

1 **Supplemental information**

2 **Comparative Genomics of Syntrophic Branched-Chain Fatty Acid Degrading Bacteria**

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18 **Materials and Methods**

19 Clustered regularly interspaced short palindromic repeats (CRISPRs) were identified
20 using the CRISPRs web server (6). Alignment of the translated amino acid sequences and
21 construction of maximum likelihood (ML) trees of acyl-CoA dehydrogenase, enoyl-CoA
22 hydratase, 3-hydroxyacyl-CoA dehydrogenase, acetyl-CoA acetyltransferase, and isobutyryl-
23 CoA mutase were performed with the MEGA version 6.06 (5, 15). For phylogenetic
24 comparison of genes involved in β -oxidation pathway, we tentatively annotated acyl-CoA
25 dehydrogenase, enoyl-CoA hydratase, 3-hydroxyacyl-CoA dehydrogenase, and acetyl-CoA
26 acetyltransferase genes from draft genome sequences of *Syntrophomonas palmitatica* strain

27 JCM 14374^T (accession no. NZ_BBCE00000000) and *Syntrophomonas zehnderi* strain OL-
28 4^T (NZ_CGIH00000000) by using Prokka version 1.11 (10). The topology of the trees was
29 estimated by 1,000 bootstrap replicates (4). The Jones-Taylor-Thornton (JTT) model and
30 nearest-neighbor-interchange (NNI) were used for substitution model and heuristic method,
31 respectively (7, 14).

32

33 **Results and Discussion**

34 *Genome statistics*

35 The quality of the genome of “*Syntrophomonas wolfei* subsp. *methylbutyratica*” strain
36 4J5, *Syntrophomonas wolfei* subsp. *wolfei* strain Göttingen, and *Syntrophothermus*
37 *lipocalidus* strain TGB-C1 seems to be high (>97%) enough for the comparative genomics
38 (Table S1). Approximately 1,800 genes of the strain 4J5 were highly homologous (>90%
39 amino acid identity) to Göttingen genes, whereas approximately 1,000 genes of the strains
40 4J5 and Göttingen have significant amino acid identity (>70%) with the genes of strain TGB-
41 C1 (Fig. S3).

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43 *Central metabolism, physiology, and transport systems*

44 In accordance with the genome of strain Göttingen (11), the 4J5 and TGB-C1
45 genomes encode the Embden–Meyerhof pathway, pentose phosphate pathway, partial
46 tricarboxylic acid (TCA) cycle, citrate (Re)-synthase gene cluster, and co-factor biosynthesis
47 for central metabolism (Table S2). Bacterial core RNA polymerase (*rpoA*, *rpoB*, *rpoC*, and
48 *rpoZ*) with sigma factors including general primary 70 factors (*rpoD*), heat stress factors
49 (*rpoE*), a flagella biogenesis factor (*fliA*, *rpoF*), and a nitrogen-limitation 54 factor (*rpoN*) are
50 identified in both of the strains. The RNA genes (rRNA and tRNA) were also found (Table
51 S7). To cope with disturbances of environmental conditions, the strain 4J5 genome encodes

52 thioresdoxin, rubrerythrin, superoxide dismutase, and molecular chaperone systems. The strain
53 TGB-C1 genome harbors these systems, except for superoxide dismutase.

54 The genes encoding flagellum components, type IV pilus synthesis, chemotaxis, and
55 sporulation are found in the genomes. In addition, all of the genes required for synthesis and
56 metabolize poly- β -hydroxyalkanoate (PHA) are found in the 4J5 genome, but not in the
57 TGB-C1 genome. The PHA granules have been observed in the cells of the strain 4J5 under
58 electron microscopic observation (16), implying that the strain 4J5 may utilize PHA under
59 thermodynamically unfavorable conditions for the degradation of VFAs and BCFAs as
60 suggested by previous culture- and genome-based studies on the strain Göttingen (1, 2, 8, 11).
61 We found the genes associated with clustered regularly interspaced short palindromic repeat
62 (CRISPR) within the genomes (Table S7). Although CRISPR is known as acquired immune
63 system against phages (12, 13), the ecological role of the CRISPRs observed in the syntroph
64 genomes remains obscure due to the absence of comprehensive study on CRISPR dynamics
65 in methanogenic ecosystem.

66 A total of 105 and 68 genes/gene clusters involved in transportation, secretion, and
67 drug resistance are found in the strain 4J5 and TGB-C1 genomes, respectively (Table S3). For
68 example, there are tungstate, molybdate, ferrous iron, zinc, cobalt, phosphate, sodium,
69 potassium, amino acids, and monosaccharides transporters. The strains Göttingen, 4J5, and
70 TGB-C1 shared almost all of the transport/secretion systems with some exceptions; for
71 example, ammonia transporters (Slip_1571 and Slip_2119) were found only in the strain
72 TGB-C1, suggesting that *Syntrophothermus lipocalidus* possesses nitrogen-associated
73 physiological function (discussed in main text).

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Table S1. Genome statistics

Attribute	<i>Syntrophomonas wolfei</i> subsp. <i>metylbutyratica</i> strain 4J5	<i>Syntrophomonas wolfei</i> subsp. <i>wolfei</i> strain Göttingen	<i>Syntrophothermus</i> <i>lipocalidus</i> strain TGB- C1
Reference	This study	(11)	(3)
Status	Draft	Complete	Complete
DNA scaffold	89	1	1
DNA, total (bp)	3,194,001	2,936,195	2,405,559
DNA, G+C content	45.55%	44.87%	50.99%
Genes total number	3,073	2,677	2,440
Protein coding genes	2,964 (96.5%)	2,574 (96.2%)	2,385 (97.8%)
RNA genes	54	65	55
rRNA genes	11	19	6
tRNA genes	43	46	46
Genes with function prediction	2,184 (73.7%)	1,507 (57.1%)	1,726 (70.74%)
CRISPR			
Site number	2	5	2
Spacer number	63, 126	3, 15, 36, 61, 185	119, 152
Genome quality			
Completeness	97.35%	97.35%	98.81%
Contamination	0.04%	0.21%	0.51%

Table S2. *Syntrophomonas wolfei* subsp. *mevibutyratica* strain 4J5^T genes relevant to general function.

