

TABLE I
The 100 most abundant transcripts of both wild type (WT) and aposymbiotic (APO) strains of *Angomonas deanei*, measured as RPKM

Feature ID	Gene function (Annotation)	WT transcript abundance (RPKM - Mean)	Feature ID	Gene function (Annotation)	APO transcript abundance (RPKM - Mean)	
1	AGDE17275	hypothetical protein	39,310	AGDE17274	hypothetical protein	25,210
2	AGDE17274	hypothetical protein	25,847	AGDE17275	hypothetical protein	24,695
3	AGDE10555	beta-fructofuranosidase	7,347	AGDE14376	hypothetical protein	8,569
4	AGDE12097	glycosomal glyceraldehyde-3-phosphate partial	5,267	AGDE10555	beta-fructofuranosidase	7,893
5	AGDE00565	kinetoplastid membrane protein 11	5,265	AGDE13194	hypothetical protein	7,657
6	AGDE01837	60s ribosomal protein l22	4,916	AGDE00565	kinetoplastid membrane protein 11	6,129
7	AGDE05651	40s ribosomal protein s3a	4,858	AGDE14377	hypothetical protein	5,952
8	AGDE12439	40s ribosomal protein s23	4,795	AGDE03921	s-adenosylmethionine synthetase	5,733
9	AGDE08950	hypothetical protein	4,077	AGDE15019	hypothetical protein	5,230
10	AGDE02419	glycosomal glyceraldehyde-3-phosphate partial	4,058	AGDE08950	hypothetical protein	5,130
11	AGDE09629	pyruvate indole-pyruvate carboxylase	3,955	AGDE05874	calcium-binding protein	4,972
12	AGDE13194	hypothetical protein	3,922	AGDE01203	glycosomal phosphoenolpyruvate carboxykinase	4,122
13	AGDE11644	translation elongation factor 1-beta	3,900	AGDE09744	calcium-binding protein	4,062
14	AGDE03921	s-adenosylmethionine synthetase	3,865	AGDE11644	translation elongation factor 1-beta	3,835
15	AGDE05874	calcium-binding protein	3,741	AGDE07510	calcium-binding protein	3,808
16	AGDE08485	60s acidic ribosomal subunit protein	3,594	AGDE08517	s-adenosylmethionine synthetase	3,705
17	AGDE15019	hypothetical protein	3,567	AGDE07844	calcium-binding protein	3,696
18	AGDE10788	eukaryotic initiation factor 5a	3,566	AGDE05651	40s ribosomal protein s3a	3,598
19	AGDE14377	hypothetical protein	3,477	AGDE01837	60s ribosomal protein l22	3,525
20	AGDE00325	histone h4	3,410	AGDE08485	60s acidic ribosomal subunit protein	3,294
21	AGDE09744	calcium-binding protein	3,126	AGDE12439	40s ribosomal protein s23	3,142
22	AGDE02676	40s ribosomal protein s9	3,079	AGDE02676	40s ribosomal protein s9	3,096
23	AGDE09466	beta-fructofuranosidase	3,064	AGDE12685	40s ribosomal protein	3,048
24	AGDE05681	40s ribosomal protein	3,005	AGDE14768	conserved hypothetical protein	2,989
25	AGDE07844	calcium-binding protein	2,853	AGDE09629	pyruvate indole-pyruvate carboxylase	2,986
26	AGDE10521	cysteine peptidase	2,851	AGDE13022	amastin	2,879
27	AGDE15370	myo-inositol-1-phosphate synthase	2,830	AGDE03102	40s ribosomal protein l14	2,853
28	AGDE08517	s-adenosylmethionine synthetase	2,788	AGDE10788	eukaryotic initiation factor 5a	2,697
29	AGDE04958	ubiquitin ribosomal protein s27a	2,730	AGDE03560	calpain-like cysteine peptidase	2,673
30	AGDE01084	eukaryotic initiation factor 5a	2,687	AGDE03923	60s ribosomal protein l11 (l16)	2,670
31	AGDE14376	hypothetical protein	2,679	AGDE05681	40s ribosomal protein	2,668
32	AGDE02314	40s ribosomal protein s13	2,677	AGDE02314	40s ribosomal protein s13	2,657
33	AGDE13022	amastin	2,644	AGDE05973	60s ribosomal protein l19	2,633
34	AGDE10805	40s ribosomal protein	2,605	AGDE00500	calpain-like cysteine peptidase	2,606

