

Supplemental Table S1. Primers used in gene disruption and complementation.

Underlined regions indicate restriction enzyme sites.

Primer name	Primer sequence 5' - 3'
AcuM-F4	TTAG <u>GTACCT</u> CGAATGCCGTTTCCTCCTG
AcuM-F3	TTAT <u>CTAGA</u> ATGGCCATGTGCTACGGGCT
AcuM-F2	GTCGTGACTGGGAAAACCTGGCGATTGGGAGAAATTCGGTGCT
AcuM-F1	TGCCCAACTCTATAGCAA
HY	GGATGCCTCCGCTCGAAGTA
YG	CGTTGCAAGACCTGCCTGAA
HYG-F	AGCGGATAACAATTTACACAGGA
AcuM-VER-UP	ACTATCAAGTCGAAATGGAC
AcuM-VER-R	AATCGTCTCATGCTCAGATG
HY-VER	TCGGTTTCAGGCAGGTCTTG
AcuM-REV-F	ATT <u>CTCGAGAC</u> CTAGATGACTATTCGCAA
AcuM-REV-R	AAT <u>CTCGAGA</u> ACTGTCAGCAGATATTGCC
AcuM-REV-VER-F	ACAGCAGGTGGTTACAACCTCTC
AcuM-REV-VER-R	ACCTATTATCATCTGCCATCAGC
Afu1g02860F4	TG <u>CAAGCTT</u> AGGTAAGACAGGAACCGAGAGG
Afu1g02860F3	TTAT <u>CTAGAT</u> GTTGTCACGGGTCACAGGA
Afu1g02860F2	GTCGTGACTGGGAAAACCTGGCGTGACTGATCCTTAGAGAATGTATG
Afu1g02860F1	TCTTCCTCCAGTCTCGACATC
Afu1g02860-VER-UP	TCTGCACCACGAGCATATGT
Afu1g02860-VER-R	AGTCGAGGTGCATCCTGGGT
Afu1g04140F4	TTAG <u>GTACCT</u> GACCTCGTGTACATCAAGACC
Afu1g04140F3	TTAT <u>CTAGAT</u> TCTCAGTGGGGAACGTGCATC
Afu1g04140F2	GTCGTGACTGGGAAAACCTGGCGTCCACTAGAGTCTATCTGCTG
Afu1g04140F1	TCTGCGCATACCGCGTCGAC

Afu1g04140-VER-UP	TGGCGTCTGGCAGCTGATTG
Afu1g04140-VER-R	TGAAGCGCTCGAACATCGTC
Afu2g04600F4	TTAGGT <u>ACC</u> ATGGTTGTCATCACTCGGAG
Afu2g04600F3	TTAT <u>CTAG</u> ATTGAGGCAGATCCCTGAATG
Afu2g04600F2	GTCGTGACTGGGAAAACCTGGCGATCCTCTACTATCAAGGTGATCG
Afu2g04600F1	AGCAGAAGGAGCAACTGTCC
Afu2g04600-VER-UP	TTGGATAGCTTACCCGTTTG
Afu2g04600-VER-R	TCAGGTCCCAGATGCAGCAC
Afu2g16310F4	ATT <u>CTGAG</u> TCGCTAGATGACTGGGATCG
Afu2g16310F3	TTA <u>ACTAG</u> TTCACACTCTATACGTCTCG
Afu2g16310F2	GTCGTGACTGGGAAAACCTGGCGATGTAACCAAGCGCTCCAAC
Afu2g16310F1	TGTCCAAGTCTGCAGAGATACC
Afu2g16310-VER-UP	ATGACACAGGCTTACAGATC
Afu2g16310-VER-R	TGTATCACGAACAGACTG
Afu4g09710F4	AATGGT <u>ACC</u> ACTTCCTGTTGTCGGTTCGA
Afu4g09710F3	AATA <u>AGCT</u> TAGCAACACGTCTCTATCGGT
Afu4g09710F2	TCGTTTTACAACGTCGTGACTGGGAAAACCTGGCGTGATGGGACTCGTGCCACTT
Afu4g09710F1	TGATCTGCTTGCAGACTACT
Afu4g09710-VER-UP	TCGACCATCTGATCCATCAC
Afu4g09710-VER-R	AGGACGATTCGACCGAATAG
Afu5g06190F4	TTAGGT <u>ACC</u> ACCGTCACGTCAATATCGCC
Afu5g06190F3	TGCA <u>AGCT</u> TAGTCTATATGGCTATGATCC
Afu5g06190F2	GTCGTGACTGGGAAAACCTGGCGAGCAGTAACCTGTGGATAATCG
Afu5g06190F1	ACTCCGTAGAATGATGTTGCTG
Afu5g06190-VER-UP	AAGCAGAGCCTTGCTCATTC
Afu5g06190-VER-R	TCCGACAATCTTGCGCAACA
Afu5g10130F4	TTAGGTACCTGACCCTGCTAGTATCTTCCAG
Afu5g10130F3	TTAACTAGTTGAGTCTAGTTCAAGTGTCCAG

Afu5g10130F2	GTCGTGACTGGGAAAACCCTGGCGAGACGCACACCAGAAGTAGT
Afu5g10130F1	TCGATATCCTGGTCTCCTGC
Afu5g10130-VER-UP	TCAGCTGGTACTGAAGGACGA
Afu5g10130-VER-R	ATGCAACTCTCAAGCTCGAG
Afu6g07170F4	ATTGGTACCACACAGACGTTACACTATGG
Afu6g07170F3	TAAACTAGTAGCGTTGCACAAGTTCGACA
Afu6g07170F2	TCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTGAGCCAGCTGGTGTCTAAC
Afu6g07170F1	ACTATCTGCAGAAGTGTTGC
Afu6g07170-VER-UP	TCTTGCCTAGGACGATACTG
Afu6g07170-VER-R	AGCACAATCAGCTTGGTCAC
Afu6g09930F4	TCTGAAGTTCTTCGAGGACC
Afu6g09930F3	TCCTGTGTGAAATTGTTATCCGCTGAGTGAAGTCGATACGACGG
Afu6g09930F2	GTCGTGACTGGGAAAACCCTGGCGAGTAGGATGATTCGGGTCAAC
Afu6g09930F1	ATCAGGCTGCTGAAGCTATCC
Afu6g09930-VER-UP	AGCAGAGCAACGGACTGTTC
Afu6g09930-VER-R	ATCCCATCCAGCTGTCAG
Afu8g05460F4	TTAGGTACCAAGTGTCTGACTTTGAATCGCTC
Afu8g05460F3	TGCAAGCTTACTCTCCGTGGCTTCCAATC
Afu8g05460F2	GTCGTGACTGGGAAAACCCTGGCGAGAGCAGTGATAGCAGTCCG
Afu8g05460F1	ACCCCACTCAAGTAGTAAGCAG
Afu8g05460-VER-UP	AGGCTTGAGACGAATAGTGC
Afu8g05460-VER-R	TCATATCCGGAAGAGGACGAG
Afu2g10770F4	TTAGGTACCAGCTCCGGTCTCAGACAAGA
Afu2g10770F3	ATTACTAGTTATCTCAGCCGGAAGTGAAG
Afu2g10770F2	TCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGATCATTGCATTGTCAGGACC
Afu2g10770F1	ACACTACGCTGTGCTGTTGG
Afu2g10770-VER-UP	ACAACAGACAACTGCGTGAG
Afu2g10770-VER-R	TCGTGTGATTGCGATGGTCA

SreA-gate1	CACCAATAGTAGCAAGAACAAACAG
SreA-gate2	CGCTCAGAACAACCGTACAA
SreA-gate3	CACCCTTGCCTTTTTTTGTCTC
SreA-gate4	ACAACCACACCCTCGACTTC
SreA-ext1	TCCGTTTGAATTGTCCTTTG
SreA-ext4	GCACCTTCACCCTCAACTTC
BL	TGATGAACAGGGTCACGTC
LE	AAGTTGACCAGTGCCGTTCC

---

Primers used in real-time RT-PCR verification.

