protein
Afu2g13850	-3.77	-5.46	-4.17	protein phosphatase regulatory subunit (Gac1), putative
Afu2g13870	-2.5	-3.04	-3.33	mitochondrial carrier protein, putative
Afu2g13980	-2.08	-2.41	-1.6	ATP dependent RNA helicase (Dbp9), putative
Afu2g13990	-1.54	-2.13	-2.78	hypothetical protein
Afu2g14090	-2.39	-2.9	-2.15	extragenic suppressor of the bimD6 mutation
Afu2g14110	-3.63	-3.81	-3.24	sulfur metabolite repression control protein SconB, putative
Afu2g14130	-1.96	-2.39	-2.46	ubiquitin C-terminal hydrolase, putative
Afu2g14190	-2.31	-2.61	-2.46	Mitochondrial import inner membrane translocase subunit TIM23, putative
Afu2g14320	-2.68	-3.11	-3.53	HHE domain protein
Afu2g14330	-4.16	-5.06	-3.97	hypothetical protein
Afu2g14700	-1.59	-2.2		hypothetical protein
Afu2g14720	-1.66	-2.21	-1.79	HAPB
Afu2g14800	-2.42	-3.32	-2.4	HLH transcription factor (Hpa3), putative
Afu2g14860	-1.63	-2.2		epoxide hydrolase, putative
Afu2g14890	-2.07	-2.44	-3.18	conserved hypothetical protein
Afu2g15000	-2.09	-3.13	-1.71	Mechanosensitive ion channel family
Afu2g15130	-2.98	-2.16	-2.34	ABC multidrug transporter, putative
Afu2g15140	-1.23	-2.24	-2.63	MSF drug transporter, putative
Afu2g15270	-1.77	-2.31		conserved hypothetical protein
Afu2g15440	-2.01	-2.6	-1.97	integral membrane protein, putative
Afu2g15480	-1.63	-2.79	-2.31	hypothetical protein
Afu2g15610	-1.59	-2.15	-1.19	mitochondrial DNA-directed RNA polymerase, putative
Afu2g15660	-1.12	-1.56	-2.69	aldehyde dehydrogenase family protein, putative
Afu2g15670	-1.65	-2.5	-2.18	hypothetical protein
Afu2g15680	-3.02	-2.75	-2.9	transcription initiation factor iia small chain
Afu2g15690	-2.05	-1.92	-1.75	conserved hypothetical protein
Afu2g15760	-1.65	-1.78	-2.3	poly(A)+ RNA transport protein (UbaA), putative
Afu2g15770	-1.77	-2.35	-2.45	conserved hypothetical protein
Afu2g15780	-1.69	-2.16	-2.34	Ca2+ dependent mitochondrial carrier protein, putative
Afu2g15800	-3.18	-3.73	-3.63	conserved hypothetical protein
Afu2g15880	-1.39	-2.07	-1.82	mitotic spindle checkpoint protein (Mad2B), putative
Afu2g15890	-2.07	-2.93	-1.87	RING finger protein, putative
Afu2g15960	-2.97	-3.41	-2.88	nucleotide binding protein Nbp35, putative

Afu2g15970	-1.6	-2.08	-2.16	phosphatidylethanolamine methyltransferase
Afu2g16000	-0.9	-2.17		hypothetical protein
Afu2g16020	-0.68	-1.26	-2.38	t-complex protein 1, alpha subunit, putative
Afu2g16090	-1.78	-1.85	-2.76	karyopherin alpha subunit, putative
Afu2g16180	-3.34	-4.07	-3.57	hypothetical protein
Afu2g16410	-2.56	-3.41	-3.76	hypothetical protein
Afu2g16420	-2.05	-2.8	-2.33	conserved hypothetical protein
Afu2g16440	-2.15	-2.48	-0.53	hypothetical protein
Afu2g16690	-1.26	-2.08	-1.87	SNF7 family protein
Afu2g16700	-1.54	-1.73	-2.13	DNA repair protein (RadR), putative
Afu2g16750	-2.19	-2.84	-2.17	nonsense-mediated mRNA decay protein 3
Afu2g16770	-1.24	-1.83	-2.15	mitochondrial carrier protein (Leu5), putative
Afu2g16810	-2.44	-3.47	-3.18	PHD finger domain protein, putative
Afu2g16930	-2.55	-3.98	-2.94	succinate:fumarate antiporter (Acr1), putative
Afu2g16940	-1.31	-1.6	-2.09	conserved hypothetical protein
Afu2g17060	-2.42	-2.39	-1.54	60S ribosome subunit biogenesis protein (Nip7), putative
Afu2g17130	-1.34	-2.27	-1.92	protein kinase regulator Ste50
Afu2g17220	-2.4	-3.18	-2.87	C2H2 transcription factor (AmdX), putative
Afu2g17480	-2	-3.71	-2.3	amino acid transporter, putative
Afu2g17520	-2.3	-0.73	-0.34	GNAT family N-acetyltransferase, putative
Afu2g18080	-1.63	-4.66	-2.34	LINE-1 class reverse transcriptase, RNaseH, putative
Afu3g00200	-2.53	-3.68	-3.29	hexose transporter protein
Afu3g00220	-1.6	-2.01	-1.95	hexose transporter protein
Afu3g00240	-2.08	-2.78	-2.5	TPR domain protein
Afu3g00250	-2.27	-3.34	-3.31	salicylate hydroxylase, putative
Afu3g00330	-1.11	-2.46	-2.59	hypothetical protein
Afu3g00440	-1.58	-2.22	-1.8	F-box domain protein
Afu3g00500	-3.51	-5.18	-4	integral membrane protein
Afu3g00640	-2.81	-3.79	-3.61	conserved hypothetical protein
Afu3g00810	-4.35	-4.68	-3.87	cholestenol delta-isomerase, putative
Afu3g00820	-2.59	-2.78	-2.6	putative exported protein
Afu3g00860	-1	-2.01	-2.75	hypothetical protein
Afu3g01030	-1.89	-3		RTA1 domain protein, putative
Afu3g01160	-2.05	-2.19	-1.99	iron-sulfur cluster-binding protein, rieske family domain protein
Afu3g01300	-3.23	-4.24	-3.39	hypothetical protein
Afu3g01440	-1.67	-2.47	-1.66	DUF1212 domain membrane protein

Afu3g01790	-1.37	-1.76	-2.06	isoflavone reductase family protein
Afu3g01800	-1.59	-2.09	-2.19	GPI anchored dioxygenase, putative
Afu3g01820	-1.02	-2.09	-1.71	amino acid permease
Afu3g02090	-1.57	-2.5	-2.47	beta-xylosidase
Afu3g02140	-3.42	-3.9	-2.89	large conductance mechanosensitive channel, putative
Afu3g02320	-2.02	-2.89	-2.41	C2H2 finger domain protein (Kin17), putative
Afu3g02550	-3.64	-3.29	-4.02	conserved hypothetical protein
Afu3g02710	-1.59	-2.08	-1.8	zinc-binding oxidoreductase, putative
Afu3g03040	-3.43	-4.95	-3.86	conserved hypothetical protein
Afu3g03070	-1.52	-2.82		MYND domain protein, putative
Afu3g03120	-0.79	-3.43	-1.83	NA
Afu3g03230	-1.76	-3.31	-2.39	hypothetical protein
Afu3g03300	-1.85	-2.7	-2.27	FAD binding domain protein
Afu3g03460	-2.96	-3.9	-1.9	HAD superfamily hydrolase, putative
Afu3g03940	-2.01	-2.69	-2.93	2,3-diketo-5-methylthio-1-phosphopentane phosphatase, putative
Afu3g04010	-1.42	-2.33	-2.32	MFS transporter, putative
Afu3g04060	-2	-2.56	-1.95	SNF7 family protein (Fti1), putative
Afu3g04110	-1.68	-2.27	-2.26	rRNA processing protein (Bystin), putative
Afu3g04300	-2.84	-3.43	-2.68	hypothetical protein
Afu3g04310	-3.35	-4.07	-4.04	snoRNA binding protein, putative
Afu3g05330	-3.01	-3.3	-3.16	R3H and G-patch domain protein, putative
Afu3g05390	-2.08	-2.35	-1.47	protein-L-isoaspartate O-methyltransferase
Afu3g05460	-2.62	-2.8	-2.76	60S ribosomal protein L20, putative
Afu3g05520	-1.85	-2.2	-1.71	oxysterol binding protein (Orp8), putative
Afu3g05550	-2.43	-2.29	-2.63	OTU-like cysteine protease, putative
Afu3g05560	-2.21	-2.32	-2.13	RSC complex subunit (RSC1), putative
Afu3g05760	-1.86	-2.5	-2.42	C6 transcription factor (Fcr1), putative
Afu3g05820	-1.17	-1.82	-2.01	Zinc finger, ZZ type domain protein
Afu3g05960	-0.4	-1.31	-2.15	hypothetical protein
Afu3g06000	-2.76	-5.02	-4.07	conserved hypothetical protein
Afu3g06010	-2.32	-2.86	-2.97	Nucleolar essential protein 1, putative
Afu3g06060	-0.62	-1.42	-2.12	Flap endonuclease, putative
Afu3g06090	-1.69	-2.68	-2.64	transcription initiation factor TFIID subunit 12, putative
Afu3g06100	-1.22	-1.68	-2.35	conserved hypothetical protein
Afu3g06110	-1.48	-1.84	-2.3	proteasome regulatory particle subunit (RpnC), putative

Afu3g06230	-1.99	-3.23	-1.67	hypothetical protein
Afu3g06250	-0.67	-2.34	-1.4	hypothetical protein
Afu3g06260	-1.59	-2	-1.78	translation initiation factor SUI1
Afu3g06270	-2.03	-2.82	-3.14	hypothetical protein
Afu3g06320	-2.41	-2.68	-2.79	conserved hypothetical protein
Afu3g06380	-2.95	-3.4	-3.13	hypothetical protein
Afu3g06400	-3.42	-4.28	-3.98	hypothetical protein
Afu3g06430	-1.7	-2.8	-2.65	GDP/GTP exchange factor Sec2p, putative
Afu3g06470	-2.29	-3.52	-2.89	DHHC zinc finger membrane protein, putative
Afu3g06480	-2.12	-2.6	-2.24	SET domain containing protein
Afu3g06540	-3.36	-4.71	-3.99	3'-phosphoadenosine-5'-phosphosulfate reductase
Afu3g06580	-1.17	-2.28	-1.2	WD repeat protein
Afu3g06690	-3.24	-4.12	-3.73	Rho GTPase Rho3
Afu3g06760	-1.77	-2.27	-2.15	ribosomal protein L37
Afu3g06770	-3.89	-4.76	-4.08	zinc knuckle domain protein
Afu3g06880	-1.73	-1.92	-2.25	SDP3
Afu3g06890	-1.4	-2.07	-1.9	RNA rocognition motif containing protein
Afu3g06950	-2.52	-2.53	-2.66	mitochondrial carrier protein (Rim2), putative
Afu3g07000	-1.32	-2.32	-1.5	conserved hypothetical protein
Afu3g07070	-2.18	-2.25	-1.15	MYB DNA-binding domain protein
Afu3g07110	-1.55	-1.99	-2.08	class III chitinase, putative
Afu3g07180	-2.68	-3.91	-3.49	pantothenate kinase, putative
Afu3g07240	-1.93	-2.48	-3.28	multidomain presynaptic cytomatrix related protein
Afu3g07680	-1.69	-2.75	-2.26	ran GTPase activating protein 1 (RNA1 protein)
Afu3g07840	-2.49	-2.66		hypothetical protein
Afu3g08030	-1.28	-1.67	-2.28	Met-10+ like-protein, putative
Afu3g08160	-1.24	-2.1	-2.79	eukaryotic translation initiation factor eIF4A, putative
Afu3g08240	-2.02	-1.89	-1.86	conserved hypothetical protein
Afu3g08280	-1.78	-1.92	-2.36	cell cycle regulatory protein (Srw1), putative
Afu3g08390	-2.09	-2.73	-2.55	tRNA dihydrouridine synthase (Smm1), putative
Afu3g08430	-1.22	-1.71	-2.14	mitochondrial phosphate carrier protein, putative
Afu3g08450	-2.76	-4.2	-2.81	hypothetical protein
Afu3g08580	-2.19	-1.94	-1.55	glycine-rich RNA-binding protein, putative
Afu3g08630	-1.79	-2.48		coactivator bridging factor 1 (Mbf1), putative
Afu3g08640	-0.68	-1.53	-2.26	eukaryotic translation initiation factor 3 subunit 2i, putative
Afu3g08670	-2.6	-3.29	-3.46	related to L-fucose permease
Afu3g08710	-1.52	-2.38	-1.52	protein kinase domain-containing protein

Afu3g08880	-1.53	-2.32	-2.75	conserved hypothetical protein
Afu3g08920	-2.01	-3.31	-2.13	hypothetical protein
Afu3g08990	-2.52	-3.04	-2.76	hypothetical protein
Afu3g09080	-1.89	-1.98	-2.27	Hypothetical protein
Afu3g09360	-1.96	-3.23	-3.32	vacuolar sorting ATPase Vps4, putative
Afu3g09380	-1.35	-2.08	-1.86	SGT1 protein, putative
Afu3g09410	-1.05	-3.74	-1.86	reverse transcriptase
Afu3g09430	-1.78	-4.21	-2.59	LINE-1 class reverse transcriptase, RNaseH, putative
Afu3g09770	-1.55	-1.88	-2.02	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) protein
Afu3g09820	-1.3	-2.27	-1.88	C2H2 transcription factor, putative
Afu3g09900	-1.53	-2.62	-1.81	GTPase-activating protein, putative
Afu3g09960	-1.94	-2.3	-2.91	aureobasidin resistance protein Aur1
Afu3g09980	-2.52	-2.7	-1.81	hypothetical protein
Afu3g10100	-1.18	-3.34	-1.89	Sfrs4 protein
Afu3g10110	-1.53	-1.88	-2.44	electron transfer flavoprotein-ubiquinone oxidoreductase
Afu3g10120	-3.45	-5.43	-4.53	TATA-box binding protein
Afu3g10150	-3.27	-4.48	-4.27	hypothetical protein
Afu3g10180	-1.98	-3.62	-3.15	HEC/Ndc80p family protein
Afu3g10240	-1.44	-1.83	-2.29	Ccr4-Not transcription complex subunit (NOT1), putative
Afu3g10320	-2.84	-3.21	-2.36	Zinc finger, C3HC4 type (RING finger) domain protein
Afu3g10340	-2.06	-2.44	-2.35	Rho GTPase Rho 2, putative
Afu3g10410	-2.07	-2.49	-2.12	conserved serine-rich protein
Afu3g10420	-1.81	-2.41	-1.9	conserved hypothetical protein
Afu3g10520	-1.61	-2.19	-2.03	serine/threonine protein kinase (Prp4), putative
Afu3g10530	-3.68	-5.16	-4.49	protein serine/threonine kinase (Ran1), putative
Afu3g10620	-1.46	-2.53	-3.07	transcription initiation protein
Afu3g10880	-3.21	-3.63	-2.85	anion exchange family protein
Afu3g10930	-2.24	-2.9	-2.77	bZIP transcription factor (MeaB), putative
Afu3g10960	-2.11	-2.51	-2.5	cell wall protein, putative
Afu3g11010	-1.71	-2.58	-1.18	suppressor of meiotic silencing
Afu3g11170	-2.06	-2.1	-1.62	hypothetical protein
Afu3g11210	-2.05	-1.85	-2.38	YagE family protein
Afu3g11230	-1.93	-1.98	-2.14	hypothetical protein
Afu3g11250	-2.11	-3.07	-1.99	C2H2 transcription factor (Swi5), putative

Afu3g11290	-1.12	-2.17		hypothetical protein
Afu3g11310	-2.74	-3.26	-2.8	hypothetical protein
Afu3g11330	-3.59	-4.73	-4.26	bZIP transcription factor (AtfA), putative
Afu3g11340	-2.14	-2.35	-1.9	transthyretin domain protein
Afu3g11390	-1.23	-1.58	-2.48	proteasome regulatory particle subunit Rpt3, putative
Afu3g11410	-2.16	-2.43	-1.69	RNA Polymerase II CTD phosphatase Fcp1, putative
Afu3g11530	-2.54	-3.47	-3.86	DnaJ domain protein
Afu3g11610	-2.75	-2.77	-2.65	nucleosome binding protein (Nhp6a), putative
Afu3g11730	-2.16	-2.68	-2.96	hypothetical protein
Afu3g11870	-2.28	-2.95	-2.68	F-box and WD40 domain protein, putative
Afu3g11890	-0.85	-2.32	-0.59	thermolabile L-asparaginase, putative
Afu3g12000	-1.27	-2.14	-1.15	hypothetical protein
Afu3g12050	-2.02	-2.94	-2.83	F-box domain protein
Afu3g12100	-2.21	-2.51	-1.94	trehalose synthase (Ccg-9), putative
Afu3g12220	-1.08	-2.42	-1.11	ABC transporter, putative
Afu3g12260	-2.05	-1.6	-1.9	hypothetical protein
Afu3g12350	-1.81	-2.14	-1.43	stress response RCI peptide, putative
Afu3g12370	-1.45	-1.39	-2.33	Vacuolar ATP synthase 16 kDa proteolipid subunit, putative
Afu3g12380	-1.15	-1.98	-2.43	hypothetical protein
Afu3g12400	-2	-2.75	-2.97	G protein complex alpha subunit (GanA), putative
Afu3g12490	-2.07	-2.34	-2.08	protein arginine methyltransferase 3
Afu3g12500	-1.81	-2.36	-2.24	conserved hypothetical protein
Afu3g12510	-1.93	-2.18	-2.82	vesicular fusion ATPase, putative
Afu3g12530	-3.63	-4.74	-3.74	sensor histidine kinase/response regulator, putative
Afu3g12550	-2.09	-2.39	-2.25	sensor histidine kinase/response regulator, putative
Afu3g12570		-2.86	-2.96	conserved hypothetical protein
Afu3g12670	-1.53	-2.17		serine/threonine protein kinase, putative
Afu3g12700	-2.3	-2.4	-2.5	DUF250 domain membrane protein
Afu3g12830	-1.64	-2.6	-1.69	RTA1 domain protein, putative
Afu3g12930	-1.69	-2.91	-2.57	dimethylallyl tryptophan synthase (GliD), putative
Afu3g13090	-2.07	-2.65	-1.71	hypothetical protein
Afu3g13100	-2.44	-3.06	-2.24	hypothetical protein
Afu3g13160	-3.43	-4.11	-3.08	hypothetical protein
Afu3g13180	-1.74	-2.31	-2.97	hypothetical protein
Afu3g13470	-3.49	-3.56	-3.22	sulfate transporter, putative
Afu3g13480	-2.04	-3.13	-3.38	translation initiation factor 2 alpha subunit, putative
Afu3g13770	-1.96	-1.92	-2.98	vacuolar segregation protein (Pep7), putative

Afu3g13810	-2.29	-1.91	-3.06	integral membrane protein, putative
Afu3g13850	-2.77	-2.91	-3.47	LRP16 family protein
Afu3g14270	-1.42	-1.86	-2.21	aldo-keto reductase (AKR), putative
Afu3g14340	-2.16	-1.15	-1.1	mitotic spindle checkpoint protein (Mad2), putative
Afu3g14350	-1.52	-2.25	-2.07	GTP binding protein Guf1, putative
Afu3g14430	-1.66	-1.77	-2.07	NEDD8 conjugating enzyme (UbcL), putative
Afu3g14540	-2.73	-3.75	-3.47	heat shock protein HSP30, putative
Afu3g14550	-3.73	-4.27	-3.71	DNA repair protein (Rex1), putative
Afu3g14810	-1.12	-2.17	-0.42	pathogenicity associated protein PEP2, putative
Afu3g14900	-2.04	-2.46	-2.54	hypothetical protein
Afu3g15050	-1.45	-2.51	-2.18	Flavin-binding monooxygenase, putative
Afu3g15370	-1.72	-4.34	-2.26	LINE-1 class reverse transcriptase, RNaseH, putative
Afu4g00180	-1.2	-2.09	-1.67	fatty acid oxygenase, putative
Afu4g00450	-2.13	-3.73	-4.5	hypothetical protein
Afu4g00720	-0.71	-2.15	-1.91	protein phosphatase 2C, putative
Afu4g00730	-3.1	-4.93	-4.05	HHE domain protein
Afu4g00740	-2.32	-4.17	-2.93	hypothetical protein
Afu4g00820	-1.39	-4.12	-1.98	reverse transcriptase, RNaseH
Afu4g00860	-2.04	-4.33	-2.27	conserved hypothetical protein
Afu4g01010	-1.44	-2.39	-1.75	C6 transcription factor, putative
Afu4g01560	-3.29	-2.17	-1.79	MFS myo-inositol transporter, putative
Afu4g05830	-1.98	-2.3	-2.97	IDI2
Afu4g05860	-2.79	-2.92	-2.56	mitochondrial NADH-ubiquinone oxidoreductase 20 kD subunit, putative
Afu4g05870	-3.48	-4.55	-3.55	oxidoreductase, short-chain dehydrogenase/reductase family
Afu4g05880	-1.91	-2.51	-1.42	Mpp10 protein superfamily
Afu4g05920	-2.06	-1.85	-1.84	mitochondrial protein sorting (Msf1), putative
Afu4g06030	-1.03	-1.05	-2.08	hypothetical protein
Afu4g06100	-2.57	-3.38	-2.6	conserved hypothetical protein
Afu4g06170	-2.29	-2.97	-2.55	conserved hypothetical protein
Afu4g06260	-3.35	-3.83	-3.35	mating-type switch/DNA repair protein Swi10, putative
Afu4g06280	-1.62	-2.62	-2.21	hypothetical protein
Afu4g06360	-2.31	-2.74	-2.46	conserved hypothetical protein
Afu4g06530	-2.09	-2.24	-1.61	bZIP transcription factor (MetR), putative
Afu4g06550	-1.53	-2.65	-2.98	RING finger domain protein (Znf1), putative
Afu4g06580	-2.53	-3.12	-2.44	hypothetical protein

Afu4g06730	-2.03	-1.96	-1.97	hypothetical protein
Afu4g06770	-1.79	-2.58	-2.38	iron-sulfur cofactor synthesis protein nifU, putative
Afu4g06790	-1.83	-1.98	-2	ubiquinol-cytochrome c reductase complex 14 kDa protein
Afu4g06830	-2.67	-3.11	-2.77	SUMO conjugating enzyme (UbcI), putative
Afu4g06950	-1.76	-2.23	-2.7	related to (VAMP)-associated protein
Afu4g07030	-2.15	-1.26	-1.87	hypothetical protein
Afu4g07090	-2.23	-2.68	-2.04	C2H2 finger domain protein, putative
Afu4g07160	-2.54	-3.13	-3	ATP dependent RNA helicase (Dob1), putative
Afu4g07230	-3	-3.25	-3.62	RecQ family helicase RecQ, putative
Afu4g07490	-3.22	-4.35	-3.98	hypothetical protein
Afu4g07550	-2.55	-3.21	-3.1	G-patch domain protein (Spp2), putative
Afu4g07580	-1.96	-3.16	-3.81	translation initiation factor EF-2 gamma subunit, putative
Afu4g07620	-1.84	-1.82	-2.27	hypothetical protein
Afu4g07650	-2.28	-1.96	-2.53	peptidyl-prolyl cis-trans isomerase (CypB), putative
Afu4g07660	-2.45	-3.6	-2.1	ATP dependent RNA helicase (Dbp1), putative
Afu4g07880	-2.24	-3.33	-2.56	conserved hypothetical protein
Afu4g07930	-2.1	-2.79	-2.98	hypothetical protein
Afu4g08040	-1.32	-1.46	-2.27	RAB GTPase Ypt5, putative
Afu4g08390	-1.75	-2.62	-1.58	hypothetical protein
Afu4g08440	-3.21	-4.13	-4.17	Patatin-like serine hydrolase, putative
Afu4g08450	-1.6	-2.61	-2.87	conserved hypothetical protein
Afu4g08490	-1.64	-1.91	-2.28	acyl-CoA dehydrogenase, putative
Afu4g08780	-3.28	-4.16	-3.29	hypothetical protein
Afu4g08790	-2.28	-2.4	-2.59	conserved hypothetical protein
Afu4g08860	-1.19	-2.79	-1.56	hypothetical protein
Afu4g08890	-0.36	-2.75	-1.12	aldo-keto reductase family protein, putative
Afu4g08900	-2.33	-3.77	-3.18	CDK-activating kinase assembly factor MAT1
Afu4g08910	-2.31	-2.25	-2.44	hypothetical protein
Afu4g08930	-1.52	-2.01	-0.99	nucleolar GTPase, putative
Afu4g08950	-1.35	-1.72	-2.12	NA
Afu4g08960	-2.01	-3.22	-3.22	GPI anchored protein, putative
Afu4g08970	-1.88	-2.26	-2.03	PAP2 domain protein
Afu4g09040	-2.51	-3.09	-2.5	high affinity methionine permease
Afu4g09050	-2.1	-2.73	-1.94	serine/threonine protein kinase (Pdd7p), putative
Afu4g09140	-2.96	-3.38	-3.69	ornithine aminotransferase
Afu4g09700	-1.55	-2.23	-1.68	hypothetical protein

Afu4g09910	-1.7	-2.36	-2.28	conserved hypothetical protein
Afu4g09960	-1.62	-2.15	-0.96	conserved hypothetical protein
Afu4g10100	-0.86	-2.48	-1.95	FAD binding domain protein
Afu4g10110	-3.23	-3.57	-3.65	homeobox transcription factor, putative
Afu4g10280	-2.46	-3.24	-2.9	histidine containing phosphotransmitter protein, putative
Afu4g10310	-1.63	-2.08	-1.78	hypothetical protein
Afu4g10350	-2.09	-2.82	-2.22	polyubiquitin (UbiD), putative
Afu4g10460	-2.43	-3.23	-3.01	homocitrate synthase
Afu4g10690	-2.72	-3.53	-3	Iron-sulfur cluster assembly accessory protein
Afu4g10790	-2.29	-3.42	-2.6	phosphoribosyl diphosphate synthase isoform 4
Afu4g10810	-1.56	-2.17	-1.8	hypothetical protein
Afu4g10870	-1.33	-2.16	-1.28	NA
Afu4g11130	-2.32	-2.5	-2.16	conserved hypothetical protein
Afu4g11140	-2.48	-2.77	-2.65	DNA polymerase iota, putative
Afu4g11280	-2.83	-3.06	-3.86	DUF409 domain protein
Afu4g11360	-2.34	-2.77	-3.05	glycerol-3-phosphate acyltransferase Sct1, putative
Afu4g11480	-3.83	-4.35	-3.66	C2H2 finger domain protein, putative
Afu4g11520	-1.16	-1.42	-2.17	hypothetical protein
Afu4g11560	-2.73	-3.08	-2.8	vacuolar protein sorting-associated protein vps13
Afu4g11630	-2.01	-2.05	-1.9	hypothetical protein
Afu4g11710	-3.6	-5.55	-4.61	oxidoreductase, zinc-binding dehydrogenase family superfamily
Afu4g11770	-1.31	-1.46	-2.01	hypothetical protein
Afu4g11850	-2.32	-2.4	-2.94	C6 finger domain protein, putative
Afu4g11860	-2.42	-2.74	-2.42	formin binding protein 21
Afu4g11960	-3.91	-4.37	-3.34	Iron only hydrogenase large subunit, C-terminal domain containing protein
Afu4g11980	-1.81	-2.22	-1.78	anthranilate phosphoribosyltransferase
Afu4g12040	-1.96	-2.27	-3.37	oxidosqualene:lanosterol cyclase
Afu4g12110	-2.41	-3.16	-2.49	TPR domain protein
Afu4g12360	-1.43	-1.8	-2.04	prefoldin subunit 1, putative
Afu4g12390	-3.25	-4	-2.83	cell differentiation protein (Rcd1), putative
Afu4g12400	-2.09	-2.57	-1.99	PHD finger domain protein, putative
Afu4g12550	-1.82	-2.42	-2.2	hypothetical protein
Afu4g12640	-2.42	-3.01	-3.05	RGS domain protein (Rax1), putative
Afu4g12650	-2.16	-2.52	-2.9	histone acetyltransferase (Gcn5), putative

Afu4g12720	-1.65	-2.12	-1.69	phosphoesterase, putative
Afu4g12760	-2.26	-2.94	-2.23	SAM binding motif containing protein
Afu4g13010	-1.76	-1.9	-2.53	conserved hypothetical protein
Afu4g13120	-2.55	-4.42	-3.91	glutamine synthetase
Afu4g13150	-2.4	-2.84	-2.5	DUF159 domain protein
Afu4g13210	-3.14	-4.08	-3.28	hypothetical protein
Afu4g13230	-2.62	-2.72	-2.21	regulatory protein weta
Afu4g13300	-2.99	-3.46	-3.71	hypothetical protein
Afu4g13340	-3.2	-3.35	-2.94	DUF907 domain protein
Afu4g13380	-2.08	-1.71	-1.66	conserved hypothetical protein
Afu4g13400	-2.39	-2.47	-2.94	glycosyltransferase family 28, putative
Afu4g13450	-1.52	-2.07	-2.02	RNA methyltransferase, TrmH family family
Afu4g13460	-1.85	-2.92	-2.44	SNF2 family helicase/ATPase, putative
Afu4g13510	-1.12	-2.21	-0.99	isocitrate lyase
Afu4g13530	-1.09	-1.87	-2.03	Trehalase
Afu4g13550	-1.87	-1.62	-2.53	short chain dehydrogenase/reductase family
Afu4g13610	-1.47	-2.43	-2.17	hypothetical protein
Afu4g13620	-1.53	-2.61	-1.11	hypothetical protein
Afu4g13660	-1.67	-3.16	-3.24	MFS multidrug resistance transporter, putative
Afu4g13820	-0.8	-2.1	-0.76	multidrug transporter, putative
Afu4g13860	-1.75	-2.58	-2.3	extracellular salicylate hydroxylase/monooxygenase, putative
Afu4g13910	-1.26	-1.71	-2.01	conserved hypothetical protein
Afu4g14370	-0.65	-2.93	-0.21	LINE-1 class reverse transcriptase, RNase H, putative
Afu4g14450	-1.28	-2.04	-1.41	D-mannonate oxidoreductase
Afu4g14630	-3.85	-5.52	-3.51	FAD binding domain protein
Afu4g14640	-3.02	-3.82	-3.42	low affinity iron transporter, putative
Afu4g14760	-3.18	-3.94	-2.88	ABC multidrug transporter, putative
Afu4g14770	-3.1	-4.59	-2.95	squalene-hopene-cyclase, putative
Afu4g14850	-0.62	-2.15	-1.28	extracellular 3-ketosteroid 1-dehydrogenase, putative
Afu4g14860	-2.29	-3.76	-1.83	NA
Afu4g14870	-1.72	-4.61	-2.68	LINE-1 class reverse transcriptase, RNaseH, putative
Afu5g00160	-2.07	-4.41	-1.54	MFS polyamine transporter, putative
Afu5g00240	-2.62	-3.87	-3.36	hypothetical protein
Afu5g00250	-2.95	-4.33	-3.54	hypothetical protein
Afu5g00290	-1.94	-1.51	-2.28	C6 transcription factor, putative
Afu5g00760	-3.09	-2.77	-3.13	chitin synthase C
Afu5g00770	-2.24	-0.6	-1.53	integral membrane protein, putative

Afu5g00790	-2.9	-2.17	-2.15	ABC multidrug transporter, putative
Afu5g00800	-3.89	-4.29	-3.98	conserved hypothetical protein
Afu5g00810	-3.23	-5.02	-4.03	hypothetical protein
Afu5g00880	-2.85	-3.45	-3.53	hypothetical protein
Afu5g00890	-2.04	-2.14	-2.22	hypothetical protein
Afu5g01020	-2.77	-2.92	-3.35	DUF858 domain protein
Afu5g01270	-2.84	-3.09	-2.75	C6 transcription factor, putative
Afu5g01290	-1.79	-2.36	-2.19	zinc-binding oxidoreductase, putative
Afu5g01340	-3.03	-4.43	-3.99	lysophospholipase, putative
Afu5g01430	-1.43	-2.03	-1.02	ThiJ/PfpI family protein
Afu5g01510	-1.41	-2.93	-1.43	amino acid transporter
Afu5g01640	-1.81	-3.37	-1.46	ankyrin repeat protein
Afu5g01650	-2.65	-2.55	-1.01	bZIP transcription factor JlbA/IDI-4, putative
Afu5g01740	-2.33	-3.42	-3.53	deoxyhypusine synthase, putative
Afu5g01800	-2.05	-2.28	-2.17	DNA repair protein rad14
Afu5g01930	-2.41	-3.48	-3.07	hypothetical protein
Afu5g01950	-2.1	-2.63	-2.92	histone H2A
Afu5g01980	-2.15	-2.47	-2.51	histone deacetylase hda1
Afu5g02070	-2.32	-3.32	-2.61	hypothetical protein
Afu5g02110	-2.09	-3.81	-3.15	hypothetical protein
Afu5g02150	-0.89	-1.21	-2.37	proteasome component Pre6, putative
Afu5g02200	-1.87	-2.14	-1.74	Mitochondrial import inner membrane translocase subunit (TIM22), putative
Afu5g02240	-2.21	-1.85	-3.02	NAD dependent epimerase/dehydratase family protein
Afu5g02300	-1.79	-2.03	-1.9	peroxidase, putative
Afu5g02390	-0.82	-2.43	-2.3	Auxin Efflux Carrier superfamily
Afu5g02400	-3.72	-4.71	-4.36	catabolite degradation protein, putative
Afu5g02410	-2.09	-3.14	-3.06	DEAD/DEAH box helicase, putative
Afu5g02480	-1.43	-1.94	-2.46	glycogen synthase
Afu5g02530	-0.9	-1.53	-2.63	ribokinase
Afu5g02560	-2.29	-3.36	-2.61	SCS1 product
Afu5g02680	-1.67	-1.53	-2.19	NA
Afu5g02800	-2	-2.64	-2.22	C6 transcription factor, putative
Afu5g02880	-4.49	-5.59	-4.51	C6 transcription factor, putative
Afu5g02890	-3.18	-4.02	-3.69	conserved hypothetical protein
Afu5g02910	-1.57	-2.23	-2.33	SET translocation
Afu5g02970	-2.65	-1.8	-2.04	LCCL domain protein
Afu5g03060	-1.86	-2.49	-2.32	hypothetical protein

Afu5g03140	-3	-3.61	-3.52	GTP cyclohydrolase I, putative
Afu5g03160	-1.06	-1.65	-2.1	protein kinase, putative
Afu5g03200	-2.03	-2.25	-2.26	Ulp1 protease family protein
Afu5g03250	-1.58	-2.16	-2.45	ubiquitin C-terminal hydrolase (HAUSP), putative
Afu5g03270	-2.25	-3.01	-2.75	hypothetical protein
Afu5g03330	-1.69	-2.13	-2.95	conserved hypothetical protein
Afu5g03340	-2.36	-3.11	-2.66	hypothetical protein
Afu5g03350	-1.44	-1.93	-2.38	glutamine dependent NAD+ synthetase, putative
Afu5g03390	-2.76	-3.39	-3.26	conserved hypothetical protein
Afu5g03430	-1.58	-2.37	-2.49	PHD transcription factor (Rum1), putative
Afu5g03570	-1.7	-1.67	-2.24	mitochondrial large ribosomal subunit protein L1, putative
Afu5g03840	-1	-1.86	-2.33	oxidoreductase, short chain dehydrogenase/reductase family
Afu5g03870	-2.28	-2.3	-2	conserved hypothetical protein
Afu5g03930	-2.28	-3.93	-3.02	alcohol dehydrogenase, putative
Afu5g04100	-1.71	-2.06	-1.74	PQ loop repeat protein
Afu5g04120	-1.81	-2.06	-2.01	SIR2 family histone deacetylase, putative
Afu5g04260	-3.6	-4.88	-3.9	arginine transporter, putative
Afu5g04380	-2.33	-2.85	-2.25	conserved hypothetical protein
Afu5g04410	-2.35	-2.11	-1.43	hypothetical protein
Afu5g04440	-1.55	-2.22	-2.28	nucleolar RNAse III, putative
Afu5g05480	-3.8	-4.37	-3.88	Rheb GTPase RhbA
Afu5g05540	-2.1	-2.12	-2.54	nucleosome assembly protein
Afu5g05590	-1.85	-2.41	-2.38	aspartokinase
Afu5g05600	-3.25	-3.44	-2.75	forkhead transcription factor (Sep1), putative
Afu5g05610	-3.85	-4.78	-3.74	cell cycle control protein Cwf14, putative
Afu5g05680	-2.25	-2.99	-2.72	peptide chain release factor eRF/aRF, subunit 1
Afu5g05710	-1.72	-2.14	-1.81	pseudouridylate synthase family protein
Afu5g05720	-2.01	-1.52	-1.92	conserved hypothetical protein
Afu5g05750	-2.18	-2.65	-2.61	protein kinase, putative
Afu5g05770	-1.16	-1.42	-2.23	1,3-beta-glucan biosynthesis protein, putative
Afu5g05780	-2.88	-3.53	-3.27	hypothetical protein
Afu5g05790	-2.61	-3	-2.92	ubiquitin ligase subunit HrtA, putative
Afu5g05900	-1.59	-2.45	-2.88	protein kinase (Chm1), putative
Afu5g06040	-0.97	-1.17	-2.4	UV excision repair protein (RadW), putative
Afu5g06060	-3.31	-3.35	-3.91	sulfur metabolism regulator SkpA, putative
Afu5g06070	-2.49	-2.81	-2.03	ABC multidrug transporter Mdr1

Afu5g06090	-0.88	-1.29	-2.2	type-III integral membrane protein (Ytp1), putative
Afu5g06140	-3.65	-4.41	-3.56	histone acetyltransferase, putative
Afu5g06170	-2.43	-2.97	-2.71	conserved hypothetical protein
Afu5g06190	-1.83	-2.77	-3.69	sexual development transcription factor SteA
Afu5g06240	-0.95	-2.03	-1.69	alcohol dehydrogenase, putative
Afu5g06260	-1.84	-2.62	-2.73	SNF2 family helicase/ATPase (Ino80), putative
Afu5g06330	-2.51	-2.94	-3.28	RSC complex subunit (Sth1), putative
Afu5g06340	-2.39	-2.77	-2.52	BAR domain protein
Afu5g06370	-2.72	-3.69	-3.26	hypothetical protein
Afu5g06400	-2	-2.79	-2.79	hypothetical protein
Afu5g06410	-1.38	-1.54	-2.32	C2H2 transcription factor (AmdA), putative
Afu5g06470	-2.16	-2.06	-1.87	serine/threonine protein kinase, putative
Afu5g06510	-2.11	-2		GTP binding protein, putative
Afu5g06700	-1.66	-2.47	-3.03	serine/threonine protein phosphatase PPT1
Afu5g06980	-1.43	-1.64	-2.3	hypothetical protein
Afu5g07020	-2.28	-3.47	-3.26	ABC transporter, putative
Afu5g07050	-1.46	-1.45	-2.29	proteasome regulatory particle subunit Rpt2, putative
Afu5g07060	-2.8	-3.82	-3.61	WD repeat protein
Afu5g07110	-1.68	-2.49	-0.98	integral membrane protein
Afu5g07210	-2.92	-4.45	-4.3	homoserine O-acetyltransferase, putative
Afu5g07250	-2.93	-3.78	-2.72	DUF300 domain protein, putative
Afu5g07450	-2.65	-2.65	-3.26	hypothetical protein
Afu5g07590	-2.24	-1.62	-1.01	hypothetical protein
Afu5g07720	-3.06	-3.67	-3.4	CCCH and RING finger protein
Afu5g07760	-1.95	-2.08	-1.98	tetracycline-efflux transporter, putative
Afu5g07800	-1.85	-2.35	-2.26	hypothetical protein
Afu5g07860	-2.6	-2.81	-2.09	phosphatase family protein
Afu5g07880	-2.34	-3.69	-3.69	a-pheromone receptor PreA
Afu5g07940	-3.09	-3.75	-3.21	hypothetical protein
Afu5g08020	-2.92	-4.08	-4	HLH DNA binding protein (Penr2), putative
Afu5g08060	-1.74	-2.02	-2.51	importin 13, putative
Afu5g08200	-2.06	-3.11	-1.48	hypothetical protein
Afu5g08300	-1.52	-1.38	-2.39	alpha-actinin, sarcomeric (f-actin cross linking protein)
Afu5g08330	-3.17	-3.64	-3.11	RNA binding protein
Afu5g08400	-1.75	-1.52	-2.51	NA
Afu5g08410	-2.55	-2.99		PQ loop repeat protein
Afu5g08550	-2.08	-2.48	-2.69	Rho guanyl nucleotide exchange factor (Rom2), putative

Afu5g08570	-2.35	-3.77	-3.08	cAMP-dependent protein kinase catalytic subunit, putative
Afu5g08580	-1.53	-2.37	-2.11	alpha-1,6-mannosyltransferase subunit (Och1), putative
Afu5g08680	-1.06	-1.63	-2.14	mitochondrial GTPase (YlqF), putative
Afu5g08710	-2.12	-2.57	-1.88	hypothetical protein
Afu5g08740	-2.2	-2.8	-3.48	DHHC zinc finger membrane protein
Afu5g08910	-1.2	-0.92	-2.21	3-methylcrotonyl-CoA carboxylase subunit alpha (MccA), putative
Afu5g08930	-1.11	-0.83	-2.07	isovaleryl-CoA dehydrogenase IvdA, putative
Afu5g09000	-1.91	-2.47	-1.99	sister chromatid cohesion protein (Eso1), putative
Afu5g09060	-1.82	-2.47	-2.18	RNA binding protein, putative
Afu5g09090	-1.03	-2.05		ATP binding protein, putative
Afu5g09100	-2.27	-3.04	-1.84	MAP kinase, putative
Afu5g09110	-2.75	-3.74	-2.84	NA
Afu5g09370	-2.25	-2.61	-2.56	hypothetical protein
Afu5g09440	-2.74	-2.76	-1.58	amino acid permease, putative
Afu5g09580	-1.03	-2.24	-1.52	conidial hydrophobin Hyp1/RodA
Afu5g09640	-1.98	-2.58	-2.62	conserved fungal protein
Afu5g09650	-2.16	-2.22	-2.33	small monomeric GTPase (Gtr1), putative
Afu5g09770	-3	-4.28	-3.58	hypothetical protein
Afu5g09850	-0.92	-2.4	-2.16	tRNA exportin, putative
Afu5g09920	-2.08	-2.83	-2.79	peptidase, putative
Afu5g10160	-1.4	-2.22	-1.81	actVA 4 protein
Afu5g10190	-1.49	-1.72	-2.28	hypothetical protein
Afu5g10200	-2.46	-3.4	-3.26	hypothetical protein
Afu5g10210	-1.95	-2.79	-1.83	hypothetical protein
Afu5g10260	-0.7	-1.97	-2.06	NA
Afu5g10590	-3.42	-3.21	-2.13	stress response RCI peptide, putative
Afu5g10620	-1.99	-2.42	-2.34	CBF/NF-Y family transcription factor, putative
Afu5g10690	-2.63	-4.78	-4.05	monosaccharide transporter
Afu5g10770	-2.23	-2.65	-2.56	topisomerase II associated protein pat1 homolog
Afu5g10910	-3.3	-3.22	-4.02	hypothetical protein
Afu5g10920	-2.12	-2.98	-3.55	DUF221 domain protein, putative
Afu5g10950	-2.47	-2.68	-2.4	hypothetical protein
Afu5g11010	-2.14	-2.25	-1.78	nucleoside diphosphatase (Ynd1), putative
Afu5g11020	-1.77	-2.57	-1.91	ammonium transporter
Afu5g11080	-2.52	-2.85	-2.62	MSF multidrug transporter, putative
Afu5g11090	-2.96	-3.33	-3.01	conserved hypothetical protein

Afu5g11130	-2.01	-1.19		PAXNEB protein superfamily
Afu5g11150	-0.4	-2.18	-2.2	ribonuclease P protein subunit p29
Afu5g11260	-1.93	-2.29	-2.05	siderophore transcription factor SreA
Afu5g11350	-2.83	-2.68	-2.45	conserved hypothetical protein
Afu5g11500	-0.96	-1.4	-3.13	conserved hypothetical protein
Afu5g11510	-1.47	-2.6	-2.54	hypothetical protein
Afu5g11520	-3.66	-4.49	-3.91	serine/threonine protein kinase (Nrc-2), putative
Afu5g11580	-1.53	-2.36	-1.84	transcription factor TFIIH subunit Tfb4, putative
Afu5g11650	-1.44	-2.51	-1.09	conserved hypothetical protein
Afu5g11680	-2.62	-2.98	-1.5	hypothetical protein
Afu5g11690	-3.45	-4.44	-3.89	related to protein tyrosine phosphatase PPS1
Afu5g11770	-1.91	-2.66	-2.14	hypothetical protein
Afu5g11800	-1.3	-2.05		NA
Afu5g11840	-2.15	-3.28	-2.97	protein kinase, putative
Afu5g11920	-1.55	-1.47	-2.26	Vacuolar ATP synthase subunit D, putative
Afu5g11970	-1.85	-1.81	-2.51	protein kinase c, putative
Afu5g12050	-2.57	-3.26	-3.38	DNA ligase, putative
Afu5g12070	-1.14	-2	-1.71	conserved hypothetical protein
Afu5g12090	-1.89	-3.11	-1.86	conserved hypothetical protein
Afu5g12100	-3.57	-4.04	-3.16	pmt2 methyltransferase
Afu5g12110	-3.03	-3.34	-3.5	conserved hypothetical protein
Afu5g12150	-3.72	-4.16	-3.87	PH domain protein
Afu5g12160	-1.94	-1.81	-2.15	alpha-1,2-mannosyltransferase (Kre5), putative
Afu5g12180	-1.79	-1.89	-2.11	Ran/spi1 binding protein
Afu5g12230	-2.3	-3.23	-2.88	MYND domain protein (SamB), putative
Afu5g12280	-1.76	-2.69		hypothetical protein
Afu5g12440	-2.41	-2.83	-3.16	cell cycle control protein (Cwf23), putative
Afu5g12580	-2.78	-3.55	-3.38	GTP binding protein (GTPBP1), putative
Afu5g12590	-1.23	-2.19	-1.41	solid-state culture expressed protein (Aos23), putative
Afu5g12630	-3.86	-3.95	-3.71	hypothetical protein
Afu5g12640	-2.78	-4.02	-3.4	DNA polymerase gamma
Afu5g12830	-2.11	-1.72	-1.58	lipoprotein, putative
Afu5g12910	-1.56	-2.02	-1.7	small nuclear ribonucleoprotein SmD2, putative
Afu5g13240	-1.58	-1.92	-2.03	related to transcription factor KCS1
Afu5g13270	-2.19	-2.38	-2.21	PalH
Afu5g13310	-1.97	-2.01	-2.54	C6 transcription factor, putative
Afu5g13480	-1.39	-2.3	-2.17	U1 small nuclear ribonucleoprotein 70 kDa
Afu5g13560	-2.09	-3.14	-2.68	FHA domain protein

Afu5g13590	-1.69	-2.16		conserved hypothetical protein
Afu5g13600	-1.92	-2.09	-2.06	vacuolar protein sorting vps16, putative
Afu5g13610	-2.16	-2.04	-2.59	conserved hypothetical protein
Afu5g13620	-2.29	-1.39	-1.17	ubiquitin C-terminal hydrolase, putative
Afu5g13760	-1.52	-2.36	-2.64	hypothetical protein
Afu5g13860	-1.16	-2	-2.14	mlo3 protein
Afu5g13870	-3.3	-4.34	-4.05	mlo3 protein
Afu5g13900	-1.81	-1.74	-2.36	transposase
Afu5g13930	-2.58	-3.48	-3.47	CCCH finger DNA binding protein, putative
Afu5g14020	-2.69	-3.92	-3.17	hypothetical protein
Afu5g14080	-2.72	-3.26	-3.05	hypothetical protein
Afu5g14320	-1.34	-2.09	-1.71	hypothetical protein
Afu5g14350	-3.57	-3.87	-4.04	c-24(28) sterol reductase
Afu5g14860	-1.48	-2.28	-2.37	cytochrome P450
Afu5g14900	-1.93	-1.91	-2.1	hypothetical protein
Afu5g15010	-1.9	-1.67	-2.13	arsenite permease (ArsB), putative
Afu5g15040	-1.32	-1.68	-2.31	hypothetical protein
Afu6g00120	-2.19	-2.78	-2.58	C6 transcription factor, putative
Afu6g00460	-1.61	-2.86	-2.4	hypothetical protein
Afu6g00520	-1.83	-2.12	-1.65	conserved hypothetical protein
Afu6g00680	-2.15	-0.04	-1.36	hypothetical protein
Afu6g00770	-4.65	-6.66	-4.74	extracellular arabinanase, putative
Afu6g00780	-1.71	-4.46	-2.21	LINE-1 class reverse transcriptase, RNaseH, putative
Afu6g02020	-3.63	-4.7	-4.27	hypothetical protein
Afu6g02070	-3.15	-3.87	-2.78	phospholipid-translocating P-type ATPase domain-containing protein
Afu6g02110	-3.21	-4.05	-3.91	SRF-type transcription factor (Umc1), putative
Afu6g02190	-1.47	-2.34	-2.51	transcriptional activator (PtaC), putative
Afu6g02330	-0.75	-2.05	-1.37	hypothetical protein
Afu6g02420	-2.8	-2.66	-3.33	ubiquitin conjugating enzyme (UbcM), putative
Afu6g02430	-1.11	-2.83	-1.83	hypothetical protein
Afu6g02520	-1.97	-2.79	-3.22	Eukaryotic initiation factor 1A, putative
Afu6g02550	-1.66	-2.08	-1.3	magnesium ion transporter (Mrs2), putative
Afu6g02640	-3.59	-3.86	-3.96	hypothetical protein
Afu6g02650	-1.48	-2.19	-2.1	hypothetical protein
Afu6g02660	-1.51	-1.68	-2.04	conserved hypothetical protein
Afu6g02680	-3.49	-4.81	-3.84	ankyrin repeat and BTB/POZ domain protein
Afu6g02740	-2.1	-2.84	-2.5	hypothetical protein

Afu6g02810	-3.24	-2.61	-3.01	Ctr copper transporter family family
Afu6g02820	-2.13	-2.18	-2.66	metalloreductase, putative
Afu6g02840	-2.32	-1.6	-1.7	serine/threonine protein kinase, putative
Afu6g02990	-0.87	-2.09	-1.46	short chain dehydrogenase/reductase, putative
Afu6g03010	-1.74	-2.29		C2H2 finger domain protein (Zms1), putative
Afu6g03080	-1.63	-1.47	-2.03	ABC multidrug transporter, putative
Afu6g03120	-1.16	-3.06	-2.1	hypothetical protein
Afu6g03130	-2.58	-2.7	-2.49	hypothetical protein
Afu6g03210	-2.14	-2.91	-3.88	conidiation-specific protein 10
Afu6g03360	-2.04	-2.09	-1.44	oxidoreductase, zinc-binding
Afu6g03370	-3.7	-5.45	-4.29	oxidoreductase, short-chain dehydrogenase/reductase family
Afu6g03740	-1.58	-1.86	-2.29	c5 cytosine methyltransferase DmtA
Afu6g03750	-1.95	-2.45	-2.26	amidophosphoribosyltransferase
Afu6g03760	-2.07	-1.79	-2.39	conserved hypothetical protein
Afu6g04000	-2.01	-2	-2.4	GTPase activating protein (Tsc2), putative
Afu6g04050	-2.49	-2.01	-2.06	D123 proteins, putative
Afu6g04260	-1.68	-2.38	-2.21	mak16 protein
Afu6g04270	0.1	-2.04	-3.36	fructose symporter
Afu6g04310	-3.17	-4.11	-3.42	Pumilio 2
Afu6g04340	-1.3	-2.48	-1.92	hypothetical protein
Afu6g04350	-1.32	-2.08	-1.4	hypothetical protein
Afu6g04360	-2.12	-2.64	-2.07	ABC drug exporter AtrF
Afu6g04390	-4.09	-5.44	-4.66	conserved hypothetical protein
Afu6g04400	-2.36	-2.7	-3.21	transcription factor TFIIIB component, putative
Afu6g04470	-1.57	-2.78	-2.59	hypothetical protein
Afu6g04490	-1.18	-2.16	-2.01	camp independent regulatory protein
Afu6g04500	-1.1	-2.4	-2.25	FOG1 protein
Afu6g04520	-1.37	-2.06	-2.43	SET domain protein
Afu6g04580	-1.83	-2.07	-1.65	NIF domain protein
Afu6g04630	-2.07	-2.38	-1.64	conserved hypothetical protein
Afu6g04680	-1.72	-2.25	-2.63	MIPC synthase subunit (SurA), putative
Afu6g04820	-2.09	-2.47	-1.59	para-aminobenzoate synthase PabaA
Afu6g04940	-1.4	-2.14	-1.89	proline-rich cytokinesis protein SepA, putative
Afu6g04950	-2.25	-2.82	-1.72	mitochondrial GTPase (Mss1), putative
Afu6g05100	-1.93	-2.22	-2.84	6-phosphofructo-2-kinase, putative
Afu6g05110	-0.72	-1.55	-2.2	mitochondrial import receptor subunit (tom40), putative