Feature ID	Gene function (Annotation)	WT transcript abundance (RPKM - Mean)	Feature ID	Gene function (Annotation)	APO transcript abundance (RPKM - Mean)	
35	AGDE07943	hypothetical protein	2,536	AGDE11775	60s ribosomal protein l7a	2,551
36	AGDE14768	conserved hypothetical protein	2,528	AGDE09466	beta-fructofuranosidase	2,438
37	AGDE12685	40s ribosomal protein	2,504	AGDE00524	aldehyde mitochondrial precursor	2,375
38	AGDE08044	protein disulfide isomerase	2,470	AGDE04284	glutamate dehydrogenase	2,302
39	AGDE03793	ribosomal protein s29	2,421	AGDE10494	amal	2,292
40	AGDE07510	calcium-binding protein	2,401	AGDE07943	hypothetical protein	2,266
41	AGDE15443	g-amastin	2,389	AGDE10521	myristoylated protein 3	2,264
42	AGDE07941	elongation factor 1-alpha	2,377	AGDE04196	60s acidic ribosomal protein p2	2,230
43	AGDE02059	60s ribosomal protein l27a l29	2,364	AGDE03670	60s ribosomal protein l18a	2,230
44	AGDE05615	40s ribosomal protein s15a	2,326	AGDE12965	d-amastin	2,202
45	AGDE03670	60s ribosomal protein l18a	2,294	AGDE01084	eukaryotic initiation factor 5a	2,194
46	AGDE00500	calpain-like cysteine peptidase	2,289	AGDE10805	40s ribosomal protein	2,187
47	AGDE14033	hypothetical protein	2,283	AGDE04017	proton motive atpase 1	2,166
48	AGDE00524	aldehyde mitochondrial precursor	2,251	AGDE02155	heat shock protein 70	2,134
49	AGDE04017	proton motive atpase 1	2,245	AGDE15370	myo-inositol-1-phosphate synthase	2,124
50	AGDE04779	argininosuccinate synthase	2,245	AGDE12097	glycosomal glyceraldehyde-3-phosphate partial	2,111
51	AGDE04193	alcohol dehydrogenase	2,210	AGDE04958	ubiquitin ribosomal protein s27a	2,082
52	AGDE06563	60s ribosomal protein l7a	2,206	AGDE07674	p-type h+-atpase	2,059
53	AGDE09068	inositol-3-phosphate synthase	2,197	AGDE03780	40s ribosomal protein s15a	2,055
54	AGDE03560	calpain-like cysteine peptidase	2,133	AGDE07941	elongation factor 1-alpha	2,027
55	AGDE01203	glycosomal phosphoenolpyruvate carboxykinase	2,108	AGDE09563	polyubiquitin	1,993
56	AGDE16970	hypothetical protein	2,046	AGDE00325	histone h4	1,988
57	AGDE03102	40s ribosomal protein l14	2,028	AGDE07279	heat-shock protein hsp70	1,970
58	AGDE07934	atp-dependent phosphofructokinase	2,023	AGDE05482	ribosomal protein s20	1,965
59	AGDE04235	beta tubulin	2,000	AGDE05221	ribosomal protein s20	1,955
60	AGDE04196	60s acidic ribosomal protein p2	1,987	AGDE06563	60s ribosomal protein l7a	1,940
61	AGDE06523	hypothetical protein	1,957	AGDE14375	circumsporozoite protein	1,910
62	AGDE05482	ribosomal protein s20	1,936	AGDE03362	alpha tubulin	1,904
63	AGDE05221	ribosomal protein s20	1,932	AGDE10549	glycosomal phosphoenolpyruvate carboxykinase	1,880
64	AGDE05973	60s ribosomal protein l19	1,932	AGDE01346	hypothetical protein	1,839
65	AGDE12965	d-amastin	1,907	AGDE14033	hypothetical protein	1,808
66	AGDE02155	heat shock protein 70	1,903	AGDE09786	activated protein kinase c receptor	1,794
67	AGDE07477	pyruvate indole-pyruvate carboxylase	1,901	AGDE03793	ribosomal protein s29	1,768
68	AGDE08102	40s ribosomal protein s12	1,884	AGDE17226	nucleoside diphosphate kinase b	1,755
69	AGDE00554	40s ribosomal protein s12	1,856	AGDE13180	hypothetical protein	1,725
70	AGDE10067	fructose-bisphosphate glycosomal	1,853	AGDE07979	60s ribosomal protein l11 (l16)	1,722

