Table 7. *M. smithii* genes in the significantly enriched GO categories listed in Table 6

■ - member of GO category
□ - not a member of GO category

ENRICHED COMPARED TO SEQUENCED ARCHAEA AND/OR NON-GUT METHANOGENS							
SURFACE VARIATION	***M. smithii* genes**	**Annotation**	**GO:0007047 - cell wall organization and biogenesis**	**GO:0042545 - cell wall modification**	**GO:0030599 - pectinesterase activity**	**GO:0042546 - cell wall biosynthesis**	**GO:0009252 - peptidoglycan biosynthesis**
	MSM0052	adhesin-like protein	■	■	■	□	□
	MSM0118	cell wall biosynthesis protein, MurD-like peptide ligase family	■	□	□	■	■
	MSM0266	adhesin-like protein	■	■	■	□	□
	MSM0359	cell wall biosynthesis protein, MurD-like peptide ligase family	■	□	□	■	■
	MSM0360	cell wall biosynthesis protein, phospho-N-acetylmuramoyl-pentapeptide-transferase family	■	□	□	■	■
	MSM1111	adhesin-like protein	■	■	■	□	□
	MSM1112	adhesin-like protein	■	■	■	□	□
	MSM1113	adhesin-like protein	■	■	■	□	□
	MSM1190	cell wall biosynthesis protein, UDP-N-acetylmuramate-alanine ligase family	■	□	□	■	■
	MSM1191	cell wall biosynthesis protein, MurD-like peptide ligase family	■	□	□	■	■
	MSM1327	predicted CDP-glycerol:poly(glycerophosphate) glycerophosphotransferase	■	□	□	■	□
	MSM1585	adhesin-like protein	■	■	■	□	□
	MSM1586	adhesin-like protein	■	■	■	□	□
	MSM1587	adhesin-like protein	■	■	■	□	□
	MSM1590	adhesin-like protein	■	■	■	□	□
	MSM1594	glycosyltransferase/CDP-glycerol:poly(glycerophosphate) glycerophosphotransferase, GT2 family	■	□	□	■	□
	MSM1602	glycosyltransferase/CDP-glycerol:poly(glycerophosphate) glycerophosphotransferase, GT2 family	■	□	□	■	□
CENTRAL METABOLISM	***M. smithii* genes**	**Annotation**	**GO:0006082 - organic acid metabolism**	**GO:0006730 - one-carbon compound metabolism**	**GO:0045333 - cellular respiration**	**GO:0015948 - methanogenesis**	**GO:0019321 - pentose metabolism**
	MSM0027	glutamate synthase, domain 2 with rubredoxin	■	□	□	□	□
	MSM0071	methionyl-tRNA synthetase, MetG	■	□	□	□	□
	MSM0082	heterodisulfide reductase, subunit A, HdrA	□	■	■	■	□
	MSM0089	pyrroline-5-carboxylate reductase (NADP oxidoreductase, coenzyme F420-dependent), ProC	■	□	□	□	□
	MSM0102	cobalamin-independent methionine synthase, MetE	■	□	□	□	□
	MSM0154	homoserine dehydrogenase, ThrA	■	□	□	□	□

MSM0160	asparagine synthetase, AsnB	■				
MSM0174	O-acetylhomoserine sulfhydrylase (PLP-dependent), MET17	■				
MSM0175	homoserine O-acetyltransferase, MetX	■				
MSM0214	threonine synthase (pyridoxal-phosphate dependent), ThrC	■				
MSM0216	tryptophanyl-tRNA synthetase, TrpS	■				
MSM0231	3-dehydroquinate dehydratase	■				
MSM0265	O-acetylhomoserine sulfhydrylase	■				
MSM0268	cysteinyl-tRNA synthetase, CysS	■				
MSM0270	serine acetyltransferase, CysE	■				
MSM0271	cysteine synthase, CysK	■				
MSM0273	EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)	■				
MSM0275	valyl-tRNA synthetase, ValS	■				
MSM0277	phenylalanyl-tRNA synthetase, beta subunit, PheT	■				
MSM0286	glycerol 1-phosphate dehydrogenase (Dehydroquinate synthase-like family)	■				
MSM0287	prolyl-tRNA synthetase, ProS	■				
MSM0307	sugar kinase (ribokinase/pfkB superfamily)					■
MSM0308	formylmethanofuran:tetrahydromethanopterin formyltransferase, FtrC		■			
MSM0334	L-asparaginase, GatD,	■				
MSM0343	GMP synthase (glutamine-hydrolysing), subunit A, GuaA	■				
MSM0350	2-isopropylmalate synthase, LeuA	■				
MSM0368	glutamate synthase (NADPH), subunit 2	■				
MSM0371	predicted glutamine amidotransferase involved in pyridoxine biosynthesis, Pdx2	■				
MSM0373	isocitrate/isopropylmalate dehydrogenase, LeuB	■				
MSM0375	acetylglutamate kinase, ArgB	■				
MSM0379	glutamate N-acetyltransferase, ArgJ	■				
MSM0388	amino acid regulator	■				
MSM0393	fumarate reductase, iron-sulfur protein			■		
MSM0403	glycyl-tRNA synthetase	■				
MSM0415	uridylate kinase, PyrH	■				
MSM0457	D-3-phosphoglycerate dehydrogenase, SerA	■				
MSM0488	carbamoylphosphate synthase, large subunit, CarB	■				
MSM0489	carbamoylphosphate synthase, small subunit, CarA	■				
MSM0513	tyrosyl-tRNA synthetase, TyrS	■				
MSM0516	corrinoid protein (methionine synthase-related), MtaC	■				
MSM0518	methylcobalamin:coenzyme M methyltransferase, MtaA		■			
MSM0556	dihydropteroate synthase	■				
MSM0572	H(2)-forming N5,N10-methylenetetrahydromethanopterin dehydrogenase (coenzyme F420-dependent), Mth		■	■	■	
MSM0573	biotin synthetase, BioB	■				
MSM0604	predicted archaeal aspartate/glutamate/uridylate kinase	■				
MSM0619	alanyl-tRNA synthetase, AlaS	■				
MSM0627	tetrahydromethanopterin S-methyltransferase, subunit H, MtrH		■			
MSM0641	prephenate dehydrogenase (NADP+)	■				

