

**SUPPLEMENTARY MATERIAL**

**QUANTITATIVE PROTEOMIC AND MICROARRAY ANALYSIS OF THE  
ARCHAEON *METHANOSARCINA ACETIVORANS* GROWN WITH ACETATE  
VERSUS METHANOL\***

**Lingyun Li<sup>‡,§</sup>, Qingbo Li<sup>¶,§,||</sup>, Lars Rohlin<sup>†,§</sup>, UnMi Kim<sup>†</sup>, Kirsty Salmon<sup>†</sup>, Tomas Rejtar<sup>‡</sup>,  
Robert P. Gunsalus<sup>†</sup>, Barry L. Karger<sup>‡</sup>, and James G. Ferry<sup>¶,#</sup>**

Table S1. Proteins with at least 3-fold, and transcripts with at least 2.5-fold, differential abundance, in acetate- *versus* methanol-grown *M. acetivorans*.

Loci	Annotation <sup>a</sup>	Proteome		Transcriptome (Me/Ac) <sup>b,d</sup>
		No. of peptides	(Me/Ac) <sup>b</sup>	
MA0007	conserved hypothetical protein		ND	0.36
MA0010	formyl-methanofuran:tetrahydromethanopterin N-formyltransferase	10	23 ± 4	10.71
MA0023	zinc ABC transporter, solute-binding lipoprotein	5	40 ± 10	ND
MA0028	predicted protein		ND	0.25
MA0032	pyruvate synthase, subunit alpha		ND	3.03
MA0033	pyruvate synthase, subunit delta	2	3.0 ± 0.1	5.06
MA0034	pyruvate synthase, subunit gamma		ND	4.54
MA0036	signal sequence peptidase		ND	2.85
MA0038	predicted protein	5	0.11 ± 0.04	ND
MA0039	conserved hypothetical protein	5	0.13 ± 0.03	ND
MA0040	conserved hypothetical protein		ND	3.11
MA0045	predicted protein		ND	0.25
MA0046	predicted protein	4	3.8 ± 0.6	ND
MA0054	conserved hypothetical protein	9	7.4 ± 0.6	ND
MA0056	conserved hypothetical protein	3	7 ± 4	ND
MA0057	conserved hypothetical protein	3	5.6 ± 0.1	ND
MA0072	anaerobic ribonucleoside-triphosphate reductase	17	5.1 ± 0.8	ND
MA0076	translation initiation factor 2B, subunit 1		ND	2.81
MA0086	Hsp60	18	5 ± 1	8.52
MA0092	conserved hypothetical protein		ND	3.60
MA0090	phenylalanyl-tR synthetase, subunit alpha	11	6 ± 2	ND
MA0097	glycyl-tR synthetase	10	6 ± 1	3.26

MA0111	predicted protein		ND	4.52
MA0118	histidinol-phosphate aminotransferase	8	4.1 ± 0.8	ND
MA0119	acetylornithine aminotransferase		ND	3.44
MA0123	predicted protein		ND	0.32
MA0130	phosphoribosylformylglycinamide cyclo-ligase	7	8 ± 4	ND
MA0134	predicted protein	3	0.16 ± 0.01	ND
MA0137	dCMP deaminase	2	6 ± 3	ND
MA0144	monomethylamine methyltransferase	4	4.7 ± 0.9	ND
MA0146	methylcobalamin:CoM methyltransferase isozyme A	3	7 ± 1	6.13
MA0152	predicted protein		ND	4.61
MA0183	ribosomal protein L10e	8	7 ± 3	ND
MA0194	alanyl-tR synthetase		ND	2.65
MA0201	3-isopropylmalate dehydrogenase		ND	4.60
MA0202	3-isopropylmalate dehydratase	7	3.6 ± 0.2	ND
MA0204	conserved hypothetical protein		ND	0.31
MA0206	conserved hypothetical protein		ND	2.68
MA0208	pseudouridylate synthase		ND	0.34
MA0211	predicted protein		ND	2.52
MA0215	predicted protein	3	0.12 ± 0.01	0.04
MA0217	ATP phosphoribosyltransferase	7	9 ± 3	ND
MA0218	N-(5-phospho-D-ribosylformimino)-5-amino-1-(5-phosphoribosyl)-4-imidazole carboxamide isomerase	3	4.9 ± 0.7	ND
MA0237	predicted protein		ND	0.14
MA0244	conserved hypothetical protein		ND	3.66
MA0246	4-hydroxybenzoate decarboxylase	7	4.1 ± 0.7	ND
MA0247	hypothetical protein (multi-domain)		ND	0.08
MA0269	Methyl-THMPT:CoM methyltransferase (MtrH), subunit H	10	0.31 ± 0.1 <sup>c</sup>	ND
MA0270	Methyl-THMPT:CoM methyltransferase (MtrG), subunit G	2	0.3 ± 0.1 <sup>c</sup>	ND
MA0272	Methyl-THMPT:CoM methyltransferase (MtrA), subunit A	5	0.3 ± 0.1 <sup>c</sup>	ND
MA0273	Methyl-THMPT:CoM methyltransferase (MtrB), subunit B	3	0.20 ± 0.03 <sup>c</sup>	ND
MA0274	Methyl-THMPT:CoM methyltransferase (MtrC), subunit C	2	0.3 ± 0.1 <sup>c</sup>	ND
MA0275	Methyl-THMPT:CoM methyltransferase (MtrD), subunit D	2	0.2 ± 0.05 <sup>c</sup>	ND
MA0276	Methyl-THMPT:CoM methyltransferase (MtrE), subunit E		ND	0.25
MA0284	hypothetical protein (multi-domain)		ND	3.84
MA0285	hypothetical protein (multi-domain)		ND	3.87
MA0302	oligopeptide ABC transporter, solute-binding protein	3	7 ± 1	ND
MA0336	cell surface protein		ND	6.14
MA0337	conserved hypothetical protein		ND	0.26
MA0339	conserved hypothetical protein	3	3.1 ± 0	ND
MA0390	predicted protein		ND	2.64
MA0435	predicted protein		ND	0.16
MA0439	fructose-bisphosphate aldolase	4	3.8 ± 0.4	ND
MA0440	dCTP deaminase	2	4 ± 0.2	0.11
MA0464	predicted protein	2	0.02 ± 0.01	0.21
MA0477	predicted protein	4	0.2 ± 0.1	0.26
MA0487	predicted protein		ND	0.14
MA0492	predicted protein		ND	3.67