Feature ID	Gene function (Annotation)	WT transcript abundance (RPKM - Mean)	Feature ID	Gene function (Annotation)	APO transcript abundance (RPKM - Mean)	
71	AGDE03780	40s ribosomal protein s15a	1,848	AGDE06789	60s ribosomal protein l27a l29	1,696
72	AGDE07738	60s ribosomal protein l18a	1,847	AGDE08044	protein disulfide isomerase	1,653
73	AGDE10417	activated protein kinase c receptor	1,832	AGDE04779	argininosuccinate synthase	1,653
74	AGDE03362	alpha tubulin	1,820	AGDE13179	hypothetical protein	1,625
75	AGDE07283	calpain-like cysteine peptidase	1,809	AGDE15968	40s ribosomal protein s21	1,602
76	AGDE09786	activated protein kinase c receptor	1,799	AGDE04235	beta tubulin	1,584
77	AGDE05045	60s ribosomal protein l36	1,735	AGDE07283	calpain-like cysteine peptidase	1,579
78	AGDE04641	cyclophilin a	1,729	AGDE05615	40s ribosomal protein s15a	1,574
79	AGDE17226	nucleoside diphosphate kinase b	1,711	AGDE02419	glycosomal glyceraldehyde-3-phosphate partial	1,562
80	AGDE02533	40s ribosomal protein s11	1,707	AGDE05634	ubiquitin ribosomal protein s27a	1,550
81	AGDE00667	60s ribosomal protein l36	1,686	AGDE02152	40s ribosomal protein	1,549
82	AGDE04164	iron superoxide dismutase	1,654	AGDE03620	argininosuccinate synthase	1,549
83	AGDE07279	heat-shock protein hsp70	1,648	AGDE13309	hypothetical protein	1,519
84	AGDE06596	ribosomal protein l1a	1,626	AGDE13304	high cysteine membrane protein group 2	1,515
85	AGDE14034	hypothetical protein	1,608	AGDE09570	hypothetical protein	1,503
86	AGDE15968	40s ribosomal protein s21	1,606	AGDE11697	60s ribosomal protein	1,458
87	AGDE11342	fructose-bisphosphate glycosomal	1,600	AGDE08102	40s ribosomal protein s12	1,452
88	AGDE02152	40s ribosomal protein	1,595	AGDE11094	40s ribosomal protein s10	1,435
89	AGDE06376	40s ribosomal protein s24e	1,594	AGDE09758	pyruvate phosphate dikinase	1,435
90	AGDE10494	ama1 protein	1,572	AGDE06523	hypothetical protein	1,432
91	AGDE10551	ribosomal protein s25	1,568	AGDE12914	hypothetical protein	1,406
92	AGDE09563	polyubiquitin	1,565	AGDE07477	pyruvate indole-pyruvate carboxylase	1,383
93	AGDE06789	60s ribosomal protein l27a l29	1,549	AGDE00554	40s ribosomal protein s12	1,373
94	AGDE11094	40s ribosomal protein s10	1,543	AGDE02059	60s ribosomal protein l27a l29	1,347
95	AGDE07979	60s ribosomal protein l11 (l16)	1,522	AGDE10678	hypothetical protein	1,346
96	AGDE07674	p-type h+-atpase	1,497	AGDE15802	hypothetical protein	1,333
97	AGDE08528	60s ribosomal subunit protein l31	1,493	AGDE05636	60s ribosomal protein l28	1,320
98	AGDE04284	glutamate dehydrogenase	1,492	AGDE04499	ubiquitin-fusion protein	1,315
99	AGDE03173	60s ribosomal protein l22	1,479	AGDE13186	hypothetical protein	1,301
100	AGDE03923	60s ribosomal protein l11 (l16)	1,450	AGDE01887	ribosomal protein l15	1,301

