

**Supplementary Table 6.** Classification of highly expressed (>2 fold) proteins in MBMA compared with HMM by clusters of orthologous groups

COG function	Accession no.	Gene function	Fold change	<i>P</i> -value	Included in other group
C (Energy production and conversion)	QKZ07892	Mannitol-1-phosphate 5-dehydrogenase	-	-	-
	QKZ07901	Mannitol dehydrogenase family protein	-	-	-
	QKZ09552	Gallate dioxygenase	-	-	-
	QKZ09729	FAD-binding oxidoreductase	-	-	-
	QKZ10463	Sorbitol-6-phosphate dehydrogenase	-	-	-
	QKZ10832	Glutaredoxin 3	-	-	-
	QKZ09590	D-amino acid dehydrogenase	6.25	0.009628918	-
	QKZ10814	Ferredoxin--NADP(+) reductase	5.59	0.000556291	-
	QKZ09900	Phosphate acetyltransferase	3.42	6.28376E-05	-
	QKZ09179	NAD(P)/FAD-dependent oxidoreductase	2.75	0.003071567	-
	QKZ09474	2-Hydroxyacid dehydrogenase	2.25	0.011850534	-
	QKZ08555	NADPH-dependent assimilatory sulfite reductase flavoprotein subunit	2.20	0.03415209	-
E (Amino acid metabolism and transport)	QKZ08360	Amidino transferase	-	-	-
	QKZ08410	Ornithine decarboxylase	-	-	-
	QKZ09346	Lactoylglutathione lyase	-	-	-
	QKZ10187	D-Glycero-beta-D-manno-heptose 1,7-bisphosphate 7-phosphatase	-	-	-
	QKZ10683	Homoserine O-succinyltransferase	8.11	2.78497E-05	-
	QKZ10797	Bifunctional aspartate kinase/homoserine dehydrogenase II	4.83	0.047121557	-
	QKZ10796	Methylenetetrahydrofolate reductase	3.32	0.000166556	-
	QKZ10798	Cystathionine gamma-synthase	2.15	0.02840569	-
QKZ08617	3-Deoxy-7-phosphoheptulonate synthase	2.04	0.044430156	-	
F (Nucleotide metabolism and transport)	QKZ09325	Kinase/pyrophosphorylase	-	-	-
	QKZ09814	Cytidine deaminase	-	-	-
	QKZ10109	NAD(+) kinase	-	-	-
	QKZ10223	dGTPase	-	-	-
	QKZ10378	Inosine/xanthosine triphosphatase	-	-	-
	QKZ10048	Glutamine-hydrolyzing GMP synthase	2.73	0.004043702	-
	QKZ10049	IMP dehydrogenase	2.65	0.002241629	-
	QKZ09899	Acetate kinase	2.36	0.005160779	-
QKZ10372	Homoserine kinase	2.28	0.035368125	-	
G (Carbohydrate metabolism and transport)	QKZ07884	Sugar ABC transporter ATP-binding protein	-	-	-
	QKZ08033	Glycogen phosphorylase	-	-	-
	QKZ08066	Phosphoglycolate phosphatase	-	-	-
	QKZ08852	Aldolase	-	-	-
	QKZ09306	Fructosamine kinase family protein	-	-	-
	QKZ09985	Phosphocarrier protein Hpr	-	-	-
	QKZ10464	PTS glucitol/sorbitol transporter subunit IIA	-	-	-
QKZ10465	PTS glucitol/sorbitol transporter subunit IIB	-	-	-	