MSM0653	histidinol-phosphate aminotransferase, HisC	■				
MSM0719	phosphoserine phosphatase, HAD family, SerB	■				
MSM0722	2-isopropylmalate synthase, LeuA	■				
MSM0723	3-isopropylmalate dehydratase, LeuC	■				
MSM0727	S-adenosylhomocysteine hydrolase (adenosylhomocysteinase), AhcY		■			
MSM0829	aspartate-semialdehyde dehydrogenase, Asd	■				
MSM0830	dihydrodipicolinate reductas, DapB	■				
MSM0832	aspartokinase, alpha subunit	■				
MSM0834	chorismate mutase	■				
MSM0835	archaeal shikimate kinase	■				
MSM0847	archaeal 3-isopropylmalate dehydratase, small subunit, LeuD	■				
MSM0858	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide (ProFAR) isomerase, HisA	■				
MSM0860	aspartate-semialdehyde dehydrogenase, ArgC	■				
MSM0878	pyruvoyl-dependent arginine decarboxylase, PdaD	■				
MSM0888	glutamate dehydrogenase (NADP+), GdhA	■				
MSM0902	methyl-coenzyme M reductase, alpha subunit, McrA		■	■	■	
MSM0903	methyl-coenzyme M reductase, gamma subunit, McrG		■	■	■	
MSM0904	methyl-coenzyme M reductase, D subunit, McrD		■	■	■	
MSM0905	methyl-coenzyme M reductase, beta subunit, McrB		■	■	■	
MSM0939	pyruvate carboxylase, subunit B, PycB	■				
MSM0965	3-hydroxyacyl-CoA dehydrogenase, FadB	■				
MSM0967	glutamyl-tRNA reductase, HemA	■				
MSM0987	tyrosine decarboxylase, MfnA	■				
MSM0988	phosphoenolpyruvate synthase, PpsA	■				
MSM1001	methyl viologen-reducing hydrogenase, delta subunit, MvhD		■	■	■	
MSM1007	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit H, MtrH		■			
MSM1008	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit G, MtrG		■	■	■	
MSM1011	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit B, MtrB		■	■	■	
MSM1012	N5-methyl-tetrahydromethanopterin:coenzyme M methyltransferase, subunit C, MtrC		■	■	■	
MSM1015	methyl-coenzyme M reductase, alpha subunit, McrA		■	■	■	
MSM1016	methyl-coenzyme M reductase, gamma subunit, McrG		■	■	■	
MSM1017	methyl-coenzyme M reductase, C subunit, McrC		■	■	■	
MSM1018	methyl-coenzyme M reductase, D subunit, McrD		■	■	■	
MSM1019	methyl-coenzyme M reductase, beta subunit, McrB		■	■	■	
MSM1052	prephenate dehydratase, PheA	■				
MSM1084	argininosuccinate synthase, ArgG	■				