Expression means of the 100 most abundant transcripts quantified by reads per gene kb per million of mapped reads (RPKM) obtained from three independent biological replicates from aposymbiotic (APO) strain and wild type (WT) strain of *Angomonas deanei* on exponential growth. AGDE: *A. deanei* sequence feature (SRA Accession: PRJNA279893).

TABLE II
Differential gene expression between *Angomonas deanei* aposymbiotic (APO) and wild type (WT) strains. List of gene transcripts down regulated in APO strain

Feature ID	Fold change	Gene function (Annotation)	FDR p-value
AGDE02219	-119	ribosomal protein l27	5.5E-20
AGDE01379	-122	aconitase	1.2E-16
AGDE04780	-134	glycosomal phosphoenolpyruvate carboxykinase	1.2E-15
AGDE11451	-170	delta-1-pyrroline-5-carboxylate dehydrogenase	3.5E-15
AGDE00951	-126	myosin XXI	3.5E-15
AGDE01738	-37	pyrroline-5-carboxylate synthetase-like protein	3.5E-14
AGDE05250	-276	serine threonine kinase-like protein	3.8E-14
AGDE04771	-877	elongation factor tu	1.8E-13
AGDE07812	-34	60s ribosomal protein	3.4E-11
AGDE12291	-42	conserved hypothetical protein	6.9E-10
AGDE13031	-56	poly ADP-ribose polymerase	2.2E-09
AGDE16801	-39	hypothetical protein	2.7E-09
AGDE01355	-48	sre-2/carboxylase carrier protein	4.7E-09
AGDE00619	-58	profilin	1.4E-07
AGDE09078	-29	squalene synthase	1.4E-07
AGDE12173	-47	conserved hypothetical protein	2.1E-07
AGDE09437	-101	serine threonine protein phosphatase catalytic subunit	2.7E-07
AGDE10173	-19	conserved hypothetical protein	4.1E-07
AGDE11664	-93	glycosomal phosphoenolpyruvate carboxykinase	5.3E-07
AGDE06268	-20	dihydrolipoamide dehydrogenase	5.5E-07
AGDE07437	-21	p450 reductase	7.5E-07
AGDE17104	-11	rhodanase-like protein	1.5E-06
AGDE16921	-35	conserved hypothetical protein	2.1E-06
AGDE06828	-48	vacuolar atp synthase subunit c	2.7E-06
AGDE08262	-14	conserved hypothetical protein	3.8E-06
AGDE12242	-44	conserved hypothetical protein	7.6E-06
AGDE16972	-284	hypothetical protein	1.1E-05
AGDE07356	-6	camp specific phosphodiesterase	1.9E-05
AGDE06718	-5	P27 protein	3.6E-05
AGDE10206	-10	2-oxoglutarate e3-like protein	5.5E-05
AGDE03552	-6	coproporphyrinogen iii oxidase	0.0001
AGDE07260	-41	d-3-phosphoglycerate dehydrogenase-like protein	0.0001
AGDE17201	-10	high cysteine membrane protein	0.0001
AGDE03214	-152	conserved hypothetical protein	0.0002