Locus Tag	Gene Product Name	BLAST top hit in <i>Syntrophomonas wolfei</i> strain Goettingen		BLAST top hit in <i>Syntrophomonas lipocalidis</i> strain TGB-C1			
		Gene ID and annotation	Identity (%)	e-Value	Gene ID and annotation	Identity (%)	e-Value
Glycolysis / TCA cycle							
SWMB_00127	glkA, glucose	638137153 Swol_0259 glucokinase (EC 2.7.1.2)	93.2	0	646854887 Slip_1859 glucokinase (EC 2.7.1.2)	43.6	2E-61
SWMB_00126	pgi-pmi; glucosyl/inositol-6-phosphate isomerase	638138500 Swol_0260 bifunctional phosphoglucoase/phosphomannose isomerase (EC 5.3.1.8; EC 5.3.1.9)	95.6	0	646854886 Slip_1858 bifunctional phosphoglucoase/phosphomannose isomerase (EC 5.3.1.8; EC 5.3.1.9)	59.1	8E-46
SWMB_00515	glpK, fructose-1,6-bisphosphatase II	638139293 Swol_2409 hypothetical protein	98.2	0	646855333 Slip_2308 fructose-1,6-bisphosphatase, class II	76.9	0
SWMB_02090	pfkA, PFK, 6-phosphofruktokinase I	638139023 pfkA 6-phosphofruktokinase (EC 2.7.1.11)	97.8	0	646854513 pfkA 6-phosphofruktokinase (EC 2.7.1.11)	60.8	6E-133
SWMB_02719	pfkB, PFK, 6-phosphofruktokinase I	638139030 pfkB 6-phosphofruktokinase (EC 2.7.1.11)	98.1	0	646854145 pfkB 6-phosphofruktokinase (EC 2.7.1.11)	67.9	2E-166
SWMB_00513	FBA, fbaA, fructose-bisphosphate aldolase, class II	638139295 Swol_2411 fructose-bisphosphate aldolase (EC 4.12.1.3)	97.9	0	646855335 Slip_2310 fructose-bisphosphate aldolase (EC 4.1.2.13)	78.8	6E-166
SWMB_00112	TPI, tpiA, triosephosphate isomerase (TIM)	638137167 tpiA triosephosphate isomerase (EC 5.3.1.1)	92.8	0	646854878 tpiA triosephosphate isomerase (EC 5.3.1.1)	54.4	8E-93
SWMB_00114	GAPDH, gapA, glyceraldehyde 3-phosphate dehydrogenase	638137166 Swol_0272 glyceraldehyde 3-phosphate dehydrogenase (NAD ⁺) (EC 1.2.1.12)	98.5	0	646854880 Slip_1852 glyceraldehyde 3-phosphate dehydrogenase (NAD ⁺) (EC 1.2.1.12)	58.5	3E-147
SWMB_00113	PKC, pck, phosphoglycerate kinase	638137166 pck phosphoglycerate kinase (EC 2.7.2.3)	98.4	0	646854879 pck phosphoglycerate kinase (EC 2.7.2.3)	59.5	4E-175
SWMB_00111	gpmI, 2,3-bisphosphoglycerate-independent phosphoglycerate mutase	638137165 gpmI phosphoglycerate mutase (EC 5.4.2.1)	95.5	0	646854877 gpmI phosphoglycerate mutase (EC 5.4.2.1)	68.4	0
SWMB_00845	apM, 2,3-bisphosphoglycerate-independent phosphoglycerate mutase	638138180 Swol_1301 phosphoglycerate mutase (EC 5.4.2.1)	94.8	0	646853321 Slip_0290 phosphoglycerate mutase (EC 5.4.2.1)	56.1	3E-166
SWMB_00110	ENO, eno, enolase; phosphopyruvate hydratase	638137169 eno enolase (EC 4.2.1.11)	97.7	0	646854876 eno enolase (EC 4.2.1.11)	73.5	0
SWMB_02089	pyk, pyruvate kinase	638138922 Swol_2040 pyruvate kinase (EC 2.7.1.40)	97.9	0	646854732 Slip_1701 pyruvate kinase (EC 2.7.1.40)	61.7	0
SWMB_02328	pyruvate, phosphopyruvate kinase	638138392 Swol_1512 pyruvate phosphate dikinase (EC 2.7.9.1)	96.5	0	646854654 Slip_1625 pyruvate phosphate dikinase (EC 2.7.9.1)	75.2	0
SWMB_02693	pyruvate, pyruvate carboxylase	638137403 Swol_0519 pyruvate carboxylase, PYKA	97.6	0	646853453 Slip_0423 CoA-carboxylase, biotin carboxylase	48.6	6E-129
SWMB_02193	hydro-lyases, Fe-S type, tartarate/fumarate subfamily, beta region	638138505 Swol_1628 Fumarate hydratase beta subunit	98.1	1E-150	646855078 Slip_2051 hydro-lyase, Fe-S type, tartarate/fumarate subfamily, beta subunit	35.0	3E-29
SWMB_02194	hydro-lyases, Fe-S type, tartarate/fumarate subfamily, alpha region	638138506 Swol_1629 Fumarate hydratase alpha subunit	95.1	0	646855079 Slip_2052 hydro-lyase, Fe-S type, tartarate/fumarate subfamily, alpha subunit	30.6	2E-36
SWMB_01460	DL-D, pdhI, dihydrolipoamide dehydrogenase	638138860 Swol_1978 dihydrolipoamide dehydrogenase (EC 1.8.1.4)	94.4	0	646855207 Slip_2184 dihydrolipoamide dehydrogenase (EC 1.8.1.4)	39.4	3E-102
SWMB_00330	korD, 2-oxoglutarate ferredoxin oxidoreductase subunit delta	638138281 Swol_1401 4Fe-4S ferredoxin, iron-sulfur binding	37.1	3E-11	646855091 Slip_0043 4Fe-4S ferredoxin iron-sulfur binding domain protein	69.0	7E-40
SWMB_00331	korC, 2-oxoglutarate ferredoxin oxidoreductase subunit gamma	638138283 Swol_0038 2-oxoglutarate ferredoxin oxidoreductase, gamma subunit (EC 1.2.2.3)	95.9	6E-135	646853090 Slip_0042 Pyruvate/ketoglutarate oxidoreductase	65.1	6E-87
SWMB_00332	korB, 2-oxoglutarate ferredoxin oxidoreductase subunit beta	638138284 Swol_0037 2-oxoglutarate ferredoxin oxidoreductase, beta subunit (EC 1.2.2.3)	100.0	0	646853089 Slip_0041 thiamine pyrophosphate protein domain protein TPP-binding protein	79.3	7E-159
SWMB_00333	korA, 2-oxoglutarate ferredoxin oxidoreductase subunit alpha	638138285 Swol_0036 putative keto-oxoal ferredoxin oxidoreductase, alpha subunit	98.3	0	646853088 Slip_0040 pyruvate flavodoxin/ferredoxin oxidoreductase domain protein	77.4	0
SWMB_00728	korD, 2-oxoglutarate ferredoxin oxidoreductase subunit delta	638138281 Swol_1401 4Fe-4S ferredoxin, iron-sulfur binding	93.0	3E-45	646854802 Slip_1773 4Fe-4S ferredoxin iron-sulfur binding domain protein	59.1	1E-26
SWMB_00729	korA, 2-oxoglutarate ferredoxin oxidoreductase subunit alpha	638138280 Swol_1400 2-oxo-oxoal ferredoxin oxidoreductase, alpha subunit	97.7	0	646854801 Slip_1772 pyruvate flavodoxin/ferredoxin oxidoreductase domain protein	58.7	2E-93
SWMB_00730	korB, 2-oxoglutarate ferredoxin oxidoreductase subunit beta	638138279 Swol_1399 putative keto-oxoal ferredoxin oxidoreductase, beta subunit	98.4	0	646854800 Slip_1771 thiamine pyrophosphate protein domain protein TPP-binding protein	75.1	3E-145
SWMB_00731	korC, 2-oxoglutarate ferredoxin oxidoreductase subunit gamma	638138278 Swol_1398 2-oxoglutarate ferredoxin oxidoreductase gamma subunit	93.4	1E-127	646854799 Slip_1770 2-oxoglutarate ferredoxin oxidoreductase, gamma subunit (EC 1.2.2.3)	62.2	2E-82
					646853257 Slip_0223 fumarate reductase/succinate dehydrogenase flavoprotein domain protein		
re-citrate synthase gene cluster							
SWMB_01738	isocitrate dehydrogenase [NADP]	638137267 Swol_0378 isocitrate dehydrogenase (NADP) (EC 1.1.1.42)	97.9	0	646853542 Slip_0511 isocitrate dehydrogenase (NADP) (EC 1.1.1.42)	81.3	0
SWMB_01739	2,3-dimethylmalate dehydratase small subunit	638137266 Swol_0377 leuD 3-isopropylmalate dehydratase, small subunit (EC 4.2.1.3)	98.8	6E-121	646853541 Slip_0510 leuD 3-isopropylmalate dehydratase, small subunit	80.1	2E-99
SWMB_01740	2,3-dimethylmalate dehydratase large subunit	638137265 Swol_0376 leuC 3-isopropylmalate dehydratase, large subunit (EC 4.2.1.3)	97.8	0	646853540 Slip_0509 leuC homoacemate hydratase family protein	78.7	0
SWMB_01741	putative re-citrate synthase	638137264 Swol_0375 hypothetical protein	97.4	0	646853539 Slip_0508 homocitrate synthase	76.3	0
Pentose phosphate pathway							
SWMB_00140	tdkA, tdkB, transketolase	638137140 Swol_0244 transketolase subunit B (EC 2.2.1.1)	96.5	0	646854901 Slip_1873 transketolase subunit B (EC 2.2.1.1)	67.1	3E-157
SWMB_00141	tdkA, tdkB, transketolase	638137139 Swol_0243 transketolase subunit A (EC 2.2.1.1)	95.6	0	646854902 Slip_1874 transketolase subunit A (EC 2.2.1.1)	70.6	6E-138
SWMB_00514	tdkA, tdkB, transaldolase	638139294 tdkA transaldolase (EC 2.2.1.2)	96.1	2E-155	646855334 tdkA transaldolase (EC 2.2.1.2)	72.5	1E-116
SWMB_02744	PRP, ppsA, ribose-phosphate 3-epimerase	638138098 Swol_1233 ribose-5-phosphate 3-epimerase (EC 5.1.3.1)	98.8	0	646853901 Slip_0765 ribose-5-phosphate 3-epimerase (EC 5.1.3.1)	58.7	2E-93
SWMB_00294	PRP, ppsA, ribose-phosphate pyrophosphokinase	638138097 Swol_1376 pyruvate ferredoxin oxidoreductase, delta subunit (EC 1.2.1.7)	97.8	0	646853149 Swol_0765 ribose-phosphate pyrophosphokinase	76.6	5E-170
SWMB_01013	ppm-pgm, phosphomannomutase / phosphoglucomutase	638139034 Swol_2154 phosphomannomutase (EC 5.4.2.8)	94.0	0	646853797 Slip_0765 phosphomannomutase (EC 5.4.2.8)	69.4	0