Gene name	Locus	Forward primer (5' - 3')	Reverse primer (5' - 3')
<i>hapX</i>	Afu5g03920	AACAGTCCAGACGTCTTG	TGGTGTGAATTGGGACAG
<i>sreA</i>	Afu5g11260	TGATGACCACTACCGATAC	ATCGGTGGATGATGTGGTC
<i>sidA</i>	Afu2g07680	AGTGGCAGCATCGCATCC	TTGAACCTTGCTCAGGAG
<i>sidC</i>	Afu1g17200	TCATCATGCATCATGCTC	TCAGTAGCTTCGGATGAG
<i>SidD</i>	Afu3g03420	TGCTACTGTAGTGCGGTC	TCTACCACGATGTAAGCG
<i>sidG</i>	Afu3g03650	ATGGTTCGCTATGCCTTC	AGCGACTTCGAGTCATGC
<i>sidF</i>	Afu3g03400	TCACTCATGGTGGTCGAC	ATCGTAGTGTGCTCCGTAG
	Afu3g03390	TGAGTCTGACGAGTCCTG	CAGTAACGTGTCCTTGTC
<i>sirB</i>	Afu3g03640	ACTACTGCTATGCCAGCT	ATCTCGCACATAACGATG
<i>sit1</i>	Afu7g06060	TCTACACC GTTCTCATTG	TGATTCTGTCATGATTGG
	Afu7g04730	ATGACTGGCTACATGACC	ATCTGGCACATAATCACG
<i>fre2</i>	Afu1g17270	TGCACGTCCAACCTCGGTT	TCAGACTACGGCATTGAG
<i>ftr2</i>	Afu5g03800	TCGTATGACATCCGACAG	ACGATCACCGCAATCCAG
<i>acuM</i>	Afu2g12330	TGTGAAAGGCTACGCTCGCT	TCTGCCATCTCCTTGTTGCC
<i>acuF</i>	Afu6g07720	TGATGATGAGCACTGCTG	ATCGCTGAGGAGGAT
<i>Fbp1</i>	Afu4g11310	AGCTCGTCATCACCATGC	TCAGCGACCATGCTGCCA
<i>tef1</i>	Afu1g06390	GTGACTCCAAGAACGATCC	AGA ACTTGCAAGCAATGTGG

---

## Down-regulated at 18 or 24h

Table 2

Locus	Comm_Name	Genes down-regulated in the acuM deletion mutant (Log2 values)							
		18 h WT1	18 h WT2	18 h Comp1	18 h Comp2	24 h WT1	24 h WT2	24 h Comp1	24 h Comp2
Afu1g00490	biotin-dependent 2-oxo acid dehydrogenases acyltransferase, putative	NaN	-0.564	-0.558	-0.435	-0.397	-0.061	-0.119	0.093
Afu1g00810	Asp f7-like allergen, putative	-0.610	-0.870	-0.572	-0.519	-0.342	0.158	-0.461	-0.755
Afu1g01480	MFS peptide transporter (Ptr2), putative	-0.334	-0.410	-0.406	-0.338	-0.176	-0.402	-0.048	-0.352
Afu1g02340	hypothetical protein	-0.557	-0.345	-0.425	-0.460	-0.178	-0.233	-0.296	-0.290
Afu1g02730	mitochondrial phosphate carrier protein (Ptp), putative	-1.610	-1.306	-1.391	-0.807	-0.861	-0.997	-0.951	-1.234
Afu1g02880	Phosphotransferase enzyme family domain protein	-0.446	-0.664	-0.382	-0.415	-0.747	-0.677	-0.611	-0.363
Afu1g03150	c-14 sterol reductase	-2.311	-0.538	-1.852	-0.814	-0.595	-0.702	-0.547	-0.921
Afu1g03610	hypothetical protein	-3.863	-2.430	-3.059	-2.039	-1.417	-1.059	-4.044	-1.250
Afu1g05390	mitochondrial ADP,ATP carrier protein (Ant), putative	-0.818	-0.721	-0.618	-0.292	-0.761	-0.819	-0.683	-0.927
Afu1g05950	integral membrane protein	-0.897	-0.570	-0.945	-1.205	-0.565	-0.614	-0.553	-0.973
Afu1g06020	DnaJ domain protein	-0.723	-0.484	-0.676	-0.601	-0.093	0.050	-0.258	0.004
Afu1g06040	sterol o-acyltransferase (APE2), putative	-1.004	-0.720	-1.124	-1.566	-0.582	-0.404	-0.163	-1.544
Afu1g07400	hypothetical protein	-0.658	-0.958	-0.730	-0.832	-0.021	-0.208	-0.326	-0.264
Afu1g07480	coproporphyrinogen III oxidase, putative	-2.594	-1.515	-2.190	-1.156	-0.330	-0.003	-1.230	-0.082
Afu1g09050	phospholipid methyltransferase	-0.717	-0.844	-0.619	-0.567	-0.416	-0.441	-0.144	-0.032
Afu1g09470	aminotransferase, class V, putative	-0.498	-0.047	-0.428	-0.799	-0.527	-0.680	-0.372	-0.539
Afu1g10120	ABC transporter permease protein	-1.477	-1.365	-1.925	-1.251	-0.168	0.082	0.275	-0.005
Afu1g10130	adenosylhomocysteinase	-1.756	-2.054	-2.039	-1.584	-0.004	-0.211	-0.058	-0.149
Afu1g10210	hypothetical protein	-0.664	-0.585	-0.622	-0.577	-0.101	0.018	-0.526	-0.249
Afu1g10350	phosphoglycerate kinase PgkA, putative	-0.770	-1.033	-0.511	-0.751	-0.910	-0.451	-1.003	-0.817
Afu1g10380	nonribosomal peptide synthase Afpes1	-2.311	-2.256	-2.084	-1.120	-1.091	-1.115	-0.607	-0.393
Afu1g10390	ABC multidrug transporter, putative	-3.610	-2.798	-2.922	-1.744	-1.122	-1.370	NaN	-0.965
Afu1g10630	S-adenosylmethionine synthetase	-1.926	-2.279	-1.990	-1.751	-0.016	-0.131	0.037	-0.256
Afu1g10780	glycine cleavage system T protein	-0.645	-0.919	-1.092	-0.977	0.115	0.130	0.230	0.097
Afu1g11550	ethanolamine kinase, putative	-0.516	-0.494	-0.362	-0.449	-0.434	-0.379	-0.301	-0.110
Afu1g11920	SH3 domain protein, putative	-0.547	-0.500	-0.542	-0.470	0.057	-0.176	-0.076	0.179
Afu1g11930	protein kinase, putative	-1.375	-0.644	-0.869	-0.826	-0.440	-0.581	-0.473	-0.327
Afu1g12070	glycine cleavage system H protein	-1.029	-0.891	-1.606	-1.001	-0.124	-0.043	0.071	0.055
Afu1g12350	extracellular fruiting body protein, putative	-1.780	-1.342	-1.636	-1.086	-0.818	-0.745	-1.446	-1.313
Afu1g12690	ABC multidrug transporter Mdr4	-0.528	-0.461	-0.490	-0.307	-0.321	-0.308	0.028	-0.078
Afu1g12800	isocitrate dehydrogenase, NAD-dependent	-0.272	-0.342	-0.006	0.114	-0.273	-0.303	-0.283	-0.273
Afu1g14280	C6 finger domain protein, putative	-0.453	-0.166	-0.431	-0.727	-0.400	-0.509	-0.398	-0.587
Afu1g14930	hypothetical protein	-2.421	-0.716	-2.023	-0.988	-1.382	-0.938	-1.188	-1.684
Afu1g15140	mitochondrial phosphate carrier protein (Mir1), putative	-2.091	-1.453	-1.766	-1.040	-1.651	-1.901	-1.529	-2.265
Afu1g16030	conserved hypothetical protein	-0.303	0.643	-0.369	0.121	-0.851	-0.744	-0.813	-0.650
Afu1g16080	hypothetical protein	-0.337	-0.335	-0.257	-0.324	0.047	0.157	0.164	0.148
Afu1g16190	cell wall glucanase Crf1	-1.327	-1.164	-1.353	-0.910	-0.700	0.056	-1.811	-0.806
Afu1g16280	mitochondrial F1F0-ATP synthase g subunit, putative	-0.753	-0.933	-0.516	-0.584	-0.497	-0.510	-0.776	-0.740
Afu1g17060	HLH DNA binding domain protein, putative	-1.056	-0.616	-1.110	-1.057	-0.364	-0.266	-0.348	-0.794
Afu1g17180	pyridine nucleotide-disulphide oxidoreductase, putative	-1.645	-0.743	-1.838	-1.362	-0.593	-0.690	0.200	-0.517
Afu1g17190	long-chain-fatty-acid-CoA ligase, putative	-1.769	-1.042	-1.700	-1.382	-0.926	-1.197	-0.168	-1.042
Afu1g17270	ferric-chelate reductase (Fre2), putative	-1.699	-1.214	-1.804	-2.004	-1.277	-1.523	-1.007	-1.297