Afu6g05120	-2.78	-3.09	-3.52	glycogen synthase kinase-3, putative
Afu6g05140	-3.1	-3.7	-3.15	sterol delta 5,6-desaturase ERG3
Afu6g05180	-2.71	-3.3	-2.43	splicing factor 3b subunit 4
Afu6g05240	-1.98	-2.71	-2.56	SUMO ligase SizA, putative
Afu6g05280	-1.25	-2.33	-2.87	mei2 protein
Afu6g05320	-1.45	-1.62	-2.34	purine nucleoside phosphorylase I, inosine and guanosine-specific
Afu6g05330	-2.46	-2.72	-2.01	hypothetical protein
Afu6g05350	-1.66	-2.57	-2.42	aspartic-type endopeptidase (OpsB), putative
Afu6g06380	-1.97	-2.56	-2.43	methyltransferase, putative
Afu6g06390	-3.26	-2.45	-3.14	hypothetical protein
Afu6g06400	-2.18	-2.76	-2.45	Rho GTPase activator (Bem3), putative
Afu6g06420	-2.86	-3.79	-3.54	mitochondrion biogenesis protein (Mdm31), putative
Afu6g06490	-1.64	-1.87	-2.35	U1 small nuclear ribonucleoprotein A, putative
Afu6g06540	-1.88	-2.05	-1.83	proteasome component (Ecm29), putative
Afu6g06550	-1.49	-2.2	-2.16	SNF2 family helicase/ATPase, putative
Afu6g07150	-2.39	-3.08	-2.14	actin binding protein, putative
Afu6g07160	-2.27	-2.48	-2.71	IZH family channel protein (Izh3), putative
Afu6g07290	-1.43	-2.15	-2.86	endosomal cargo receptor (Erv14), putative
Afu6g07330	-2.91	-3.27	-2.51	methionine aminopeptidase, type I, putative
Afu6g07420	-2.09	-2.84	-2.35	F-box domain protein
Afu6g07440	-3.01	-3.87	-2.65	1-phosphatidylinositol-3-phosphate 5-kinase (Fab1), putative
Afu6g07530	-1.35	-2.11	-2.07	bZIP transcription factor, putative
Afu6g07660	-1.36	-2.42	-1.14	hypothetical protein
Afu6g07800	-1.13	-1.88	-2.09	C6 finger domain protein, putative
Afu6g08030	-2.88	-2.99	-2.91	hypothetical protein
Afu6g08130	-0.65	-1.39	-2.22	hypothetical protein
Afu6g08260	-1.83	-2.5	-1.91	conserved hypothetical protein
Afu6g08270	-2.27	-1.83	-1.82	hypothetical protein
Afu6g08290	-2.18	-2.06	-3.16	ADP-ribosylation factor family protein
Afu6g08320	-1.61	-2.5	-2.4	conserved hypothetical protein
Afu6g08450	-1.78	-2.22	-2.67	conserved hypothetical protein
Afu6g08540	-1.93	-2.21	-1.64	C6 finger domain protein, putative
Afu6g08600	-1.31	-2.41	-2.31	transcription factor TFIID complex 145 kDa subunit, putative
Afu6g08920	-1.04	-1.52	-2.32	assimilatory sulfite reductase
Afu6g08980	-0.85	-2.01	-1.81	FF domain protein

Afu6g09000	-1.91	-2.87	-2.99	PHD finger domain protein, putative
Afu6g09160	-1.28	-1.7	-2.26	ubiquitin conjugating enzyme, putative
Afu6g09200	-2.88	-2.01	-2.25	conserved hypothetical protein
Afu6g09310	-1.98	-1.26	-2.3	class V chitinase, putative
Afu6g09340	-1.58		-2.21	hypothetical protein
Afu6g09460	-1.89	-3.01	-2.18	NA
Afu6g09470	-1.55	-4.43	-2.21	reverse transcriptase, RNaseH, putative
Afu6g09570	-1.6	-3.45	-1.07	conserved hypothetical protein
Afu6g09930	-2.87	-3.11	-3.45	bZIP transcription factor (AP-1), putative
Afu6g09940	-2.13	-1.84	-2.14	transposase
Afu6g10020	-1.86	-2.24	-2.42	Hypothetical nuclear protein
Afu6g10050	-1.79	-1.42	-2.95	small oligopeptide transporter, OPT family
Afu6g10150	-3.76	-4.03	-3.35	hypothetical protein
Afu6g10180	-1.15	-2.29		hypothetical protein
Afu6g10190	-2.28	-3.64		hypothetical protein
Afu6g10240	-1.67	-3.13	-2.39	sensor histidine kinase/response regulator Fos-1
Afu6g10270	-1.41	-2.6		NA
Afu6g10460	-2.37	-2.85	-2.23	ceramide synthase membrane component (Lag1), putative
Afu6g10470	-2.11	-2.48	-2.66	zinc finger protein ZPR1
Afu6g10500	-3.44	-4.36	-2.72	conserved hypothetical protein
Afu6g10720	-2.27	-3.14		alpha-ketoglutarate-dependent taurine dioxygenase
Afu6g10780	-2.66	-3.32	-3.17	carboxylesterase, putative
Afu6g10790	-3.73	-4.55	-4.06	MFS amine transporter, putative
Afu6g10800	-2.67	-2.59	-2.39	carboxylesterase, putative
Afu6g10840	-2.35	-2.72	-2.71	hypothetical protein
Afu6g10860	-2.7	-2.88	-3.1	hypothetical protein
Afu6g10900	-2.57	-3.77	-3.42	UV-endonuclease UVE-1
Afu6g10940	-1.65	-1.94	-2.56	conserved hypothetical protein
Afu6g10950	-2.12	-4.11	-3.29	NA
Afu6g11060	-2.04	-2.1	-1.66	DnaJ domain protein
Afu6g11070	-2.5	-3.05	-2.75	DEAD box RNA helicase (Hca4), putative
Afu6g11180	-1.02	-2.16	-1.28	conserved hypothetical protein
Afu6g11220	-1.56	-2.03	-0.72	TBC domain protein, putative
Afu6g11250	-1.77	-2.75	-1.77	C2H2 finger domain protein, putative
Afu6g11430	-0.92	-1.25	-2.06	aldehyde dehydrogenase, putative
Afu6g11450	-1.9	-2.1	-2.14	C6 transcription factor, putative
Afu6g11670	-2.4	-3.86	-4.45	conserved hypothetical protein

Afu6g11690	-0.74	-3.08	-3.02	NA
Afu6g12020	-0.64	-2.15	-1.46	C2H2 finger domain protein, putative
Afu6g12260	-1.5	-1.97	-2	NA
Afu6g12270	-1.38	-2.43		ubiquitin C-terminal hydrolase, putative
Afu6g12290	-1.42	-2.4	-2.5	PH domain protein
Afu6g12340	-1.52	-2.09	-1.49	GTPase activating protein (BUD2/CLA2), putative
Afu6g12430	-1.77	-1.88	-2.08	Ran-interacting protein MOG1, putative
Afu6g12440	-2.23	-2.28	-2.3	conserved hypothetical protein
Afu6g12540	-2.33	-2.32	-2.75	RING finger protein
Afu6g12600	-2.16	-2.98	-2.93	WD repeat protein
Afu6g12610	-1.31	-1.27	-2	rhomboid family protein, putative
Afu6g12640	-3.17	-4.07	-3.14	conserved hypothetical protein
Afu6g12650	-2.33	-2.78	-1.82	conserved hypothetical protein
Afu6g12840	-1	-2.04	-1.1	kinesin family protein
Afu6g12950	-2.17	-2.8	-2.3	alpha,alpha-trehalose-phosphate synthase subunit TPS1, putative
Afu6g12970	-1.88	-2.25	-2.14	nuclear migration protein NudF
Afu6g13010	-1.73	-2.62	-2.81	GTP binding protein (EngB), putative
Afu6g13020	-2.68	-2.87	-2.64	AP-3 adaptor complex subunit sigma, putative
Afu6g13030	-2.09	-1.95	-2.69	cell division control protein Cdc4, putative
Afu6g13130	-2.48	-2.77	-2.88	transcription initiation factor TFIIE, beta subunit, putative
Afu6g13200	-2.5	-2.04	-2.48	autophagy regulatory protein (Gsa11/Atg2), putative
Afu6g13440	-2.26	-2.41		choline sulfatase, putative
Afu6g13470	-1.26	-2.1	-1.82	conserved hypothetical protein
Afu6g13670	-2.68	-3.78	-3.62	conserved hypothetical protein
Afu6g14130	-1.66	-1.33	-2.37	ubiquitin conjugating enzyme, putative
Afu6g14250	-2.79	-3.42	-3.76	endosomal integral membrane protein (P24a), putative
Afu6g14260	-1.74	-2.03	-1.55	conserved hypothetical protein
Afu6g14270	-2.08	-1.5	-1.12	hypothetical protein
Afu6g14290	-1.48	-2.29		conserved hypothetical protein
Afu6g14660	-1.63	-4.4	-2.14	reverse transcriptase, RNaseH
Afu7g00270	-3.75	-4.64	-3.95	FAD binding monooxygenase, putative
Afu7g00290	-0.68	-2.48	-1.44	cytochrome P450 monooxygenase, putative
Afu7g00300	-2.3	-2.58	-1.53	squalene-hopene-cyclase, putative
Afu7g00390	-1.66	-2.03	-1.52	MFS multidrug transporter, putative
Afu7g00400	-2.62	-3.18	-3.19	hypothetical protein
Afu7g00410	-2.16	-2.54	-2.41	C6 transcription factor, putative

Afu7g00470	-2.25	-3.01	-2.4	hypothetical protein
Afu7g00960	-0.65	-2.08	-1.25	extracellular cysteine-rich protein, putative
Afu7g00990	-2.46	-3.78	-2.75	integral membrane protein
Afu7g01250	-1.16	-2.19		hypothetical protein
Afu7g01350	-2.33	-3.28	-2.1	hypothetical protein
Afu7g01380	-2.47	-2.92	-2.43	anaphase promoting complex subunit Apc11, putative
Afu7g01430	-2.77	-4.44	-3.58	opsin 1
Afu7g01470	-2.03	-3.35	-2.79	integral membrane protein, Mpv17/PMP22 family, putative
Afu7g01560	-1.58	-2.45	-1.77	FAD dependent oxidoreductase, putative
Afu7g01620	-1.46	-2.38	-2.67	hypothetical protein
Afu7g01630	-1.48	-1.82	-2.13	hypothetical protein
Afu7g01650	-0.93	-2.24	-1.19	related to ARCA protein, putative
Afu7g01720	-0.05	-1.44	-2	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase
Afu7g01850	-3.41	-3.56	-3.66	RNA polymerase Rpc34 subunit superfamily
Afu7g01920	-2.74	-3.65	-3.15	DNA-dependent RNA polymerase II RPB140
Afu7g02090	-2.18	-2.07	-2.99	membrane associated DnaJ chaperone, putative
Afu7g02170	-2.35	-3.07	-3.51	RNA binding protein, putative
Afu7g02210	-2.63	-3.03	-2.19	conserved hypothetical protein
Afu7g02280	-2.19	-2.47		small nucleolar ribonucleoprotein complex subunit, putative
Afu7g02320	-1.48	-1.86	-2.83	hypothetical protein
Afu7g02370	-1.78	-2.67	-1.88	SNF2 family helicase/ATPase (Swr1), putative
Afu7g02390	-1.63	-2.47	-2.08	hypothetical protein
Afu7g02420	-1.3	-2.12	-2.25	malate dehydrogenase, putative
Afu7g02440	-2.15	-3.62	-3.38	extracellular conserved glycine-rich protein
Afu7g02600	-2.62	-3.08	-3.19	hypothetical protein
Afu7g02610	-1.81	-3.7	-1.89	WD repeat protein
Afu7g02620	-3.7	-4.17	-4.24	DNA-directed RNA polymerases N/8 kDa subunit superfamily
Afu7g03650	-1.94	-2.14	-2.19	conserved hypothetical protein
Afu7g03700	-1.89	-1.45	-2.44	diacylglycerol acyltransferase type 2A
Afu7g03770	-3.65	-5.22	-3.43	hypothetical protein
Afu7g03780	-2.27	-3.07	-3.03	YT521-B-like splicing factor, putative
Afu7g03820	-1.9	-2.2	-1.72	DNA excision repair protein (Rad16), putative
Afu7g03830	-2.2	-2.7	-2.22	related to nucleotide exsicion repair protein RAD7
Afu7g03860	-1.8	-2.21	-2.6	RPB11a protein
Afu7g03910	-1.73	-2.4	-1.71	C2H2 zinc finger protein

Afu7g03930	-1.77	-2.34	-2.31	hypothetical protein
Afu7g03940	-1.13	-2.26	-1.41	alpha,alpha-trehalose phosphate synthase subunit TPS3, putative
Afu7g04000	-1.19	-2.03	-1.43	hypothetical protein
Afu7g04010	-1.37	-2.3	-1.88	conserved hypothetical protein
Afu7g04030	-1.8	-2.7	-3.11	hypothetical protein
Afu7g04100	-1.77	-2.33	-2.34	conserved hypothetical protein
Afu7g04130	-1.47	-2.86	-1.62	Trf5
Afu7g04140	-2.45	-2.79	-2.54	L-galactose dehydrogenase (L-GalDH), putative
Afu7g04150	-2.44	-2.77	-2.17	CGI-136 protein
Afu7g04300	-1.85	-2.56	-3.14	RhoGAP and Fes/CIP4 domain protein
Afu7g04320	-1.9	-2.13	-2.35	UBX domain protein (Ubx5), putative
Afu7g04340	-0.5	-1.12	-2.05	C6 transcription factor, putative
Afu7g04490	-2.06	-2.29	-2.19	Ribosomal protein S28e
Afu7g04640	-2.43	-2.88	-3.18	conserved hypothetical protein
Afu7g04660	-1.92	-2.78	-2.68	BEM46 protein
Afu7g04810	-0.62	-2.06		hypothetical protein
Afu7g04860	-1.95	-2.61	-2.71	dimethyladenosine transferase
Afu7g04930	-4.4	-5.37	-4.34	alkaline serine protease (PR1), putative
Afu7g04950	-2.02	-2.81	-2.63	lipase, putative
Afu7g05020	-1.94	-2.89	-2.46	polysaccharide export protein (CAP59), putative
Afu7g05050	-2.14	-3.27	-3.01	hypothetical protein
Afu7g05180	-2.4	-4.44	-2.07	defensin domain protein, putative
Afu7g05210	-1.42	-2.32	-2.58	CTP synthase
Afu7g05330	-1.61	-1.86	-2.15	hypothetical protein
Afu7g05380	-0.86	-1.5	-2.27	conserved hypothetical protein
Afu7g05430	-2.73	-3.94	-4.24	nonsense-mediated mRNA decay factor (Upf2), putative
Afu7g05460	-1.66	-2.07	-1.51	conserved hypothetical protein
Afu7g05490	-3.95	-5.16	-2.76	hypothetical protein
Afu7g05500	-4.01	-4.8	-3.78	theta class glutathione S-transferase
Afu7g05520	-2.15	-2.42	-1.18	hypothetical protein
Afu7g05760	-0.59	-2.28	-0.74	hypothetical protein
Afu7g05810	-0.55	-1.49	-2.04	29kD B ribonucleoprotein, putative
Afu7g05860	-2.16	-2.54	-3.2	Zinc finger, C3HC4 type (RING finger) domain protein
Afu7g05920	-1.24	-2.3	-1.05	stearic acid desaturase (SdeA), putative
Afu7g05980	-2.67	-2.55	-2.83	small nuclear ribonucleoprotein SmE, putative

Afu7g06240	-2.34	-2.78	-1.59	hypothetical protein
Afu7g06260	-3.81	-3.22	-3.02	alcohol dehydrogenase, zinc-containing
Afu7g06270	-2.36	-1.64	-1.74	cyanamide hydratase
Afu7g06300	-0.49	-1.55	-2.07	hypothetical protein
Afu7g06310	-0.37	-2.23	-1	hypothetical protein
Afu7g06440	-0.7	-2.06	-1.15	F-box domain protein
Afu7g06840	-4.43	-5.85	-4.75	class III aminotransferase
Afu7g06870	-2.58	-4.25	-4.26	Tf1-like reverse transcriptase, integrase, putative
Afu7g06880	-0.94	-2.23	-1.28	hypothetical protein
Afu7g06890	-3.88	-4.72	-3.51	Dyp-type peroxidase family protein
Afu7g06900	-2.15	-3.06	-3.33	branched-chain amino acid aminotransferase, putative
Afu7g07010	-2.36	-1.28	-0.84	hypothetical protein
Afu7g07150	-1.38	-3.48	-2.67	NA
Afu7g07160	-1.01	-2.21	-1.24	NA
Afu7g08220	-2.2	-2.98	-2.53	hypothetical protein
Afu7g08260	-1.83	-3.27	-1.4	hypothetical protein
Afu7g08280	-3.09	-1.68	-1.4	hypothetical protein
Afu7g08390	-0.81	-2.19	-1.3	hypothetical protein
Afu7g08410	-2.55	-2.93	-2.34	Tc1-mariner transposase, putative
Afu7g08470	-1.15	-1.53	-2.26	peroxisomal copper amine oxidase, putative
Afu7g08500	-0.52	-2.93	-1.04	NACHT and WD40 domain protein
Afu7g08540	-1.34	-2.48	-2.25	ankyrin repeat protein
Afu8g00310	-1.48	-4.15	-2.58	LINE-1 class reverse transcriptase, RNaseH, putative
Afu8g00330	-1.59	-3.69	-2.17	endonuclease/reverse transcriptase/RNaseH, putative
Afu8g00460	-1.87	-2.35	-2.3	methionine aminopeptidase, type I, putative
Afu8g00520	-1.12	-2.18		integral membrane protein
Afu8g00620	-0.63	-2.17		dimethylallyl tryptophan synthase, putative
Afu8g00970	-1.79	-2.53	-2.69	hypothetical protein
Afu8g01040	-2.05	-4.85	-2.7	reverse transcriptase, RNaseH
Afu8g01260	-2.51	-2.58	-2.84	hypothetical protein
Afu8g01330	-2.89	-5.1	-3.44	hypothetical protein
Afu8g01340	-3.43	-3.9	-4.13	MFS sugar transporter, putative
Afu8g01480	-2.62	-2.76	-2.41	potassium channel, putative
Afu8g01520	-1.02	-2.75	-2.23	Pectinesterase family
Afu8g01530	-1.88	-3.81	-3.19	HHE domain protein
Afu8g01570	-2.22	-2.43	-2.17	ADP-ribosylglycohydrolase family protein
Afu8g01610	-1.17	-2.03	-1.78	hypothetical protein
Afu8g01820	-1.42	-2.24	-1.53	hypothetical protein

Afu8g01890	-1.35	-2.49	-1.86	Na+/H+ exchanger family protein, putative
Afu8g02170	-1.83	-2.81	-2.29	C6 finger domain protein, putative
Afu8g02190	-1.45	-2.79	-2.35	hypothetical protein
Afu8g02260	-3.39	-4.4	-3	neutral amino acid permease
Afu8g02270	-3.94	-4.84	-4.01	dihydrodipicolinate synthetase family protein
Afu8g02280	-3.13	-3.05	-2.12	C6 transcription factor, putative
Afu8g02290	-4.13	-5.48	-4.08	conserved hypothetical protein
Afu8g02310	-2.51	-2.41	-2.37	aldehyde dehydrogenase ALDH
Afu8g02650	-1.88	-2.99	-2.99	ABC multidrug transporter, putative
Afu8g02690	-2.62	-3.1	-3.52	alphaN-acetylglucosamine transferase
Afu8g02720	-2.87	-3.27	-2.17	Hex2 protein
Afu8g02740	-2.13	-1.6	-2.25	hypothetical protein
Afu8g02750	-2.24	-1.63	-0.95	nucleolar protein CgrA
Afu8g02810	-3	-3.75	-3.73	conserved hypothetical protein
Afu8g02830	-2.28	-2.13	-2.21	UPD-GlcNAc transporter (Mnn2-2), putative
Afu8g02860	-1.59	-2	-1.94	amp deaminase
Afu8g03930	-1.77	-3.5	-2.82	Hsp70 chaperone (HscA), putative
Afu8g03950	-1.91	-2.34	-2.55	hypothetical protein
Afu8g03980	-1.51	-1.61	-2.63	DUF59 domain protein
Afu8g04040	-0.63	-1.27	-2.07	CPSF A subunit, putative
Afu8g04060	-0.85	-1.18	-2.05	NA
Afu8g04070	-2.01	-2.54	-3.09	glucosamine-6-phosphate deaminase, putative
Afu8g04130	-1.7	-4.54	-2.31	C6 transcription factor (Ctf1B), putative
Afu8g04150	-2.44	-3.72	-3.21	MFS transporter, putative
Afu8g04160	-2.18	-2.63	-2.73	folylpolyglutamate synthetase; FPGS
Afu8g04180	-1.49	-2.2	-2.82	C2H2 zinc finger protein
Afu8g04290	-1.82	-3.68	-2.13	C2H2 finger domain protein, putative
Afu8g04470	-2.06	-2.36	-1	MFS transporter, putative
Afu8g04490	-2.29	-3.38	-3.14	hypothetical protein
Afu8g04550	-3.07	-4.29	-4	sulfonate biosynthesis enzyme, putative
Afu8g04560	-2.24	-1.75	-2.63	integral membrane protein
Afu8g04570	-1.72	-2.62	-3.13	PWWP domain protein
Afu8g04690	-1.63	-2.45	-2.02	hol1 protein
Afu8g04780	-2.94	-3.83	-3.97	24 kDa intrinsic membrane protein
Afu8g04810	-1.36	-2.36	-3.09	casein kinase, putative
Afu8g04820	-1.84	-2.83	-3.48	ribonuclease P complex subunit p30, putative
Afu8g04920	-0.66	-2.19	-2.14	LEA domain protein
Afu8g04980	-1.86	-2.9	-3	hypothetical protein

Afu8g05050	-1.25	-2.47	-1.18	hypothetical protein
Afu8g05100	-1.8	-2.37	-2.64	hypothetical protein
Afu8g05120	-4.41	-5.51	-4.77	hypothetical protein
Afu8g05130	-2.59	-3.16	-1.72	hypothetical protein
Afu8g05160	-1.67	-2.31	-2.45	peroxisomal membrane protein (Pex13), putative
Afu8g05170	-1.94	-2.5	-1.75	autophagy protein Apg6, putative
Afu8g05270	-2.25	-2.45	-2.38	C6 transcription factor, putative
Afu8g05360	-2.45	-2.71	-2.38	conserved hypothetical protein
Afu8g05400	-1.33	-2.41	-1.98	hypothetical protein
Afu8g05430	-1.01	-2.43	-2.24	hypothetical protein
Afu8g05470	-0.61	-2.28	-1.44	hypothetical protein
Afu8g05480	-2.35	-2.96	-3.07	CCCH zinc finger protein
Afu8g05490	-1.75	-1.99	-2.33	transcription initiation factor iif, beta subunit
Afu8g05770	-2.95	-3.69	-3.07	hypothetical protein
Afu8g05780	-2.63	-3.43	-4.6	NACHT and Ankyrin domain protein
Afu8g05900	-1.35	-1.52	-2.19	hypothetical protein
Afu8g06040	-3.75	-5.08	-3.52	hypothetical protein
Afu8g06080	-2.71	-4.65	-2.86	flavohemoprotein, putative
Afu8g06290	-1.59	-4.36	-1.99	LINE-1 class reverse transcriptase, RNaseH, putative
Afu8g07150	-1.79	-2.99	-1.13	arsenic resistance protein ArsH, putative
Afu8g07210	-2.26	-3.27	-2.69	hydroxymethylglutaryl-CoA synthase

Table AD.1.5: List of down-regulated genes in the ATCC46645 time course. Genes significantly down-regulated were included if showing a fold change of -2 on a $\log_2$ scale at least in one of the time point datasets. T0 vs T4 = 4 hrs, T0 vs T8 hrs = 8 hrs, T0 vs T16 = 16 hrs.

ORFs	T4 vs T0	T8 vs T0	T16 vs T0	Description	Annotation
Afu7g08280	-3.09	-1.68	-1.4	hypothetical protein	
Afu1g14800	-2.74	-0.86	0.13	hypothetical protein	
Afu2g12630	-2.71	0.24	-1.18	allergen Asp F13	
Afu2g04210	-2.67	-1.37	-1.55	conserved hypothetical protein	
Afu2g01120	-2.53	-1.9	-1.67	DNA repair protein, putative	DNA-(apurinic or apyrimidinic site) lyase activity///DNA repair///base-excision repair///nucleus///mitochondrion///oxidized pyrimidine base lesion DNA N-glycosylase activity///oxidized purine base lesion DNA N-glycosylase activity///"base-excision repair, AP site formation"

Afu1g02200	-2.51	-1.95		F-box domain protein	
Afu1g03380	-2.43	-1.3	-1.6	UDP-N-acetylglucosaminyltransferase	
Afu7g06270	-2.36	-1.64	-1.74	cyanamide hydratase	cellular component unknown///molecular function unknown
Afu7g07010	-2.36	-1.28	-0.84	hypothetical protein	
Afu6g02840	-2.32	-1.6	-1.7	serine/threonine protein kinase, putative	protein serine/threonine kinase activity///cell cycle///cytoplasm///protein amino acid phosphorylation
Afu2g17520	-2.3	-0.73	-0.34	GNAT family N-acetyltransferase, putative	N-acetyltransferase activity///secondary metabolic process///metabolic process
Afu5g13620	-2.29	-1.39	-1.17	ubiquitin C-terminal hydrolase, putative	protein deubiquitination///cytoplasm///ubiquitin-specific protease activity
Afu6g08270	-2.27	-1.83	-1.82	hypothetical protein	
Afu5g00770	-2.24	-0.6	-1.53	integral membrane protein, putative	
Afu5g07590	-2.24	-1.62	-1.01	hypothetical protein	
Afu8g02750	-2.24	-1.63	-0.95	nucleolar protein CgrA	ribosome biogenesis///nucleolus///pathogenesis///growth or development of symbiont in host
Afu1g15530	-2.21	-1.28	-1.83	lactam utilization protein LamB, putative	
Afu3g08580	-2.19	-1.94	-1.55	glycine-rich RNA-binding protein, putative	ribosomal small subunit assembly///single-stranded DNA binding///nucleolus///rRNA processing///nucleus///RNA binding
Afu1g10960	-2.18	-1.7	-1.9	Mago nashi domain protein	
Afu3g14340	-2.16	-1.15	-1.1	mitotic spindle checkpoint protein (Mad2), putative	nuclear pore///mitotic cell cycle spindle assembly checkpoint///molecular function unknown///condensed nuclear chromosome kinetochore
Afu6g00680	-2.15	-0.04	-1.36	hypothetical protein	
Afu4g07030	-2.15	-1.26	-1.87	hypothetical protein	
Afu2g10540	-2.11	-1.91	-1.28	hypothetical protein	
Afu5g12830	-2.11	-1.72	-1.58	lipoprotein, putative	
Afu6g14270	-2.08	-1.5	-1.12	hypothetical protein	
Afu4g13380	-2.08	-1.71	-1.66	conserved hypothetical protein	
Afu1g17440	-2.06	-1.44		ABC drug exporter AbcA	response to drug///xenobiotic-transporting ATPase activity///ABC-type efflux porter activity///multidrug transport///plasma membrane
Afu4g05920	-2.06	-1.85	-1.84	mitochondrial protein sorting (Msf1), putative	mitochondrion///biological process unknown///molecular function unknown
Afu3g122	-2.05	-1.6	-1.9	hypothetical protein	

60					
Afu2g15690	-2.05	-1.92	-1.75	conserved hypothetical protein	

Table AD.1.6: 30 ORFs with the lowest $\log_2$ values between the down-regulated genes unique to the 4 hrs time point of the ATCC46645 time course.

ORFs	T4 vs T0	T8 vs T0	T16 vs T0	Description	Annotation
Afu8g06290	-1.59	-4.36	-1.99	LINE-1 class reverse transcriptase, RNaseH, putative	
Afu4g00820	-1.39	-4.12	-1.98	reverse transcriptase, RNaseH	
Afu3g09410	-1.05	-3.74	-1.86	reverse transcriptase	
Afu7g02610	-1.81	-3.7	-1.89	WD repeat protein	
Afu6g09570	-1.6	-3.45	-1.07	conserved hypothetical protein	
Afu5g01640	-1.81	-3.37	-1.46	ankyrin repeat protein	
Afu3g10100	-1.18	-3.34	-1.89	Sfrs4 protein	mRNA export from nucleus///cytoplasm///nucleus///mRNA binding
Afu7g08260	-1.83	-3.27	-1.4	hypothetical protein	
Afu3g06230	-1.99	-3.23	-1.67	hypothetical protein	
Afu5g12090	-1.89	-3.11	-1.86	conserved hypothetical protein	cellular component unknown///biological process unknown///molecular function unknown
Afu3g01030	-1.89	-3		RTA1 domain protein, putative	biological process unknown///molecular function unknown///integral to membrane
Afu8g07150	-1.79	-2.99	-1.13	arsenic resistance protein ArsH, putative	FMN reductase activity///electron transport
Afu1g16430	-1.42	-2.95	-1.81	hypothetical protein	
Afu4g14370	-0.65	-2.93	-0.21	LINE-1 class reverse transcriptase, RNase H, putative	
Afu5g01510	-1.41	-2.93	-1.43	amino acid transporter	plasma membrane///neutral amino acid transmembrane transporter activity///neutral amino acid transport///amino acid permease activity
Afu7g08500	-0.52	-2.93	-1.04	NACHT and WD40 domain protein	GTP binding///programmed cell death
Afu2g08680	-1.68	-2.9	-1.46	hypothetical protein	
Afu7g04130	-1.47	-2.86	-1.62	Trf5	DNA-directed DNA polymerase activity///sister chromatid cohesion///nucleus
Afu6g02430	-1.11	-2.83	-1.83	hypothetical protein	
Afu3g03070	-1.52	-2.82		MYND domain protein, putative	chromatin modification///"regulation of transcription, DNA-dependent"///zinc ion binding
Afu5g10210	-1.95	-2.79	-1.83	hypothetical protein	
Afu4g08860	-1.19	-2.79	-1.56	hypothetical protein	
Afu2g05980	-1.85	-2.77		conserved hypothetical protein	cellular component unknown///biological process unknown///molecular function unknown

Afu6g11250	-1.77	-2.75	-1.77	C2H2 finger domain protein, putative	
Afu4g08890	-0.36	-2.75	-1.12	aldo-keto reductase family protein, putative	cellular component unknown///aldo-keto reductase activity///cellular aldehyde metabolic process
Afu5g12280	-1.76	-2.69		hypothetical protein	
Afu1g15720	-1.11	-2.68	-1.83	importin beta-1 subunit	nuclear pore///protein import into nucleus///cytoplasm///protein transmembrane transporter activity
Afu2g09460	-1.95	-2.68		potassium transporter	

Table AD.1.7: 30 ORFs with the lowest $\log_2$ values between the down-regulated genes unique to the 8 hrs time point of the ATCC46645 time course.

ORFs	T4 vs T0	T8 vs T0	T16 vs T0	Description	Annotation
Afu2g01110	-1.11	-1.35	-3.34	hypothetical protein	
Afu5g11500	-0.96	-1.4	-3.13	conserved hypothetical protein	
Afu3g13770	-1.96	-1.92	-2.98	vacuolar segregation protein (Pep7), putative	Golgi to vacuole transport///cytoplasm///extrinsic to plasma membrane///vesicle fusion///vesicle docking during exocytosis///external side of endosome membrane///zinc ion binding
Afu6g10050	-1.79	-1.42	-2.95	small oligopeptide transporter, OPT family	sulfur metabolic process///oligopeptide transporter activity///integral to plasma membrane///endoplasmic reticulum
Afu1g02410	-1.56	-1.94	-2.88	AAA family ATPase Reptin, putative	chromatin remodeling complex///snoRNA metabolic process///regulation of transcription from RNA polymerase II promoter///nucleus///ATPase activity///35S primary transcript processing
Afu7g02320	-1.48	-1.86	-2.83	hypothetical protein	
Afu2g11740	-1.17	-1.7	-2.82	LON domain serine protease, putative	proteolysis///response to heat///ATP-dependent peptidase activity///mitochondrial matrix
Afu2g16090	-1.78	-1.85	-2.76	karyopherin alpha subunit, putative	nucleocytoplasmic transport///cytoplasm///nucleus///protein transmembrane transporter activity
Afu1g04500	-1.55	-1.86	-2.76	hypothetical protein	
Afu1g08790	-1.57	-1.5	-2.76	exportin KapK	mRNA export from nucleus///protein export from nucleus///nucleus///ribosomal large subunit export from nucleus///protein transmembrane transporter activity
Afu2g15660	-1.12	-1.56	-2.69	aldehyde dehydrogenase family protein, putative	cytoplasm///3-chloroallyl aldehyde dehydrogenase activity

Afu2g02600	-1.5	-1.84	-2.68	hypothetical protein	
Afu8g03980	-1.51	-1.61	-2.63	DUF59 domain protein	cytoplasm///transcription
Afu5g02530	-0.9	-1.53	-2.63	ribokinase	ribokinase activity///cytoplasm///nucleus///ATP binding///D-ribose metabolic process
Afu2g04250	-1.12	-1.01	-2.62	C6 finger domain protein, putative	
Afu1g09950	-1.49	-1.91	-2.6	casein kinase II beta subunit CKB2	establishment of cell polarity (sensu Saccharomyces)///flocculation///protein kinase CK2 activity///G1/S transition of mitotic cell cycle///regulation of transcription from RNA polymerase I promoter///regulation of transcription from RNA polymerase III promoter///protein amino acid phosphorylation///response to DNA damage stimulus///protein kinase CK2 complex///G2/M transition of mitotic cell cycle///cellular ion homeostasis
Afu1g05460	-1.91	-1.79	-2.6	hypothetical protein	
Afu2g08620	-1.58	-1.87	-2.56	20S cyclosome subunit (BimA/Nuc2/Cdc27), putative	ubiquitin-dependent protein catabolic process///ubiquitin-protein ligase activity///regulation of progression through cell cycle///spindle pole body///anaphase-promoting complex///mitotic metaphase/anaphase transition///protein binding///cyclin catabolic process///mitotic sister chromatid segregation///mitotic spindle elongation///regulation of exit from mitosis
Afu6g10940	-1.65	-1.94	-2.56	conserved hypothetical protein	
Afu4g13010	-1.76	-1.9	-2.53	conserved hypothetical protein	cytoplasm///biological process unknown///molecular function unknown
Afu4g13550	-1.87	-1.62	-2.53	short chain dehydrogenase/reductase family	sporulation (sensu Saccharomyces)///fatty acid catabolic process///peroxisomal matrix///"2,4-dienoyl-CoA reductase (NADPH) activity"
Afu5g11970	-1.85	-1.81	-2.51	protein kinase c, putative	actin filament organization///cell wall organization///protein kinase cascade///protein amino acid phosphorylation///signal transduction///protein kinase C activity
Afu3g11390	-1.23	-1.58	-2.48	proteasome regulatory particle subunit Rpt3, putative	ubiquitin-dependent protein catabolic process///endopeptidase activity///ATPase activity///proteasome regulatory

					particle///"proteasome regulatory particle, base subcomplex"
Afu5g02480	-1.43	-1.94	-2.46	glycogen synthase	cytoplasm///glycogen metabolic process///glycogen (starch) synthase activity
Afu1g02770	-1.61	-1.1	-2.45	hypothetical protein	
Afu3g10110	-1.53	-1.88	-2.44	electron transfer flavoprotein-ubiquinone oxidoreductase	NADH catabolism///"oxidoreductase activity, acting on the CH-NH group of donors, quinone or similar compound as acceptor"///mitochondrion
Afu7g03700	-1.89	-1.45	-2.44	diacylglycerol acyltransferase type 2A	lipid particle///lipid storage///triglyceride biosynthetic process///diacylglycerol O-acyltransferase activity
Afu3g12380	-1.15	-1.98	-2.43	hypothetical protein	
Afu2g06280	-1.58	-1.87	-2.41	oligosaccharyl transferase subunit (gamma), putative	oligosaccharyltransferase complex///dolichyl-diphosphooligosaccharide-protein glycotransferase activity///protein amino acid N-linked glycosylation///protein amino acid glycosylation///protein complex assembly///integral to membrane

Table AD.1.8: 30 ORFs with the lowest $\log_2$ values between the down-regulated genes unique to the 16 hrs time point of the ATCC46645 time course.

AD.2 *A. fumigatus* ATCC46645 Δ*pacC* mutant transcript profile during initiation of murine infection

Locus	T0 vs T4	T0 vs T8	T0 vs T16	Common Name
Afu1g00420	0.1	1.88	2.38	carboxypeptidase S1, putative
Afu1g00460	1.98	2.09	2.37	choline oxidase, putative
Afu1g01050	2.5	0.76	0.56	conserved hypothetical protein
Afu1g01190	3.38	1.72	2.57	hypothetical protein
Afu1g01220	2.36	1.84	2.81	conserved hypothetical protein
Afu1g01300	-2.06	0.56	3.21	GPI anchored protein, putative
Afu1g01310	-1.35	0.57	2.84	carboxylesterase, putative
Afu1g01360	0.69	1.08	2.02	conserved hypothetical protein
Afu1g01430	2.35	2.18	2.59	hypothetical protein
Afu1g01450	1.78	2.66	3.79	toxin biosynthesis protein, putative
Afu1g01530	-0.6	1.95	2.03	GrpB domain protein

Afu1g01540	1.48	3.52	4.32	Endonuclease/Exonuclease/phosphatase family family
Afu1g01550	-0.88	1.05	2.06	high affinity zinc ion transporter, putative
Afu1g01610	1.02	0.88	2.08	hypothetical protein
Afu1g01730	2.27	1.47	2.33	glycosyl hydrolase, putative
Afu1g01740	3.16	2	2.48	t-complex protein 1, beta subunit, putative
Afu1g01800	2.22	2.28	2.5	MFS transporter, putative
Afu1g02070	2.58	2.46	2.43	cytochrome c1, heme protein precursor
Afu1g02370	2	1.11	1.04	fumarylacetoacetate hydrolase family protein
Afu1g02480	1.55	1.73	2.02	plasma membrane ATPase, putative
Afu1g02550	3.85	3.76	3.39	tubulin alpha-1 subunit
Afu1g02570	2.16	1.42	1.71	aspartyl-tRNA synthetase, cytoplasmic
Afu1g02580	2.15	1.23	1.22	lipase, putative
Afu1g02730	2.44	1.8	1.98	mitochondrial phosphate carrier protein (Ptp), putative
Afu1g02780	2.62	0.23	-0.33	L-asparaginase
Afu1g02820	3.15	2.06	1.82	Y20 protein
Afu1g02880	3.8	2.84	3.5	Phosphotransferase enzyme family domain protein
Afu1g02890	1.8	3.63	3.03	dUTPase (Dut), putaive
Afu1g02900	2.42	2.16	2.65	pyridoxal kinase, putative
Afu1g02910	2.97	3.92	3.85	hypothetical protein
Afu1g02930	1.36	3.01	2.63	Ca2+ binding protein (calmodulin), putative
Afu1g03060	2.56	2.59	3.23	F-actin capping protein beta subunit
Afu1g03120	1.46	2.29	2.22	hypothetical protein
Afu1g03440	2.66	1.3	1.45	peroxisomal carrier protein, putative
Afu1g03510	2.52	1.73	1.52	ATP synthase gamma chain, mitochondrial precursor, putative
Afu1g03530	0.65	2.08	2.13	glucose transporter, putative
Afu1g03550	3.52	2.75	2.52	mitochondrial dihydroxy acid dehydratase, putative
Afu1g03560	2.29	1.48	2.04	peroxisomal protein car1
Afu1g03570	4.61	5.22	5.61	acid phosphatase PHOa
Afu1g03610	2.39	2.54	1.78	hypothetical protein
Afu1g03620	2.69	1.58	1.45	vanillin dehydrogenase, putative
Afu1g03630	3.6	5.62	5.83	GPI anchored serine-threonine rich protein
Afu1g03660	2.89	2.07	2.3	acid phosphatase, putative
Afu1g03740	2.2	2.1	1.98	prostate-specific membrane antigen
Afu1g03800	2.18	1.14	1.01	C6 transcription factor, putative
Afu1g03890	1.04	1.11	2.31	alpha/beta hydrolase, putative
Afu1g03910	2.89	0.98	0.68	hypothetical protein
Afu1g03920	2.99	1.05	0.97	DNA replication licensing factor Mcm3, putative
Afu1g03950	2.06	0.92	0.94	cytochrome P450 sterol C-22 desaturase, putaitve

Afu1g04080	2.12	1.02	0.97	GARP complex subunit (Sac2), putative
Afu1g04130	1.62	2.31	2.71	FG-GAP repeat protein, putative
Afu1g04300	2.09	2.56	3.22	hypothetical protein
Afu1g04430	1.96	2.67	4.36	conserved hypothetical protein
Afu1g04460	2.13	1.35	2.16	lysyl-tRNA synthetase, putative
Afu1g04510	2.87	1.08	0.62	hypothetical protein
Afu1g04520	2.82	0.89	0.49	Hypothetical protein
Afu1g04540	2.19	1.69	0.99	NADH-cytochrome b5 reductase precursor
Afu1g04620	2.39	2.7	2.75	alcohol dehydrogenase, zinc-containing, putative
Afu1g04890	2.78	2.39	1.78	translocon subunit
Afu1g05080	2.84	1.28	1.27	ribosomal protein P0
Afu1g05100	1.74	2.06	1.88	GARP complex subunit Vps53, putative
Afu1g05170	0.64	0.27	2.11	related to monocarboxylate transporter
Afu1g05280	2.51	2.58	3.15	conserved hypothetical protein
Afu1g05320	1.56	2.16	1.94	disulfide isomerase, putative
Afu1g05520	3.2	3.58	3.95	mandelate racemase/muconate lactonizing enzyme family protein
Afu1g05580	2.29	2.29	2.42	glycogenin
Afu1g05630	3.06	2.74	2.88	40s ribosomal protein s3
Afu1g05640	2.67	1.07	0.99	protein phosphatase
Afu1g05670	2.26	1.82		conserved hypothetical protein
Afu1g05720	2.53	0.79	0.79	c-14 sterol reductase
Afu1g05790	2.63	4.79	5.28	GPI anchored serine-rich protein
Afu1g05870	2.34	2.57	3.52	scs3 protein
Afu1g05930	1.8	1.61	2.21	serine/threonine protein kinase, putative
Afu1g05940	1.48	3.22	4.11	conserved hypothetical protein
Afu1g05960	1.61	2.56	2.93	Peptidase family M28 family
Afu1g05980	1.27	1.33	2.14	AMP-binding domain protein, putative
Afu1g06200	2.31	1.8	2.36	Mn2+ homeostasis protein (Per1), putative
Afu1g06210	2.8	2.05	1.94	N-acetylglucosamine-phosphate mutase
Afu1g06240	2.77	3.01	3.47	riboflavin synthase, alpha subunit
Afu1g06250	3.38	2.48	2.74	CAIB/BAIF family enzyme
Afu1g06530	2.64	1.83	2.12	mitochondrial carrier protein (Ymc1), putative
Afu1g06680	1.22	2.01	1.56	VHS domain protein
Afu1g06710	2.64	1.01	1.07	t-complex protein 1, eta subunit, putative
Afu1g06940	2.68	2.5	2.46	chorismate synthase
Afu1g06960	3.02	1.46	1.28	pyruvate dehydrogenase complex alpha subunit, putative
Afu1g07080	2.04	0.83	1	tRNA-specific adenosine-34 deaminase subunit Tad3, putative
Afu1g07110	2.14	1.75	1.99	related to export control protein CHS7

Afu1g07130	4.02	3.55	3.53	dienelactone hydrolase family protein
Afu1g07140	2.3	0.41	0.31	c-24(28) sterol reductase
Afu1g07200	2.45	2.77	2.46	mitochondrial cytochrome b2, putative
Afu1g07330	2.97	1.56	2.07	dihydroxy-acid dehydratase, putative
Afu1g07340	1.76	1.14	2	cytochrome P450, putative
Afu1g07380	2.94	2.1	2.21	NADH-dependent glutamate synthase (GLT1), putative
Afu1g07400	1.78	1.82	2.01	hypothetical protein
Afu1g07430	0.44	2.13	2.05	hypothetical protein
Afu1g07480	2.55	1.52	1.08	coproporphyrinogen III oxidase, putative
Afu1g07520	2.85	2.86	2.54	dimeric dihydrodiol dehydrogenase, putative
Afu1g07560	1.86	1.45	2.44	MYB DNA-binding domain protein
Afu1g07700	1.38	1.72	2.15	MFS monosaccharide transporter, putative
Afu1g08810	2.23	0.6	0.28	glycerol-3-phosphate dehydrogenase, mitochondrial
Afu1g08840	1.58	2.38	1.84	guanylate kinase
Afu1g08850	2.92	3.25	1.46	septin
Afu1g08880	0.88	2.27	2.06	heavy metal ion transporter, putative
Afu1g08950	1.96	2.06	1.86	DUF431 domain protein
Afu1g09010	2.43	2.37	1.73	methionyl-tRNA synthetase
Afu1g09480	1.49	2.37	1.68	vacuolar protein sorting 29, putative
Afu1g09510	1.63	2.69	3.24	GPI anchored serine-threonine rich protein
Afu1g09690	0.61	1.87	2.37	tRNA ligase
Afu1g09760	2.19	1.99	1.46	UPF0171 domain protein
Afu1g09810	1.9	3.59	3.8	PUA RNA binding domain protein, putative
Afu1g09820	2.1	1.46	1.51	DUF1339 domain protein
Afu1g09830	2.66	2.11	1.9	Hsc70 cochaperone (SGT), putative
Afu1g09910	2.99	2.3	2.32	glucose transporter, putative
Afu1g09960	1.91	1.85	2.14	conserved hypothetical protein
Afu1g10020	3.65	4.68	3.93	reverse transcriptase, RNaseH
Afu1g10030	0.95	2.26	2.62	hypothetical protein
Afu1g10100	1.48	2.45	2.23	3-oxoacyl-(acyl-carrier-protein) reductase
Afu1g10350	2.57	2.22	1.14	phosphoglycerate kinase PgkA, putative
Afu1g10400	2.34	1.67	1.31	hypothetical protein
Afu1g10520	1.97	1.91	2.43	hypothetical protein
Afu1g10530	2.36			hypothetical protein
Afu1g10570	2.25	2.58	3.23	glycerol-3-phosphate phosphatase (GppA), putative
Afu1g10590	-0.37	0.85	2.22	GPI anchored protein, putative
Afu1g10780	2.98	4.08	3.99	glycine cleavage system T protein
Afu1g10790	2.07	2.22	2.4	alpha-1,2-mannosidase family protein, putative

Afu1g10800	2.49	3.26	3.25	thioesterase family protein
Afu1g10820	0.84	1.98	2.14	adenylylsulfate kinase
Afu1g10900	2.25	2.44	2.87	conserved hypothetical protein
Afu1g10910	4.09	3.87	3.92	tubulin beta, putative
Afu1g10930	5.28	3.26	2.04	ammonium transporter
Afu1g11010	2.22	1.95	3.12	oxidoreductase, short chain dehydrogenase/reductase family superfamily
Afu1g11040			2.01	hypothetical protein
Afu1g11250	4.5	3.8	4.37	amidohydrolase, putative
Afu1g11450	2.66	1.95	2.9	myosin class II heavy chain (MHC), putative
Afu1g11480	4.02	5.08	4.81	hypothetical protein
Afu1g11530	3.29	3.27	3.81	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase
Afu1g11540	1.35	1.73	2.05	CORD and CS domain protein
Afu1g11550	3.51	2.08	1.98	ethanolamine kinase, putative
Afu1g11810	2.24	1.8	2.38	hypothetical protein
Afu1g11820	1.44	1.91	2.58	MFS transporter, putative
Afu1g11830	3.27	3.25	2.86	MFS quinate transporter (QutD), putative
Afu1g11890	2.16	0.37	0.17	serine palmitoyltransferase 2, putative
Afu1g12050	1.56	2.5	3.3	acetyltransferase, GNAT family family
Afu1g12070	1.78	1.67	2.39	glycine cleavage system H protein
Afu1g12100	2.62	1.45	1.64	hypothetical protein
Afu1g12190	1.67	2.33	2.31	conserved hypothetical protein
Afu1g12240	2.86	4.72	4.79	MFS peptide transporter, putaitve
Afu1g12290	2.18	3.7	3.13	possible NADH-ubiquinone oxidoreductase
Afu1g12310	2.5	2.26	3.61	GABA permease GabA
Afu1g12350	1.69	2.92	2.49	extracellular fruiting body protein, putative
Afu1g12380	2.08	1.1	1.04	WD repeat protein
Afu1g12440	1.42	1.15	2.01	isoflavone reductase family protein CipA, putative
Afu1g12510	2.44	2.66	3.66	isoflavone reductase family protein
Afu1g12620	-0.11	0.58	2	MFS toxin efflux pump (AflT), putative
Afu1g12630	2.82	2.77	2.9	mannosylphosphate transferase (Mnn4), putative
Afu1g12690	4.75	4.03	4.06	ABC multidrug transporter Mdr4
Afu1g12830	2.12	1.21	0.94	nitrate reductase NiaD
Afu1g12840	2.93	1.23	1.03	nitrite reductase
Afu1g12920	4.32	3.23	3.24	glycogen phosphorylase 1; possible glycogen phosphorylase
Afu1g13090	2.24	1.63	2.16	anthranilate synthase multifunctional protein
Afu1g13230	-0.22	2.09	2.42	conserved hypothetical protein
Afu1g13330	2.98	3.11	2.55	Arp2/3 complex subunit (Arp2), putative

Afu1g13490	2.11	2.29	2.16	spermidine synthase
Afu1g13500	4.44	3.73	2.11	transketolase TktA
Afu1g13690	2.01	0.98	0.44	WD repeat protein
Afu1g13720	2.09	1.97	1.07	intracellular protein transport protein (UsoA), putative
Afu1g13740	2.58	1.76	2.44	pentafunctional polypeptide (AroM), putative
Afu1g13780	1.68	3.76	3.3	histone H4
Afu1g13930	2.91	2.78	2.84	Leucine carboxyl methyltransferase superfamily
Afu1g13940	2.36	1.45	1.78	SUN domain protein (Adg3), putative
Afu1g14120	2.09	0.83	-0.22	nuclear segregation protein (Bfr1), putative
Afu1g14200	2.6	1.67	1.95	mitochondrial processing peptidase beta subunit, putative
Afu1g14210	3.13	2.73	2.93	putative nucleoside-diphosphate-sugar epimerase
Afu1g14240	2.09	2.26	2.82	conserved hypothetical protein
Afu1g14260	2.14	2.4	2.4	related to TGF beta receptor associated protein 1
Afu1g14350	2.92	3.43	3.18	2-deoxy-D-gluconate 3-dehydrogenase, putative
Afu1g14380	1.95	2.86	3.07	3-ketoacyl-acyl carrier protein reductase
Afu1g14390	2.62	4.4	4.57	zinc binding dehydrogenase family protein
Afu1g14400	2.47	2.99	2.77	glyoxylate reductase
Afu1g14530	2.3	2.66	3.07	general amidase-B
Afu1g14540	2.52	3.11	2.7	oxidoreductase, short-chain dehydrogenase/reductase family
Afu1g14550	5.29	6.65	6.03	Mn superoxide dismutase MnSOD
Afu1g14560	0.62	2.33	2.33	alpha-mannosidase
Afu1g14650	2.31	0.34	0.15	WD repeat protein
Afu1g14710	2.34	1.42	0.52	beta-glucosidase 1
Afu1g14980	2.68	2.22	3.03	hypothetical protein
Afu1g15050	3.05	2.24	1.73	Hsp70 chaperone (Orp150), putative
Afu1g15150	2.1	1.05	1.55	alpha-amylase (amyE)
Afu1g15180	2.6	1.91	1.19	conserved hypothetical protein
Afu1g15260	2.76	0.42	0.32	hypothetical protein
Afu1g15290	3.09	2.61	3.27	hypothetical protein
Afu1g15300	3.58	3.3	3.17	choline transport protein, putative
Afu1g15310	2.22	1.39	1.91	sna41 protein
Afu1g15320	2.2	1.49	1.83	NA
Afu1g15330	2.92	4.32	4.37	T10O22.24
Afu1g15470	2.49	1.84	2.22	C6 transcription factor (UaY), putative
Afu1g15550	2.43	1.86	2.83	homeobox and C2H2 transcription factor, putative
Afu1g15660	1.68	1.21	2.15	hypothetical protein
Afu1g15780	2.38	1.7	1.74	3-isopropylmalate dehydrogenase
Afu1g15860	2.04	1.4	0.38	Coatomer subunit delta, putative

Afu1g15950	2.07	0.7	0.3	MAP kinase kinase (Pbs2), putative
Afu1g16190	2.1	1.89	1.32	cell wall glucanase Crf1
Afu1g16250	3.87	5.94	5.07	alpha-glucosidase B
Afu1g16270	2.29	2.02	1.84	xylitol dehydrogenase XdhB, putative
Afu1g16480	2.7	2.81	2.48	acid phosphatase, putative
Afu1g16500	2.03	0.8	0.39	small monomeric GTPase (Gtr2), putative
Afu1g16640	1.47	2.72	3.18	hypothetical protein
Afu1g16670	2.71	3.04	3.23	hypothetical protein
Afu1g16760	0.98	3.12	3.38	acetyltransferase, GNAT family family
Afu1g16770	0.99	3.25	3.24	amidase
Afu1g17050	1.66		2.19	hypothetical protein
Afu1g17110	2.17	0.79	1.52	long chain fatty alcohol oxidase, putative
Afu1g17140	2.32	2.27	2.9	voltage-gated K+ channel beta subunit (KCNAB), putative
Afu1g17170	4.13	4.7	5.17	alpha-ketoglutarate-dependent taurine dioxygenase
Afu1g17180	5.7	6.51	6.73	pyridine nucleotide-disulphide oxidoreductase, putative
Afu1g17190	4.02	4.52	4.4	long-chain-fatty-acid-CoA ligase, putative
Afu1g17200	3.76	4.16	4.37	nonribosomal peptide synthase, putative
Afu1g17270	2.61	2.97	4.05	ferric-chelate reductase (Fre2), putative
Afu1g17420	1.07	0.97	2	hypothetical protein
Afu1g17470	0.62	1.9	2.88	high affinity nitrate transporter NrtB
Afu1g17480	1.51	3.63	4.37	conserved hypothetical protein
Afu1g17490	2.76	3.55	3.92	glucokinase regulator family protein, putative
Afu1g17510	1.92	1.67	2.23	lipase/esterase, putative
Afu1g17530	2.95	2.97	3.93	MFS transporter, putative
Afu1g17540	0.85	0.67	2.12	hypothetical protein
Afu1g17590	1.8	2.32	3.9	phosphoesterase superfamily protein
Afu1g17640	1.31	1.33	3.45	melanin biosynthesis transcription factor RegA
Afu1g17650	1.8	1.93	3.4	short chain dehydrogenase, putative
Afu1g17670	1.47	0.67	2.44	salicylate hydroxylase, putative
Afu1g17700	3.89	4.32	4.52	short chain dehydrogenase, putative
Afu2g00230	2.38	1.62	1.98	NADH oxidoreductase Amid, putative
Afu2g00260	3.26	1.89	2.25	phenylacetaldoxime dehydratase family protein, putative
Afu2g00320	2.67	2.72	2.91	sterol delta 5,6-desaturase, putative
Afu2g00570	-0.68	1	2.03	GNAT family acetyltransferase, putative
Afu2g00620	2.12	1.77	2.64	hypothetical protein
Afu2g00640	2.66	3.98	4.93	beta-N-hexosaminidase, putative
Afu2g00690	1.13	5.03	4.96	glucan 1,4-alpha-glucosidase, putative
Afu2g00710	1.83	4.18	4.39	alpha-amylase, putative