SWMB_02559	deobP, phosphopentomutase	638137487 deobP phosphopentomutase	93.3	0	646853524 deobP phosphopentomutase	60.8	9E-171
SWMB_01012	ppm-pgm, phosphomannomutase / phosphoglucomutase	638139034 Swol_2154 phosphomannomutase (EC 5.4.2.8)	94.0	0	646853797 Slip_0765 phosphomannomutase (EC 5.4.2.8)	69.4	0
SWMB_02912	ppm-pgm, phosphomannomutase / phosphoglucomutase	638139034 Swol_2154 phosphomannomutase (EC 5.4.2.8)	94.0	0	646853797 Slip_0765 phosphomannomutase (EC 5.4.2.8)	69.4	0
SWMB_00294	PRP, ppsA, ribose-phosphate pyrophosphokinase	638138097 Swol_1376 pyruvate ferredoxin oxidoreductase, delta subunit (EC 1.2.1.7)	97.8	0	646853149 Swol_0765 ribose-phosphate pyrophosphokinase	76.6	5E-170
SWMB_02011	deoC, DERA, deoxyribose-phosphate aldolase	638138440 deoC Deoxyribose-phosphate aldolase	93.2	2E-150	646854663 deoC deoxyribose-phosphate aldolase	48.6	9E-62
					646855321 Slip_2294 sugar-phosphate isomerase, RpiB/LacA/LacB family		
					646853351 Slip_0321 PflB domain protein		
Amplimeric reactions							
SWMB_02089	pyk, pyruvate kinase	638138922 Swol_2040 pyruvate kinase (EC 2.7.1.40)	97.9	0	646854732 Slip_1701 pyruvate kinase (EC 2.7.1.40)	61.7	0
SWMB_02328	pyruvate, orthophosphate dikinase	638138392 Swol_1512 pyruvate phosphate dikinase (EC 2.7.9.1)	96.5	0	646854654 Slip_1625 pyruvate phosphate dikinase (EC 2.7.9.1)	75.2	0
SWMB_00006	porI, pyruvate ferredoxin oxidoreductase beta subunit	638138254 Swol_1374 pyruvate ferredoxin oxidoreductase, beta subunit	96.5	0			
SWMB_00007	porC, pyruvate ferredoxin oxidoreductase alpha subunit	638138255 Swol_1375 pyruvate ferredoxin oxidoreductase, alpha subunit (EC 1.2.1.7)	94.0	0			
SWMB_00008	porF, pyruvate ferredoxin oxidoreductase delta subunit	638138256 Swol_1376 pyruvate ferredoxin oxidoreductase, delta subunit (EC 1.2.1.7)	94.1	2E-70			
SWMB_00009	porG, pyruvate ferredoxin oxidoreductase gamma subunit	638138257 Swol_1377 pyruvate ferredoxin oxidoreductase, gamma subunit (EC 1.2.1.7)	93.8	1E-137			
SWMB_00921	porC, pyruvate ferredoxin oxidoreductase gamma subunit	638139117 Swol_2237 pyruvate ferredoxin oxidoreductase, gamma subunit (EC 1.2.1.7)	95.7	1E-121			
SWMB_00922	porF, pyruvate ferredoxin oxidoreductase delta subunit	638139116 Swol_2236 pyruvate ferredoxin oxidoreductase, delta subunit	96.5	7E-58			
SWMB_00923	porC, pyruvate ferredoxin oxidoreductase gamma subunit	638139115 Swol_2235 2-oxo-oxoal ferredoxin oxidoreductase, alpha subunit	99.2	0			
SWMB_00924	porF, pyruvate ferredoxin oxidoreductase beta subunit	638139114 Swol_2234 2-ketocacid ferredoxin oxidoreductase beta subunit	99.0	0			
SWMB_02955	aldelyde dehydrogenase (NAD ⁺)	63931138 Swol_0319 Aldelyde dehydrogenase	88.5	0			
SWMB_01418	Phosphoenolpyruvate synthase (2.7.9.2)						
SWMB_01420	Phosphoenolpyruvate synthase (2.7.9.2)						
SWMB_02538	Phosphoenolpyruvate synthase (2.7.9.2)						
SWMB_02598	Phosphoenolpyruvate synthase (2.7.9.2)						
RNA polymerase							
SWMB_00505	DNA-directed RNA polymerase subunit delta	638139048 Swol_2420 hypothetical protein	90.9	6E-50	646855343 Slip_2318 hypothetical protein	43.6	1E-17
SWMB_00509	DNA-directed RNA polymerase subunit beta	638139222 pfkA DNA-directed RNA polymerase subunit beta (EC 2.7.7.6)	98.3	0	646855267 pfkA DNA-directed RNA polymerase subunit beta (EC 2.7.7.6)	81.4	0
SWMB_00590	DNA-directed RNA polymerase subunit beta'	638139221 pfkB DNA-directed RNA polymerase subunit beta' (EC 2.7.7.6)	98.9	0	646855266 pfkB DNA-directed RNA polymerase subunit beta' (EC 2.7.7.6)	79.5	0
SWMB_00625	DNA-directed RNA polymerase subunit alpha	638139185 rpoA DNA-directed RNA polymerase subunit alpha (EC 2.7.7.6)	99.7	0	646855230 rpoA DNA-directed RNA polymerase subunit alpha (EC 2.7.7.6)	75.6	5E-177
SWMB_02752	DNA-directed RNA polymerase subunit omega	638138111 rpoZ DNA-directed RNA polymerase subunit omega (EC 2.7.7.6)	95.8	6E-35	646853888 rpoZ DNA-directed RNA polymerase subunit omega (EC 2.7.7.6)	64.4	9E-22
Sigma factor / anti-sigma factor							
SWMB_00121	rpoN, RNA polymerase sigma-54 factor	638137158 Swol_0265 RNA polymerase, sigma 54 subunit, RpoN/SigL	96.8	0	646854882 Slip_1854 RNA polymerase, sigma 54 subunit, RpoN/SigL	53.7	0
SWMB_00232	rpoC, RNA polymerase sigma-70 factor, ECF subfamily	638137032 Swol_0132 RNA polymerase, sigma-24 subunit, RpoE	89.2	1E-129	646854990 Slip_1965 RNA polymerase, sigma-24 subunit, RpoE	58.2	1E-41
SWMB_00233	mycothiol system anti-sigma-R factor	638137031 Swol_0131 putative transmembrane anti-sigma factor	91.3	0	646854992 Slip_1967 putative transmembrane anti-sigma factor	33.2	1E-71
SWMB_00495	Sigma-W factor	638137032 Swol_0132 RNA polymerase, sigma-24 subunit, RpoE	96.5	0	646854430 Slip_1410 RNA polymerase, sigma-24 subunit, ECF subfamily	35.0	1E-22
SWMB_00576	RNA polymerase sporulation-specific sigma factor	638139237 Swol_2351 RNA polymerase, sigma 30 subunit, SigH	100.0	0	646855281 Slip_2255 RNA polymerase, sigma 30 subunit, SigH	84.4	3E-130
SWMB_00768	rpoC, RNA polymerase sigma-70 factor, ECF subfamily	638137032 Swol_0132 RNA polymerase, sigma-24 subunit, RpoE	27.3	1E-48	646854430 Slip_1410 RNA polymerase, sigma-24 subunit, ECF subfamily	21.8	6E-07
SWMB_01098	Putative anti-sigma factor antagonist BtrV	638138944 Swol_2062 anti-sigma-F factor antagonist (stage II sporulation protein AA)	96.0	1E-64	646853556 Slip_0525 anti-sigma regulatory factor, SpoIIAA	31.5	9E-09
SWMB_01044	rpoC, RNA polymerase sigma-70 factor, ECF subfamily	638138940 Swol_2058 RNA polymerase, sigma-24 subunit, RpoE	97.1	1E-121	646854430 Slip_1410 RNA polymerase, sigma-24 subunit, ECF subfamily	26.5	1E-08
SWMB_01123	sigma-70 RNA polymerase sigma factor	638137818 Swol_0944 RNA polymerase sigma factor	91.8	1E-162	646853625 Slip_0594 putative RNA polymerase, sigma 28 subunit, FliA/WhiG subfamily	32.4	1E-19
SWMB_01321	RNA polymerase sigma factor for flagellar operon FliA	638137746 Swol_0878 RNA polymerase sigma 28 subunit, RpoG/SigF	96.6	0	646854014 Slip_0982 RNA polymerase, sigma 28 subunit, SigD/FliA/WhiG	63.1	6E-107
SWMB_01365	RNA polymerase sporulation-specific sigma factor	638137706 Swol_0836 RNA polymerase, sigma subunit, RpoG/SigG	99.6	3E-167	646853841 Slip_0808 RNA polymerase, sigma subunit, RpoG/SigG	80.2	6E-134
SWMB_01367	RNA polymerase sigma-35 factor precursor	638137705 Swol_0835 RNA polymerase, sigma 29 subunit, SigE	98.3	7E-173	646853840 Slip_0807 RNA polymerase, sigma 29 subunit, SigE	79.3	3E-124
SWMB_01423	rpoC, RNA polymerase sigma-70 factor, ECF subfamily	638138901 Swol_2019 RNA polymerase, sigma-24 subunit, RpoE	99.5	9E-142	646854990 Slip_1965 RNA polymerase, sigma-24 subunit, RpoE	45.0	3E-47
SWMB_01424	mycothiol system anti-sigma-R factor	638138900 Swol_2018 putative transmembrane anti-sigma factor	91.2	0	646854431 Slip_1411 hypothetical protein	27.2	0.0001
SWMB_01571	Putative anti-sigma factor antagonist BtrV	638138678 Swol_1795 anti-sigma regulatory factor, SpoIIAA	90.0	3E-65	646853556 Slip_0525 anti-sigma regulatory factor, SpoIIAA	22.3	0.0008
SWMB_01574	rpoC, RNA polymerase sigma-70 factor, ECF subfamily	638138674 Swol_1791 RNA polymerase, sigma-24 subunit, RpoE	91.3	1E-127	646854430 Slip_1410 RNA polymerase, sigma-24 subunit, ECF subfamily	27.2	1E-09
SWMB_01607	Anti-sigma-V factor RsvF	638138645 Swol_1762 hypothetical protein	92.5	3E-173	646853840 Slip_0807 RNA polymerase, sigma 29 subunit, SigE	44.7	1E-13
SWMB_01650	RNA polymerase sigma-28 factor precursor	638137385 Swol_0501 sigma 28 (flagella/sporulation)	95.2	1E-86	646854323 Slip_0393 RNA polymerase, sigma 27/28 subunit, RpsK/SigK	67.8	1E-53
SWMB_01951	Anti-sigma-W factor RsvF	63931177 Swol_1624 hypothetical protein	94.9	7E-155	646855347 Slip_2322 S-layer domain protein	25.0	0.00008
SWMB_02043	Putative anti-sigma factor antagonist BtrV	63813867					

