

Supplementary Table 4. Classification of more (>2 fold) expressed proteins in *AcAypAc* using clusters of orthologous groups

COG function	Accession no.	Gene function	Fold change	P-value	Included in other group
C (Energy production and conversion)	ATG94438	D-glycerate dehydrogenase	0.4	0.026	
	ATG94924	FAD-binding oxidoreductase	0.34	0.035	
	ATG96066	D-amino acid dehydrogenase	0.29	0.007	
	ATG93705	Glycerophosphodiester phosphodiesterase		*	
	ATG94865	Cytochrome-c oxidase, cbb3-type subunit I		*	
	ATG95327	Cytochrome c4		*	
	ATG96225	Methylmalonate-semialdehyde dehydrogenase (CoA acylating)		*	
	ATG94221	Fe(2+)-trafficking protein		*	O
	ATG97061	Redoxin		*	O
E (Amino Acid metabolism and transport)	ATG95126	Aspartate-semialdehyde dehydrogenase	0.47	0.004	
	ATG94307	Glycine cleavage system aminomethyltransferase T	0.38	0.001	
	ATG93205	Aminotransferase	0.32	0.009	
	ATG94308	Glycine cleavage system protein H		*	
	ATG94419	Prephenate dehydrogenase/arogenate dehydrogenase family protein		*	
	ATG95182	Tryptophan 2,3-dioxygenase		*	
	ATG96889	Branched-chain amino acid ABC transporter substrate-binding protein		*	
F (Nucleotide metabolism and transport)	ATG95391	Dihydroorotase	0.43	0.007	
	ATG93781	AAA family ATPase		*	
	ATG94528	Thymidylate kinase		*	
G (Carbohydrate metabolism and transport)	ATG96356	Type I glyceraldehyde-3-phosphate dehydrogenase	0.42	0.005	
	ATG95874	Phosphoenolpyruvate--protein phosphotransferase		*	
	ATG96638	PTS fructose transporter subunit EIIBC		*	
	ATG96676	Trehalose-phosphatase		*	
	ATG96128	NAD-dependent dehydratase		*	M
H (Translation)	ATG93863	Quinolinate synthase NadA	0.39	0.031	
	ATG95140	Pyridoxine 5'-phosphate synthase	0.35	0.016	
	ATG93712	Glutamyl-tRNA reductase		*	
	ATG93864	3-Methyl-2-oxobutanoate hydroxymethyltransferase		*	
	ATG93881	Pantetheine-phosphate adenylyltransferase		*	
	ATG95634	16S rRNA (cytidine(1402)-2'-O)-methyltransferase		*	
I (Lipid metabolism)	ATG92771	Hypothetical protein CQB05_00805		*	
	ATG93582	Acetyl/propionyl-CoA carboxylase subunit alpha		*	
	ATG94022	Alpha/beta hydrolase		*	
	ATG94067	Enoyl-CoA hydratase		*	
	ATG95418	Enoyl-CoA hydratase		*	
	ATG95630	NAD(P)-dependent oxidoreductase		*	
	ATG95244	3-Oxoacyl-ACP reductase	0.41	0.035	Q