## Down-regulated at 18 or 24h

Afu2g01260	HLH transcription factor, putative	-0.508	0.256	-0.406	-0.037	-0.577	-0.396	-0.405	-0.397
Afu2g01720	conserved hypothetical protein	-0.728	0.411	-0.050	0.193	-0.482	-0.508	-0.471	-0.554
Afu2g01890	CAT5 protein	-1.020	-0.317	-1.050	-0.486	-0.417	-0.386	-0.540	-0.452
Afu2g02110	MSF monosaccharide transporter, putative	-0.333	-0.273	-0.295	-0.342	-0.077	-0.062	-0.199	0.195
Afu2g03020	MYB DNA-binding domain protein	-2.172	-2.055	-1.442	-1.450	-0.184	-0.381	-0.643	-0.517
Afu2g03420	mitochondrial translocase complex component (Tim50), putative	-0.247	0.074	-0.165	0.100	-0.259	-0.251	-0.268	-0.285
Afu2g03860	plasma membrane low affinity zinc ion transporter, putative	-0.804	-0.642	-0.599	-0.590	0.102	0.141	-0.964	0.180
Afu2g03990	hypothetical protein	-1.380	-1.430	-1.309	-1.893	-0.799	-1.004	-0.744	-1.289
Afu2g05050	hypothetical protein	-1.269	-0.986	-1.095	-1.073	-1.027	-0.523	-1.098	-0.747
Afu2g05060	alternative oxidase	-4.573	-3.104	-4.252	-3.959	-3.605	-2.903	-3.792	-4.351
Afu2g05400	sugar hydrolase, putative	-0.522	-0.580	-0.623	-0.347	-0.245	0.078	-0.123	0.213
Afu2g05720	conserved hypothetical protein	-1.504	-0.985	-1.375	-0.726	-0.360	-0.188	-0.033	-0.095
Afu2g05730	siderochrome-iron transporter (MirC), putative	-1.363	-0.642	-1.373	-1.063	-0.266	-0.436	-0.112	-0.586
Afu2g07620	cystathionine beta-synthase, putative	-1.362	-2.094	-1.514	-1.331	-0.471	-0.412	-0.100	-0.160
Afu2g07670	palmitoyltransferase (SidR), putative	-0.875	-0.597	-0.903	-0.634	-0.163	-0.649	0.062	-0.640
Afu2g07680	L-ornithine N5-oxygenase SidA	-2.381	-1.582	-2.406	-1.644	-0.566	-0.849	0.245	-0.740
Afu2g07810	cytosolic hydroxymethyltransferase, putative	-0.729	-0.899	-1.072	-1.025	-0.110	-0.269	-0.110	-0.167
Afu2g08010	conserved hypothetical protein	-0.737	-0.812	-0.918	-0.649	-0.404	0.082	-0.871	-0.582
Afu2g08080	conserved hypothetical protein	-0.706	-0.725	-0.392	-0.534	-0.190	-0.091	-0.199	-0.270
Afu2g08280	NADP-dependent malic enzyme	-3.339	-3.714	-2.822	-2.904	-1.824	-2.457	-1.556	-2.913
Afu2g09220	hypothetical protein	-0.560	-0.465	-0.556	-0.415	-0.056	0.107	-0.041	0.084
Afu2g09290	antigenic mitochondrial protein HSP60, putative	-0.835	-0.076	-0.145	0.092	-0.483	-0.468	-0.320	-0.526
Afu2g09330	C6 finger domain protein, putative	-2.216	-1.827	-1.131	-1.387	-0.100	-0.093	-0.248	-0.159
Afu2g09340	fungal specific trascription factor, putative	-1.381	-1.397	NaN	NaN	-0.022	-0.004	NaN	NaN
Afu2g09350	endo-beta-1,6-glucanase, putative	-2.206	-1.699	-1.173	-1.242	-0.211	-0.390	NaN	-0.735
Afu2g10660	mannitol-1-phosphate dehydrogenase	-0.842	-0.894	-1.079	-0.887	-0.400	0.108	-0.348	-0.297
Afu2g11300	G2882	-0.671	-1.649	-1.225	-1.341	0.346	0.107	0.448	0.135
Afu2g11790	conserved hypothetical protein	-0.733	-0.923	-0.606	-0.694	-0.213	-0.266	-0.521	-0.400
Afu2g11900	pyruvate dehydrogenase kinase	-1.293	-1.023	-0.946	-1.222	-0.283	-0.520	-0.148	-0.246
Afu2g12330	conserved hypothetical protein	-2.754	-2.214	-2.997	-2.963	-2.206	-2.653	-2.453	-2.656
Afu2g12450	hydroxymethylglutaryl-CoA lyase	-0.445	-0.397	-0.478	-0.350	-0.320	-0.095	-0.312	0.322
Afu2g12910	PtaB protein, putative	-0.575	-0.538	-0.402	-0.480	-0.001	-0.083	-0.077	0.051
Afu2g13110	cytochrome c	-1.687	-0.684	-1.460	-0.726	-0.977	-0.930	-1.397	-1.890
Afu2g14970	Gamma-butyrobetaine hydroxylase subfamily, putative	-0.652	-0.780	-0.599	-0.381	0.082	0.023	-0.048	0.129
Afu2g16000	hypothetical protein	-0.972	-0.773	-0.654	-0.749	0.032	0.115	-0.207	-0.162
Afu2g16860	membrane transporter	-0.627	-0.355	-0.477	-0.527	-0.128	-0.075	NaN	-0.229
Afu2g16930	succinate:fumarate antiporter (Acr1), putative	-0.641	NaN	-0.529	-0.833	-0.764	-0.565	-0.213	-0.563
Afu2g17000	PT repeat family protein	-0.717	-0.580	-0.402	-0.476	-0.137	0.126	-0.251	-0.353
Afu2g17300	glutathione S-transferase	-0.988	NaN	-0.590	-0.712	-0.254	-0.253	NaN	-0.644
Afu2g17320	conserved hypothetical protein	-1.109	-1.091	-1.038	-0.483	-0.242	-0.356	-0.050	-0.305
Afu2g17330	serine peptidase, family S28, putative	-0.826	-0.642	-0.660	-0.435	-0.293	-0.392	-0.237	-0.160
Afu3g00310	extracellular phytase, putative	-0.633	-0.637	-0.666	-0.372	-0.253	-0.174	-0.534	-0.196
Afu3g00510	GPI anchored cell wall protein, putative	0.035	-0.125	0.285	0.226	-0.497	-0.751	-0.557	-0.415
Afu3g00820	putative exported protein	-1.273	-0.210	-0.542	-0.197	-0.524	-0.725	-0.733	-0.380
Afu3g00860	hypothetical protein	-0.331	-0.542	-0.469	-0.606	-0.644	-0.214	-0.644	-0.528