SWMB_00182	flgD flagellar hook-associated protein 2	638137094 Swol_0197 Flagellar capping protein-like protein	36.8	4E-25	646854931 Slip_1904 flagellar hook-associated 2 domain protein	42.6	4E-28
SWMB_00184	Flagellar assembly factor Flw3	638137092 flw3 hypothetical protein	54.5	2E-50	646854933 flw3 protein of unknown function DUF188	47.7	1E-43
SWMB_00186	Flagellin	638137090 Swol_0193 Flagellin and related hook-associated protein-like protein	35.9	3E-13	646854936 Slip_1909 flagellar hook-associated protein 3	48.0	6E-51
SWMB_00187	flgK flagellar hook-associated protein 1 FlgK	638137089 Swol_0192 Flagellar hook-associated protein-like protein	83.0	0	646854937 Slip_1910 flagellar hook-associated protein FlgK	43.6	1E-50
SWMB_00189	Flagellar biosynthesis anti-sigma factor FlgM	638137087 Swol_0190 anti-sigma-28 factor, FlgM family	95.9	3E-54	646854939 Slip_1912 anti-sigma-28 factor, FlgM family	46.5	5E-19
SWMB_00190	Flagellar operon protein	638137086 Swol_0189 flagellar protein	98.6	1E-99	646854940 Slip_1913 flagellar protein	50.4	1E-42
SWMB_00551	flgG flagellar basal-body rod protein FlgG	638137257 Swol_2373 flagellar basal-body rod protein (flgG-2)	94.7	4E-171	646854931 Slip_2273 flagellar basal-body rod protein FlgG	52.9	2E-82
SWMB_00656	Flagellar biosynthetic protein FlhB	638138554 Swol_1476 flagellar biosynthesis	98.9	8E-57	646853949 Slip_0916 type III secretion exporter	68.6	9E-36
SWMB_01125	Flagellar rod assembly protein/muramidine FlgJ	638137820 Swol_0946 hypothetical protein	92.4	3E-79	646853757 Slip_0725 flagellar protein FlgJ	49.3	1E-23
SWMB_01126	flgK flagellar basal-body rod protein FlgK	638137821 Swol_0947 flagellar basal-body rod protein FlgK	95.8	0	646853758 Slip_0726 flagellar basal-body rod protein FlgK	63.2	1E-122
SWMB_01321	flhA RNA polymerase sigma factor for flagellar operon FlhA	638137746 Swol_0878 RNA polymerase, sigma 28 subunit, SigD/FlhA/WhiG	97.3	0	646854014 Slip_0982 RNA polymerase, sigma 28 subunit, SigD/FlhA/WhiG	63.1	6E-107
SWMB_01328	Flagellin site-determining protein YlhJ	638137399 Swol_0871 flagellin	96.8	0	646854007 Slip_0973 CysH-type ac-diamide synthase	57.8	2E-25
SWMB_01329	Flagella-associated GTP-binding protein	638137738 Swol_0870 hypothetical protein	93.8	0	646854006 Slip_0974 flagellar biosynthetic protein FlhF	43.1	4E-113
SWMB_01330	Flagellar biosynthesis protein FlhA	638137737 Swol_0869 flagella-associated protein	96.0	0	646854005 Slip_0973 flagellar biosynthesis protein FlhA	70.0	0
SWMB_01331	Flagellar biosynthetic protein FlhB	638137736 Swol_0868 flagellar biosynthesis/type III secretory pathway protein	96.8	0	646854004 Slip_0972 flagellar biosynthetic protein FlhB	58.7	2E-155
SWMB_01332	Flagellar biosynthetic protein FlhR	638137735 Swol_0867 flagellar biosynthetic protein FlhR	96.1	8E-172	646854003 Slip_0971 flagellar biosynthetic protein FlhR	50.6	2E-89
SWMB_01333	Flagellar biosynthetic protein FlhQ	638137734 Swol_0866 hypothetical protein	97.2	3E-55	646854002 Slip_0970 flagellar biosynthetic protein FlhQ	57.8	2E-25
SWMB_01334	Flagellar biosynthetic protein FlhP precursor	638137733 Swol_0865 flagellar biosynthetic protein	97.1	4E-166	646854001 Slip_0969 flagellar biosynthetic protein FlhP	69.8	4E-118
SWMB_01335	Flagella biosynthesis protein FlhZ	638137732 Swol_0864 hypothetical protein	91.9	1E-138	646854000 Slip_0968 hypothetical protein	37.4	7E-32
SWMB_01337	Flagellar motor switch protein FlhN	638137730 Swol_0862 CheC, inhibitor of MCP methylation	91.5	0	646853998 Slip_0966 CheC, inhibitor of MCP methylation	57.3	2E-151
SWMB_01338	Flagellar motor switch protein FlhM	638137729 Swol_0861 hypothetical protein	99.1	0	646853997 Slip_0965 flagellar motor switch protein FlhM	62.5	9E-161
SWMB_01339	Flagellar basal-body-associated protein FlhI	638137728 Swol_0860 flagellar protein (FlhI)-like protein	96.9	2E-109	646853996 Slip_0964 flagellar basal-body-associated protein FlhI	51.9	4E-51
SWMB_01340	Flagellar protein (FlhD)	638137727 Swol_0859 hypothetical protein	95.3	1E-38	646853995 Slip_0963 flagellar FlhD family protein	61.9	6E-24
SWMB_01341	Flagellar hook protein FlgE	638137726 Swol_0858 flagellar hook protein	59.4	8E-130	646853994 Slip_0962 flagellar hook-basal body protein	40.1	9E-49
SWMB_01342	Flagellar operon protein	638137725 Swol_0857 hypothetical protein	93.8	4E-61	646853993 Slip_0961 flagellar operon protein	54.3	9E-39
SWMB_01343	Flagellar basal body rod modification protein	638137724 Swol_0856 flagellar hook capping protein-like protein	83.3	9E-106	646853992 Slip_0960 flagellar hook capping protein	43.0	3E-34
SWMB_01344	Flagellar hook-length control protein FlhK	638137723 Swol_0855 flagellar hook-length control protein-like protein	57.2	3E-94	646853991 Slip_0959 flagellar hook-length control protein	40.3	2E-21
SWMB_01346	Flagellar export protein FlhJ	638137721 Swol_0853 hypothetical protein	96.0	3E-82	646853989 Slip_0957 flagellar export protein FlhJ	35.4	7E-18
SWMB_01347	flhI flagellin-specific ATP synthase	638137720 Swol_0852 type III secretion system ATPase, FlhI-YscN (EC 3.6.1.5)	96.6	0	646853988 Slip_0956 type III secretion system ATPase, FlhI-YscN (EC 3.6.1.5)	70.7	0
SWMB_01348	flhI flagellar assembly protein FlhI	638137719 Swol_0851 flagellar biosynthesis/type III secretory pathway protein-like protein	92.1	0	646853987 Slip_0955 flagellar assembly protein FlhI>Type III secretion system HrpE	40.0	1E-38
SWMB_01349	Flagellar motor switch protein Flg	638137718 Swol_0850	92.1	0	646853986 Slip_0954 flagellar motor switch protein Flg	75.1	8E-173
SWMB_01350	Flagellar M-ring protein	638137717 Swol_0849 flagellar M-ring protein FlhF	93.9	0	646853985 Slip_0953 flagellar M-ring protein FlhF	45.3	1E-17
SWMB_01351	Flagellar hook-basal body complex protein FlhE	638137716 flhE flagellar hook-basal body protein	85.3	9E-58	646853984 flhE flagellar hook-basal body complex protein FlhE	52.4	7E-29
SWMB_01353	Flagellar basal body rod protein FlgB	638137715 Swol_0846 hypothetical protein	91.3	8E-88	646853982 Slip_0950 flagellar basal-body rod protein FlgB	48.2	1E-38
SWMB_01934	Flagellum site-determining protein YlhJ	638138085 Swol_1211 nucleotide-binding protein	47.5	5E-82	646853371 Slip_0341 ATPase-like, ParA/Mnd	52.0	1E-89
SWMB_02893	Flagellar motor switch protein	638137721 Swol_0853 CheC, inhibitor of MCP methylation	95.8	5E-139	646854012 Slip_0980 CheC, inhibitor of MCP methylation	25.3	2E-45
SWMB_02606	Flagellar assembly protein P	638137151 Swol_0257 hypothetical protein	82.1	0	646853757 Slip_0725 flagellar protein FlgJ		
					646853758 Slip_0726 flagellar basal-body rod protein FlgG		
					646853983 Slip_0951 flagellar basal-body rod protein FlgC		
					646853984 Slip_0952 flhE flagellar hook-basal body complex subunit FlhE		
					646854932 Slip_1908 flagellin domain protein		
					646854932 Slip_1905 carbon source regulator, CsrA (could also regulate swarming and quorum sensing)		
Pilin							
SWMB_02048	cpaF, pilA, pilN assembly protein CpaF	638137415 Swol_0531 type II secretion system protein E	34.9	5E-10	646854946 Slip_1919 type II secretion system protein E	31.0	5E-40
SWMB_02057	Tip pilus assembly protein CpaA	638139006 Swol_2126 butyryl-CoA dehydrogenase (EC 1.3.99.2)	27.7	0.009	646854215 Slip_1187 Peptidyl pyridase	29.6	0.0010
SWMB_02441	Fimbrial assembly protein (PilN)	638137424 Swol_0540 hypothetical protein	94.6	4E-98	646854206 Slip_1178 Fimbrial assembly family protein	25.7	2E-00002
SWMB_02442	type IV pilus assembly protein PilM	638137423 Swol_0539 Tip pilus assembly protein ATPase PilM-like protein	89.4	0	646853433 Slip_0403 Tip pilus assembly protein ATPase PilM	16.3	0.00002