Afu2g00720	0.42	1.26	2.15	aldehyde dehydrogenase, putative
Afu2g00750	1.89	2.23	3.17	oxidoreductase, 2OG-Fe(II) oxygenase family, putative
Afu2g00770	2.18	2.47	3.22	salicylate hydroxylase
Afu2g00790	0.46	1.64	2.12	hypothetical protein
Afu2g00820	1.18	2.95	3.48	extracellular GDSL-like lipase/acylhydrolase, putative
Afu2g00880	0.73	2.29	2.21	conserved hypothetical protein
Afu2g00890	0.43	2.2	1.62	hypothetical protein
Afu2g01010	1.71	2.08	1.64	myo-inositol-phosphate synthase, putative
Afu2g01030	1.62	2.72	2.88	1-aminocyclopropane-1-carboxylate deaminase, putative
Afu2g01040	2.71	2.66	3.17	formaldehyde dehydrogenase
Afu2g01070	1.45	2.59	2.87	GPI-anchor biosynthesis protein (Pig-F), putative
Afu2g01240	3.65	2.06	1.74	beta-D-fructofuranoside fructohydrolase
Afu2g01280	2.2	4.27	3.73	D-mandelate dehydrogenase, putative
Afu2g01300	2.35	3.86	4.05	conserved hypothetical protein
Afu2g01310	1.94	3.12	3.36	EF-hand domain protein
Afu2g01320	2.49	3.57	3.94	P-type ATPase, putative
Afu2g01360	0.54	1.38	2.04	nucleotide-binding GAF domain protein
Afu2g01380	0.99	2.45	4.22	GNAT family acetyltransferase, putative
Afu2g01430	2.06	1.1	1.13	hypothetical protein
Afu2g02050	2.54	2.56	1.76	peptidyl-prolyl cis-trans isomerase, putative
Afu2g02100	2.91	1.89	1.76	dihydrolipoamide dehydrogenase
Afu2g02440	3.03	2.47	3.5	conserved hypothetical protein
Afu2g02490	0.98	1.85	2.4	hypothetical protein
Afu2g02590	3.94	2.67	2.07	aspartyl-tRNA synthetase
Afu2g02790	3.5	1.06	1.72	NA
Afu2g02800	2.19	0.25	0.53	NA
Afu2g02810	3.36	2.17	2.41	alcohol dehydrogenase, zinc-containing, putative
Afu2g02870	1.01	1.56	2.12	hypothetical protein
Afu2g02950	4.02	3.28	3.01	aldehyde reductase, putative
Afu2g03010	2.36	2.23	1.48	cytochrome c subunit Vb, putative
Afu2g03100	0.56	1.11	2.04	conserved hypothetical protein
Afu2g03270	2.32		2.01	glycosyl hydrolase, putative
Afu2g03330	1.17	1.98	2.06	phytanoyl-CoA dioxygenase family protein
Afu2g03450	0.87	2.07	1.85	hypothetical protein
Afu2g03510	1.86	3.02	3.39	pheromone processing carboxypeptidase (Sxa2), putative
Afu2g03540	2.14	1.67	1.94	conserved hypothetical protein
Afu2g03550	2.45	1.38	1.72	NA
Afu2g03580	2.59	1.31	0.42	phenylalanyl-tRNA synthetase beta chain cytoplasmic

Afu2g03730	2.79	3.44	2.06	Ctr copper transporter family protein
Afu2g03830	3.74	3.92	4.19	allergen Asp F4
Afu2g03860	3.2	3.58	4.14	plasma membrane low affinity zinc ion transporter, putative
Afu2g03870	0.69	1.94	2.01	FKBP-type peptidyl-prolyl isomerase, putative
Afu2g03990	1.51	2.52	3.1	hypothetical protein
Afu2g04060	1.58	1.55	2.58	NADH:flavin oxidoreductase/NADH oxidase family protein
Afu2g04230	0.67	2.3	1.41	fumarylacetoacetate hydrolase FahA
Afu2g04300	1.86	2.3	2.29	lipase/esterase, putative
Afu2g04310	2.21	1.76	2.19	argininosuccinate synthase
Afu2g04490	1.09	1.98	2.69	D-3-phosphoglycerate dehydrogenase
Afu2g04520	1.33	2.67	2.76	Fe-containing alcohol dehydrogenase, putative
Afu2g04540	1.76	2.94	3.54	hypothetical protein
Afu2g04570	2.46	3.27	3.44	BNR/Asp-box repeat domain protein
Afu2g04590	3.35	3.2	4.23	alcohol dehydrogenase, putative
Afu2g04600	2.3	2.43	3.33	C6 transcription factor, putative
Afu2g04620	2	1.32	1.18	ER Hsp70 chaperone BiP, putative
Afu2g04700	2.68	2.01	1.17	RNA binding effector protein (Scp160), putative
Afu2g04710	1.55	1.77	2.23	cytochrome b5, putative
Afu2g04980	2.03	2.45	2.63	tyrosine decarboxylase, putative
Afu2g05080	1.01	1.65	2.88	hypothetical protein
Afu2g05150	1.26	4.48	4.79	cell wall galactomannoprotein Mp2
Afu2g05180	1.04	1.13	2.26	NF-X1 finger and helicase domain protein, putative
Afu2g05260	2.49	2.42	2.99	salicylate hydroxylase
Afu2g05290	1.72	1.55	2.87	isoflavone reductase family protein
Afu2g05310	-0.04	1.28	2.09	C6 transcription factor, putative
Afu2g05340	2.43	2.49	3.18	1,3-beta-glucanosyltransferase, putative
Afu2g05350	2.21	0.74	0.68	major facilitator superfamily protein superfamily
Afu2g05360	2.18	1.23	1.16	C6 transcription factor, putative
Afu2g05400	1.3	2.01	2.69	sugar hydrolase, putative
Afu2g05450	2.12	1.21	0.68	64 kDa mitochondrial NADH dehydrogenase
Afu2g05590	2.02	2.63	3.12	ubiquitin C-terminal hydrolase L3
Afu2g05750	1.73	1.68	2.83	agmatinase, putative
Afu2g05800	2.75	2.95	3.46	IdgA domain protein
Afu2g05820	1.62	2.49	3.08	Riboflavin kinase, putative
Afu2g05880	2.71	1.18	0.6	ammonium transporter MEAA
Afu2g05910	2.75	1.86	1.49	hexokinase Kxk, putative
Afu2g06100	2.41	1.6	1.24	DUF907 domain protein
Afu2g06150	3.2	3.11	1.12	disulfide isomerase, putative

Afu2g06260	2.09	2.21	2.25	hypothetical protein
Afu2g07500	2.8	2.48	2.55	prolidase pepP, putative
Afu2g07570	2.61	1.46	1.63	glutamate 5-kinase, putative
Afu2g07630	2.28	2.09	2.06	vacuolar H+\/Ca2+ exchanger
Afu2g07680	4.44	4.31	4.65	L-ornithine N5-oxygenase SidA
Afu2g07750	0.01	1.88	3.26	haloacid dehalogenase, type II
Afu2g07760	1.94	1.04	2.04	hypothetical protein
Afu2g07780	1.18	2.01	3.05	acyl-CoA synthetase, putative
Afu2g07810	2.33	2.86	3.31	cytosolic hydroxymethyltransferase, putative
Afu2g07820	1.42	2.06	2.63	MOSC domain protein
Afu2g07910	1.42	1.8	2.54	myo-inositol transporter
Afu2g07940	0.93	2.66	2.54	NADPH-cytochrome P450 reductase (CprA), putative
Afu2g08120	0.95	1.34	2.01	MFS monosaccharide transporter (Hxt8), putative
Afu2g08220	2.17	1.04	1.31	hypothetical protein
Afu2g08230	2.03		1.7	MFS transporter, putative
Afu2g08300	3.7	3.07	2.66	DnaJ domain protein, putative
Afu2g08350	2.25	0.97	1.63	allantoate permease
Afu2g08470	0.56	2.49	1.93	GTP binding protein (Bud4), putative
Afu2g08550	3.16	4.11	3.86	peptidyl-prolyl cis/trans isomerase
Afu2g08560	2.41	1.12	1.2	hypothetical protein
Afu2g08800	1.97	2.92	3.25	amino acid permease (Dip5), putative
Afu2g08820	2.39	2.62	4.32	hypothetical protein
Afu2g08950	0.15	1.79	2.7	isochorismatase family hydrolase, putative
Afu2g08970	2.15	0.95	1.41	hydroxyethylthiazole kinase;
Afu2g09060	2.67	2.98	3.73	DNA replication licensing factor Mcm4, putative
Afu2g09070	2.55	2.32	1.41	DUF221 domain protein, putative
Afu2g09150	2.59	1.6	0.95	adenosine deaminase
Afu2g09620	2.45	2.7	3.06	phytanoyl-CoA dioxygenase family protein
Afu2g09670	0.64	2.22	2	SNARE protein (Ufe1), putative
Afu2g09680	2.53	2.24	2.96	PB1 domain protein, putative
Afu2g09780	2.15	2.64	2.66	hypothetical protein
Afu2g09790	3.88	2.72	1.21	glucose-6-phosphate isomerase
Afu2g09810	3.58	3.56	2.81	mandelate racemase/muconate lactonizing enzyme family protein
Afu2g09850	3.1	3.67	3.25	oxidoreductase, 2-nitropropane dioxygenase family, putative
Afu2g09940	2.35	1.21	1.12	hypothetical protein
Afu2g10070	2.64	1.84	1.8	carbamoyl-phosphate synthase, large subunit
Afu2g10190	1.68	2.2	2.3	hypothetical protein
Afu2g10220	3.46	3.43	2.87	glycerol dehydrogenase, putative

Afu2g10240	2.43	2.87	2.94	NAD binding Rossmann fold oxidoreductase, putative
Afu2g10280	2.66	2.36	2.15	ketoreductase
Afu2g10450	2.57	1.38	1	prephenate dehydrogenase
Afu2g10580	0.32	2.19	1.75	hypothetical protein
Afu2g10610	2.31	1.61	0.74	COPI vesicle coat beta' subunit, putative
Afu2g10650	1.71	2.4	1.66	enoyl-CoA hydratase
Afu2g10660	3.28	2.4	2.04	mannitol-1-phosphate dehydrogenase
Afu2g10730	1.84	3.03	2.7	DNA polymerase alpha catalytic subunit, putative
Afu2g10910	2.05	3.54	4.4	maltose permease
Afu2g10920	1.86	3.58	3.67	enoyl-CoA hydratase/isomerase family protein
Afu2g10950	3	3.35	4.23	hypothetical protein
Afu2g10960	2.83	2.38	3.12	alcohol dehydrogenase, putative
Afu2g11010	3.04	2.99	2.82	dihydroorotate reductase PyrE, putative
Afu2g11060	0.08	2.08	1.59	Acyl CoA binding protein family
Afu2g11150	2.58	2.18	1.46	secretory pathway gdp dissociation inhibitor
Afu2g11490	1.75	1.94	2.78	acetylglutamate synthase
Afu2g11520	3.77	2.11	0.88	MFS monosaccharide transporter, putative
Afu2g11540	3.83	2.18	2.48	ketoreductase, putative
Afu2g11580	2.67	1.49	2.29	mfs-multidrug-resistance transporter
Afu2g11600	2.48	2.49	2.9	oxidoreductase, putative
Afu2g11850	2.56	1.03	0.52	large subunit ribosomal protein L3
Afu2g12550	2.41	0.82	0.22	multidrug resistant protein, putative
Afu2g12740	1.25	2.41	4.03	methyltransferase, putative
Afu2g12760	1.41	2.68	2.46	conserved hypothetical protein
Afu2g12790	3.32	3.69	5.31	monocarboxylate transporter-like protein
Afu2g12850	1.64	3.22	3.81	1,3-beta-glucanosyltransferase Gel3
Afu2g12940	1.84	1.81	2	conserved hypothetical protein
Afu2g13160	0.49	2.14	3.15	hypothetical protein
Afu2g13170	1.8	2.59	3.15	hypothetical protein
Afu2g13240	2.08	1.29	0.81	V-type ATPase, B subunit, putative
Afu2g13250	2.05	0.62	0.38	bifunctional tryptophan synthase TRPB
Afu2g13270	0.33	2.78	2.99	alcohol dehydrogenase, putative
Afu2g13290	1.77	2.89	3.61	GYF domain protein
Afu2g13450	2.88	2.78	2.76	dynactin, putative
Afu2g13580	2.17	2.5	3.18	conserved hypothetical protein
Afu2g13800	2.2	2.2	3.04	malate dehydrogenase
Afu2g14390	2.08	3.29	3.77	methyltransferase, putative
Afu2g14410	2.49	1.32	1.89	dioxygenase, putative

Afu2g14510	1.68	1.68	2.32	hypothetical protein
Afu2g14590	3.54	2.54	2.22	MFS monosaccharide transporter, putative
Afu2g14600	2.84	2.02	2.42	ab-hydrolase associated lipase family
Afu2g14740	1.25	2.64	2.7	DUF821 domain protein
Afu2g14790	1.36	2.3	3.1	hypothetical protein
Afu2g14850	1.16	2.84	2.86	enoyl-CoA hydratase/isomerase family protein
Afu2g14910	2.4	1.54	1.36	alpha-1,6-mannosyltransferase subunit, putative
Afu2g14920	3.11	3.8	3.97	protein kinase, putative
Afu2g14930	2.66	1.81	2.6	alanine racemase
Afu2g14970	3.36	2.93	2.62	Gamma-butyrobetaine hydroxylase subfamily, putative
Afu2g14990	2.33	3.21	2.98	tubulin alpha-2 subunit
Afu2g15240	2.5	4.88	5.66	small oligopeptide transporter, OPT family
Afu2g15490	2.81	2.58	2.87	TPR domain protein
Afu2g15550	2.82	1.49	2.46	molybdenum cofactor biosynthesis protein Gephyrin, putative
Afu2g15850	2.16	2.92	3.75	phytanoyl-CoA dioxygenase family protein
Afu2g15900	0.97	2.24	2.33	conserved hypothetical protein
Afu2g15930	2.43	2.1	2.89	alcohol dehydrogenase, zinc-containing
Afu2g16010	2.16	0.52	-0.38	prolyl-tRNA synthetase
Afu2g16060	1.49	1.58	2.14	conserved hypothetical protein
Afu2g16120	3.23	2.23	1.99	translocon-associated protein, alpha subunit, putative
Afu2g16200	0.49	1.95	2.14	uracil phosphoribosyltransferase
Afu2g16380	2.11	1.64	1.68	conserved hypothetical protein
Afu2g16540	1.38	2.31	2.77	C2H2 finger domain protein, putative
Afu2g16620	2.34	1	0.99	protein kinase, putative
Afu2g16720	2.11	1.59	1.29	DUF1237 domain protein
Afu2g16820	3.61	2.09	1.17	curved DNA-binding protein (42 kDa protein)
Afu2g17000	2.92		1.27	PT repeat family protein
Afu2g17010	1.75	2.31	1.87	NA
Afu2g17070	1.89	2.18	2.27	DUF298 domain protein
Afu2g17080	2.05	1.66	1.29	integral membrane protein 25D9-6
Afu2g17300	0.89	2.18	3.46	glutathione S-transferase
Afu2g17320	4.59	5.29	5.74	conserved hypothetical protein
Afu2g17330	1.92	2.48	3.47	serine peptidase, family S28, putative
Afu2g17360	1.64	1.63	2.32	monocarboxylate transporter (Mct), putative
Afu2g17400	3.24	3.57	3.85	C-3 sterol dehydrogenase/C-4 decarboxylase
Afu2g17430	1.16	0.85	2.22	oxidoreductase, 2-nitropropane dioxygenase family, putative
Afu2g17450	1.23	2.23	2.77	3-hydroxyanthranilate 3,4-dioxygenase
Afu2g17460	0.93	1.99	2.38	aldehyde dehydrogenase, putative

Afu2g17600	2	1.98	1.02	polyketide synthetase PksP
Afu2g17630	-0.01	2.44	2.15	hypothetical protein
Afu2g17660	2.25	1.55	1.74	C4-dicarboxylate transporter/malic acid transport protein, putative
Afu2g17770	0.51	1.87	2.24	conserved hypothetical protein
Afu2g17790	1.22	2.24	3.04	amino acid transporter, putative
Afu2g17800	0.23	2.18	2.73	C6 transcription factor, putative
Afu2g17830	-0.2	1.75	4.06	hypothetical protein
Afu2g17840	0.81	2.87	4.72	MFS transporter, putative
Afu2g17930	-0.26	2.53	2.95	integral membrane protein
Afu2g18030	1.83	2.54	3.01	catalase, putative
Afu2g18050	-0.07	1.13	3.26	FAD binding oxidoreductase, putative
Afu3g00290	0.83	1.33	2.07	3-hydroxyacyl-CoA dehydrogenase, putative
Afu3g00310	2.31	1.64	1.56	extracellular phytase, putative
Afu3g00320	1.15	3	1.92	endo-1,4-beta-xylanase (XlnA), putative
Afu3g00350	0.92	2.25	1.58	hypothetical protein
Afu3g00420	0.73	1.49	3.73	acetyl xylan esterase (Axe1), putative
Afu3g00430	2.19	1.45	2.48	high-affinity glucose transporter, putative
Afu3g00470	1.87	3.86	5.04	endo-1,4-beta-xylanase, putative
Afu3g00520	0.8	2.42	2.56	SIR2 family histone deacetylase, putative
Afu3g00560	-0.24	1.15	2.03	conserved hypothetical protein
Afu3g00590	2.2	2.18	2.45	Asp-hemolysin
Afu3g00680	3.6	3.18	3.39	copper amine oxidase
Afu3g00690	2		0.32	C6 transcription factor, putative
Afu3g00740	4.12	3.88	4.14	2-dehydropantoate 2-reductase, putative
Afu3g00750	2.74	4.23	3.77	short-chain dehydrogenase/reductase, putative
Afu3g00900	4.13	4.86	4.97	alpha-amylase AmyA
Afu3g00960	-1.5	1.55	2.11	conserved hypothetical protein
Afu3g00990	2.27	2.1	2.14	flavin-binding monooxygenase, putative
Afu3g01110	2.34	1.24	1.5	GMP synthase
Afu3g01170	-0.22	0.14	2.1	cystathionine beta-lyase
Afu3g01180	0.96	1.16	3.48	sarcosine oxidase, putative
Afu3g01220	0.87	1.69	2.63	aspartic-type endopeptidase, putative
Afu3g01230	2.92	3.39	4.44	sugar transporter-like protein
Afu3g01240	-2.58	0.46	2.52	hypothetical protein
Afu3g01280	0.29	1.75	3.31	alpha/beta hydrolase, putative
Afu3g01320	2.19	3.64	3.97	homocysteine S-methyltransferase, putative
Afu3g01330	1.75	2.61	2.68	class II aldolase/adducin domain protein
Afu3g01370	3.44	5.08	5.33	MFS transporter, putative

Afu3g01450	1.47	2.15	1.84	3-methyl-2-oxobutanoate dehydrogenase, putative
Afu3g01490	2.57	3.15	4.53	alcohol dehydrogenase, putative
Afu3g01500	-0.18	2.09	3.33	integral membrane protein
Afu3g01530	-0.03	2.56	4.2	phosphatidylglycerol specific phospholipase, putative
Afu3g01580	0.18	2.52	3.58	GMC oxidoreductase, putative
Afu3g01590	0.98	1.28	2.03	hypothetical protein
Afu3g01610	0.33	3.03	3.53	hypothetical protein
Afu3g01660	2.02	3.46	3.73	putative hydrolase
Afu3g01670	0.35		2.82	MFS hexose transporter, putative
Afu3g01700	1.73	1.61	2.65	maltose permease
Afu3g01780	2.23	1.7	1.76	alcohol dehydrogenase, putative
Afu3g01810	2.54	2.57	3.04	F-box domain protein
Afu3g01950	1.16	1.85	2.06	alcohol dehydrogenase, zinc-containing
Afu3g02040	3.37	3.62	4	glycosyl hydrolase, putative
Afu3g02130	0.49	0.87	2.45	oxidoreductase, zinc-binding, putative
Afu3g02240	2.56	1.33	1.51	aromatic-L-amino-acid decarboxylase
Afu3g02250	1.76	3.15	3.98	conserved hypothetical protein
Afu3g02270	3.42	3.7	1.71	mycelial catalase Cat1
Afu3g02280	4	4.74	4.77	alpha,alpha-trehalose glucohydrolase, putative
Afu3g02360	2.1	2.29	1.2	FAD dependent oxidoreductase superfamily
Afu3g02890	2.69	1.83	2.1	MFS sugar transporter, putative
Afu3g02940	5.04	5.54	5.48	allergen, putative
Afu3g02970	0.98	4.32	4.99	aspergillopepsin, putative
Afu3g02980	3.06	2.66	3.03	metalloreductase, putative
Afu3g03000	1.27	2.6	3.25	phosphatidylethanolamine-binding protein, putative
Afu3g03010	2.04	4.44	4.82	phosphate-repressible phosphate permease
Afu3g03020	3.18	3.18	2.72	phosphoglucomutase, putative
Afu3g03330	2.36	3.76	6.03	mitochondrial enoyl reductase, putative
Afu3g03350	0.67	3.46	5.24	nonribosomal peptide synthase, putative
Afu3g03360	1.02	2.71	5.12	hypothetical protein
Afu3g03390	5.34	5.37	5.87	siderophore biosynthesis lipase/esterase, putative
Afu3g03400	4.88	5.58	5.49	siderophore biosynthesis acetylase AceI, putative
Afu3g03410	5.2	6.21	6.25	enoyl-CoA hydratase/isomerase family protein
Afu3g03420	4.42	6.45	6.07	hypothetical protein
Afu3g03430	4.32	5.73	5.71	ABC multidrug transporter SitT, putative
Afu3g03440	5.85	6.29	6.55	MFS family siderophore transporter, putative
Afu3g03450	2.82	2.77	3.4	cytochrome P450 pisatin demethylase, putative
Afu3g03600	1.29	2.9	3.72	carboxyl esterase A

Afu3g03640	3.3	5.11	2.99	siderochrome-iron transporter (MirB), putative
Afu3g03660	4.77	2.49	3.8	esterase superfamily protein
Afu3g03670	3.85	3.34	4.08	ABC multidrug transporter, putative
Afu3g03700	5.21	6.69	6.7	Sugar transporter subfamily
Afu3g03710	3.36	1.44	2.4	D-aminopeptidase putative
Afu3g03810	1.9	1.25	3.48	hypothetical protein
Afu3g03820	3.66	4.09	5.47	MFS transporter, putative
Afu3g03830	2.83	2.89	3.89	hypothetical protein
Afu3g03850	0.93	1.44	2.31	hypothetical protein
Afu3g03860	3.82	3.43	4.91	3-hydroxyacyl-CoA dehydrogenase, putative
Afu3g04170	2.94	1.5	1.67	pyruvate dehydrogenase E1 beta subunit, putative
Afu3g04220	2.71	1.71	1.07	fatty acid synthase beta subunit, putative
Afu3g05450	2.79	1.99	2.07	glutamate carboxypeptidase, putative
Afu3g05880	1.26	1.78	2.52	oxysterol binding protein (Osh3), putative
Afu3g06530	4.2	3.4	3.43	ATP sulphurylase
Afu3g06650	2.44	1.81	1.91	aminoalcoholphosphotransferase
Afu3g06660	2.29	1.78	1.04	NIPSNAP1 protein
Afu3g06730	1.67	2.54	2.56	MFS sugar transporter, putative
Afu3g06740	1.27	2.18	2.23	C6 transcription factor (Gal4), putative
Afu3g07020	0.43	1.88	2.59	annexin ANXC4
Afu3g07140	2.21	3	3.85	developmental regulator FluG
Afu3g07150	2.94	3.89	4.88	succinate-semialdehyde dehydrogenase, putative
Afu3g07160	0.54	1.11	2.43	class V chitinase, putative
Afu3g07310	2.18	2.93	3.08	conserved hypothetical protein
Afu3g07400	1.11	2.12	2.67	hypothetical protein
Afu3g07410	3.05	3.23	3.48	isoamyl alcohol oxidase
Afu3g07640	1.85	1.27	2.64	plasma membrane H+-ATPase
Afu3g07790	2.51	1.54	1.59	argininosuccinate lyase
Afu3g07830	2.08	0.24	-0.6	t-complex protein 1, delta subunit, putative
Afu3g07870	2.52	3.32	3.29	extracellular serine-rich protein
Afu3g07890	1.96	2.48	3	endo alpha-1,4 polygalactosaminidase, putative
Afu3g07910	2.48	3.68	3.88	UDP-glucose 4-epimerase, putative
Afu3g08060	1.27	1.26	2.49	DUF1338 domain protein
Afu3g08110	0.29	3.13	2.96	cell wall protein, putative
Afu3g08150	1.3	1.76	2.11	hypothetical protein
Afu3g08290	3.9	2.73	2.24	aspartyl aminopeptidase
Afu3g08300	2.1	1.45	1.15	DNA replication factor C subunit Rfc2, putative
Afu3g08310	3.08	2.41	1.95	4-nitrophenylphosphatase

Afu3g08380	2.56	1.68	1.25	inorganic diphosphatase, putative
Afu3g08610	1.4	2.35	2.37	DUF124 domain protein
Afu3g09050	2.06			exonuclease I, putative
Afu3g09140	1.8	3.26	4.36	endo 1,5-alpha-arabinase
Afu3g09150	2.11	3.3	4.25	oxidoreductase, short chain dehydrogenase/reductase family
Afu3g09220	1.81	2.24	2.12	fatty acid hydroxylase, putative
Afu3g09330	2.54	1.49	1.17	conserved hypothetical protein
Afu3g09550	2.4	1.23	1.38	calcium/calmodulin dependent protein kinase, putative
Afu3g09690	1.5	1	2.11	extracellular thaumatin domain protein, putative
Afu3g09700	2.21	2.07	2.16	Sec23/Sec24 family protein
Afu3g09710	1.68	2.05	1.93	amino acid permease
Afu3g09720	2.67	2.27	1.65	cleavage and polyadenylylation specificity factor, putative
Afu3g09740	3.21	2.91	3.13	integral plasma membrane protein, putative
Afu3g10300	2.55	1.74	1.27	galactokinase
Afu3g10390	1.18	1.54	2.23	conserved hypothetical protein
Afu3g10540	0.06	0.82	2.13	3-oxoacyl-(acyl-carrier-protein) reductase, putative
Afu3g10790	2.01	1.34	1.22	hypothetical protein
Afu3g10910	1	1.66	2.49	glutaminase A
Afu3g10920	2.67	1.61	0.77	telomere and ribosome associated protein Stm1, putative
Afu3g11280	2.69	3.17	3.33	class V chitinase, putative
Afu3g11480	1.94	3	3.13	mitochondrial methylglutaconyl-CoA hydratase (Auh), putative
Afu3g11510	1.7	1.8	2.29	O-acetyltransferase, putative
Afu3g11640	3.66	3.56	4.17	homoserine dehydrogenase
Afu3g11650	1.36	3.97	5.15	hypothetical protein
Afu3g11770	1.07	2.08	2.97	hypothetical protein
Afu3g11780	2.46	2.82	3.13	beta-N-acetylglucosaminidase, putative
Afu3g11790	2.84	3.39	3.28	galactose-proton symport, putative
Afu3g11850	2.51	1.02	1.61	hypothetical protein
Afu3g11900	2.23	3.45	3.19	oxidoreductase, zinc-binding
Afu3g11920	1.37	2.52	1.73	dihydrodipicolinate synthetase family protein
Afu3g12170	2.29	3.12	3.62	MFS sugar transporter, putative
Afu3g12210	2.07	1	1.65	carboxypeptidase Y, putative
Afu3g12250	0.93	2.05	2.43	protein-tyrosine phosphatase, putative
Afu3g12330	2.04	1.63	0.3	phosphatidyl synthase
Afu3g12420	2.7	2.08	1.42	endothelin-converting enzyme
Afu3g12430	2.11	1.64	1.72	guanine nucleotide exchange factor, putative
Afu3g12460	2.66	2.45	1.72	conserved hypothetical protein
Afu3g12600	0.76	1.79	2.39	beta-glucosidase 1

Afu3g12610	0.69	1.58	2.11	hypothetical protein
Afu3g12620	2.32	3.92	4.66	acyl-CoA:6-aminopenicillanic-acid-acyltransferase, putative
Afu3g12770	1.75	2.18	2.18	putative nucleoside-diphosphate-sugar epimerase
Afu3g12790	2.21	3.23	3.2	conserved glutamic acid-rich protein
Afu3g12800	3.2	2.03	1.93	conserved hypothetical protein
Afu3g12840	1.11	2.33	2.45	Signal peptidase I
Afu3g13030	2.07	0.86	0.71	t-complex protein 1, gamma subunit, putative
Afu3g13080	-0.07	0.53	2.05	hypothetical protein
Afu3g13110	-1.01	2.19	1.85	extracellular serine-threonine rich protein
Afu3g13120	2.61	1.77	2.46	porphobilinogen deaminase
Afu3g13180	2.13	0.11	-0.53	hypothetical protein
Afu3g13240	1.33	3.03	2.21	aldose 1-epimerase, putative
Afu3g13260	1.66	1.81	2.01	related to DNA repair endonuclease rad2
Afu3g13320	3.47	1.88	1.33	40S ribosomal protein S0, putative
Afu3g13390	2.07	1.8	1.4	Vacuolar ATP synthase subunit d, putative
Afu3g13980	3.11	2.86	2.59	glucose transporter
Afu3g14030	1.09	1.63	2.18	alkaline phosphatase
Afu3g14170	1.77	2.26	2.86	high-affinity hexose transporter
Afu3g14180	2.99	2.99	2.13	hypothetical protein
Afu3g14190	2.08	2.46	2.04	hypothetical protein
Afu3g14200	1.32	3.36	2.14	hypothetical protein
Afu3g14320	2.45	1.96	2.04	Golgi transport protein Sly1, putative
Afu3g14440	1.36	2.47	1.86	cytochrome c oxidase family protein
Afu3g14460	1.22	1.12	2.01	Rad51 family DNA repair protein, putative
Afu3g14470	1.77	1.59	2.4	Pyridoxal-phosphate dependent enzyme, putative
Afu3g14510	1.63	2.9	3.66	rhamnogalacturonan acetylesterase, putative
Afu3g14520	2.07	2.29	2	enoyl-CoA hydratase/isomerase family protein
Afu3g14570	2	1.89	2.78	histidine acid phosphatase, putative
Afu3g14590	2.66	2.93	3.48	copper amine oxidase
Afu3g14600	0.58	1.38	2.02	fungal specific transcription factor, putative
Afu3g14650	0.32	2.8	2.55	hypothetical protein
Afu3g14660	0.48	2.23	1.74	hypothetical protein
Afu3g14670	1.76	1.72	3.47	MFS transporter, putative
Afu3g14680	-1	2.86	2.69	lysophospholipase Plb3
Afu3g14730	0.18	1.06	2.1	LysR family regulatory protein, putative
Afu3g14740	1.22	1.38	2.28	conserved hypothetical protein
Afu3g14920	2.92	3.23	3.38	LaeA-like methyltransferase, putative
Afu3g15210	0.78	3.63	3.4	endo-1,4-beta-xylanase, putative

Afu3g15230	2.85	1.55	2.38	general amidase, putative
Afu3g15340	0.48	1.29	2.14	hypothetical protein
Afu4g00150	3.93	4.5	4.84	MFS maltose transporter, putative
Afu4g00370	2.19	2.11	2.33	general amidase, putative
Afu4g00390	0.79	3.05	3.38	glycosyl hydrolase, putative
Afu4g00460	2.13	1.73	1.32	chlorohydrolase family protein, putative
Afu4g00610	2.16	4.53	5.4	aryl-alcohol dehydrogenase, putative
Afu4g00620	2.04	1.39	1.79	glycosyl hydrolase, putative
Afu4g00630	2.11		1.41	aminotransferase, putative
Afu4g00700	1.97	2.43	2.73	oxidoreductase, zinc-binding
Afu4g00800	4.81	4.53	4.35	MFS monosaccharide transporter, putative
Afu4g00830	1	2.35	2.47	MFS peptide transporter, putative
Afu4g00980	-1.95	2.73	3.2	hypothetical protein
Afu4g00990	1.28	3.05	4.4	MFS quinate transporter, putative
Afu4g01000	-0.05	1.4	2.39	MFS transporter, putative
Afu4g01060	0.05	1.13	2.34	hypothetical protein
Afu4g01070	1.01	1.7	3.53	acid phosphatase, putative
Afu4g01140	2.45	3.28	4.36	MFS multidrug transporter, putative
Afu4g01280	0.73	1.19	2.3	hypothetical protein
Afu4g01290	1.87	4.41	4.68	endo-chitosanase, pseudogene
Afu4g01370	1.06	1.94	3.82	hypothetical protein
Afu4g01440	-0.27	0.77	4.05	glutathione S-transferase family protein
Afu4g01470	0.86	2.14	3.31	C6 finger domain protein, putative
Afu4g01550	2.71	3.36	3.58	aldehyde dehydrogenase, putative
Afu4g01580	1.04	2.59	1.82	ankyrin repeat protein
Afu4g05940	2.21	2.17	2.82	phosphoethanolamine
Afu4g05970	1.48	1.82	2.77	para-hydroxybenzoate-polyprenyltransferase precursor
Afu4g06020	1.71	1.92	2.01	cyclin dependent kinase inhibitor (Nuc-2), putative
Afu4g06190	2.27	2.26	2.94	fungal specific transcription factor, putative
Afu4g06380	2.72	1.91	2.13	sterol carrier protein, putative
Afu4g06460	2.12	3.01	3.65	pentafunctional AROM polypeptide, putative
Afu4g06640	0.23	3.53	4.07	acid sphingomyelinase
Afu4g06670	2.74	2.21	2.24	allergen Asp F7
Afu4g06860	1.75	3.26	3.23	conserved hypothetical protein
Afu4g06910	3.31	3.04	2.91	outer mitochondrial membrane protein porin
Afu4g07010	2.51	1.36	1.55	hydrolase, TatD family protein, putative
Afu4g07080	2.01	0.55	0.49	dual specificity phosphatase, putative
Afu4g07130	2.67	1.99	1.67	diphosphomevalonate decarboxylase

Afu4g07140	2.14	1.39	1.51	iki3 protein
Afu4g07190	2.24	1.6	1.31	ornithine carbamoyltransferase
Afu4g07320	0.34	1.45	2.11	conserved hypothetical protein
Afu4g07460	2.23	1.51	1.13	cytoskeleton organisation protein (Dec1), putative
Afu4g07690	4.01	2.73	2.58	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
Afu4g07710	2.11	1.85	2.37	pyruvate carboxylase, putative
Afu4g07740	2.17	0.81	0.44	small nuclear ribonucleoprotein SmB, putative
Afu4g07760	2.31	0.98	0.54	Transmembrane amino acid transporter protein family
Afu4g07790	1.38	2.08	2.26	hypothetical protein
Afu4g07810	1.96	1.98	2.56	L-serine dehydratase, putative
Afu4g07940	2.68	3.37	3.54	oxidoreductase, 2-nitropropane dioxygenase family, putative
Afu4g07990	2.22	0.99	1.59	CobW domain protein
Afu4g08010	1.4	0.98	2.02	ornithine decarboxylase
Afu4g08020	1.4	2.01	2.34	hypothetical protein
Afu4g08030	2.17	0.99	0.66	conserved hypothetical protein
Afu4g08070	2.4	0.9	0.2	peptide N-myristoyl transferase (Nmt1)
Afu4g08170	1.82	2.61	3.32	succinate-semialdehyde dehydrogenase, putative
Afu4g08240	2.21	0.49	0.01	alcohol dehydrogenase, zinc-containing
Afu4g08320	2.08	0.53	-0.5	tyrosyl-tRNA synthetase, mitochondrial precursor (tyrosine--tRNA ligase) (tyrrs)
Afu4g08460	2.14	0.21	0.18	conserved hypothetical protein
Afu4g08580	2.86	3.26	2.96	antioxidant protein LsfA
Afu4g08600	3.04	2.82	2.3	aldehyde dehydrogenase, putative
Afu4g08610	2.54	2.22	2.29	regucalcin homolog [imported]
Afu4g08710	4.02	3.93	4.39	short chain dehydrogenase, putative
Afu4g09200	2.42	2	3.37	hypothetical protein
Afu4g09210	1.79	2.49	2.82	phosphate transporter
Afu4g09300	0.41	2.15	3.44	hypothetical protein
Afu4g09320	1.2	4.13	3.32	antigenic dipeptidyl-peptidase Dpp4
Afu4g09350	3.08	2.45	2.92	hypothetical protein
Afu4g09360	3.12	2.67	3.1	ATP synthase proteolipid P2, putative
Afu4g09390	1.68	2.15	0.87	conserved hypothetical protein
Afu4g09440	0.75	1.5	2.31	sodium P-type ATPase, putative
Afu4g09450	0.13	2.74	3.21	hypothetical protein
Afu4g09560	1.41	2.75	3.02	ZIP Zinc transporter, putative
Afu4g09580	1.6	3.65	4.1	major allergen Asp F2
Afu4g09790	2.76	0.56	0.54	hypothetical protein

Afu4g10120	2.41	2.39	3	C6 finger domain protein, putative
Afu4g10130	2	3.91	4.06	alpha-amylase (Amy1), putative
Afu4g10140	1.19	2.34	2.48	glucoamylase
Afu4g10150	4.91	6.35	5.88	alpha-glucosidase
Afu4g10160	2.8	3.57	3.75	C6 transcription factor (AmyR), putative
Afu4g10230	1.56	2.24	3.42	conserved hypothetical protein
Afu4g10410	3.17	2.74	3.06	aspartate aminotransferase, putative
Afu4g10830	2.07	0.5	0.76	SNF2 family helicase, putative
Afu4g10840	2.02	1.62	1.3	conserved hypothetical protein
Afu4g11050	2.31	1.48	0.91	NADH-ubiquinone oxidoreductase, subunit F, putative
Afu4g11190	2.66	2.01	2.23	kynurenine aminotransferase, putative
Afu4g11240	2.67	2.22	2.83	alpha-aminoadipate reductase large subunit, putative
Afu4g11320	0.61	1.57	2.43	hypothetical protein
Afu4g11330	1.98	2.07	1.93	Aha1 domain family
Afu4g11340	3.04	1.76	1.32	saccharopine dehydrogenase
Afu4g11380	2.25	1.86	2.86	hypothetical protein
Afu4g11400	0.66	2.18	2.52	cell surface receptor/MFS transporter (FLVCR), putative
Afu4g11460	3.2	2.72	2.99	aminotransferase, classes I and II, putative
Afu4g11550	4.05	3.21	2.51	hypothetical protein
Afu4g11620	2.35	3.92	3.85	conserved hypothetical protein
Afu4g11750	1.13	2.16	2	hypothetical protein
Afu4g11780	2.01	1.44	1.69	major facilitator superfamily, putative
Afu4g11870	2.38	1.29	1.16	tubulin-specific chaperone, putative
Afu4g11890	2.67	2.16	2.09	serine/threonine protein kinase, putative
Afu4g11910	2.66	1.37	0.83	N-terminal acetyltransferase catalytic subunit (NAT1), putative
Afu4g12000	2.84	2.46	1.79	phosphatidylinositol phospholipase C
Afu4g12150	2.31	2.71	2.42	HIT domain protein
Afu4g12170	2.62	1.58	1.74	ribosomal protein L2
Afu4g12370	1.7	1.96	2.71	hypothetical protein
Afu4g12450	2.05	0.91	1.04	lysine-rich protein
Afu4g12570	2.06	1.94	2.02	C6 transcription factor, putative
Afu4g12670	1.98	2.18	1.73	DNA repair protein rad1, putative
Afu4g12840	3.42	3.35	2.87	class II aldolase/adducin domain protein
Afu4g12850	3.23	2.8	2.47	calnexin
Afu4g12880	2.17	3.22	2.76	hypothetical protein
Afu4g12900	1.99	2.15	2.08	alpha-1,6-mannosyltransferase subunit (Ecm39), putative
Afu4g12920	2.16	0.57	0.5	histidyl-tRNA synthetase, mitochondrial precursor
Afu4g12930	2.02	1.03	0.58	ubiquinone biosynthesis monooxgenase (Coq6), putative

Afu4g13080	2.62	2.25	1.8	monosaccharide transporter
Afu4g13090	2.24	2.07	3.2	MFS transporter, putative
Afu4g13170	2.25	1.36	1.08	guanine nucleotide-binding protein subunit, putative
Afu4g13390	2.99	1.79	1.53	actin-related protein ArpA
Afu4g13520	0.38	1.53	2.13	oxidoreductase, short-chain dehydrogenase/reductase family
Afu4g13580	3.51	3.91	3.44	gamma-glutamyltranspeptidase
Afu4g13720	2.28	1.71	1.47	MAP kinase (MpkA), putative
Afu4g13770	2.32	1.95	3.29	glycosyl hydrolase, putative
Afu4g13780	1.41	1.26	3.02	polyphenol monooxygenase, putative
Afu4g13880	4.11	1.84	0.85	ankyrin repeat protein
Afu4g13900	3.93	2.78	2.37	MFS transporter, putative
Afu4g13930	1.72	1.83	2.37	CRAL/TRIO domain protein
Afu4g13950	-0.11	1.68	2.47	GNAT family acetyltransferase, putative
Afu4g13960	2.54	1.97	2.78	2-dehydropantoate 2-reductase
Afu4g14000	2.41	5.62	5.86	tripeptidyl peptidase A
Afu4g14010	3.21	3.38	4.91	oxidoreductase, short chain dehydrogenase/reductase family superfamily
Afu4g14070	0.37	1.45	3.55	glycosyl transferase, putative
Afu4g14090	1.62	2.92	4.49	UDP-glucose 4-epimerase
Afu4g14120	1.62	2.15	1.85	cutinase, putative
Afu4g14150	0.77	1	2.58	Diacylglycerol acyltransferase family
Afu4g14420	1.53	2.92	3.57	secreted glycosyl hydrolase, putative
Afu4g14670	1.8	2.39	3.62	MFS quinate transporter, putative
Afu4g14730	-0.32	2.32	3.32	GNAT family acetyltransferase, putative
Afu4g14800	0.86	1.44	2.23	short chain dehydrogenase, putative
Afu5g00220	2.08	2.04	2.14	hypothetical protein
Afu5g00290	5.04	4.97	5.13	C6 transcription factor, putative
Afu5g00300	4.94	4.59	4.18	zinc-binding oxidoreductase, putative
Afu5g00310	3.73	2.28	1.5	flavin-containing monooxygenase, putative
Afu5g00390	2.52	2.58	3.35	hypothetical protein
Afu5g00480	2.41	2.51	3.56	fructan beta-fructosidase, putative
Afu5g00550	0.47	1.39	2.57	endoglycoceramidase, putative
Afu5g00600	1.12	1.8	2.69	NPP1 domain protein, putative
Afu5g00640	1.82	2.39	1.97	peroxisomal dehydratase, putative
Afu5g00710	0.67	2.19	3.3	GABA permease, putative
Afu5g00720	1.37	2.54	2.12	acetyltransferase, GNAT family family
Afu5g00980	3.06	2.27	3.03	multidrug resistant protein
Afu5g01000	2.43	2.05	2.28	oxidoreductase, 2OG-Fe(II) oxygenase family, putative

Afu5g01030	1.99	2.6	4.39	glyceraldehyde 3-phosphate dehydrogenase (Ccg-7), putative
Afu5g01090	2.07	0.93	1.75	UPF0075 domain protein
Afu5g01200	0.72	5.02	6.25	carboxypeptidase S1, putative
Afu5g01320	0.81	1.96	3.25	phosphate permease
Afu5g01440	0.7	2.87	2.77	allergen, putative
Afu5g01580	1.44	3.26	1.3	oxidoreductase, short chain dehydrogenase/reductase family
Afu5g01600	1.29	2.63	4.08	PHP domain protein
Afu5g01630	2.78	2.85	3.27	major facilitator superfamily
Afu5g01690	0.89	2.27	1.71	conserved hypothetical protein
Afu5g01880	3.36	3.27	3.31	conserved hypothetical protein
Afu5g01910	1.47	2.15	3.25	aldo-keto reductase (AKR), putative
Afu5g01970	2.16	1.16	1.54	glyceraldehyde 3-phosphate dehydrogenase GpdA
Afu5g02020	3.25	3.46	2	aldehyde reductase (GliO), putative
Afu5g02230	3.06	1.46	1.41	actin interacting protein 2
Afu5g02310	1.12	1.3	2.03	alpha/beta hydrolase, putative
Afu5g02350	2.52	3.34	3.16	hydrolase, carbon-nitrogen family, putative
Afu5g02450	3.18	1.83	0.57	farnesyl-pyrophosphate synthetase
Afu5g02490	2.02	1.4	1.52	zinc-binding oxidoreductase, putative
Afu5g02510	2.17	1.65	1.42	conserved hypothetical protein
Afu5g02700	1.13	0.55	2.23	multidrug resistant protein
Afu5g02750	1.39	2.13	1.9	cytochrome c oxidase subunit Va, putative
Afu5g02790	2.05	1.3	1.61	amino acid permease
Afu5g02830	1.71	1.17	2.12	NA
Afu5g02840	2.9	2.14	2.54	sugar transporter family protein, putative
Afu5g02850	3.62	4.17	4.49	conserved hypothetical protein
Afu5g02930	3.45	4.11	5	lysophospholipase, putative
Afu5g02940	3.94	3.71	2.71	choline transport protein Ctr, putative
Afu5g02950	3.19	2.59	2.99	conserved hypothetical protein
Afu5g02960	2.64	3.26	2.97	hypothetical protein
Afu5g03020	3.43	2.05	1.84	60s ribosomal protein l2
Afu5g03030	2	1.31	0.9	C6 transcription factor, putative
Afu5g03080	2.4	2.1	1.89	septin
Afu5g03110	2.3	2.54	2.13	conserved hypothetical protein
Afu5g03130	3.07	1.33	0.82	chromatin assembly factor 1 subunit C, putative
Afu5g03380	2.81	1.68	1.82	flavin dependent monooxygenase, putative
Afu5g03470	2.61	1.29	0.65	tRNA-guanine transglycosylases, various specificities domain protein
Afu5g03490	2.34	3	2.32	nucleoside diphosphate kinase

Afu5g03500	3.05	2.41	2.51	alpha glucosidase II, alpha subunit, putative
Afu5g03540	1.61	1.6	2.43	pyridine nucleotide-disulphide oxidoreductase, class II, putative
Afu5g03550	3.55	2.57	2.87	plasma membrane H(+)ATPase, putative
Afu5g03560	2.02	1.4	0.4	glutamyl-tRNA synthetase
Afu5g03750	3.44	4.85	4.82	WW domain protein
Afu5g03760	3.22	4.36	3.62	class III chitinase ChiA1
Afu5g03780	0.89	2.42	4.05	L-PSP endoribonuclease family protein (Brt1), putative
Afu5g03800	2.8	2.26	3.08	high-affinity iron permease CaFTR2
Afu5g03920	2.1	0.75	0.89	bZIP transcription factor (HapX), putative
Afu5g03990	2.1	0.91	0.61	aspartyl aminopeptidase
Afu5g04080	2.57	1.44	1.43	oxidosqualene:lanosterol cyclase
Afu5g04210	3.14	1.61	2.07	ubiquinol-cytochrome C reductase complex core protein 2, putative
Afu5g04220	2.12	1.12	2.3	mitochondrial DNA replication protein (Yhm2), putative
Afu5g04230	2.24	1.33	1.39	citrate synthase, eukaryotic
Afu5g04240	2.19	0.29	0.49	RNA binding protein Nrd1, putative
Afu5g04250	3.67	3.38	2.73	homocysteine synthase, putative
Afu5g04330	2.24	1.41	2.13	aminopeptidase, putative
Afu5g05810	3.23	1.54	1.3	homoserine kinase
Afu5g05820	2.77	0.79	0.61	homoserine kinase
Afu5g06300	2.43	0.74	0.37	Pex3p
Afu5g06420	2.57	1.95	1.99	MAP kinase kinase kinase Ste11
Afu5g06500	3.05	2.55	2.44	acyl-CoA dehydrogenase family protein
Afu5g06530	2.13	1.34	1.85	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
Afu5g06600	2.18	1.21	1.75	SNF2 family helicase/ATPase, putative
Afu5g06610	1.93	2.09	2.32	glutathione synthetase
Afu5g06670	1.74	2.75	3.23	related to L-fucose permease, putative
Afu5g06680	0.02	2.87	2.61	4-aminobutyrate aminotransferase
Afu5g06910	0.85	3.53	4.6	DUF636 domain protein
Afu5g06990	2.08		1.6	catecholamine-O-methyltransferase, putative
Afu5g07290	2.54	1.72	1.71	NADPH-dependent FMN and FAD containing oxidoreductase
Afu5g07300	1.91	2.56	2.87	electron transfer flavoprotein, beta subunit [imported]
Afu5g07330	2.92	2.53	2.68	carboxypeptidase S1, putative
Afu5g07400	3.13	2.48	1.93	phenylacetyl-CoA ligase PclA, putative
Afu5g07550	1.6		2.27	hypothetical protein
Afu5g07560	1.89	1.46	2.14	capsular associated protein, putative
Afu5g07580	1.37	1.69	2.61	methylmalonyl-CoA decarboxylase, alpha subunit, putative
Afu5g07600	2.46	1.28	2.04	SH2-containing inositol 5-phosphatase 2
Afu5g07610	1.1	2.48	3.35	NA

Afu5g07620	2.44	3.38	3.91	DUF1212 domain membrane protein
Afu5g07630	1.86	2.13	2.93	ubiE/COQ5 methyltransferase, putative
Afu5g07640	1.28	2.12	2.65	RNA 3'-terminal phosphate cyclase, putative
Afu5g07690	1.99	2.3	1.75	conserved hypothetical protein
Afu5g07700	-0.13	2.07	1.93	NA
Afu5g07710	2.04		0.98	nuclear migration protein (ApsA), putative
Afu5g08050	2.21	0.38	0.73	aminopeptidase P, putative
Afu5g08120	1.5	2.53	3.42	arginine biosynthesis bifunctional protein ArgJ
Afu5g08250	2.54	2.16	2.82	hypothetical protein
Afu5g08610	2.97	1.91	1.42	ThiF domain protein, putative
Afu5g08620	2.1	1.55	2.13	Ser/Thr protein phosphatase family
Afu5g08630	2.23	1.84	2.21	LCCL domain protein
Afu5g08770	2.34	1.65	2.45	hypothetical protein
Afu5g08800	1.24	1.58	2.93	hypothetical protein
Afu5g08810	0.98	2.01	3.26	epoxide hydrolase, putative
Afu5g08830	1.17	3.84	3.42	HEX1
Afu5g08900	1.73	2.65	2.46	D-arabinitol dehydrogenase ArbD, putative
Afu5g08950	1.26	1.62	2.03	RAS small monomeric GTPase (Rsr1), putative
Afu5g08990	2.68			transcription factor RfeG, putative
Afu5g09020	3.31	2.45	2.71	WSC domain protein, putative
Afu5g09070	0.89	2.31	1.67	hypothetical protein
Afu5g09130	3.06	3.62	3	polysaccharide deacetylase family protein
Afu5g09140	3.7	3.91	3.71	amidase, putative
Afu5g09150	3.24	2.92	2.87	oxidoreductase, short-chain dehydrogenase/reductase family
Afu5g09250	2.58	1.62	1.05	transcription factor (Snd1/p100), putative
Afu5g09280	3.17	1.77	2.87	conserved hypothetical protein
Afu5g09290	3.27	3.34	3.6	NAD-dependent 15-hydroxyprostaglandin dehydrogenase
Afu5g09330	2.5	4.46	4.26	CipC protein
Afu5g09340	1.77	3.41	3.21	Phospholipase/Carboxylesterase superfamily
Afu5g09400	4.78	4.97	4.73	carbonyl reductase, putative
Afu5g09530	1.64	2.22	2.41	conserved hypothetical protein
Afu5g09560	1.32	1.28	2.23	ankyrin repeat protein (Yar1), putative
Afu5g09600	2.17	2.63	2.15	2-nitropropane dioxygenase family oxidoreductase, putative
Afu5g09720	2.22	0.93	1.73	flavin containing polyamine oxidase, putative
Afu5g09790	1.93	1.63	2.37	beta-lactamase
Afu5g09800	1.57	2.64	3.77	hypothetical protein
Afu5g09860	2.2	2.5	2.25	esterase, putative
Afu5g10010	3.3	4.95	4.53	extracellular serine-threonine rich protein