MA0538	peptidase family protein U32		ND	2.90
MA0539	predicted protein	2	$0.3 \pm 0.1$	0.06
MA0571	predicted protein		ND	4.83
MA0587	glutamyl-tR synthetase	8	$5 \pm 2$	ND
MA0595	ribosomal protein L18e	5	$5 \pm 1$	ND
MA0596	ribosomal protein L13p	3	$6 \pm 2$	ND
MA0597	ribosomal protein S9p	7	$4.8 \pm 0.5$	ND
MA0600	ribosomal protein S2p	8	$5 \pm 1$	2.78
MA0609	R -binding protein		ND	0.33
MA0644	translation initiation factor 2B, subunit alpha		ND	3.23
MA0646	ribosomal protein L44e	3	$4.4 \pm 0.5$	8.17
MA0651	conserved hypothetical protein	7	$9 \pm 3$	ND
MA0653	predicted protein	11	$3.8 \pm 0.7$	ND
MA0656	2-5 R ligase		ND	0.22
MA0669	replication factor C, small subunit	8	$6 \pm 2$	ND
MA0671	Tungsten formylmethanofuran dehydrogenase (FwdG), subunit G	2	$14 \pm 2$	ND
MA0676	biotin operon repressor/biotin-pyruvate carboxylase ligase		ND	0.33
MA0685	sulfite reductase		ND	0.15
MA0705	aldehyde dehydrogenase		ND	0.23
MA0706	predicted protein		ND	0.13
MA0709	conserved hypothetical protein		ND	2.99
MA0715	conserved hypothetical protein		ND	0.13
MA0719	conserved hypothetical protein		ND	2.56
MA0746	conserved hypothetical protein		ND	4.25
MA0791	hypothetical protein		ND	2.56
MA0792	arginine deiminase		ND	3.35
MA0808	homocysteine desulfhydrase		ND	0.39
MA0814	predicted protein	7	$0.18 \pm 0.04$	ND
MA0821	conserved hypothetical protein		ND	0.29
MA0827	predicted protein	5	$5 \pm 1$	3.80
MA0834	formylmethanofuran dehydrogenase, subunit B		ND	0.32
MA0835	formylmethanofuran dehydrogenase, subunit D		ND	5.53
MA0840	dipeptide ABC transporter, solute-binding protein		ND	2.92
MA0859	hypothetical protein (multi-domain)		ND	3.68
MA0872	cobN/magnesium chelatase family protein	6	$0.14 \pm 0.05$	0.31
MA0873	PQQ enzyme repeat domain protein	10	$0.12 \pm 0.03$	ND
MA0875	predicted protein		ND	0.30
MA0880	dipeptide ABC transporter, dipeptide-binding protein		ND	0.32
MA0882	magnesium chelatase subunit	9	$20 \pm 10$	ND
MA0904	predicted protein	4	$5.1 \pm 0.4$	4.99
MA0913	imidazoleglycerol-phosphate synthase, subunit H	3	$8 \pm 3$	ND
MA0923	ribosomal protein S8e	3	$8 \pm 4$	3.91
MA0936	conserved hypothetical protein		ND	2.88
MA0937	ABC transporter, ATP-binding protein		ND	2.89
MA0940	conserved hypothetical protein	2	$4 \pm 1$	ND
MA0942	histidinol-phosphate aminotransferase		ND	3.48