MSM1092	formylmethanofuran:tetrahydromethanopterin formyltransferase, Ftr		■			
MSM1103	phosphoribosyl-ATP pyrophosphohydrolase, HisE	■				
MSM1141	tryptophan synthase, alpha subunit, TrpA	■				
MSM1142	tryptophan synthase, beta subunit, TrpB	■				
MSM1143	indole-3-glycerol phosphate synthase, TrpC	■				
MSM1144	anthranilate phosphoribosyltransferase, TrpD	■				
MSM1145	anthranilate/para-aminobenzoate synthase component II, TrpG	■				
MSM1159	glutamine amidotransferase, HisH	■				
MSM1172	leucyl-tRNA synthetase, LeuS	■				
MSM1179	shikimate 5-dehydrogenase, AroE	■				
MSM1181	histidyl-tRNA synthetase, HisS	■				
MSM1182	phosphoribosyl-AMP cyclohydrolase, HisI	■				
MSM1202	branched-chain-amino-acid aminotransferase, IlvE	■				
MSM1204	coenzyme F420-dependent methylenetetrahydromethanopterin dehydrogenase, Mtd		■	■	■	
MSM1206	imidazoleglycerol-phosphate dehydrogenase, HisB	■				
MSM1214	threonyl-tRNA synthetase, ThrS	■				
MSM1222	ketol-acid reductoisomerase, IlvC	■				
MSM1224	acetolactate synthase, small subunit (regulatory), IlvH	■				
MSM1226	ornithine carbamoyltransferase, ArgF	■				
MSM1231	arginyl-tRNA synthetase, ArgS	■				
MSM1236	aspartyl-tRNA synthetase, AspS	■				
MSM1237	dihydroxy-acid dehydratase, IlvD	■				
MSM1238	histidinol dehydrogenase, HisD	■				
MSM1242	tryptophan synthase, beta subunit, TrpB	■				
MSM1246	isopropylmalate synthase, LeuA	■				
MSM1261	ATP phosphoribosyltransferase, HisG	■				
MSM1263	aspartate carbamoyltransferase, PyrB	■				
MSM1298	3-isopropylmalate dehydrogenase, LeuB	■				
MSM1299	3-isopropylmalate dehydratase, small subunit, LeuD	■				
MSM1300	3-isopropylmalate dehydratase, large subunit, LeuC	■				
MSM1327	predicted CDP-glycerol:poly(glycerophosphate) glycerophosphotransferase	■				■
MSM1337	glycine hydroxymethyltransferase, GlyA	■				
MSM1340	archaeal S-adenosylmethionine synthetase, MetK		■			
MSM1341	isoleucyl-tRNA synthetase, IleS	■				
MSM1364	imidazoleglycerol-phosphate synthase, HisF	■				
MSM1368	N-acetylornithine aminotransferase, ArgD	■				
MSM1371	diaminopimelate decarboxylase, LysA	■				
MSM1372	diaminopimelate epimerase, DapF	■				
MSM1387	lysyl-tRNA synthetase (class I), LysS	■				
MSM1389	sugar kinase, ribokinase/pfkB superfamily					■
MSM1396	tungsten formylmethanofuran dehydrogenase, subunit E, FwdE		■	■	■	

	MSM1404	formate dehydrogenase, alpha subunit, FdhA	■	■				
	MSM1414	tungsten formylmethanofuran dehydrogenase, subunit C, FwdC		■	■	■		
	MSM1418	glutamine synthetase, GlnA	■					
	MSM1440	predicted archaeal kinase	■					
	MSM1452	glutamyl-tRNA synthetase, GltX	■					
	MSM1461	methyl viologen-reducing hydrogenase, delta subunit, MvhD		■	■	■		
	MSM1474	chorismate synthase, AroC	■					
	MSM1478	phenylalanyl-tRNA synthetase, PheS	■					
	MSM1594	glycosyltransferase/CDP-glycerol:poly(glycerophosphate) glycerophosphotransferase, GT2 family	■				■	
	MSM1602	glycosyltransferase/CDP-glycerol:poly(glycerophosphate) glycerophosphotransferase, GT2 family	■				■	
	MSM1636	ProFAR isomerase-related protein	■					
	MSM1710	seryl-tRNA synthetase, SerS	■					
	MSM1713	predicted regulatory protein, amino acid-binding ACT domain family	■					
COFACTOR/ VITAMIN METABOLISM	***M. smithii* genes**	**Annotation**	**GO:0046872 - metal ion binding**	**GO:0005506 - iron ion binding**	**GO:0050661 - NADP binding**	**GO:0006767 - water-soluble vitamin metabolism**	**GO:0042727 - riboflavin and derivative biosynthesis**	**GO:0008703 - 5-amino-6-(5-phosphoribosylamino)uracil reductase**
	MSM0027	glutamate synthase, domain 2 with rubredoxin	■					
	MSM0029	putative calcium-binding protein	■					
	MSM0052	adhesin-like protein			■	■	■	■
	MSM0065	riboflavin-specific deaminase			■	■	■	■
	MSM0079	CofH protein (7,8-didemethyl-8-hydroxy-5-deazariboflavin (FO)/F420 biosynthesis)	■	■				
	MSM0082	heterodisulfide reductase, subunit A, HdrA	■	■				
	MSM0084	heterodisulfide reductase, subunit C, HdrC	■	■				
	MSM0085	putative ferredoxin	■	■				
	MSM0101	precorrin-3 methylase, CbiF				■		
	MSM0107	hydrogenase expression/formation protein, HypB	■					
	MSM0108	hydrogenase nickel incorporation protein, HypA	■					
	MSM0129	nicotinamide mononucleotide adenylyltransferase, NadR				■		
	MSM0131	molybdenum-binding protein, MopI	■					
	MSM0135	coenzyme F420-reducing hydrogenase, beta subunit	■	■				
	MSM0136	putative ferredoxin	■	■				
	MSM0148	predicted oxidoreductase, aldo/keto reductase family	■	■				
	MSM0153	predicted phosphoglycerate mutase	■					
	MSM0187	rubredoxin	■					
	MSM0188	rubredoxin	■					
	MSM0198	inorganic pyrophosphatase	■					
	MSM0203	nucleoside diphosphate kinase, Ndk	■					
	MSM0209	ferredoxin	■	■				
	MSM0218	iron dependent transcriptional regulator (Fe2+-binding)	■	■				
	MSM0238	precorrin-6B methylase, CbiT				■		