Afu5g10020	3.59	3.7	4.82	sensor histidine kinase/response regulator, putative
Afu5g10280	2.92	2.77	2.65	oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor
Afu5g10290	2.77	3.37	3.36	fructose-bisphosphate aldolase, putative
Afu5g10320	3.59	2.33	3.94	toxin biosynthesis protein (GliH), putative
Afu5g10340	2.83	2.22	3.32	MFS transporter, putative
Afu5g10350	1.65	2.15	2.53	conserved hypothetical protein
Afu5g10430	1.47	1.69	2.28	MSF multidrug transporter, putative
Afu5g10450	2.02	1.06	0.88	hypothetical protein
Afu5g10460	2.37	0.43	0.76	hypothetical protein
Afu5g10520	1.36	2.48	3.83	alpha-1,2-mannosidase family protein
Afu5g10550	3.13	2.16	1.66	ATP synthase F1, beta subunit, putative
Afu5g10560	3.43	3.56	3.31	cytochrome c oxidase subunit V
Afu5g10580	3.57		1.54	SH3 domain protein
Afu5g10890	2.39	2.47	2.79	DNA replication licensing factor Mcm6, putative
Afu5g10960	0.93	1.37	2.08	conserved hypothetical protein
Afu5g11230	2.17	1.41	1.66	RAS small monomeric GTPase Ras
Afu5g11240	4.23	3.84	4.06	oxidoreductase, short chain dehydrogenase/reductase family
Afu5g11400	2.74	2.13	2.16	mRNA cleavage factor complex II protein Clp1, putative
Afu5g11430	1.65	1.56	2.34	quinone oxidoreductase, putative
Afu5g11440	1.62	1.46	2.37	hypothetical protein
Afu5g11610	3.33	2.51	2.55	shk1 kinase-binding protein 1
Afu5g11810	0.44	2.06	1.97	cytoplasmic dynein heavy chain
Afu5g11850	3.49	3.48	3.83	mitochondrial carrier protein (Pet8), putative
Afu5g11940	2.74	1.58	1.52	beta-tubulin cofactor D, putative
Afu5g12370	2.91	1.69	1.55	WD repeat protein
Afu5g12460	2.9	1.94	2.18	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase, putative
Afu5g12480	3.95	3.5	3.74	short chain dehydrogenase/reductase family
Afu5g12620	2.63	0.87	0.56	CorA family metal ion transporter, putative
Afu5g12660	3.18			phosphotidylinositol kinase Tel1, putative
Afu5g12690	3.25	3.35	3.24	dihydroxyacetone kinase (DakA), putative
Afu5g12720	2.22	2.3	3	ABC drug transporter, putative
Afu5g12770	2.88	3.38	1.89	metallo-beta-lactamase family protein
Afu5g12790	1.94	2.04	2.58	mitochondrial 3-hydroxyisobutyryl-CoA hydrolase, putative
Afu5g12860	1.48	2.51	3.49	hypothetical protein
Afu5g12940	0.07	0.47	2.04	arylsulfatase, putative
Afu5g13000	2.91	1.58	1.15	CRAL/TRIO domain protein

Afu5g13060	-0.65	0.58	2.16	DUF1275 domain protein
Afu5g13170	3.61	2.42	2.6	MATE efflux family protein subfamily, putative
Afu5g13180	5.53			agmatinase, putative
Afu5g13300	5	6.42	6.94	aspartic endopeptidase Pep1
Afu5g13370	2.38	1.97	1.75	mitochondrial DNA helicase (Pif1), putative
Afu5g13450	2.58	1.92	1.17	triosephosphate isomerase
Afu5g13570	1.17	1.11	2.06	conserved hypothetical protein
Afu5g13640	0.25	1.37	2.06	thioredoxin, putative
Afu5g13800	1.36	3.07	3.66	transcriptional regulator, putative
Afu5g13810	3.22	3.71	3.56	transulfuration enzyme family protein, putative
Afu5g13920	1.68	2.23	2.05	p21 protein
Afu5g13940	1.11	1.7	2.29	FAD dependent oxidoreductase superfamily
Afu5g14060	1.77	2.12	1.84	Rho GTPase Rho4, putative
Afu5g14230	0.86	2.08	3.11	C6 transcription factor, putative
Afu5g14240	1.7	2.98	4.42	ThiJ/PfpI family protein
Afu5g14500	2.2	2.55	3.79	MFS transporter, putative
Afu5g14510	2.05	3.09	4.3	beta-lactamase, putative
Afu5g14530	0.79	2.06	3.7	C6 transcription factor, putative
Afu5g14550	3.07	3.44	3.78	beta-galactosidase, putative
Afu5g14660	-1.68	1.03	2.4	GABA permease, putative
Afu5g14680	2.11	4.13	3.24	hypothetical protein
Afu5g14690	1.96	3.12	2.26	phosphorylase, putative
Afu5g14720	2.79	1.83	1.91	conserved hypothetical protein
Afu5g15030	2.17	1.33	1.74	arsenic resistance protein ArsH
Afu6g00140	1.33	1.72	2.12	hypothetical protein
Afu6g00240	2.6	2.8	3.42	4-hydroxyphenylpyruvate dioxygenase, putative
Afu6g00260	5.59	4.13	5.19	phosphatidylserine decarboxylase family protein
Afu6g00290	1.52	4.06	5.59	aminotransferase, putative
Afu6g00300	2.22	2.53	3.56	serine palmitoyltransferase 1, putative
Afu6g00310	0.98	3.21	4.13	serine carboxypeptidase (CpdS), putative
Afu6g00430	-0.12	3.83	4.2	IgE-binding protein
Afu6g00580	2.86	1.89	3.17	ankyrin repeat protein
Afu6g00600	1.61	1.9	2.54	hypothetical protein
Afu6g00620	3.53	4.82	4.95	GPI anchored hypothetical protein
Afu6g00630	5.07	5.49	6.15	MFS transporter, putative
Afu6g00640	4.19	4.5	5.41	integral membrane protein
Afu6g00650	3.14	3.42	4.05	hypothetical protein
Afu6g00660	2.1	0.06	0.02	conserved hypothetical protein

Afu6g00680	0.81	2.87	2.56	hypothetical protein
Afu6g00710	2.13	3.02	3.86	MFS transporter, putative
Afu6g00740	1.97	2.81	2.23	hypothetical protein
Afu6g00750	1.45	3.52	3.21	pyruvate decarboxylase, putative
Afu6g01820	2.79	3.05	4.55	MFS transporter, putative
Afu6g01830	1.59	1.98	3.34	O-methyltransferase, putative
Afu6g01840	1.14	2.52	2.59	C6 transcription factor, putative
Afu6g01850	0.51	1.31	2.32	hypothetical protein
Afu6g01900	0.39	1.57	2.27	hypothetical protein
Afu6g01940	2	1	0.22	conserved hypothetical protein
Afu6g02030	1.62	2.72	3.29	aminotransferase, putative
Afu6g02230	2.68	1.82	1.4	glucokinase GlkA, putative
Afu6g02240	2.37	2.09	2.18	protein kinase, putative
Afu6g02260	2.38	3.51	3.22	hypothetical protein
Afu6g02400	0.81	2.16	2.61	MFS drug efflux pump, putative
Afu6g02410	2.1	1.72	1.53	WD repeat protein
Afu6g02470	1.97	2.25	1.9	fumarate hydratase, putative
Afu6g02560	2.09	1.52	1.88	alpha-galactosidase
Afu6g02600	3.53	2.93	3.09	phosphoglycerate mutase family protein
Afu6g02610	2.32	1.44	1.45	conserved hypothetical protein
Afu6g02750	1.64	2.13	1.32	nascent polypeptide-associated complex (NAC) subunit, putative
Afu6g02850	0.49	1.42	2.2	C6 finger domain protein, putative
Afu6g02890	2.25	1.8	2.05	hypothetical protein
Afu6g02910	2.34	1.78	2.09	acetylglutamate kinase, putative
Afu6g02940	2.2	2.19	2.38	chitin synthase activator (Chs3), putative
Afu6g02980	2.81	2.24	0.32	extracellular exo-polygalacturonase, putative
Afu6g03040	2.66	1.76	2.13	MSF multidrug transporter, putative
Afu6g03060	3.5	4.2	4.15	monosaccharide transporter
Afu6g03100	0.28	1.44	2.02	hypothetical protein
Afu6g03170	3.76	4.93	5.49	NA
Afu6g03180	3.47	4.57	5.01	hypothetical protein
Afu6g03190	1.93	4.63	5.31	hypothetical protein
Afu6g03200	1.62	4.06	4.38	solute symporter family transporter
Afu6g03230	0.82	2.97	2.07	cell wall glucanase, putative
Afu6g03260	1.85	2.17	2.49	aspartic endopeptidase (AP1), putative
Afu6g03340	1.15	2.58	2.82	hypothetical protein
Afu6g03350	-1.74	0.69	2.16	acetyltransferase, GNAT family, putative
Afu6g03420	3.05	3.43	3.37	trehalose synthase, putative

Afu6g03470	0.32	2.25	3.42	ABC multidrug transporter, putative
Afu6g03510	0.72	1.36	2.13	polyamine oxidase, putative
Afu6g03520	3.07	2.57	2.79	short-chain dehydrogenase/reductase family protein, putative
Afu6g03560	0.98	1.86	2.09	IgE-binding protein, putative
Afu6g03570	2.7	2.94	3.56	beta-glucosidase 3
Afu6g03590	2.12	2.76	2.57	methylcitrate synthase
Afu6g03600	2.18	2.75	2.28	integral membrane protein (Pth11), putative
Afu6g03680	2.1	3.89	4.01	hypothetical protein
Afu6g04040	1.89	2.61	2.48	peroxisomal D3,D2-enoyl-CoA isomerase
Afu6g04250	2.7	3.35	3.33	Protein required for hyphal anastomosis
Afu6g04270	4.39	2.49	2.59	fructose symporter
Afu6g04380	2.07	0.32	-0.11	molecular chaperone (ABC1), putative
Afu6g04570	2.17	0.66	0.5	elongation factor 1-gamma 2
Afu6g04740	2.28	1.29	1.15	actin, putative
Afu6g04800	2.35	2.8	2.79	lysine decarboxylase-like protein
Afu6g04900	2.58	2.1	1.95	sucrose cleavage family protein
Afu6g04920	3.31	3.59	3.08	NAD-dependent formate dehydrogenase
Afu6g05000	2	1.33	0.88	Glycosyl hydrolases family 32 superfamily
Afu6g05030	2.62	3.8	3.65	polysaccharide deacetylase family protein
Afu6g05130	2.49	2.28	2.54	snRNA cap binding complex subunit (Gcr3), putative
Afu6g05210	2.35	2.32	2.45	malate dehydrogenase, NAD-dependent
Afu6g06360	-0.81	-0.31	2.26	mating alpha-pheromone PpgA
Afu6g06460	2.17	2.23	3.08	fumarylacetoacetate hydrolase family protein
Afu6g06690	2.52	2.66	3.03	CFEM domain protein, putative
Afu6g06700	0.64	1.38	2.17	hypothetical protein
Afu6g06770	3.62	2.67	2.26	enolase
Afu6g06870	0.29	1.21	2.44	casein kinase I homolog, putative
Afu6g07120	0.65	1.8	2.04	nuclear movement protein
Afu6g07340	2.99	2.34	2.13	kynurenine 3-monooxygenase
Afu6g07380	2.01	1.43	0.41	conserved hypothetical protein
Afu6g07430	3.17	1.85	1.76	pyruvate kinase
Afu6g07490	3.81	2.55	2.69	WD repeat protein
Afu6g07540	3.07	1.79	2.46	t-complex protein 1, epsilon subunit, putative
Afu6g07560	2.87	2.63	2.3	hypothetical protein
Afu6g07610	1.8	1.75	2.12	hypothetical protein
Afu6g07620	3.07	3.28	3.38	GDP-mannose pyrophosphorylase A
Afu6g07640	2.74	1.86	1.93	lysyl-tRNA synthetase
Afu6g07670	2.23	0.88	0.42	cytochrome c oxidase assembly protein cox15

Afu6g07740	1.72	1.68	2.12	peroxisomal biogenesis factor (PEX11), putative
Afu6g07750	2.8	3.51	3.32	MFS phospholipid transporter (Git1), putative
Afu6g07760	3.31	2.28	1.74	proteasome regulatory particle subunit (RpnG), putative
Afu6g07770	2.63	2.6	3.25	alanine aminotransferase, putative
Afu6g08000	2	2.18	2.75	general amidase
Afu6g08050	2.6	1.25	0.63	6-phosphogluconate dehydrogenase, decarboxylating
Afu6g08160	1.38	2.3	2.51	MOSC domain protein
Afu6g08440	2.88	2.71	2.73	protoporphyrinogen oxidase, putative
Afu6g08470	1.85	1.76	3.12	glycerol kinase, putative
Afu6g08490	-0.36	1.25	3.4	inorganic diphosphatase, putative
Afu6g08610	1.54	2.09	1.63	RNA methylase family protein, putative
Afu6g08620	2.42	2.15	1.78	Golgi reassembly stacking protein, putative
Afu6g08640	1.88	1.7	2.66	metallopeptidase Mip1
Afu6g08660	2.76	3.08	3.52	hypotetical protein
Afu6g08700	0.29	2.5	2.68	beta glucosidase, putative
Afu6g08710	1.79	2.62	3.43	alkaline phosphatase, putative
Afu6g08840	1.41	2.15	2.42	beta-mannosidase
Afu6g09260	2.18	1.87	2.69	sensor histidine kinase/response regulator, putative
Afu6g09420	1.84	1.04	2.36	conserved hypothetical protein
Afu6g09720	0.01		2.24	methyltransferase GliN
Afu6g09730	1.82	1.16	2.29	cytochrome P450 oxidoreductase GliF
Afu6g09860	1.18	2.63	2.99	hypothetical protein
Afu6g09880	1.36	0.88	2.11	monocarboxylate transporter-like protein
Afu6g09910	2.68	2.57	3.36	glutaminase A
Afu6g09970	1.25	2.16	2.75	oxidoreductase, short chain dehydrogenase/reductase family
Afu6g09990	2.3	1.11	1.71	importin beta-4 subunit, putative
Afu6g10060	1.35	2.07	1.45	F-actin capping protein alpha-1 subunit
Afu6g10070	0.89	1.74	2.11	PEX11 domain protein
Afu6g10080	1.5	3.24	3.55	conserved hypothetical protein
Afu6g10090	2.3	2.92	3.48	D-isomer specific 2-hydroxyacid dehydrogenase family protein
Afu6g10100	1.88	2.24	3.89	related to monocarboxylate transporter, putative
Afu6g10130	0.29	1.08	2.12	N,O-diacetyl muramidase, putative
Afu6g10160	1.88	2.42	3.31	hypothetical protein
Afu6g10210	2.56	2.66	2.83	guanine deaminase, putative
Afu6g10220	2.22	2.47	2.56	small oligopeptide transporter, OPT family
Afu6g10260	2	1.37	0.46	aldehyde reductase (AKR1), putative
Afu6g10340	3.12	3.01	3.89	hypothetical protein
Afu6g10440	2.05	1.69	0.57	hypothetical protein

Afu6g10450	2.25	2.67	1.32	hypothetical protein
Afu6g10660	4.05	2.85	2.64	ATP-citrat-lyase
Afu6g10880	2.17	2.38	1.43	acyl-CoA dehydrogenase, putative
Afu6g11020	3.02	3.48	3.76	3-hydroxyisobutyrate dehydrogenase
Afu6g11190	1.46	1.48	2.01	protein kinase (VPS15), putative
Afu6g11210	1.02	2.3	2.59	3-oxoacyl-(acyl-carrier-protein) reductase
Afu6g11330	2.17	2.6	3.13	histidine acid phosphatase, putative
Afu6g11340	3.86	3	3.75	peroxisomal AMP binding enzyme, putative
Afu6g11420	2.46	3.21	3.66	conserved hypothetical protein
Afu6g11490	2.64	2.95	3.42	NUDIX domain protein
Afu6g11500	2.55	3.15	3.87	dipeptidase, putative
Afu6g11680	1.88	2.27	3.52	thiamine pyrophosphate enzyme, putative
Afu6g11700	2.49	0.97	0.63	hypothetical protein
Afu6g11720	2.32	1.59	2.59	hypothetical protein
Afu6g11860	2.18	0.57	0.91	hypothetical protein
Afu6g11880	1.59	1.3	2.29	conserved hypothetical protein
Afu6g12030	2.79	0.82	1.88	putative rhamnosidase
Afu6g12040	2.26	1.5	2.02	maltose permease, putative
Afu6g12110	0.91	1.15	2.82	salicylate synthetase, putative
Afu6g12120	1.52	2.83	3.81	BNR/Asp-box repeat domain protein
Afu6g12130	0.22	0.84	2.33	C6 transcription factor, putative
Afu6g12150	0.35	1.07	2.05	bZIP transcription factor (Atf7), putative
Afu6g12160	2.92	2.24	1.72	C6 transcription factor, putative
Afu6g12170	0.04	2.09	1.04	FKBP-type peptidyl-prolyl isomerase, putative
Afu6g12180	3.53	2.48	1.77	conserved hypothetical protein
Afu6g12230	1.77	1.95	2.03	conserved hypothetical protein
Afu6g12250	2.86	3.02	3.4	succinyl-CoA:3-ketoacid-coenzyme A transferase (ScoT), putative
Afu6g12300	2.4	1.57	2.54	RNP domain protein
Afu6g12390	2.32	0.91	0.73	serine palmitoyl CoA transferase subunit LcbA
Afu6g12400	2.72	2.16	2.27	1,3-beta-glucan synthase catalytic subunit FksP
Afu6g12420	0.97	2.65	2.32	SprT family metallopeptidase, putative
Afu6g12550	2.8	1.23	0.5	mitochondrial carrier protein, putative
Afu6g12580	2.81	2.58	2.99	anthranilate synthase component I
Afu6g12670	4.46	3.37	3.74	beta-alanine synthase, putative
Afu6g12680	0.62	2.26	1.36	HIT domain protein
Afu6g12700	2.05	1.46	1.25	hypothetical protein
Afu6g12760	2.53	2.93	3.44	GPI transamidase component (GAA1), putative
Afu6g12790	3.03	2.56	2.1	NADH-ubiquinone oxidoreductase 39 kDa subunit, putative

Afu6g12880	1.81	1.76	2.24	hypothetical protein
Afu6g13160	3.01	2.79	2.21	serine/threonine protein kinase, putative
Afu6g13400	1.23	2.93	2.35	arsenate reductase (Arc2), putative
Afu6g13590	3.29	2.58	2.93	3-isopropylmalate dehydrogenase
Afu6g13610	0.05	1.16	2.39	endo-1,4-beta-xylanase, putative
Afu6g13700	1.5	2.82	3.13	hypothetical protein
Afu6g13710	3.26	3.13	3.79	hypothetical protein
Afu6g13750	0.84	2.39	2.03	ferric-chelate reductase, putative
Afu6g13760	0.98	1.48	2.2	alpha-1,2-mannosidase, putative subfamily
Afu6g13790	0.93	1.03	2.12	monooxigenase
Afu6g13830	2.23	2.29	3.37	oxidoreductase, short chain dehydrogenase/reductase family
Afu6g13850	0.81	1.86	2.98	GTPase activating protein (Evi5), putative
Afu6g13900	2.83	1.6	1.54	conserved hypothetical protein
Afu6g14010	2.71	4.77	4.44	GPI anchored protein, putative
Afu6g14020	1.9	3.14	3.02	conserved hypothetical protein
Afu6g14040	2.21	2	1.92	glycosyl transferase, putative
Afu6g14050	1.14	1.66	2.05	FAD binding domain protein
Afu6g14060	1.09	3.35	3.83	hypothetical protein
Afu6g14090	2.35	1.94	0.9	CFEM domain protein, putative
Afu6g14180	2.76	2.31	2.18	beta-1,4-mannosyltransferase (Alg1), putative
Afu6g14330	1.91	2.59	2.63	5-oxo-L-prolinase, putative
Afu6g14390	0.43	2	3.51	extracelular cellulose binding protein (Cip2), putative
Afu6g14400	2.27	1.55	2.87	conserved hypothetical protein
Afu6g14410	2.54	1.1	1.37	amidase family protein
Afu6g14420	0.55	2.1	2.17	disintegrin-like metalloproteinase, putative
Afu6g14440	3.73	5.03	5.13	MFS monosaccharide transporter, putative
Afu6g14480	2.04	3.48	5.04	alpha-1,3-mannosyltransferase, putative
Afu6g14490	0.33	2.09	2.85	beta-glucosidase, putative
Afu6g14500	0.16	3.16	4.71	MFS sugar transporter, putative
Afu6g14510	3.01	2.85	2.83	monooxygenase, putative
Afu6g14530	1.47	3.23	4.07	L-cystine transporter, putative
Afu7g00380	1.18	4.27	4.63	GNAT family acetyltransferase, putative
Afu7g00540	0.7	2.13	2.2	integral membrane protein
Afu7g00550	2.93	2.25	3.2	NACHT and WD40 domain protein
Afu7g00690	0.53	0.09	2.22	aminotransferase, putative
Afu7g00700	2.11	2.3	3.05	aldo-keto reductase (AKR13), puatative
Afu7g00710	2.01	3.24	1.89	oxalate/formate antiporter, putative
Afu7g00780	-0.67	1.05	2.59	MFS monocarboxylate transporter, putative

Afu7g00820	0.84	2.23	3.15	hypothetical protein
Afu7g00850	1.61	3.07	3.68	acetyltransferase, GNAT family, putative
Afu7g00910	2.91	2.02	3.27	peptide transporter MTD1
Afu7g01000	0.52	1.71	2	aldehyde dehydrogenase, putative
Afu7g01010	-0.61	1.03	2.59	alcohol dehydrogenase, putative
Afu7g01070	0.22	1.58	2.28	endo-1,4-beta-mannosidase
Afu7g01090	1.87	3.67	4.2	proline permease
Afu7g01160	0.53	2.01	0.86	cytochrome P450 alkane hydroxylase, putative
Afu7g01180	1	1.18	2.04	extracellular lipase, putative
Afu7g01240	1.08	2.95	4.03	phytase, putative
Afu7g01300	1.77	2.23	2.9	mannosyltransferase (PIG-M), putative
Afu7g01310	2.29	1.77	2.08	C6 transcription factor, putative
Afu7g01460	3.08	1.52	1.99	ribosomal protein S5
Afu7g01530	2	0.94	0.22	fadD36
Afu7g01590	3.06	2.74	2.59	cystathionine gamma-synthase
Afu7g01600	2.83	2.22	2.24	hypothetical protein
Afu7g01680	1.13	2.27	2.65	hypothetical protein
Afu7g01690	1.99	3.58	3.5	acetamidase
Afu7g01720	2.34	0.33	0.4	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase
Afu7g01740	0.86	2.84	3.97	sugar transporter, putative
Afu7g01860	2.19	3.22	2.64	heat shock protein (Sti1), putative
Afu7g01880	2.66	1.8	1.05	nicotinate phosphoribosyltransferase
Afu7g01930	0.71	2.03	2.54	sexual development protein EsdC, putative
Afu7g02180	3.18	2.07	2.63	UDP-N-acetylglucosamine pyrophosphorylase
Afu7g02340	0.75	3.33	3.13	L-PSP endoribonuclease family protein (Hmf1), putative
Afu7g03970	2.68	2.81	2.94	hypothetical protein
Afu7g03990	2.17	1.84	2.09	uridylate kinase
Afu7g04010	2.03	1.04	0.57	conserved hypothetical protein
Afu7g04070	2.21	0.77	1.16	phospho-2-dehydro-3-deoxyheptonate aldolase
Afu7g04110	2.33	1.53	0.75	protein kinase C substrate, putative
Afu7g04180	2.52	2.58	2.8	amine oxidase
Afu7g04190	2.32	0.55	0.32	cyclopropane-fatty-acyl-phospholipid synthase, putative
Afu7g04280	-0.09	2.05	2.25	small nuclear ribonucleoprotein (LSM5), putative
Afu7g04500	3.48	3.46	3.84	ATP phosphoribosyltransferase
Afu7g04570	3.02	5.42	5.33	Na/K ATPase alpha 1 subunit, putative
Afu7g04580	2.39	3.23	3.8	TBC domain protein, putative
Afu7g04600	2.26	1.64	1.77	Rho guanyl nucleotide exchange factor, putative
Afu7g04690	0.98	1.25	2.04	FAD dependent sulfhydryl oxidase Erv2, putative

Afu7g04720	2.43	2.91	3.49	alpha-1,2-mannosidase, putative
Afu7g04730	5.74	6.46	6.78	siderochrome-iron transporter, putative
Afu7g04760	2.43	2.72	3.06	gamma-glutamyltranspeptidase
Afu7g04800	1.56	2.34	2.75	hypothetical protein
Afu7g04820	2.2	1.3	1.44	C6 transcription factor, putative
Afu7g04900	0.99	1.93	2.15	MSF multidrug transporter, putative
Afu7g04910	4.74	6.5	5.6	phosphatidylglycerol specific phospholipase C, putative
Afu7g04960	-0.01	1.37	3.11	N-acetyltransferase, GNAT family, putative
Afu7g04970	0.96	2.52	2.35	metalloreductase, putative
Afu7g05070	3.32	2.76	3.34	FAD dependent oxidoreductase, putative
Afu7g05080	3.13	3.19	3.44	C6 transcription factor, putative
Afu7g05090	3.35	3.41	4.51	glucuronyl hydrolase, putative
Afu7g05100	1.85	3.71	5.05	hexose transporter protein
Afu7g05130	1.44	1.74	2.07	O-methyltransferase
Afu7g05150	4.25	3.67	4.97	hypothetical protein
Afu7g05160	1.48	1.4	2.78	fumarylacetoacetate hydrolase family protein
Afu7g05300	2.48	3.29	3.46	hypothetical protein
Afu7g05370	3.52	2.83	2.35	septin AspB
Afu7g05410	2.18	1.68	1.56	thiamine pyrophosphokinase
Afu7g05440	2.08	0.98	0.94	TOS4, putative
Afu7g05450	3.96	5.03	5.08	SUN domain protein (Uth1), putative
Afu7g05470	2.17	2.55	2.5	electron transfer flavoprotein alpha subunit, putative
Afu7g05550	3.76	3.81	4.43	sugar transporter family protein
Afu7g05610	1.71	2.81	3.07	glucanase, putative
Afu7g05690	2.2	1.71	2.12	NA
Afu7g05720	3.56	2.01	1.79	pyruvate dehydrogenase complex, dihydrolipoamide acetyltransferase component, putative
Afu7g06080	2.12	2.79	2.69	ubiE/COQ5 methyltransferase, putative
Afu7g06140	2.27	5.21		beta-D-glucoside glucohydrolase
Afu7g06160	0.6	2.7	3.62	hypothetical protein
Afu7g06360	-0.23	1.33	2.04	hypothetical protein
Afu7g06380	5.81	7.05	6.43	maltase
Afu7g06390	4.16	5.05	5.54	maltose permease
Afu7g06520	2.13	1.48	1.81	CAIB/BAIF family enzyme
Afu7g06680	1.41	2.47	4.27	AAA family ATPase, putative
Afu7g06740	0.44	1.34	2.43	endoglucanase, putative
Afu7g06750	2.79	5.26	5.42	phosphoglycerate mutase family protein, putative
Afu7g06760	3	2.67	2.8	CRAL/TRIO domain protein

Afu7g06770	2.97	2.06	1.33	hypothetical protein
Afu7g06810	3.93	5.21	5.51	L-amino acid oxidase LaoA, putative
Afu7g06820	0.52	0.75	2.03	galactose oxidase, putative
Afu7g08530	2.58	4.09	3.47	hypothetical protein
Afu7g08540	2.99	1.8	1.59	ankyrin repeat protein
Afu8g00110	2.08	1.72	3.05	oxidoreductase, 2OG-Fe(II) oxygenase family, putative
Afu8g00240	0.63	1.36	2.51	cytochrome P450 monooxygenase, putative
Afu8g00280	0.59	1.14	2.04	short-chain dehydrogenase, putative
Afu8g00370	-0.4	0.65	2.97	polyketide synthase, putative
Afu8g00390	-0.14		2.03	O-methyltransferase, putative
Afu8g00420	-1.42	0.45	2.97	C6 finger transcription factor, putative
Afu8g00430	-1.7	0.1	2.87	conserved hypothetical protein
Afu8g00500			2.35	acetate-CoA ligase, putative
Afu8g00540	0.92	2.12	5.52	hybrid polyketide synthase/nonribosomal peptide synthase, putative
Afu8g00550		1.4	4.92	SirN-like methyltransferase, putative
Afu8g00560	1.32	1.97	4.67	cytochrome P450, putative
Afu8g00570	1.44	0.94	2.55	alpha/beta hydrolase, putative
Afu8g00610	0.46	3.46	3.28	cell surface protein Mas1, putative
Afu8g00640	2.36	1.79	2.2	glycosyl transferase, putative
Afu8g00700	0.79	1.12	2.06	class III chitinase ChiA2
Afu8g00720	2.42	2.14	2.39	amino acid transporter, putative
Afu8g00760	1.47	3.03	3.37	cytochrome P450, putative
Afu8g00770	3.38	5.56	5.39	sugar transporter family protein
Afu8g00790	2.02	3.87	2.91	hypothetical protein
Afu8g00840	1.25	2.08	2.5	amino acid permease, putative
Afu8g00850	2.74	3.66	3.75	dihydroorotase, homodimeric type
Afu8g00890	2.8	1.65	2.94	glucose transporter
Afu8g00910	-0.24	0.51	2.24	conserved hypothetical protein
Afu8g00980	0.07	1.78	2.31	hypothetical protein
Afu8g01030	1.34	1.51	2.65	hypothetical protein
Afu8g01160	2.84	3.37	3.84	tartrate dehydrogenase, putative
Afu8g01580	3.63	4.33	4.68	aminotransferase, classes I and II family
Afu8g01670	0.86	1.89	2.04	bifunctional catalase-peroxidase Cat2
Afu8g01710	3.8	4.74	5.37	antigenic thaumatin domain protein, putative
Afu8g01780	3.07	3.59	3.84	nitrilase, putative
Afu8g01850	-1.36	1.55	2.27	phosphate-repressible phosphate permease
Afu8g01920	-0.05	2.95	2.4	hypothetical protein
Afu8g01970	1.21	2.14	1.93	extracellular endo-polygalacturonase, putative

Afu8g02010	1.88	1.95	2.36	MFS sugar transporter, putative
Afu8g02030	2.43	3.35	4.01	conserved hypothetical protein
Afu8g02090	0.4	2.57	2.87	nucleotide-sugar transporter family protein
Afu8g02200	1.26	3.74	4.18	proline permease
Afu8g02440	1.34	3.15	3.12	C-4 methyl sterol oxidase, putative
Afu8g02450	-0.87	2.27	2.72	hypothetical protein
Afu8g02550	-0.71	2.6	2.46	Ptr2-like MFS peptide transporter, putative
Afu8g02560	-0.53	0.96	2.94	glyceraldehyde-3-phosphate dehydrogenase, putative
Afu8g02610	1.94	1.56	2.13	cytochrome P450 monooxygenase, putative
Afu8g02620	2.68	2.22	2.5	CobW domain protein
Afu8g02760	2.05	1.86	2.76	mitochondrial ornithine carrier protein (AmcA), putative
Afu8g04000	3.17	2.85	3.26	acetyl-coa acetyltransferase
Afu8g04370	3.07	2.34	3.15	GPI anchored protein, putative
Afu8g04380	2.95	3.51	3.65	conserved hypothetical protein
Afu8g04430	2.55	1.84	0.57	oligosaccharyl transferase subunit (Stt3), putative
Afu8g04480	0.71	3.49	4.17	hexose transporter protein
Afu8g04650	0.92	2	2.29	3-hydroxyanthranilate 3,4-dioxygenase
Afu8g04670	2.04	1.51	1.26	serine/threonine protein kinase, putative
Afu8g04700	2.59	4.27	3.95	conserved hypothetical protein
Afu8g04710	2.99	4.33	4.65	xylosidase
Afu8g05040	0.27	2.1	2.6	dihydrodipicolinate synthetase family protein
Afu8g05080	2.5	2.2	2.05	hypothetical protein
Afu8g05280	2.05	2.69	1.75	QDE2 protein
Afu8g05310	0.35	2.12	1.36	DUF962 domain protein
Afu8g05320	3.25	2.1	2.35	mitochondrial F1 ATPase subunit alpha, putative
Afu8g05440	2.41	2.14	2.09	mitochondrial ATPase subunit ATP4, putative
Afu8g05530	2.62	2.31	2.08	soluble fumarate reductase (Osm1), putative
Afu8g05570	2.46	1.78	1.83	transcription factor (Sin3), putative
Afu8g05610	3.5	4.71	4.51	cell wall glucanase (Scw11), putative
Afu8g05630	1.48	2.04	1.73	chitin synthase F
Afu8g05680	1.6	2.73	2.97	serine/threonine protein kinase, putative
Afu8g05690	0.62	2.5	2.83	acetyltransferase, GNAT family family
Afu8g05710	3.54	1.71	2.44	MFS sugar transporter Stl1, putative
Afu8g05760	2.07	1.35	1.49	dehydrogenase
Afu8g05800	-0.24	3	2.07	C6 finger domain protein, putative
Afu8g05850	2.69	3.18	3.56	FAD dependent oxidoreductase superfamily
Afu8g05970	2.3	1.48	2.1	TRI7, putative
Afu8g06090	0.01	1.45	2.58	amino acid permease, putative

Afu8g06130	1.65	1.63	2.29	FluG family protein
Afu8g06160	2.63		0.44	conserved hypothetical protein
Afu8g06410	2.27	1.81	2.48	MFS multidrug transporter, putative
Afu8g06440	-0.27	1.71	2.74	fructosyl amino acid oxidase, putative
Afu8g06460	0.01	2.14	2.6	C6 transcription factor, putative
Afu8g06470	1.16	3.97	4.75	N,N-dimethylglycine oxidase
Afu8g06560	1.54	3.5	4.56	DUF895 domain membrane protein
Afu8g06570	-0.2	2.68	4.31	acetyl xylan esterase, putative
Afu8g06580	0.43	2.62	3.91	GABA permease
Afu8g06590	-0.13	2.54	3.53	hypothetical protein
Afu8g06680		1.87	2.3	acyl-CoA thioesterase
Afu8g06700	1.45	2.26	1.72	annexin ANXC3.1
Afu8g06760	2.96	2.97	3.69	integral membrane protein
Afu8g06770	3.27	3.8	4.17	conserved hypothetical protein
Afu8g06850	0.26	0.97	2.3	conserved hypothetical protein
Afu8g06870	3.03	3.23	3.25	MFS sugar transporter, putative
Afu8g06930	3.18	1.65	1.3	C6 transcription factor, putative
Afu8g07030	2.25	1.55	2.31	endo-1,4-beta-mannosidase, putative
Afu8g07080	-0.46	3.24	-0.25	elastinolytic metalloproteinase Mep
Afu8g07090	3.11	5.75	5.99	extracellular proline-serine rich protein
Afu8g07240	3.27	3.05	3.62	MFS maltose permease, putative
Afu8g07320	0.07	0.9	2.21	hypothetical protein

Table AD.2.1: List of up-regulated genes in the ATCC46645 Δ*pacC* time course. Genes significantly up-regulated were included if showing a fold change of +2 on a $\log_2$ scale at least in one of the time point datasets. T0 vs T4 = 4 hrs, T0 vs T8 hrs = 8 hrs, T0 vs T16 = 16 hrs.

ORFs	**T4 vs T0**	**T8 vs T0**	**T16 vs T0**	**Annotation**	**Functional classification**
Afu4g13880	4.11	1.84	0.85	ankyrin repeat protein	
Afu5g10580	3.57		1.54	SH3 domain protein	
Afu3g13320	3.47	1.88	1.33	40S ribosomal protein S0, putative	structural constituent of ribosome///ribosomal small subunit assembly///translation///cytosolic small ribosomal subunit (sensu Eukaryota)
Afu5g05810	3.23	1.54	1.3	homoserine kinase	
Afu5g12660	3.18			phosphotidylinositol kinase Tel1, putative	inositol or phosphatidylinositol kinase activity///telomere maintenance via telomerase///nucleus///response to DNA damage stimulus

Afu5g02450	3.18	1.83	0.57	farnesyl-pyrophosphate synthetase	isoprenoid biosynthetic process///cytosol///farnesyl diphosphate biosynthetic process///geranyltranstransferase activity///dimethylallyltranstransferase activity///ergosterol biosynthetic process
Afu8g06930	3.18	1.65	1.3	C6 transcription factor, putative	
Afu6g07430	3.17	1.85	1.76	pyruvate kinase	cytosol///pyruvate metabolic process///pyruvate kinase activity///glycolysis
Afu7g01460	3.08	1.52	1.99	ribosomal protein S5	structural constituent of ribosome///regulation of translational fidelity///translation///cytosolic small ribosomal subunit (sensu Eukaryota)
Afu5g03130	3.07	1.33	0.82	chromatin assembly factor 1 subunit C, putative	chromatin silencing at telomere///H3/H4 histone acetyltransferase activity///chromatin assembly or disassembly///cytoplasm///nucleus
Afu5g02230	3.06	1.46	1.41	actin interacting protein 2	D-lactate dehydrogenase (cytochrome) activity///mitochondrial matrix///biological process unknown
Afu4g11340	3.04	1.76	1.32	saccharopine dehydrogenase	lysine biosynthetic process via aminoadipic acid///"saccharopine dehydrogenase (NADP+, L-glutamate-forming) activity"///"saccharopine dehydrogenase (NAD+, L-lysine-forming) activity"///cytoplasm///lysine biosynthetic process
Afu1g06960	3.02	1.46	1.28	pyruvate dehydrogenase complex alpha subunit, putative	pyruvate dehydrogenase (acetyl-transferring) activity///pyruvate dehydrogenase complex///pyruvate metabolic process///mitochondrion
Afu4g13390	2.99	1.79	1.53	actin-related protein ArpA	sporulation (sensu Saccharomyces)///mitochondrion inheritance///budding cell apical bud growth///protein secretion///actin filament reorganization during cell cycle///exocytosis///structural constituent of cytoskeleton///endocytosis///histone acetyltransferase complex///cell wall organization///establishment of mitotic spindle orientation///response to osmotic stress///regulation of transcription from RNA polymerase II promoter///vacuole inheritance///vesicle transport along actin filament///cytokinesis///actin filament///histone acetylation///budding cell isotropic bud growth
Afu7g08540	2.99	1.8	1.59	ankyrin repeat protein	
Afu1g03920	2.99	1.05	0.97	DNA replication licensing factor Mcm3, putative	pre-replicative complex///DNA replication initiation///chromatin binding///cytoplasm///DNA

					unwinding during replication///ATP-dependent DNA helicase activity///nucleus///pre-replicative complex assembly
Afu5g08610	2.97	1.91	1.42	ThiF domain protein, putative	biological process unknown///coenzyme binding
Afu3g04170	2.94	1.5	1.67	pyruvate dehydrogenase E1 beta subunit, putative	pyruvate dehydrogenase (acetyl-transferring) activity///pyruvate dehydrogenase complex///pyruvate metabolic process///mitochondrion///binding
Afu1g12840	2.93	1.23	1.03	nitrite reductase	nitrate assimilation///nitrite reductase (NO-forming) activity
Afu2g17000	2.92		1.27	PT repeat family protein	
Afu2g02100	2.91	1.89	1.76	dihydrolipoamide dehydrogenase	valine catabolic process///glycine catabolic process///acetyl-CoA biosynthetic process from pyruvate///L-serine biosynthetic process///leucine catabolic process///mitochondrial matrix///mitochondrial pyruvate dehydrogenase complex///isoleucine catabolic process///dihydrolipoyl dehydrogenase activity
Afu5g12370	2.91	1.69	1.55	WD repeat protein	histone-lysine N-methyltransferase activity///mRNA cleavage and polyadenylation specificity factor complex///"termination of RNA polymerase II transcription, poly(A)-independent"///"termination of RNA polymerase II transcription, poly(A)-coupled"///histone methylation
Afu5g13000	2.91	1.58	1.15	CRAL/TRIO domain protein	lipid particle///response to drug///sterol biosynthetic process///phosphatidylinositol transporter activity///phospholipid transport///cytoplasm///microsome
Afu1g03910	2.89	0.98	0.68	hypothetical protein	
Afu1g04510	2.87	1.08	0.62	hypothetical protein	
Afu1g05080	2.84	1.28	1.27	ribosomal protein P0	structural constituent of ribosome///translation///translational elongation///ribosomal large subunit assembly///cytosolic large ribosomal subunit (sensu Eukaryota)
Afu6g13900	2.83	1.6	1.54	conserved hypothetical protein	
Afu1g04520	2.82	0.89	0.49	Hypothetical protein	
Afu5g03380	2.81	1.68	1.82	flavin dependent monooxygenase, putative	protein folding///endoplasmic reticulum membrane///monooxygenase activity
Afu6g12550	2.8	1.23	0.5	mitochondrial carrier protein, putative	RNA splicing///carrier activity///mitochondrion///transport

Table AD.2.2 30 ORFs having the highest $\log_2$ among up-regulated genes unique to the 4 hrs time point of the ATCC46645 Δ*pacC* time course.

ORFs	T4 vs T0	T8 vs T0	T16 vs T0	Annotation	Functional classification
Afu5g01580	1.44	3.26	1.3	oxidoreductase, short chain dehydrogenase/reductase family	
Afu8g07080	-0.46	3.24	-0.25	elastinolytic metalloproteinase Mep	pathogenesis///endopeptidase activity
Afu3g00320	1.15	3	1.92	endo-1,4-beta-xylanase (XlnA), putative	xylan metabolic process
Afu4g01580	1.04	2.59	1.82	ankyrin repeat protein	
Afu3g11920	1.37	2.52	1.73	dihydrodipicolinate synthetase family protein	catalytic activity///metabolic process
Afu2g08470	0.56	2.49	1.93	GTP binding protein (Bud4), putative	GTP binding///cellular bud site selection///axial cellular bud site selection
Afu3g14440	1.36	2.47	1.86	cytochrome c oxidase family protein	
Afu2g10650	1.71	2.4	1.66	enoyl-CoA hydratase	
Afu5g00640	1.82	2.39	1.97	peroxisomal dehydratase, putative	enoyl-CoA hydratase activity///3-hydroxyacyl-CoA dehydrogenase activity///peroxisomal matrix///fatty acid beta-oxidation
Afu1g08840	1.58	2.38	1.84	guanylate kinase	GMP metabolic process///cytoplasm///nucleus///guanylate kinase activity
Afu1g09480	1.49	2.37	1.68	vacuolar protein sorting 29, putative	endosome///"retrograde transport, endosome to Golgi"///molecular function unknown
Afu5g09070	0.89	2.31	1.67	hypothetical protein	
Afu5g07690	1.99	2.3	1.75	conserved hypothetical protein	
Afu2g04230	0.67	2.3	1.41	fumarylacetoacetate hydrolase FahA	tyrosine catabolic process///L-phenylalanine catabolic process///fumarylacetoacetase activity
Afu5g01690	0.89	2.27	1.71	conserved hypothetical protein	
Afu6g12680	0.62	2.26	1.36	HIT domain protein	nucleotide metabolic process///nucleotide binding///cytoplasm///nucleus///hydrolase activity
Afu8g06700	1.45	2.26	1.72	annexin ANXC3.1	
Afu3g00350	0.92	2.25	1.58	hypothetical protein	
Afu6g02470	1.97	2.25	1.9	fumarate hydratase, putative	tricarboxylic acid cycle///fumarate hydratase activity///fumarate metabolic process///cytosol///mitochondrial matrix
Afu3g14660	0.48	2.23	1.74	hypothetical protein	
Afu2g00890	0.43	2.2	1.62	hypothetical protein	
Afu3g131	-1.01	2.19	1.85	extracellular serine-	

10				threonine rich protein	
Afu2g10580	0.32	2.19	1.75	hypothetical protein	
Afu4g12670	1.98	2.18	1.73	DNA repair protein rad1, putative	
Afu1g05320	1.56	2.16	1.94	disulfide isomerase, putative	protein disulfide isomerase activity///fungal-type vacuole///protein folding
Afu4g14120	1.62	2.15	1.85	cutinase, putative	
Afu3g01450	1.47	2.15	1.84	3-methyl-2-oxobutanoate dehydrogenase, putative	Binding
Afu4g09390	1.68	2.15	0.87	conserved hypothetical protein	
Afu8g01970	1.21	2.14	1.93	extracellular endo-polygalacturonase, putative	pectin catabolic process///pseudohyphal growth///extracellular region///polygalacturonase activity

Table AD.2.3: 30 ORFs with the highest log$_2$ values between the up-regulated genes unique to the 8 hrs time point of the ATCC46645 Δ*pacC* time course.

ORFs	T4 vs T0	T8 vs T0	T16 vs T0	Annotation	Functional classification
Afu8g00550		1.4	4.92	SirN-like methyltransferase, putative	
Afu8g00560	1.32	1.97	4.67	cytochrome P450, putative	oxidoreductase activity///metabolic process
Afu2g17830	-0.2	1.75	4.06	hypothetical protein	
Afu4g01440	-0.27	0.77	4.05	glutathione S-transferase family protein	regulation of nitrogen utilization///soluble fraction///transcription corepressor activity
Afu4g01370	1.06	1.94	3.82	hypothetical protein	
Afu3g00420	0.73	1.49	3.73	acetyl xylan esterase (Axe1), putative	cellulose binding///xylan metabolic process///acetylxylan esterase activity
Afu4g14070	0.37	1.45	3.55	glycosyl transferase, putative	transferase activity, transferring glycosyl groups
Afu4g01070	1.01	1.7	3.53	acid phosphatase, putative	acid phosphatase activity///response to stress
Afu3g01180	0.96	1.16	3.48	sarcosine oxidase, putative	
Afu3g03810	1.9	1.25	3.48	hypothetical protein	
Afu3g14670	1.76	1.72	3.47	MFS transporter, putative	nicotinamide mononucleotide transport///nicotinamide mononucleotide permease activity///integral to plasma membrane
Afu1g17640	1.31	1.33	3.45	melanin biosynthesis transcription factor RegA	melanin biosynthetic process///"regulation of transcription, DNA-dependent"///transcription factor activity///nucleus///zinc ion binding
Afu1g17650	1.8	1.93	3.4	short chain dehydrogenase, putative	oxidoreductase activity///cytoplasm///metabolic

					process
Afu6g08490	-0.36	1.25	3.4	inorganic diphosphatase, putative	phosphate metabolic process///inorganic diphosphatase activity///cytosol
Afu6g01830	1.59	1.98	3.34	O-methyltransferase, putative	
Afu3g01280	0.29	1.75	3.31	alpha/beta hydrolase, putative	
Afu2g07750	0.01	1.88	3.26	haloacid dehalogenase, type II	
Afu2g18050	-0.07	1.13	3.26	FAD binding oxidoreductase, putative	FAD binding
Afu5g01320	0.81	1.96	3.25	phosphate permease	integral to plasma membrane///inorganic phosphate transmembrane transporter activity///phosphate transport
Afu1g01300	-2.06	0.56	3.21	GPI anchored protein, putative	
Afu6g08470	1.85	1.76	3.12	glycerol kinase, putative	cytoplasm///glycerol kinase activity///glycerol metabolic process
Afu7g04960	-0.01	1.37	3.11	N-acetyltransferase, GNAT family, putative	N-acetyltransferase activity///metabolic process
Afu4g13780	1.41	1.26	3.02	polyphenol monooxygenase, putative	
Afu6g13850	0.81	1.86	2.98	GTPase activating protein (Evi5), putative	Rab GTPase activator activity///cytosol
Afu8g00370	-0.4	0.65	2.97	polyketide synthase, putative	3-oxoacyl-[acyl-carrier-protein] synthase activity///polyketide synthase activity
Afu8g00420	-1.42	0.45	2.97	C6 finger transcription factor, putative	DNA binding
Afu8g02560	-0.53	0.96	2.94	glyceraldehyde-3-phosphate dehydrogenase, putative	lipid particle///fungal-type cell wall///cytoplasm///cytosol///gluconeogenesis///glycolysis///glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity
Afu5g08800	1.24	1.58	2.93	hypothetical protein	
Afu2g05080	1.01	1.65	2.88	hypothetical protein	
Afu1g17470	0.62	1.9	2.88	high affinity nitrate transporter NrtB	

Table AD.2.4: 30 ORFs with the highest log$_2$ values among up-regulated genes unique to the 16 hrs time point of the ATCC46645 Δ*pacC* time course.