	QKZ10466	Glucitol/sorbitol permease IIC component	-	-	-
	QKZ07886	Sugar ABC transporter substrate-binding protein	3.40	0.010164031	-
	QKZ10931	Glycoside hydrolase family 68 protein	2.73	0.000269996	-
	QKZ07893	PTS mannitol transporter subunit IICBA	2.40	0.000542532	-
H (Coenzyme metabolism)	QKZ08652	Methylthioribulose 1-phosphate dehydratase	-	-	-
	QKZ08859	Lipoyl synthase	-	-	-
	QKZ09773	Glucose-1-phosphate thymidyltransferase RfbA	-	-	-
	QKZ09918	Bifunctional tetrahydrofolate synthase/dihydrofolate synthase	-	-	-
	QKZ10545	Bifunctional ADP-dependent NAD(P)H-hydrate dehydratase/ NAD(P)H-hydrate epimerase	-	-	-
	QKZ10713	Bifunctional biotin--[acetyl-CoA-carboxylase] ligase/biotin operon repressor BirA	-	-	-
	QKZ10951	tRNA dihydrouridine synthase DusB	-	-	-
	QKZ10970	Uroporphyrinogen-III C-methyltransferase	-	-	-
	QKZ11089	Bifunctional phosphopantothenoylcysteine decarboxylase/phospho- pantothenate--cysteine ligase CoaBC	-	-	-
	QKZ10219	Bifunctional uridylyltransferase/uridylyl-removing protein GlnD	2.75	0.029393695	-
I (Lipid me- tabolism)	QKZ09161	Phosphate acyltransferase PlsX	-	-	-
	QKZ09439	Carboxylesterase/lipase family protein	-	-	-
J (Translation)	QKZ08105	50S ribosomal protein L23	-	-	-
	QKZ08566	tRNA pseudouridine(13) synthase TruD	-	-	-
	QKZ08867	Ribosome silencing factor	-	-	-
	QKZ09215	tRNA 2-thiouridine(34) synthase MnmA	-	-	-
	QKZ09529	Threonylcarbamoyl-AMP synthase	-	-	-
	QKZ09604	RidA family protein	-	-	-
	QKZ08655	S-methyl-5-thioribose-1-phosphate isomerase	3.10	0.018603451	-
		QKZ08764	P-II family nitrogen regulator	-	-
K (Transcrip- tion)	QKZ09740	Lrp/AsnC family transcriptional regulator	-	-	-
	QKZ10178	Transcriptional repressor MprA	-	-	-
	QKZ10734	HTH-type transcriptional regulator MetR	-	-	-
	QKZ08233	DEAD/DEAH box helicase	-	-	L
	QKZ09662	Chemotaxis response regulator CheY	2.84	0.004442898	T
	QKZ10881	Bifunctional GTP diphosphokinase/guanosine-3',5'-bis pyrophos- phate 3'-pyrophosphohydrolase	2.24	0.019934822	T
L (Replication and repair)	QKZ08523	Exodeoxyribonuclease V subunit gamma	-	-	-
	QKZ08781	DNA polymerase III subunit gamma/tau	-	-	-
	QKZ10652	Replicative DNA helicase	-	-	-
	QKZ10744	DNA helicase II	2.68	0.047390726	-