MSM0262	desulfoferrodoxin (dfx)							
MSM0262	desulfoferrodoxin (dfx)							
MSM0266	adhesin-like protein							
MSM0272	endonuclease III							
MSM0284	ribose 5-phosphate isomerase, RpiA							
MSM0289	phosphomethylpyrimidine kinase (HMPP-kinase), ThiD							
MSM0306	polyferredoxin, iron-sulfur binding							
MSM0310	polyferredoxin, iron-sulfur binding							
MSM0311	polyferredoxin, iron-sulfur binding							
MSM0312	[NiFe]-hydrogenase-3-type complex, large subunit/NADH:quinone oxidoreductase (complex I), subunit 49K/NdhH/NuoD							
MSM0331	2-oxoisovalerate ferredoxin oxidoreductase, delta subunit							
MSM0357	conserved hypothetical membrane protein (possible Zinc-binding)							
MSM0368	glutamate synthase (NADPH), subunit 2							
MSM0376	alcohol dehydrogenase (zinc-binding), GroES-like							
MSM0385	anaerobic magnesium-protoporphyrin IX monomethyl ester cyclase, Elongator protein 3/MiaB/NifB family							
MSM0392	indolepyruvate ferredoxin oxidoreductase, alpha subunit							
MSM0393	fumarate reductase, iron-sulfur protein							
MSM0395	ferredoxin, iron-sulfur binding							
MSM0409	C4-type Zinc-finger protein							
MSM0424	transcription initiation factor TFIIB (zinc-binding)							
MSM0491	nicotinate-nucleotide pyrophosphorylase (carboxylating), NadC							
MSM0494	quinolinate synthetase, subunit A, NadA							
MSM0516	corrinoid protein (methionine synthase-related), MtaC							
MSM0517	methyltransferase activation protein, MapA							
MSM0517	methyltransferase activation protein, MapA							
MSM0538	pyruvate formate-lyase activating enzyme, PflA							
MSM0543	DNA repair photolyase, SplB							
MSM0544	predicted Fe-S oxidoreductase							
MSM0558	pyruvate:ferredoxin oxidoreductase, delta subunit, PorD							
MSM0561	formate dehydrogenase, iron-sulfur subunit							
MSM0562	formate dehydrogenase, iron-sulfur subunit							
MSM0573	biotin synthetase, BioB							
MSM0579	polyferredoxin, iron-sulfur binding							
MSM0583	cobalt ABC transporter, permease component, CbiM							
MSM0585	cobalt ABC transporter, permease component, CbiQ							
MSM0607	predicted ATPase, RNase L inhibitor family							
MSM0607	predicted ATPase, RNase L inhibitor family							
MSM0609	ferredoxin, iron-sulfur binding							
MSM0616	adhesin-like protein							

MSM0617	thiamine biosynthesis ATP pyrophosphatase, ThiI				■		
MSM0644	thiamine biosynthesis protein, ThiC				■		
MSM0652	pyruvate formate-lyase activating enzyme, PflA	■	■				
MSM0657	phosphoglycerate mutase, AP superfamily	■					
MSM0696	Fe-S oxidoreductase	■					
MSM0723	3-isopropylmalate dehydratase, LeuC	■	■				
MSM0723	3-isopropylmalate dehydratase, LeuC						
MSM0728	predicted oxidoreductase, aldo/keto reductase family	■	■				
MSM0771	cobalt ABC transporter, permease component, CbiQ				■		
MSM0783	tungsten formylmethanofuran dehydrogenase, subunit F, FwdF	■	■				
MSM0784	ferredoxin	■	■				
MSM0787	Fe-S oxidoreductase	■	■				
MSM0796	heterodisulfide reductase, subunit C, HdrC	■	■				
MSM0808	nitrogenase iron-molybdenum cofactor biosynthesis protein, NifB	■	■				
MSM0829	aspartate-semialdehyde dehydrogenase, Asd			■			
MSM0837	cobalamin biosynthesis protein D, CbiD				■		
MSM0842	histone acetyltransferase, radical SAM superfamily	■	■				
MSM0845	2-methylthioadenine synthetase, MiaB	■	■				
MSM0849	molybdenum cofactor biosynthesis-related protein, MoaA	■	■				
MSM0865	putative glucose-methanol-choline oxidoreductase (FAD-dependent)	■	■				
MSM0892	putative zinc-binding protein	■					
MSM0895	cation transport ATPase, HAD family	■					
MSM0896	precorrin-6X reductase, CbiJ				■		
MSM0916	hydroxyethylthiazole kinase, ThiM				■		
MSM0917	thiamine monophosphate synthase, ThiE	■			■		
MSM0922	Fe-S oxidoreductase	■	■				
MSM0928	2-oxoglutarate ferredoxin oxidoreductase, delta subunit, KorD	■	■				
MSM0933	cobalamin-5-phosphate synthase, CobS				■		
MSM0960	cation transport ATPase, HAD family	■					
MSM0961	heavy-metal cation transporting ATPase	■					
MSM0962	glyceraldehyde 3-phosphate dehydrogenase, GapA			■			
MSM0998	polyferredoxin, MvhB	■	■				
MSM0999	methyl viologen-reducing hydrogenase, alpha subunit, MvhA	■					
MSM1020	Fe-S oxidoreductase, Radical SAM family	■	■				
MSM1035	FO synthase subunit 1 (SAM-dependent), CofG (F420 biosynthesis)	■	■				
MSM1043	dihydroorotate dehydrogenase electron transfer subunit, PyrK	■	■				
MSM1055	coenzyme PQQ synthesis protein, SAM family	■	■				
MSM1063	energy-converting hydrogenase B, subunit N, EhbN	■					
MSM1065	energy-converting hydrogenase B, subunit L, EhbL	■	■				
MSM1066	energy-converting hydrogenase B, subunit K, EhbK	■	■				