## Down-regulated at 18 or 24h

Afu3g01400	ABC multidrug transporter, putative	-0.045	-0.541	0.191	-0.135	-0.685	-0.677	-0.401	-0.596
Afu3g01450	3-methyl-2-oxobutanoate dehydrogenase, putative	-0.416	-0.517	-0.628	-0.664	-0.379	-0.207	-0.039	0.442
Afu3g01580	GMC oxidoreductase, putative	-1.562	-1.950	-1.300	-1.363	-0.386	-0.090	-0.333	-0.195
Afu3g01590	hypothetical protein	-0.845	-1.215	-0.622	-0.737	-0.189	-0.094	-0.441	-0.055
Afu3g01990	DUF636 domain protein	-1.113	-0.062	-1.050	-0.594	-1.174	-0.960	-1.155	-0.927
Afu3g02000	C6 transcription factor, putative	-2.094	-0.617	-2.056	-1.083	-1.675	-1.542	-1.311	-1.683
Afu3g02830	ankyrin repeat protein	-0.766	-0.744	-0.521	-0.686	-0.226	-0.297	-0.360	-0.232
Afu3g03280	FAD binding monooxygenase, putative	-2.349	-0.922	-2.076	-2.523	-0.828	-1.094	-1.330	-1.885
Afu3g03400	siderophore biosynthesis acetylase Acel, putative	-2.261	-1.916	-1.652	-1.276	-1.280	-1.132	-0.702	-1.140
Afu3g03410	enoyl-CoA hydratase/isomerase family protein	-2.807	-1.629	-2.107	-1.325	-1.424	-1.567	-0.907	-1.237
Afu3g03440	MFS family siderophore transporter, putative	-2.499	-0.323	-2.392	-1.141	-1.110	-1.374	-0.593	-1.528
Afu3g03640	siderochrome-iron transporter (MirB), putative	-2.777	-0.940	-2.832	-1.399	-1.407	-1.125	-1.695	-1.519
Afu3g03650	acetyltransferase, GNAT family, putative	-2.351	-0.962	-1.875	-1.212	-0.934	-0.927	-0.879	-0.930
Afu3g05620	Fot1 family transposase, putative	-0.379	-0.409	-0.347	-0.465	-0.158	-0.021	-0.431	0.094
Afu3g06240	hypothetical protein	-0.439	-0.475	-0.329	-0.514	0.009	-0.004	-0.114	0.013
Afu3g06250	hypothetical protein	-0.528	-0.573	-0.429	-0.462	-0.057	-0.157	0.026	0.062
Afu3g06600	siroheme synthase, putative	-0.431	-0.774	-0.722	-0.534	0.167	0.127	0.482	0.077
Afu3g07300	ABC multidrug transporter, putative	0.031	-0.417	-0.376	-0.714	-0.370	-0.342	-0.263	-0.318
Afu3g07980	conserved hypothetical protein	-1.141	-0.769	-0.915	-0.510	-0.187	0.066	-0.304	-0.236
Afu3g08110	cell wall protein, putative	-1.762	-0.515	-1.754	-0.851	-1.045	-0.742	-1.483	-1.273
Afu3g08530	MFS drug transporter, putative	-0.320	-0.298	-0.344	-0.283	0.160	-0.206	-0.051	-0.243
Afu3g08650	C1-THFS protein	-1.145	-0.709	-1.416	-0.944	-0.242	-0.263	-0.027	0.104
Afu3g09210	endonuclease/exonuclease/phosphatase family protein	NaN	-0.356	-0.324	-0.402	-0.346	-0.060	-0.090	-0.236
Afu3g09380	SGT1 protein, putative	-0.423	-0.327	-0.599	-0.716	-0.442	-0.545	-0.383	-0.693
Afu3g09660	hypothetical protein	-0.934	-1.006	-0.750	-0.551	0.071	0.142	-0.186	0.225
Afu3g09690	extracellular thaumatin domain protein, putative	0.149	1.128	0.255	0.643	-2.404	-1.651	-1.652	-1.008
Afu3g11430	arginase	-3.212	-2.651	-2.331	-0.915	-3.382	-3.407	-2.701	-1.879
Afu3g11700	ubiquitin C-terminal hydrolase, putative	-1.448	-0.967	-0.870	-1.192	-1.227	-0.968	-0.788	-0.889
Afu3g12100	trehalose synthase (Ccg-9), putative	-1.280	-0.870	-0.904	-1.045	-0.281	-0.291	-0.310	-0.446
Afu3g12180	C6 transcription factor, putative	-1.018	-1.052	-0.923	-0.869	0.004	0.127	0.097	0.176
Afu3g12190	RING finger domain protein, putative	-1.429	-1.597	-1.282	-0.940	0.332	0.376	0.725	-0.131
Afu3g12330	phosphatidyl synthase	-0.794	0.454	-1.308	-0.572	-0.932	-0.700	-1.103	-0.978
Afu3g13450	oxidoreductase, short chain dehydrogenase/reductase family superfamily	-0.116	0.310	-0.197	0.190	-0.352	-0.396	-0.379	-0.296
Afu3g14460	Rad51 family DNA repair protein, putative	-0.368	-0.463	-0.321	-0.339	0.254	-0.062	-0.192	0.030
Afu4g05920	mitochondrial protein sorting (Msf1), putative	-1.640	-0.171	-1.239	-0.723	-1.160	-1.339	-1.056	-1.844
Afu4g06610	hypothetical protein	0.145	-0.341	0.055	-0.102	-0.543	-0.737	-0.913	-0.619
Afu4g06620	Glutamate/Leucine/Phenylalanine/Valine dehydrogenase, putative	-3.340	-1.842	-2.819	-2.260	-1.197	-1.004	-2.523	-2.349
Afu4g06670	allergen Asp F7	-0.402	-0.652	-0.529	-0.624	-0.371	0.009	-0.918	-0.732
Afu4g06700	GPI anchored cell wall protein, putative	-0.391	-0.339	-0.450	-0.301	0.054	0.014	-0.381	-0.238
Afu4g06760	ubiquinone biosynthesis protein, putative	-1.385	-0.789	-1.253	-1.151	-0.768	-1.099	-0.656	-1.383
Afu4g06910	outer mitochondrial membrane protein porin	-0.480	-0.998	-0.370	-0.505	-0.623	-0.532	-0.741	-0.558
Afu4g06940	Des-1 protein	-0.489	-0.330	-0.546	-0.529	-0.115	-0.117	-0.269	-0.169
Afu4g07050	L-lactate dehydrogenase	-1.185	-1.074	-0.883	-1.274	-0.342	-0.795	-0.210	-0.838
Afu4g07060	acyl-CoA thioester hydrolase, putative	-1.758	-1.748	-1.585	-1.929	-1.042	-1.394	-0.916	-1.661
Afu4g07300	hypothetical protein	-1.000	-1.086	-1.222	-0.865	-0.310	0.027	-1.236	-0.765

## Down-regulated at 18 or 24h

Afu4g07360	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase	-1.032	-1.780	-1.748	-1.494	0.329	0.198	0.349	0.038
Afu4g07810	L-serine dehydratase, putative	-1.061	0.293	-1.254	-1.361	-1.669	-2.089	-1.269	-1.668
Afu4g08710	short chain dehydrogenase, putative	-2.117	0.926	-1.393	0.165	-0.937	-1.378	-1.187	-0.899
Afu4g09320	antigenic dipeptidyl-peptidase Dpp4	-0.738	-0.791	-1.012	-0.535	-0.285	0.016	-0.245	0.169
Afu4g09350	hypothetical protein	-2.349	-2.065	-2.089	-1.723	-1.454	-1.403	-2.004	-1.782
Afu4g09360	ATP synthase proteolipid P2, putative	-2.440	-2.315	-2.068	-1.752	-1.545	-1.607	-1.987	-1.855
Afu4g09560	ZIP Zinc transporter, putative	-0.403	-0.428	-0.390	-0.349	-0.262	0.127	-0.524	-0.247
Afu4g09960	conserved hypothetical protein	-1.348	-0.432	-1.175	-0.963	-0.639	-0.941	-0.546	-1.088
Afu4g10120	C6 finger domain protein, putative	-1.149	-0.745	-0.829	-0.639	-1.734	-0.933	-0.806	0.188
Afu4g10410	aspartate aminotransferase, putative	-1.542	-1.884	-1.101	-1.452	-1.064	-0.746	-1.187	-1.097
Afu4g10990	transporter protein smf2	-0.714	-0.779	-0.568	-0.908	-0.569	-0.796	-0.963	-0.550
Afu4g11310	fructose-1,6-bisphosphatase	-2.150	-1.492	-1.976	-2.677	-1.384	-1.311	-0.737	-2.193
Afu4g11680	conserved hypothetical protein	-0.458	-0.436	-0.330	-0.321	-0.159	0.039	-0.351	-0.075
Afu4g11720	phosphatidyl synthase	-1.529	-1.706	-1.713	-1.226	-1.909	-1.539	-2.535	-2.243
Afu4g12440	sulfate transporter family protein	-1.762	-1.116	-1.393	-0.667	-1.104	-0.959	-1.138	-0.844
Afu4g13510	isocitrate lyase	-1.973	1.006	-1.578	-0.808	-1.968	-2.074	-1.542	-2.067
Afu4g14060	conserved hypothetical protein	-1.263	-0.549	-0.930	-1.305	-1.169	-1.209	-1.635	-0.897
Afu4g14090	UDP-glucose 4-epimerase	-0.430	-0.313	-0.316	-0.379	-0.194	0.011	-0.556	-0.307
Afu4g14230	MFS transporter, putative	-1.393	-1.446	-1.181	-0.984	0.142	-0.302	-0.189	-0.288
Afu4g14240	O-methyltransferase	-1.937	-1.363	-1.405	-0.670	NaN	NaN	NaN	NaN
Afu4g14450	D-mannonate oxidoreductase	-0.195	1.890	-0.391	0.376	-0.881	-0.866	-0.944	-1.278
Afu5g00550	endoglycoceramidase, putative	-0.696	-1.206	-0.661	-0.788	-0.483	-0.110	-0.884	-0.417
Afu5g00770	integral membrane protein, putative	-0.393	-0.609	-0.558	-0.413	0.296	0.291	-0.085	-0.157
Afu5g02470	thiamine biosynthesis protein (Nmt1), putative	-1.744	-1.638	-1.353	-1.718	-1.207	-0.782	-1.247	-0.841
Afu5g02820	hypothetical protein	-1.531	-2.131	-1.623	-1.407	-0.441	0.129	-0.744	-0.393
Afu5g02840	sugar transporter family protein, putative	-1.099	-0.977	-1.336	-0.983	-0.299	-0.339	-0.415	-0.199
Afu5g02850	conserved hypothetical protein	-1.006	-1.293	-1.174	-1.050	-0.324	-0.283	-0.058	-0.028
Afu5g02860	integral membrane protein, putative	-0.723	-1.602	-1.184	-0.928	-0.126	-0.087	0.009	0.095
Afu5g02950	conserved hypothetical protein	-0.806	-1.204	-0.753	-0.667	0.237	-0.375	-0.102	-0.346
Afu5g02960	hypothetical protein	-0.665	-1.048	-0.663	-0.613	0.216	-0.303	-0.032	-0.238
Afu5g03030	C6 transcription factor, putative	-0.802	-1.154	-0.724	-0.890	-0.184	-0.265	-0.360	-0.306
Afu5g03760	class III chitinase ChiA1	-0.703	-1.076	-0.695	-0.976	-0.523	0.135	-1.737	-0.832
Afu5g03800	high-affinity iron permease CaFTR2	-2.083	-0.931	-1.612	-1.275	0.100	-1.029	-0.335	-1.373
Afu5g03920	bZIP transcription factor (HapX), putative	-1.918	-0.792	-1.892	-1.479	-0.840	-1.214	-0.645	-1.576
Afu5g03930	alcohol dehydrogenase, putative	-2.047	-1.323	-1.824	-1.969	-1.206	-1.768	-1.193	-1.992
Afu5g04220	mitochondrial DNA replication protein (Yhm2), putative	-1.105	-1.464	-1.278	-1.175	-1.139	-0.996	-1.359	-1.431
Afu5g04230	citrate synthase, eukaryotic	-0.708	-0.685	-0.487	-0.440	-0.635	-0.568	-0.806	-1.097
Afu5g04250	homocysteine synthase, putative	-1.871	-0.907	-2.019	-1.636	-0.241	-0.511	-0.142	-0.391
Afu5g06240	alcohol dehydrogenase, putative	-2.194	-2.242	-1.565	-1.279	NaN	NaN	NaN	NaN
Afu5g07480	hypothetical protein	-0.751	-0.807	-0.477	-0.517	-0.013	0.031	-0.165	-0.050
Afu5g07490	steroid monooxygenase [imported]	-0.499	-0.545	-0.309	-0.473	-0.053	0.024	NaN	0.088
Afu5g07630	ubiE/COQ5 methyltransferase, putative	-0.539	-0.814	-0.508	-0.743	-0.537	-0.414	-1.557	-0.944
Afu5g08210	dolichyl-phosphate beta-glucosyltransferase, putative	-0.680	-0.517	-0.371	-0.681	-0.267	-0.231	-0.295	-0.429
Afu5g08770	hypothetical protein	-0.752	-0.477	-0.736	-0.726	-0.583	-0.130	-1.117	-0.219
Afu5g09520	conserved hypothetical protein	-0.556	-1.199	-0.448	-0.780	-0.880	-0.801	-0.804	-0.682