MA0943	histidyl-tR synthetase		ND	2.86
MA0949	ribosomal protein S15p	4	5 ± 1	3.30
MA0950	ferric enterobactin transport ATP-binding protein	4	14 ± 4	ND
MA0957	hypothetical protein (multi-domain)		ND	0.26
MA0958	conserved hypothetical protein	5	5 ± 1	ND
MA0968	eif5A-deoxyhypusine synthase		ND	0.37
MA0985	predicted protein		ND	0.37
MA0991	predicted protein		ND	0.32
MA1017	conserved hypothetical protein		ND	0.38
MA1030	NAD <sup>+</sup> synthase (glutamine-hydrolyzing)	5	0.1 ± 0.05	ND
MA1032	serine O-acetyltransferase	4	0.27 ± 0.05	ND
MA1033	predicted protein		ND	0.25
MA1050	transposase		ND	0.20
MA1072	ribosomal protein L3p	8	10 ± 6	ND
MA1073	ribosomal protein L4	6	6 ± 2	ND
MA1074	ribosomal protein L23p	2	6 ± 1	0.12
MA1075	ribosomal protein L2p	3	6.1 ± 0.7	3.43
MA1076	ribosomal protein S19p	5	7 ± 3	ND
MA1077	ribosomal protein L22p	3	6 ± 2	ND
MA1078	ribosomal protein S3p	6	5 ± 2	4.30
MA1079	ribosomal protein L29p	3	4.8 ± 0.2	ND
MA1081	ribosomal protein S17p	2	4.4 ± 0.5	3.52
MA1082	ribosomal protein L14p	2	6 ± 1	3.36
MA1083	ribosomal protein L24p	5	5 ± 2	ND
MA1084	ribosomal protein S4e	6	7 ± 3	4.10
MA1085	ribosomal protein L5p	4	5 ± 1	3.85
MA1087	ribosomal protein S8	3	4.1 ± 0.4	ND
MA1088	ribosomal protein L6p	4	6 ± 1	5.57
MA1089	ribosomal protein L32e	4	4.9 ± 0.8	5.22
MA1090	ribosomal protein L19e	2	5 ± 2	4.42
MA1091	ribosomal protein L18p	5	7 ± 3	2.98
MA1092	ribosomal protein S5	3	4 ± 1	3.15
MA1093	ribosomal protein L30p		ND	3.19
MA1094	ribosomal protein L15p	3	5 ± 1	ND
MA1108	ribosomal protein S13p	3	7 ± 1	ND
MA1109	ribosomal protein S4p	9	5 ± 1	4.41
MA1110	ribosomal protein S11p	6	6 ± 2	3.76
MA1111	NAD-directed R polymerase, subunit D	2	3.9 ± 0.5	ND
MA1112	NAD-directed R polymerase, subunit D	2	4.5 ± 0.7	ND
MA1130	iron ABC transporter, solute-binding protein	5	28 ± 6	ND
MA1138	hydrogenase expression/formation protein		ND	2.55
MA1141	F <sub>420</sub> -nonreducing hydrogenase		ND	6.32
MA1173	GDP-mannose 4,6-dehydratase		ND	2.92
MA1174	GDP-mannose 4,6-dehydratase		ND	2.84
MA1185	UDP-glucose 4-epimerase		ND	3.66
MA1231	iron(III) ABC transporter, solute-binding protein		ND	0.08
MA1255	ribosomal protein S10p	4	4.3 ± 0.4	3.23

