

Figure S1: Naphthol concentration calibration curve at wavelength of 540 nm

Figure S2: RNA gel-electrophoresis image

Figure S3: Bioanalyzer RNA gel-electrophoresis image

Table S1: The specific growth rate (μ , day⁻¹), and the doubling time (t_d , days) for each individual concentration. All standard deviations are within 5% of the μ_{\max} (day⁻¹).

Days	Specific growth rate (μ , day ⁻¹)					Doubling time (t_d , days)				
	0 μM	3 μM	5 μM	6 μM	10 μM	0 μM	3 μM	5 μM	6 μM	10 μM
0	-0.10	-0.08	-0.22	-0.14	-0.03	NA	NA	NA	NA	NA
1	0.11	0.15	0.13	0.20	0.31	NA	NA	NA	NA	NA
2	0.24	0.27	0.35	0.41	0.53	NA	NA	NA	1.67 (40 hours)	1.30 (31 hours)
3	0.31	0.30	0.38	0.38	0.38	2.25 (54 hours)	2.32 (56 hours)	1.80 (43 hours)	NA	NA
4	0.22	0.23	0.30	0.28	0.27	NA	NA	NA	NA	NA
5	0.17	0.19	0.23	0.22	0.23	NA	NA	NA	NA	NA
6	0.14	0.14	0.18	0.16	0.15	NA	NA	NA	NA	NA
7	0.10	0.10	0.13	0.12	0.11	NA	NA	NA	NA	NA
8	0.05	0.05	0.08	0.07	0.06	NA	NA	NA	NA	NA
9	0.00	-0.01	0.03	0.01	0.00	NA	NA	NA	NA	NA
10	-0.07	-0.08	-0.04	-0.07	-0.08	NA	NA	NA	NA	NA

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 across the	NA	GO:0016021 GO:0005886	NA

membrane

Cell wall biosynthesis/regulation/degradation							
CQW49_00125	NA	A0A2D2CUV8	CDP-alcohol phosphatidyltransferase	Biosynthesis	NA	GO:0016021	GO:0016740
CQW49_13240	NA	A0A2D2D5S9	Peptidoglycan glycosyltransferase	Shape/ size/ protection	GO:0009252	GO:0016021	GO:0008955 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>	A0A2D2CY	Aminotransferase	Mbn	GO:0009058	NA	GO:0008483

G3 ase class I and production GO:0030170
II

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>	A0A2D2D6S7	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>	A0A2D2CV	Copper resistance	Putative involvement in	GO:0006825	GO:0005886	GO:0046872

CQW49_20210		13	protein	copper uptake		GO:0042597	GO:0020037
		A0A2D2D4L4				GO:0016021	GO:0009055
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.

Table S3: StringDb enrichment statistics (Excel file)

Table S4: Network analysis between the enriched genes (Excel file)

Table S5: Forward and reverse primers of gene sets used in expression studies.

Operon	Gene Id	Gene names	Protein accession ID	Primer name	qPCR Primer sequence (5'→ 3')
sMMO	NA	<i>mmoX</i>	CAA39068.2	Forward	TGGAGTGCTCGGTCAATCTG
				Reverse	GACACCACGGTCTGGTAGCC
	NA	<i>mmoR</i>	CAD61955.1	Forward	GACCGCTCTGCGCAAAGCC
				Reverse	CCCTCATAGCCGAACAATTCG
pMMO	NA	<i>mmoC</i>	CAB45257.1	Forward	AGGAGGAGGACGGCAAGGTT C
				Reverse	AGCACGAGACGCACGACATT GG
	NA	<i>pmo operon</i>	U31650.2	Forward	GCGTTCTTCTCGGGCTTCG
				Reverse	CGGCCTCACTCGTCTTCTCC
pMMO	NA	<i>pmoA</i>	AAA87220.2	Forward	TGCTGATCGGGGAGTGGATC
				Reverse	ACGTGCGGACGAAGTGGAA
	NA	<i>pmoB</i>	AAF37894.1	Forward	ACATGGCCGACTTCAAGGATC C
				Reverse	TCGCTGATGCGAAGATAAGAA CG
pMMO	NA	<i>pmoC</i>	AAF37893.1	Forward	TGGAAGACCCGTGACCGC
				Reverse	ATGTGCGACGGCGTGAAGT
<i>Mbn</i> operon (methanobactin)	CQW49_07125	NA	ATQ67685.1	Forward	AGGAAATCGACATCTGCGCT
				Reverse	GGAGATTGCAATTCGGCTCG
	CQW49_07130	NA	ATQ67686.1	Forward	FCCGCAGATCCGCCATATGAT
				Reverse	ATACGCAGATACGCCTGTCTG
	CQW49_07135	NA	ATQ67687.1	Forward	CATAGCGGCTGTCTGAAGGAA
				Reverse	GCCAATAAGGCGGAGATCGT
	CQW49_07140	NA	ATQ67688.1	Forward	AGAGAATATCGGCGAGACGC
				Reverse	TTTGACGACGCTGTTCGAGA
	CQW49_07175	NA	ATQ67694.1	Forward	GCAAATTCGGATCGGCGAAA
				Reverse	CGAGCAGAGCTCCTATGACG
	CQW49_07180	NA	ATQ67695.1	Forward	GTAGAGGATGAACGCCTCGC
				Reverse	CAATTGCCTCGTCTTCGGTG
<i>Mbn</i> operon (methanobactin)	CQW49_07120	NA	ATQ67684.1	Forward	GTGAGAGCCTGACGTTCTC
				Reverse	GCAATCACCAGAAACGCTCC
	CQW49_07160	<i>mbnB</i>	ATQ70273.1	Forward	AGGGGAAAATATCGCGCAGT
				Reverse	AGGACACGCTCGATTTCTG
	CQW49_07155	<i>mbnC</i>	ATQ67691.1	Forward	AAAGCTCCAGTCGAAAGCGA
				Reverse	TATCAGCCTTCGGGCCTACT
	NA	<i>mbnA</i>	From literature	Forward	TGGAAACTCCCTTAGGAGGAA
				Reverse	CTGCACGGATAGCACGAAC
	CQW49_07170	<i>TonB</i>	ATQ67693.1	Forward	GTAGAGGATGAACGCCTCGC
				Reverse	GCAATCACCAGAAACGCTCC
Reference gene	CQW49_06935	16S rRNA	ATQ67650.1	Forward	TAGGCGGATTGTTAAGTCAGG
				Reverse	ATTTACCTCTACACTCGCAG

NA: Not Applicable

Note: The complete genome of *Methylosinus trichosporium* OB3b for the primer designing of the gene set was retrieved from the GenBank accession ID: CP023737.1.