## Down-regulated at 18 or 24h

Afu5g10650	pyridoxamine phosphate oxidase, putative	-0.773	-0.926	-0.564	-0.696	-0.348	-0.278	-0.060	-0.146
Afu5g10660	pentatricopeptide repeat protein	-3.029	-1.744	-2.471	-2.131	-1.632	-1.736	-1.739	-2.417
Afu5g10950	hypothetical protein	-0.583	-0.581	-0.446	-0.421	-0.051	-0.117	-0.161	0.210
Afu5g10960	conserved hypothetical protein	-0.548	-0.350	-0.456	-0.382	-0.232	-0.211	-0.131	-0.102
Afu5g11320	thioredoxin, putative	-0.695	-0.562	-0.740	-0.492	0.080	-0.035	-0.107	-0.032
Afu5g11630	hypothetical protein	-0.391	-0.478	-0.391	-0.414	-0.100	-0.237	-0.117	-0.469
Afu5g14330	CPRD8 protein	-0.911	-0.935	-0.857	-0.672	0.091	NaN	NaN	-1.010
Afu5g14340	oxidoreductase, short-chain dehydrogenase/reductase family, putative	-1.186	-0.744	-1.085	-0.654	-0.234	-0.245	-0.779	-0.405
Afu5g14650	RING finger protein	-1.344	-0.862	-1.017	-0.787	-0.633	-0.578	-1.226	-0.923
Afu5g14660	GABA permease, putative	-1.185	-0.871	-0.950	-0.802	-0.743	-0.458	-1.197	-0.903
Afu5g14680	hypothetical protein	-3.575	-1.995	-2.501	-1.602	-0.525	-0.916	-2.174	-1.420
Afu5g14690	phosphorylase, putative	-0.846	-0.652	-0.851	-0.705	-0.263	0.051	-0.217	-0.139
Afu5g14930	conserved hypothetical protein	-0.283	0.545	-0.351	0.176	-0.815	-0.679	-0.787	-0.644
Afu6g00270	conserved hypothetical protein	-0.342	-0.303	-0.305	-0.276	-0.277	-0.008	-0.301	-0.051
Afu6g02280	allergen Asp F3	-0.629	-0.447	-0.597	-0.442	-0.460	-0.167	-0.605	-0.301
Afu6g02470	fumarate hydratase, putative	-1.293	-1.460	-0.975	-1.225	-0.678	-0.676	-0.529	-0.553
Afu6g02480	esterase, putative	-0.604	-0.850	-0.553	-0.659	-0.753	-0.423	-0.924	-0.435
Afu6g02500	Null	-0.400	-0.556	-0.401	-0.358	-0.139	-0.018	-0.367	-0.005
Afu6g02690	C2H2 finger domain protein, putative	-0.469	-0.493	-0.377	-0.403	-0.570	-0.150	-0.725	-0.410
Afu6g03530	glutamine synthetase	-1.083	-0.695	-0.926	-1.170	-0.666	-0.541	-0.634	-0.416
Afu6g03540	malate synthase A	-1.522	-0.030	-1.300	-0.971	-0.971	-0.719	NaN	-1.164
Afu6g03670	biotin synthase, putative	-0.323	-0.361	-0.373	-0.411	-0.263	0.107	-0.610	-0.092
Afu6g04820	para-aminobenzoate synthase PabaA	-0.846	-1.072	-0.807	-0.741	-0.153	-0.225	-0.298	-0.326
Afu6g04920	NAD-dependent formate dehydrogenase	-1.512	-1.108	-1.271	-0.677	-0.289	-0.416	0.352	0.172
Afu6g05080	ABC transporter, putative	-1.260	-1.158	-1.051	-0.872	-0.278	-0.111	-0.217	0.016
Afu6g06800	peptidase, putative	-0.574	-0.822	-0.997	-0.633	-0.266	-0.090	0.450	0.114
Afu6g06840	hypothetical protein	-1.252	-1.399	-1.147	-1.367	-0.505	-0.399	-0.525	-0.753
Afu6g07720	phosphoenolpyruvate carboxykinase (ATP)	-3.872	-3.849	-3.872	-5.113	-3.878	-4.419	-3.466	-4.346
Afu6g07770	alanine aminotransferase, putative	-1.858	-1.610	-1.386	-1.559	-1.171	-1.095	-1.073	-1.206
Afu6g07780	Copper fist DNA binding domain protein	-0.537	-0.386	-0.705	-0.518	-0.487	-0.290	-0.100	-0.345
Afu6g07790	hypothetical protein	-0.222	-0.225	-0.288	-0.295	-0.330	-0.275	-0.329	-0.344
Afu6g07900	carbon catabolite repression protein CreD, putative	-1.668	-1.019	-1.327	-1.290	-0.572	-0.754	-0.571	-1.288
Afu6g08360	thiazole biosynthesis enzyme	-1.124	-0.977	-1.224	-1.393	-0.887	-0.621	-0.967	-0.972
Afu6g08470	glycerol kinase, putative	-0.854	0.115	-0.979	-0.909	-1.183	-1.265	-0.894	-0.888
Afu6g08630	hypothetical protein	-0.651	-0.906	-0.550	-0.540	-0.531	-0.568	-0.767	-0.684
Afu6g08750	delta-1-pyrroline-5-carboxylate dehydrogenase	-2.282	-1.449	-2.109	-1.198	-1.861	-1.515	-1.948	-0.650
Afu6g08760	proline oxidase	-2.754	-1.525	-2.538	-1.214	-2.046	-1.476	-2.411	-0.495
Afu6g08850	ubiquinone biosynthesis methyltransferase Coq5, putative	-1.071	-0.720	-0.776	-0.840	-0.377	-0.401	-0.644	-0.759
Afu6g08920	assimilatory sulfite reductase	-1.002	-0.753	-1.065	-0.577	0.648	0.218	0.738	-0.044
Afu6g10450	hypothetical protein	-0.918	-0.797	-0.974	-0.547	-0.397	-0.144	-0.585	-0.204
Afu6g11100	basic amino acid transporter, putative	-1.237	-0.773	-0.949	-0.659	0.148	-0.280	NaN	-0.155
Afu6g11200	DENN (AEX-3) domain protein	-0.387	-0.601	-0.440	-0.515	-0.070	-0.028	-0.333	-0.169
Afu6g12200	hypothetical protein	-1.016	-0.602	-0.805	-0.758	-0.480	-0.434	-0.397	-0.434
Afu6g12880	hypothetical protein	-0.310	-0.266	-0.361	-0.311	-0.311	0.006	-0.669	-0.402
Afu6g13140	3,4-dihydroxy-2-butanone 4-phosphate synthase	-0.746	-0.945	-0.712	-0.768	-0.354	-0.482	-0.593	-0.706