MA1256	translation elongation factor 1, subunit alpha		ND	4.10
MA1257	translation elongation factor 2	12	5 ± 2	ND
MA1258	ribosomal protein S7p	9	6 ± 2	3.92
MA1260	transcription termination factor NusA	4	4.8 ± 0.8	ND
MA1261	ribosomal protein L30e	2	5 ± 2	4.73
MA1262	NAD-directed R polymerase, subunit D		ND	0.07
MA1265	NAD-directed R polymerase, subunit B		ND	37.00
MA1278	conserved hypothetical protein		ND	2.72
MA1279	conserved hypothetical protein		ND	3.43
MA1288	23S R methyltransferase J		ND	2.53
MA1303	predicted protein		ND	10.99
MA1310	predicted protein		ND	6.87
MA1316	sodium:proline symporter (proline permease)		ND	0.31
MA1339	conserved hypothetical protein		ND	0.31
MA1341	FMN-binding protein	5	12 ± 2	ND
MA1342	P-type copper-transporting ATPase	7	5 ± 1	ND
MA1343	predicted protein		ND	0.14
MA1364	O-linked N-acetylglucosamine transferase		ND	0.05
MA1384	6-phospho-3-hexuloisomerase		ND	2.93
MA1395	transcriptional regulator, CopG family	4	6 ± 2	0.24
MA1405	predicted protein		ND	2.64
MA1418	hypothetical protein		ND	3.15
MA1421	predicted protein		ND	0.33
MA1423	conserved hypothetical protein	3	12 ± 3	ND
MA1432	hypothetical protein (multi-domain)		ND	0.19
MA1439	NAD <sup>+</sup> pyrophosphatase		ND	0.18
MA1446	ribosomal protein L21e	2	5 ± 1	ND
MA1448	conserved hypothetical protein	2	16 ± 2	ND
MA1454	cell surface lipoprotein	2	0.17 ± 0.01	ND
MA1456	predicted protein	5	4.1 ± 0.4	3.54
MA1457	conserved hypothetical protein		ND	2.92
MA1462	universal stress protein	5	4.4 ± 0.7	ND
MA1465	predicted protein		ND	0.09
MA1471	translation elongation factor 1, subunit beta		ND	3.00
MA1484	geranylgeranyl reductase	6	5.4 ± 0.9	ND
MA1486	MoaA/NifB/PqqE family protein		ND	2.72
MA1488	conserved hypothetical protein		ND	2.69
MA1489	conserved hypothetical protein	3	20 ± 10	ND
MA1490	conserved hypothetical protein		ND	3.13
MA1494	predicted protein		ND	3.76
MA1495	F <sub>420</sub> H <sub>2</sub> dehydrogenase, subunit FpoA		ND	8.75
MA1496	F <sub>420</sub> H <sub>2</sub> dehydrogenase, subunit FpoB		ND	6.87
MA1498	F <sub>420</sub> H <sub>2</sub> dehydrogenase, subunit FpoD	4	15 ± 4	ND
MA1499	F <sub>420</sub> H <sub>2</sub> dehydrogenase, subunit FpoH	3	26 ± 1	2.97
MA1500	F <sub>420</sub> H <sub>2</sub> dehydrogenase, subunit FpoI		ND	4.98
MA1501	F <sub>420</sub> H <sub>2</sub> dehydrogenase, subunit FpoJ		ND	6.40
MA1502	F <sub>420</sub> H <sub>2</sub> dehydrogenase, subunit FpoJ		ND	6.75

MA1503	F <sub>420</sub> H <sub>2</sub> dehydrogenase, subunit FpoK		ND	7.08
MA1504	F <sub>420</sub> H <sub>2</sub> dehydrogenase, subunit FpoL		ND	5.33
MA1506	F <sub>420</sub> H <sub>2</sub> dehydrogenase, subunit FpoN		ND	0.14
MA1521	ribosomal protein L7ae	4	5.2 ± 0.7	7.80
MA1524	nucleoside-diphosphate kinase	3	6 ± 2	5.79
MA1525	translation initiation factor If2	4	5 ± 2	5.08
MA1526	ribosomal protein S6e	4	5 ± 0.7	3.36
MA1560	predicted protein		ND	3.40
MA1568	predicted protein		ND	0.06
MA1569	Pap2 superfamily protein	2	12 ± 2	ND
MA1574	superoxide dismutase		ND	0.14
MA1615	methylcobamide:CoM methyltransferase isozyme M		ND	0.20
MA1654	intracellular protease	3	0.19 ± 0.05	ND
MA1662	predicted protein		ND	0.04
MA1666	integral membrane protein		ND	0.31
MA1671	conserved hypothetical protein		ND	7.88
MA1676	predicted protein	2	4 ± 1	ND
MA1684	aspartyl-tR synthetase	10	4 ± 1	4.51
MA1685	unknown		ND	0.34
MA1710	methenyltetrahydromethanopterin cyclohydrolase		ND	5.64
MA1714	aldehyde ferredoxin oxidoreductase		ND	0.17
MA1737	predicted protein		ND	0.26
MA1744	conserved hypothetical protein	2	9 ± 3	ND
MA1748	cobalt ABC transporter, permease protein		ND	0.21
MA1754	cell surface protein		ND	0.23
MA1756	cell surface protein		ND	0.27
MA1758	hypothetical protein (multi-domain)		ND	0.18
MA1760	hypothetical protein (multi-domain)		ND	0.20
MA1764	cell surface protein		ND	0.12
MA1775	ribosomal protein L37ae	2	4.4 ± 0.5	ND
MA1776	tR nucleotidyltransferase		ND	2.77
MA1784	ribosomal protein L15e	3	6.6 ± 0.8	ND
MA1794	metallo-beta-lactamase		ND	0.39
MA1795	predicted protein		ND	2.60
MA1798	predicted protein		ND	0.20
MA1816	aspartate aminotransferase		ND	3.11
MA1817	riboflavin synthase, subunit alpha		ND	2.90
MA1820	glycerol-3-phosphate cytidyltransferase		ND	0.32
MA1821	conserved hypothetical protein	4	4.8 ± 0.7	ND
MA1826	conserved hypothetical protein		ND	3.06
MA1835	conserved hypothetical protein		ND	0.28
MA1837	predicted protein		ND	3.26
MA1848	UbiE/COQ5 methyltransferase	3	0.08 ± 0.05	ND
MA1897	predicted protein		ND	0.25
MA1901	alcohol dehydrogenase ( NADP <sup>+</sup> )		ND	0.19
MA1909	hypothetical protein	3	20 ± 10	ND
MA1937	carbon-nitrogen hydrolase		ND	4.11

