

Table S2: Methanobactin-mediated cellular genes, and the physical protein-protein interactions (PPIs) between the methanobactin synthesis cassette genes (*mbnB* and *mbnC*), MMOs and other enriched genes.

Gene ID/ ORF	Gene name	UNIPROT ID	Protein names	Function	GO term (Cellular Location)	GO term (Biological Process)	GO term (Molecular Process)
Transport system/ signal transduction							
CQW49_16885	NA	A0A2D2D2Z0	Efflux transporter periplasmic adaptor subunit	Tripartite efflux assemblies	NA	NA	NA
CQW49_11995	<i>LptC</i>	A0A2D2D0J1	LPS export ABC transporter periplasmic protein	Tripartite efflux assemblies	GO:0005887	NA	GO:0015221
CQW49_12590	NA	A0A2D2D0V5	Apolipoprotein acyltransferase	Nutrient uptake/ signal transduction/ adhesion	GO:0042157 GO:0006869	GO:0016021 GO:0005576	GO:0008289 GO:0016746
CQW49_01190	NA	A0A2D2CV99	Cytochrome c	Electron transfer and energy transduction			GO:0020037 GO:0009055
CQW49_18585	NA	A0A2D2D697	Cytochrome b	Electron transfer and energy transduction	GO:0022904	GO:0016021	
CQW49_03150	NA	A0A2D2CW27	Symporter-like protein	Transport of two different molecules across the cell membrane in the same direction	NA	GO:0016021	GO:0022857
CQW49_19365	NA	A0A2D2D4B1	Porin	Passive diffusion of selective molecules across the membrane	NA	NA	NA
CQW49_15440	NA	A0A2D2D294	Permease	Catalyzes the transport of substance	NA	GO:0016021	NA

				across the membrane		GO:0005886	
Cell wall biosynthesis/regulation/degradation							
CQW49_00125	NA	A0A2D2CUV8	CDP-alcohol phosphatidyltransferase	Biosynthesis	NA	GO:0016021	GO:0016740
							GO:0008955
CQW49_13240	NA	A0A2D2D5S9	Peptidoglycan glycosyltransferase	Shape/ size/ protection	GO:0009252	GO:0016021	GO:0008658
							GO:0004180
CQW49_15485	NA	A0A2D2D281	Peptidoglycan-binding protein	Degradation	NA	NA	NA
Methanobactin genes							
CQW49_19010	<i>mbnT</i>	A0A2D2D407	TonB-dependent receptor	substrate-specific transport across the outer membrane	NA	GO:0009279	NA
CQW49_07140	<i>mbnH</i>	A0A2D2CY67	Metallo-mystery pair system four-Cys motif protein	Copper homeostasis	NA	NA	NA
CQW49_16895	<i>mbnM</i>	A0A2D2D5Z2	TolC family protein	Export mechanism (multidrug resistance efflux pump)	NA	NA	GO:0015562
CQW49_16840	NA	A0A2D2D311	RNA polymerase subunit sigma-24	Efficient binding of RNA to promoter and regulates transcription	GO:0006352	NA	GO:0003677 GO:0016987
CQW49_09150	NA	A0A2D2CZ69	Class I SAM-dependent methyltransferase	Transfer of methyl groups	GO:0032259	NA	GO:0008168
CQW49_07150	<i>mbnM</i>	A0A2D2CY63	Multidrug resistance protein NorM	Export of substances across the membrane	NA	GO:0016021	GO:0042910 GO:0015297