## Down-regulated at 18 or 24h

Afu6g13790	monooxygenase	-1.896	-2.546	-1.337	-1.793	0.011	-0.606	NaN	-0.794
Afu6g14060	hypothetical protein	-0.556	-0.679	-0.506	-0.428	-0.005	-0.033	-0.351	-0.640
Afu6g14530	L-cystine transporter, putative	-1.794	-1.817	-1.847	-1.698	-0.992	-1.476	-1.473	-1.522
Afu7g01010	alcohol dehydrogenase, putative	-1.525	-0.905	NaN	-0.772	-0.364	0.248	NaN	NaN
Afu7g04730	siderochrome-iron transporter, putative	-2.308	-0.518	-1.482	-0.821	-0.930	-0.870	-0.677	-1.006
Afu7g04930	alkaline serine protease (PR1), putative	-0.864	-0.496	-0.571	-0.842	0.142	-0.081	0.184	0.277
Afu7g05060	MgtC/SapB family membrane protein	-1.923	-2.113	NaN	NaN	NaN	NaN	NaN	NaN
Afu7g05450	SUN domain protein (Uth1), putative	-0.754	-0.590	-0.732	-0.567	0.020	0.317	-0.255	-0.027
Afu7g05500	theta class glutathione S-transferase	-1.628	-0.122	-0.863	-0.756	-0.446	-0.650	-0.607	-0.538
Afu7g05710	hypothetical protein	-0.723	-0.567	-0.554	-0.430	-0.332	-0.263	-0.488	-0.633
Afu7g05800	fructose-2,6-bisphosphatase	-0.732	-0.590	-0.564	-0.681	-0.644	-0.608	-0.117	-0.806
Afu7g05880	hypothetical protein	-0.628	-0.763	-0.681	-0.633	0.078	0.010	-0.069	-0.138
Afu7g06060	siderochrome-iron transporter (Sit1), putative	-1.738	-0.142	-1.644	-0.957	-1.052	-0.803	-1.061	-1.373
Afu7g06100	acyl-coenzyme A oxidase I, peroxisomal, component A	-0.241	-0.736	-0.316	-0.513	-0.686	-0.371	-0.542	-0.428
Afu7g06780	hypothetical protein	-0.977	-0.597	-0.704	-0.671	-1.804	-0.708	-2.538	-1.447
Afu7g07090	zinc knuckle domain protein	-0.899	0.326	-0.579	0.093	-0.372	-0.462	-0.693	-0.587
Afu7g08660	Fot1 family transposase, putative	-0.384	-0.384	-0.342	-0.535	-0.189	-0.038	-0.461	0.078
Afu8g01070	Lathosterol oxidase, putative	-0.573	-0.817	-0.631	-0.531	-0.082	-0.215	-0.423	-0.068
Afu8g01730	Glycosyl transferase family 8 domain containing protein	-1.197	-0.713	-1.138	-1.126	-0.404	-0.565	-0.728	-0.780
Afu8g02100	beta-glucosidase, putative	-0.431	-0.512	-0.574	-0.345	-0.379	-0.333	0.008	-0.163
Afu8g02190	hypothetical protein	-1.036	-1.337	-0.683	-0.772	-0.023	0.108	NaN	0.199
Afu8g04370	GPI anchored protein, putative	-0.726	-0.569	-0.904	-0.482	-0.404	-0.210	-1.068	-0.807
Afu8g04630	C4-dicarboxylate transporter/malic acid transport protein, putative	-1.472	-0.944	-1.525	-1.579	-0.526	-0.333	-1.289	-0.916
Afu8g05610	cell wall glucanase (Scw11), putative	-0.957	-0.860	-0.925	-0.608	-0.087	0.217	-0.497	-0.276
Afu8g05850	FAD dependent oxidoreductase superfamily	-0.848	-0.878	-0.565	-0.488	-0.020	0.244	-0.583	-0.036
Afu8g05970	TRI7, putative	NaN	-1.008	-0.952	NaN	NaN	NaN	NaN	NaN
Afu8g06020	glutamate decarboxylase	-0.740	-0.677	-0.565	-0.424	-0.105	-0.140	-0.308	0.155
Afu8g06360	alpha-1,3-glucanase, putative	NaN	NaN	NaN	-0.377	-0.103	0.195	NaN	-0.156
Afu8g07130	AhpC/TSA family thioredoxin peroxidase, putative	-0.869	-0.606	-1.154	-0.906	0.010	0.139	-0.726	-0.302

## Up-regulated at 18 or 24h

Locus	Comm_Name	Genes up-regulated in the acuM deletion mutant (Log2 values)							
		18 h WT1	18 h WT2	18 h Comp1	18 h Comp2	24 h WT1	24 h WT2	24 h Comp1	24 h Comp2
Afu1g01690	cytochrome P450 alkane hydroxylase, putative	0.487	-0.118	0.189	-0.041	0.876	0.822	0.970	0.730
Afu1g01800	MFS transporter, putative	1.422	0.579	0.785	0.373	0.883	0.733	1.349	1.025
Afu1g02410	AAA family ATPase Reptin, putative	0.389	0.378	0.414	0.409	-0.002	0.064	-0.001	0.007
Afu1g02600	hypothetical protein	0.461	0.578	0.556	0.411	0.473	0.336	0.328	0.248
Afu1g02770	hypothetical protein	2.139	2.757	1.772	1.258	1.343	0.990	1.479	1.681
Afu1g02890	dUTPase (Dut), putative	0.725	0.534	0.638	0.557	-0.059	0.044	-0.056	0.043
Afu1g03910	hypothetical protein	0.544	0.408	0.516	0.388	0.287	0.089	0.201	0.187
Afu1g04560	urease, putative	0.799	0.306	0.141	0.101	0.789	0.709	0.651	0.665
Afu1g05610	protein phosphotase 2a 65kd regulatory subunit	0.510	-0.014	0.481	0.076	0.332	0.409	0.393	0.313
Afu1g07200	mitochondrial cytochrome b2, putative	0.578	0.438	0.515	0.361	0.324	0.652	0.322	0.611
Afu1g07430	hypothetical protein	1.898	1.051	1.558	0.697	0.451	0.353	0.445	0.353
Afu1g09580	conserved hypothetical protein	0.659	0.740	0.477	0.760	0.206	0.112	0.674	0.066
Afu1g10580	homeobox transcription factor, putative	1.371	1.237	1.100	0.684	0.122	0.265	0.222	0.198
Afu1g11000	C6 transcription factor, putative	0.291	NaN	0.316	0.273	0.032	0.066	0.122	0.278
Afu1g11190	eukaryotic translation elongation factor eEF-1 beta, putative	0.578	0.763	0.661	0.486	0.258	0.011	0.262	-0.031
Afu1g15490	MFS multidrug transporter, putative	1.275	0.930	0.787	0.799	0.133	0.043	0.062	-0.571
Afu1g15870	DNA topoisomerase IV subunit A, putative	0.350	0.339	0.450	0.363	0.277	-0.071	0.282	0.437
Afu1g16250	alpha-glucosidase B	2.870	2.691	2.267	1.585	0.891	0.819	1.109	1.099
Afu1g17470	high affinity nitrate transporter NrtB	2.662	NaN	1.541	NaN	1.531	2.221	1.259	0.969
Afu1g17480	conserved hypothetical protein	0.701	-0.099	0.817	-0.041	0.650	0.861	0.553	0.590
Afu2g00540	carboxyphosphoenolpyruvate phosphonmutase, putative	0.973	-0.398	1.107	-1.144	1.449	1.520	0.904	0.698
Afu2g00960	NACHT and Ankyrin domain protein	2.901	1.753	1.757	1.081	0.473	0.550	0.364	0.625
Afu2g02080	C2H2 finger domain protein, putative	1.071	1.197	0.786	1.053	0.071	-0.250	-0.026	-0.704
Afu2g02250	allantoinase	0.681	1.099	0.736	0.717	0.798	0.507	0.840	0.580
Afu2g02660	DNA topoisomerase III, putative	NaN	-0.357	0.324	0.261	0.395	0.313	0.413	0.372
Afu2g03230	alpha-amylase AmyA	1.156	0.310	0.793	0.167	0.525	0.357	0.506	0.582
Afu2g07400	mitochondrial carrier protein, putative	0.410	0.337	0.415	0.338	0.054	-0.032	0.065	0.049
Afu2g07970	ribosomal protein L19	0.540	0.390	0.531	0.641	-0.047	0.038	-0.205	-0.281
Afu2g10230	myo-inositol oxygenase	2.943	3.779	1.190	1.605	0.412	0.368	0.532	0.463
Afu2g11270	alpha-1,3-glucan synthase, putative	1.867	1.919	1.650	1.559	0.054	0.294	0.143	0.090
Afu2g14750	endo-arabinase, putative	2.975	3.153	1.950	1.812	0.245	0.395	0.595	0.677
Afu2g15390	flug protein	0.939	0.997	0.633	0.631	0.009	-0.107	-0.041	-0.086
Afu2g17530	conidial pigment biosynthesis oxidase Arb2/brown2	2.509	1.751	2.317	1.228	0.106	-0.252	0.122	0.035
Afu2g17540	pigment biosynthesis oxidase Abr1/brown 1	2.651	2.544	1.966	1.796	0.063	-0.332	0.073	0.088
Afu2g17580	conidial pigment biosynthesis scytalone dehydratase Arp1	2.799	1.986	2.217	1.307	0.205	-0.090	0.167	0.280
Afu2g18000	short chain dehydrogenase, putative	1.235	1.410	1.123	0.768	0.378	-0.674	0.325	0.112
Afu2g18030	catalase, putative	2.168	2.649	1.981	1.828	0.020	-0.246	0.339	0.274
Afu3g02340	CBF/NF-Y family transcription factor, putative	0.753	0.557	0.605	0.562	0.320	0.003	0.308	-0.024
Afu3g05520	oxysterol binding protein (Orp8), putative	0.412	0.454	0.342	0.360	-0.057	-0.038	0.089	0.069
Afu3g05530	condensin complex component cnd1	0.420	0.111	0.450	0.036	0.414	0.425	0.451	0.455
Afu3g06760	ribosomal protein L37	0.601	0.479	0.563	0.804	0.021	-0.144	-0.317	-0.372
Afu3g08040	polymerase (RNA) II (DNA directed) polypeptide D	0.699	0.473	0.655	0.373	1.221	1.068	0.888	0.806
Afu3g08050	C6 transcription factor (OTam), putative	0.029	-0.314	0.074	-0.228	0.585	0.503	0.389	0.477