MA1940	predicted protein	2	0.15 ± 0.03	0.08
MA1981	conserved hypothetical protein		ND	3.85
MA1998	predicted protein	4	0.26 ± 0.07	0.14
MA2003	sodium-dependent transporter		ND	0.28
MA2004	FtsJ-like methyltransferase	3	6.6 ± 0.4	ND
MA2039	predicted protein		ND	3.13
MA2044	predicted protein		ND	3.46
MA2046	conserved hypothetical protein		ND	2.98
MA2059	4-carboxymuconolactone decarboxylase		ND	0.13
MA2084	cob(I)alamin adenosyltransferase		ND	0.37
MA2097	predicted protein		ND	2.76
MA2143	carbamoyl-phosphate synthase (glutamine-hydrolyzing), large subunit	11	5 ± 2	2.88
MA2144	carbamoyl-phosphate synthase (glutamine-hydrolyzing), small subunit	7	5 ± 2	ND
MA2145	glycine betaine/L-proline ABC transporter, ATP-binding protein		5 ± 1	ND
MA2149	Fe(III) dicitrate ABC transporter, permease		ND	0.37
MA2161	conserved hypothetical protein		ND	3.97
MA2229	predicted protein		ND	3.61
MA2252	conserved hypothetical protein		ND	0.002
MA2273	predicted protein		ND	0.29
MA2298	predicted protein		ND	0.23
MA2299	predicted protein		ND	0.28
MA2320	metallo-beta-lactamase		ND	0.32
MA2334	predicted protein		ND	0.11
MA2349	phosphate-binding protein		ND	0.38
MA2373	predicted protein		ND	3.42
MA2375	arylsulfatase		ND	0.19
MA2389	conserved hypothetical protein		ND	0.22
MA2390	predicted protein		ND	0.03
MA2392	predicted protein		ND	0.13
MA2410	formate acetyltransferase activating enzyme		ND	0.33
MA2427	conserved hypothetical protein		ND	0.12
MA2441	H <sup>+</sup> -transporting ATP synthase, subunit beta		ND	0.31
MA2456	predicted protein	2	0.06 ± 0.02	ND
MA2510	DNA topoisomerase, type I	4	3.9 ± 0.6	ND
MA2522	predicted protein		ND	0.15
MA2536	carbonic anhydrase (Cam)	2	0.11 ± 0.03 <sup>c</sup>	ND
MA2574	hypothetical protein (multi-domain)		ND	0.32
MA2589	predicted protein		ND	2.61
MA2595	predicted protein		ND	0.27
MA2615	conserved hypothetical protein	4	15 ± 4	ND
MA2628	glycogen debranching enzyme		ND	3.09
MA2636	conserved hypothetical protein	2	0.1 ± 0.06	ND
MA2655	MuT/NUDIX protein		ND	0.30
MA2678	predicted protein		ND	0.22