MSM1099	biotin synthase related protein	■	■				
MSM1106	hydrogenase maturation factor, HypF	■					
MSM1111	adhesin-like protein			■	■	■	■
MSM1112	adhesin-like protein			■	■	■	■
MSM1122	coenzyme F420-reducing hydrogenase, gamma subunit, FrhG	■	■				
MSM1123	coenzyme F420-reducing hydrogenase, delta subunit, FrhD	■					
MSM1124	coenzyme F420-reducing hydrogenase, alpha subunit, FrhA	■					
MSM1127	cation transport ATPase, HAD family	■					
MSM1138	predicted glutamine amidotransferase, CobB/CobQ-like family				■		
MSM1153	cation transport ATPase, HAD family	■					
MSM1167	cobalt precorrin-6Y C5,15-methyltransferase, CbiE				■		
MSM1171	ammonia-dependent NAD+ synthetase, NadE				■		
MSM1174	heat shock protein HtpX (Zn-dependent)	■					
MSM1179	shikimate 5-dehydrogenase, AroE			■			
MSM1198	O-sialoglycoprotein endopeptidase	■					
MSM1200	phosphoribosyltransferase, CobT				■		
MSM1215	cobyrinic acid a,c-diamide synthase, CbiA				■		
MSM1223	carbonic anhydrase	■					
MSM1230	transcriptional regulator, MarR family	■	■				
MSM1234	cobalt-precorrin-8X methylmutase, CbiC				■		
MSM1238	histidinol dehydrogenase, HisD	■					
MSM1239	predicted DNA-binding protein	■	■				
MSM1241	chromosome partitioning ATPase				■		
MSM1254	cobyric acid synthase				■		
MSM1256	3,4-dihydroxy-2-butanone 4-phosphate synthase, RibB				■	■	
MSM1266	cobalamin biosynthesis protein D, CobD				■		
MSM1267	cobalamin biosynthesis protein G, CbiG				■		
MSM1273	cobalt precorrin-3B C17-methyltransferase, CbiH				■		
MSM1283	thiamine monphosphate kinase, ThiL				■		
MSM1284	pyruvate formate-lyase activating enzyme, PflA	■	■				
MSM1296	riboflavin synthase, beta subunit, RibH				■	■	
MSM1300	3-isopropylmalate dehydratase, large subunit, LeuC	■	■				
MSM1301	predicted Fe-S oxidoreductase	■	■				
MSM1336	heterodisulfide reductase, subunit A, HdrA	■	■				
MSM1338	archaeal flavoprotein	■	■				
MSM1348	rubrerythrin	■					
MSM1351	precorrin-2 C20-methyltransferase, CbiL				■		
MSM1354	DNA-directed RNA polymerase subunit M, RpoM	■					
MSM1380	NADP-dependent alcohol dehydrogenase	■					
MSM1386	cytosine deaminase	■					
MSM1388	thiamine biosynthesis protein, ThiC				■		
MSM1404	formate dehydrogenase, alpha subunit, FdhA	■					
MSM1405	formate dehydrogenase, beta subunit, FdhB	■	■				