## Up-regulated at 18 or 24h

Afu3g10080	serine/threonine protein kinase, putative	0.406	0.479	0.488	0.352	0.126	-0.024	0.201	0.136
Afu3g12220	ABC transporter, putative	1.412	1.083	1.173	0.849	0.373	0.496	0.689	0.153
Afu3g12230	hypothetical protein	2.024	1.593	1.282	1.150	0.391	-0.064	0.637	0.067
Afu3g12710	conserved hypothetical protein	0.538	0.483	0.538	0.380	0.297	0.093	0.548	0.378
Afu3g13090	hypothetical protein	1.652	1.335	1.147	0.770	0.383	0.202	0.597	0.461
Afu3g13210	protein kinase domain-containing protein	1.319	1.101	1.164	0.633	0.423	0.289	0.392	0.636
Afu4g00210	polyketide synthase, putative	2.934	3.001	2.594	2.035	0.544	0.258	1.052	0.473
Afu4g00230	oxidoreductase, 2OG-Fe(II) oxygenase family, putative	2.074	2.129	2.082	1.922	0.336	0.255	0.782	0.394
Afu4g00510	hypothetical protein	2.408	2.024	1.813	1.698	0.336	-0.114	0.418	0.139
Afu4g06880	conserved hypothetical protein	2.758	3.311	2.109	1.783	0.405	0.140	0.736	0.210
Afu4g10070	class I alpha-mannosidase	0.763	0.825	0.473	0.284	0.341	0.358	0.293	0.377
Afu4g10130	alpha-amylase (Amy1), putative	2.839	1.289	2.221	0.835	1.383	0.951	1.698	1.256
Afu4g10140	glucoamylase	2.614	2.134	1.815	1.325	0.666	0.552	1.057	1.030
Afu4g10150	alpha-glucosidase	4.558	3.210	3.396	2.734	1.656	1.562	1.476	1.211
Afu4g12520	hypothetical protein	0.954	0.200	0.871	0.104	0.497	0.430	0.554	0.533
Afu4g13530	Trehalase	0.452	0.507	0.476	0.482	0.004	-0.139	0.211	-0.031
Afu4g14530	glutathione S-transferase, putative	1.924	1.535	1.395	0.989	0.199	-0.238	0.243	-0.010
Afu4g14770	squalene-hopene-cyclase, putative	2.545	0.899	2.009	0.400	0.731	0.622	1.013	1.177
Afu4g14840	transferase family protein	1.527	NaN	0.575	NaN	0.676	0.636	0.833	1.118
Afu4g14850	extracellular 3-ketosteroid 1-dehydrogenase, putative	1.801	0.519	0.820	0.544	0.835	0.523	0.948	0.938
Afu5g01420	conserved hypothetical protein	1.785	0.524	1.164	0.340	1.041	0.592	0.646	0.660
Afu5g01490	hypothetical protein	1.773	1.545	1.365	1.104	0.165	-0.301	0.249	0.128
Afu5g01580	oxidoreductase, short chain dehydrogenase/reductase family	0.775	0.572	0.578	0.435	-0.061	0.237	0.062	0.433
Afu5g02520	DNA replication licensing factor Mcm5, putative	0.628	0.615	0.509	0.483	0.417	0.331	0.383	0.071
Afu5g02770	hypothetical protein	2.011	2.038	1.650	1.081	0.553	0.280	0.879	0.450
Afu5g03280	hypothetical protein	1.456	0.000	1.156	-0.110	0.712	0.422	0.502	0.609
Afu5g06230	gaba-specific permease	0.156	-0.576	0.330	-0.270	0.372	0.410	0.506	0.442
Afu5g06290	MFS transporter, putative	1.199	0.734	0.505	0.690	0.715	0.463	0.929	0.714
Afu5g06610	glutathione synthetase	-0.068	-1.667	-0.206	-0.216	0.500	0.505	0.616	0.452
Afu5g06680	4-aminobutyrate aminotransferase	0.713	1.025	0.901	0.592	0.211	0.138	0.778	0.547
Afu5g07360	peroxisomal copper amine oxidase	1.156	0.697	1.235	NaN	0.546	0.521	0.538	0.636
Afu5g08180	hypothetical protein	3.400	2.853	2.491	1.980	1.026	0.526	0.999	0.622
Afu5g10890	DNA replication licensing factor Mcm6, putative	0.584	0.559	0.475	0.428	0.152	0.466	0.400	0.158
Afu5g11020	ammonium transporter	2.385	0.523	2.164	0.604	1.607	1.466	1.637	1.547
Afu5g11600	CRO1 protein	1.220	1.562	1.152	0.795	0.572	0.300	0.809	0.264
Afu5g14850	conserved hypothetical protein	1.506	1.966	1.026	1.274	0.111	0.131	0.726	0.426
Afu6g00770	extracellular arabinanase, putative	2.590	2.045	1.810	1.185	-0.456	-0.202	-0.471	0.044
Afu6g02450	ribosomal S30/ubiquitin fusion	0.538	0.527	0.538	0.687	0.021	0.013	-0.240	-0.271
Afu6g03060	monosaccharide transporter	2.227	2.739	1.519	1.539	0.714	1.473	0.246	0.719
Afu6g03510	polyamine oxidase, putative	0.805	0.452	0.562	0.845	0.957	0.893	1.206	1.329
Afu6g03870	hypothetical protein	2.884	2.930	2.153	1.800	0.712	0.327	0.792	0.630
Afu6g03880	hypothetical protein	2.600	2.383	1.922	1.271	0.643	0.406	0.836	0.643
Afu6g06530	hypothetical protein	1.724	1.457	1.641	1.256	0.222	0.216	0.735	0.848
Afu6g06580	Eukaryotic phosphomannomutase	0.436	0.322	0.391	0.396	-0.009	-0.086	-0.081	0.110
Afu6g07260	purine-cytosine permease, putative	2.382	1.554	1.834	1.394	0.271	0.237	0.686	0.445

