Supplementary File 6. Spectral count (S.c.) statistics for proteins involved in central metabolism of *Methylobacillus flagellatus*

Gene name (Mfla identifier)	Protein/ function	S.c. ratio MA/ Me (log2)	S.c. Sum (log2)	Raw counts MA	Raw counts Me
Methanol oxidation					
mxaF (mfla_2044)	MDH large subunit	0.527	12.931	2885	2837
mxaJ (mfla_2043)	essential for MDH function	0.290	9.510	252	297
mxaG (mfla_2042)	cytochrome, electron acceptor from MDH	-0.622	8.679	104	225
mxaI (mfla_2041)	MDH small subunit	2.365	6.763	44	27
mxaR (mfla_2040)	unknown	0.181	9.019	176	222
mxaS (mfla_2039)	unknown	1.882	5.936	30	11
mxaA (mfla_2038)	essential for Ca^{2+} insertion into MDH	0.347	6.590	35	39
mxaC (mfla_2037)	essential for Ca^{2+} insertion into MDH	1.057	5.433	20	11
mxaK (mfla_2036)	essential for Ca^{2+} insertion into MDH	-0.013	5.537	14	21
mxaL (mfla_2035)	essential for Ca^{2+} insertion into MDH	1.402	5.983	28	15
mxaD (mfla_2034)	unknown	-1.144	8.729	83	263
xoxF (mfla_2314)	MxaF homolog	1.724	6.345	38	16
xoxJ (mfla_2313)	MxaJ homolog	0.639	5.992	24	22
xoxG (mfla_2312)	MxaG homolog	0.733	5.075	12	11
mfla_344	MxaF homolog	3.274	3.763	7	1
mfla_1451	MxaF homolog	-	-	-	-
mfla_1450	MxaG homolog	-	-	-	-
mfla_1717	MxaF homolog	0.418	3.776	4	6
Pyrroloquinoline quinone (PQQ) biosynthesis					
pqqA (mfla_0021)	PQQ synthesis	-	-	-	-
pqqB (mfla_1683)	PQQ synthesis	-0.836	5.643	12	27
pqqC (mfla_1682)	PQQ synthesis	-1.249	7.653	43	120
pqqD (mfla_1681)	PQQ synthesis	-0.577	3.852	2	9
pqqE (mfla_1680)	PQQ synthesis	0.008	5.437	13	19
pqqF (mfla_0734)	PQQ synthesis	-0.099	8.708	196	125

pqqG (mfla_0735)	PQQ synthesis	0.687	8.247	114	116
Methylamine oxidation (methylamine dehydrogenase, MADH)					
mauF (mfla_0547)	unknown	-	-	-	-
mauB (mfla_0548)	MADH large subunit	6.529	12.602	3830	59
mauE (mfla_0549)	essential for small subunit maturation	-	4.691	18	-
mauD (mfla_0550)	essential for small subunit maturation	6.716	10.047	671	5
mauA (mfla_0551)	MADH small subunit	-	7.785	140	-
mauG (mfla_0552)	TTQ biosynthesis	-	7.524	115	-
mauL (mfla_0553)	unknown	-	-	-	-
mauM (mfla_0554)	unknown	-	5.720	31	-
mauN (mfla_0555)	unknown	-	3.720	7	-
azu (mfla_0556)	electron acceptor from MADH	4.723	8.239	184	5
Methylamine oxidation (N-methylglutamate pathway)					
mgdA (mfla_0452)	N-methylglutamate DH sub. A	5.132	8.427	19	-
mgdB (mfla_0453)	N-methylglutamate DH sub. B	-	3.621	7	-
mgdC (mfla_0454)	N-methylglutamate DH sub. C	6.159	7.581	112	1
mgdD (mfla_0455)	N-methylglutamate DH sub. D	-	4.302	11	-
gma (mfla_0456)	γ-glutamylmethylamide synthase	4.597	7.451	100	4
mgsA (mfla_0457)	N-methylglutamate synthase sub. A	5.132	8.427	203	4
mgsB (mfla_0458)	N-methylglutamate synthase sub. B	-	6.812	65	-
mgsC (mfla_0459)	N-methylglutamate synthase sub. C	4.429	8.631	226	12
H_4MPT-linked formaldehyde oxidation					
fhcB (mfla_1662)	Fhc, subunit B	-0.140	8.467	106	171
fhcA (mfla_1663)	Fhc, subunit A	0.265	9.594	267	310
fhcD (mfla_1664)	Fhc, subunit D	0.163	8.426	114	148
fhcC (mfla_1665)	Fhc, subunit C	0.624	9.891	365	335
mptG (mfla_1661)	β-RFAP	-1.353	7.980	45	161
mtdB (mfla_1660)	methylene H_4MPT dehydrogenase	-0.352	10.703	460	848
orfY (mfla_1659)	unknown	0.171	5.076	13	12