SWMB_02443	pilP, pilQ, peptidase (prepilin peptidase) / N-methyltransferase	638137422 Swol_0538 type 4 prepilin peptidase 1 (EC3.4.23.43) Aspartic peptidase MEROPS family 3	93.4	5E-135	646854215 Slip_1187 Prepilin peptidase	38.6	4E-47
SWMB_02447	major pilin subunit	638137416 Swol_0534 hypothetical protein	100.0	3E-99	646853418 Slip_1186 hypothetical protein	40.0	2E-09
SWMB_02448	type IV pilus assembly protein PilC	638137417 Swol_0533 type II secretion system protein	99.8	0	646853295 Slip_1014 type IV secretion system F domain protein	41.3	1E-97
SWMB_02449	twitching motility protein PilT	638137416 Swol_0532 twitching motility protein	99.3	0	646854216 Slip_1188 twitching motility protein	48.6	1E-115
SWMB_02450	type IV pilus assembly protein PilB	638137415 Swol_0531 type II secretion system protein E	92.1	0	646853431 Slip_0401 type II secretion system protein E (CspE)	51.7	2E-146
SWMB_00028	putative protein encoded in hypervariable junctions of pilus gene clusters	638137455 Swol_0572 hypothetical protein	42.7	5E-24			
SWMB_01569	putative protein encoded in hypervariable junctions of pilus gene clusters	638137455 Swol_0572 hypothetical protein	30.2	0.00007			
SWMB_01647	putative protein encoded in hypervariable junctions of pilus gene clusters	638137455 Swol_0572 hypothetical protein	39.3	0			
SWMB_02440	type IV pilus assembly protein PilO	638137425 Swol_0541 hypothetical protein	84.2	4E-159			
SWMB_02444	Tip pilus assembly protein PilX	638137421 Swol_0537 hypothetical protein	91.2	4E-89			
SWMB_02445	Type II secretory pathway, component PilQ	638137420 Swol_0536 hypothetical protein	97.4	6E-110			
SWMB_02446	putative type IV pilin N-term methylation site GFxxxE	638137419 Swol_0535 hypothetical protein	99.3	2E-101			
SWMB_03047	putative protein encoded in hypervariable junctions of pilus gene clusters	638137455 Swol_0572 hypothetical protein	23.7	0.0004			
SWMB_02458	Vernu, Chiton cassette protein D				646853426 Slip_0396 pilin assembly protein	37.0	2E-23
					646854951 Slip_1924 peptidase A2/A4 prepilin type IV		
					646854952 Slip_1925 PilP/Fap pilin component		
					646854008 Slip_0976 type IV pilus assembly PilZ		
					646854046 Slip_1014 type IV secretion system PilZ		
					646853435 Slip_0405 Pilus assembly protein, PilO		
					646853434 Slip_0404 Fimbrial assembly family protein		
					646853432 Slip_0402 Type 4 fimbrial biogenesis protein PilX, N-terminal domain		
					646854218 Slip_1190 PilT protein domain protein		
Sporulation							
SWMB_00101	Sporulation-specific N-acetylmuramoyl-L-alanine amidase	638137026 Swol_0126 N-acetylmuramoyl-L-alanine amidase	36.6	3E-20	646853299 Slip_0268 cell wall hydrolase/autolysin	35.0	1E-20
SWMB_00122	Sporulation transcription regulator WhiA	638137157 whiA hypothetical protein	95.9	0	646854883 whiA protein of unknown function DUF1979	50.0	5E-100
SWMB_00269	Stage II sporulation protein E	638136995 Swol_0093 Phosphoprotein phosphatase	94.8	0	646853450 Slip_1189 phosphoprotein phosphatase	42.6	0
SWMB_00274	spore coat biosynthesis protein YabQ	638136988 Swol_0086 hypothetical protein	97.4	4E-83	646853519 Slip_0115 Spore coat biosynthesis protein, YabQ	49.8	1E-42
SWMB_00275	Spore protein YabP	638136987 Swol_0085 hypothetical protein	100.0	4E-59	646853158 Slip_0114 sporulation protein YabP	44.4	1E-23
SWMB_00281	Stage II sporulation protein F	638136983 Swol_0081 stage V sporulation protein B	97.7	0	646853154 Slip_0110 polysaccharide biosynthesis protein	66.7	0
SWMB_00282	Stage V sporulation protein T	638136982 Swol_0080 transcriptional regulator, AbrB family	98.9	2E-130	646853153 Slip_0109 transcriptional regulator, AbrB family	73.9	8E-92
SWMB_00283	Spore germination protein YadE	638136981 Swol_0079 hypothetical protein	93.6	0	646853328 Slip_0297 spore germination protein	28.4	7E-23
SWMB_00284	Spore germination protein B1	638136980 Swol_0078 germination protein	99.4	4E-85	646853329 Slip_0296 CpaA spore germination protein	49.9	9E-99
SWMB_00285	Spore germination protein B3 precursor	638136979 Swol_0077 hypothetical protein	91.9	0	646853327 Slip_0296 germination protein, GerX/C family	36.4	1E-86
SWMB_00286	Spore germination protein B3 precursor	638136977 Swol_0075 hypothetical protein	88.7	0	646853327 Slip_0296 germination protein, GerX/C family	33.8	1E-67
SWMB_00289	Spore germination protein (amino acid permease)	638136976 Swol_0074 hypothetical protein	88.0	0	646854095 Slip_1063 spore germination protein	23.6	1E-14
SWMB_00298	stage II sporulation protein R	638136966 Swol_0073 pro-sigma-E processing factor spoRR	96.8	1E-134	646853414 Slip_1010 stage II sporulation protein R	58.3	2E-56
SWMB_00313	sporulation initiation protein YhcY/Yhl family	638136955 Swol_0052 hypothetical protein	91.1	2E-111	646853318 Slip_0057 sporulation initiation protein, YhcY/Yhl	39.8	5E-14
SWMB_00376	Stage II sporulation protein J	638136954 Swol_0051 hypothetical protein	98.1	6E-156	646854507 Slip_2382 protein translocase subunit yJcE	54.2	9E-95
SWMB_00382	Sporulation initiation inhibitor protein YscA	638139452 Swol_2568 chromosome segregation ATPase	97.3	0	646855401 Slip_2376 chromosome segregation ATPase	65.6	1E-124
SWMB_00387	putative sporulation protein YycC	638139447 Swol_2563 YycC	93.1	5E-142	646855394 Slip_2369 sporulation protein YycC	55.7	3E-66
SWMB_00404	Sporulation kinase E	638139431 Swol_2546 Signal transduction histidine kinase-like protein	20.3	0.0007	646854510 Slip_1119 putative PAS/PAC sensor protein	23.4	0.00065
SWMB_00512	Sporulation initiation phosphotransferase F	638139296 Swol_2042 response regulator receiver protein	99.3	0	646853329 Slip_0296 CpaA spore germination protein	49.9	9E-99
SWMB_00576	Stage 0 sporulation protein H	638139237 Swol_2351 RNA polymerase, sigma 30 subunit, SigH	100.0	1E-159	646855281 Slip_2254 RNA polymerase, sigma 30 subunit, SigH	84.4	8E-130
SWMB_00669	Sporulation initiation inhibitor protein soj	638138334 Swol_1454 chromosome partitioning protein	93.5	0	646854760 Slip_1729 Cofribin acid ac-diamide synthase	68.1	5E-131
SWMB_00717	putative spore protein YtlJ	638138294 Swol_1414 hypothetical protein	100.0	3E-98	646853383 Slip_0552 sporulation protein YtlJ	66.1	1E-55
SWMB_00719	Spore maturation protein A	638138293 Swol_1413 nucleoside recognition protein	97.5	2E-137	646853384 Slip_0553 nucleoside recognition domain protein	71.4	3E-63
SWMB_00815	stage II sporulation protein P	638138292 Swol_1412 nucleoside recognition protein	98.3	4E-124	646853385 Slip_0554 nucleoside recognition domain protein	74.2	5E-69
SWMB_00833	Stage IV sporulation protein A	638138203 Swol_1322 hypothetical protein	97.7	0	646854498 Slip_1476 stage II sporulation protein P	47.6	3E-106
SWMB_00886	Stage III sporulation protein E	638138140 Swol_1265 DNA translocase FtsK	95.7	0	646854070 Slip_1038 DNA translocase FtsK	53.4	0
SWMB_01127	sporulation protein, YlmC/YlmH family	638137822 Swol_0948 hypothetical protein	97.9	3E-63	646853384 Slip_0553 nucleoside recognition domain protein	64.5	4E-32
SWMB_01186	Stage V sporulation protein B2	638137856 Swol_0903 SpoVx	99.3	0	646853411 Slip_1080 A.A.A. ATPase germination domain protein	63.5	4E-122
SWMB_01255	Spore germination protein	638137923 Swol_1052 SpoE germination protein-like protein	99.1	0	646853068 Slip_0022 Spore germination protein-like Gmad2	58.6	1E-106
SWMB_01258	Sporulation kinase E	638137925 Swol_1054 PAS/PAC sensor signal transduction histidine kinase (EC 2.7.1.33)	89.2	0	646853849 Slip_0816 PAS/PAC sensor signal transduction histidine kinase (EC 2.7.1.33)	24.9	4E-21
SWMB_01267	Sporulation protein YumB	638137797 Swol_0931 hypothetical protein	98.2	4E-155	646853750 Slip_0723 sporulation protein YumB	51.7	4E-66
SWMB_01281	Small, acid-soluble spore proteins, alpha beta type	638137798 Swol_0918 hypothetical protein	98.3	5E-36	646854098 Slip		