Locus	T0 vs T4	T0 vs T8	T0 vs T16	Common Name
Afu1g00140	-2.92	-1.94	-1.39	Fot5 transposase, putative
Afu1g00170	-4.99	-3.59	-4.58	hypothetical protein
Afu1g00410	-1.92	-1.95	-2.19	C6 transcription factor, putative
Afu1g00550	-2.41	-0.67	-1.09	conserved hypothetical protein
Afu1g00600	-2.86	-1.71	-2.05	LMBR1 domain protein, putative

Afu1g00880	-1.42	-1.5	-2.06	reverse transcriptase, RNaseH, putative
Afu1g00910	-4.67	-3.73	-3.92	conserved hypothetical protein
Afu1g00980	-1.93	-1.79	-2.53	FAD-dependent oxidase, putative
Afu1g01180	-4.33	-2.72	-2.66	isoamyl alcohol oxidase
Afu1g01300	-2.06	0.56	3.21	GPI anchored protein, putative
Afu1g01500	-4	-3.36	-3.32	short-chain dehydrogenase/reductase family protein, putative
Afu1g01950	-2.02	-1.47	-1.02	hypothetical protein
Afu1g01970	-1.62	-2.4	-2.51	mutant VeA1 protein
Afu1g02000	-1.68	-1.9	-2.16	DNA mismatch repair protein Msh4, putative
Afu1g02120	-2.99	-2.84	-1.92	F-box domain protein
Afu1g02130	-1.34	-2.27	-2.79	DUF221 domain protein, putative
Afu1g02280	-2.99	-2.2	-2.61	conserved hypothetical protein
Afu1g02620	-3.07	-1.13	-1.38	hypothetical protein
Afu1g02640	-1.28	-2.36	-2.33	conserved hypothetical protein
Afu1g02940	-1.34	-1.25	-2.01	mitotic check point protein (Bub2), putative
Afu1g02950	-2.37	-1.52	-0.99	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) protein
Afu1g03010	-1.75	-2.37	-2.31	cell cycle control protein (Cwf22), putative
Afu1g03020	-2.38	0.42	-0.6	My026 protein
Afu1g03030	-2.17	-2.4	-3.32	hypothetical protein
Afu1g03090	-1.14	-1.82	-2.81	conserved hypothetical protein
Afu1g03110	-2.93	-1.95	-2.26	60S ribosomal protein L29, putative
Afu1g03150	-1.17	-1.95	-2.69	c-14 sterol reductase
Afu1g03190	-2.03	-1.47	-1.63	hypothetical protein
Afu1g03210	-3.02	-2.81	-3.38	MYB family conidiophore development protein FlbD, putative
Afu1g03220	-2.24		-1.41	hypothetical protein
Afu1g03230	-2.33	-1.58	-1.88	ABC multidrug transporter, putative
Afu1g03330	-2.57	-2.79	-2.25	hypothetical protein
Afu1g03360	-3.36	-2.1	-2.12	hypothetical protein
Afu1g03410	-1.06	-1.2	-2.66	DNA primase large subunit
Afu1g03500	-1.79	-2.56	-2.47	topoisomerase I
Afu1g03600	-2.39	-2.32	-2.86	exo-beta-1,3-glucanase (Exg1), putative
Afu1g03650	-2.37	-2.21	-2.62	hypothetical protein
Afu1g03710	-1.57	-1.95	-2.28	C2H2 finger domain protein, putative
Afu1g03830	-2.75	-2.21	-3.46	prefoldin subunit 2, putative
Afu1g04100	-2.13	-2.15	-0.35	hypothetical protein
Afu1g04220	-2.18	-1.25	-0.87	hypothetical protein
Afu1g04230	-2.76	-2.46	-2.71	mitoribosomal protein YmL27

Afu1g04410	-0.98	-2.58	-2.52	conserved hypothetical protein
Afu1g04670	-1.09	-1.59	-2.52	related to suppressor protein PSP1
Afu1g04750	-2.24	-2.73	-2.68	cyclin
Afu1g04850	-1.42	-1.41	-2.1	8 kDa cytoplasmic dynein light chain
Afu1g04860	-4.07	-2.47	-3.33	hypothetical protein
Afu1g04930	-2.28	-2.48	-2.24	hypothetical protein
Afu1g04970	0.01	-1.69	-2.21	Patatin-like serine hydrolase, putative
Afu1g05040	-1.2	-2.27	-1.45	protein mitochondrial targeting protein (Mas1), putative
Afu1g05250	-2.28	-1.43	-1.79	hypothetical protein
Afu1g05370	-2.06	-1.2	-0.17	conserved hypothetical protein
Afu1g05400	-3.76	-1.93	-1.63	hypothetical protein
Afu1g05560	-0.97	-1.92	-2.35	GTP binding protein, putative
Afu1g05660	-2.01	-1.85	-1.72	hypothetical protein
Afu1g05680	-2.05	-2.83	-2.6	hypothetical protein
Afu1g05850	-2.44	-3.71	-4.25	erythromycin esterase family protein
Afu1g06020	-2.23	-2.11	-1.69	DnaJ domain protein
Afu1g06100	-3.21	-1.67	-2	glutaredoxin
Afu1g06190	-2.36	-3.97	-4.2	hnrnp arginine n-methyltransferase
Afu1g06220	-1.74	-2.21	-1.32	ATP-dependent RNA helicase , putative
Afu1g06350	-1.87	-2.31	-2.84	virulence related protein (Cap20), putative
Afu1g06380	-2.75	-1.59	-1.77	RNA polymerase III subunit CII
Afu1g06400	-0.98	-1.75	-2.28	cAMP-dependent protein kinase-like, putative
Afu1g06580	-3.45	-1.19	-1.78	high expression lethality protein (Hel10), putative
Afu1g06590	-2.84	-1.71	-1.69	phosphoglycerate mutase family protein, putative
Afu1g06640	-1.41	-2.06	-2.27	zinc-binding oxidoreductase, putative
Afu1g06690	-0.07	-1.67	-2.22	RLI and DUF367 domain protein
Afu1g06720	-1.77	-1.72	-2.52	histone acetyltransferase Spt10, putative
Afu1g06740	-1.3	-1.32	-2.03	hypothetical protein
Afu1g06990	-4.49	-0.73	-3.27	NA
Afu1g07470	-3.18	-2.39	-2.72	autophagic death protein IDI-7, putative
Afu1g07730	-2.82	-2.62	-3.08	metalloprotease MEP1
Afu1g07740	-0.84	-1.62	-2.02	LEM3/CDC50 family protein
Afu1g07750	-3.27	-2.31	-2.47	FUN19 protein
Afu1g08800	-2.05	-1.06	-1.81	cytochrome P450 phenylacetate hydroxylase, putative
Afu1g08870	-2.28	-3.09	-3.68	hypothetical protein
Afu1g09060	-1.8	-2.15	-2.28	conserved hypothetical protein
Afu1g09140	-1.95	-3.22	-2.98	hypothetical protein
Afu1g09360	-2.37	-0.5	-0.92	DUF1242 domain protein, putative

Afu1g09430	-1.08	-2.04	-1.17	conserved hypothetical protein
Afu1g09500	-1.36	-2.18	-3.21	ubiquitin-protein ligase (Rsp5), putative
Afu1g09670	-2.08	-2.46	-2.27	HLH transcription factor (GlcD gamma), putative
Afu1g09750	-1.21	-1.7	-2.74	aldehyde reductase (AKR1), putative
Afu1g09940	-1.64	-1.99	-2.37	protein required for survival at high temperature during stationary phase, putative
Afu1g10040	-0.85	-1.57	-2.65	HMG box protein, putative
Afu1g10090	-2.27	-1.02	-1.4	hypothetical protein
Afu1g10300	-4.43	-2.29	-1.6	hypothetical protein
Afu1g10610	-1.97	-2.11	-1.75	hypothetical protein
Afu1g10850	-2.68	-1.27	-1.88	ubiquitin-like modifier SUMO, putative
Afu1g10880	-0.29	-0.68	-2	P-type calcium ATPase, putative
Afu1g10950	-2.72	-3.45	-4.32	conserved hypothetical protein
Afu1g10960	-1.89	-1.19	-2.2	Mago nashi domain protein
Afu1g11220	-2.43	-0.9	-1.55	GPI anchored protein, putative
Afu1g11240	-2.11	-2.12	-2.53	hypothetical protein
Afu1g11330	-3.34	-2.07	-1.16	lactonohydrolase, putative
Afu1g11370	-2.5	-1.39	-1.13	versicolorin B synthase, putative
Afu1g11430	-2.19	-0.94	-1.56	hypothetical protein
Afu1g11460	-1.64	-2.32	-2.09	1,3-beta-glucanosyltransferase Bgt1
Afu1g11490	-0.53	-1.57	-2.28	vacuolar endopolyphosphatase, putative
Afu1g11560	-3.97	-3.42	-3.99	4-hydroxyphenylpyruvate dioxygenase, putative
Afu1g11720	-3.38	-3.29	-3.74	conserved hypothetical protein
Afu1g11860	-1.85	-2.76	-2.76	mitochondrial import receptor subunit tom22
Afu1g11930	-2.63	-2.45	-2.36	protein kinase, putative
Afu1g12270	-2.26	-0.07	-0.62	hypothetical protein
Afu1g12340	-2.61	-3.04	-2.76	carnitine acetyl transferase
Afu1g12360	-2.35	-0.88	-0.4	hypothetical protein
Afu1g12410	-2.47	-2.61	-2.99	salicylate hydroxylase
Afu1g12420	-2.28	-2.51	-2.52	hypothetical protein
Afu1g12460	-3.03	-1.58	-1.95	isoflavone reductase family protein
Afu1g12810	-1.49	-2.02	-2.81	hypothetical protein
Afu1g12900	-1.04	-1.93	-2.67	Leucine Rich Repeat domain protein
Afu1g12960	-0.6	-1.43	-2.45	SCF ubiquitin ligase complex subunit CulA, putative
Afu1g12980	-1.88	-2.39	-3.37	conserved hypothetical protein
Afu1g12990	-1.33	-1.71	-2.34	membrane protein, putative
Afu1g13050	-2.52	-3.16	-3.2	C2H2 transcription factor, putative
Afu1g13060	-1.02	-2.24	-1.97	regulator of nonsense transcripts, putative

Afu1g13120	-2.23	-2.07	-2.8	hypothetical protein
Afu1g13350	-2.36	-2.62	-4.1	transporter, putative
Afu1g13360	-2.97	-2.08	-0.83	C4-dicarboxylate transporter/malic acid transport protein, putative
Afu1g13400	-3.34	-2.76	-2.76	conserved hypothetical protein
Afu1g13460	-0.85		-2.07	conserved hypothetical protein
Afu1g13530	-2.21	-1.2	-1.39	hypothetical protein
Afu1g13550	-2.91	-1.55	-2.85	hypothetical protein
Afu1g13560	-0.29	-1.31	-2.38	hypothetical protein
Afu1g13660	-1.03	-1.79	-2.24	phenol 2-monooxygenase, putative
Afu1g13850	-1.15	-2.26	-2.17	conserved hypothetical protein
Afu1g13880	-2.38	-3.1	-3.05	NAF1 domain family
Afu1g13910	-1.49	-1.64	-2.4	TFIIH complex helicase (RAD3), putative
Afu1g13970	-1.4	-1.45	-2.03	MFS transporter, putative
Afu1g14000	-5.49	-3.48	-3.71	hypothetical protein
Afu1g14050	-3.32	-3.63	-3.81	F-box domain protein
Afu1g14060	-3.05	-2.25	-2.26	C2H2 finger domain protein, putative
Afu1g14070	-2.61	-1.79	-2.03	chromosome segregation protein BIR1, putative
Afu1g14160	-3.03	-1.72	-1.7	hypothetical protein
Afu1g14300	-1.92	-1.99	-2.5	Fasciclin domain family
Afu1g14310	-0.64	-1.4	-2.19	poly(A)-binding protein-dependent poly(A) ribonuclease, putative
Afu1g14330	-4.28	-4.3	-5.29	ABC transporter, putative
Afu1g14630	-1.7	-2.05	-1.89	tRNAHis guanylyltransferase, putative
Afu1g14640	-2.46	-1.64	-1.17	hypothetical protein
Afu1g14660	-1.81	-2.96	-3.26	regulator of secondary metabolism LaeA
Afu1g14740	-2.38	-3.32	-3.24	TFIIA alpha/beta
Afu1g14750	-2.54	-3.37	-3.47	C2H2 transcription factor (Sfp1), putative
Afu1g14770	-1.05	-1.96	-2.91	tRNA dihydrouridine synthase, putative
Afu1g14820	-3.36	-1.7	-0.83	hypothetical protein
Afu1g14840	-2.61	-1.76	-1.94	Ser/Thr protein phosphatase superfamily
Afu1g14910	-2.05	-1.82	-1.73	YKL529
Afu1g15190	-2.23	-0.93	-1.12	hypothetical protein
Afu1g15340	-0.84	-2.27	-3.11	polymerase
Afu1g15390	-1.63	-2.13	-2.34	DUF1014 domain protein
Afu1g15410	-3.5	-3.92	-4.53	CUE domain protein, putative
Afu1g15430	-2.73	-1.99	-3.01	lipase/esterase, putative
Afu1g15530	-2.89	-1.28	0.64	lactam utilization protein LamB, putative
Afu1g15570	-2.15	-2.04	-2.19	ubiquitin-conjugating enzyme, putative
Afu1g15620	-1.49	-2.82	-2.72	DEAD box RNA helicase HelA, putative

Afu1g15650	-3.76	-2.39	-3.04	hypothetical protein
Afu1g15690	-4.46	-1.85	-1.18	conserved hypothetical protein
Afu1g15710	-2.86	-2.92	-3.7	cyclosome/APC complex component Cut20/Apc4, putative
Afu1g15720	-0.81	-1.97	-2.41	importin beta-1 subunit
Afu1g15790	-0.29	-1.59	-2.14	ecylglycaid-PDC
Afu1g15810	-1.05	-1.7	-2.18	RNA splicing factor (Pad-1), putative
Afu1g15820	-1.98	-3.21	-3.26	fatty acid hydroxylase, putative
Afu1g15840	-0.82	-2.26	-2.08	hypothetical protein
Afu1g15850	-1.75	-2.78	-3.59	C6 transcription factor, putative
Afu1g15870	-0.73	-1.85	-2.26	DNA topoisomerase IV subunit A, putative
Afu1g15890	-0.88	-2.24	-3.21	SacI domain protein
Afu1g15940	0.51	-1.3	-2.07	Auxin Efflux Carrier superfamily
Afu1g16080	-3.07	-1.71	-2.35	hypothetical protein
Afu1g16140	-2.88	-1.79	-2.75	hypothetical protein
Afu1g16160	-2.12	-0.61	-0.48	C6 transcription factor, putative
Afu1g16430	-1.66	-1.76	-2.35	hypothetical protein
Afu1g16450	-5.36	-3.33	-4.18	hypothetical protein
Afu1g16520	-3	-1.92	-2.33	hypothetical protein
Afu1g16530	-3.55	-2.75	-2.95	NA
Afu1g16550	-1.02	-1.99	-2.22	dihydrouridine synthase family protein, putative
Afu1g16570	-2.01	-2.14	-2.59	G4P04 protein
Afu1g16710	-0.2	-2.37	-3.55	fatty acid elongase (Gig30), putative
Afu1g16780	-1.73	-1.76	-2.29	protein kinase (Lkh1), putative
Afu1g16790	-1.23	-2.26	-2.67	related to tpa inducible protein, putative
Afu1g16850	-1.3	-2.21	-1.94	sur2 protein
Afu1g16930	-2.03	-2.82	-3.33	phosphatidylserine decarboxylase, putative
Afu1g16940	-3.58	-3.97	-4.09	DEAD/DEAH box helicase, putative
Afu1g16960	-1.98	-2.21	-3.02	hypothetical protein
Afu1g16990	-1.85	-2.05	-2.82	mRNA splicing factor (Prp18), putative
Afu1g17060	-3.16	-3.92	-4.29	HLH DNA binding domain protein, putative
Afu1g17080	-2.3	-1.3	-0.57	acetyltransferase, GNAT family, putative
Afu1g17280	-2.18	-1.74	-1.11	hypothetical protein
Afu1g17290	-4.15	-3.48	-3.35	conserved hypothetical protein
Afu1g17360	-2.53	-3.29	-4.02	bZIP transcription factor (BACH2), putative
Afu1g17370	-4.11	-2.26	-3.32	chaperone/heat shock protein Hsp9, putative
Afu1g17380	-3.13	-3.7	-4.35	3-oxoacyl-(acyl-carrier-protein) reductase, putative
Afu1g17430	-2.25	-3.2	-3.53	tyrosinase
Afu1g17440	-2.36	-1.8	-2.31	ABC drug exporter AbcA

Afu1g17460	-2	-2.01	-2.02	C6 transcription factor, putative
Afu1g17680	-2.28	-0.83	0.5	MFS transporter, putative
Afu2g00160	-4.03	-3.12	-2.56	hypothetical protein
Afu2g00170	-3.92	-3.29	-3.55	glutathione-dependent formaldehyde dehydrogenase
Afu2g00200	-5.8	-5.74	-6.99	catalase, putative
Afu2g00220	-0.71	-1.12	-2.06	aminopeptidase, putative
Afu2g00290	-2.49	-1.26	-2.57	hypothetical protein
Afu2g00440	-2.63	-1.64	-0.84	hypothetical protein
Afu2g00470	-2.34	-2.38	-2.21	C6 transcription factor, putative
Afu2g00580	-2.36	0.44	0.37	hypothetical protein
Afu2g00650	-2.12	-2.19	-2.14	arabinosidase
Afu2g00940	-1.71	-2.84	-2.36	hypothetical protein
Afu2g01050	-1.75	-1.48	-2.42	mitochondrial intermembrane space translocase subunit Tim9, putative
Afu2g01120	-3.36	-2.56	-1.57	DNA repair protein, putative
Afu2g01150	-3.17	-2.6	-3.12	conserved hypothetical protein
Afu2g01670	-1.77	-2.22	-2.78	hypothetical protein
Afu2g01880	-2.24	-1.23	-0.41	Low molecular weight phosphotyrosine protein phosphatase family
Afu2g01900	-0.69	-1.54	-2.24	Rtf1p, putative
Afu2g02020	-2.97	-2.81	-2.81	formamidase
Afu2g02030	-1.91	-2.39	-2.04	fructosyl amine:oxygen oxidoreductase
Afu2g02060	-2.53	-2.14	-2.23	D-tyrosyl-tRNA(Tyr) deacylase
Afu2g02180	-1.26	-1.93	-2.11	hypothetical protein
Afu2g02270	-3.33	-0.87	-1.22	ribosomal protein S14p/S29e
Afu2g02290	-1.3	-2.58	-2.96	hypothetical protein
Afu2g02390	-2.14	-1.67	-1.47	hypothetical protein
Afu2g02570	-0.8	-1.96	-2.02	F-box domain protein
Afu2g02600	-0.71	-1.98	-2.27	hypothetical protein
Afu2g02660	-2.13	-1.59	-1.37	DNA topoisomerase III, putative
Afu2g02690	-2.59	-2.45	-2.65	fungal specific transcription factor, putative
Afu2g02700	-2.93	-1.95	-1.42	mitochondrial DnaJ chaperone (Tim14), putative
Afu2g02710	-2.66	-1.78	-1.09	60S ribosomal protein (Rlp24), putative
Afu2g02760	-1.25	-1.56	-2.1	protein-tyrosine phosphatase, putative
Afu2g02830	-1.35	-1.39	-2.22	hypothetical protein
Afu2g02840	-1.37	-1.58	-2.04	TBC domain protein, putative
Afu2g02850	-1.8	-2.58	-3.05	serine/threonine protein kinase, putative
Afu2g03030	-0.88	-1.77	-2.15	pre-mRNA splicing factor (PRP8), putative

Afu2g03070	-3.15	-2.99	-2.81	hypothetical protein
Afu2g03080	-2.26	-1.87	-1.68	WD repeat protein
Afu2g03090	-1.71	-2.36	-3.01	vacuolar ABC heavy metal transporter (Hmt1), putative
Afu2g03150	-4.87	-2.81	-2.04	kinesin family protein
Afu2g03470	-2.04	-0.35	-0.37	hypothetical protein
Afu2g03620	-2.84	-1.44	-1.55	oxidoreductase, short-chain dehydrogenase/reductase family
Afu2g03750	-2.08	-1.97	-1.98	DNA excision repair protein (Rad26L), putative
Afu2g03850	-2.43	-2.53	-2.04	hypothetical protein
Afu2g03950	-1.82	-3.33	-3.96	serine/threonine protein phosphatase, putative
Afu2g04050	-1.99	-2.39	-2.53	hypothetical protein
Afu2g04100	-0.14	-1.61	-2	hypothetical protein
Afu2g04170	-1.54	-2.13	-2.14	conserved hypothetical protein
Afu2g04200	-2.11	-0.27	-0.71	4-hydroxyphenylpyruvate dioxygenase, putative
Afu2g04210	-3.75	-0.92	-0.87	conserved hypothetical protein
Afu2g04250	-1.54	-2.41	-2.25	C6 finger domain protein, putative
Afu2g04260	-2.95	-0.6	-0.71	transcription factor, putative
Afu2g04270	-2.06	-1.73	0.26	mitochondrial inner membrane translocase subunit (TIM17), putative
Afu2g04320	-0.73	-2.04	-1.8	NADH-dependent flavin oxidoreductase, putative
Afu2g04730	-4.03	-2.84	-3.14	NA
Afu2g04740	-0.44	-1.8	-2.71	vacuolar sorting-associated protein (Vps27), putative
Afu2g04750	-2.26	-2.73	-3.23	hypothetical protein
Afu2g04780	-1.12	-1.94	-2.3	WD repeat protein
Afu2g04870	-1.33	-1.91	-2.41	dehydrogenase complex alpha subunit, putative
Afu2g04880	-4.17	-3.45	-4.54	DUF77 domain protein
Afu2g05050	-2.78	-0.75	-1.09	hypothetical protein
Afu2g05060	-4.01	-2.35	-2.05	alternative oxidase
Afu2g05120	-2.35	-1.85	-2.36	hypothetical protein
Afu2g05240	-2.49	-1.21	-0.58	conserved hypothetical protein
Afu2g05250	-1.8	-2.95	-3.22	RfeD
Afu2g05330	0.21	-1.43	-2.16	vacuolar H+\/Ca2+ exchanger
Afu2g05440	-1.29	-1.55	-2.08	Hypothetical protein
Afu2g05480	-2.49	-2.04	-1.65	DNA-directed RNA polymerase I 13.1 kDa polypeptide, putative
Afu2g05530	-2.43	-2.71	-2.95	histone acetyltransferase (Esa1), putative
Afu2g05550	-1.07	-1.69	-2.21	conserved hypothetical protein
Afu2g05620	-1.31	-1.53	-2.24	conserved hypothetical protein
Afu2g05630	-0.86	-1.7	-2.6	hypothetical protein
Afu2g05640	-2.12	-1.55	-1.91	hypothetical protein

Afu2g05700	-5.08	-1.83	-1.95	hypothetical protein
Afu2g05730	-1.23	-2.4	-2.04	siderochrome-iron transporter (MirC), putative
Afu2g05830	-2.24	-0.3	-1.12	C6 finger domain protein, putative
Afu2g05940	-1.15	-1.8	-2.01	conserved hypothetical protein
Afu2g05970	-1.25	-1.85	-2.24	PHD finger and JmjC domain protein, putative
Afu2g05980	-2.13	-2.16	-1.99	conserved hypothetical protein
Afu2g06010	-2.54	-2.02	-2.06	alkaline lipase, putative
Afu2g06050	-1.54	-2.16	-3.04	conserved hypothetical protein
Afu2g06060	-0.91	-1.65	-2.15	transcriptional co-activator (Hfi1/Ada1), putative
Afu2g06070	-1.97	-2.78	-3.2	NA
Afu2g06290	-4.71	-4.55	-4.99	nuclear division rft1 protein
Afu2g07460	-3	-2.72	-3.31	RNA polymerase II transcriptional coactivator, putative
Afu2g07610	-0.17	-1.79	-2.8	alcohol dehydrogenase PAN2
Afu2g07620	-0.36	-1.57	-2.04	cystathionine beta-synthase, putative
Afu2g07840	-2.29	-0.37	-0.91	competence/damage-inducible protein CinA, putative
Afu2g07890	-2.4	-1.15	-1.49	conserved hypothetical protein
Afu2g08080	-1.73	-2.84	-3.14	conserved hypothetical protein
Afu2g08090	-2.9	-0.19	-0.5	hypothetical protein
Afu2g08150	-2.58	-1.9	-2.58	NEDD8-like protein (RubA), putative
Afu2g08170	-1.74	-1.92	-2.8	hypothetical protein
Afu2g08520	-3.1	-1.74	-1.82	50S ribosomal protein L14
Afu2g08660	-2.14	-1.51	-2.4	conserved hypothetical protein
Afu2g08680	-3.93	-1.96	-1.45	hypothetical protein
Afu2g08730	-2.39	-1.7	-1.74	hypothetical protein
Afu2g08740	-1.99	-2.26	-1.54	ZIP metal ion transporter, putative
Afu2g08780	-1.49	-2.17	-2.08	guanyl-nucleotide exchange factor, putative
Afu2g08990	-1.07	-1.87	-2.2	eukaryotic translation initiation factor 5
Afu2g09190	-1.27	-1.62	-2.17	hypothetical protein
Afu2g09460	-0.96	-1.59	-2.43	potassium transporter
Afu2g09510	-4.33	-3.84	-4.29	hypothetical protein
Afu2g09530	-1.81	-1.93	-2.18	PUTATIVE SIGNAL PEPTIDE PROTEIN
Afu2g09630	-0.89	-1.67	-2.79	hypothetical protein
Afu2g09820	-0.12	-1.7	-2.03	conserved hypothetical protein
Afu2g09880	-3.17	-2.61	-2.26	hypothetical protein
Afu2g09890	-2.77	-3.34	-3.8	conserved hypothetical protein
Afu2g09990	-1.98	-3.02	-3.35	hypothetical protein
Afu2g10020	-2.63	-1.34	-2.14	hypothetical protein
Afu2g10030	-2.86	-2.97	-4.11	vip1 protein

Afu2g10050	-1.51	-2.2	-2.76	hypothetical protein
Afu2g10110	-1.99	-2.54	-3.37	hypothetical protein
Afu2g10120	-1.5	-2.65	-3.59	YjeF domain protein
Afu2g10130	-6.69	-4.64	-5.2	phase-specific adhesin, putative
Afu2g10310	-2.43	-2.86	-2.54	DUF408 domain protein
Afu2g10330	-2.09	-2.66	-2.32	conserved hypothetical protein
Afu2g10490	-1.29	-1.7	-2.35	hypothetical protein
Afu2g10540	-2.26	-1.93	-1.63	hypothetical protein
Afu2g10550	-3.08	-3.38	-3.28	C2H2 transcription factor (RfeC), putative
Afu2g10750	-1.5	-1.97	-2.21	RNA helicase (Dbp), putative
Afu2g10770	-2.35	-2.18	-2.67	C2H2 transcription factor (Con7), putative
Afu2g10900	-1.01	-1.5	-2.16	autophagy related lipase (Atg15), putative
Afu2g10980	-3	-3.31	-3.91	ADP-ribosylation factor, putative
Afu2g11090	-2.1	-1.44	-1.29	DNA replication complex GINS protein (Psf2), putative
Afu2g11100	-3.3	-3.03	-3.07	AMFR protein, putative
Afu2g11180	-1.54	-1.99	-2.65	developmental regulator FlbA
Afu2g11210	-1.66	-1.9	-2.1	PHD finger and SET domain protein, putative
Afu2g11250	-1.58	-2.42	-1.56	aryl-alcohol dehydrogenase (AAD), putative
Afu2g11310	-2.22	-1.71	-1.11	NTP binding protein, putative
Afu2g11390	-1.52	-1.69	-2.27	hypothetical protein
Afu2g11650	-2.8	-1.12	-1.77	hypothetical protein
Afu2g11660	-2.27	-2.33	-2.46	Rad4 family protein
Afu2g11770	-1.5	-1.86	-2.01	hypothetical protein
Afu2g11840	-1.5	-1.58	-2	transcriptional corepressor (Cyc8), putative
Afu2g12130	-2.37	-1.1	-0.69	conserved hypothetical protein
Afu2g12140	-1.16	-1.51	-2.09	voltage-gated chloride channel, putative
Afu2g12220	-1.75	-2.56	-2.96	DNA replication factor C subunit Rfc1, putative
Afu2g12230	-2	-1.27	-1.33	mitochondrial large ribosomal subunit protein L16, putative
Afu2g12370	-2.05	-1.64	-1.06	conserved hypothetical protein
Afu2g12440	-2.31	-2.69	-2.5	Dph2l1 protein
Afu2g12460	-3.71	-2.16	-1.88	conserved hypothetical protein
Afu2g12530	-2.31	-2.01	-3.02	carnitine acetyl transferase
Afu2g12630	-4.18	-0.96	-1.65	allergen Asp F13
Afu2g12780	-2.78	-0.55	-0.92	von Willebrand domain protein
Afu2g13040	-1.39	-2.45	-2.85	mitochondrial co-chaperone GrpE, putative
Afu2g13060	-5.54	-3.22	-3.54	calcineurin binding protein, putative
Afu2g13110	-2.16	-0.82	-1.53	cytochrome c
Afu2g13370	-1.65	-1.65	-2.04	55 kDa type II phosphatidylinositol 4-kinase

Afu2g13380	-0.28	-1.31	-2.01	GATA transcription factor (AreB), putative
Afu2g13390	-1.48	-2.67	-3.18	MFS transporter, putative
Afu2g13400	-1.46	-2.19	-2.41	TDE domain protein, putative
Afu2g13760	-1.64	-1.92	-2.15	plasma membrane SNARE protein (Sec9), putative
Afu2g13830	-2.16	-1.84	-2.28	conserved hypothetical protein
Afu2g13850	-2.3	-3.43	-3.76	protein phosphatase regulatory subunit (Gac1), putative
Afu2g13870	-1.26	-2.65	-2.78	mitochondrial carrier protein, putative
Afu2g13970	-1.75	-2.24	-2.01	conserved hypothetical protein
Afu2g13990	-0.81	-1.71	-2.3	hypothetical protein
Afu2g14090	-0.6	-1.76	-2.08	extragenic suppressor of the bimD6 mutation
Afu2g14110	-2.13	-2.51	-3.38	sulfur metabolite repression control protein SconB, putative
Afu2g14130	-1.31	-2.12	-2.09	ubiquitin C-terminal hydrolase, putative
Afu2g14150	-1.26	-1.66	-2.07	endo-arabinanase, putative
Afu2g14320	-3.68	-3.35	-4.42	HHE domain protein
Afu2g14330	-5.97	-4.81	-5.97	hypothetical protein
Afu2g14340	-3.53	-3.38	-4.06	hypothetical protein
Afu2g14480	-2.29	-1.17	-0.08	oxidoreductase, FAD-binding, putative
Afu2g14530	-2.43	-0.9	-2	esterase D
Afu2g14610	-2.38	0.57	0.02	Oxalate decarboxylase
Afu2g14720	-1.81	-2.13	-2.51	HAPB
Afu2g14780	-2.12	-1.75	-1.82	conserved hypothetical protein
Afu2g14800	-2.04	-1.35	-1.48	HLH transcription factor (Hpa3), putative
Afu2g14820	-2.02	-1.35	-0.59	hypothetical protein
Afu2g14960	-2.66	-2.7	-2.6	thioredoxin, putative
Afu2g15000	-1.1	-1.97	-2.08	Mechanosensitive ion channel family
Afu2g15110	-2.47	-1.92	-2	C2H2 finger domain protein, putative
Afu2g15130	-4.12	-3.08	-2.61	ABC multidrug transporter, putative
Afu2g15140	-2.55	-2.36	-2.23	MSF drug transporter, putative
Afu2g15150	-2.28	-1.26	-0.93	choline transport protein, putative
Afu2g15270	-4.41	-3.57	-3.79	conserved hypothetical protein
Afu2g15440	-0.81	-1.83	-2.38	integral membrane protein, putative
Afu2g15480	-1.65	-2.96	-3.69	hypothetical protein
Afu2g15650	0.78	-0.69	-2.66	DUF323 domain protein
Afu2g15670	-2.47	-2.45	-2.67	hypothetical protein
Afu2g15680	-4.19	-2.34	-3.81	transcription initiation factor iia small chain
Afu2g15740	-0.39	-1.51	-2.03	oxidoreductase, short chain dehydrogenase/reductase family
Afu2g15760	0.18	-0.96	-2.34	poly(A)+ RNA transport protein (UbaA), putative
Afu2g15770	-1.01	-1.94	-2.76	conserved hypothetical protein

Afu2g15800	-3.35	-3.31	-3.78	conserved hypothetical protein
Afu2g15810	-2.11	-1.11	-1.96	conserved hypothetical protein
Afu2g15960	-2.53	-2.36	-2.95	nucleotide binding protein Nbp35, putative
Afu2g16180	-1.78	-2.27	-1.73	hypothetical protein
Afu2g16190	-3.19	-0.81	-0.47	hypothetical protein
Afu2g16240	-2.23	-1.25	-0.45	cell division control protein Cdc25, putative
Afu2g16410	-0.97	-2.19	-2.27	hypothetical protein
Afu2g16440	-1.53	-2.1	-1.71	hypothetical protein
Afu2g16740	-0.59	-1.4	-2.24	hypothetical protein
Afu2g16810	-2.19	-2.87	-3.08	PHD finger domain protein, putative
Afu2g16930	-2.31	-2.33	-1.58	succinate:fumarate antiporter (Acr1), putative
Afu2g16980	-2.6	-1.08	-0.71	hypothetical protein
Afu2g17060	-2.47	-1.89	-1.9	60S ribosome subunit biogenesis protein (Nip7), putative
Afu2g17210	-3.5	-1.48	-2.65	hypothetical protein
Afu2g17220	-2.07	-2.31	-2.08	C2H2 transcription factor (AmdX), putative
Afu2g17310	-2.54	-1.11	-1.7	hypothetical protein
Afu2g17380	-2.93	-2.41	-2.53	hypothetical protein
Afu2g17480	-1.72	-1.99	-2.28	amino acid transporter, putative
Afu2g17510	-2.31	-1.05	-1.27	hypothetical protein
Afu2g17520	-3.51	-1.97	-1.44	GNAT family N-acetyltransferase, putative
Afu2g17850	-2.26	-2.16	-2.88	conserved hypothetical protein
Afu2g18080	-5.78	-2.7	-4.36	LINE-1 class reverse transcriptase, RNaseH, putative
Afu3g00140	-1.86	-2.25	-2.41	hypothetical protein
Afu3g00150	-2.24	-2.63	-2.73	short-chain dehydrogenase/oxidoreductase, putative
Afu3g00240	-0.77	-1.79	-2.28	TPR domain protein
Afu3g00250	-0.77	-2.11	-2.52	salicylate hydroxylase, putative
Afu3g00330	-0.22	-1.65	-2.04	hypothetical protein
Afu3g00500	-4.63	-4.41	-5	integral membrane protein
Afu3g00630	-2.03	-1.17	-1.02	conserved hypothetical protein
Afu3g00640	-2.26	-3.74	-3.54	conserved hypothetical protein
Afu3g00730	-2.31	0.22	1.13	conserved hypothetical protein
Afu3g00800	-1.36	-2.08	-1.71	oxidoreductase, 2OG-Fe(II) oxygenase family, putative
Afu3g00810	-6.16	-4.5	-6.19	cholestenol delta-isomerase, putative
Afu3g00820	-3.9	-3.36	-4.15	putative exported protein
Afu3g00970	-2.57	-0.55	-1.29	hypothetical protein
Afu3g01160	-0.92	-1.94	-2.44	iron-sulfur cluster-binding protein, rieske family domain protein
Afu3g01210	-2.74	-2.47	-1	ThiJ/PfpI family protein
Afu3g01240	-2.58	0.46	2.52	hypothetical protein

Afu3g01300	-5.81	-4.65	-5.26	hypothetical protein
Afu3g01400	-5.59	-3.77	-4.06	ABC multidrug transporter, putative
Afu3g01410	-4.36	-3.01	-3.23	polyketide synthase, putative
Afu3g01820	-1.72	-1.53	-2.15	amino acid permease
Afu3g02090	-2.72	-3.39	-2.87	beta-xylosidase
Afu3g02140	-5.63	-4.47	-4.52	large conductance mechanosensitive channel, putative
Afu3g02320	-1.02	-2.22	-2.49	C2H2 finger domain protein (Kin17), putative
Afu3g02550	-2.7	-1.63	-3.07	conserved hypothetical protein
Afu3g02570	-2.16	-1.49	-2.11	polyketide synthase, putative
Afu3g02780	-0.39	-2.35	-2.87	multidrug transporter, putative
Afu3g03040	-5.97	-3.53	-4.34	conserved hypothetical protein
Afu3g03070	-2.1	-1.21	-1.83	MYND domain protein, putative
Afu3g03120	-4.76	-2.78	-3.35	NA
Afu3g03230	-2.99	-3.37	-3.59	hypothetical protein
Afu3g03290	-3.13	-1.03	-0.83	hypothetical protein
Afu3g03460	-3.78	-3.16	-3.68	HAD superfamily hydrolase, putative
Afu3g03570	-2.12	-2.76	-3.53	67 kDa myosin-cross-reactive antigen family protein
Afu3g03580	-0.56	-1.76	-2.54	Transferase family superfamily
Afu3g03720	-3.05	-1.04	-0.73	hypothetical protein
Afu3g03750	-2.6	-0.05	-0.8	hypothetical protein
Afu3g03940	0.18	-1.4	-2.44	2,3-diketo-5-methylthio-1-phosphopentane phosphatase, putative
Afu3g03960	-3.41	-2.86	-3.81	hypothetical protein
Afu3g03980	-0.74	-1.93	-2.28	cytochrome P450 monooxygenase, putative
Afu3g04000	-2.44	-1.83	-2.27	light regulation of gametogenesis6 protein
Afu3g04060	-1.48	-2.05	-2.61	SNF7 family protein (Fti1), putative
Afu3g04300	-1.01	-1.98	-2.29	hypothetical protein
Afu3g04310	-1.06	-2.73	-3.01	snoRNA binding protein, putative
Afu3g05330	-2.08	-2.39	-2.8	R3H and G-patch domain protein, putative
Afu3g05390	-2.98	-2.52	-2.85	protein-L-isoaspartate O-methyltransferase
Afu3g05400	-0.77	-1.34	-2.1	DnaJ and TPR domain protein
Afu3g05550	-0.69	-1.93	-2.38	OTU-like cysteine protease, putative
Afu3g05560	-1.97	-2.06	-2.52	RSC complex subunit (RSC1), putative
Afu3g05760	-0.49	-2.02	-2.23	C6 transcription factor (Fcr1), putative
Afu3g05820	-0.28	-1.3	-2.26	Zinc finger, ZZ type domain protein
Afu3g06000	-2.69	-3.03	-4.17	conserved hypothetical protein
Afu3g06090	-0.79	-1.53	-2.13	transcription initiation factor TFIID subunit 12, putative
Afu3g06150	-2.09	-1.51	-1.74	NA
Afu3g06230	-2.96	-3.18	-2.74	hypothetical protein

Afu3g06260	-1.39	-1.59	-2.63	translation initiation factor SUI1
Afu3g06380	-2.23	-2.67	-2.64	hypothetical protein
Afu3g06400	-3.01	-3.14	-2.82	hypothetical protein
Afu3g06430	-2.2	-1.95	-1.92	GDP/GTP exchange factor Sec2p, putative
Afu3g06470	-0.64	-1.65	-2.26	DHHC zinc finger membrane protein, putative
Afu3g06480	-1.76	-2.92	-3.42	SET domain containing protein
Afu3g06500	-2.38	-2.31	-2.29	Complex 1 protein (LYR family) family
Afu3g06540	-0.91	-2.19	-3.68	3'-phosphoadenosine-5'-phosphosulfate reductase
Afu3g06690	-1.36	-2.42	-2.98	Rho GTPase Rho3
Afu3g06760	-2.5	-1.75	-1.9	ribosomal protein L37
Afu3g06770	-2.99	-3.55	-3.84	zinc knuckle domain protein
Afu3g06940	-3.52	-2.66	-2.36	C2H2 zinc finger domain protein, putative
Afu3g06950	-1.45	-2.26	-1.53	mitochondrial carrier protein (Rim2), putative
Afu3g07070	-2.17	-0.7	0.18	MYB DNA-binding domain protein
Afu3g07180	-0.73	-2.05	-2.57	pantothenate kinase, putative
Afu3g07530	-2.57	-2.19	-1.63	pH signal transduction protein PalI, putative
Afu3g07570	-2.25	-0.48	-1.09	conserved hypothetical protein
Afu3g07650	-2.06	-1.37	-1.84	pectin methyl esterase, putative
Afu3g07680	-1.23	-2.54	-1.39	ran GTPase activating protein 1 (RNA1 protein)
Afu3g07730	-2.54	-1.25	-1.3	hypothetical protein
Afu3g07800	-2.06	-1.11	-0.15	hypothetical protein
Afu3g07840	-2.66	-2.87	-3.86	hypothetical protein
Afu3g07900	-2.07	-0.18	-1.68	conserved hypothetical protein
Afu3g08040	-2.97	-1.46	-1.95	polymerase (RNA) II (DNA directed) polypeptide D
Afu3g08390	-3.29	-2.93	-3.76	tRNA dihydrouridine synthase (Smm1), putative
Afu3g08450	-1.62	-2.07	-2.19	hypothetical protein
Afu3g08520	-2.4	-2	-2.07	SRF-type transcription factor (RlmA), putative
Afu3g08620	-2.13	-1.25	-1.6	csh3 protein
Afu3g08630	-2.99	-2.55	-2.68	coactivator bridging factor 1 (Mbf1), putative
Afu3g08670	-1.1	-2.05	-1.22	related to L-fucose permease
Afu3g08720	-1.03	-1.65	-2.52	hypothetical protein
Afu3g08750	-1.52	-1.99	-2.7	conserved hypothetical protein
Afu3g08880	-0.54	-2.01	-3.23	conserved hypothetical protein
Afu3g08920	-4.47	-4.65	-4.54	hypothetical protein
Afu3g08990	-2.72	-2.81	-2.79	hypothetical protein
Afu3g09080	-0.9	-1.78	-2.19	Hypothetical protein
Afu3g09190	-2.21	-1.78	-1.99	aldehyde reductase I (ARI), putative
Afu3g09410	-3.75	-1.64	-2.4	reverse transcriptase

Afu3g09430	-5.3	-2.82	-4.23	LINE-1 class reverse transcriptase, RNaseH, putative
Afu3g09640	-2.51	-1.83	-2.35	camp independent regulatory protein
Afu3g09870	-2.43	-1.76	-2.69	hypothetical protein
Afu3g09960	-2.3	-2.27	-2.41	aureobasidin resistance protein Aur1
Afu3g09980	-3.57	-1.81	-1.93	hypothetical protein
Afu3g10100	-1.94	-2.15	-2.37	Sfrs4 protein
Afu3g10120	-2.16	-3.3	-3.52	TATA-box binding protein
Afu3g10130	-1.04	-1.83	-2.52	sarcosine oxidase, putative
Afu3g10150	-1.44	-3.17	-3.81	hypothetical protein
Afu3g10320	-1.8	-2.76	-3.39	Zinc finger, C3HC4 type (RING finger) domain protein
Afu3g10370	-3.28	-1.8	-3.59	conserved hypothetical protein
Afu3g10410	-3.65	-3.11	-3.64	conserved serine-rich protein
Afu3g10480	-0.4	-1.16	-2.79	conserved hypothetical protein
Afu3g10500	-2.85	-2.57	-3.01	hypothetical protein
Afu3g10510	-4.55	-2.17	-1.75	hypothetical protein
Afu3g10530	-3.38	-4.03	-4.48	protein serine/threonine kinase (Ran1), putative
Afu3g10690	-4.73	-3.19	-4.59	calcium-translocating P-type ATPase(PMCA-type),putative
Afu3g10760	-0.28	-1.77	-2.45	phosphoketolase, putative
Afu3g10770	-2.28	-1.68	-1.6	RTA1 domain protein, putative
Afu3g11150	-1.21	-2	-2.79	conserved hypothetical protein
Afu3g11170	-2.06	-2.25	-2.6	hypothetical protein
Afu3g11180	-3.71	-2.73	-2.57	DNA binding protein
Afu3g11230	-1.51	-1.53	-2.15	hypothetical protein
Afu3g11250	-1.05	-2.16	-3.26	C2H2 transcription factor (Swi5), putative
Afu3g11270	-2.18	-1.92	-2.09	hypothetical protein
Afu3g11310	-0.88	-1.9	-2.05	hypothetical protein
Afu3g11330	-1.36	-2.7	-3.75	bZIP transcription factor (AtfA), putative
Afu3g11340	-3.35	-2.1	-2.14	transthyretin domain protein
Afu3g11410	-1.53	-2.37	-3.07	RNA Polymerase II CTD phosphatase Fcp1, putative
Afu3g11530	-1.58	-2.33	-2.9	DnaJ domain protein
Afu3g11540	-1.02	-1.41	-2.04	RE68879p
Afu3g11550	-2.9	-2.5	-3.18	LEA domain protein
Afu3g11610	-2.22	-2.18	-2.33	nucleosome binding protein (Nhp6a), putative
Afu3g11870	-2.37	-2.32	-1.61	F-box and WD40 domain protein, putative
Afu3g11880	-5.7	-2.28	-2.24	hypothetical protein
Afu3g11890	-2.97	-2.09	-2	thermolabile L-asparaginase, putative
Afu3g12000	-5.26	-3.57	-3.18	hypothetical protein
Afu3g12050	-0.82	-1.3	-2.09	F-box domain protein

Afu3g12190	-3.24	-2.33	-2.4	RING finger domain protein, putative
Afu3g12220	-2.89	-1.79	-2.11	ABC transporter, putative
Afu3g12260	-3.23	-1.59	-2.99	hypothetical protein
Afu3g12270	-3.98	-2.2	-3.42	glutathione peroxidase family protein
Afu3g12390	-2.21	-2.37	-1.65	hypothetical protein
Afu3g12410	-3.69	-2.56	-2.53	DNA binding protein
Afu3g12510	-0.44	-1.65	-2.08	vesicular fusion ATPase, putative
Afu3g12530	-1.32	-2.48	-3.84	sensor histidine kinase/response regulator, putative
Afu3g12570	-2.55	-2.24	-2.29	conserved hypothetical protein
Afu3g12830	-2.81	-2.01	-2.45	RTA1 domain protein, putative
Afu3g12920	-2.24	-1.06	-0.88	nonribosomal peptide synthase (GliP), putative
Afu3g12930	-2.95	-3.26	-3.05	dimethylallyl tryptophan synthase (GliD), putative
Afu3g12940	-0.97	-1.54	-2.2	C6 transcription factor, putative
Afu3g13010	-2.31	-1.91	-2.03	conserved hypothetical protein
Afu3g13100	-2.27	-2.52	-2.15	hypothetical protein
Afu3g13160	-2.29	-2.93	-3.34	hypothetical protein
Afu3g13220	-2.04	-1.39	-1.83	hypothetical protein
Afu3g13470	-1.4	-2.13	-2.23	sulfate transporter, putative
Afu3g13480	-0.09	-1.78	-2.37	translation initiation factor 2 alpha subunit, putative
Afu3g13510	-1.51	-0.54	-2.1	flavin containing amine oxidase, putative
Afu3g13530	-1.87	-2.01	-2.08	NA
Afu3g13540	-1.85	-2.11	-1.31	NA
Afu3g13580	-1.46	-2.4	-2.35	dynamin GTPase, putative
Afu3g13600	-2.67	-1.94	-2.5	C6 transcription factor, putative
Afu3g13650	-1.99	-2.03	-1.38	integral membrane protein
Afu3g13810	-1.48	-2.37	-2.48	integral membrane protein, putative
Afu3g14270	-1.35	-2.06	-2.28	aldo-keto reductase (AKR), putative
Afu3g14480	-1.27	-2.48	-2.2	hypothetical protein
Afu3g14490	-0.36	-1.41	-2.15	Ketol-acid reductoisomerase
Afu3g14540	-3.72	-2.34	-1.97	heat shock protein HSP30, putative
Afu3g14550	-4.37	-2.71	-3.21	DNA repair protein (Rex1), putative
Afu3g14620	-5.12	-3.67	-3.7	extracellular endo-1,5-alpha-L-arabinase, putative
Afu3g14810	-4.02	-3.41	-2.61	pathogenicity associated protein PEP2, putative
Afu3g14820	-2.48	-2.06	-1.81	4-hydroxyphenylpyruvate dioxygenase, putative
Afu3g14860	-1.48	-2.18	-1.74	hypothetical protein
Afu3g14870	-4.14	-4.02	-4.18	hypothetical protein
Afu3g14900	-1.42	-1.72	-2.32	hypothetical protein
Afu3g15040	-2.15	-2.21	-3.06	xenobiotic compound monooxygenase, DszA family

Afu3g15050	-2.15	-2.59	-3.34	Flavin-binding monooxygenase, putative
Afu3g15160	-2.16	-2.69	-2.22	hypothetical protein
Afu3g15170	-1.92	-3.45	-3.53	molybdenum cofactor biosynthesis protein (MoeA), putative
Afu3g15190	-2.14	-0.81	-1.56	periplasmic nitrate reductase, putative
Afu3g15330	-3.71	-1.91	-2.71	hypothetical protein
Afu3g15370	-5.37	-2.77	-4.01	LINE-1 class reverse transcriptase, RNaseH, putative
Afu3g15380	-2.42	-2.04	-2.2	conserved hypothetical protein
Afu4g00180	-4.79	-3.96	-4.37	fatty acid oxygenase, putative
Afu4g00280	-2.39	-0.77	-0.75	hypothetical protein
Afu4g00450	-2.98	-3.84	-4.29	hypothetical protein
Afu4g00710	-1.89	-2.77	-3.6	C6 transcription factor, putative
Afu4g00720	-1.27	-2.8	-4.17	protein phosphatase 2C, putative
Afu4g00730	-5.14	-5.1	-6.21	HHE domain protein
Afu4g00740	-4.29	-5.6	-6.02	hypothetical protein
Afu4g00820	-6.07	-2.45	-4.18	reverse transcriptase, RNaseH
Afu4g00860	-4.56	-4.64	-5.36	conserved hypothetical protein
Afu4g00870	-2.49	-0.66	-0.55	antigenic cell wall galactomannoprotein, putative
Afu4g00930	-2.76	-1.39	-1.67	CorA family metal ion transporter, putative
Afu4g00940	-1.86	-1.6	-2.27	short chain dehydrogenase, putative
Afu4g01240	-2.72	-1.57	-1.62	hypothetical protein
Afu4g05860	-2.31	-1.89	-2.55	mitochondrial NADH-ubiquinone oxidoreductase 20 kD subunit, putative
Afu4g05870	-3.14	-3.51	-4.42	oxidoreductase, short-chain dehydrogenase/reductase family
Afu4g05880	-1.21	-1.93	-2.1	Mpp10 protein superfamily
Afu4g05900	-2.84	-1.65	-2.52	conserved hypothetical protein
Afu4g05990	-1.71	-1.49	-2.33	conserved hypothetical protein
Afu4g06170	-3.37	-2.29	-2.84	conserved hypothetical protein
Afu4g06260	-1.42	-2.07	-2.14	mating-type switch/DNA repair protein Swi10, putative
Afu4g06360	-3.27	-2.88	-3.21	conserved hypothetical protein
Afu4g06530	-1.3	-1.77	-2.99	bZIP transcription factor (MetR), putative
Afu4g06550	-1.56	-1.81	-2.14	RING finger domain protein (Znf1), putative
Afu4g06580	-3.18	-1.89	-2.18	hypothetical protein
Afu4g06730	-1.9	-2.19	-2.84	hypothetical protein
Afu4g06770	-2.15	-1.89	-2.19	iron-sulfur cofactor synthesis protein nifU, putative
Afu4g06830	-3.29	-2.72	-3.37	SUMO conjugating enzyme (UbcI), putative
Afu4g06900	0.33	-1.39	-2.13	asparagine synthetase (glutamine-hydrolyzing) 2
Afu4g06950	-0.08	-0.9	-2.18	related to (VAMP)-associated protein
Afu4g07230	-1.75	-2.2	-3.12	RecQ family helicase RecQ, putative

Afu4g07490	-0.94	-2.32	-2.7	hypothetical protein
Afu4g07550	-1.52	-2.6	-2.87	G-patch domain protein (Spp2), putative
Afu4g07650	-1.18	-1.37	-2.04	peptidyl-prolyl cis-trans isomerase (CypB), putative
Afu4g07660	-2.65	-3.36	-2.77	ATP dependent RNA helicase (Dbp1), putative
Afu4g07850	-1.77	-1.62	-2.28	endoglucanase, putative
Afu4g07880	-1.22	-2.04	-2.25	conserved hypothetical protein
Afu4g07930	-1.29	-2.65	-2.47	hypothetical protein
Afu4g08150	-1.73	-1.78	-2.21	hypothetical protein
Afu4g08380	-2.79	-2.54	-1.39	hypothetical protein
Afu4g08390	-2.14	-2	-2.38	hypothetical protein
Afu4g08410	-0.1	-1.61	-2.15	mannose-6-phosphate isomerase, class I
Afu4g08440	-1.06	-2.54	-3.45	Patatin-like serine hydrolase, putative
Afu4g08490	-1.62	-1.51	-2.2	acyl-CoA dehydrogenase, putative
Afu4g08510	-1.83	-1.7	-2.04	NA
Afu4g08750	-3.58	-1.58	-1.25	hypothetical protein
Afu4g08780	-1.6	-2.91	-3.66	hypothetical protein
Afu4g08790	-2.61	-2.63	-3.21	conserved hypothetical protein
Afu4g08800	-1.68	-2.26	-2.04	ABC a-pheromone efflux pump AtrD
Afu4g08850	-3.9	-1.43	-1.72	hypothetical protein
Afu4g08890	-3.1	-2.02	-1.95	aldo-keto reductase family protein, putative
Afu4g08900	-1.13	-2.23	-2.66	CDK-activating kinase assembly factor MAT1
Afu4g08910	-1.89	-2.07	-2.2	hypothetical protein
Afu4g08960	0.03	-1.72	-3.59	GPI anchored protein, putative
Afu4g09100	-2.17	-1.86	-1.24	DnaJ domain protein
Afu4g09140	-1.24	-1.97	-3.2	ornithine aminotransferase
Afu4g09250	-3.2	-2.41	-2.42	hypothetical protein
Afu4g09670	-2.22	-1.71	-1.75	hypothetical protein
Afu4g09920	-3.79	-1.16	0.7	conserved hypothetical protein
Afu4g10040	-0.56	-1.24	-2.1	Tlg SNARE complex subunit (Tlg2), putative
Afu4g10110	-2.49	-3.28	-3.83	homeobox transcription factor, putative
Afu4g10280	-1.53	-2.48	-3.51	histidine containing phosphotransmitter protein, putative
Afu4g10310	-0.18	-1.37	-2.06	hypothetical protein
Afu4g10340	-2.91	-1.59	-1.68	C6 finger domain protein, putative
Afu4g10530	-2.01	-1.19	-1.67	hypothetical protein
Afu4g10540	-2.52	-2.84	-2.89	bdf1 protein
Afu4g10610	-2.76	0.2	0.24	hypothetical protein
Afu4g10690	-1.99	-2.5	-2.09	Iron-sulfur cluster assembly accessory protein
Afu4g10790	-1.6	-2.68	-3.58	phosphoribosyl diphosphate synthase isoform 4

Afu4g10810	-1.09	-2.13	-1.94	hypothetical protein
Afu4g11110	-0.44	-1.29	-2.92	C2 domain protein
Afu4g11140	-1.03	-1.5	-2.25	DNA polymerase iota, putative
Afu4g11270	-2.79	-2.81	-2.46	hypothetical protein
Afu4g11280	-3.57	-3.54	-4.28	DUF409 domain protein
Afu4g11480	-2.2	-3.03	-2.93	C2H2 finger domain protein, putative
Afu4g11560	-0.62	-1.67	-2.54	vacuolar protein sorting-associated protein vps13
Afu4g11630	-1.51	-1.69	-2.63	hypothetical protein
Afu4g11670	-2.17	-0.14	-1.64	hypothetical protein
Afu4g11710	-5.43	-4.92	-5.94	oxidoreductase, zinc-binding dehydrogenase family superfamily
Afu4g11860	-2.99	-3.04	-2.93	formin binding protein 21
Afu4g11960	-3.57	-3.51	-3.38	Iron only hydrogenase large subunit, C-terminal domain containing protein
Afu4g11970	-3.3	-2.39	-1.96	metallothionein-I gene transcription activator
Afu4g12040	-1.04	-2.23	-3.48	oxidosqualene:lanosterol cyclase
Afu4g12050	-1.5	-1.57	-2.1	thermoresistant gluconokinase
Afu4g12390	-1.37	-2.19	-2.9	cell differentiation protein (Rcd1), putative
Afu4g12490	-4.51	-2.92	-3.94	guanine nucleotide exchange factor VPS9, putative
Afu4g12510	-2.77	-1.82	-0.26	hypothetical protein
Afu4g12550	-1.62	-2.13	-1.64	hypothetical protein
Afu4g12760	-1.55	-1.8	-2.11	SAM binding motif containing protein
Afu4g12910	-2.22	-1.75	-2.19	ubiquitin C-terminal hydrolase CreB
Afu4g13120	-1.55	-2.45	-2.19	glutamine synthetase
Afu4g13150	-0.92	-2.03	-2.69	DUF159 domain protein
Afu4g13180	-0.11	-1.37	-2.05	TPR repeat protein
Afu4g13210	-3.57	-3.84	-3.99	hypothetical protein
Afu4g13220	-3.04	-3.16	-2.65	hypothetical protein
Afu4g13230	-3.81	-3.47	-3.65	regulatory protein weta
Afu4g13240	-1.99	-1.06	-2.03	conserved hypothetical protein
Afu4g13300	-1.77	-2.59	-2.84	hypothetical protein
Afu4g13340	-1.34	-1.71	-2.1	DUF907 domain protein
Afu4g13350	-2.44	-0.92	-0.82	U1 small nuclear ribonucleoprotein C, putative
Afu4g13460	-1.84	-2	-2.26	SNF2 family helicase/ATPase, putative
Afu4g13610	-3.06	-1.63	-1.89	hypothetical protein
Afu4g13620	-2.58	-1.76	-1.81	hypothetical protein
Afu4g13750	-3.03	-0.23	-0.31	Deuterolysin metalloprotease, putative
Afu4g13820	-3.03	-1.63	-2.12	multidrug transporter, putative
Afu4g13970	-3.39	-2.55	-0.42	conserved hypothetical protein