MA2711	conserved hypothetical protein	5	0.2 ± 0.1	ND
MA2717	NifU protein	2	7 ± 1	ND
MA2719	conserved hypothetical protein		ND	0.40
MA2792	predicted protein		ND	0.33
MA2813	peptidylprolyl isomerase		ND	3.25
MA2819	conserved hypothetical protein	2	0.18 ± 0.03	ND
MA2846	conserved hypothetical protein		ND	0.31
MA2868	heterodisulfide reductase (HdrA), subunit A	4	0.2 ± 0.1	ND
MA2896	threonyl-tR synthetase	3	4.1 ± 0.8	2.53
MA2912	AMP-binding protein	4	8 ± 4	ND
MA2923	conserved hypothetical protein	6	0.09 ± 0.01	0.09
MA2933	conserved hypothetical protein		ND	0.10
MA2971	monomethylamine corrinoid protein		ND	3.99
MA2978	predicted protein		ND	0.23
MA2982	predicted protein	5	0.12 ± 0.04	ND
MA2984	predicted protein		ND	0.03
MA2985	predicted protein		ND	0.15
MA2986	anthranilate synthase, component II		ND	2.52
MA2989	anthranilate phosphoribosyltransferase		ND	6.33
MA2990	tryptophan synthase, subunit alpha		ND	10.46
MA2991	tryptophan synthase, subunit beta		ND	4.16
MA2992	indole-3-glycerol-phosphate synthase		ND	6.29
MA3006	formaldehyde-activating enzyme		ND	2.64
MA3008	phosphoglycerate mutase family protein		ND	3.03
MA3026	predicted protein		ND	0.38
MA3034	uroporphyrinogen-III synthase	3	3.6 ± 0.6	ND
MA3035	coenzyme PQQ synthesis protein E	4	6 ± 2	ND
MA3045	predicted protein		ND	0.39
MA3048	oligopeptide ABC transporter, solute-binding protein		ND	3.26
MA3052	valyl-tR synthetase		ND	3.48
MA3067	chemotaxis protein-glutamate methylesterase		ND	0.35
MA3075	2-oxoacid ferredoxin oxidoreductase, subunit alpha		ND	0.32
MA3092	conserved hypothetical protein	3	0.09 ± 0.01	ND
MA3113	predicted protein		ND	0.33
MA3133	cell surface protein		ND	0.40
MA3140	mannose-1-phosphate guanylyltransferase (GDP)		ND	3.14
MA3141	predicted protein		ND	2.74
MA3152	carboxymuconolactone decarboxylase		ND	0.27
MA3165	hypothetical protein	4	0.2 ± 0.1	ND
MA3169	glutamate dehydrogenase ( NAD(P)H <sup>+</sup> )		ND	0.25
MA3186	predicted protein		ND	0.07
MA3213	predicted protein		ND	0.18
MA3250	cobyric acid synthase	5	9 ± 3	ND
MA3252	ornithine cyclodeaminase		ND	0.18
MA3260	O-Glc c transferase, p110 subunit	9	12 ± 9	ND
MA3261	FxsA protein		ND	0.33
MA3264	cysteine desulphurase		ND	0.27



MA3280	predicted protein		ND	0.24
MA3289	endopeptidase La	10	11 ± 5	ND
MA3300	predicted protein		ND	0.38
MA3302	conserved hypothetical protein	5	0.004 ± 0.002	ND
MA3307	orotate phosphoribosyltransferase	5	6 ± 2	ND
MA3315	predicted protein		ND	0.20
MA3317	arylsulfatase regulator	4	0.12 ± 0.01	ND
MA3322	conserved hypothetical protein	3	20 ± 10	ND
MA3334	conserved hypothetical protein	2	0.07 ± 0.01	ND
MA3342	2-isopropylmalate synthase	3	5 ± 1	ND
MA3343	conserved hypothetical protein		ND	0.38
MA3345	glyceraldehyde 3-phosphate dehydrogenase (phosphorylating)		ND	0.25
MA3378	predicted protein	2	3.3 ± 0.2	ND
MA3382	glutamate-ammonia ligase	7	4 ± 1	24.17
MA3387	predicted protein		ND	2.73
MA3408	pyruvate water dikinase		ND	0.16
MA3416	ribosomal protein S3Ae	3	5 ± 1	6.13
MA3418	conserved hypothetical protein	3	6 ± 3	ND
MA3439	sulfite reductase, beta subunit	4	12 ± 4	5.36
MA3449	conserved hypothetical protein	2	40 ± 30	ND
MA3454	conserved hypothetical protein		ND	3.17
MA3455	nickel ABC transporter, solute-binding protein	3	20 ± 10	4.01
MA3467	methyltransferase		ND	0.26
MA3475	predicted protein	2	8 ± 3	ND
MA3476	predicted protein		ND	4.85
MA3477	ferrous iron transport protein B	8	30 ± 10	34.15
MA3482	MoaA/NifB/PqqE family protein		ND	0.06
MA3498	hydantoinase		ND	3.66
MA3520	glycine hydroxymethyltransferase		ND	3.16
MA3522	phosphoribosylglycinamide formyltransferase	2	3.8 ± 0.7	ND
MA3547	predicted protein		ND	3.13
MA3556	predicted protein		ND	0.17
MA3562	glucokinase		ND	0.28
MA3568	predicted protein		ND	0.11
MA3569	predicted protein		ND	0.08
MA3576	predicted protein	2	4 ± 0	ND
MA3606	acetate kinase	8	0.02 ± 0.01 <sup>c</sup>	0.05
MA3607	phosphotransacetylase	9	0.06 ± 0.03 <sup>c</sup>	0.09
MA3631	cobalamin biosynthesis protein	3	20 ± 7	ND
MA3632	cadmium efflux ATPase		ND	2.96
MA3661	predicted protein	2	240 ± 90	ND
MA3667	conserved hypothetical	4	0.02 ± 0.01	ND
MA3679	predicted protein		ND	0.23
MA3684	conserved hypothetical protein		ND	0.37
MA3689	conserved hypothetical protein	5	4 ± 0.8	ND
MA3694	conserved hypothetical protein		ND	3.86