	MSM1406	molybdopterin cofactor biosynthesis protein A, MoaA	■	■				
	MSM1408	tungsten formylmethanofuran dehydrogenase, subunit E, FwdE	■	■				
	MSM1409	tungsten formylmethanofuran dehydrogenase, subunit F, FwdF	■	■				
	MSM1410	tungsten formylmethanofuran dehydrogenase, subunit G, FwdG	■	■				
	MSM1411	tungsten formylmethanofuran dehydrogenase, subunit D, FwdD	■					
	MSM1436	ferredoxin	■	■				
	MSM1446	predicted hydroxylamine reductase, Hcp	■	■				
	MSM1450	predicted oxidoreductase, aldo/keto reductase family	■	■				
	MSM1460	energy-converting hydrogenase B, subunit K, EhbK	■	■				
	MSM1462	formate dehydrogenase, beta subunit, FdhB	■	■				
	MSM1488	cobalt ABC transporter, permease component, CbiM				■		
	MSM1497	predicted coenzyme PQQ synthesis protein	■	■				
	MSM1565	cobyric acid synthase, CobQ				■		
	MSM1567	adhesin-like protein			■	■	■	■
	MSM1590	adhesin-like protein			■	■	■	■
	MSM1606	arylsulfatase regulator, AslB	■	■				
	MSM1608	predicted oxidoreductase, aldo/keto reductase family	■	■				
	MSM1618	cobalamin biosynthesis protein M, CbiM				■		
	MSM1619	cobalt ABC transporter, substrate-binding component, CbiN				■		
	MSM1620	cobalt ABC transporter, permease component, CbiQ				■		
	MSM1622	archaeal riboflavin synthase, RibC				■	■	
	MSM1626	predicted fumarate reductase	■	■				
	MSM1655	hypothetical protein (phage)	■					
	MSM1700	predicted ferredoxin	■	■				
	MSM1712	predicted ferritin	■	■				
	MSM1720	DNA-directed RNA polymerase, subunit M, RpoM	■					
	MSM1733	rubrerythrin	■					
	MSM1792	nicotinate phosphoribosyltransferase				■		
AMINO ACID METABOLISM	***M. smithii* genes**	**Annotation**	**GO:0006519 - amino acid and derivative metabolism**	**GO:0008652 - amino acid biosynthesis**				
	MSM0027	glutamate synthase, domain 2 with rubredoxin	■	■				
	MSM0071	methionyl-tRNA synthetase, MetG	■					
	MSM0089	pyrroline-5-carboxylate reductase (NADP oxidoreductase, coenzyme F420-dependent), ProC	■	■				
	MSM0102	cobalamin-independent methionine synthase, MetE	■	■				
	MSM0154	homoserine dehydrogenase, ThrA	■	■				
	MSM0160	asparagine synthetase, AsnB	■	■				
	MSM0174	O-acetylhomoserine sulfhydrylase (PLP-dependent), MET17	■					
	MSM0175	homoserine O-acetyltransferase, MetX	■	■				

MSM0214	threonine synthase (pyridoxal-phosphate dependent), ThrC		
MSM0216	tryptophanyl-tRNA synthetase, TrpS		
MSM0231	3-dehydroquinate dehydratase		
MSM0265	O-acetylhomoserine sulfhydrylase		
MSM0268	cysteinyl-tRNA synthetase, CysS		
MSM0270	serine acetyltransferase, CysE		
MSM0271	cysteine synthase, CysK		
MSM0273	EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)		
MSM0275	valyl-tRNA synthetase, ValS		
MSM0277	phenylalanyl-tRNA synthetase, beta subunit, PheT		
MSM0286	glycerol 1-phosphate dehydrogenase (Dehydroquinate synthase-like family)		
MSM0287	prolyl-tRNA synthetase, ProS		
MSM0334	L-asparaginase, GatD		
MSM0343	GMP synthase (glutamine-hydrolysing), subunit A, GuaA		
MSM0368	glutamate synthase (NADPH), subunit 2		
MSM0371	predicted glutamine amidotransferase involved in pyridoxine biosynthesis, Pdx2		
MSM0373	isocitrate/isopropylmalate dehydrogenase, LeuB		
MSM0375	acetylglutamate kinase, ArgB		
MSM0379	glutamate N-acetyltransferase, ArgJ		
MSM0388	amino acid regulator		
MSM0403	glycyl-tRNA synthetase		
MSM0415	uridylate kinase, PyrH		
MSM0457	D-3-phosphoglycerate dehydrogenase, SerA		
MSM0488	carbamoylphosphate synthase, large subunit, CarB		
MSM0489	carbamoylphosphate synthase, small subunit, CarA		
MSM0513	tyrosyl-tRNA synthetase, TyrS		
MSM0516	corrinoid protein (methionine synthase-related), MtaC		
MSM0604	predicted archaeal aspartate/glutamate/uridylate kinase		
MSM0619	alanyl-tRNA synthetase, AlaS		
MSM0641	prephenate dehydrogenase (NADP+)		
MSM0653	histidinol-phosphate aminotransferase, HisC		
MSM0719	phosphoserine phosphatase, HAD family, SerB		
MSM0723	3-isopropylmalate dehydratase, LeuC		
MSM0829	aspartate-semialdehyde dehydrogenase, Asd		
MSM0830	dihydrodipicolinate reductas, DapB		
MSM0832	aspartokinase, alpha subunit		
MSM0834	chorismate mutase		
MSM0835	archaeal shikimate kinase		
MSM0847	archaeal 3-isopropylmalate dehydratase, small subunit, LeuD		
MSM0858	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide (ProFAR) isomerase, HisA		
MSM0860	aspartate-semialdehyde dehydrogenase, ArgC		
MSM0876	arginase/agmatinase/formimionoglutamate hydrolase, SpeB		
MSM0878	pyruvoyl-dependent arginine decarboxylase, PdaD		