Afu4g14180	-3.39	-0.72	-0.33	hypothetical protein
Afu4g14370	-4.52	-1.01	-3.44	LINE-1 class reverse transcriptase, RNase H, putative
Afu4g14380	-3.04	-1.51	-1.95	conserved hypothetical protein
Afu4g14450	-1.77	-2.37	-1.91	D-mannonate oxidoreductase
Afu4g14510	-1.12	-1.31	-2.01	hypothetical protein
Afu4g14630	-1.15	-2.96	-3.2	FAD binding domain protein
Afu4g14760	-5.77	-3.33	-4.46	ABC multidrug transporter, putative
Afu4g14770	-4.35	-2.81	-2.17	squalene-hopene-cyclase, putative
Afu4g14860	-4.37	-1.81	-2.94	NA
Afu4g14870	-5.9	-2.83	-4.46	LINE-1 class reverse transcriptase, RNaseH, putative
Afu5g00160	-4.01	-3.92	-4.57	MFS polyamine transporter, putative
Afu5g00170	-2.15	-1.85	-2.01	extracellular serine treonine rich protein
Afu5g00650	-3.18	0.58	-0.85	hypothetical protein
Afu5g00760	-0.83	-1.5	-2.4	chitin synthase C
Afu5g00770	-2.15	-1.99	-2.83	integral membrane protein, putative
Afu5g00790	-5.99	-4.5	-5.44	ABC multidrug transporter, putative
Afu5g00800	-4.17	-3.28	-4.73	conserved hypothetical protein
Afu5g00810	-6.76	-5.33	-6.4	hypothetical protein
Afu5g00870	-2.12	-0.93	-1.96	hypothetical protein
Afu5g01020	-1.51	-2.1	-1.5	DUF858 domain protein
Afu5g01190	-3.51	-1.72	1.15	conserved hypothetical protein
Afu5g01220	-2.28	-1.92	-1.47	hypothetical protein
Afu5g01270	-2.68	-2.67	-3.4	C6 transcription factor, putative
Afu5g01280	-3.31	-2.41	-2.64	conserved hypothetical protein
Afu5g01290	-2.36	-3.05	-2.56	zinc-binding oxidoreductase, putative
Afu5g01300	-2.6	-1.93	-1.41	integral membrane protein
Afu5g01340	-2.79	-3.69	-3.68	lysophospholipase, putative
Afu5g01430	-3.69	-2.83	-3.34	ThiJ/PfpI family protein
Afu5g01500	-1.25	-2.18	-1.65	homocysteine S-methyltransferase, putative
Afu5g01510	-1.52	-2.59	-2.37	amino acid transporter
Afu5g01520	-2.1	-1.93	-0.94	major facilitator superfamily protein superfamily
Afu5g01620	-2.14	0.61	0.63	extracellular proline-rich protein
Afu5g01640	-2.2	-1.84	-2.31	ankyrin repeat protein
Afu5g01650	-2.82	-1.73	-0.77	bZIP transcription factor JlbA/IDI-4, putative
Afu5g01670	-2.51	-1.76	-1.98	hypothetical protein
Afu5g01740	-2.34	-2.39	-2.38	deoxyhypusine synthase, putative
Afu5g01840	-1.61	-0.85	-2.07	conserved hypothetical protein
Afu5g01930	-4.66	-3.51	-3.84	hypothetical protein

Afu5g01990	-2.48	0.89	1	BYS1 domain protein, putative
Afu5g02100	-2.47	-1.38	-2.09	hypothetical protein
Afu5g02110	-1.54	-3.09	-3.8	hypothetical protein
Afu5g02200	-2.64	-2.03	-1.04	Mitochondrial import inner membrane translocase subunit (TIM22), putative
Afu5g02260	-2.22	-2.27	-2.37	ABC multidrug transporter, putative
Afu5g02300	-4.03	-3.43	-3.57	peroxidase, putative
Afu5g02320	-2.99	-0.02	-0.26	hypothetical protein
Afu5g02330	-2.51	1.31	1.12	major allergen Asp F1
Afu5g02380	-1.77	-1.93	-2.31	conserved hypothetical protein
Afu5g02390	-0.5	-2.23	-3.03	Auxin Efflux Carrier superfamily
Afu5g02400	-2.51	-3.98	-5.01	catabolite degradation protein, putative
Afu5g02410	-0.68	-2.24	-2.16	DEAD/DEAH box helicase, putative
Afu5g02430	-0.8	-1.35	-2.34	ATP dependent DNA ligase domain protein
Afu5g02560	-2.3	-2.19	-2.5	SCS1 product
Afu5g02580	-2.03	-1.76	-1.65	cell cycle control protein Cwf16, putative
Afu5g02610	-3.13	-2.21	-2.04	cytochrome P450, putative
Afu5g02880	-7.28	-5.53	-6.46	C6 transcription factor, putative
Afu5g02890	-2.46	-3.61	-3.46	conserved hypothetical protein
Afu5g03140	-2.33	-3.11	-3.18	GTP cyclohydrolase I, putative
Afu5g03170	-2.69	-0.74	-1.39	hypothetical protein
Afu5g03230	-3.1	-2	-2.74	stress response RCI peptide, putative
Afu5g03250	-0.86	-1.73	-2.34	ubiquitin C-terminal hydrolase (HAUSP), putative
Afu5g03270	-2.95	-2.14	-3.08	hypothetical protein
Afu5g03330	0.78	-0.47	-2.25	conserved hypothetical protein
Afu5g03340	-2.37	-2.4	-2.37	hypothetical protein
Afu5g03350	-0.02	-1.17	-2.21	glutamine dependent NAD+ synthetase, putative
Afu5g03390	-2.26	-2.65	-3.17	conserved hypothetical protein
Afu5g03430	0.53	-1	-2.23	PHD transcription factor (Rum1), putative
Afu5g03460	0	-1.33	-2.07	thymidylate kinase
Afu5g03620	-3.8	-2.83	-2.53	endonuclease/transposase
Afu5g03870	-2.17	-1.94	-1.36	conserved hypothetical protein
Afu5g03930	-1.57	-3.06	-3.8	alcohol dehydrogenase, putative
Afu5g03940	-1.43	-2.42	-3.41	alpha-1,3-glucanase, putative
Afu5g04040	-4.66	-2.16	-3	conserved hypothetical protein
Afu5g04060	-2.07	-2.32	-1.67	ubiquitin conjugating enzyme (UbcH), putative
Afu5g04070	-2.11	-1.4	-1.42	Spo11
Afu5g04260	-1.91	-2.63	-1.81	arginine transporter, putative

Afu5g04380	-3.43	-2.89	-3.62	conserved hypothetical protein
Afu5g04410	-1.63	-1.88	-2.56	hypothetical protein
Afu5g05480	-4.02	-4.33	-5.24	Rheb GTPase RhbA
Afu5g05600	-1.56	-2.08	-2.65	forkhead transcription factor (Sep1), putative
Afu5g05610	-3.6	-3.67	-4.29	cell cycle control protein Cwf14, putative
Afu5g05750	-3.01	-2.89	-3.1	protein kinase, putative
Afu5g05780	-2.01	-2.75	-3.29	hypothetical protein
Afu5g05790	-1.95	-2.12	-2.37	ubiquitin ligase subunit HrtA, putative
Afu5g05910	-2.16	-1.62	-1.9	hypothetical protein
Afu5g06040	-0.29	-1.04	-2	UV excision repair protein (RadW), putative
Afu5g06060	-2.73	-2.67	-3.37	sulfur metabolism regulator SkpA, putative
Afu5g06070	-2.71	-2.02	-2.24	ABC multidrug transporter Mdr1
Afu5g06140	-3.15	-3.56	-3.79	histone acetyltransferase, putative
Afu5g06170	-1.2	-2.16	-1.41	conserved hypothetical protein
Afu5g06260	-2.15	-2.26	-3	SNF2 family helicase/ATPase (Ino80), putative
Afu5g06330	-1.62	-2.23	-1.93	RSC complex subunit (Sth1), putative
Afu5g06340	-1.93	-2.69	-2.56	BAR domain protein
Afu5g06370	-0.86	-2.57	-2.67	hypothetical protein
Afu5g06380	-2.06	-1.51	-1.51	hypothetical protein
Afu5g06400	-1.24	-2.38	-2.26	hypothetical protein
Afu5g06470	-2.06	-1.86	-1.89	serine/threonine protein kinase, putative
Afu5g06650	-2.08	-0.62	-1.29	hypothetical protein
Afu5g06690	-2.04	-1.07	-0.5	transcriptional elongation protein Spt4, putative
Afu5g06820	-3.1	-0.37	-1.16	hypothetical protein
Afu5g07020	-0.38	-2.15	-2.4	ABC transporter, putative
Afu5g07060	-1.67	-2.91	-2.81	WD repeat protein
Afu5g07110	-2.05	-2.36	-3.15	integral membrane protein
Afu5g07210	-0.97	-2.59	-2.63	homoserine O-acetyltransferase, putative
Afu5g07250	-1.41	-2.05	-2.12	DUF300 domain protein, putative
Afu5g07310	-2.21	-1.8	-2.09	DUF500 domain protein
Afu5g07460	-2.94	-2.28	-1.69	hypothetical protein
Afu5g07590	-2.32	-1.04	-0.63	hypothetical protein
Afu5g07720	-2.93	-3.3	-2.57	CCCH and RING finger protein
Afu5g07760	-0.43	-1.36	-2.01	tetracycline-efflux transporter, putative
Afu5g07860	-1.37	-2.35	-3.04	phosphatase family protein
Afu5g07870	-1.98	-2.02	-1.49	hypothetical protein
Afu5g07880	-2.22	-3.07	-3.32	a-pheromone receptor PreA
Afu5g07940	-3.91	-3.79	-4.33	hypothetical protein

Afu5g08020	-1.83	-2.86	-2.99	HLH DNA binding protein (Penr2), putative
Afu5g08170	-2.05	-1.67	-1.7	autophagocytosis protein Aut1, putative
Afu5g08200	-0.42	-2.04	-1.14	hypothetical protein
Afu5g08220	-1.27	-2.04	-2.41	hypothetical protein
Afu5g08330	-2.67	-2.7	-3.16	RNA binding protein
Afu5g08550	-1.54	-1.78	-2.13	Rho guanyl nucleotide exchange factor (Rom2), putative
Afu5g08570	0.76	-1.35	-2.05	cAMP-dependent protein kinase catalytic subunit, putative
Afu5g08710	-1.39	-2.27	-2.69	hypothetical protein
Afu5g09060	-2.27	-2.13	-2.3	RNA binding protein, putative
Afu5g09100	-1.56	-2.15	-2.22	MAP kinase, putative
Afu5g09110	-4.23	-3.72	-3.96	NA
Afu5g09170	-1.22	-2.06	-2.47	C2H2 finger domain protein, putative
Afu5g09200	-2.3	-1.99	-1.18	ubiquitin conjugating enzyme (UbcC), putative
Afu5g09230	-0.36	-1.24	-2.43	transaldolase
Afu5g09310	-1.98	-1.86	-2.05	Bax Inhibitor family protein
Afu5g09370	-2.01	-2.23	-1.65	hypothetical protein
Afu5g09440	-3.81	-2.78	-2.12	amino acid permease, putative
Afu5g09690	-2.81	-0.53	-1.52	hypothetical protein
Afu5g09710	-3.08	-1.39	-1.59	separin, putative
Afu5g09770	-2.24	-2.96	-3.29	hypothetical protein
Afu5g09780	-1.05	-1.6	-2.31	MSF multidrug transporter, putative
Afu5g09920	-1.42	-2.3	-2.41	peptidase, putative
Afu5g10160	-2.77	-2.98	-2.5	actVA 4 protein
Afu5g10180	-2.54	-2.02	-1.37	monooxygenase, putative
Afu5g10190	-2.53	-1.96	-1.34	hypothetical protein
Afu5g10200	-2.67	-2.81	-3.01	hypothetical protein
Afu5g10210	-3.23	-2.81	-2.18	hypothetical protein
Afu5g10250	-3.85	-1.57	-1.92	hypothetical protein
Afu5g10260	-2.12	-1.8	-2.23	NA
Afu5g10270	-4.4	-3.02	-2.9	heat shock protein, HSP20 family
Afu5g10420	-0.18	-1.19	-2.23	nitrate reductase, putative
Afu5g10590	-2.06	-1.68	-3	stress response RCI peptide, putative
Afu5g10620	-2.05	-1.57	-2.02	CBF/NF-Y family transcription factor, putative
Afu5g10690	0.25	-2.18	-2.77	monosaccharide transporter
Afu5g10770	-1.68	-2.41	-2.58	topisomerase II associated protein pat1 homolog
Afu5g10800	-3.46	-2.59	-2.27	G-patch domain protein, putative
Afu5g10830	-1.94	-1.95	-2.35	RNA helicase-like splicing factor (HRH1), putative
Afu5g10850	-1.14	-1.53	-2.08	hypothetical protein

Afu5g10920	0.34	-1.61	-2.55	DUF221 domain protein, putative
Afu5g11020	-1.27	-2.3	-2.25	ammonium transporter
Afu5g11080	-1.69	-1.97	-2.18	MSF multidrug transporter, putative
Afu5g11090	-2.26	-2.54	-2.78	conserved hypothetical protein
Afu5g11120	-2.21	-1.28	-1.18	DNA-directed RNA polymerases i, ii, and iii 145 kDa polypeptide
Afu5g11190	-2.63	-1.29	-1.39	hypothetical protein
Afu5g11250	-2.01	-2.52	-2	polyglutamate biosynthesis protein, putative
Afu5g11260	-3.06	-2.58	-2.91	siderophore transcription factor SreA
Afu5g11510	-1.46	-2.08	-2.02	hypothetical protein
Afu5g11520	-1.81	-2.64	-3.29	serine/threonine protein kinase (Nrc-2), putative
Afu5g11680	-3.75	-3.41	-3.36	hypothetical protein
Afu5g11690	-0.47	-1.62	-2.33	related to protein tyrosine phosphatase PPS1
Afu5g11840	-0.16	-1.73	-2.3	protein kinase, putative
Afu5g12050	-0.95	-1.87	-2.26	DNA ligase, putative
Afu5g12070	-1.01	-1.61	-2.15	conserved hypothetical protein
Afu5g12090	-3.35	-3.11	-3.5	conserved hypothetical protein
Afu5g12100	-1.87	-2.39	-2.69	pmt2 methyltransferase
Afu5g12110	-2.35	-2.99	-3	conserved hypothetical protein
Afu5g12120	-2.11	-2.08	-2.9	autophagy protein Apg16, putative
Afu5g12150	-2.24	-2.39	-3.05	PH domain protein
Afu5g12180	-0.61	-1.05	-2.22	Ran/spi1 binding protein
Afu5g12230	-3.46	-2.91	-2.96	MYND domain protein (SamB), putative
Afu5g12440	-1.99	-2.82	-3.23	cell cycle control protein (Cwf23), putative
Afu5g12580	-1.88	-2.59	-3.33	GTP binding protein (GTPBP1), putative
Afu5g12590	-1.65	-2.17	-2.12	solid-state culture expressed protein (Aos23), putative
Afu5g12630	-3.76	-3	-3.56	hypothetical protein
Afu5g12640	-0.68	-1.82	-2.4	DNA polymerase gamma
Afu5g13050	-3.27	-1.52	-2.24	kinesin family protein
Afu5g13070	-2.47	-2.12	-1.76	hypothetical protein
Afu5g13270	-1.63	-2.51	-2.82	PalH
Afu5g13560	-0.01	-1.59	-2.33	FHA domain protein
Afu5g13590	-0.87	-2.06	-2.14	conserved hypothetical protein
Afu5g13630	-2.73	-1.15	-0.56	EF-hand superfamily protein
Afu5g13760	-2.53	-2.16	-2.23	hypothetical protein
Afu5g13840	-3.13	-2.32	-3.18	NUDIX domain, putative
Afu5g13870	-3.36	-4.53	-4.97	mlo3 protein
Afu5g13930	-1.06	-2.36	-2.64	CCCH finger DNA binding protein, putative
Afu5g13950	-2.08	-0.68	-1.5	conserved hypothetical protein

Afu5g14020	-0.73	-2.43	-2.73	hypothetical protein
Afu5g14070	-2	-0.87	-1.56	conserved hypothetical protein
Afu5g14080	-1.47	-2.68	-2.4	hypothetical protein
Afu5g14200	-1.94	-2.13	-2.75	hypothetical protein
Afu5g14210	-3.1	-0.83	-1.65	glucose-repressible gene protein-related protein
Afu5g14290	-3.58	-2.68	-2.73	C6 transcription factor, putative
Afu5g14300	-1.27	-2.57	-2.78	alpha,alpha-trehalose-phosphate synthase subunit, putative
Afu5g14310	-1.6	-2.49	-2.17	short chain dehydrogenase/reductase family protein
Afu5g14320	-2.68	-3.25	-2.55	hypothetical protein
Afu5g14340	-2.55	-0.75	0.63	oxidoreductase, short-chain dehydrogenase/reductase family, putative
Afu5g14350	-3.96	-4.67	-4.92	c-24(28) sterol reductase
Afu5g14650	-2.32	0.74	1.89	RING finger protein
Afu5g14830	-2.47	-1.49	-1.64	glyoxalase family protein
Afu5g14930	-2.4	-0.32	-0.32	conserved hypothetical protein
Afu5g14990	-3.23	-1.98	-2.49	hypothetical protein
Afu5g15010	-1.73	-1.94	-2.22	arsenite permease (ArsB), putative
Afu6g00170	-2.07	-0.99	-0.04	hypothetical protein
Afu6g00460	-2.75	-3.23	-2.99	hypothetical protein
Afu6g00770	-3.74	-3.94	-4.51	extracellular arabinanase, putative
Afu6g00780	-5.48	-2.79	-4.18	LINE-1 class reverse transcriptase, RNaseH, putative
Afu6g01980	-3.65	-2.05	-2.51	haemolysin-III family protein
Afu6g02020	-3.66	-3.58	-4.66	hypothetical protein
Afu6g02070	-1.29	-2.07	-2.56	phospholipid-translocating P-type ATPase domain-containing protein
Afu6g02110	-2.24	-2.55	-2.99	SRF-type transcription factor (Umc1), putative
Afu6g02290	-3.49	-1.95	-3.11	hypothetical protein
Afu6g02330	-2.5	-2.22	-1.96	hypothetical protein
Afu6g02420	-1.3	-1.48	-2.49	ubiquitin conjugating enzyme (UbcM), putative
Afu6g02580	-3.92	-3.55	-3.82	hypothetical protein
Afu6g02640	-1.59	-2.36	-2.26	hypothetical protein
Afu6g02660	-1.32	-1.79	-2.31	conserved hypothetical protein
Afu6g02680	-3.25	-3.92	-4.69	ankyrin repeat and BTB/POZ domain protein
Afu6g02820	-1.11	-1.98	-3.09	metalloreductase, putative
Afu6g02830	-2.67	-0.98	-0.85	hypothetical protein
Afu6g03080	-3.86	-3.11	-3.54	ABC multidrug transporter, putative
Afu6g03090	-3.65	-2.89	-2.99	cytochrome P450 alkane hydroxylase, putative
Afu6g03120	-1.9	-2.28	-2.52	hypothetical protein

Afu6g03130	-4.14	-3.76	-4.22	hypothetical protein
Afu6g03140	-4.34	-3.78	-3.75	isp4 protein, putative
Afu6g03210	-5.13	-3.77	-5.61	conidiation-specific protein 10
Afu6g03320	-2.35	-1.26	0.7	MFS drug transporter, putative
Afu6g03370	-1.54	-2.62	-2.17	oxidoreductase, short-chain dehydrogenase/reductase family
Afu6g03400	-2.22	0.23	0.14	hypothetical protein
Afu6g03800	-2.11	-0.37	-0.67	hypothetical protein
Afu6g03890	-0.28	-1.36	-2.09	catalase A
Afu6g04310	-1.64	-2.26	-2.57	Pumilio 2
Afu6g04360	-2.29	-2.39	-1.92	ABC drug exporter AtrF
Afu6g04390	-3.06	-4	-4.72	conserved hypothetical protein
Afu6g04470	-4.13	-2.82	-3.11	hypothetical protein
Afu6g04580	-1.7	-1.52	-2.35	NIF domain protein
Afu6g04630	-2.37	-2.17	-1.95	conserved hypothetical protein
Afu6g04820	-2.61	-2.31	-1.24	para-aminobenzoate synthase PabaA
Afu6g04950	-1.12	-1.72	-2.52	mitochondrial GTPase (Mss1), putative
Afu6g05100	-0.66	-1.52	-2.04	6-phosphofructo-2-kinase, putative
Afu6g05120	-0.93	-1.89	-2.96	glycogen synthase kinase-3, putative
Afu6g05140	-1	-2.45	-2.89	sterol delta 5,6-desaturase ERG3
Afu6g05180	-1.97	-2.76	-3.2	splicing factor 3b subunit 4
Afu6g05330	-2.03	-1.78	-2.72	hypothetical protein
Afu6g06540	-2.27	-2.41	-2.08	proteasome component (Ecm29), putative
Afu6g06550	-1.67	-2.01	-1.45	SNF2 family helicase/ATPase, putative
Afu6g06730	-3.41	-2.04	-1.69	l-fucose permease, putative
Afu6g06790	0.12	-1.39	-2.41	mannosyl-oligosaccharide alpha-1,2-mannosidase
Afu6g07170	-1.85	-1.6	-2.18	conserved hypothetical protein
Afu6g07330	-2.05	-3.07	-3.88	methionine aminopeptidase, type I, putative
Afu6g07440	-2.62	-3.1	-3.08	1-phosphatidylinositol-3-phosphate 5-kinase (Fab1), putative
Afu6g07530	-0.29	-1.01	-2.25	bZIP transcription factor, putative
Afu6g07790	-3.66	-1.5	-1.39	hypothetical protein
Afu6g07830	-1.86	-1.82	-2.82	stromal membrane-associated protein
Afu6g08020	-1.95	-1.62	-3.26	ABC transporter, putative
Afu6g08030	-1.57	-2.26	-2.72	hypothetical protein
Afu6g08180	-2.21	-0.15	-0.05	hypothetical protein
Afu6g08270	-2.3	-1.5	-1.69	hypothetical protein
Afu6g08570	-2.29	-0.74	-0.88	DNA damage repair protein Mus42, putative
Afu6g08730	-0.46	-1.54	-2.03	6-phosphogluconate dehydrogenase, decarboxylating
Afu6g08980	-0.16	-1	-2.21	FF domain protein

Afu6g09020	-1.98	-2.59	-2.98	GPI transamidase component Gpi16, putative
Afu6g09090	-2.67	-1.38	-2.38	conserved hypothetical protein
Afu6g09100	-1.31	-1.02	-2.3	hypothetical protein
Afu6g09310	-3.13	-1.89	-1.82	class V chitinase, putative
Afu6g09340	-3.81	-2.23	-3.15	hypothetical protein
Afu6g09460	-3.07	-1.55	-2.28	NA
Afu6g09470	-5.73	-2.67	-3.9	reverse transcriptase, RNaseH, putative
Afu6g09490	-2.42	-1.17	-1.21	NA
Afu6g09570	-2.46	-3.21	-2.26	conserved hypothetical protein
Afu6g09930	-0.94	-1.66	-2.75	bZIP transcription factor (AP-1), putative
Afu6g09940	-1.06	-1.26	-2.32	transposase
Afu6g10050	-2.14	-1.33	-1.16	small oligopeptide transporter, OPT family
Afu6g10150	-3.71	-2.95	-3.22	hypothetical protein
Afu6g10180	-2.51	-2.13	-2.42	hypothetical protein
Afu6g10190	-2.83	-2.31	-2.26	hypothetical protein
Afu6g10240	-0.04	-2.05	-2.5	sensor histidine kinase/response regulator Fos-1
Afu6g10270	-0.1	-1.92	-2.36	NA
Afu6g10290	-2.36	-1.44	-1.74	receptor L domain protein
Afu6g10500	-1.87	-2.87	-2.19	conserved hypothetical protein
Afu6g10530	-2.73	-0.8	-0.73	transcriptional elongation regulator (Elongin C), putative
Afu6g10720	-2.71	-3.52	-4.19	alpha-ketoglutarate-dependent taurine dioxygenase
Afu6g10780	-2.39	-1.83	-2.04	carboxylesterase, putative
Afu6g10790	-4.09	-3.78	-4.12	MFS amine transporter, putative
Afu6g10800	-1.98	-2.44	-2.75	carboxylesterase, putative
Afu6g10840	-3.91	-2.92	-3.34	hypothetical protein
Afu6g10860	-3.2	-2.76	-2.35	hypothetical protein
Afu6g10900	-2.07	-3.24	-4.45	UV-endonuclease UVE-1
Afu6g10950	-3.63	-2.62	-3.22	NA
Afu6g11060	-2.36	-1.67	-1.49	DnaJ domain protein
Afu6g11180	-2.05	-1.4	-1.93	conserved hypothetical protein
Afu6g11250	-1.26	-1.82	-2.21	C2H2 finger domain protein, putative
Afu6g11550	-3.13	-2.9	-2.28	hypothetical protein
Afu6g11670	-1.07	-3.18	-3.12	conserved hypothetical protein
Afu6g11690	-3.21	-2.06	-2.48	NA
Afu6g11810	-2.52	-1.59	-2.11	RTA1 domain protein, putative
Afu6g12000	-3.13	-1.46	-1.74	hypothetical protein
Afu6g12010	-1.64	-1.5	-2.58	glycosyl hydrolase, family 3, putative
Afu6g12200	-3.06	-0.29	-0.33	hypothetical protein

Afu6g12220	-3.24	-2.34	-2.35	isochorismatase family hydrolase, putative
Afu6g12290	-0.1	-0.99	-2.17	PH domain protein
Afu6g12430	-2.91	-2.39	-2.56	Ran-interacting protein MOG1, putative
Afu6g12440	-2.39	-2.53	-2.83	conserved hypothetical protein
Afu6g12450	-2.78	-1.91	-3.65	chaperone/heat shock protein Hsp12, putative
Afu6g12460	-3.07	-2.05	-3.6	conserved hypothetical protein
Afu6g12540	-1.04	-1.72	-2.36	RING finger protein
Afu6g12570	-0.85	-1.72	-2.01	EH domain binding protein epsin 2
Afu6g12640	-2.66	-3.42	-3.22	conserved hypothetical protein
Afu6g12650	-2.95	-2.36	-1.73	conserved hypothetical protein
Afu6g12920	-2.05	-1.14	-1.64	C2H2 finger domain protein, putative
Afu6g13000	-2.48	-1.57	-1.48	NA
Afu6g13020	-3.66	-2.94	-3.23	AP-3 adaptor complex subunit sigma, putative
Afu6g13060	-2.1	-1.14	-2.3	conserved hypothetical protein
Afu6g13130	-0.99	-1.53	-2.13	transcription initiation factor TFIIE, beta subunit, putative
Afu6g13220	-4.08	-3.45	-3.11	hypothetical protein
Afu6g13290	-3.03	-2.78	-3.49	SNF2 family helicase/ATPase, putative
Afu6g13380	-3.05	-0.72	0.66	hypothetical protein
Afu6g13430	-2.6	-1.41	-1.63	multispanning membrane protein, putative
Afu6g13440	-2.87	-2.41	-2.81	choline sulfatase, putative
Afu6g13470	-1.08	-2.09	-2.06	conserved hypothetical protein
Afu6g13580	-2.63	-1.67	-1.59	hypothetical protein
Afu6g13670	-0.51	-2.3	-2.64	conserved hypothetical protein
Afu6g13780	-2.94	-0.74	0.04	multidrug resistant protein, putative
Afu6g13840	-2.1	1.64	1.84	conserved hypothetical protein
Afu6g13940	-3.49	-3.25	-2.86	P450-monooxygenase, putative
Afu6g14130	-3.01	-2.27	-2.84	ubiquitin conjugating enzyme, putative
Afu6g14270	-2.15	-1.34	-2.26	hypothetical protein
Afu6g14380	-2.75	-1.23	-0.78	hypothetical protein
Afu6g14540	-3.06	1.05	1.46	endo-1,3(4)-beta-glucanase, putative
Afu6g14630	-2.13	-1.99	-2.36	conserved hypothetical protein
Afu6g14660	-5.41	-2.64	-3.95	reverse transcriptase, RNaseH
Afu7g00100	-2.09	-1.63	-1.4	LINE-1 class reverse transcriptase, RNaseH, putative
Afu7g00120	-2.21	-0.65	0.2	metallo-beta-lactamase domain protein
Afu7g00180	-2.21	-0.96	0.36	NAD dependent epimerase/dehydratase, putative
Afu7g00220	-3.4	-3.07	-1.63	plasma membrane hexose transporter, putative
Afu7g00270	-1.82	-3.32	-3.46	FAD binding monooxygenase, putative
Afu7g00300	-2.49	-2.47	-1.38	squalene-hopene-cyclase, putative

Afu7g00390	-3.2	-2.55	-2.07	MFS multidrug transporter, putative
Afu7g00400	-4.61	-3.35	-3.33	hypothetical protein
Afu7g00410	-4.57	-3.16	-2.56	C6 transcription factor, putative
Afu7g00450	-3	-1.5	-1.19	GPI anchored protein, putative
Afu7g00470	-2.86	-3.07	-3.21	hypothetical protein
Afu7g00740	-2.37	-1.85	-2.25	protein kinase, putative
Afu7g00860	-2.22	-1.21	-1.3	lipoxygenase, putative
Afu7g00870	-2.26	-1.33	-1.19	exonuclease, putative
Afu7g00880	-2.05	-1.71	-1.45	hypothetical protein
Afu7g00960	-2.11	-1.65	-2.19	extracellular cysteine-rich protein, putative
Afu7g00980	-2.96	-2.08	0.66	NA
Afu7g00990	-3.02	-2.57	-0.72	integral membrane protein
Afu7g01030	-2.29	-0.88	-0.44	Calcium-transporting ATPase 1 (PMC1), putative
Afu7g01120	-3.91	-2.26	-1.91	NA
Afu7g01250	-1.44	-2.14	-1.62	hypothetical protein
Afu7g01350	-1.07	-2.34	-2.54	hypothetical protein
Afu7g01380	-3.38	-1.67	-2.4	anaphase promoting complex subunit Apc11, putative
Afu7g01430	-1.88	-2.94	-3.66	opsin 1
Afu7g01440	-1.05	-1.86	-2.44	hypothetical protein
Afu7g01470	-2.02	-1.56	-1.24	integral membrane protein, Mpv17/PMP22 family, putative
Afu7g01620	-1.23	-2.34	-2.58	hypothetical protein
Afu7g01640	-2.01	-1.97	-2.61	C6 transcription factor, putative
Afu7g01780	-4.61	-1.95	-2.67	hypothetical protein
Afu7g01800	-2.59	-1.73	-1.94	AT DNA binding protein, putative
Afu7g01810	-3.13	-2.38	-2.41	C6 transcription factor, putative
Afu7g01850	-2.26	-2.31	-2.62	RNA polymerase Rpc34 subunit superfamily
Afu7g01920	-2.09	-2.56	-3.61	DNA-dependent RNA polymerase II RPB140
Afu7g02010	-4.82	-1.12	0.76	hypothetical protein
Afu7g02050	-1.13	-1.47	-2.38	hypothetical protein
Afu7g02160	-2.52	-1.37	-1.68	DDE superfamily endonuclease/transposase
Afu7g02170	-1.36	-2.35	-2.38	RNA binding protein, putative
Afu7g02210	-2.32	-2.7	-2.94	conserved hypothetical protein
Afu7g02330	-2.18	-1.66	-1.98	hypothetical protein
Afu7g02390	-2.46	-2.27	-2.77	hypothetical protein
Afu7g02420	-1.1	-2.36	-3.21	malate dehydrogenase, putative
Afu7g02440	-2.75	-2.92	-3.18	extracellular conserved glycine-rich protein
Afu7g02600	-0.01	-1.56	-2.32	hypothetical protein
Afu7g02610	-0.25	-2.09	-2.21	WD repeat protein

Afu7g02620	-3.13	-3.07	-3.37	DNA-directed RNA polymerases N/8 kDa subunit superfamily
Afu7g03770	-2.48	-3.48	-3.88	hypothetical protein
Afu7g03780	-2.22	-2.49	-2.92	YT521-B-like splicing factor, putative
Afu7g03820	-1.69	-2.37	-1.84	DNA excision repair protein (Rad16), putative
Afu7g03910	-2.01	-2.08	-2.96	C2H2 zinc finger protein
Afu7g04030	-2.97	-2.14	-2.14	hypothetical protein
Afu7g04100	-1.77	-2.03	-2.24	conserved hypothetical protein
Afu7g04140	-1.77	-2.24	-2.83	L-galactose dehydrogenase (L-GalDH), putative
Afu7g04150	-1.94	-2.38	-1.98	CGI-136 protein
Afu7g04640	-2.17	-2.28	-2.02	conserved hypothetical protein
Afu7g04710	-2.72	-1.87	-1.26	NF-X1 finger transcription factor, putative
Afu7g04860	-1.03	-2.06	-1.41	dimethyladenosine transferase
Afu7g04880	-2.5	-2.23	-1.72	UDP-glucose,sterol transferase
Afu7g04930	-5.13	-4.92	-4.84	alkaline serine protease (PR1), putative
Afu7g04950	-1.81	-4.22	-4.45	lipase, putative
Afu7g05050	-1.9	-3.11	-3.38	hypothetical protein
Afu7g05200	-3.72	-2.53	-3.04	conserved hypothetical protein
Afu7g05230	-2.18	-1.01	-2.03	conserved hypothetical protein
Afu7g05430	-0.59	-2.27	-2.87	nonsense-mediated mRNA decay factor (Upf2), putative
Afu7g05490	-5.31	-4.11	-5.03	hypothetical protein
Afu7g05500	-3.04	-3.41	-3.98	theta class glutathione S-transferase
Afu7g05650	-3	-1.89	-2.16	glutamine-serine rich protein MS8, putative
Afu7g05660	-1.96	-2.11	-1.05	elongation factor EF-3, putative
Afu7g05830	-2.6	-2.1	-0.39	MFS sugar transporter, putative
Afu7g05910	-1.86	-2.03	-2.41	purine permease, putative
Afu7g05980	-1.45	-2	-2.99	small nuclear ribonucleoprotein SmE, putative
Afu7g06040	-2.41	-0.16	-0.19	integral membrane protein, putative
Afu7g06260	-2.49	-3.31	-3.08	alcohol dehydrogenase, zinc-containing
Afu7g06270	-2.87	-2.56	-2.96	cyanamide hydratase
Afu7g06280	-2.78	-2.59	-2.79	conserved hypothetical protein
Afu7g06320	-1.26	-2.07	-2.1	C6 transcription factor, putative
Afu7g06450	-2.12	-0.73	0.17	hypothetical protein
Afu7g06530	-2.08	-1.2	-1.62	hypothetical protein
Afu7g06640	-2.44	-1.7	-1.63	hypothetical protein
Afu7g06840	-5.4	-5.39	-5.98	class III aminotransferase
Afu7g06860	-2.08	-2.15	-1.96	hypothetical protein
Afu7g06870	-1.23	-2.95	-3.71	Tf1-like reverse transcriptase, integrase, putative
Afu7g06880	-2.43	-2.72	-3.02	hypothetical protein

Afu7g06890	-3.62	-4.22	-5.27	Dyp-type peroxidase family protein
Afu7g06900	-1.02	-3.28	-3.63	branched-chain amino acid aminotransferase, putative
Afu7g07050	-2.52	-0.44	-1.29	hypothetical protein
Afu7g07150	-3.37	-1.15	-2.71	NA
Afu7g07160	-2.01	-1.46	-1.87	NA
Afu7g07190	-2.25	-0.6	-1.45	NA
Afu7g08210	-3.59	-0.04	-2.15	reverse transcriptase, putative
Afu7g08220	-1.9	-2.01	-2.59	hypothetical protein
Afu7g08230	-2.95	-1.08	-1.7	NA
Afu7g08260	-1.71	-2	-2.52	hypothetical protein
Afu7g08280	-3.17	-1.77	-1.33	hypothetical protein
Afu7g08300	-2.9	-0.45	-1.11	hypothetical protein
Afu7g08390	-2.34	-1.85	-1.9	hypothetical protein
Afu7g08410	-4.01	-3.07	-3.87	Tc1-mariner transposase, putative
Afu7g08430	-1.83	-2.17	-2.19	hypothetical protein
Afu7g08500	-2.86	-1.12	-2.28	NACHT and WD40 domain protein
Afu7g08560	-1.66	-2.63	-3.29	hypothetical protein
Afu7g08570	-2.17	-3.59	-4.03	hypothetical protein
Afu7g08580	-2.86	-2.63	-3.74	dynamin GTPase, putative
Afu8g00310	-5.54	-2.6	-4.08	LINE-1 class reverse transcriptase, RNaseH, putative
Afu8g00330	-3.62	-1.43	-2.84	endonuclease/reverse transcriptase/RNaseH, putative
Afu8g00440	-2.3	-1.37	1.5	steroid monooxygenase, putative
Afu8g00450	-2.44	-2.16	-2.14	NA
Afu8g00460	-1.43	-2.27	-2.22	methionine aminopeptidase, type I, putative
Afu8g00520	-2.95	-1.54	1.4	integral membrane protein
Afu8g00620	-2.27	-1.71	-1.66	dimethylallyl tryptophan synthase, putative
Afu8g00970	-1.91	-1.7	-2.09	hypothetical protein
Afu8g00990	-2.65	-1.9	-2.43	F-box domain protein
Afu8g01040	-6.05	-2.92	-4.56	reverse transcriptase, RNaseH
Afu8g01260	-2.58	-2.21	-4.14	hypothetical protein
Afu8g01300	-1.76	-1.63	-2.13	hypothetical protein
Afu8g01330	-4.25	-4.21	-4.46	hypothetical protein
Afu8g01340	-2.82	-2.94	-3.38	MFS sugar transporter, putative
Afu8g01400	-4.96	-3.57	-3.66	mitochondrial carrier protein (Pet8), putative
Afu8g01410	-3.08	-2.99	-2.63	class V chitinase ChiB1
Afu8g01420	-1.79	-2.11	-1.59	quinone oxidoreductase, putative
Afu8g01480	-3.76	-3.64	-2.76	potassium channel, putative
Afu8g01520	-2.45	-3.07	-3.54	Pectinesterase family

Afu8g01530	-3.06	-2.91	-4.54	HHE domain protein
Afu8g01540	-2.5	-0.82	-1.16	hypothetical protein
Afu8g01570	-4.46	-3.41	-4.26	ADP-ribosylglycohydrolase family protein
Afu8g01600	-2.51	-1.84	-1.59	hypothetical protein
Afu8g01610	-3.28	-2.63	-2.7	hypothetical protein
Afu8g01760	-2.7	-1.6	-2.54	hypothetical protein
Afu8g01860	-2.48	-2.1	-3.11	hypothetical protein
Afu8g01930	-2.31	-1.2	-1.12	methyltransferase
Afu8g02110	-3.44	-3.02	-3.28	hypothetical protein
Afu8g02120	-2.93	-0.67	-1.5	conserved hypothetical protein
Afu8g02170	-2.42	-2.68	-2.94	C6 finger domain protein, putative
Afu8g02260	-3.29	-2.36	-1.36	neutral amino acid permease
Afu8g02270	-3.77	-3.11	-3.06	dihydrodipicolinate synthetase family protein
Afu8g02280	-2.78	-2.42	-2.07	C6 transcription factor, putative
Afu8g02290	-4.77	-3.78	-3.97	conserved hypothetical protein
Afu8g02490	-2.35	-1.18	-1.37	hypothetical protein
Afu8g02630	-2.1	-1.53	-2.86	extracellular exo-polygalacturonase, putative
Afu8g02690	-0.67	-1.83	-2.02	alphaN-acetylglucosamine transferase
Afu8g02720	-1.87	-2.41	-2.55	Hex2 protein
Afu8g02750	-2.25	-1.45	-1.25	nucleolar protein CgrA
Afu8g02810	-1.09	-2.26	-2.49	conserved hypothetical protein
Afu8g03930	-0.14	-2.1	-2.72	Hsp70 chaperone (HscA), putative
Afu8g04020	-1.27	-1.27	-2.08	conserved hypothetical protein
Afu8g04030	-2.3	-1.59	-1.88	LMBR1 domain protein, putative
Afu8g04130	-1.76	-1.69	-2.04	C6 transcription factor (Ctf1B), putative
Afu8g04150	-2.06	-2.67	-2.04	MFS transporter, putative
Afu8g04160	-1.2	-2.01	-2.08	folylpolyglutamate synthetase; FPGS
Afu8g04280	-2.63	-0.84	-2.04	conserved hypothetical protein
Afu8g04290	-2.51	-2.68	-2.25	C2H2 finger domain protein, putative
Afu8g04540	-1.51	-1.48	-2.21	C6 transcription factor, putative
Afu8g04550	-2.69	-3.62	-4.06	sulfonate biosynthesis enzyme, putative
Afu8g04560	-0.44	-1.07	-2.05	integral membrane protein
Afu8g04570	0.01	-1.72	-2.75	PWWP domain protein
Afu8g04630	-1.99	-2.05	-1.83	C4-dicarboxylate transporter/malic acid transport protein, putative
Afu8g04780	-1.14	-2.19	-2.74	24 kDa intrinsic membrane protein
Afu8g04860	-2.42	-2.81	-3.34	GPI anchored glycoprotein, putative
Afu8g04870	-1.64	-2.54	-2.77	NAD binding Rossmann fold oxidoreductase, putative
Afu8g04910	-2.02	-1.73	-2.44	choline transport protein, putative

Afu8g04920	-2.25	-3.06	-5.49	LEA domain protein
Afu8g05030	-4.35	-1.96	-2.2	hypothetical protein
Afu8g05050	-2.15	-1.33	-1.84	hypothetical protein
Afu8g05120	-2.44	-4.26	-4.77	hypothetical protein
Afu8g05130	-2.91	-2.53	-2.69	hypothetical protein
Afu8g05140	-1.29	-1.43	-2.48	oxidoreductin
Afu8g05360	-1.93	-2.35	-2.15	conserved hypothetical protein
Afu8g05380	-2.32	-1.91	-2.18	hypothetical protein
Afu8g05470	-2.54	-1.53	-1.53	hypothetical protein
Afu8g05480	-1.84	-2.05	-3.25	CCCH zinc finger protein
Afu8g05490	-1.27	-1.65	-2.34	transcription initiation factor iif, beta subunit
Afu8g05770	-4.79	-3.91	-4.06	hypothetical protein
Afu8g05780	-2	-2.84	-3.09	NACHT and Ankyrin domain protein
Afu8g05870	-3.59	-2.74	-2.77	2-haloalkanoic acid dehalogenase, putative
Afu8g05880	-4.37	-2.35	-2.23	10 kDa chaperonin (GroES/Cpn10), putative
Afu8g06030	-2.06	-2.41	-3	alpha-1,3-glucanase, putative
Afu8g06040	-3.6	-3.31	-3.25	hypothetical protein
Afu8g06080	-3.22	-4.13	-4.33	flavohemoprotein, putative
Afu8g06290	-5.39	-2.74	-4.07	LINE-1 class reverse transcriptase, RNaseH, putative
Afu8g06450	-2.87	0.87	0.96	Rieske 2Fe-2S family protein, putative
Afu8g06840	-2.32	-1.66	-0.82	oxidoreductase, short chain dehydrogenase/reductase family
Afu8g07050	-2.68	-1.89	-1.25	hypothetical protein
Afu8g07110	-1.96	-2.08	-1.32	alanyl-tRNA synthetase, putative
Afu8g07150	-3.11	-2.83	-3.19	arsenic resistance protein ArsH, putative
Afu8g07210	-1.83	-2.74	-3.09	hydroxymethylglutaryl-CoA synthase

Table AD.2.5: List of down-regulated genes in the ATCC46645 Δ*pacC* time course. Genes significantly down-regulated were included if showing a fold change of -2 on a log$_2$ scale at least in one of the time point datasets. T0 vs T4 = 4 hrs, T0 vs T8 hrs = 8 hrs, T0 vs T16 = 16 hrs.

ORFs	T4 vs T0	T8 vs T0	T16 vs T0	Annotation	Functional classification
Afu2g05700	-5.08	-1.83	-1.95	hypothetical protein	
Afu7g02010	-4.82	-1.12	0.76	hypothetical protein	cytoplasm///"tryptophan 2,3-dioxygenase activity"///NAD biosynthetic process
Afu1g15690	-4.46	-1.85	-1.18	conserved hypothetical protein	
Afu2g12630	-4.18	-0.96	-1.65	allergen Asp F13	
Afu2g08680	-3.93	-1.96	-1.45	hypothetical protein	

Afu4g08850	-3.9	-1.43	-1.72	hypothetical protein	
Afu5g10250	-3.85	-1.57	-1.92	hypothetical protein	
Afu4g09920	-3.79	-1.16	0.7	conserved hypothetical protein	
Afu1g05400	-3.76	-1.93	-1.63	hypothetical protein	
Afu2g04210	-3.75	-0.92	-0.87	conserved hypothetical protein	
Afu6g07790	-3.66	-1.5	-1.39	hypothetical protein	
Afu4g08750	-3.58	-1.58	-1.25	hypothetical protein	
Afu3g09980	-3.57	-1.81	-1.93	hypothetical protein	
Afu2g17520	-3.51	-1.97	-1.44	GNAT family N-acetyltransferase, putative	N-acetyltransferase activity///secondary metabolic process///metabolic process
Afu5g01190	-3.51	-1.72	1.15	conserved hypothetical protein	
Afu1g06580	-3.45	-1.19	-1.78	high expression lethality protein (Hel10), putative	programmed cell death
Afu4g14180	-3.39	-0.72	-0.33	hypothetical protein	
Afu1g14820	-3.36	-1.7	-0.83	hypothetical protein	
Afu2g02270	-3.33	-0.87	-1.22	ribosomal protein S14p/S29e	structural constituent of ribosome///translation///mitochondrial small ribosomal subunit
Afu2g16190	-3.19	-0.81	-0.47	hypothetical protein	
Afu5g00650	-3.18	0.58	-0.85	hypothetical protein	
Afu7g08280	-3.17	-1.77	-1.33	hypothetical protein	
Afu6g09310	-3.13	-1.89	-1.82	class V chitinase, putative	chitinase activity///chitin catabolic process
Afu6g12000	-3.13	-1.46	-1.74	hypothetical protein	
Afu3g03290	-3.13	-1.03	-0.83	hypothetical protein	
Afu2g08520	-3.1	-1.74	-1.82	50S ribosomal protein L14	structural constituent of ribosome///translation///mitochondrial large ribosomal subunit
Afu5g06820	-3.1	-0.37	-1.16	hypothetical protein	
Afu5g14210	-3.1	-0.83	-1.65	glucose-repressible gene protein-related protein	
Afu5g09710	-3.08	-1.39	-1.59	separin, putative	spindle///mitotic sister chromatid separation///cytoplasm///nucleus///regulation of exit from mitosis///cysteine-type endopeptidase activity
Afu1g02620	-3.07	-1.13	-1.38	hypothetical protein	

Table AD.2.6: 30 ORFs with the lowest $\log_2$ values among down-regulated genes unique to the 4 hrs time point of the ATCC46645 Δ*pacC* time course.

ORFs	T4 vs T0	T8 vs T0	T16 vs T0	Annotation	Functional classification
Afu5g04260	-1.91	-2.63	-1.81	arginine transporter, putative	basic amino acid transmembrane transporter activity///arginine permease activity///lysine permease activity///basic amino acid transport///plasma membrane
Afu3g07680	-1.23	-2.54	-1.39	ran GTPase activating protein 1 (RNA1 protein)	rRNA metabolic process///ribosomal subunit export from nucleus///rRNA export from nucleus///protein import into nucleus///cytosol///nucleus///Ran GTPase activator activity

Afu2g11250	-1.58	-2.42	-1.56	aryl-alcohol dehydrogenase (AAD), putative	cellular component unknown///aryl-alcohol dehydrogenase activity///cellular aldehyde metabolic process
Afu7g04150	-1.94	-2.38	-1.98	CGI-136 protein	mitochondrion///protein import into mitochondrial matrix///molecular function unknown
Afu7g03820	-1.69	-2.37	-1.84	DNA excision repair protein (Rad16), putative	nucleotide-excision repair, DNA damage recognition///repairosome///nucleotide-excision repair factor 4 complex///DNA-dependent ATPase activity
Afu4g14450	-1.77	-2.37	-1.91	D-mannonate oxidoreductase	mannitol dehydrogenase activity///cellular component unknown
Afu1g05040	-1.2	-2.27	-1.45	protein mitochondrial targeting protein (Mas1), putative	Hsp70/Hsc70 protein regulator activity///cytosol///protein targeting to mitochondrion///chaperone regulator activity///ATPase activator activity
Afu2g16180	-1.78	-2.27	-1.73	hypothetical protein	
Afu2g08740	-1.99	-2.26	-1.54	ZIP metal ion transporter, putative	zinc ion transport///cellular zinc ion homeostasis///zinc ion transmembrane transporter activity///vacuolar membrane
Afu3g06950	-1.45	-2.26	-1.53	mitochondrial carrier protein (Rim2), putative	mitochondrial genome maintenance///mitochondrion///transporter activity
Afu1g13060	-1.02	-2.24	-1.97	regulator of nonsense transcripts, putative	nucleic acid binding///"nuclear-transcribed mRNA catabolic process, nonsense-mediated decay"///polysome///cytoplasm///ATP-dependent helicase activity///mRNA catabolic process///ATPase activity///regulation of translational termination
Afu5g06330	-1.62	-2.23	-1.93	RSC complex subunit (Sth1), putative	chromatin remodeling///DNA helicase activity///meiosis///nucleus///ATPase activity
Afu1g16850	-1.3	-2.21	-1.94	sur2 protein	sphingolipid biosynthetic process///sphingosine hydroxylase activity///endoplasmic reticulum///sphingolipid metabolic process
Afu1g06220	-1.74	-2.21	-1.32	ATP-dependent RNA helicase , putative	nucleolus///35S primary transcript processing///ATP-dependent RNA helicase activity
Afu5g01500	-1.25	-2.18	-1.65	homocysteine S-methyltransferase, putative	cytoplasm///homocysteine S-methyltransferase activity///sulfur amino acid metabolic process
Afu3g14860	-1.48	-2.18	-1.74	hypothetical protein	
Afu5g06170	-1.2	-2.16	-1.41	conserved hypothetical protein	
Afu7g01250	-1.44	-2.14	-1.62	hypothetical protein	
Afu4g10810	-1.09	-2.13	-1.94	hypothetical protein	
Afu4g12550	-1.62	-2.13	-1.64	hypothetical protein	
Afu1g10610	-1.97	-2.11	-1.75	hypothetical protein	
Afu8g01420	-1.79	-2.11	-1.59	quinone oxidoreductase, putative	oxidoreductase activity///zinc ion binding///metabolic process

Afu7g05660	-1.96	-2.11	-1.05	elongation factor EF-3, putative	cytosolic ribosome (sensu Eukaryota)///translational elongation///ATPase activity///translation elongation factor activity
Afu2g16440	-1.53	-2.1	-1.71	hypothetical protein	
Afu5g01020	-1.51	-2.1	-1.5	DUF858 domain protein	S-adenosylmethionine-dependent methyltransferase activity///cytoplasm///biological process unknown
Afu3g00800	-1.36	-2.08	-1.71	oxidoreductase, 2OG-Fe(II) oxygenase family, putative	oxidoreductase activity///metabolic process
Afu8g07110	-1.96	-2.08	-1.32	alanyl-tRNA synthetase, putative	
Afu7g04860	-1.03	-2.06	-1.41	dimethyladenosine transferase	nucleolus///rRNA modification///35S primary transcript processing///"rRNA (adenine-N6,N6-)-dimethyltransferase activity"
Afu3g08670	-1.1	-2.05	-1.22	related to L-fucose permease	

Table AD.2.7: 30 ORFs with the lowest $\log_2$ values among down-regulated genes unique to the 8 hrs time point of the ATCC46645 Δ*pacC* time course.

ORFs	T4 vs T0	T8 vs T0	T16 vs T0	Annotation	Functional classification
Afu4g08960	0.03	-1.72	-3.59	GPI anchored protein, putative	
Afu6g08020	-1.95	-1.62	-3.26	ABC transporter, putative	ATP-binding cassette (ABC) transporter activity///transport///integral to membrane
Afu4g09140	-1.24	-1.97	-3.2	ornithine aminotransferase	arginine catabolic process///cytoplasm///nucleus///ornithine-oxo-acid transaminase activity
Afu6g02820	-1.11	-1.98	-3.09	metalloreductase, putative	oxidoreductase activity, oxidizing metal ions, NAD or NADP as acceptor///transition metal ion transport///integral to membrane///cellular iron ion homeostasis
Afu4g06530	-1.3	-1.77	-2.99	bZIP transcription factor (MetR), putative	regulation of sulfur metabolic process///transcription///transcription factor activity///nucleus
Afu6g05120	-0.93	-1.89	-2.96	glycogen synthase kinase-3, putative	proteolysis///sporulation (sensu Saccharomyces)///glycogen synthase kinase 3 activity///cytoplasm///protein amino acid phosphorylation///response to stress
Afu4g11110	-0.44	-1.29	-2.92	C2 domain protein	cellular component unknown///biological process unknown///molecular function unknown
Afu1g14770	-1.05	-1.96	-2.91	tRNA dihydrouridine synthase, putative	tRNA modification///cytoplasm///nucleus///tRNA dihydrouridine synthase activity

Afu6g07830	-1.86	-1.82	-2.82	stromal membrane-associated protein	clathrin-coated vesicle///ER to Golgi vesicle-mediated transport///ARF GTPase activator activity///intra-Golgi vesicle-mediated transport
Afu1g03090	-1.14	-1.82	-2.81	conserved hypothetical protein	fungal-type vacuole///biological process unknown///molecular function unknown
Afu2g07610	-0.17	-1.79	-2.8	alcohol dehydrogenase PAN2	oxidoreductase activity///metabolic process
Afu2g08170	-1.74	-1.92	-2.8	hypothetical protein	
Afu3g10480	-0.4	-1.16	-2.79	conserved hypothetical protein	
Afu2g09630	-0.89	-1.67	-2.79	hypothetical protein	
Afu2g15770	-1.01	-1.94	-2.76	conserved hypothetical protein	cell wall organization///cytoplasm///molecular function unknown
Afu8g04570	0.01	-1.72	-2.75	PWWP domain protein	
Afu6g09930	-0.94	-1.66	-2.75	bZIP transcription factor (AP-1), putative	response to drug///response to oxidative stress///cytoplasm///transcription///transcription factor activity///nucleus
Afu1g09750	-1.21	-1.7	-2.74	aldehyde reductase (AKR1), putative	aldo-keto reductase activity///cytoplasm///nucleus///cellular aldehyde metabolic process
Afu2g04740	-0.44	-1.8	-2.71	vacuolar sorting-associated protein (Vps27), putative	protein retention in Golgi apparatus///endosome///protein binding///zinc ion binding
Afu3g08750	-1.52	-1.99	-2.7	conserved hypothetical protein	cytoplasm///biological process unknown///molecular function unknown
Afu1g03150	-1.17	-1.95	-2.69	c-14 sterol reductase	endoplasmic reticulum///ergosterol biosynthetic process///C-14 sterol reductase activity
Afu1g12900	-1.04	-1.93	-2.67	Leucine Rich Repeat domain protein	negative regulation of microtubule depolymerization///cell wall organization///microtubule///structural constituent of cytoskeleton
Afu2g15650	0.78	-0.69	-2.66	DUF323 domain protein	
Afu1g03410	-1.06	-1.2	-2.66	DNA primase large subunit	DNA replication initiation///lagging strand elongation///"DNA replication, synthesis of RNA primer"///alpha DNA polymerase:primase complex///alpha DNA polymerase activity///DNA synthesis during DNA repair
Afu1g10040	-0.85	-1.57	-2.65	HMG box protein, putative	
Afu2g11180	-1.54	-1.99	-2.65	developmental regulator FlbA	regulation of sporulation resulting in formation of a cellular spore///pheromone-dependent signal transduction involved in conjugation with cellular fusion///response to pheromone during conjugation with cellular fusion///response to stress
Afu3g06260	-1.39	-1.59	-2.63	translation initiation factor SUI1	ribosome///translation initiation factor activity///translational initiation
Afu4g11630	-1.51	-1.69	-2.63	hypothetical protein	
Afu2g05630	-0.86	-1.7	-2.6	hypothetical protein	

Afu6g12010	-1.64	-1.5	-2.58	glycosyl hydrolase, family 3, putative	carbohydrate metabolic process///"hydrolase activity, hydrolyzing O-glycosyl compounds"

Table AD.2.8: 30 ORFs with the lowest $\log_2$ values between the down-regulated genes unique to the 16 hrs time point of the ATCC46645 Δ*pacC* time course.