Feature ID	Fold change	Gene function (Annotation)	FDR p-value
AGDE05533	-4	camp specific phosphodiesterase	0.0002
AGDE03177	-20	proteasome beta 3 subunit	0.0002
AGDE00606	-55	conserved hypothetical protein	0.0003
AGDE08631	-10	40s ribosomal protein s8	0.0003
AGDE17124	-136	hypothetical protein	0.0005
AGDE07145	-29	conserved hypothetical protein	0.0007
AGDE07360	-29	u2 splicing auxiliary factor	0.0007
AGDE12090	-6	aldose 1 epimerase	0.0007
AGDE04864	-4	sterol 24-c-methyltransferase	0.0007
AGDE07550	-28	conserved hypothetical protein	0.0007
AGDE09287	-38	udp-glucose pyrophosphorylase	0.0008
AGDE06160	-15	n-myristoyl transferase	0.0008
AGDE17058	-9	hypothetical protein	0.0009
AGDE17084	-202	hypothetical protein	0.0010
AGDE16802	-126	hypothetical protein	0.0010
AGDE05062	-20	conserved hypothetical protein	0.0011
AGDE03215	-4	coproporphyrinogen iii oxidase	0.0011
AGDE01118	-127	conserved hypothetical protein	0.0011
AGDE14744	-125	FAD linked oxidase	0.0017
AGDE06230	-24	glycosomal phosphoenolpyruvate carboxykinase	0.0022
AGDE10976	-9	metal-ion transporter	0.0023
AGDE07908	-5	mitochondrial isocitrate dehydrogenase	0.0025
AGDE11864	-19	cyclin 9	0.0028
AGDE08758	-3	conserved hypothetical protein	0.0028
AGDE03939	-4	mitochondrial isocitrate dehydrogenase	0.0031
AGDE06048	-25	conserved hypothetical protein	0.0031
AGDE07651	-24	rna-binding protein	0.0032
AGDE00952	-5	aldose 1 epimerase	0.0033
AGDE11769	-5	squalene monooxygenase-like protein	0.0033
AGDE17193	-115	conserved hypothetical protein	0.0046
AGDE06650	-4	mitochondrial phosphate transporter	0.0047
AGDE02757	-4	a chain radiation-reduced tryparedoxin-i	0.0048
AGDE03018	-5	rad51 protein	0.0051
AGDE02649	-22	ethanolamine phosphotransferase	0.0054
AGDE17249	-12	prostaglandin f synthase	0.0054
AGDE10667	-21	conserved hypothetical protein	0.0056
AGDE10579	-5	ubiquitin hydrolase	0.0065