	MSM0888	glutamate dehydrogenase (NADP+), GdhA		
	MSM0967	glutamyl-tRNA reductase, HemA		
	MSM1052	prephenate dehydratase, PheA		
	MSM1084	argininosuccinate synthase, ArgG		
	MSM1103	phosphoribosyl-ATP pyrophosphohydrolase, HisE		
	MSM1141	tryptophan synthase, alpha subunit, TrpA		
	MSM1142	tryptophan synthase, beta subunit, TrpB		
	MSM1143	indole-3-glycerol phosphate synthase, TrpC		
	MSM1144	anthranilate phosphoribosyltransferase, TrpD		
	MSM1145	anthranilate/para-aminobenzoate synthase component II, TrpG		
	MSM1159	glutamine amidotransferase, HisH		
	MSM1172	leucyl-tRNA synthetase, LeuS		
	MSM1179	shikimate 5-dehydrogenase, AroE		
	MSM1181	histidyl-tRNA synthetase, HisS		
	MSM1182	phosphoribosyl-AMP cyclohydrolase, HisI		
	MSM1202	branched-chain-amino-acid aminotransferase, IlvE		
	MSM1206	imidazoleglycerol-phosphate dehydrogenase, HisB		
	MSM1214	threonyl-tRNA synthetase, ThrS		
	MSM1222	ketol-acid reductoisomerase, IlvC		
	MSM1224	acetolactate synthase, small subunit (regulatory), IlvH		
	MSM1226	ornithine carbamoyltransferase, ArgF		
	MSM1231	arginyl-tRNA synthetase, ArgS		
	MSM1236	aspartyl-tRNA synthetase, AspS		
	MSM1237	dihydroxy-acid dehydratase, IlvD		
	MSM1238	histidinol dehydrogenase, HisD		
	MSM1242	tryptophan synthase, beta subunit, TrpB		
	MSM1261	ATP phosphoribosyltransferase, HisG		
	MSM1263	aspartate carbamoyltransferase, PyrB		
	MSM1298	3-isopropylmalate dehydrogenase, LeuB		
	MSM1299	3-isopropylmalate dehydratase, small subunit, LeuD		
	MSM1300	3-isopropylmalate dehydratase, large subunit, LeuC		
	MSM1337	glycine hydroxymethyltransferase, GlyA		
	MSM1341	isoleucyl-tRNA synthetase, IleS		
	MSM1364	imidazoleglycerol-phosphate synthase, HisF		
	MSM1368	N-acetylornithine aminotransferase, ArgD		
	MSM1371	diaminopimelate decarboxylase, LysA		
	MSM1372	diaminopimelate epimerase, DapF		
	MSM1387	lysyl-tRNA synthetase (class I), LysS		
	MSM1418	glutamine synthetase, GlnA		
	MSM1440	predicted archaeal kinase		
	MSM1452	glutamyl-tRNA synthetase, GltX		
	MSM1474	chorismate synthase, AroC		
	MSM1478	phenylalanyl-tRNA synthetase, PheS		
	MSM1615	deoxyhypusine synthase, Dys		
	MSM1636	ProFAR isomerase-related protein		
	MSM1710	seryl-tRNA synthetase, SerS		
	MSM1713	predicted regulatory protein, amino acid-binding ACT domain family		

DEPLETED COMPARED TO SEQUENCED ARCHAEA AND/OR NON-GUT METHANOGENS

ENVIRONMENTAL SENSING	*M. smithii* genes	Annotation	GO:0004672 - protein kinase activity	GO:0007165 - signal transduction	GO:0000160 - two-component signal transduction
	MSM0485	universal stress protein, UspA	■	■	
	MSM0525	predicted unusual protein kinase, ubiquinone biosynthesis protein-related, AarF	■		
	MSM0869	GTPase, GTP1/OBG family		■	
	MSM0896	precorrin-6X reductase, CbiJ			■
	MSM0952	serine/threonine protein kinase, RIO1 family	■		
	MSM1198	O-sialoglycoprotein endopeptidase	■		

TRANSCRIPTIONAL CONTROL	*M. smithii* genes	Annotation	GO:0006350 - transcription	GO:0019222 - regulation of metabolism	GO:0045449 - regulation of transcription
	MSM0067	conserved hypothetical protein	■	■	■
	MSM0069	conserved hypothetical protein	■	■	■
	MSM0094	predicted transcription regulator (TetR family)	■	■	■
	MSM0196	archaeal DNA-dependent RNA polymerase, subunit E, RpoE	■		
	MSM0197	archaeal DNA-dependent RNA polymerase, subunit E, RpoE	■		
	MSM0218	iron dependent transcriptional regulator (Fe2+-binding)	■	■	■
	MSM0233	nitrogen regulatory protein P-II, GlnK		■	
	MSM0288	conserved hypothetical protein (DUF121 daomain)	■	■	■
	MSM0334	L-asparaginase, GatD,		■	
	MSM0364	transcriptional regulator (nickel-responsive), NikR	■	■	■
	MSM0413	transcriptional regulator, MarR family	■	■	■
	MSM0424	transcription initiation factor TFIIB (zinc-binding)	■	■	■
	MSM0600	transcriptional regulator, MarR family	■	■	■
	MSM0624	transcription antiterminator, NusG	■	■	■
	MSM0631	transcription initiation factor IIE, alpha subunit	■		
	MSM0650	transcriptional regulator, TetR/AcrR family	■	■	■
	MSM0720	transcription initiation factor TFIID TATA binding protein	■	■	■
	MSM0767	selenocysteine synthase, SelA		■	
	MSM0775	transcriptional regulator, AraC family	■	■	■
	MSM0817	predicted transcriptional regulator	■	■	■
	MSM0896	precorrin-6X reductase, CbiJ	■	■	■
	MSM0908	DNA-dependent RNA polymerase, subunit A, RpoA	■		
	MSM0909	DNA-dependent RNA polymerase, subunit A', RpoA	■		
	MSM0910	DNA-dependent RNA polymerase, subunit B', RpoB	■		
	MSM0911	DNA-dependent RNA polymerase, subunit B, RpoB	■		
	MSM0912	DNA-dependent RNA polymerase, subunit H, RpoH	■		
	MSM1032	transcriptional regulator, Lrp family	■	■	■