AD.3 *A. fumigatus* ATCC46645 Δ*pacC*/ATCC46645 $\log_2$ ratio comparison during initiation of murine infection

Locus	T0 vs T4	T0 vs T8	T0 vs T16	Common Name
Afu1g00300	0.86	1.76	1.68	Ankyrin repeat protein
Afu1g00420	1.19	2.51	3.73	carboxypeptidase S1, putative
Afu1g00480	1.18	0.97	1.61	glucosamine-6-phosphate deaminase, putative
Afu1g00540	1.37	0.83	1.81	beta-N-acetylglucosaminidase, putative
Afu1g01050	1.80	0.79	1.57	conserved hypothetical protein
Afu1g01220	1.57	0.23	0.41	conserved hypothetical protein
Afu1g01260		0.26	1.56	MFS transporter, putative
Afu1g01430	1.20	1.20	1.67	hypothetical protein
Afu1g01450	0.51	1.66	3.17	toxin biosynthesis protein, putative
Afu1g01730	2.43	2.13	2.35	glycosyl hydrolase, putative
Afu1g01800	0.86	0.89	1.82	MFS transporter, putative
Afu1g01850	1.17	1.26	1.51	hypothetical protein
Afu1g02730	1.89	1.83	1.82	mitochondrial phosphate carrier protein (Ptp), putative
Afu1g02770	0.49	0.39	1.82	hypothetical protein
Afu1g03440	0.99	0.20	1.59	peroxisomal carrier protein, putative
Afu1g03490	2.61	1.83	1.83	conserved hypothetical protein
Afu1g03570	3.70	5.10	5.09	acid phosphatase PHOa
Afu1g03730	0.84	0.62	2.19	MFS transporter, putative
Afu1g03800	1.59	0.80	0.33	C6 transcription factor, putative
Afu1g04520	1.53	0.26	0.48	Hypothetical protein
Afu1g05170	0.94	0.59	1.93	related to monocarboxylate transporter
Afu1g05550	0.83	0.31	1.53	conserved hypothetical protein
Afu1g05670	2.63	1.78		conserved hypothetical protein
Afu1g05790	0.81	1.33	1.53	GPI anchored serine-rich protein

Afu1g06900	0.67	0.54	1.55	C2H2 transcription factor (Crz1), putative
Afu1g06980	1.51	0.95	0.97	mitochondrial small ribosomal subunit protein S4, putative
Afu1g06990	-2.81	1.85	-1.80	NA
Afu1g07140	1.65	0.10		c-24(28) sterol reductase
Afu1g07350	1.71	1.26	0.54	RNA12 protein, putative
Afu1g08800	-0.98	1.80	-0.66	cytochrome P450 phenylacetate hydroxylase, putative
Afu1g08910	1.02	0.84	2.64	conserved hypothetical protein
Afu1g09140	2.02	0.65		hypothetical protein
Afu1g09630	1.36	0.65	1.68	PAB1 binding protein (Pbp1), putative
Afu1g10130	1.55	0.80	1.19	adenosylhomocysteinase
Afu1g10210	1.56	0.71	0.75	hypothetical protein
Afu1g10220	2.07	1.44	0.52	hypothetical protein
Afu1g10310	1.73	0.56	0.97	RNase L inhibitor of the ABC superfamily, putative
Afu1g10630	1.54	1.34	1.48	S-adenosylmethionine synthetase
Afu1g10950	1.58	0.79	0.44	conserved hypothetical protein
Afu1g11060	2.09	1.90	2.11	ubiquitin domain protein, putative
Afu1g11250	3.06	1.53	2.96	amidohydrolase, putative
Afu1g11280	1.34	1.24	1.90	oxidoreductase, putative
Afu1g11760	2.25	0.98	1.30	hypothetical protein
Afu1g11890	2.28	1.14	0.63	serine palmitoyltransferase 2, putative
Afu1g12240	2.38	4.67	4.83	MFS peptide transporter, putaitve
Afu1g12900	1.58	1.08	0.78	Leucine Rich Repeat domain protein
Afu1g12930	1.56	1.02	0.43	G protein complex alpha subunit GpaB
Afu1g12950	1.65	1.19	0.98	mKIAA0241 protein
Afu1g13060	0.78	0.22	1.58	regulator of nonsense transcripts, putative
Afu1g13310	0.78	1.51	1.30	hypothetical protein
Afu1g13660	0.74	1.00	1.59	phenol 2-monooxygenase, putative
Afu1g13980	1.96	0.30	1.51	conserved hypothetical protein
Afu1g14890	1.74	0.51	0.20	cpdP protein, putative
Afu1g15260	1.71			hypothetical protein
Afu1g15340	1.78	1.16	0.74	polymerase
Afu1g15440	2.43	2.29	1.82	alpha-1,3-glucan synthase, putative
Afu1g15650	-1.87	1.53		hypothetical protein

Afu1g15850	1.82	1.39	0.56	C6 transcription factor, putative
Afu1g15940	2.10	1.67	1.75	Auxin Efflux Carrier superfamily
Afu1g16920	2.17	2.27	1.25	beta-xylosidase A
Afu1g17430	1.75	0.25		tyrosinase
Afu1g17440	0.67	-0.02	1.92	ABC drug exporter AbcA
Afu1g17480	-0.12	1.00	1.81	conserved hypothetical protein
Afu1g17490	0.85	0.43	1.59	glucokinase regulator family protein, putative
Afu1g17670	-0.21		1.87	salicylate hydroxylase, putative
Afu2g00140	1.14	1.07	2.44	FAD monooxygenase, putative
Afu2g00150	2.46	1.87	0.85	catecholamine-O-methyltransferase, putative
Afu2g00170	0.64	1.55	1.34	glutathione-dependent formaldehyde dehydrogenase
Afu2g00180	1.65	2.35	2.35	neutral amino acid permease
Afu2g00260	0.75	-0.34	1.74	phenylacetaldoxime dehydratase family protein, putative
Afu2g00430	1.02	1.37	1.68	exo-beta-1,3-glucanase, putative
Afu2g00680	0.69	1.48	1.80	glycosyl hydrolase, putative
Afu2g00690	0.86	3.87	4.29	glucan 1,4-alpha-glucosidase, putative
Afu2g00710		2.77	3.15	alpha-amylase, putative
Afu2g01110	-0.46	0.07	2.23	hypothetical protein
Afu2g01230	0.13	0.48	1.63	dihydrodipicolinate synthetase family protein
Afu2g01330	0.91	0.10	1.78	exosome complex subunit Rrp46, putative
Afu2g01410	0.47	0.13	1.96	aldo-keto reductase, putative
Afu2g01430	1.14	0.74	1.65	hypothetical protein
Afu2g02570	0.97	0.53	1.59	F-box domain protein
Afu2g03490	1.55	0.96	0.02	calcium/calmodulin-dependent protein kinase, putative
Afu2g03510	2.10	2.60	3.27	pheromone processing carboxypeptidase (Sxa2), putative
Afu2g03860	2.98	3.33	4.04	plasma membrane low affinity zinc ion transporter, putative
Afu2g03920	1.59	0.18		G1/S-specific cyclin, putative
Afu2g04000	1.72	1.15	-0.15	Png1p
Afu2g04080	0.65	0.84	2.14	GPR/FUN34 family protein
Afu2g04100	1.70	1.04		hypothetical protein
Afu2g05250	1.58	0.68		RfeD
Afu2g05320	1.04	1.70	1.83	ion transporter
Afu2g05330	2.74	2.14		vacuolar H+\/Ca2+ exchanger

Afu2g05840	1.24	1.79	1.61	multidrug transporter, putative
Afu2g05880	1.57	0.89	-0.19	ammonium transporter MEAA
Afu2g06080	1.58	1.05	1.52	GTPase activating protein (Gyp1), putative
Afu2g08820	1.02	1.34	2.62	hypothetical protein
Afu2g09150	1.65	1.26	0.76	adenosine deaminase
Afu2g09350	0.36	1.04	1.75	endo-beta-1,6-glucanase, putative
Afu2g09820	1.20	0.73	1.76	conserved hypothetical protein
Afu2g09860	3.36	4.37	4.33	purine-cytosine permease
Afu2g10110	0.99	0.41	1.55	hypothetical protein
Afu2g10690	1.58	2.54	3.41	MFS phosphate transporter, putative
Afu2g11420	1.08	0.47	2.41	MFS transporter, putative
Afu2g11580	2.42	1.18		mfs-multidrug-resistance transporter
Afu2g11620	1.67	1.10	1.78	alpha-glucosidase, putative
Afu2g11740	0.60	0.14	1.74	LON domain serine protease, putative
Afu2g11920	1.52	0.68	1.55	hypothetical protein
Afu2g12550	2.67	0.90	0.15	multidrug resistant protein, putative
Afu2g12850	0.24	2.91	2.60	1,3-beta-glucanosyltransferase Gel3
Afu2g13050	0.15	-0.12	1.65	arylesterase/monoxygenase
Afu2g13390	1.39	0.68	1.53	MFS transporter, putative
Afu2g13510	2.20	0.91	1.67	DUF300 domain protein, putative
Afu2g14330	-0.18	1.50	1.14	hypothetical protein
Afu2g14460	0.30	0.57	1.63	oxidoreductase, short-chain dehydrogenase/reductase family
Afu2g14470	0.82	0.44	1.71	oxidoreductase, FAD-binding, putative
Afu2g14590	2.10	1.51	0.96	MFS monosaccharide transporter, putative
Afu2g14760	1.72	1.08	0.23	BCS1-like ATPase, putative
Afu2g15240	1.82	3.91	5.28	small oligopeptide transporter, OPT family
Afu2g15380	-0.08	-0.44	1.53	hypothetical protein
Afu2g16060	1.44	1.47	1.93	conserved hypothetical protein
Afu2g16180	1.29	1.38	1.64	hypothetical protein
Afu2g16540	2.51	4.03	1.39	C2H2 finger domain protein, putative
Afu2g16860	2.54	3.40	3.14	membrane transporter
Afu2g16930	-0.10	0.64	1.51	succinate:fumarate antiporter (Acr1), putative
Afu2g17140	-0.72	0.35	1.89	conserved hypothetical protein

Afu2g17480	2.08	2.84	1.69	amino acid transporter, putative
Afu2g17600	0.57	1.14	1.82	polyketide synthetase PksP
Afu2g17630	0.10	1.41	1.91	hypothetical protein
Afu2g17730	1.67	2.51	3.17	MFS multidrug transporter, putative
Afu2g17770	1.50	3.49	3.71	conserved hypothetical protein
Afu2g17780	2.38	1.97	2.61	hypothetical protein
Afu2g17790	3.90	5.42	5.17	amino acid transporter, putative
Afu2g17800	2.69	4.33	3.94	C6 transcription factor, putative
Afu2g17830		1.96	3.39	hypothetical protein
Afu2g17840		2.37	3.27	MFS transporter, putative
Afu2g17860	0.97	-0.06	1.72	C6 transcription factor, putative
Afu2g18080	-2.85	1.57	-1.03	LINE-1 class reverse transcriptase, RNaseH, putative
Afu3g00470	1.78	4.62	5.05	endo-1,4-beta-xylanase, putative
Afu3g00550		2.81	2.32	hypothetical protein
Afu3g00560	1.75	2.20	1.51	conserved hypothetical protein
Afu3g00690	1.84	0.66		C6 transcription factor, putative
Afu3g00860	0.77	0.95	1.55	hypothetical protein
Afu3g01940	1.35	2.59	2.49	MFS multidrug transporter, putative
Afu3g01950	0.42	1.33	1.51	alcohol dehydrogenase, zinc-containing
Afu3g02040	3.75	5.25	4.76	glycosyl hydrolase, putative
Afu3g02090	0.14	-0.48	1.53	beta-xylosidase
Afu3g02130			2.24	oxidoreductase, zinc-binding, putative
Afu3g02640	0.58	0.83	2.22	nucleoside-diphosphate-sugar epimerase family protein
Afu3g02970	1.64	4.99	4.89	aspergillopepsin, putative
Afu3g03040	-0.07	1.28	2.21	conserved hypothetical protein
Afu3g03290	-0.08	1.62	1.73	hypothetical protein
Afu3g03330	-0.17	3.24	3.83	mitochondrial enoyl reductase, putative
Afu3g03350	0.82	3.37	4.84	nonribosomal peptide synthase, putative
Afu3g03360	0.26	2.40	4.29	hypothetical protein
Afu3g03600	0.58	1.69	1.60	carboxyl esterase A
Afu3g03660	1.64		0.91	esterase superfamily protein
Afu3g03700	0.04	0.82	2.11	Sugar transporter subfamily
Afu3g03710	2.74	0.96	1.10	D-aminopeptidase putative
Afu3g03720	0.12	0.77	1.52	hypothetical protein

Afu3g04010	1.52	1.41	2.24	MFS transporter, putative
Afu3g04310	1.64	0.54	0.83	snoRNA binding protein, putative
Afu3g05700	0.19	-0.01	2.27	Sec7 domain containing protein
Afu3g05760	1.09	0.82	1.52	C6 transcription factor (Fcr1), putative
Afu3g05780	1.48	1.56	1.29	GATA transcription factor (LreA), putative
Afu3g06000	1.57	1.44	1.21	conserved hypothetical protein
Afu3g06010	1.54	0.97	1.58	Nucleolar essential protein 1, putative
Afu3g06540	1.51	0.47	1.05	3'-phosphoadenosine-5'-phosphosulfate reductase
Afu3g06720	0.97	1.93	1.60	ThiJ/PfpI family protein
Afu3g07400	-0.16	1.95	1.99	hypothetical protein
Afu3g07410	1.49	2.43	2.40	isoamyl alcohol oxidase
Afu3g07420	0.00	1.40	2.96	hypothetical protein
Afu3g08160	1.45	0.86	1.92	eukaryotic translation initiation factor eIF4A, putative
Afu3g08990	1.87	2.08	2.09	hypothetical protein
Afu3g09360	1.85	1.42	1.36	vacuolar sorting ATPase Vps4, putative
Afu3g09960	0.70	0.64	1.51	aureobasidin resistance protein Aur1
Afu3g10120	1.39	1.08	1.57	TATA-box binding protein
Afu3g10150	1.53	0.84	0.83	hypothetical protein
Afu3g10620	1.33	1.52	2.61	transcription initiation protein
Afu3g10760	1.58	1.05	-0.77	phosphoketolase, putative
Afu3g11070	1.64	1.09	0.25	pyruvate decarboxylase PdcA, putative
Afu3g11250	1.65	0.85	0.81	C2H2 transcription factor (Swi5), putative
Afu3g11330	1.63	1.41	1.72	bZIP transcription factor (AtfA), putative
Afu3g11590	1.79			Taz1-interacting factor 1 (TAF1), putative
Afu3g11790	0.62	0.90	1.77	galactose-proton symport, putative
Afu3g12170	0.41	0.64	1.65	MFS sugar transporter, putative
Afu3g12530	1.57	1.18	0.37	sensor histidine kinase/response regulator, putative
Afu3g12580	-0.43	0.35	1.72	related to hexose transporter protein, putative
Afu3g12620	0.89	0.79	1.58	acyl-CoA:6-aminopenicillanic-acid-acyltransferase, putative
Afu3g12960	1.56	1.43	0.91	cytochrome P450 monooxigenase (GliC), putative
Afu3g13080	0.23	0.12	1.50	hypothetical protein
Afu3g13180	1.89	0.32	0.86	hypothetical protein
Afu3g13240	1.00	2.12	2.29	aldose 1-epimerase, putative

Afu3g13570	0.42	0.78	1.54	conserved hypothetical protein
Afu3g13580	2.40	1.51	0.49	dynamin GTPase, putative
Afu3g13610	1.47	1.81	0.52	oxidoreductase, zinc-binding, putative
Afu3g13640	1.56	2.27	2.09	extracellular serine-rich protein
Afu3g13670	0.38	0.46	1.51	siderochrome-iron transporter, putative
Afu3g13810	1.81	0.96	1.93	integral membrane protein, putative
Afu3g13850	1.66	0.70	0.61	LRP16 family protein
Afu3g14170	1.00	0.81	2.51	high-affinity hexose transporter
Afu3g14180	1.81	1.87	0.79	hypothetical protein
Afu3g14190	1.87	1.76	0.24	hypothetical protein
Afu3g14200	0.88	2.54	0.62	hypothetical protein
Afu3g14210	0.64	1.79	0.35	hypothetical protein
Afu3g14540	1.04	2.05	2.63	heat shock protein HSP30, putative
Afu3g14720	1.07	1.90	1.59	MFS transporter, putative
Afu3g14730	0.60	1.35	2.49	LysR family regulatory protein, putative
Afu3g14740	1.17	1.47	2.20	conserved hypothetical protein
Afu3g14920	2.36	0.99	1.54	LaeA-like methyltransferase, putative
Afu4g00150	1.10	1.88	2.83	MFS maltose transporter, putative
Afu4g00820	-2.94	1.68	-1.27	reverse transcriptase, RNaseH
Afu4g00980	-1.06	2.50	1.94	hypothetical protein
Afu4g00990	-0.20	2.01	2.41	MFS quinate transporter, putative
Afu4g01290	-0.27	1.05	2.02	endo-chitosanase, pseudogene
Afu4g01360	0.46	0.28	2.89	MFS transporter of unkown specificity
Afu4g01370	-0.37	0.63	2.70	hypothetical protein
Afu4g01380	0.90	0.90	2.87	4-nitrophenylphosphatase, putative
Afu4g01390	0.86	1.82	1.53	C6 transcription factor, putative
Afu4g01440	0.02	1.12	4.19	glutathione S-transferase family protein
Afu4g01450	0.08	-0.39	1.56	phospho-2-dehydro-3-deoxyheptonate aldolase
Afu4g01470	1.08	3.70	2.80	C6 finger domain protein, putative
Afu4g01480	1.14	1.85	3.51	MSF transporter, putative
Afu4g01580	1.13	1.30	1.79	ankyrin repeat protein
Afu4g06030	1.65	0.71	0.22	hypothetical protein
Afu4g06620	1.31	1.49	1.57	Glutamate/Leucine/Phenylalanine/Valine dehydrogenase, putative

Afu4g07080	1.73	0.66	1.10	dual specificity phosphatase, putative
Afu4g07490	1.73	0.76	1.75	hypothetical protein
Afu4g07580	1.47	0.85	1.57	translation initiation factor EF-2 gamma subunit, putative
Afu4g07760	1.52	0.91	-0.13	Transmembrane amino acid transporter protein family
Afu4g08420	0.61	0.97	1.51	hypothetical protein
Afu4g08440	1.57	1.04	1.23	Patatin-like serine hydrolase, putative
Afu4g08460	1.72	0.54	1.32	conserved hypothetical protein
Afu4g08650	1.63	0.54		hypothetical protein
Afu4g08780	1.87	1.00	0.89	hypothetical protein
Afu4g08790	1.58	1.07	1.03	conserved hypothetical protein
Afu4g08960	1.68	1.09	0.57	GPI anchored protein, putative
Afu4g08970	1.70	1.53	1.28	PAP2 domain protein
Afu4g09150	0.63	1.09	1.55	ABC multidrug transporter, putative
Afu4g09190	1.62	0.31	0.36	S-adenosyl-methionine-sterol-C- methyltransferas
Afu4g09640	-0.09	1.93	1.60	GAJ protein, putative
Afu4g09790	2.02	0.27	0.87	hypothetical protein
Afu4g10120	2.70	1.44	3.59	C6 finger domain protein, putative
Afu4g10130	1.14	3.70	3.86	alpha-amylase (Amy1), putative
Afu4g10140	0.76	1.66	1.84	glucoamylase
Afu4g10150	2.01	2.49	3.19	alpha-glucosidase
Afu4g10790	1.58	1.22	1.07	phosphoribosyl diphosphate synthase isoform 4
Afu4g11130	1.63	0.79	0.41	conserved hypothetical protein
Afu4g11720	1.72	1.13	0.64	phosphatidyl synthase
Afu4g12470	0.71	1.06	1.59	bZIP transcription factor CpcA
Afu4g13120	1.42	1.63	2.30	glutamine synthetase
Afu4g13390	1.09	0.66	2.72	actin-related protein ArpA
Afu4g13660	0.35	1.82	3.16	MFS multidrug resistance transporter, putative
Afu4g13770		1.02	2.71	glycosyl hydrolase, putative
Afu4g13780	0.81	0.82	2.07	polyphenol monooxygenase, putative
Afu4g14000	3.53	4.98	5.63	tripeptidyl peptidase A
Afu4g14150	0.16	0.58	1.69	Diacylglycerol acyltransferase family
Afu4g14380	1.19	0.92	1.58	conserved hypothetical protein
Afu4g14640	0.49	2.27	2.48	low affinity iron transporter, putative
Afu4g14650	-0.27	1.41	3.24	ribokinase

Afu4g14660	-0.89	1.29	2.46	conserved hypothetical protein
Afu4g14670	-0.17	1.13	2.95	MFS quinate transporter, putative
Afu4g14800	1.10	1.13	2.07	short chain dehydrogenase, putative
Afu4g14870	-2.93	1.69	-1.14	LINE-1 class reverse transcriptase, RNaseH, putative
Afu5g00550		0.74	2.33	endoglycoceramidase, putative
Afu5g00600	1.39	0.89	1.79	NPP1 domain protein, putative
Afu5g00700		0.12	1.84	hypothetical protein
Afu5g00730	0.53	2.25	2.69	H /K ATPase alpha subunit, putative
Afu5g00930	1.89	0.52		amino acid permease, putative
Afu5g00980	2.29	1.60	1.23	multidrug resistant protein
Afu5g01010	-0.23	0.51	3.15	hypothetical protein
Afu5g01030	2.42	-0.61	0.47	glyceraldehyde 3-phosphate dehydrogenase (Ccg-7), putative
Afu5g01190	0.08	1.26	3.69	conserved hypothetical protein
Afu5g01200	0.98	2.30	5.16	carboxypeptidase S1, putative
Afu5g01320	0.70	1.11	2.40	phosphate permease
Afu5g01330	1.18	2.25	2.55	acid phosphatase
Afu5g01340	2.15	1.48	2.03	lysophospholipase, putative
Afu5g01420	0.14	-0.43	1.66	conserved hypothetical protein
Afu5g01600	0.33	0.38	2.30	PHP domain protein
Afu5g02280	2.00	1.17	0.98	endo-1,3(4)-beta-glucanase, putative
Afu5g02400	2.02	0.70	0.45	catabolite degradation protein, putative
Afu5g02600	1.24	1.06	1.96	conserved hypothetical protein
Afu5g02700	0.62	1.32	2.88	multidrug resistant protein
Afu5g02920	0.49	0.41	1.75	nitrogen metabolite repression regulator NmrA
Afu5g03010	0.23	0.44	1.53	conserved hypothetical protein
Afu5g03330	1.84	0.82	0.13	conserved hypothetical protein
Afu5g03430	1.70	1.09	0.89	PHD transcription factor (Rum1), putative
Afu5g03510	0.87	0.81	1.91	PQ loop repeat protein
Afu5g03750	2.50	2.64	3.03	WW domain protein
Afu5g03920	1.54	0.24	0.86	bZIP transcription factor (HapX), putative
Afu5g04260	1.32	1.04	1.51	arginine transporter, putative
Afu5g06070	1.43	2.13	1.27	ABC multidrug transporter Mdr1
Afu5g06090	1.14	0.74	1.79	type-III integral membrane protein (Ytp1), putative

Afu5g06190	1.15	0.90	1.89	sexual development transcription factor SteA
Afu5g06290	2.30	1.58	2.88	MFS transporter, putative
Afu5g06670	1.59	2.24	2.82	related to L-fucose permease, putative
Afu5g06980	1.60	0.25	0.90	hypothetical protein
Afu5g07210	1.54	0.99	1.63	homoserine O-acetyltransferase, putative
Afu5g07250	2.24	1.72	1.65	DUF300 domain protein, putative
Afu5g07320	2.08	0.80	0.78	poly(ADP)-ribose polymerase PARP, putative
Afu5g07450	1.57	1.03	1.62	hypothetical protein
Afu5g07740	0.17	1.33	1.54	DSB repair complex subunit Ku70, putative
Afu5g08570	1.63	1.17		cAMP-dependent protein kinase catalytic subunit, putative
Afu5g08580	1.63	0.99	1.22	alpha-1,6-mannosyltransferase subunit (Och1), putative
Afu5g08770	1.86	0.20	0.43	hypothetical protein
Afu5g09020	1.42	0.44	1.78	WSC domain protein, putative
Afu5g09330		3.44	1.94	CipC protein
Afu5g09340	-0.12	1.78	1.94	Phospholipase/Carboxylesterase superfamily
Afu5g10320	2.04	2.75	2.64	toxin biosynthesis protein (GliH), putative
Afu5g10340	1.82	2.31	2.19	MFS transporter, putative
Afu5g10350	1.89	3.17	3.59	conserved hypothetical protein
Afu5g10360	1.79	0.66		actin-binding protein fragmin, putative
Afu5g10420	1.17	1.54	0.22	nitrate reductase, putative
Afu5g10460	2.05	0.48		hypothetical protein
Afu5g10690	1.62	1.17	0.48	monosaccharide transporter
Afu5g10960	-0.21	0.20	1.84	conserved hypothetical protein
Afu5g11240	0.66	0.52	1.68	oxidoreductase, short chain dehydrogenase/reductase family
Afu5g11500	0.37	-0.84	2.03	conserved hypothetical protein
Afu5g11840	1.80	0.71	0.67	protein kinase, putative
Afu5g13040	1.78	0.63	0.45	translation initiation factor eif-2b delta subunit
Afu5g13090	1.68	1.03	1.94	alpha-1,2-mannosyltransferase, putative
Afu5g13300	2.60	4.37	5.72	aspartic endopeptidase Pep1
Afu5g13560	1.63	0.92	0.84	FHA domain protein
Afu5g13970	0.53	1.56	0.58	conserved hypothetical protein
Afu5g14020	1.59	1.25	0.67	hypothetical protein

Afu5g14300	1.79	0.02	-0.52	alpha,alpha-trehalose-phosphate synthase subunit, putative
Afu5g14340	0.43	0.66	2.82	oxidoreductase, short-chain dehydrogenase/reductase family, putative
Afu5g14510	1.49	1.22	3.27	beta-lactamase, putative
Afu5g14810	1.27	0.76	1.73	pyruvate decarboxylase, putative
Afu5g14840	0.90	1.52	1.85	hypothetical protein
Afu6g00160	2.29	1.61	2.41	Ser/Thr protein phosphatase family protein
Afu6g00220	1.69	2.45	2.41	fungal specific transcription factor, putative
Afu6g00230	2.49	1.72	1.92	isoflavone reductase family protein
Afu6g00260	2.10	0.98	2.00	phosphatidylserine decarboxylase family protein
Afu6g00310	0.33	2.74	3.92	serine carboxypeptidase (CpdS), putative
Afu6g00430	2.28	2.25	3.48	IgE-binding protein
Afu6g00630	1.61	0.64	1.00	MFS transporter, putative
Afu6g00640	1.32	0.82	1.55	integral membrane protein
Afu6g00660	2.27	1.27	1.52	conserved hypothetical protein
Afu6g00780	-2.77	1.73	-1.04	LINE-1 class reverse transcriptase, RNaseH, putative
Afu6g02400	0.62	1.83	2.09	MFS drug efflux pump, putative
Afu6g02740	1.68	0.69	0.36	hypothetical protein
Afu6g03060	0.62	0.85	2.18	monosaccharide transporter
Afu6g03230	2.30	3.14	1.82	cell wall glucanase, putative
Afu6g03260	2.10	1.83	2.98	aspartic endopeptidase (AP1), putative
Afu6g03360	3.41	2.83	2.31	oxidoreductase, zinc-binding
Afu6g03370	2.52	1.37	2.28	oxidoreductase, short-chain dehydrogenase/reductase family
Afu6g03680	0.83	1.18	1.85	hypothetical protein
Afu6g04270	3.10	3.23	4.35	fructose symporter
Afu6g04300	2.12	0.93	1.74	conserved hypothetical protein
Afu6g04500	1.95	1.02	0.47	FOG1 protein
Afu6g04550	0.30	0.05	1.91	hypothetical protein
Afu6g04670	1.05	1.74		DER1 protein, putative
Afu6g06460	0.46	0.71	1.73	fumarylacetoacetate hydrolase family protein
Afu6g06470	-0.76	1.27	2.88	heat shock protein HSP30, putative
Afu6g06640	1.48	2.06	2.05	FK506 suppressor Sfk1, putative
Afu6g06840	0.72	0.82	1.65	hypothetical protein

Afu6g07470	1.25	1.00	1.52	conserved hypothetical protein
Afu6g07750	1.91	1.99	2.46	MFS phospholipid transporter (Git1), putative
Afu6g07900	1.65	1.17	0.53	carbon catabolite repression protein CreD, putative
Afu6g07970	0.55	0.46	2.09	calpain-like protein
Afu6g08290	-0.25	-0.03	1.61	ADP-ribosylation factor family protein
Afu6g08770	1.54	1.59	1.22	ankyrin repeat protein
Afu6g08840	-0.25	0.43	1.69	beta-mannosidase
Afu6g09200	0.30	1.11	1.55	conserved hypothetical protein
Afu6g09880	-0.62	-0.17	2.43	monocarboxylate transporter-like protein
Afu6g10130	0.03	1.43	3.11	N,O-diacetyl muramidase, putative
Afu6g10160	1.57	3.42	2.12	hypothetical protein
Afu6g10580	0.22	0.53	2.78	antigenic CFEM domain protein, putative
Afu6g11670	1.74	0.75	1.70	conserved hypothetical protein
Afu6g11860	1.59	0.98	0.05	hypothetical protein
Afu6g12110	0.67	0.31	1.72	salicylate synthetase, putative
Afu6g12120	0.64	1.18	2.19	BNR/Asp-box repeat domain protein
Afu6g12270	1.77	0.43		ubiquitin C-terminal hydrolase, putative
Afu6g12390	1.09	0.31	1.50	serine palmitoyl CoA transferase subunit LcbA
Afu6g12550	1.62	0.65	1.02	mitochondrial carrier protein, putative
Afu6g12840	1.61	0.27	0.17	kinesin family protein
Afu6g12900	0.61	0.36	1.86	mitochondrial carrier protein, putative
Afu6g12930	0.94	1.05	1.69	mitochondrial aconitate hydratase, putative
Afu6g13070	1.51	1.03	0.67	UDP-galactose transporter, putative
Afu6g13180	0.07	0.31	1.52	CECR1 family adenosine deaminase, putative
Afu6g13190	0.63	0.67	1.79	H+/nucleoside cotransporter
Afu6g13670	1.91	1.44	1.13	conserved hypothetical protein
Afu6g13710	2.23	2.27	2.41	hypothetical protein
Afu6g13740	-0.18	0.02	1.99	hypothetical protein
Afu6g14010	1.33	3.95	3.96	GPI anchored protein, putative
Afu6g14020	1.71	2.28	2.93	conserved hypothetical protein
Afu6g14040	1.60	1.99		glycosyl transferase, putative
Afu6g14050	1.31	1.91	3.56	FAD binding domain protein
Afu6g14250	1.60	0.88	1.10	endosomal integral membrane protein (P24a), putative
Afu6g14280	2.44	1.08	0.43	hypothetical protein

Afu6g14440	2.29	3.41	4.33	MFS monosaccharide transporter, putative
Afu6g14480	0.69	0.91	1.59	alpha-1,3-mannosyltransferase, putative
Afu6g14540	-1.78	2.01	1.99	endo-1,3(4)-beta-glucanase, putative
Afu6g14660	-2.96	1.86	-1.16	reverse transcriptase, RNaseH
Afu7g00120	0.14	0.82	1.86	metallo-beta-lactamase domain protein
Afu7g00150	0.08	0.62	2.27	FAD-dependent monooxygenase, putative
Afu7g00160	-0.27	-0.17	2.12	polyketide synthase, putative
Afu7g00170	0.76	0.28	1.65	dimethylallyl tryptophan synthase (GliD), putative
Afu7g00230	0.06	-0.78	1.57	MFS multidrug transporter, putative
Afu7g00270	2.07	0.42	-0.02	FAD binding monooxygenase, putative
Afu7g00910	0.10	0.19	2.19	peptide transporter MTD1
Afu7g00990	-0.91	0.51	1.60	integral membrane protein
Afu7g01490	2.34	3.67	4.51	MFS peptide transporter, putative
Afu7g01600	0.91	0.40	1.53	hypothetical protein
Afu7g01720	2.19	1.44	2.67	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase
Afu7g01930	2.36	2.26	2.88	sexual development protein EsdC, putative
Afu7g01960	1.60	0.92		conserved hypothetical protein
Afu7g02600	1.53	0.65	0.57	hypothetical protein
Afu7g04190	1.94			cyclopropane-fatty-acyl-phospholipid synthase, putative
Afu7g04570	0.97	2.73	3.31	Na/K ATPase alpha 1 subunit, putative
Afu7g04730	2.00	1.25	2.00	siderochrome-iron transporter, putative
Afu7g04810	1.22	1.62	2.06	hypothetical protein
Afu7g04910	3.92	6.05	5.28	phosphatidylglycerol specific phospholipase C, putative
Afu7g04930	3.08	2.02	3.63	alkaline serine protease (PR1), putative
Afu7g04950	3.93	2.62	2.60	lipase, putative
Afu7g05090	-0.91	0.47	1.53	glucuronyl hydrolase, putative
Afu7g05100	-1.67	0.72	2.55	hexose transporter protein
Afu7g05130	1.27	1.33	1.70	O-methyltransferase
Afu7g05140	0.46	0.63	2.12	class III chitinase, putative
Afu7g05210	0.78	0.19	1.62	CTP synthase
Afu7g05260	1.49	0.85	1.75	transformer-SR ribonucleoprotein
Afu7g05370	1.44	1.20	1.68	septin AspB
Afu7g05380	1.67	1.19	0.72	conserved hypothetical protein
Afu7g05430	1.67	0.99	1.82	nonsense-mediated mRNA decay factor (Upf2), putative

Afu7g05550	4.18	6.32	5.59	sugar transporter family protein
Afu7g05580	1.23	1.50	-0.48	hypothetical protein
Afu7g06140	-0.09	0.43	1.72	beta-D-glucoside glucohydrolase
Afu7g06380	0.68	0.77	1.52	maltase
Afu7g06450	0.37	1.26	1.68	hypothetical protein
Afu7g06570	1.37	1.85	2.46	zinc/cadmium resistance protein
Afu7g06680	0.03	0.56	1.88	AAA family ATPase, putative
Afu7g06750	-1.27	0.92	1.54	phosphoglycerate mutase family protein, putative
Afu7g06840	1.10	0.79	2.40	class III aminotransferase
Afu7g06900	1.81	0.56	1.48	branched-chain amino acid aminotransferase, putative
Afu7g08250	1.53	1.23	0.64	conserved hypothetical protein
Afu7g08540	2.51	2.20	2.05	ankyrin repeat protein
Afu7g08570	1.90	1.08		hypothetical protein
Afu8g00280	1.37	1.76	1.75	short-chain dehydrogenase, putative
Afu8g00290	0.80	1.05	1.69	conserved hypothetical protein
Afu8g00310	-2.66	1.61	-1.24	LINE-1 class reverse transcriptase, RNaseH, putative
Afu8g00370		0.46	2.34	polyketide synthase, putative
Afu8g00390			2.46	O-methyltransferase, putative
Afu8g00420	-0.89	0.73	2.11	C6 finger transcription factor, putative
Afu8g00430		0.62	2.58	conserved hypothetical protein
Afu8g00440	-0.88	-0.05	1.76	steroid monooxygenase, putative
Afu8g00480			2.57	phytanoyl-CoA dioxygenase family protein
Afu8g00490			1.93	polyketide synthase, putative
Afu8g00520			3.05	integral membrane protein
Afu8g00540	-0.31	0.52	3.90	hybrid polyketide synthase/nonribosomal peptide synthase, putative
Afu8g00550		0.77	3.19	SirN-like methyltransferase, putative
Afu8g00560	0.81	0.58	4.28	cytochrome P450, putative
Afu8g00570	0.74	0.50	1.81	alpha/beta hydrolase, putative
Afu8g00640	1.15	1.41	2.73	glycosyl transferase, putative
Afu8g00680	0.37	0.64	2.55	glycosyl transferase, group 2 family protein
Afu8g00700	0.41	1.46	2.47	class III chitinase ChiA2
Afu8g00720	0.86	1.19	1.91	amino acid transporter, putative
Afu8g00760	-0.30	0.78	1.59	cytochrome P450, putative

Afu8g00770	1.30	2.20	3.02	sugar transporter family protein
Afu8g00820	0.93	1.03	1.86	rhamnogalacturonase, putative
Afu8g01040	-2.45	1.67	-0.98	reverse transcriptase, RNaseH
Afu8g01230	-0.72	0.58	2.23	conserved transmembrane protein
Afu8g01260	3.47	4.50	3.94	hypothetical protein
Afu8g01540	0.34	0.46	1.89	hypothetical protein
Afu8g01630		0.80	1.70	pyridine nucleotide-disulphide oxidoreductase family protein
Afu8g01970	2.88	4.26	3.67	extracellular endo-polygalacturonase, putative
Afu8g02040	2.54	3.96	4.15	glycosyl transferase, putative
Afu8g02050	2.97	4.34	4.13	hypothetical protein
Afu8g02060	3.72	5.27	5.05	glycan biosynthesis protein (PigL), putative
Afu8g02070	3.19	4.38	4.19	glycosyl transferase, putative
Afu8g02090	2.60	4.36	4.32	nucleotide-sugar transporter family protein
Afu8g02130	2.29	3.44	2.97	1,3-beta-glucanosyltransferase, putative
Afu8g02140	0.51	1.63	0.90	ankyrin repeat protein
Afu8g02420	-0.50	0.04	1.83	hypothetical protein
Afu8g04060	1.24	0.93	1.69	NA
Afu8g04070	1.16	1.08	1.87	glucosamine-6-phosphate deaminase, putative
Afu8g04110	0.81	0.39	1.55	DUF895 domain membrane protein
Afu8g04120	1.04	2.30	3.33	carboxypeptidase S1, putative
Afu8g04550	1.28	1.13	1.95	sulfonate biosynthesis enzyme, putative
Afu8g04810	1.75	0.61	1.65	casein kinase, putative
Afu8g05120	1.69			hypothetical protein
Afu8g05170	1.60	-0.03	0.75	autophagy protein Apg6, putative
Afu8g05710	1.83	0.56	1.02	MFS sugar transporter Stl1, putative
Afu8g05780	1.05	0.57	2.70	NACHT and Ankyrin domain protein
Afu8g06090	-0.31	1.27	3.44	amino acid permease, putative
Afu8g06160	1.90	0.29	1.44	conserved hypothetical protein
Afu8g06410	1.24	1.32	2.00	MFS multidrug transporter, putative
Afu8g06490	0.70	0.83	1.74	conserved hypothetical protein
Afu8g06560	1.98	2.36	3.51	DUF895 domain membrane protein
Afu8g06570	-0.22	2.34	3.75	acetyl xylan esterase, putative
Afu8g06580	1.09	2.89	4.02	GABA permease

Afu8g06590	1.26	3.58	4.27	hypothetical protein
Afu8g06760	1.68	1.29	1.93	integral membrane protein
Afu8g06870	1.76	2.95	3.32	MFS sugar transporter, putative
Afu8g06930	2.41	0.95		C6 transcription factor, putative
Afu8g06970	1.11	0.59	1.65	beta-glucosidase
Afu8g07120		0.98	2.23	beta-1,6-glucanase, putative
Afu8g07200	0.77	1.15	1.86	neutral amino acid permease
Afu8g07260	1.76	-0.16		conserved hypothetical protein

Table AD.3.1: List of up-regulated genes in the ATCC46645 Δ*pacC*/ATCC46645 dataset. Genes significantly up-regulated were included if showing a fold change of +1.5 on a $\log_2$ scale at least in one of the time point datasets. T0 vs T4 = 4 hrs, T0 vs T8 hrs = 8 hrs, T0 vs T16 = 16 hrs.

ORFs	T4	T8	T16	Annotation	Functional classification
Afu3g03710	2.737714	0.957446	1.103734	D-aminopeptidase putative	
Afu2g12550	2.6694	0.903991	0.152785	multidrug resistant protein, putative	integral to plasma membrane///multidrug transporter activity///response to toxin
Afu6g14280	2.442983	1.081611	0.427854	hypothetical protein	
Afu2g11580	2.423186	1.176501		mfs-multidrug-resistance transporter	drug transport///drug transporter activity///integral to membrane
Afu5g01030	2.418955	-0.61028	0.467242	glyceraldehyde 3-phosphate dehydrogenase (Ccg-7), putative	lipid particle///fungal-type cell wall///cytoplasm///cytosol///gluconeogenesis///glycolysis///glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity
Afu8g06930	2.411022	0.946438		C6 transcription factor, putative	
Afu1g11890	2.281586	1.140555	0.633299	serine palmitoyltransferase 2, putative	serine C-palmitoyltransferase complex///membrane fraction///sphingolipid biosynthetic process///microsome///serine C-palmitoyltransferase activity
Afu1g11760	2.246248	0.9831	1.297836	hypothetical protein	
Afu5g07320	2.084854	0.796519	0.775437	poly(ADP)-ribose polymerase PARP, putative	ascospore formation///programmed cell death///nucleus///protein amino acid ADP-ribosylation
Afu7g00270	2.070118	0.416592	-0.01619	FAD binding monooxygenase, putative	cellular aromatic compound metabolic process///monooxygenase activity

Afu1g10220	2.065073	1.435086	0.516343	hypothetical protein	
Afu5g10460	2.051653	0.475156		hypothetical protein	
Afu1g09140	2.01708	0.652077		hypothetical protein	
Afu4g09790	2.016705	0.268105	0.871365	hypothetical protein	
Afu5g02400	2.016294	0.700609	0.454573	catabolite degradation protein, putative	cytoplasm///nucleus///molecular function unknown///negative regulation of gluconeogenesis
Afu5g02280	1.999782	1.171611	0.981543	endo-1,3(4)-beta-glucanase, putative	hydrolase activity, hydrolyzing O-glycosyl compounds///fungal-type cell wall///"1,3-beta-glucan metabolic process"
Afu6g04500	1.953883	1.023767	0.46636	FOG1 protein	AMP-activated protein kinase activity///protein amino acid phosphorylation///nucleus///signal transduction///cell adhesion///filamentous growth
Afu7g04190	1.941314			cyclopropane-fatty-acyl-phospholipid synthase, putative	cyclopropane-fatty-acyl-phospholipid synthase activity///lipid biosynthetic process
Afu6g13670	1.911538	1.441284	1.128986	conserved hypothetical protein	endoplasmic reticulum///biological process unknown///molecular function unknown
Afu7g08570	1.898359	1.07764		hypothetical protein	
Afu8g06160	1.895054	0.290622	1.44473	conserved hypothetical protein	
Afu3g13180	1.894706	0.32358	0.858888	hypothetical protein	
Afu5g00930	1.885961	0.523825		amino acid permease, putative	amino acid transport///plasma membrane///amino acid permease activity///amino acid transmembrane transporter activity
Afu4g08780	1.872012	0.998307	0.890531	hypothetical protein	
Afu5g08770	1.862777	0.197912	0.426802	hypothetical protein	
Afu3g09360	1.851611	1.418699	1.364285	vacuolar sorting ATPase Vps4, putative	protein retention in Golgi apparatus///late endosome to vacuole transport///cytoplasm///endoplasmic reticulum///ATPase activity
Afu3g00690	1.84368	0.663801		C6 transcription factor, putative	transcription factor activity///regulation of transcription
Afu5g03330	1.838389	0.817449	0.125998	conserved hypothetical protein	
Afu8g05710	1.827636	0.560392	1.016054	MFS sugar transporter Stl1, putative	membrane///transporter activity///transport
Afu1g15850	1.817327	1.394791	0.559448	C6 transcription factor, putative	transcription factor activity///nucleus///regulation of transcription

Table AD.3.2: 30 ORFs with the highest $\log_2$ values between the up-regulated genes unique to the 4 hrs time point of the ATCC46645 Δ*pacC*/ATCC46645 comparison.

ORFs	T4	T8	T16	Description	Annotation
Afu3g14200	0.876814	2.538769	0.615371	hypothetical protein	
Afu5g06070	1.432669	2.127281	1.265371	ABC multidrug transporter Mdr1	ATP-binding cassette (ABC) transporter activity///pathogenesis///integral to plasma membrane///ATP binding///transport
Afu6g14660	-2.9557	1.860377	-1.1636	reverse transcriptase, RNaseH	
Afu3g13610	1.467361	1.807056	0.521209	oxidoreductase, zinc-binding, putative	
Afu1g08800	-0.9773	1.799103	-0.65998	cytochrome P450 phenylacetate hydroxylase, putative	oxidoreductase activity///metabolic process
Afu3g14210	0.640494	1.786179	0.348299	hypothetical protein	
Afu6g04670	1.053427	1.736744		DER1 protein, putative	
Afu6g00780	-2.77278	1.728312	-1.04089	LINE-1 class reverse transcriptase, RNaseH, putative	
Afu4g14870	-2.931	1.691895	-1.14393	LINE-1 class reverse transcriptase, RNaseH, putative	
Afu4g00820	-2.93653	1.675784	-1.27336	reverse transcriptase, RNaseH	
Afu8g01040	-2.45291	1.671414	-0.97913	reverse transcriptase, RNaseH	
Afu8g02140	0.512359	1.629873	0.902237	ankyrin repeat protein	molecular function unknown
Afu8g00310	-2.66174	1.614126	-1.23683	LINE-1 class reverse transcriptase, RNaseH, putative	
Afu2g18080	-2.84645	1.569657	-1.02842	LINE-1 class reverse transcriptase, RNaseH, putative	
Afu5g13970	0.525837	1.560481	0.575816	conserved hypothetical protein	
Afu3g05780	1.480159	1.555111	1.289243	GATA transcription factor (LreA), putative	response to light stimulus///blue light signaling pathway///signal transducer activity///transcription factor activity///nucleus///zinc ion binding///regulation of transcription
Afu2g00170	0.643133	1.549262	1.33784	glutathione-dependent formaldehyde dehydrogenase	cellular component unknown///D-xylulose reductase activity///monosaccharide metabolic process
Afu5g10420	1.172004	1.537118	0.217866	nitrate reductase, putative	endoplasmic reticulum///biological process unknown///molecular function unknown
Afu1g15650	-1.86523	1.525741		hypothetical protein	
Afu1g13310	0.780711	1.513824	1.296539	hypothetical protein	

Afu2g14330	-0.18024	1.502973	1.139134	hypothetical protein	
Afu7g05580	1.228544	1.501547	-0.48059	hypothetical protein	phospholipase D activity///phospholipid metabolic process///response to osmotic stress

Table AD.3.3: 23 up-regulated ORFs unique to the 8 hrs time point of the ATCC46645 Δ*pacC*/ATCC46645 comparison.

ORFs	T4	T8	T16	Description	Annotation
Afu8g00560	0.805217	0.577403	4.282449	cytochrome P450, putative	oxidoreductase activity///metabolic process
Afu4g01440	0.015722	1.117132	4.187358	glutathione S-transferase family protein	regulation of nitrogen utilization///soluble fraction///transcription corepressor activity
Afu8g00540	-0.30856	0.518624	3.902841	hybrid polyketide synthase/nonribosomal peptide synthase, putative	polyketide synthase activity
Afu5g01190	0.076751	1.259981	3.6873	conserved hypothetical protein	
Afu8g06090	-0.30684	1.265351	3.444201	amino acid permease, putative	plasma membrane///choline transport///choline transmembrane transporter activity
Afu5g14510	1.48869	1.216701	3.268445	beta-lactamase, putative	beta-lactamase activity///beta-lactam antibiotic catabolic process///response to antibiotic
Afu4g14650	-0.26748	1.413061	3.242713	ribokinase	ribokinase activity///cytoplasm///nucleus///ATP binding///D-ribose metabolic process
Afu8g00550		0.771255	3.193361	SirN-like methyltransferase, putative	
Afu5g01010	-0.22811	0.50861	3.152844	hypothetical protein	
Afu6g10130	0.025108	1.425918	3.105561	N,O-diacetyl muramidase, putative	
Afu8g00520			3.050442	integral membrane protein	
Afu3g07420	-5.79E-04	1.395135	2.955786	hypothetical protein	
Afu4g14670	-0.17023	1.131038	2.948804	MFS quinate transporter, putative	mannose transmembrane transporter activity///hexose transport///fructose transmembrane transporter activity///plasma membrane///glucose transmembrane transporter activity
Afu4g01360	0.458923	0.279962	2.88947	MFS transporter of unkown specificity	cellular component unknown///biological process

					unknown///molecular function unknown
Afu6g06470	-0.75911	1.273413	2.883151	heat shock protein HSP30, putative	
Afu5g02700	0.621452	1.316531	2.878638	multidrug resistant protein	drug transport///drug transporter activity///integral to membrane
Afu4g01380	0.900303	0.899762	2.870861	4-nitrophenylphosphatase, putative	protein amino acid dephosphorylation///alkaline phosphatase activity///histone dephosphorylation///cytoplasm///nucleus///4-nitrophenylphosphatase activity
Afu5g14340	0.427511	0.663077	2.821667	oxidoreductase, short-chain dehydrogenase/reductase family, putative	sporulation (sensu Saccharomyces)///fatty acid catabolic process///peroxisomal matrix///"2,4-dienoyl-CoA reductase (NADPH) activity"
Afu6g10580	0.21607	0.526281	2.783088	antigenic CFEM domain protein, putative	
Afu8g00640	1.150127	1.409414	2.733811	glycosyl transferase, putative	
Afu4g13390	1.091511	0.660816	2.722349	actin-related protein ArpA	sporulation (sensu Saccharomyces)///mitochondrion inheritance///budding cell apical bud growth///protein secretion///actin filament reorganization during cell cycle///exocytosis///structural constituent of cytoskeleton///endocytosis///histone acetyltransferase complex///cell wall organization///establishment of mitotic spindle orientation///response to osmotic stress///regulation of transcription from RNA polymerase II promoter///vacuole inheritance///vesicle transport along actin filament///cytokinesis///actin filament///histone acetylation///budding cell isotropic bud growth
Afu4g13770		1.017059	2.711048	glycosyl hydrolase, putative	carbohydrate metabolic process///"hydrolase activity, hydrolyzing O-glycosyl compounds"
Afu8g05780	1.047412	0.574622	2.698992	NACHT and Ankyrin domain protein	GTP binding///protein binding
Afu4g01370	-0.36595	0.627445	2.696766	hypothetical protein	

Afu1g08910	1.019169	0.841916	2.640441	conserved hypothetical protein	
Afu2g08820	1.017503	1.344053	2.623839	hypothetical protein	
Afu8g00430		0.61711	2.581202	conserved hypothetical protein	
Afu8g00480			2.573668	phytanoyl-CoA dioxygenase family protein	
Afu7g05100	-1.66823	0.722887	2.553792	hexose transporter protein	mannose transmembrane transporter activity///hexose transport///fructose transmembrane transporter activity///plasma membrane///glucose transmembrane transporter activity
Afu8g00680	0.37096	0.644718	2.552493	glycosyl transferase, group 2 family protein	carbohydrate metabolic process///"transferase activity, transferring glycosyl groups"

Table AD.3.4: 30 ORFs with the highest $\log_2$ values between the up-regulated genes unique to the 16 hrs time point of the ATCC46645 Δ*pacC*/ATCC46645 comparison.