MA3695	ribosomal protein S24e	4	6 ± 1	ND
MA3705	O-sialoglycoprotein endopeptidase		ND	2.62
MA3731	cytidyltransferase		ND	2.88
MA3732	F <sub>420</sub> H <sub>2</sub> dehydrogenase, subunit FpoF	5	4.2 ± 0.8	ND
MA3733	F <sub>420</sub> -dependent N <sup>5</sup> ,N <sup>10</sup> -methylene-tetrahydromethanopterin reductase	11	9 ± 4	7.11
MA3751	3-isopropylmalate dehydratase		ND	4.66
MA3762	predicted protein		ND	0.24
MA3785	predicted protein		ND	0.03
MA3786	dihydroorotate dehydrogenase, electron transfer subunit		ND	2.57
MA3869	conserved hypothetical protein		ND	2.74
MA3886	prolyl-tR synthetase		ND	2.58
MA3915	UbiE/COQ5 methyltransferase	3	7 ± 2	ND
MA3917	ammonium transporter		ND	5.92
MA3918	ammonium transporter		ND	4.09
MA3921	hemin ABC transporter, permease protein		ND	2.93
MA3956	ATP-dependent R helicase	5	20 ± 10	ND
MA3961	predicted protein	2	0.05 ± 0.01	ND
MA3967	methylcoenzyme M reductase system, component A2		ND	0.12
MA3969	PcrB family protein		ND	2.74
MA3980	predicted protein		ND	0.07
MA3990	MutT related protein		ND	0.34
MA4017	conserved hypothetical protein		ND	0.07
MA4028	predicted protein		ND	0.07
MA4039	conserved hypothetical protein		ND	0.30
MA4040	conserved hypothetical protein	5	7 ± 2	3.75
MA4041	acyl carrier protein synthase	4	17 ± 4	ND
MA4042	acetyl-CoA C-acyltransferase	6	12 ± 5	2.53
MA4044	adenylate cyclase	4	6 ± 1	ND
MA4047	proteinase IV	2	4 ± 1	ND
MA4048	seryl-tR synthetase	4	5 ± 2	ND
MA4058	predicted protein		ND	0.27
MA4080	predicted protein		ND	0.07
MA4081	conserved hypothetical protein		ND	2.58
MA4096	predicted protein		ND	0.40
MA4101	glutamate 5-kinase		ND	3.19
MA4110	prefoldin, subunit alpha		ND	2.58
MA4111	ribosomal protein LX	2	5 ± 2	ND
MA4112	translation initiation factor 6	3	5.3 ± 0.9	3.21
MA4113	ribosomal protein L31e	2	6 ± 2	3.81
MA4116	conserved hypothetical protein		ND	4.13
MA4117	ribosomal protein S19e	5	6 ± 2	3.72
MA4118	adenylosuccinate synthase	6	5 ± 1	4.34
MA4142	predicted protein	2	0.14 ± 0.05	ND
MA4147	metallo-beta-lactamase family protein		ND	0.31
MA4152	H <sup>+</sup> -transporting ATP synthase, (AtpH) subunit H	2	0.32 ± 0.1 <sup>c</sup>	ND
MA4153	H <sup>+</sup> -transporting ATP synthase, (AtpI) subunit I	8	0.10 ± 0.05 <sup>c</sup>	6.16