CQW49_07145	<i>mbnN</i>	A0A2D2CYG3	Aminotransferase class I and II	Mbn production	GO:0009058	NA	GO:0008483 GO:0030170
Methane monooxygenases							
CQW49_01225	<i>pmoB</i>	A0A2D2D5S7	Methane monooxygenase/ammonia monooxygenase subunit B	Methane oxidation	NA	GO:0016021	GO:0004497
CQW49_01220	<i>pmoA</i>	A0A2D2D011	Methane monooxygenase/ammonia monooxygenase subunit A	Methane oxidation	NA	GO:0016021	GO:0004497
CQW49_19210	<i>pmoC</i>	A0A2D2D657	Methane monooxygenase/ammonia monooxygenase subunit C	Methane oxidation	NA	GO:0016021	GO:0004497
CQW49_12480	<i>mmoX</i>	A0A2D2D5X0	Methane monooxygenase component A alpha chain	Methane oxidation	GO:0006725	NA	GO:0004497
CQW49_12470	<i>mmoB</i>	A0A2D2D0T8	Methane monooxygenase regulatory protein B	Regulator of electron flow through the soluble mmo complex/switching the enzyme from oxidase to hydroxylase	GO:0006725	NA	GO:0004497
CQW49_12460	<i>mmoD</i>	A0A2D2D0X7	Soluble methane monooxygenase-binding protein MmoD	Conformational changes within the hydroxylase catalytic center	NA	NA	GO:0004497
CQW49_12475	<i>mmoR</i>	A0A2D2D5X7	Methane monooxygenase reductase subunit	shuttles electrons from NADH to the active site of hydroxylase	GO:0006725	NA	GO:0016709
Copper-associated							

CQW49_01240	<i>copD</i>	A0A2D2CV13	Copper resistance protein	Putative involvement in copper uptake	GO:0006825	GO:0005886	GO:0046872
CQW49_20210		A0A2D2D4L4				GO:0042597	GO:0020037
CQW49_02930	<i>copC</i>	A0A2D2D5A2	Copper resistance protein	Putative involvement in copper uptake	GO:0046688 GO:0006825	GO:0042597	GO:0005507
Hypothetical genes / domain containing genes¹							
CQW49_18195	NA	A0A2D2D3P3	Uncharacterized protein	NA	NA	GO:0016021	NA
CQW49_17470	NA	A0A2D2D3N0	MaoC-like domain-containing protein	NA	NA	NA	NA
CQW49_16865	NA	A0A2D2D3D0	GSCFA domain-containing protein	NA	NA	NA	NA
CQW49_16540	NA	A0A2D2D367	Uncharacterized protein	NA	NA	GO:0016021	NA
CQW49_16090	NA	A0A2D2D2J0	Uncharacterized protein	NA	NA	NA	NA
CQW49_14355	NA	A0A2D2D1T4	DGQHR domain-containing protein	NA	NA	NA	NA
CQW49_02010	NA	A0A2D2CVS6	DUF2232 domain-containing protein	NA	NA	GO:0016021	NA
CQW49_12920	NA	A0A2D2D107	Uncharacterized protein	NA	NA	NA	NA
CQW49_12835	NA	A0A2D2D1C4	Uncharacterized protein	NA	NA	GO:0016021	NA
CQW49_11915	NA	A0A2D2D0I2	Uncharacterized protein	NA	NA	NA	NA
CQW49_11245	NA	A0A2D2D096	Uncharacterized protein	NA	NA	GO:0016021	NA

CQW49_01770	NA	A0A2D2CV C1	DUF2147 domain- containing protein	NA	NA	NA	NA
CQW49_10090	NA	A0A2D2CZ P3	YIP1 family protein	NA	NA	GO:0016021	NA
CQW49_09945	NA	A0A2D2CZ H7	Uncharacteriz ed protein	NA	NA	NA	NA
CQW49_08865	NA	A0A2D2CZ B0	NfeD domain- containing protein	NA	NA	GO:0016021	NA
CQW49_06205	NA	A0A2D2CX U2	SPOR domain- containing protein	NA	NA	NA	GO:0042834
CQW49_06135	NA	A0A2D2CX S9	DUF2336 domain- containing protein	NA	NA	NA	NA
CQW49_00040	NA	A0A2D2CU X7	DUF202 domain- containing protein	NA	NA	GO:0016021	NA

Note: More details are included in text under section 3.5. ¹Their roles need to be validated experimentally.