	MSM1087	NAD-dependent protein deacetylase, SIR2 family	
	MSM1107	predicted transcriptional regulator	
	MSM1126	predicted transcriptional regulator, ArsR family	
	MSM1137	DNA polymerase sliding clamp subunit, PCNA family, Pcn	
	MSM1207	molybdate transport system regulatory protein	
	MSM1230	transcriptional regulator, MarR family	
	MSM1315	predicted transcriptional regulator	
	MSM1350	predicted transcriptional regulator, ArsR family	
	MSM1354	DNA-directed RNA polymerase subunit M, RpoM	
	MSM1356	DNA-directed RNA polymerase, subunit L, RpoL	
	MSM1376	DNA-directed RNA polymerase subunit F	
	MSM1390	transcriptional regulator, LysR family	
	MSM1408	tungsten formylmethanofuran dehydrogenase, subunit E, FwdE	
	MSM1428	DNA-directed RNA polymerase, subunit D, RpoD	
	MSM1432	DNA-directed RNA polymerase, subunit N, RpoN	
	MSM1433	DNA-directed RNA polymerase, subunit K, RpoK	
	MSM1499	predicted transcriptional regulator	
	MSM1631	predicted DNA-directed RNA polymerase II, subunit RPC10	
	MSM1720	DNA-directed RNA polymerase, subunit M, RpoM	
	MSM1763	predicted DNA-directed RNA polymerase, subunit M, RpoM	
	MSM1764	conserved hypothetical protein	
	MSM1765	conserved hypothetical protein	
PHOSPHATE METABOLISM	***M. smithii* genes**	**Annotation**	**GO:0006796 - phosphate metabolism**
	MSM0060	predicted archaeal kinase (GHMP kinase family)	
	MSM0198	inorganic pyrophosphatase	
	MSM0313	[NiFe]-hydrogenase-3-type complex, small subunit/NADH:quinone oxidoreductase (complex I), subunit PSST/NdhK/NuoB	
	MSM0433	archaeal/vacuolar-type H+-transporting ATP synthase, subunit D	
	MSM0434	archaeal/vacuolar-type H+-transporting ATP synthase, subunit B	
	MSM0435	archaeal/vacuolar-type H+-transporting ATP synthase, subunit A	
	MSM0436	archaeal/vacuolar-type H+-transporting ATP synthase, subunit F	
	MSM0437	archaeal/vacuolar-type H+-transporting ATP synthase, subunit C	
	MSM0438	archaeal/vacuolar-type H+-transporting ATP synthase, subunit E	
	MSM0439	archaeal/vacuolar-type H+-transporting ATP synthase, subunit K	
	MSM0525	predicted unusual protein kinase, ubiquinone biosynthesis protein-related, AarF	

	MSM0835	archaeal shikimate kinase	
	MSM0842	histone acetyltransferase, radical SAM superfamily	
	MSM0848	predicted archaeal sugar kinase, GHMP kinase family	
	MSM0952	serine/threonine protein kinase, RIO1 family	
	MSM0988	phosphoenolpyruvate synthase, PpsA	
	MSM1000	methyl viologen-reducing hydrogenase, gamma subunit, MvhG	
	MSM1064	energy-converting hydrogenase B, subunit M, EhbM	
	MSM1071	energy-converting hydrogenase B, subunit F, EhbF	
	MSM1072	energy-converting hydrogenase B, subunit E, EhbE	
	MSM1122	coenzyme F420-reducing hydrogenase, gamma subunit, FrhG	
	MSM1198	O-sialoglycoprotein endopeptidase	
	MSM1424	polyphosphate kinase, ppk	
	MSM1439	mevalonate kinase	
RECOMBINATION	***M. smithii* genes**	**Annotation**	**GO:0006310 - DNA recombination**
	MSM0002	integrase-recombinase protein	
	MSM0428	integrase-recombinase protein, phage integrase family	
	MSM0611	DNA repair protein, RadB	
	MSM0645	ATP-dependent DNA ligase, Cdc9	
	MSM1333	DNA repair protein RadA, RadA	
	MSM1523	transposase	
	MSM1640	DNA intergrase/recombinase, phage integrase family	
	MSM1742	predicted integrase, phage integrase-like family	