Feature ID	Fold change	Gene function (Annotation)	FDR p-value	Feature ID	Fold change	Gene function (Annotation)	FDR p-value
AGDE09555	-3	cytochrome p450-like protein	0.0071	AGDE11280	-13	conserved hypothetical protein	0.0221
AGDE03011	-6	coproporphyrinogen iii oxidase	0.0080	AGDE09294	-3	p450 reductase	0.0223
AGDE02136	-24	glycosomal phosphoenolpyruvate carboxykinase	0.0086	AGDE03369	-35	vacuolar atp synthase subunit c	0.0226
AGDE16194	-103	transcriptional regulator	0.0089	AGDE00406	-4	chaperonin alpha subunit	0.0226
AGDE05429	-5	conserved hypothetical protein	0.0091	AGDE07534	-4	phenylalanine-4-hydroxylase	0.0226
AGDE00762	-14	conserved hypothetical protein	0.0097	AGDE01335	-4	hypothetical protein	0.0235
AGDE00627	-11	lysophospholipase	0.0099	AGDE16613	-5	conserved hypothetical protein	0.0242
AGDE00497	-4	mitogen-activated protein kinase 3	0.0100	AGDE06541	-4	mitochondrial isocitrate dehydrogenase	0.0244
AGDE05100	-3	mitogen-activated protein kinase	0.0100	AGDE11267	-3	squalene monooxygenase-like protein	0.0246
AGDE07028	-23	conserved hypothetical protein	0.0112	AGDE07797	-4	cytosolic malate dehydrogenase	0.0252
AGDE16193	-43	hypothetical protein	0.0116	AGDE01319	-6	n-myristoyltransferase	0.0277
AGDE07816	-8	protein kinase	0.0118	AGDE08574	-33	conserved hypothetical protein	0.0278
AGDE06949	-3	fatty acid hydrolase	0.0124	AGDE07060	-95	serine threonine protein phosphatase type 5	0.0283
AGDE03376	-23	40s ribosomal protein s15	0.0127	AGDE02444	-3	conserved hypothetical protein	0.0298
AGDE01304	-25	conserved hypothetical protein	0.0140	AGDE16763	-3	ABC-type transport system	0.0313
AGDE06436	-26	conserved hypothetical protein	0.0142	AGDE07987	-3	glycosomal membrane protein	0.0317
AGDE07443	-10	hypothetical protein, unknown function	0.0142	AGDE05390	-3	carnitine	0.0328
AGDE14046	-3	folic acid/methotrexate transporter	0.0142	AGDE09947	-11	haloacid dehalogenase hydrolase	0.0329
AGDE09900	-23	chaperonin mitochondrial precursor	0.0145	AGDE05545	-4	ecotin	0.0331
AGDE00411	-17	proteasome regulatory non-atp-ase subunit	0.0145	AGDE05787	-23	u2 splicing auxiliary	0.0384
AGDE08887	-5	conserved hypothetical protein	0.0149	AGDE12335	-21	conserved hypothetical protein	0.0384
AGDE02570	-12	protein kinase	0.0155	AGDE05577	-6	conserved hypothetical protein	0.0384
AGDE04064	-5	cytochrome b-domain protein	0.0157	AGDE10917	-3	aldehyde dehydrogenase	0.0384
AGDE06428	-3	glutamamyl carboxypeptidase	0.0157	AGDE06888	-3	heat shock protein	0.0384
AGDE06369	-18	conserved hypothetical protein	0.0159	AGDE17001	-4	conserved hypothetical protein	0.0392
AGDE07859	-4	ribosomal protein l1a	0.0159	AGDE10708	-4	lathosterol oxidase-like protein	0.0395
AGDE17113	-3	rhodanese-like protein	0.0165	AGDE00061	-3	conserved hypothetical protein	0.0400
AGDE08063	-36	proteasome regulatory non-atp-ase subunit	0.0174	AGDE01243	-6	rna polymerase b subunit rpb8	0.0401
AGDE00995	-3	folate/biopterin transporter	0.0178	AGDE10382	-3	protein kinase	0.0404
AGDE06960	-6	dynein light chain	0.0192	AGDE10777	-20	conserved hypothetical protein	0.0404
AGDE00596	-3	arginase	0.0193	AGDE01232	-3	60s ribosomal protein l12	0.0420
AGDE06554	-3	nucleolar protein	0.0198	AGDE11341	-44	cytochrome c oxidase assembly protein	0.0425
AGDE07616	-3	polyprenol reductase	0.0203	AGDE06734	-26	iron superoxide dismutase	0.0457
AGDE00155	-3	dihydrolipoamide dehydrogenase	0.0204	AGDE09251	-3	enolase	0.0458
AGDE01259	-10	ras-related protein rab-14	0.0207	AGDE11134	-3	heat shock protein atpase subunit	0.0479
AGDE16806	-13	hypothetical protein	0.0212	AGDE02848	-3	acetyl- synthetase	0.0482
AGDE08085	-11	protein kinase	0.0212	AGDE11243	-3	dihydrolipoamide dehydrogenase	0.0496

AGDE: *Angomonas deanei* sequence feature (SRA Accession: PRJNA279893).