## Up-regulated at 18 or 24h

Afu6g08390	conserved hypothetical protein	0.410	0.692	0.508	0.611	-0.666	-0.243	-0.538	-0.392
Afu6g09410	conserved hypothetical protein	1.220	0.742	1.118	0.674	-0.258	-0.123	0.045	0.240
Afu6g09720	methyltransferase GliN	-0.940	-3.726	-1.219	-2.788	0.749	0.720	0.748	0.397
Afu6g11160	isopentenyl-diphosphate delta-isomerase	0.540	-0.207	0.601	0.179	0.640	0.633	0.480	0.831
Afu6g12050	nonribosomal peptide synthase, putative	2.480	1.885	2.257	1.591	0.372	0.517	0.546	0.500
Afu6g12060	MAK1-like monooxygenase, putative	2.099	NaN	1.888	NaN	0.274	0.668	0.574	0.450
Afu6g12070	FAD binding domain protein	3.116	2.902	2.313	1.952	0.489	0.310	0.628	0.437
Afu6g13940	P450-monooxygenase, putative	1.601	1.640	1.047	1.458	-0.143	-0.051	0.037	0.035
Afu6g13970	FAD-dependent monooxygenase (PaxM), putative	1.563	1.133	0.931	0.981	0.111	0.153	0.213	-0.018
Afu7g01590	cystathionine gamma-synthase	0.807	0.748	0.461	0.265	0.388	0.565	0.528	0.506
Afu7g02180	UDP-N-acetylglucosamine pyrophosphorylase	0.902	0.935	0.670	0.521	-0.120	-0.055	0.113	0.258
Afu7g02510	hypothetical protein	0.608	0.469	0.480	0.448	-0.062	-0.079	0.013	-0.047
Afu7g04070	phospho-2-dehydro-3-deoxyheptonate aldolase	0.463	0.658	0.491	0.463	0.355	0.233	0.224	-0.004
Afu7g05180	defensin domain protein, putative	4.219	0.782	2.514	1.049	1.687	1.659	1.859	2.032
Afu7g06380	maltase	2.534	2.426	2.185	1.449	0.861	0.367	1.491	1.151
Afu7g06450	hypothetical protein	1.536	-0.020	1.243	NaN	0.869	1.340	1.126	1.165
Afu7g06860	hypothetical protein	0.525	0.475	0.408	0.366	0.233	0.096	0.051	0.174
Afu7g06870	Tf1-like reverse transcriptase, integrase, putative	0.627	0.711	0.663	0.475	0.289	0.127	0.139	0.133
Afu7g06880	hypothetical protein	0.653	0.738	0.666	0.452	0.191	0.045	0.122	0.079
Afu7g08600	hypothetical protein	2.176	1.491	1.581	1.470	0.198	0.063	0.195	0.085
Afu8g00100	aspartate-tRNA ligase, putative	1.719	1.842	1.548	1.489	-0.067	-0.298	0.605	0.583
Afu8g00110	oxidoreductase, 2OG-Fe(II) oxygenase family, putative	1.802	2.163	1.278	1.319	-0.091	-0.383	0.544	0.311
Afu8g00390	O-methyltransferase, putative	1.853	2.000	2.199	1.140	-1.537	0.008	-1.642	-0.157
Afu8g00400	conserved hypothetical protein	1.587	0.992	1.480	0.889	-1.282	0.033	-1.535	-0.191
Afu8g00740	cytochrome P450, putative	0.604	0.479	0.754	0.583	-0.516	-0.634	0.187	0.136
Afu8g01980	hypothetical protein	2.384	2.454	1.551	1.246	0.185	-0.077	0.063	0.232
Afu8g02620	CobW domain protein	0.858	0.945	0.845	0.502	0.141	0.548	-0.822	0.027
Afu8g04290	C2H2 finger domain protein, putative	1.545	1.605	1.248	1.063	0.444	0.047	0.345	0.186
Afu8g04890	hypothetical protein	0.310	0.350	0.560	0.411	0.499	0.507	0.395	0.468
Afu8g06030	alpha-1,3-glucanase, putative	1.609	1.817	1.269	1.551	-0.101	-0.022	0.197	-0.078
Afu8g06080	flavoheprotein, putative	0.524	NaN	0.639	0.524	0.790	0.826	0.884	0.336

### Real-time PCR verification

Real-time PCR verification of microarray results. Organisms grown in RPMI medium for 18 h  
Gene expression levels are presented in terms of the absolute ratio of the mutant strains to strain Af293.

Locus	Name/function	$\Delta acuM$	$\Delta acuM::acuM$
2g07680	L-ornithine N <sup>5</sup> -oxygenase	0.18	0.58
3g03400	Siderophore biosynthesis acetylase Acel	0.43	1.07
3g03390	Siderophore biosynthesis lipase/esterase	0.86	1.30
3g03640	Siderophore transporter	0.82	1.02
7g06060	Siderophore transporter (Sit1)	0.77	1.45
7g04730	Siderophore transporter	0.66	0.93
1g17270	Ferric-chelate reductase	0.47	0.97
5g03800	High-affinity iron permease FtrA	0.55	1.43
5g03920	bZIP transcription factor (HapX)	0.61	1.04

Real-time PCR verification of microarray results.

Organisms grown in Sabrouaud Dextrose broth with 25  $\mu$ M phenanthroline for 24 h.

Gene expression levels are presented in terms of the absolute ratio of the mutant strains to strain Af293.

Locus	Name/function	$\Delta acuM$	$\Delta acuM::acuM$
1g17270	Ferric-chelate reductase	0.21	0.89
5g03800	High-affinity iron permease FtrA	0.51	0.81
1g17200	Nonribosomal peptide synthase	0.34	0.86
2g05730	Siderophore transporter (MirC)	0.43	0.74
5g03920	bZIP transcription factor (HapX)	0.34	1.18
3g03640	Siderophore transporter	0.26	0.77
2g07680	L-ornithine N <sup>5</sup> -oxygenase	0.45	0.76
3g03350	Nonribosomal peptide synthase SidE	0.56	1.01

Specific Go Terms

**Table 3.** Expression levels of genes annotated to specific GO terms

		<b>18 hour<sup>a</sup></b>	<b>24 hour<sup>b</sup></b>
<b>siderophore-iron transport</b>			
Afu3g03440	MFS family siderophore transporter	0.33	0.45
Afu3g03640	siderochrome-iron transporter (MirB)	0.25	0.37
Afu7g04730	siderochrome-iron transporter	0.41	0.55
Afu7g06060	siderochrome-iron transporter (Sit1)	0.46	0.48
<b>glutamate biosynthesis</b>			
Afu1g12800	isocitrate dehydrogenase, NAD-dependent	0.92	0.82
Afu4g06620	Glutamate/Leucine/Phenylalanine/Valine dehydrogenase	0.17	0.29
Afu5g04230	citrate synthase, eukaryotic	0.67	0.58
Afu6g08750	delta-1-pyrroline-5-carboxylate dehydrogenase	0.30	0.36
<b>iron ion homeostasis</b>			
Afu3g03440	MFS family siderophore transporter	0.33	0.45
Afu3g03640	siderochrome-iron transporter (MirB)	0.25	0.37
Afu7g04730	siderochrome-iron transporter	0.41	0.55
Afu7g06060	siderochrome-iron transporter (Sit1)	0.46	0.48
<b>glyoxylate cycle</b>			
Afu1g09470	aminotransferase, class V, putative	0.74	0.69
Afu4g13510	isocitrate lyase	0.56	0.27
<b>gluconeogenesis</b>			
Afu1g10350	phosphoglycerate kinase PgkA, putative	0.59	0.58
Afu4g11310	fructose-1,6-bisphosphatase	0.24	0.38
Afu6g07720	phosphoenolpyruvate carboxykinase (ATP)	0.06	0.06
Afu7g05800	fructose-2,6-bisphosphatase	0.64	0.69
<b>methionine metabolism</b>			
Afu1g10130	adenosylhomocysteinase	0.28	0.93
Afu1g10630	S-adenosylmethionine synthetase	0.25	0.94
Afu2g11300	G2882	0.43	1.20
Afu3g06600	siroheme synthase	0.65	1.16
Afu5g04250	homocysteine synthase	0.33	0.80
<b>one-carbon compound metabolism</b>			
Afu1g10780	glycine cleavage system T protein	0.53	1.10

### Specific Go Terms

Afu1g12070	glycine cleavage system H protein	0.46	0.99
Afu2g07810	cytosolic hydroxymethyltransferase	0.54	0.89

<sup>a, b</sup> the combined results of four replicates microarray analysis.  
Gene expression changes in  $\Delta acuM$  are the absolute ratio compared to wild-type and *acuM* complemented strains.