

Supplementary Table 3. Classification of more (>2 fold) expressed proteins in *Acidovorax citrulli* (*Ac*) using clusters of orthologous groups

COG function	Accession no.	Gene function	Fold change	P-value	Included in other group
C (Energy production and conversion)	ATG94299	Catalase		*	
	ATG96545	Acyl-CoA dehydrogenase		*	
	ATG96540	Isovaleryl-CoA dehydrogenase	2.2	0.05	
E (Amino Acid metabolism and transport)	ATG93315	DNA-binding protein YbiB		*	
	ATG93779	ImmA/IrrE family metallo-endopeptidase		*	
	ATG94324	Pyridoxal phosphate-dependent aminotransferase		*	
	ATG95965	ABC transporter substrate-binding protein		*	
	ATG96931	ABC transporter substrate-binding protein		*	
F (Nucleotide metabolism and transport)	ATG94739	Glutathione ABC transporter substrate-binding protein GsiB	2.06	0.01	
	ATG93517	Phosphoribosylglycinamide formyltransferase		*	
G (Carbohydrate metabolism and transport)	ATG93526	C4-dicarboxylate ABC transporter substrate-binding protein		*	
H (Coenzyme transport and metabolism)	ATG94575	Di-trans,poly-cis-decaprenylcistransferase		*	
	ATG95464	Phosphomethylpyrimidine synthase ThiC		*	
	ATG93694	Bifunctional demethylmenaquinone methyltransferase/2-methoxy-6-polyprenyl-1,4-benzoquinol methylase UbiE	2.03	0.048	
I (Lipid metabolism)	ATG92720	NAD(P)-dependent oxidoreductase		*	Q
	ATG92960	Acetyl/propionyl/methylcrotonyl-CoA carboxylase subunit alpha		*	
	ATG96554	Methylcrotonoyl-CoA carboxylase		*	
J (Translation)	ATG94018	Transcription elongation factor GreAB		*	
	ATG93713	Peptide chain release factor 1	3.62	0.014	
K (Transcription)	ATG93642	DNA-directed RNA polymerase subunit omega		*	
	ATG94247	Crp/Fnr family transcriptional regulator		*	
	ATG95003	LysR family transcriptional regulator		*	
	ATG96167	ATP-dependent DNA helicase DinG		*	L
	ATG96436	Peptidase		*	
M (Cell wall/membrane/envelop biogenesis)	ATG96918	DNA-binding response regulator		*	T
	ATG92779	Disulfide isomerase		*	
	ATG92997	Penicillin-binding protein 1A		*	
	ATG94038	Cell shape determination protein CcmA		*	
	ATG94182	D-(-)-3-hydroxybutyrate oligomer hydrolase		*	
	ATG94734	Aspartate/glutamate racemase family protein		*	
	ATG94988	Phospholipase C, phosphocholine-specific		*	
N (Cell motility)	ATG96146	Efflux RND transporter periplasmic adaptor subunit		*	
	ATG94052	Glycosyltransferase family 2 protein	2.53	0.043	
	ATG95814	Methyl-accepting chemotaxis protein		*	T
	ATG97121	Flagellar biosynthesis protein FlgI		*	

O	ATG94269	[protein-PII] uridylyltransferase		*
(post-translational modification, protein turnover, and chaperones)				
P	ATG92949	Multidrug efflux RND transporter permease subunit		*
(Inorganic ion transport and metabolism)	ATG94056	Amino acid ABC transporter permease		*
	ATG94394	ABC transporter ATP-binding protein		*
	ATG95656	ABC transporter ATP-binding protein		*
S	ATG92674	Type VI secretion system tip protein VgrG		*
(Function Unknown)	ATG93469	Tripartite tricarboxylate transporter substrate binding protein BugE		*
	ATG94886	TIGR00645 family protein		*
	ATG95338	Hypothetical protein CQB05_15975		*
	ATG95817	Lipopolysaccharide transport periplasmic protein LptA		*
	ATG95978	Type VI secretion system tip protein VgrG		*
	ATG96124	Peptidoglycan-binding protein		*
	ATG96336	Hypothetical protein CQB05_21800		*
	ATG96471	Methyl-accepting chemotaxis protein		*
	ATG96538	ABC transporter ATP-binding protein		*
	ATG97021	General secretion pathway protein GspN		*
	ATG93161	Phosphoesterase	2.51	0.048
	ATG94314	Hypothetical protein CQB05_09930	2.45	0.008
	ATG97084	Hypothetical protein CQB05_20725	2.38	0.004
U	ATG95501	Peptidoglycan-binding protein		*
(Intracellular trafficking and secretion)	ATG96307	Preprotein translocase subunit YajC		*
V	ATG95000	AcrB/AcrD/AcrF family protein		*
(Defense mechanisms)				

Asterisks indicates that the protein is only detected in Ac.