Table S4. *Syntrophomonas wolfei* subsp. *methylbutyratica* strain 4J5^T genes encoding β -oxidation pathway.

Locus tag	Gene product	Best BLAST hit in:					
		<i>Syntrophomonas wolfei</i> Goettingen			<i>Syntrophothermus lipocalidus</i> DSM 12680		
		Locus tag	%ID	e-value	Locus tag	%ID	e-value
Acyl-CoA dehydrogenase							
SWMB_00118	Acyl-CoA dehydrogenase	Swol_0268	99.2	0	Slip_0874	82.6	0
SWMB_00649	Acyl-CoA dehydrogenase	Swol_1483	98.7	0	Slip_0286	83.5	0
SWMB_01042	Acyl-CoA dehydrogenase	Swol_2126	98.7	0	Slip_0456	63.1	0
SWMB_01416	Acyl-CoA dehydrogenase	Swol_0788	99.7	0	Slip_0501	70.2	0
SWMB_01499	Acyl-CoA dehydrogenase, short-chain specific	Swol_1933	99.2	0	Slip_0881	72.0	0
SWMB_01701	Acyl-CoA dehydrogenase	Swol_0788	66.5	0	Slip_0501	73.9	0
SWMB_01732	Acyl-CoA dehydrogenase, short-chain specific	Swol_0384	97.7	0	Slip_0481	56.4	0
SWMB_01942	Acyl-CoA dehydrogenase	Swol_0788	44.3	1E-105	Slip_1241	75.3	0
SWMB_02100	Acyl-CoA dehydrogenase	Swol_2052	94.9	0	Slip_0881	71.6	0
SWMB_02510	Acyl-CoA dehydrogenase	Swol_0384	72.2	0	Slip_0481	54.9	0
Enoyl-CoA hydratase							
SWMB_00384	putative enoyl-CoA hydratase echA8	Swol_2566	87.4	3.00E-161			
SWMB_00648	2-methyl-but-2-enoyl-CoA hydratase	Swol_1484	97.3	0	Slip_2197	63.5	1.00E-120
SWMB_01414	putative enoyl-CoA hydratase echA8	Swol_0790	96.5	0	Slip_2197	63.1	1E-113
SWMB_01496	putative enoyl-CoA hydratase echA8	Swol_1936	98.9	0	Slip_2197	66.5	3E-122
SWMB_01703	2-methyl-but-2-enoyl-CoA hydratase	Swol_0790	42.3	1E-59	Slip_0502	65.6	1E-115
SWMB_02083	putative enoyl-CoA hydratase echA8	Swol_2031	97.7	0	Slip_2197	64.6	1E-115
SWMB_02134	putative enoyl-CoA hydratase echA8	Swol_0650	98.4	0			
SWMB_02508	2-methyl-but-2-enoyl-CoA hydratase	Swol_2031	67.3	9.00E-129	Slip_2197	56.9	8.00E-100
SWMB_03023	putative enoyl-CoA hydratase echA8	Swol_2031	45.8	9E-76	Slip_0502	68.0	2E-125
3-hydroxybutyryl-CoA dehydrogenase							
SWMB_00002	putative 3-hydroxybutyryl-CoA dehydrogenase	Swol_0307	99.3	0	Slip_0503	54.6	9E-107
SWMB_00647	2-methyl-3-hydroxybutyryl-CoA dehydrogenase	Swol_1485	97.5	0	Slip_0285	82.9	6E-168
SWMB_01413	putative 3-hydroxybutyryl-CoA dehydrogenase	Swol_0791	98.6	0	Slip_1415	56.8	2E-112
SWMB_01497	putative 3-hydroxybutyryl-CoA dehydrogenase	Swol_1935	99.3	0	Slip_1415	82.4	5E-172
SWMB_01704	2-methyl-3-hydroxybutyryl-CoA dehydrogenase	Swol_0435	93.0	7.00E-129	Slip_0503	71.3	7E-123
SWMB_01947	putative 3-hydroxybutyryl-CoA dehydrogenase	Swol_0435	61.8	1.00E-84	Slip_1238	73.2	2E-145
SWMB_02082	putative 3-hydroxybutyryl-CoA dehydrogenase	Swol_2030	99.3	0	Slip_0503	55.6	5E-109
SWMB_02507	2-methyl-3-hydroxybutyryl-CoA dehydrogenase	Swol_0791	68.8	9E-139	Slip_0503	54.6	5E-103
SWMB_02718	putative 3-hydroxybutyryl-CoA dehydrogenase	Swol_1171	96.8	0	Slip_1415	53.4	5E-107
Acetyl-CoA acetyltransferase							
SWMB_00001	Acetyl-CoA acetyltransferase	Swol_0308	97.5	0	Slip_0499	59.9	9E-172
SWMB_00646	2-methyl-acetoacetyl-CoA acetyltransferase	Swol_1486	97.8	0	Slip_0284	62.8	1E-163
SWMB_01415	Acetyl-CoA acetyltransferase	Swol_0789	98.0	0	Slip_0499	66.8	0
SWMB_01498	Acetyl-CoA acetyltransferase	Swol_1934	98.0	0	Slip_0880	79.8	0
SWMB_01702	2-methyl-acetoacetyl-CoA acetyltransferase	Swol_0789	74.5	0	Slip_0499	66.5	0
SWMB_01946	Acetyl-CoA acetyltransferase	Swol_0789	72.7	0	Slip_0499	68.4	0
SWMB_02099	Acetyl-CoA acetyltransferase	Swol_2051	95.7	0	Slip_0880	81.1	0
SWMB_02161	Acetyl-CoA acetyltransferase	Swol_0675	99.5	0	Slip_0499	67.3	0
SWMB_02509	2-methyl-acetoacetyl-CoA acetyltransferase	Swol_0675	62.6	0	Slip_0499	65.8	0
CoA transferase							
SWMB_00469	Succinyl-CoA:coenzyme A transferase	Swol_0436	72.0	0	Slip_0882	62.0	0
SWMB_00650	Acyl-CoA:acetate/3-ketoacid CoA transferase	Swol_1482	96.0	0	Slip_0287	80.9	0
SWMB_00651	Acyl-CoA:acetate/3-ketoacid CoA transferase	Swol_1481	99.3	0	Slip_0288	80.8	8E-167
SWMB_01218	Succinyl-CoA:coenzyme A transferase	Swol_1014	96.2	0	Slip_0882	57.3	0
SWMB_01500	Succinyl-CoA:coenzyme A transferase	Swol_1932	99.8	0	Slip_0882	56.5	0
SWMB_01699	Acyl-CoA:acetate/3-ketoacid CoA transferase	Swol_0436	97.3	0	Slip_0882	60.8	0
SWMB_01700	Acyl-CoA:acetate/3-ketoacid CoA transferase	Swol_0309	50.3	3.00E-162	Slip_0500	50.3	9E-164
SWMB_01907	Succinyl-CoA:coenzyme A transferase	Swol_1735	98.6	0	Slip_0665	40.2	2E-108
SWMB_01923	butyryl-CoA:acetate CoA-transferase	Swol_1744	95.9	1E-119	Slip_0665	31.9	1E-24
SWMB_02359	Succinyl-CoA:coenzyme A transferase	Swol_1147	96.7	0	Slip_0500	62.6	0
SWMB_02505	Acyl-CoA:acetate/3-ketoacid CoA transferase	Swol_1147	63.1	0	Slip_0500	59.2	0
SWMB_03019	butyryl-CoA:acetate CoA-transferase	Swol_1932	34.3	2E-11	Slip_0882	29.1	0.0000007
SWMB_03052	Succinyl-CoA:coenzyme A transferase	Swol_0787	98.2	4E-123	Slip_0500	73.1	0
Acetate kinase/phosphotransacetylase gene cassette							
SWMB_02801	Phosphate acetyltransferase (phosphotransacetylase)	Swol_0767	98.48	0	Slip_0902	77.9	0
SWMB_02802	Acetate kinase	Swol_0768	98.5	0	Slip_0903	82.1	0
Acyl-CoA synthetase							
SWMB_02363	Long-chain-fatty-acid--CoA ligase (for PHA metabolism?)	Swol_1144	93.6	0	Slip_0583	25.9	4E-26
SWMB_02710	Long-chain-fatty-acid--CoA ligase FadD13 (for coenzyme A biosynthesis?)	Swol_1180	99.3	0	Slip_1686	64.4	0