M (Cell wall/ membrane/en- velop biogen- esis)	QKZ08382	Type III secretion inner membrane ring lipoprotein SctJ	□-	-□	□-	
	QKZ08477	Bifunctional protein-disulfide isomerase/oxidoreductase DsbC	□-	-□	□-	
	QKZ08516	Prolipoprotein diacylglyceryl transferase	□-	-□	□-	
	QKZ08599	Lytic murein transglycosylase B	□-	-□	□-	
	QKZ08834	TonB-dependent receptor	□-	-□	□-	
	QKZ08865	Peptidoglycan DD-transpeptidase MrdA	□-	-□	□-	
	QKZ09129	LpxL/LpxP family Kdo(2)-lipid IV(A) lauroyl/palmitoleoyl acyl- transferase	□-	-□	□-	
	QKZ09398	TonB-dependent receptor	□-	-□	□-	
	QKZ09703	Lipoprotein	□-	-□	□-	
	QKZ09777	Colanic acid biosynthesis glycosyltransferase WcaL	□-	-□	□-	
	QKZ09787	Undecaprenyl-phosphate galactose phosphotransferase WbaP	□-	-□	□-	
	QKZ10191	Rcs stress response system protein RcsF	□-	-□	□-	
	QKZ10550	Miniconductance mechanosensitive channel MscM	□-	-□	□-	
	QKZ10741	Phospholipase A	□-	-□	□-	
	QKZ10764	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	□-	-□	□-	
	QKZ11074	N-acetylmuramoyl-L-alanine amidase AmiB	□-	-□	□-	
	QKZ11006	Porin	4.03	0.007519071	□-	
	QKZ10460	KpsF/GutQ family sugar-phosphate isomerase	2.72	0.01179005	□-	
	N (Cell motility)	QKZ09148	Flagellar hook protein FlgE	□-	-□	□-
		QKZ09191	Flagellar motor switch protein FliM	□-	-□	□-
QKZ09669		Flagellar motor stator protein MotA	□-	-□	□-	
QKZ09663		Chemotaxis response regulator protein-glutamate methyltransferase	□-	-□	T	
QKZ09667		Chemotaxis protein CheW	□-	-□	T	
QKZ10517		Tar ligand binding domain-containing protein	3.77	0.000455328	T	
QKZ09438		Tar ligand binding domain-containing protein	3.56	0.000613854	T	
QKZ11025		Chemotaxis protein CheA	3.36	0.006526724	T	
QKZ09666		Tar ligand binding domain-containing protein	2.24	0.014878652	T	
QKZ08369		FliM/FliN family flagellar motor switch protein	□-	-□	U	
QKZ08387	Type III secretion system outer membrane ring subunit SctC	3.96	0.035792497	U		
O (Post-transla- tional modifi- cation, protein turnover, chaperone functions)	QKZ07866	Heat shock chaperone IbpA	□-	-□	-□	
	QKZ08175	Outer membrane-stress sensor serine endopeptidase DegS	□-	-□	-□	
	QKZ10772	Peptidylprolyl isomerase PpiC	□-	-□	-□	
P (Inorganic ion transport and metabolism)	QKZ10007	Multidrug efflux RND transporter permease AcrD	□-	-□	-□	
	QKZ08083	Taurine ABC transporter substrate-binding protein	4.13	0.000170442	□-	
Q	QKZ09421	L-tyrosine/L-tryptophan isonitrile synthase family protein	□-	-□	□-	
	QKZ08086	Taurine dioxygenase	7.19	0.026116547	□-	
S	QKZ08094	Transcriptional regulator	□-	-□	□-	
	QKZ08239	Ribonuclease E inhibitor RraB	□-	-□	□-	

	QKZ08357	C-lysozyme inhibitor	□-	-□	□-
	QKZ08391	Type III secretion system chaperone	□-	-□	□-
	QKZ08396	CesT family type III secretion system chaperone	□-	-□	□-
	QKZ08605	Fructose-1-phosphate/6-phosphogluconate phosphatase	□-	-□	□-
	QKZ09062	Hypothetical protein HU055_06640	□-	-□	□-
	QKZ09397	Hypothetical protein HU055_08490	□-	-□	□-
	QKZ09778	Colanic acid biosynthesis pyruvyl transferase WcaK	□-	-□	□-
	QKZ10052	Hypothetical protein HU055_12180	□-	-□	-□
	QKZ10487	DUF1090 domain-containing protein	□-	-□	-□
	QKZ10649	YjbQ family protein	□-	-□	-□
	QKZ10820	PhzF family phenazine biosynthesis protein	□-	-□	-□
	QKZ08144	Gamma carbonic anhydrase family protein	3.90	0.006853587	□-
	QKZ08664	Esterase FrsA	2.75	0.00658637	□-
	QKZ10890	Glucose-1-phosphatase	2.53	0.011227181	□-
	QKZ07927	Insulinase family protein	2.13	0.017701158	□-
T	QKZ09199	Chemotaxis protein CheV	□-	-□	□-
	QKZ08515	Phosphoenolpyruvate--protein phosphotransferase	2.07	0.009642555	□-

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HMM, hrp inducing media; MABA, amylovoran inducing media.