MA4154	H <sup>+</sup> -transporting ATP synthase, (AtpC) subunit C	2	0.08 ± 0.03 <sup>c</sup>	ND
MA4155	H <sup>+</sup> -transporting ATP synthase, (AtpE) subunit E	7	0.13 ± 0.04 <sup>c</sup>	ND
MA4156	H <sup>+</sup> -transporting ATP synthase, (AtpC) subunit C	8	0.10 ± 0.04 <sup>c</sup>	ND
MA4157	H <sup>+</sup> -transporting ATP synthase, (AtpF) subunit F	4	0.13 ± 0.04 <sup>c</sup>	ND
MA4158	H <sup>+</sup> -transporting ATP synthase, (AtpA) subunit A	15	0.12 ± 0.05 <sup>c</sup>	ND
MA4159	H <sup>+</sup> -transporting ATP synthase, (AtpB) subunit B	8	0.14 ± 0.06 <sup>c</sup>	ND
MA4160	H <sup>+</sup> -transporting ATP synthase, (AtpD) subunit D	5	0.10 ± 0.03 <sup>c</sup>	0.27
MA4175	formylmethanofuran dehydrogenase, subunit A	2	0.14 ± 0.05	2.79
MA4176	formylmethanofuran dehydrogenase, subunit C	2	0.14 ± 0.05	6.34
MA4198	conserved hypothetical protein	3	4.1 ± 0.1	ND
MA4200	conserved hypothetical protein	3	0.2 ± 0.1	0.16
MA4216	glutamate-ammonia ligase	6	4 ± 1	6.91
MA4217	conserved hypothetical protein		ND	16.14
MA4219	conserved hypothetical protein	4	4 ± 1	15.11
MA4221	predicted protein		ND	2.58
MA4240	conserved hypothetical protein		ND	0.38
MA4244	conserved hypothetical protein	4	50 ± 20	ND
MA4245	conserved hypothetical protein	2	7.4 ± 0	2.50
MA4246	nucleotide binding protein	3	5 ± 1	ND
MA4258	precorrin-8X methylmutase	5	6 ± 1	ND
MA4259	precorrin-3B C17-methyltransferase	3	8 ± 4	ND
MA4268	proteasome-activating nucleotidase	3	4 ± 1	0.27
MA4274	ribosomal protein L11p	5	5.6 ± 0.9	ND
MA4275	ribosomal protein L1p	4	5 ± 2	4.51
MA4276	acidic ribosomal protein P0 homolog	6	6 ± 2	3.62
MA4277	ribosomal protein L12p	2	5 ± 1	ND
MA4281	predicted protein		ND	8.41
MA4318	conserved hypothetical protein		ND	0.21
MA4329	thiamine biosynthesis protein ThiC		ND	3.48
MA4333	conserved hypothetical protein		ND	0.24
MA4367	5-amino-6-(5-phosphoribosylamino) uracil reductase		ND	0.19
MA4369	hydrogenase-3 subunit (EchB homolog)		ND	2.62
MA4379	methylcobamide:CoM methyltransferase isozyme M	3	80 ± 30	29.20
MA4411	isochorismatase		ND	0.31
MA4428	conserved hypothetical protein	5	4.2 ± 0.7	5.07
MA4429	phosphoserine phosphatase		ND	4.21
MA4430	methylene-tetrahydromethanopterin dehydrogenase	3	33 ± 7	5.16
MA4431	conserved hypothetical protein		ND	0.18
MA4432	conserved hypothetical protein		ND	0.37
MA4436	conserved hypothetical protein	4	5 ± 1	ND
MA4451	predicted protein		ND	0.37
MA4459	UTP-glucose-1-phosphate uridylyltransferase	5	4.3 ± 0.8	ND
MA4472	ribosomal protein S17e	2	7 ± 3	ND
MA4477	predicted protein		ND	5.74
MA4509	predicted protein		ND	0.26
MA4513	conserved hypothetical protein		ND	2.72
MA4515	acetylglutamate kinase		ND	3.67

MA4517	conserved hypothetical protein		ND	4.63
MA4520	coenzyme F <sub>420</sub> -dependent oxidoreductase		ND	4.56
MA4547	Methyl coenzyme M reductase (McrG), gamma subunit	5	0.31 ± 0.1 <sup>c</sup>	ND
MA4550	Methyl coenzyme M reductase (McrB), beta subunit	7	0.29 ± 0.09 <sup>c</sup>	6.04
MA4591	deoxyribose-phosphate aldolase	3	5 ± 2	4.21
MA4592 <sup>c</sup>	conserved hypothetical protein	4	5 ± 1	4.36
MA4593	3-dehydroquinate dehydratase		ND	3.66
MA4608	D-arabino 3-hexulose 6-phosphate formaldehyde lyase		ND	2.97
MA4615	2-isopropylmalate synthase		ND	8.50
MA4631	D-lactate dehydrogenase		ND	3.86
MA4634	conserved hypothetical protein		ND	0.01
MA4636	NADH dehydrogenase		ND	0.12
MA4638	conserved hypothetical protein		ND	0.30
MA4640	conserved hypothetical protein		ND	8.37
MA4665	multiple resistance/pH regulation related protein B (Na <sup>+</sup> /H <sup>+</sup> )		ND	0.13
MA4673	nickel ABC transporter, permease protein		ND	2.61

<sup>a</sup>Annotations are the annotations listed at <http://www.tigr.org>.

<sup>b</sup>Ac, acetate-grown cells; Me, methanol-grown cells.

<sup>c</sup>Reported previously<sup>30</sup>.

<sup>d</sup>P values were ≤0.04 (95% confidence).

ND, Not determined.