The gray bars indicate that there are no corresponding genes with significant similarity (<20%).

Table S5. *Syntrophothermus lipocalidus* strain TGB-C1 genes encoding β -oxidation pathway.

Locus tag	Gene product	Best BLAST hit in:					
		<i>Syntrophomonas wolfei</i> Goettingen			<i>Syntrophomonas wolfei</i> subsp. <i>metylbutyratica</i> JCM14075T		
		Locus tag	%ID	e-value	Locus tag	%ID	e-value
Acyl-CoA dehydrogenase							
Slip_0286	acyl-CoA dehydrogenase	Swol_1483	84.3	0	SWMB_00649	83.5	0
Slip_0481	acyl-CoA dehydrogenase	Swol_0384	57.0	0	SWMB_02510	54.9	0
Slip_0501	acyl-CoA dehydrogenase	Swol_0788	70.2	0	SWMB_01701	73.9	0
Slip_0581	acyl-CoA dehydrogenase domain protein	Swol_0788	34.8	4.00E-66	SWMB_01701	37.4	9.00E-72
Slip_0881	acyl-CoA dehydrogenase	Swol_1933	72.1	0	SWMB_01499	72.0	0
Slip_0884	acyl-CoA dehydrogenase						
Slip_1241	Butyryl-CoA dehydrogenase	Swol_0788	44.5	9.00E-112	SWMB_01942	75.3	0
Slip_1986	acyl-CoA dehydrogenase						
Slip_1987	short-chain dehydrogenase/reductase						
Slip_2083	acyl-CoA dehydrogenase						
Slip_2087	short-chain dehydrogenase/reductase						
Enoyl-CoA hydratase							
Slip_0485	short chain enoyl-CoA hydratase						
Slip_0486	Enoyl-CoA hydratase/isomerase						
Slip_0490	Enoyl-CoA hydratase						
Slip_0502	short chain enoyl-CoA hydratase	Swol_2031	50.4	2.00E-83	SWMB_03023	68.0	2.00E-125
Slip_0580	enoyl-CoA hydratase/isomerase	Swol_2031	47.7	9.00E-79	SWMB_01498	48.1	2.00E-77
Slip_1234	3-hydroxybutyryl-CoA dehydrogenase	Swol_1936	43.5	4.00E-72	SWMB_01090	30.1	7.00E-22
Slip_1989	Enoyl-CoA hydratase/isomerase						
Slip_2089	Enoyl-CoA hydratase/isomerase	Swol_2566	36.6	5.00E-41	SWMB_00384	37.2	2.00E-44
Slip_2197	short chain enoyl-CoA hydratase	Swol_1936	67.3	3.00E-123	SWMB_01496	66.5	3.00E-122
3-hydroxybutyryl-CoA dehydrogenase							
Slip_0285	3-hydroxyacyl-CoA dehydrogenase	Swol_1485	83.7	1.00E-180	SWMB_00647	82.6	7.00E-180
Slip_0503	3-hydroxyacyl-CoA dehydrogenase	Swol_1935	55.6	4.00E-109	SWMB_01704	71.3	1.00E-150
Slip_0579	3-hydroxyacyl-CoA dehydrogenase NAD-binding protein	Swol_1935	47.3	3.00E-92	SWMB_01497	47.3	5.00E-92
Slip_1238	3-hydroxybutyryl-CoA dehydrogenase	Swol_1935	54.7	1.00E-110	SWMB_01947	73.2	2.00E-101
Slip_1415	3-hydroxybutyryl-CoA dehydrogenase	Swol_1935	82.8	2.00E-172	SWMB_01497	82.4	5.00E-172
Slip_2088	putative 3-hydroxybutyryl-CoA dehydrogenase						
Acetyl-CoA acetyltransferase							
Slip_0284	acetyl-CoA acetyltransferase	Swol_1486	62.8	2.00E-177	SWMB_00646	62.8	8.00E-178
Slip_0464	Propanoyl-CoA C-acyltransferase						
Slip_0465	Acetyl-CoA acetyltransferase						
Slip_0479	Acetyl-CoA acetyltransferase						
Slip_0499	Acetyl-CoA acetyltransferase	Swol_0675	67.0	0	SWMB_02161	67.3	0
Slip_0577	putative acetyl-CoA acetyltransferase	Swol_2051	28.2	1.00E-33	SWMB_01702	30.0	1.00E-34
Slip_0880	Acetyl-CoA acetyltransferase	Swol_2051	80.3	0	SWMB_02099	81.1	0
Slip_1111	Acetyl-CoA acetyltransferase						
Slip_1236	Acetyl-CoA acetyltransferase	Swol_2051	22.9	8.00E-11	SWMB_01703	47.1	7.00E-85
Slip_1985	acetyl-CoA acetyltransferase						
Slip_1988	acetyl-CoA acetyltransferase						
Slip_2084	Crotonobetainyl-CoA: carnitine CoA-transferase CaiB and related acyl-CoA transferases						
Slip_2085	acetyl-CoA acetyltransferase						
CoA transferase							
Slip_0098	putative acyl CoA:acetate/3-ketoacid CoA transferase, alpha subunit				SWMB_01948	72.4	6.00E-67
Slip_0099	putative acyl CoA:acetate/3-ketoacid CoA transferase, beta subunit						
Slip_0287	coenzyme A transferase	Swol_1482	78.5	0	SWMB_00650	80.9	0
Slip_0288	putative acyl CoA:acetate/3-ketoacid CoA transferase	Swol_1481	80.4	4.00E-166	SWMB_00651	80.8	8.00E-167
Slip_0500	acetyl-CoA hydrolase/transferase	Swol_0309	74.7	0	SWMB_03052	73.1	0
Slip_0578	putative CoA-transferase family III						
Slip_0665	putative 4-hydroxybutyrate CoA-transferase	Swol_1744	40.1	9.00E-109	SWMB_01907	40.2	2.00E-108
Slip_1192	coenzyme A transferase						
Slip_1193	coenzyme A transferase						
Slip_1195	putative acyl CoA:acetate/3-ketoacid CoA transferase beta subunit						
Slip_1196	putative acyl CoA:acetate/3-ketoacid CoA transferase alpha subunit						
Slip_1239	Acyl-CoA:acetate/3-ketoacid CoA transferase	Swol_1481	41.4	7.00E-54	SWMB_00651	41.4	9.00E-54
Slip_1240	Acyl-CoA:acetate/3-ketoacid CoA transferase	Swol_1482	29.1	3.00E-29	SWMB_01944	30.7	2.00E-35
Slip_1981	CoA-transferase family III domain						
Acetate kinase/phosphotransacetylase gene cassette							
Slip_0902	Phosphate acetyltransferase (phosphotransacetylase)	Swol_0767	76.7	0	SWMB_02801	77.9	0
Slip_0903	Acetate kinase	Swol_0768	82.12	0	SWMB_02802	82.1	0
Isomerization							
Slip_0757	Cob(I)alamin adenosyltransferase						
Slip_0758	Isobutyryl-CoA mutase, N-terminal domain subunit						
Slip_0759	Isobutyryl-CoA mutase, C-terminal domain subunit (cobalamin B12-binding domain protein)						
Slip_0760	LAO/AO transport system ATPase, MeaB-like protein						
Acyl-CoA synthetase							
Slip_1686	Acyl-CoA synthetase (AMP-forming)/AMP-acid ligase II (for coenzyme A biosynthesis?)	Swol_1180	64.4	0	SWMB_02710	64.4	0
Slip_0583	Acyl-CoA synthetase (AMP-forming)/AMP-acid ligase II	Swol_1180	31.1	6.00E-67	SWMB_02710	30.6	5.00E-72
Slip_0475	Acyl-CoA synthetase (AMP-forming)/AMP-acid ligase II						

The gray bars indicate that there are no corresponding genes with significant similarity (<20%).