TABLE III
Differential gene expression between *Angomonas deanei* aposymbiotic (APO) and wild type (WT) strains. List of gene transcripts up regulated in APO strain

Feature ID	Fold change	Gene function (Annotation)	FDR p-value
AGDE02714	52	ribosomal protein 11a	9.2E-21
AGDE03418	340	hypothetical protein	1.8E-18
AGDE10054	77	serine peptidase	2.7E-18
AGDE04136	41	heat shock protein 100	3.2E-12
AGDE16735	7	metacaspase	4.0E-08
AGDE03792	53	mitochondrial trypanothione	1.6E-06
AGDE04435	18	conserved hypothetical protein	4.9E-06
AGDE11862	31	vacuolar protein sorting-associated protein 4	7.7E-06
AGDE16940	7	conserved hypothetical protein	3.1E-05
AGDE16861	5	hypothetical protein	4.9E-05
AGDE12000	9	protein kinase	0.0001
AGDE08977	165	conserved hypothetical protein	0.0001
AGDE09083	7	branched-chain amino acid aminotransferase	0.0002
AGDE16676	4	conserved hypothetical protein	0.0003
AGDE00528	18	conserved hypothetical protein	0.0004
AGDE05202	8	minichromosome maintenance complex	0.0004
AGDE07150	10	vacuolar protein sorting-associated protein 4	0.0005
AGDE08997	16	conserved hypothetical protein	0.0005
AGDE05706	8	ribosomal protein 11a	0.0005
AGDE11571	7	translation factor SUI1	0.0005
AGDE14375	9	circumsporozoite protein	0.0006
AGDE17158	4	hypothetical protein	0.0008
AGDE16978	7	conserved hypothetical protein	0.0013
AGDE10823	4	protein kinase	0.0018
AGDE16514	4	conserved hypothetical protein	0.0019
AGDE04133	9	udp-glucose pyrophosphorylase	0.0029
AGDE16371	4	conserved hypothetical protein	0.0035
AGDE16675	5	conserved hypothetical protein	0.0047
AGDE11076	4	propionyl-coa carboxylase beta chain	0.0048
AGDE14602	7	conserved hypothetical protein	0.0052
AGDE16372	4	conserved hypothetical protein	0.0054
AGDE10194	10	conserved hypothetical protein	0.0056
AGDE10373	26	conserved hypothetical protein	0.0069
AGDE00415	4	conserved hypothetical protein	0.0086

Feature ID	Fold change	Gene function (Annotation)	FDR p-value
AGDE16447	4	pre-mrna splicing factor	0.0088
AGDE07680	10	conserved hypothetical protein	0.0092
AGDE15874	5	ATP-binding cassette protein subfamily A	0.0132
AGDE08430	5	branched-chain amino acid aminotransferase	0.0138
AGDE15539	4	GMP synthase	0.0138
AGDE07170	3	propionyl-coa carboxylase beta chain	0.0142
AGDE16950	6	PadR family transcriptional regulator	0.0145
AGDE00082	31	dihydrolipoamide dehydrogenase	0.0149
AGDE13187	4	glycosyltransferase group 1 family	0.0149
AGDE00804	7	hypothetical protein	0.0159
AGDE16626	4	conserved hypothetical protein THERM	0.0159
AGDE04004	5	conserved hypothetical protein	0.0166
AGDE08637	4	rna polymerase ii largest subunit	0.0172
AGDE13234	3	conserved hypothetical protein	0.0178
AGDE02425	78	conserved hypothetical protein	0.0196
AGDE15579	4	conserved hypothetical protein	0.0212
AGDE04400	5	propionyl-coa carboxylase beta chain	0.0221
AGDE13758	4	nonsense mRNA reducing factor	0.0232
AGDE14376	3	conserved hypothetical protein TGME	0.0239
AGDE15677	3	conserved hypothetical protein	0.0251
AGDE08441	4	endo exonuclease mre11	0.0270
AGDE10321	4	amastin	0.0277
AGDE15693	3	conserved hypothetical protein	0.0277
AGDE13224	4	conserved hypothetical protein	0.0301
AGDE09994	23	conserved hypothetical protein	0.0325
AGDE13223	3	conserved hypothetical protein	0.0365
AGDE15197	68	conserved hypothetical protein	0.0370
AGDE03972	6	cytochrome-b5 reductase	0.0370
AGDE10457	3	hypothetical protein	0.0375
AGDE17176	7	glutamamyl carboxypeptidase	0.0384
AGDE12339	6	conserved hypothetical protein	0.0392
AGDE02016	4	conserved hypothetical protein	0.0392
AGDE16448	4	formin	0.0399
AGDE16566	3	neurohypophysial n-terminal domain containing protein	0.0401
AGDE03338	3	prostaglandin f synthase	0.0448
AGDE15358	3	hypothetical protein	0.0456
AGDE12076	3	conserved hypothetical protein	0.0500