mch (mfla_1658)	methenyl H_4MPT cyclohydrolase	-0.888	10.018	234	620
orf5 (mfla_1657)	biosynthesis of H_4MPT	1.856	3.354	4	3
orf7 (mfla_1656)	unknown	-	2.095	-	4
fae (mfla_1652)	formaldehyde activating enzyme	-0.380	11.077	590	1077
fae (mfla_2543)	formaldehyde activating enzyme	-0.725	4.872	7	16
orf17 (mfla_1651)	unknown	-	2.095	-	4
orf1 (mfla_1650)	unknown	-	1.346	-	2
orf9 (mfla_1649)	biosynthesis of H_4MPT	-0.399	6.288	22	39
pabB (mfla_1648)	para-aminobenzoate synthase component I	0.016	5.928	19	27
pcbD (mfla_1646)	unknown	-0.749	5.732	12	29
orf21 (mfla_1647)	biosynthesis of H_4MPT	0.580	7.216	57	47
orf22 (mfla_1579)	biosynthesis of H_4MPT	-1.153	2.996	1	6
orf19 (mfla_1580)	biosynthesis of H_4MPT	-	2.600	4	-
orf20 (mfla_1581)	biosynthesis of H_4MPT	1.440	4.765	12	6
afp (mfla_1582)	dihydromethanopterin reductase	-0.317	5.484	12	22
fae2 (mfla_1524)	formaldehyde activating enzyme homolog	-1.629	10.146	176	766
fae3 (mfla_2364)	formaldehyde activating enzyme homolog	-0.028	8.321	107	139
Formate oxidation					
Fdh1A (mfla_0720)	FDH1, dehydrogenase alpha subunit	-	6.738	64	-
Fdh1B (mfla_0721)	FDH1, beta subunit	-	6.692	62	-
Fdh1C (mfla_0722)	FDH1, gamma subunit	-	1.398	1	-
Fdh1D (mfla_0719)	FDH1, accessory protein	-	-	-	-
Fdh1E (mfla_0718)	FDH1, delta subunit	-	2.621	3	-
fdh4A (mfla_0338)	FDH4	0.673	6.051	26	22
fdh4B (mfla_0337)	FDH4-associated protein	-	-	-	-
Ribulose monophosphate cycle for formaldehyde assimilation/oxidation					
hps (mfla_1654)	hexulosephosphate synthase	-0.548	12.329	1311	2728
hps (mfla_0250)	hexulosephosphate synthase	-0.274	12.910	2194	3775
hpi (mfla_1653)	hexulosephosphate isomerase	-0.302	9.111	156	284
tal (mfla_1655)	transaldolase	-0.380	11.077	823	1790
pgi (mfla_1325)	glucose 6-phosphate isomerase	-0.566	8.539	95	193
zwf (mfla_0917/1061)	glucose 6-phosphate dehydrogenase	0.106	9.998	332	432

pgl (mfla_0919/1063)	6-phosphogluconolactonase	-1.109	6.040	24	75
gndA (mfla_0918/1062)	6-phosphogluconate dehydrogenase (NAD)	0.173	10.690	617	648
gndB (mfla_2599)	6-phosphogluconate dehydrogenase (NADP)	3.393	7.128	78	10
edd (mfla_0759)	6-phosphogluconate dehydratase	0.271	8.752	147	172
eda (mfla_0760)	2-keto 3-deoxy 6-phosphogluconate aldolase	-0.371	8.239	82	153
tkt (mfla_2249)	transketolase	-0.044	12.657	2082	2925
rpe (mfla_2472)	ribulosephosphate 3-epimerase	-0.472	9.959	264	516
C3 interconversion reactions and partial citric acid cycle					
aceE (mfla_2074)	EI component, pyruvate dehydrogenase	-0.461	9.590	208	400
aceF (mfla_2075)	E2 component, pyruvate dehydrogenaser	-0.189	8.038	77	123
lpdA (mfla_2076)	E3 component, pyruvate dehydrogenase	0.018	7.477	57	81
pyk (mfla_2244)	pyruvate kinase	1.139	6.093	29	20
pgk (mfla_2247)	phosphoglycerate kinase	-0.716	7.783	52	124
gpd (mfla_2248)	glyceraldehyde phosphate dehydrogenase	-0.262	78.550	107	183
pps (mfla_2203)	PEP synthase	-0.522	10.770	463	911
pgm (mfla_2188)	phosphoglyceromutase	-0.889	8.618	86	226
eno (mfla_1909)	enolase	-1.035	10.294	269	756
tpi (mfla_2064)	triosephosphate isomerase	0.857	4.064	4	8
acnB (mfla_1817)	aconitate hydratase B	0.015	9.193	189	259
gltA (mfla_0061)	citrate synthase	-0.419	8.248	82	154
idh (mfla_2139)	isocitrate dehydrogenase	0.345	9.509	257	284
sucC (mfla_1888)	succinly-CoA sythase alpha subunit	0.742	7.852	91	72
sucD (mfla_1889)	succinly-CoA sythase beta subunit	-0.243	7.627	57	95

MA, methylamine; Me, methanol; β-RFAP, β-ribofuranosylaminobenzene 5'-phosphate synthase; FDH, formate dehydrogenase.