Locus	T0 vs T4	T0 vs T8	T0 vs T16	Common Name
Afu1g00500		-1.94		FMN dependent dehydrogenase, putative
Afu1g01370	-1.91	-0.88	-0.58	glutathione S-transferase, putative
Afu1g01540	-1.67	-1.24	-0.95	Endonuclease/Exonuclease/phosphatase family family
Afu1g02260	-0.46	0.51	-1.62	hypothetical protein
Afu1g02620	-1.68	-0.67	-0.90	hypothetical protein
Afu1g02860	-2.13	-0.05	-1.01	C2H2 transcription factor, putative
Afu1g02890	-2.11	-0.74	-1.71	dUTPase (Dut), putaive
Afu1g02930	-1.07	-0.84	-1.52	Ca2+ binding protein (calmodulin), putative
Afu1g03020	-2.41	-0.40	-1.34	My026 protein
Afu1g03150	-0.07	-1.16	-1.91	c-14 sterol reductase
Afu1g03160	-1.47	-1.00	-2.17	hypothetical protein
Afu1g03200		-0.96	-2.05	MFS transporter, putative
Afu1g03610	0.36	0.59	-1.50	hypothetical protein
Afu1g03720	-1.56	-0.83	-0.49	UPF0136 domain protein
Afu1g04130	-1.60	-0.69	-0.76	FG-GAP repeat protein, putative
Afu1g04150	-0.84	0.14	-1.64	tartrate dehydrogenase
Afu1g04310	-1.51	-0.96	-1.35	hypothetical protein

Afu1g04860	-1.50	-0.61	-0.55	hypothetical protein
Afu1g05400	-2.13	-0.09	-1.26	hypothetical protein
Afu1g05720	0.04	-1.55	-0.97	c-14 sterol reductase
Afu1g05820	-2.32	-0.67	-1.23	conserved hypothetical protein
Afu1g05940	-2.16	-0.58	-0.78	conserved hypothetical protein
Afu1g06100	-2.11	-0.23	-0.61	glutaredoxin
Afu1g06200	-1.63	-1.98	-1.38	Mn2+ homeostasis protein (Per1), putative
Afu1g06990	-2.81	1.85	-1.80	NA
Afu1g07430	-1.78	-0.70	-1.00	hypothetical protein
Afu1g09360	-1.57	-0.35	-0.92	DUF1242 domain protein, putative
Afu1g09750	-0.39	-0.55	-1.53	aldehyde reductase (AKR1), putative
Afu1g09810	-1.89	-0.90	-1.20	PUA RNA binding domain protein, putative
Afu1g10100	-1.67	0.01	-0.23	3-oxoacyl-(acyl-carrier-protein) reductase
Afu1g10300	-2.65		-0.90	hypothetical protein
Afu1g10460	-2.40	-1.51	-2.15	hypothetical protein
Afu1g10690	-0.75	-1.04	-1.53	conserved hypothetical protein
Afu1g10720	0.10	-0.13	-1.91	origin recognition complex subunit Orc1, putative
Afu1g10820	-1.73	-0.73	-0.62	adenylylsulfate kinase
Afu1g10830	0.06	-1.28	-1.53	succinyl-CoA synthetase, putative
Afu1g10930	1.24	-0.29	-2.36	ammonium transporter
Afu1g11480	-1.81	-0.87	-0.88	hypothetical protein
Afu1g11560	-1.48	-1.87	-3.74	4-hydroxyphenylpyruvate dioxygenase, putative
Afu1g11590	-1.58	-1.45	-0.24	quinate 5-dehydrogenase
Afu1g12270	-2.39	-0.42	-1.46	hypothetical protein
Afu1g12360	-2.05		-1.43	hypothetical protein
Afu1g12740	-1.75	-1.42	-1.31	hypothetical protein
Afu1g12860	-1.10	-1.03	-2.00	DUF718 domain protein
Afu1g13480	-1.90	-0.36	-0.72	ubiquinol-cytochrome C reductase complex subunit UcrQ, putative
Afu1g13550	-1.55	-0.15	-1.62	hypothetical protein
Afu1g14380	-1.52	-0.83	-0.33	3-ketoacyl-acyl carrier protein reductase
Afu1g14390	-2.16	-0.86	-0.77	zinc binding dehydrogenase family protein
Afu1g14820	-2.91	0.09	-1.15	hypothetical protein
Afu1g15040	-0.40	-0.75	-1.54	hypothetical protein

Afu1g15150	-0.40	-1.67	-1.79	alpha-amylase (amyE)
Afu1g15190	-2.27		-0.87	hypothetical protein
Afu1g15280	-1.67	-0.64	-1.32	polysaccharide deacetylase family protein
Afu1g15330	-2.22	-1.03	-0.69	T10O22.24
Afu1g15650	-1.87	1.53		hypothetical protein
Afu1g15710		-1.33	-1.60	cyclosome/APC complex component Cut20/Apc4, putative
Afu1g16250	-3.99	-1.86	-1.91	alpha-glucosidase B
Afu1g16330	-1.82	-0.14	-1.06	ribosome assembly protein Noc2, putative
Afu1g16510	-1.54	-0.47	-0.80	heme/steroid binding domain protein, putative
Afu1g17120	-1.59	-0.49	-0.61	elongation factor-1 gamma
Afu1g17150	-1.51	-2.19	-2.08	C6 transcription factor, putative
Afu1g17160	-1.44	-1.83	-1.43	transporter, putative
Afu1g17170	-1.58	-2.28	-1.45	alpha-ketoglutarate-dependent taurine dioxygenase
Afu1g17190	-0.80	-1.68	-1.51	long-chain-fatty-acid-CoA ligase, putative
Afu1g17200	-0.92	-1.34	-1.86	nonribosomal peptide synthase, putative
Afu1g17370	-2.06	0.51	-0.68	chaperone/heat shock protein Hsp9, putative
Afu1g17590	-1.65	-1.69	-0.34	phosphoesterase superfamily protein
Afu1g17680	-1.58	-0.61	-0.01	MFS transporter, putative
Afu2g00120	0.15	-1.30	-1.67	carboxyvinyl-carboxyphosphonate phosphorylmutase
Afu2g00240	-1.80	-0.62	-1.88	hypothetical protein
Afu2g00320	-0.26	-1.69	-1.75	sterol delta 5,6-desaturase, putative
Afu2g00500	-0.36	-2.76	-2.72	conserved hypothetical protein
Afu2g00520	-1.90			hypothetical protein
Afu2g00540	-2.09	-1.45	-2.67	carboxyphosphonoenolpyruvate phosphonomutase, putative
Afu2g00570	-1.35	-1.58	-1.71	GNAT family acetyltransferase, putative
Afu2g00580	-1.77	0.02	-1.04	hypothetical protein
Afu2g00720	-2.80	-2.92	-2.97	aldehyde dehydrogenase, putative
Afu2g00760	-0.53	-1.78	-2.38	pectate lyase A
Afu2g00870	-0.40	-1.52	-0.69	hypothetical protein
Afu2g01130	-2.27	-0.80	-0.12	ubiquitin conjugating enzyme (UbcJ), putative
Afu2g01280	-1.96	0.98	-0.57	D-mandelate dehydrogenase, putative
Afu2g01320	-2.86	-2.45	-2.63	P-type ATPase, putative

Afu2g01490	-0.62	-0.10	-2.43	hypothetical protein
Afu2g01990	-1.68	-0.86	-1.10	Signal recognition particle 14kD protein domain containing protein
Afu2g02090	-1.79	-1.14		methylated-DNA-protein-cysteine methyltransferase
Afu2g02270	-2.43	-0.64	-1.41	ribosomal protein S14p/S29e
Afu2g03000	-1.58	-1.20	-1.21	nucleoside transporter, putative
Afu2g03150	-1.88	-0.81	-1.70	kinesin family protein
Afu2g03470	-1.95	-0.34	-0.89	hypothetical protein
Afu2g03570	-2.08	-0.97	-1.08	transposase
Afu2g04140	-1.17	-1.00	-1.62	conserved hypothetical protein
Afu2g04210	-2.32	-1.45	-1.08	conserved hypothetical protein
Afu2g04260	-1.60	-0.67	-0.62	transcription factor, putative
Afu2g04520	-1.51	-0.43	-0.16	Fe-containing alcohol dehydrogenase, putative
Afu2g04540	-2.01	-1.04	-0.68	hypothetical protein
Afu2g04570	-2.40	-0.95	-1.33	BNR/Asp-box repeat domain protein
Afu2g04730	-2.10			NA
Afu2g05050	-1.95	-0.95	-1.05	hypothetical protein
Afu2g05080	-1.89	-0.95	0.08	hypothetical protein
Afu2g05150	-1.52	-1.01	-0.57	cell wall galactomannoprotein Mp2
Afu2g05180	-1.58	-1.14	-1.42	NF-X1 finger and helicase domain protein, putative
Afu2g05360	-1.76	-1.09	-2.04	C6 transcription factor, putative
Afu2g05700	-2.64	-0.23	-1.14	hypothetical protein
Afu2g05810	-1.56	-0.99	-1.33	dienelactone hydrolase
Afu2g07750	-1.63	-0.71	-0.29	haloacid dehalogenase, type II
Afu2g07840	-3.18	-1.80	-2.74	competence/damage-inducible protein CinA, putative
Afu2g07910	-1.67	-1.62	-1.65	myo-inositol transporter
Afu2g07940	-1.76	-0.52	-1.13	NADPH-cytochrome P450 reductase (CprA), putative
Afu2g08130	-1.67	-0.50	-1.25	ribosomal protein L41
Afu2g08180	-0.73	-1.31	-2.68	flotillin domain protein
Afu2g08320	-1.53	-0.44	-0.42	U3 small nucleolar ribonucleoprotein subunit (Imp3), putative

Afu2g08500	-1.18	-0.39	-1.52	carboxylesterase, putative
Afu2g08680	-1.76	0.25	0.03	hypothetical protein
Afu2g08880	-1.66	-0.73	-1.20	hypothetical protein
Afu2g08950	-1.64	-0.53	0.13	isochorismatase family hydrolase, putative
Afu2g09030	-2.73	-2.51	-3.13	secreted dipeptidyl peptidase
Afu2g09450	-4.15	-4.46	-4.48	carboxylic acid transport protein
Afu2g09580	-1.73	-0.54		UDP-N-acetylenolpyruvoylglucosamine reductase
Afu2g09670	-1.64	-0.35	-1.09	SNARE protein (Ufe1), putative
Afu2g10020	-2.17	-0.79	-2.44	hypothetical protein
Afu2g10580	-1.72	0.07	-0.26	hypothetical protein
Afu2g10920	-1.59	-0.76	0.49	enoyl-CoA hydratase/isomerase family protein
Afu2g11120	0.05	-0.68	-2.10	hypothetical protein
Afu2g11520	1.03	-0.50	-2.24	MFS monosaccharide transporter, putative
Afu2g11820	-1.72	-1.20	-0.73	hypothetical protein
Afu2g12020	-1.61	-1.32	-0.82	U6 snRNA-associated Sm-like protein LSM4, putative
Afu2g12600	-0.75	-1.12	-1.87	hypothetical protein
Afu2g12680	-1.58	-3.40	-4.34	conserved hypothetical protein
Afu2g12740	-1.58	-0.17	0.74	methyltransferase, putative
Afu2g12990	-1.55	-0.83	-0.89	cyclophilin
Afu2g13010	-1.69	-0.46	-1.03	cytochrome c oxidase polypeptide vib
Afu2g13160	-1.58	-0.79	-1.34	hypothetical protein
Afu2g13460	0.55	-0.06	-2.05	alpha-amylase, putative
Afu2g14490	-2.23	-4.64	-4.74	endoglucanase, putative
Afu2g14540	-1.95	-2.10	-1.82	endoglucanase, putative
Afu2g14610	-1.62	0.46	0.36	Oxalate decarboxylase
Afu2g14630	-1.18	-0.59	-1.59	cell wall glycosyl hydrolase family 88 (YteR), putative
Afu2g14850	-1.76	-0.62	-0.97	enoyl-CoA hydratase/isomerase family protein
Afu2g14950	0.08	-0.47	-1.57	exonuclease, putative
Afu2g15150	-1.53	-0.93	-0.80	choline transport protein, putative
Afu2g15510	-2.04	-1.14	-1.35	conserved hypothetical protein
Afu2g15950	-1.14	-3.27	-3.00	aspartic endopeptidase, putative
Afu2g16190	-1.59	-0.06	-0.44	hypothetical protein

Afu2g16710	-1.60	-0.93	-1.33	hypothetical protein
Afu2g16880	-2.02	-0.10	-0.65	ribosomal protein L37a
Afu2g17020	-1.04	-0.41	-1.52	NA
Afu2g17450	-0.54	-1.20	-1.56	3-hydroxyanthranilate 3,4-dioxygenase
Afu2g18080	-2.85	1.57	-1.03	LINE-1 class reverse transcriptase, RNaseH, putative
Afu3g00350	-1.73	-0.74	-1.22	hypothetical protein
Afu3g00490	-3.44	-2.56	-3.99	C6 finger domain protein, putative
Afu3g00650		-1.63	-1.55	aminopeptidase Y, putative
Afu3g00660	-2.30	-1.08	-1.52	conserved hypothetical protein
Afu3g00720	-0.69	-0.82	-1.68	DUF500 and UBA/TS-N domain protein
Afu3g00730	-1.20	-0.68	-1.60	conserved hypothetical protein
Afu3g00760	-0.66	-0.48	-1.56	GNAT family N-acetyltransferase, putative
Afu3g00770	-2.03	-2.90	-2.92	hypothetical protein
Afu3g00960	-1.83	-0.06	0.30	conserved hypothetical protein
Afu3g01210	-1.64	-1.06	-1.22	ThiJ/PfpI family protein
Afu3g01240	-2.69	-0.80	-0.76	hypothetical protein
Afu3g01280	-1.58	-1.82	-0.69	alpha/beta hydrolase, putative
Afu3g01340	-2.10	-1.18	-1.19	DUF636 domain protein
Afu3g01370	-2.06	-0.75	-1.11	MFS transporter, putative
Afu3g01430	-2.34	-0.93	-1.12	benzodiazepine receptor family protein
Afu3g01480	-1.69	-1.49	-2.67	conserved hypothetical protein
Afu3g01530	-3.17	-1.93	-1.09	phosphatidylglycerol specific phospholipase, putative
Afu3g01580	-1.69	-0.62	-0.19	GMC oxidoreductase, putative
Afu3g01610	-2.06	-0.93	-0.81	hypothetical protein
Afu3g01670		-1.98	-0.90	MFS hexose transporter, putative
Afu3g01710	-1.28	-0.57	-1.63	TPR domain protein
Afu3g02260	-1.69	-0.94	-1.44	hypothetical protein
Afu3g02270	-0.89	-0.92	-2.05	mycelial catalase Cat1
Afu3g03000	-3.04	-1.70	-2.64	phosphatidylethanolamine-binding protein, putative
Afu3g03010	-5.35	-2.99	-2.89	phosphate-repressible phosphate permease
Afu3g03070	-1.65	0.24		MYND domain protein, putative
Afu3g03110	-1.73	-0.58	-0.90	NA

Afu3g03120	-2.59	1.04	-1.36	NA
Afu3g03370	-1.51	-0.59	-0.91	cell surface protein, putative
Afu3g03640	-0.17	0.32	-2.07	siderochrome-iron transporter (MirB), putative
Afu3g03650	-0.29	-1.43	-2.03	acetyltransferase, GNAT family, putative
Afu3g03670	0.51	-1.60	-1.11	ABC multidrug transporter, putative
Afu3g03730	-0.61	-0.03	-2.36	hypothetical protein
Afu3g03770	-1.56	-0.56	-0.94	transposase
Afu3g03810	-1.66	-1.09	0.36	hypothetical protein
Afu3g03820	-1.81	-1.27	0.59	MFS transporter, putative
Afu3g03850	-1.78	-1.19	-0.57	hypothetical protein
Afu3g03860	-2.41	-1.83	0.29	3-hydroxyacyl-CoA dehydrogenase, putative
Afu3g03950	0.87		-1.58	endoglucanase, putative
Afu3g04290	-0.90		-1.57	NA
Afu3g05360	-1.72	-0.55	-0.81	histone H2A
Afu3g07140	-2.01	-0.48	-0.77	developmental regulator FluG
Afu3g07300	-1.01	-1.20	-1.86	ABC multidrug transporter, putative
Afu3g07560	-1.93	-0.57	-1.64	enoyl-CoA hydratase/isomerase family protein
Afu3g07860	-1.51	-1.50	-1.99	glycosyl transferase, putative
Afu3g07870	-3.26	-2.58	-3.09	extracellular serine-rich protein
Afu3g07900	-2.36	-1.77	-2.56	conserved hypothetical protein
Afu3g07910	-3.87	-2.69	-3.09	UDP-glucose 4-epimerase, putative
Afu3g07930	-1.53	-0.51	-0.42	putative glutathione S-transferase
Afu3g08130	-2.19	-1.97	-2.50	hypothetical protein
Afu3g08150	-1.53	-0.96	-1.08	hypothetical protein
Afu3g08850	-1.54	-0.14	0.05	FAD dependent sulfhydryl oxidase Erv1, putative
Afu3g09120	-1.80	-0.56	-0.85	hypothetical protein
Afu3g09200	-0.55	-1.38	-1.77	NA
Afu3g09410	-1.83	0.88		reverse transcriptase
Afu3g09430	-2.41	1.02	-0.84	LINE-1 class reverse transcriptase, RNaseH, putative
Afu3g10330	-2.18	-0.69	-1.09	hypothetical protein
Afu3g10500	-1.87	-2.18	-2.77	hypothetical protein
Afu3g10510	-2.75	-0.64	-0.94	hypothetical protein
Afu3g10690	-2.76	-2.37	-3.78	calcium-translocating P-type ATPase(PMCA-

				type),putative
Afu3g10990			-2.12	NA
Afu3g11480	-1.68	-0.74	-0.37	mitochondrial methylglutaconyl-CoA hydratase (Auh), putative
Afu3g11820	-1.89	-0.51	-1.08	mitochondrial oligoribonuclease, putative
Afu3g11880	-4.24	-0.67	-1.11	hypothetical protein
Afu3g11970	-3.95	-2.87	-3.87	C2H2 transcription factor PacC, putative
Afu3g12070	-0.60	-0.42	-2.34	conserved hypothetical protein
Afu3g12090	-1.94	-0.87	-2.36	hypothetical protein
Afu3g12220	-1.55	1.18	-0.98	ABC transporter, putative
Afu3g12740	-1.73	-0.82	-1.16	copper resistance-associated P-type ATPase, putative
Afu3g12790	-1.53	-1.31	-1.90	conserved glutamic acid-rich protein
Afu3g13220	-1.12	0.29	-1.80	hypothetical protein
Afu3g13600	-2.07	-1.87	-2.06	C6 transcription factor, putative
Afu3g13620	-1.20	-0.37	-1.82	conserved hypothetical protein
Afu3g13740	-2.03	-1.72	-0.40	HSP70 family protein
Afu3g13910	-2.02	-0.57	-1.22	NADH-ubiquinone oxidoreductase B18 subunit, putative
Afu3g14030	-4.81	-3.75	-3.92	alkaline phosphatase
Afu3g14600	-1.52	-0.43	-0.59	fungal specific transcription factor, putative
Afu3g14650	-1.87	0.04	-0.02	hypothetical protein
Afu3g14660	-1.75	-0.08	-0.71	hypothetical protein
Afu3g14870	0.26	-0.36	-2.03	hypothetical protein
Afu3g15080	0.42	-0.54	-1.61	hypothetical protein
Afu3g15350	-0.31		-2.00	short chain dehydrogenase family protein, putative
Afu3g15370	-2.70	1.49	-1.16	LINE-1 class reverse transcriptase, RNaseH, putative
Afu4g00750	-2.82	-2.87	-3.51	hypothetical protein
Afu4g00760	-1.43	-2.26	-3.22	hypothetical protein
Afu4g00820	-2.94	1.68	-1.27	reverse transcriptase, RNaseH
Afu4g00930	-3.90	-2.74	-3.68	CorA family metal ion transporter, putative
Afu4g01000	-1.76	-0.59	0.55	MFS transporter, putative
Afu4g01060	-1.69	-0.66	0.06	hypothetical protein
Afu4g01120	-0.25	0.13	-1.81	hypothetical protein

Afu4g01270	-1.76	-0.33	-0.34	hypothetical protein
Afu4g01560	-2.57	-3.05	-4.92	MFS myo-inositol transporter, putative
Afu4g01570	-2.33	-1.44	-2.52	neutral amino acid permease
Afu4g06420	-1.88	-0.10	-0.58	fungal specific transcription factor, putative
Afu4g06470	-0.64	0.27	-2.13	NA
Afu4g06600	-1.54	-0.91	-1.22	hypothetical protein
Afu4g06640	-2.23	-1.30	-0.65	acid sphingomyelinase
Afu4g06650	-2.45	-2.24	-2.72	hypothetical protein
Afu4g06860	-1.73	-0.82	-1.38	conserved hypothetical protein
Afu4g07150	-2.21	-0.81	-1.16	cytochrome-c oxydase chain VIIc-like protein
Afu4g07750	-1.73	-0.51	-0.86	UPF0041 domain protein
Afu4g08640	-1.72	0.13	1.35	hypothetical protein
Afu4g08680	-1.86	-0.40	-0.88	hypothetical protein
Afu4g08750	-2.05	-0.74	-0.82	hypothetical protein
Afu4g08840	-2.26	-2.97	-2.18	RING finger domain protein, putative
Afu4g08850	-1.96	-1.89	-1.92	hypothetical protein
Afu4g08890	-1.98	1.41	-0.82	aldo-keto reductase family protein, putative
Afu4g09300	-1.92	-1.39	-2.00	hypothetical protein
Afu4g09310	-2.50	-2.77	-3.89	hypothetical protein
Afu4g09320	-5.70	-3.69	-6.07	antigenic dipeptidyl-peptidase Dpp4
Afu4g09330	-1.83	-0.27	-0.67	conserved hypothetical protein
Afu4g09340	-2.63	-0.50	-0.74	hypothetical protein
Afu4g09440	-2.74	-2.05	-1.71	sodium P-type ATPase, putative
Afu4g09450	-1.78	-0.18	-0.24	hypothetical protein
Afu4g09560	-2.89	-2.24	-2.92	ZIP Zinc transporter, putative
Afu4g09580	-3.22	-2.25	-2.21	major allergen Asp F2
Afu4g09920	-3.23	-0.87	-1.61	conserved hypothetical protein
Afu4g09980	-1.59	-0.65	-1.46	cytochrome P450 monooxygenase, putative
Afu4g09990	-3.34	-3.10	-3.52	Nucleoside transporter family
Afu4g10370	-2.35	-1.62	-1.34	3-demethylubiquinone-9 3-methyltransferase
Afu4g10610	-3.23	-1.32	-1.39	hypothetical protein
Afu4g11380	-0.39	-1.59	-0.30	hypothetical protein
Afu4g11400	-1.64	-0.26	-0.22	cell surface receptor/MFS transporter (FLVCR), putative

Afu4g11620	-2.11	-0.78	-0.19	conserved hypothetical protein
Afu4g11800	-1.56	-3.83	-1.22	alkaline serine protease Alp1
Afu4g12150	-1.51	-0.82	-0.43	HIT domain protein
Afu4g12430	-1.70	-0.73	-0.42	PSF1 domain protein
Afu4g12490	-2.04	-0.33	-1.26	guanine nucleotide exchange factor VPS9, putative
Afu4g12540	-1.55	-0.67	-0.31	hypothetical protein
Afu4g13090	-0.47	-1.17	-1.54	MFS transporter, putative
Afu4g13260	-1.00	-0.66	-1.68	hypothetical protein
Afu4g13760	-2.05	-2.05	-3.66	hypothetical protein
Afu4g13820	-1.78	0.23	-1.54	multidrug transporter, putative
Afu4g13880	0.95	-0.55	-2.21	ankyrin repeat protein
Afu4g13900	0.14	-0.29	-2.20	MFS transporter, putative
Afu4g13970		-1.02	-2.35	conserved hypothetical protein
Afu4g14070	-0.47	-2.58	-2.40	glycosyl transferase, putative
Afu4g14090	-0.77	-1.74	-1.29	UDP-glucose 4-epimerase
Afu4g14180	-1.71	-1.31	-1.83	hypothetical protein
Afu4g14200			-2.53	conserved hypothetical protein
Afu4g14230	0.10	-0.42	-1.51	MFS transporter, putative
Afu4g14370	-1.78	0.83	-1.74	LINE-1 class reverse transcriptase, RNase H, putative
Afu4g14420	-2.13	-1.69	-1.07	secreted glycosyl hydrolase, putative
Afu4g14860	-1.81	1.41		NA
Afu4g14870	-2.93	1.69	-1.14	LINE-1 class reverse transcriptase, RNaseH, putative
Afu5g00100	-0.99	0.18	-1.74	hypothetical protein
Afu5g00540	-0.67	-1.82	-2.54	extracellular signaling protein FacC, putative
Afu5g00670	-1.71	-1.44	-1.48	glycosyl hydrolase family 35, putative
Afu5g00770	-0.61	-2.28	-2.71	integral membrane protein, putative
Afu5g00790	-2.39	-2.76	-3.69	ABC multidrug transporter, putative
Afu5g00810	-1.65	-0.36		hypothetical protein
Afu5g00870	-2.54	-1.90	-3.25	hypothetical protein
Afu5g01230	-0.24	-2.22	-0.06	RTA1 domain protein, putative
Afu5g01250		-1.83	-2.97	oxidoreductase, putative
Afu5g01440	-2.13	-0.71	-0.61	allergen, putative

Afu5g01570	-3.31	-2.20	-3.34	hypothetical protein
Afu5g01580	-4.90	-1.81	-3.66	oxidoreductase, short chain dehydrogenase/reductase family
Afu5g01710	-2.24	1.11	-1.78	cytochrome P450 phenylacetate 2-hydroxylase, putative
Afu5g01770	-1.73	-0.96	-0.79	conserved hypothetical protein
Afu5g01990	-1.73	-1.82	-0.75	BYS1 domain protein, putative
Afu5g02250	-1.27	-0.42	-2.14	conserved hypothetical protein
Afu5g02350	-1.89	-0.68	-1.02	hydrolase, carbon-nitrogen family, putative
Afu5g02500	-1.65	-0.73	-1.38	hypothetical protein
Afu5g02870	-1.67	-0.87	-0.22	oxidoreductase, short-chain dehydrogenase/reductase family
Afu5g02990	-1.73	-2.01	-2.90	aromatic amino acid aminotransferase, putative
Afu5g03170	-1.84	0.17		hypothetical protein
Afu5g03620	-1.73	-0.20	-0.53	endonuclease/transposase
Afu5g04040	-2.26	-0.27	-0.84	conserved hypothetical protein
Afu5g05910	-1.04	-0.79	-1.70	hypothetical protein
Afu5g06910	-2.98	-0.43	0.18	DUF636 domain protein
Afu5g06960	-1.50	-0.58	-0.31	conserved hypothetical protein
Afu5g07610	-2.17	-0.81	-1.22	NA
Afu5g07670	-1.04	-0.93	-1.75	SH3 domain signalling protein
Afu5g09130	-2.45	-0.95	-1.94	polysaccharide deacetylase family protein
Afu5g09140	-1.77	-0.52	-1.67	amidase, putative
Afu5g09150	-1.70	-0.96	-0.56	oxidoreductase, short-chain dehydrogenase/reductase family
Afu5g09530	-1.64	-1.47	-1.02	conserved hypothetical protein
Afu5g10090	-2.78	-1.33	-1.44	3-demethylubiquinone-9 3-methyltransferase, putative
Afu5g10250	-2.74	-1.61	-3.38	hypothetical protein
Afu5g10290	-1.80	-0.36	-0.38	fructose-bisphosphate aldolase, putative
Afu5g11190	-1.79	-1.77	-2.89	hypothetical protein
Afu5g12600		-1.12	-1.68	DNA excision repair protein (Rad5), putative
Afu5g13030	-1.91	-0.53	-1.13	Apc13 domain protein
Afu5g13100	-1.51	-0.15	-1.10	hypothetical protein
Afu5g13170	0.59	0.28	-1.57	MATE efflux family protein subfamily, putative

Afu5g13630	-1.57	-0.74	-0.36	EF-hand superfamily protein
Afu5g14070	-0.88	-0.50	-1.66	conserved hypothetical protein
Afu5g14210	-2.48	-0.74	-1.27	glucose-repressible gene protein-related protein
Afu5g14290	-1.13	-0.84	-2.49	C6 transcription factor, putative
Afu5g14650	-1.62	-0.93	-0.19	RING finger protein
Afu5g14680	-2.04	0.03	-3.45	hypothetical protein
Afu5g14690	-1.22	0.36	-3.56	phosphorylase, putative
Afu5g14710	0.51	-0.70	-1.83	hypothetical protein
Afu5g14780	-1.54	0.73	-1.95	heat shock trehalose synthase, putative
Afu5g14930	-1.60	0.27	-0.24	conserved hypothetical protein
Afu6g00140	-1.90	-2.33	-2.25	hypothetical protein
Afu6g00400	-0.48	-0.18	-1.73	conserved hypothetical protein
Afu6g00470	-3.85	-2.44	-3.05	plasma membrane zinc ion transporter, putative
Afu6g00710	-2.29	-1.49	-0.67	MFS transporter, putative
Afu6g00780	-2.77	1.73	-1.04	LINE-1 class reverse transcriptase, RNaseH, putative
Afu6g01850	-2.04	-0.42	0.11	hypothetical protein
Afu6g01980	-1.95	-0.31	-0.95	haemolysin-III family protein
Afu6g02040	-1.77	-0.68	-0.08	hypothetical protein
Afu6g02140	-1.29	-1.37	-1.88	peptidyl prolyl cis-trans isomerase (CypC), putative
Afu6g02220	-2.29	-0.99	-1.14	MFS toxin efflux pump, putative
Afu6g02290	-1.33	-0.83	-1.70	hypothetical protein
Afu6g02830	-1.70	-0.28	-0.89	hypothetical protein
Afu6g02960	-1.76	-0.75	-1.25	NADH-ubiquinone oxidoreductase 105 kDa subunit
Afu6g03100	-1.74	-1.16	-0.71	hypothetical protein
Afu6g03140	-1.07	-1.10	-2.09	isp4 protein, putative
Afu6g03170	-2.18	-1.43	-1.22	NA
Afu6g03190	-2.34	-0.33	0.98	hypothetical protein
Afu6g03200	-2.09	-0.56	0.24	solute symporter family transporter
Afu6g03350	-2.41	-3.60	-4.51	acetyltransferase, GNAT family, putative
Afu6g03400	-2.28	-0.67	-0.92	hypothetical protein
Afu6g03460	-2.24	-1.65	-3.11	hypothetical protein
Afu6g03480	-0.08	-2.15	-2.15	nonribosomal peptide synthetase, putative

Afu6g03490	0.35	-1.62	-1.15	phenol 2-monooxygenase, putative
Afu6g03800	-1.68	-0.09	-1.51	hypothetical protein
Afu6g04020	-2.02	-0.71	-0.97	peptidyl-tRNA hydrolase domain protein
Afu6g04370	-0.67	-0.66	-1.58	hypothetical protein
Afu6g04620	-1.89	-0.29	-0.91	NADH-ubiquinone oxidoreductase B14 subunit, putative
Afu6g04700	-1.71	-0.60	-1.27	imidazoleglycerol-phosphate dehydratase
Afu6g07480	-1.20	-0.70	-1.92	endoglucanase C
Afu6g07920	-0.76	-0.88	-1.69	acetyltransferase, GNAT family family
Afu6g08180	-1.91	-0.37	-0.68	hypothetical protein
Afu6g08560	-2.00	-0.71	-1.62	nonribosomal peptide synthase (NRPS), putative
Afu6g08630	-1.69	-0.79	-0.44	hypothetical protein
Afu6g08700	-2.44	-0.63	-1.17	beta glucosidase, putative
Afu6g08830	-1.66	-1.02	-0.53	2-oxoisovalerate dehydrogenase complex alpha subunit, putative
Afu6g09340	-1.67	1.08		hypothetical protein
Afu6g09470	-2.80	1.45	-0.98	reverse transcriptase, RNaseH, putative
Afu6g09610	-0.72	-1.14	-2.07	nonribosomal peptide synthase, putative
Afu6g09640	-1.03	-2.45	-3.79	aminotransferase GliI
Afu6g09650	-0.76	-1.97	-4.06	membrane dipeptidase GliJ
Afu6g09660			-3.31	nonribosomal peptide synthase GliP
Afu6g09670	0.29	-3.38	-6.05	cytochrome P450 oxidoreductase GliC
Afu6g09680		-4.31	-6.94	O-methyltransferase GliM
Afu6g09690	-0.58	-3.98	-7.27	glutathione S-transferase GliG
Afu6g09700	-0.12	-2.98	-6.89	gliotoxin biosynthesis protein GliK
Afu6g09710	0.62	-3.02	-5.56	MFS gliotoxin efflux pump GliA
Afu6g09720		-4.85	-7.37	methyltransferase GliN
Afu6g09730	-0.29	-4.08	-6.18	cytochrome P450 oxidoreductase GliF
Afu6g09740	-1.00	-3.30	-5.05	thioredoxin reductase GliT
Afu6g09830	-2.77	-1.17	-0.21	hypothetical protein
Afu6g10080	-2.21	-1.06	-1.58	conserved hypothetical protein
Afu6g10700	-1.90	-0.83	-1.10	chaperonin, putative
Afu6g11320	0.54	-1.38	-2.48	MFS transporter, putative
Afu6g11330	-1.77	-1.71	-1.33	histidine acid phosphatase, putative

Afu6g11390	-2.11	-2.45	-3.32	1,3-beta-glucanosyltransferase Gel2
Afu6g11600	-2.11	-0.52	-0.10	endoglucanase, putative
Afu6g11680	-1.52	-1.34	-0.90	thiamine pyrophosphate enzyme, putative
Afu6g11690	-1.70	0.72		NA
Afu6g11810	-1.75	1.34		RTA1 domain protein, putative
Afu6g12000	-1.66	-0.47	-0.79	hypothetical protein
Afu6g12150	-0.50	0.08	-1.54	bZIP transcription factor (Atf7), putative
Afu6g12170	-1.70	-0.24	-1.01	FKBP-type peptidyl-prolyl isomerase, putative
Afu6g12200	-1.63	-0.21	-1.18	hypothetical protein
Afu6g12220	-1.79	-1.20	-1.31	isochorismatase family hydrolase, putative
Afu6g12240	-4.95	-4.28	-5.19	Glycerophosphoryl diester phosphodiesterase family family
Afu6g12420	0.21	-1.00	-1.65	SprT family metallopeptidase, putative
Afu6g12450	-1.88	-0.67	-2.99	chaperone/heat shock protein Hsp12, putative
Afu6g12460	-1.83	-0.59	-2.83	conserved hypothetical protein
Afu6g12480	-0.73	-0.69	-1.68	ngg1-interacting factor 3
Afu6g12780	-0.22	-0.03	-1.53	conserved hypothetical protein
Afu6g13280	-1.61	-0.15	-0.75	Fox2 protein
Afu6g13290	-1.14	-0.79	-1.67	SNF2 family helicase/ATPase, putative
Afu6g13310	-1.49	-1.25	-1.50	26S proteasome non-ATPase regulatory subunit 9, putative
Afu6g13750	-5.45	-4.16	-5.55	ferric-chelate reductase, putative
Afu6g13760	-2.58	-2.25	-2.56	alpha-1,2-mannosidase, putative subfamily
Afu6g13780	-2.33	-0.28	-0.66	multidrug resistant protein, putative
Afu6g13840	-4.19	-1.79	-1.63	conserved hypothetical protein
Afu6g13850	-2.48	-2.32	-1.48	GTPase activating protein (Evi5), putative
Afu6g13860	-1.62	-0.56	-1.22	conserved hypothetical protein
Afu6g14000	-1.91	0.63	-0.75	Tri7-like toxin biosynthesis protein, putative
Afu6g14380	-1.66	-0.23	0.22	hypothetical protein
Afu6g14500	-4.11	-3.69	-2.59	MFS sugar transporter, putative
Afu6g14530	-3.29	-1.42	-0.67	L-cystine transporter, putative
Afu6g14540	-1.78	2.01	1.99	endo-1,3(4)-beta-glucanase, putative
Afu6g14570			-1.65	conserved hypothetical protein
Afu6g14660	-2.96	1.86	-1.16	reverse transcriptase, RNaseH

Afu7g00280	-1.16	-2.12	-2.36	conserved hypothetical protein
Afu7g00440	-2.17	-2.42	-2.77	GABA permease, putative
Afu7g00450	-3.54	-2.76	-3.11	GPI anchored protein, putative
Afu7g00580	-3.84	-3.26	-4.68	conserved hypothetical protein
Afu7g00710	-0.98	-1.09	-1.72	oxalate/formate antiporter, putative
Afu7g00780	-2.44	-1.11	-1.09	MFS monocarboxylate transporter, putative
Afu7g00960	-1.63	0.34		extracellular cysteine-rich protein, putative
Afu7g00970	-1.36	-1.33	-2.65	GPI-anchored serine-threonine rich protein
Afu7g00980	-1.87	-1.26	-0.86	NA
Afu7g01000	-1.53	-0.08	0.33	aldehyde dehydrogenase, putative
Afu7g01010	-1.90	-0.74	-0.15	alcohol dehydrogenase, putative
Afu7g01030	-2.79	-1.68	-1.61	Calcium-transporting ATPase 1 (PMC1), putative
Afu7g01040	-2.06	-1.24	-1.37	cytidine deaminase, putative
Afu7g01090	-1.61	-0.58	-0.12	proline permease
Afu7g01120	-1.29	0.16	-1.65	NA
Afu7g01440	0.22	-0.12	-1.73	hypothetical protein
Afu7g01520	-2.47	-1.02	-1.71	BolA domain protein
Afu7g01580	-2.31	-0.99	-1.20	molybdopterin synthase small subunit CnxG
Afu7g01670	-0.93	-0.49	-2.33	MFS amino acid transporter, putative
Afu7g01780	-2.87	-0.62	-1.37	hypothetical protein
Afu7g01900	-1.87	-0.09	-0.81	TOM core complex subunit Tom6, putative
Afu7g02010	-3.21	-1.72	-0.48	hypothetical protein
Afu7g02030	-1.65	-0.25	-0.87	cytochrome c oxidase assembly protein (Pet117), putative
Afu7g02220	-2.65	-1.49	-3.50	hypothetical protein
Afu7g02340	-2.22	-0.85	-1.20	L-PSP endoribonuclease family protein (Hmf1), putative
Afu7g02510	-0.59	-1.66	-1.69	hypothetical protein
Afu7g04280	-1.73	-0.60	-0.38	small nuclear ribonucleoprotein (LSM5), putative
Afu7g04560	-1.55	0.62	-0.65	hypothetical protein
Afu7g04820	0.14	-0.74	-1.82	C6 transcription factor, putative
Afu7g04970	-0.35	-1.70	-0.54	metalloreductase, putative
Afu7g04990		-2.29	-3.79	dUTP diphosphatase Dut, putative
Afu7g05010	-2.17	-0.16	-0.66	glyoxalase family protein

Afu7g05100	-1.67	0.72	2.55	hexose transporter protein
Afu7g05200	-1.51	-1.24	-2.46	conserved hypothetical protein
Afu7g05350	-1.20	-2.06	-2.45	delta-9 fatty acid desaturase; stearoyl-CoA desaturase
Afu7g05490	0.08	0.30	-2.06	hypothetical protein
Afu7g05560	0.34	-0.46	-2.20	hypothetical protein
Afu7g05610	-2.66	-2.40	-2.88	glucanase, putative
Afu7g05840	-1.62	-1.10	-0.76	amidohydrolase family protein
Afu7g05940	-1.72	-0.58	-0.20	hypothetical protein
Afu7g05950	-1.55	-0.59	-0.61	EF-hand protein
Afu7g06040	-1.74	-0.53	-1.05	integral membrane protein, putative
Afu7g06060	-1.03	-1.86	-1.76	siderochrome-iron transporter (Sit1), putative
Afu7g06160	-2.69	-2.23	-1.69	hypothetical protein
Afu7g06360	-2.03	-1.05	-1.16	hypothetical protein
Afu7g06800		-1.14	-2.74	glutamyl-tRNA(Gln) amidotransferase, subunit A
Afu7g07040	-1.78	-0.35	-1.38	hypothetical protein
Afu7g07050	-2.68	0.26	-0.82	hypothetical protein
Afu7g08210	-1.97	1.27	-1.82	reverse transcriptase, putative
Afu7g08230	-1.80	-0.33	-0.60	NA
Afu7g08300	-2.64	0.08	-0.89	hypothetical protein
Afu7g08500	-2.02	1.16	-0.49	NACHT and WD40 domain protein
Afu8g00310	-2.66	1.61	-1.24	LINE-1 class reverse transcriptase, RNaseH, putative
Afu8g00790	-1.75	-0.72	-1.01	hypothetical protein
Afu8g00830	-0.79	-1.62	-2.90	conserved hypothetical protein
Afu8g00960	-2.14	-1.11	-0.91	cytochrome P450, putative
Afu8g00980	-2.92	-2.04	-2.34	hypothetical protein
Afu8g01030	-2.53	-2.91	-2.53	hypothetical protein
Afu8g01040	-2.45	1.67	-0.98	reverse transcriptase, RNaseH
Afu8g01080	-1.24	-2.17	-2.17	hypothetical protein
Afu8g01120	-1.91	-1.07	-1.15	hypothetical protein
Afu8g01310	-1.25	-2.37	-2.42	metalloreductase, putative
Afu8g01400	-2.37	-1.96	-1.59	mitochondrial carrier protein (Pet8), putative
Afu8g01410	-0.32	-1.93	-2.55	class V chitinase ChiB1

Afu8g01840	-1.99	0.35	-1.54	hypothetical protein
Afu8g01850	-5.49	-2.47	-3.55	phosphate-repressible phosphate permease
Afu8g01920	-2.31	-0.31	-1.47	hypothetical protein
Afu8g02200	-2.00	-0.34	0.19	proline permease
Afu8g02270	-1.56	-0.76	-0.71	dihydrodipicolinate synthetase family protein
Afu8g02290	-1.60	-1.20	-0.48	conserved hypothetical protein
Afu8g02440	-1.78	-2.02	-2.57	C-4 methyl sterol oxidase, putative
Afu8g02450	-5.14	-3.62	-4.97	hypothetical protein
Afu8g02470	-0.54	-1.02	-1.59	trihydroxytoluene oxygenase
Afu8g02550	-5.64	-3.68	-2.74	Ptr2-like MFS peptide transporter, putative
Afu8g02560	-1.92	-0.63	-0.17	glyceraldehyde-3-phosphate dehydrogenase, putative
Afu8g02660	-1.94	-2.40	-2.72	chromate ion transporter, putative
Afu8g02670	-1.68	-1.78	-2.06	conserved hypothetical protein
Afu8g04280	-1.57	-0.26	-0.95	conserved hypothetical protein
Afu8g04480	-1.66	0.04	0.98	hexose transporter protein
Afu8g04920	0.08	0.67	-2.25	LEA domain protein
Afu8g05030	-2.70	-0.60	-0.99	hypothetical protein
Afu8g05040	-1.69	-0.86	-0.05	dihydrodipicolinate synthetase family protein
Afu8g05470	-1.89			hypothetical protein
Afu8g05600	-1.40	-0.34	-1.60	hypothetical protein
Afu8g05650	-1.70	-0.47	-0.61	hypothetical protein
Afu8g05690	-1.80	0.21	-0.66	acetyltransferase, GNAT family family
Afu8g05880	-1.54	-0.46	-1.12	10 kDa chaperonin (GroES/Cpn10), putative
Afu8g06130	-1.68	-0.67	-0.80	FluG family protein
Afu8g06220	-0.51	-0.11	-1.52	conserved hypothetical protein
Afu8g06290	-2.68	1.43	-1.43	LINE-1 class reverse transcriptase, RNaseH, putative
Afu8g06440	-1.88	-0.74	0.24	fructosyl amino acid oxidase, putative
Afu8g06450	-2.34	-0.49	-0.29	Rieske 2Fe-2S family protein, putative
Afu8g06470	-1.98	-0.86	-0.30	N,N-dimethylglycine oxidase
Afu8g06830	0.12	-2.01	-1.76	endoglucanase, putative
Afu8g06880	-2.98	-2.71	-2.98	pectin methylesterase, putative
Afu8g06960	-2.48	-2.86	-3.44	hypothetical protein

Afu8g07060	-0.96	-1.25	-1.79	hydrophobin, putative
Afu8g07080	-3.51	-4.13	-7.06	elastinolytic metalloproteinase Mep
Afu8g07090	-3.11	-0.87	-0.33	extracellular proline-serine rich protein
Afu8g07340	-2.05	-2.61	-2.69	HET domain protein

Table AD.3.5: List of down-regulated genes in the ATCC46645 Δ*pacC* time course. Genes significantly down-regulated were included if showing a fold change of -1.5 on a $\log_2$ scale at least in one of the time point datasets. T0 vs T4 = 4 hrs, T0 vs T8 hrs = 8 hrs, T0 vs T16 = 16 hrs.

ORFs	T4	T8	T16	Annotation	Functional classifiication
Afu3g11880	-4.23547	-0.66626	-1.10961	hypothetical protein	
Afu6g14530	-3.28847	-1.42491	-0.66835	L-cystine transporter, putative	L-cystine transport///L-cystine transmembrane transporter activity///integral to membrane
Afu4g10610	-3.22659	-1.31568	-1.39204	hypothetical protein	
Afu8g07090	-3.11086	-0.86701	-0.334	extracellular proline-serine rich protein	
Afu5g06910	-2.97962	-0.42897	0.184572	DUF636 domain protein	
Afu6g14660	-2.9557	1.860377	-1.1636	reverse transcriptase, RNaseH	
Afu4g00820	-2.93653	1.675784	-1.27336	reverse transcriptase, RNaseH	
Afu4g14870	-2.931	1.691895	-1.14393	LINE-1 class reverse transcriptase, RNaseH, putative	
Afu1g14820	-2.90572	0.091875	-1.15382	hypothetical protein	
Afu7g01780	-2.87419	-0.61664	-1.37278	hypothetical protein	
Afu2g18080	-2.84645	1.569657	-1.02842	LINE-1 class reverse transcriptase, RNaseH, putative	
Afu6g09470	-2.80126	1.447962	-0.98003	reverse transcriptase, RNaseH, putative	
Afu5g10090	-2.78253	-1.32544	-1.44416	3-demethylubiquinone-9 3-methyltransferase, putative	
Afu6g00780	-2.77278	1.728312	-1.04089	LINE-1 class reverse transcriptase, RNaseH, putative	
Afu6g09830	-2.76976	-1.17222	-0.21361	hypothetical protein	
Afu3g10510	-2.74832	-0.64028	-0.94419	hypothetical protein	
Afu3g15370	-2.70303	1.492442	-1.15501	LINE-1 class reverse transcriptase, RNaseH, putative	
Afu8g05030	-2.69522	-0.60416	-0.99184	hypothetical protein	
Afu3g01240	-2.69314	-0.7984	-0.76405	hypothetical protein	
Afu7g07050	-2.68214	0.2633	-0.81587	hypothetical protein	
Afu8g06290	-2.67744	1.428126	-1.4259	LINE-1 class reverse transcriptase, RNaseH, putative	
Afu8g00310	-2.66174	1.614126	-1.23683	LINE-1 class reverse transcriptase, RNaseH, putative	

Afu1g10300	-2.64905		-0.90146	hypothetical protein	
Afu7g08300	-2.64434	0.084216	-0.89306	hypothetical protein	
Afu2g05700	-2.64371	-0.23111	-1.14208	hypothetical protein	
Afu4g09340	-2.63448	-0.49654	-0.73921	hypothetical protein	
Afu5g14210	-2.47762	-0.73683	-1.26991	glucose-repressible gene protein-related protein	
Afu8g01040	-2.45291	1.671414	-0.97913	reverse transcriptase, RNaseH	
Afu6g08700	-2.44401	-0.63088	-1.17012	beta glucosidase, putative	carbohydrate metabolic process///"hydrolase activity, hydrolyzing O-glycosyl compounds"

Table AD.3.6: 30 ORFs with the lowest log$_2$ values between the down-regulated genes unique to the 4 hrs time point of the ATCC46645 Δ*pacC*/ATCC46645 comparison.

ORFs	T4	T8	T16	Description	Annotation
Afu5g01230	-0.24096	-2.22037	-0.05612	RTA1 domain protein, putative	fatty acid transport///phospholipid-translocating ATPase activity///plasma membrane///endoplasmic reticulum///integral to membrane
Afu3g01670		-1.9796	-0.90466	MFS hexose transporter, putative	mannose transmembrane transporter activity///hexose transport///fructose transmembrane transporter activity///plasma membrane///glucose transmembrane transporter activity///galactose transmembrane transporter activity
Afu1g00500		-1.93631		FMN dependent dehydrogenase, putative	L-lactate dehydrogenase (cytochrome) activity///mitochondrial intermembrane space///electron transport
Afu1g17160	-1.43931	-1.82537	-1.43362	transporter, putative	membrane///transporter activity///transport
Afu4g14090	-0.77326	-1.74198	-1.29176	UDP-glucose 4-epimerase	cellular component unknown///galactose metabolic process///molecular function unknown
Afu7g04970	-0.35248	-1.69981	-0.53531	metalloreductase, putative	ferric-chelate reductase activity///copper ion import///plasma membrane///iron ion transport
Afu6g03490	0.352669	-1.62026	-1.14572	phenol 2-monooxygenase, putative	cellular aromatic compound metabolic process///monooxygenase activity
Afu3g03670	0.511368	-1.59752	-1.11115	ABC multidrug transporter, putative	ATP-binding cassette (ABC) transporter activity///ATP binding///transport

Afu4g11380	-0.39018	-1.59447	-0.30184	hypothetical protein	
Afu1g05720	0.043107	-1.55012	-0.97044	c-14 sterol reductase	endoplasmic reticulum///ergosterol biosynthetic process///C-14 sterol reductase activity
Afu2g00870	-0.40115	-1.51851	-0.68898	hypothetical protein	

Table AD.3.7: 11 down-regulated ORFs unique to the 8 hrs time point of the ATCC46645 Δ*pacC*/ATCC46645 comparison.

ORFs	T4	T8	T16	Description	Annotation
Afu5g14690	-1.2196	0.362299	-3.55809	phosphorylase, putative	
Afu6g09660			-3.30507	nonribosomal peptide synthase GliP	peptide antibiotic biosynthetic process///nonribosomal peptide biosynthetic process///catalytic activity///secondary metabolic process///amino acid adenylylation by nonribosomal peptide synthase
Afu7g06800		-1.1443	-2.73912	glutamyl-tRNA(Gln) amidotransferase, subunit A	
Afu2g08180	-0.72978	-1.31112	-2.68077	flotillin domain protein	membrane
Afu7g00970	-1.36368	-1.33176	-2.65048	GPI-anchored serine-threonine rich protein	
Afu4g14200			-2.52849	conserved hypothetical protein	cellular component unknown///biological process unknown///molecular function unknown
Afu5g14290	-1.13266	-0.8413	-2.49466	C6 transcription factor, putative	transcription factor activity///nucleus///zinc ion binding///regulation of transcription
Afu6g11320	0.54134	-1.37793	-2.47886	MFS transporter, putative	integral to plasma membrane///transporter activity///transport
Afu2g01490	-0.61901	-0.09634	-2.42675	hypothetical protein	
Afu1g10930	1.244659	-0.29084	-2.36323	ammonium transporter	pseudohyphal growth///plasma membrane///ammonium transport///ammonium transmembrane transporter activity
Afu3g03730	-0.61043	-0.028	-2.36022	hypothetical protein	
Afu4g13970		-1.02177	-2.3513	conserved hypothetical protein	
Afu3g12070	-0.60208	-0.41509	-2.33994	conserved hypothetical protein	
Afu7g01670	-0.93085	-0.49365	-2.32899	MFS amino acid transporter, putative	fungal-type vacuole///transporter activity///transport
Afu8g04920	0.076836	0.667887	-2.25142	LEA domain protein	
Afu2g11520	1.030773	-0.4971	-2.23882	MFS monosaccharide transporter, putative	mannose transmembrane transporter activity///hexose transport///fructose transmembrane transporter activity///plasma

					membrane///glucose transmembrane transporter activity
Afu4g13880	0.954418	-0.54824	-2.20732	ankyrin repeat protein	
Afu4g13900	0.144009	-0.28784	-2.19808	MFS transporter, putative	nicotinamide mononucleotide transport///nicotinamide mononucleotide permease activity///integral to plasma membrane
Afu7g05560	0.338728	-0.46484	-2.19781	hypothetical protein	
Afu1g03160	-1.46566	-0.99915	-2.17325	hypothetical protein	
Afu5g02250	-1.27462	-0.41563	-2.14126	conserved hypothetical protein	
Afu2g11120	0.048098	-0.67513	-2.10403	hypothetical protein	
Afu6g03140	-1.07119	-1.10186	-2.08614	isp4 protein, putative	oligopeptide transporter activity///integral to plasma membrane///oligopeptide transport
Afu3g03640	-0.1735	0.317753	-2.07101	siderochrome-iron transporter (MirB), putative	siderophore-iron transport///siderophore-iron (ferrioxamine) uptake transmembrane transporter activity///integral to membrane///cellular iron ion homeostasis
Afu6g09610	-0.71728	-1.1404	-2.06918	nonribosomal peptide synthase, putative	nonribosomal peptide biosynthetic process///pathogenesis
Afu7g05490	0.08085	0.295737	-2.06049	hypothetical protein	
Afu2g13460	0.552806	-0.0569	-2.05493	alpha-amylase, putative	carbohydrate utilization///alpha-amylase activity
Afu1g03200		-0.95734	-2.05467	MFS transporter, putative	integral to plasma membrane///transporter activity///transport

Table AD.3.8 30 ORFs with the lowest log$_2$ values between the down-regulated genes unique to the 16 hrs time point of the ATCC46645 Δ*pacC*/ATCC46645 comparison.