J (Translation)	ATG93276	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD			*	
	ATG95932	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase GatCAB subunit C			*	
K (Transcription)	ATG93204	Transcription antitermination factor NusB	0.45	0.046		
	ATG94645	XRE family transcriptional regulator			*	
	ATG95148	RNA polymerase sigma factor RpoE			*	
	ATG95292	BolA family transcriptional regulator			*	
	ATG95903	MarR family transcriptional regulator			*	
	ATG94807	Bifunctional (p)ppGpp synthetase/guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase			*	T
L (Replication and repair)	ATG93660	DNA repair protein RecN	0.36	0.041		
	ATG95937	Exodeoxyribonuclease III	0.34	0.023		
	ATG92823	Single-stranded DNA-binding protein			*	
	ATG94483	Restriction endonuclease			*	
	ATG95618	ATP-dependent helicase			*	
M (Cell wall/membrane/envelop biogenesis)	ATG93815	Hypothetical protein CQB05_07060			*	
	ATG95350	Hypothetical protein CQB05_16045			*	
N (Cell motility)	ATG96977	Type VI secretion system protein TssL	0.49	0.044		
	ATG96505	Motility protein MotB			*	
	ATG96515	Flagellar cap protein FliD			*	
	ATG96524	Flagellar basal body protein FliL			*	
	ATG96526	Flagellar motor switch protein FliN			*	
	ATG96536	Chemotaxis protein CheD	0.43	0.017		T
	ATG92975	Chemotaxis protein			*	T
	ATG93157	Methyl-accepting chemotaxis protein			*	T
	ATG93438	Chemotaxis protein			*	T
	ATG93503	Methyl-accepting chemotaxis protein			*	T
	ATG93728	Type II secretion system F family protein	0.49	0.007		U
	ATG95626	Type IV pili twitching motility protein PilT	0.39	0.048		U
	ATG94949	Type IV pilus biogenesis/stability protein PilW			*	U
	ATG96719	Type II secretion system F family protein			*	U
	O (post-translational modification, protein turnover, and chaperones)	ATG94899	Type VI secretion system ATPase TssH	0.36	0	
ATG93010		NrdH-redoxin			*	
ATG95167		2-Oxoglutarate-dependent dioxygenase			*	
ATG95959		DNA repair protein RadA			*	
P (Inorganic ion transport and metabolism)	ATG92889	Superoxide dismutase family protein			*	
	ATG92932	Sulfate ABC transporter ATP-binding protein			*	
	ATG93703	sn-glycerol-3-phosphate import ATP-binding protein UgpC			*	
Q (Secondary Structure)	ATG96058	Glucan biosynthesis protein D			*	
	ATG95299	Outer membrane lipid asymmetry maintenance protein MlaD			*	

S (Function Unknown)	ATG94909	Type VI secretion system baseplate subunit TssK	0.21	0.016	
	ATG92737	Phosphohydrolase		*	
	ATG92865	Hypothetical protein CQB05_01415		*	
	ATG92904	Molybdopterin-dependent oxidoreductase		*	
	ATG92939	NADPH-dependent oxidoreductase		*	
	ATG93416	DUF4124 domain-containing protein		*	
	ATG93552	Hypothetical protein CQB05_05450		*	
	ATG93564	Type VI secretion system tip protein VgrG		*	
	ATG93852	DUF3460 domain-containing protein		*	
	ATG94227	DUF934 domain-containing protein		*	
	ATG94529	Aminodeoxychorismate lyase		*	
	ATG94628	DUF2158 domain-containing protein		*	
	ATG94901	Type VI secretion system baseplate subunit TssF		*	
	ATG94931	Hypothetical protein CQB05_13580		*	
	ATG95339	Peptidoglycan-binding protein		*	
	ATG95746	Hypothetical protein CQB05_18345		*	
	ATG95747	Type VI secretion system tip protein VgrG		*	
	ATG95938	2,5-Didehydrogluconate reductase DkgB		*	
	ATG96156	DUF3297 domain-containing protein		*	
	ATG96185	Hypothetical protein CQB05_20895		*	
	ATG96283	Hypothetical protein CQB05_21490		*	
	ATG96433	Tripartite tricarboxylate transporter substrate binding protein		*	
	ATG96440	Methyl-accepting chemotaxis protein		*	
	ATG96794	Hydroxyacylglutathione hydrolase		*	
	ATG97072	Hypothetical protein CQB05_19925		*	
	T (Signal Transduction)	ATG96504	Chemotaxis protein CheY	0.48	0.017
		ATG96412	Two-component system response regulator	0.43	0
ATG94313		Universal stress protein	0.41	0.021	
ATG96273		FHA domain-containing protein	0.31	0.017	
ATG95433		Sigma-54-dependent Fis family transcriptional regulator		*	
ATG96411		PAS domain-containing sensor histidine kinase		*	
U (Intracellular trafficking and secretion)	ATG96659	Carbon starvation protein A		*	
	ATG92916	MotA/TolQ/ExbB proton channel family protein		*	

Asterisks indicates that the protein is only detected in AcΔYppAc.