AGDE: *Angomonas deanei* sequence feature (SRA Accession: PRJNA279893).



TABLE IV

Enrichment of genes from functional biological process category downregulated in aposymbiotic *Angomonas deanei* strain. Gene ontology (GO) terms of biological process and the number of genes involved in each function are listed according to the p-value

	Biological processes category GO terms	Description	Number of genes	p-value
1	55114	oxidation-reduction process	418	0.0000
2	15991	ATP hydrolysis coupled proton transport	75	0.0000
3	6108	malate metabolic process	16	0.0002
4	6096	glycolysis	48	0.0014
5	6099	tricarboxylic acid cycle	35	0.0026
6	6694	steroid biosynthetic process	8	0.0029
7	46034	ATP metabolic process	9	0.0051
8	6102	isocitrate metabolic process	5	0.0066
9	6561	proline biosynthetic process	6	0.0067
10	44262	cellular carbohydrate metabolic process	16	0.0090
11	7165	signal transduction	11	0.0110
12	6633	fatty acid biosynthetic process	46	0.0139
13	8654	phospholipid biosynthetic process	7	0.0219
14	6091	generation of precursor metabolites and energy	7	0.0303
15	6007	glucose catabolic process	6	0.0330
16	6166	purine ribonucleoside salvage	5	0.0370
17	6167	AMP biosynthetic process	5	0.0370
18	6544	glycine metabolic process	8	0.0397

TABLE V

Enrichment of genes from functional biological process category upregulated in aposymbiotic *Angomonas deanei* strain. Gene ontology (GO) terms of biological process and the number of genes involved in each function are listed according to the p-value

	Biological processes category GO terms	Description	Number of genes	p-value
1	6508	proteolysis	95	0.0000
2	9987	cellular process	59	0.0002
3	10506	regulation of autophagy	5	0.0002
4	9081	branched-chain amino acid metabolic process	7	0.0023
5	7018	microtubule-based movement	93	0.0032
6	8652	cellular amino acid biosynthetic process	18	0.0045
7	6270	DNA replication initiation	14	0.0045
8	44267	cellular protein metabolic process	11	0.0047
9	44237	cellular metabolic process	70	0.0054
10	6351	transcription, DNA-dependent	24	0.0169
11	6260	DNA replication	38	0.0246
12	6310	DNA recombination	10	0.0246
13	6264	mitochondrial DNA replication	5	0.0309
14	6281	DNA repair	24	0.0336
15	44260	cellular macromolecule metabolic process	8	0.0340
16	35556	intracellular signal transduction	9	0.0351
17	6139	nucleobase-containing compound metabolic process	14	0.0363
18	6400	tRNA modification	10	0.0382
19	9396	folic acid-containing compound biosynthetic process	8	0.0453