Table S6. *Syntrophomonas wolfei* subsp. *meritlithytratica* strain 415^T genes encoding syntrophic electron flow

Locus tag in JCM14075	Predicted product	<i>Syntrophomonas wolfei</i> Goettingen			<i>Syntrophomonas lipocalculus</i> TGB-C1			Locus tag in TGB-C1	Predicted product	Closely related strain			
		Locus Tag	%ID	e-value	Locus Tag	%ID	e-value			Locus Tag	%ID	e-value	
Electron-bifurcating [FeFe] hydrogenase (H⁺ + NADH + Fd_{ox} ↔ H₂ + NAD⁺ + Fd_{ox})													
SWMB_01221	Fe-only hydrogenase	Swol_1017	98.1	0	Slip_0125	81.4	0						
SWMB_01222	NADH:UQ oxidoreductase, 51 kDa subunit	Swol_1018	98.5	0	Slip_0124	76.6	0						
SWMB_01223	NADH:UQ oxidoreductase, 24 kDa subunit	Swol_1019	98.0	8E-104	Slip_0123	73.5	2E-72						
Ferredoxin [FeFe] hydrogenase (H⁺ + Fd_{ox} ↔ H₂ + Fd_{ox})													
SWMB_00486	NADP-reducing hydrogenase subunit HndC	Swol_2436	97.5	0	Slip_0543	82.4	0						
Periplasmic [FeFe] hydrogenase (MQ ↔ H₂)													
SWMB_01505	Cytochrome b(N-terminal)/b6/pefB	Swol_1927	95.6	3E-154	Slip_1532	71.2	3E-120						
SWMB_01506	Periplasmic [Fe] hydrogenase small subunit precursor	Swol_1926	92.3	1E-79	Slip_1533	68.7	5E-57						
SWMB_01507	Periplasmic [Fe] hydrogenase large subunit	Swol_1925	93.6	0	Slip_1534	76.6	0						
Periplasmic [NiFe] hydrogenase (MQ ↔ H₂)													
SWMB_01823	Hydrogenase expression/formation protein HypE				Slip_0392	64.6	1E-158						
SWMB_01824	Hydrogenase expression/formation protein HypD				Slip_0391	67.4	1E-179						
SWMB_01825	Hydrogenase isoenzymes formation protein HypC				Slip_0390	65.3	3E-32						
SWMB_01826	[NiFe] hydrogenase maturation protein HypF				Slip_0389	63.9	0						
SWMB_01827	Hydrogenase 2 maturation protease				Slip_0388	47.4	3E-45						
SWMB_01828	putative Ni/Fe-hydrogenase 1 β-type cytochrome subunit, hyaC				Slip_0387	71.2	2E-107						
SWMB_01829	Periplasmic [NiFeSe] hydrogenase large subunit, hyaB				Slip_0386	70.5	0						
SWMB_01830	Periplasmic [NiFe] hydrogenase large subunit precursor, hyaA				Slip_0385	73.0	4E-18						
SWMB_01831	Periplasmic [NiFeSe] hydrogenase small subunit precursor				Slip_0384	76.9	0						
SWMB_01832	Hydrogenase isoenzymes nickel incorporation protein HypB				Slip_0384	59.7	1E-92						
SWMB_01833	Hydrogenase nickel incorporation protein HypA/HypF				Slip_0383	49.1	2E-37						
Energy conserving hydrogenase, Ech (H⁺ + Fd_{ox} ↔ H₂ + Fd_{ox})													
								Slip_0655	echA ech hydrogenase subunit A	Tph_c21360	41.6	3E-141	
								Slip_0656	echB ech hydrogenase subunit B	Tph_c21350	50.4	5E-87	
								Slip_0657	echC ech hydrogenase subunit C	Tph_c21340	66.2	4E-65	
								Slip_0658	echD ech hydrogenase subunit D	Tph_c21330	34.8	1E-15	
								Slip_0659	echE ech hydrogenase subunit E	Tph_c21320	54.4	5E-139	
								Slip_0660	NADH:ubiquinone reductase (H ⁺)-translocating	Tph_c21310	41.5	1E-20	
Formate dehydrogenase O (Formate ↔ MQ)													
SWMB_01402	Molybdopterin molybdenumtransferase	Swol_0802	95.5	0	Slip_0566	52.8	7E-152						
SWMB_01403	Molybdopterin molybdenumtransferase	Swol_0801	95.5	0	Slip_0567	56.9	0						
SWMB_01404	Formate dehydrogenase subunit alpha precursor, fdoG	Swol_0800	96.2	1E-152	Slip_1434	77.5	9E-115						
SWMB_01405	Formate dehydrogenase subunit alpha precursor, fdoG	Swol_0799	96.9	0	Slip_1434	70.4	0						
SWMB_01406	Formate dehydrogenase-N subunit beta, fdoH	Swol_0798	98.5	0	Slip_1433	58.1	5E-121						
SWMB_01407	Formate dehydrogenase-N subunit gamma, fdoI	Swol_0797	99.6	5E-169	Slip_1432	74.0	7E-125						
SWMB_01408	formate dehydrogenase accessory protein FdhE	Swol_0796	95.3	0	Slip_1431	35.4	1E-67						
SWMB_01533	Formate dehydrogenase subunit alpha precursor, fdoG	Swol_1826	98.5	8E-145									
SWMB_01535	Formate dehydrogenase, nitrate-insoluble, major subunit precursor, fdoG	Swol_1825	92.5	0									
SWMB_01536	Formate dehydrogenase-N subunit beta, fdoH	Swol_1824	93.3	0									
SWMB_01537	Formate dehydrogenase-O subunit gamma, fdoI	Swol_1823	96.4	3E-158									
SWMB_01538	formate dehydrogenase accessory protein FdhE	Swol_1822	93.3	4E-180									
SWMB_01539	putative molybdopterin biosynthesis protein MoeA/LysR substrate binding-d	Swol_1821	94.9	0									
Electron-bifurcating formate dehydrogenase (CO₂ + NADH + Fd_{ox} ↔ Formate + NAD⁺ + Fd_{ox})													
SWMB_02818	NADH-quinone oxidoreductase subunit E	Swol_0783	96.0	4E-103									
SWMB_02819	NADP-reducing hydrogenase subunit HndC	Swol_0784	98.3	0									
SWMB_02820	Putative formate dehydrogenase/NADH-ubiquinone oxidoreductase-G	Swol_0785	97.2	0									
SWMB_02821	Formate dehydrogenase H	Swol_0786	98.3	0									
SWMB_01527	Putative formate dehydrogenase	Swol_1831	98.6	0									
SWMB_01528	Formate dehydrogenase H	Swol_1830	98.0	0									
SWMB_01529	NADP-reducing hydrogenase subunit HndA	Swol_1829	96.6	2E-103									
SWMB_01530	NADP-reducing hydrogenase subunit HndC	Swol_1828	98.8	0									
SWMB_01228	NADP-reducing hydrogenase subunit HndC	Swol_1024	98.5	0									
SWMB_01229	NADP-reducing hydrogenase subunit HndA	Swol_1025	97.3	3E-106									
SWMB_01230	Molybdopterin molybdenumtransferase	Swol_1026	94.5	0									
SWMB_01231	bifunctional molybdenum cofactor biosynthesis protein MoeC/MogA	Swol_1027	96.5	0									
SWMB_01232	Formate dehydrogenase H	Swol_1028	98.7	0									
SWMB_01233	Putative formate dehydrogenase	Swol_1029	98.9	0									
NAD-dependent formate dehydrogenase (CO₂ + NADH ↔ Formate + NAD⁺)													
								Slip_1031	Formate dehydrogenase (NADP) alpha subunit	<i>S. wolfei</i> subsp. <i>meritlithytratica</i> JCM14075	SWMB_02820	66.7	0
								Slip_1032	Formate dehydrogenase (NADP) alpha subunit	SWMB_02821	69.4	0	
Flox-Hdr system													
SWMB_01721	Heterodisulfide reductase subunit C (HdC)	Swol_0394	100.0	4E-139	Slip_2075	63.4	2E-86						
SWMB_01720	Heterodisulfide reductase subunit B (HdB)	Swol_0395	92.1	0	Slip_2074	65.9	6E-142						
SWMB_01719	Heterodisulfide reductase subunit A (HdA)	Swol_0396	99.0	5E-144									
SWMB_01718	Heterodisulfide reductase subunit A (HdA)	Swol_0397	98.9	0	Slip_2073	75.5	0						
SWMB_01717	Hydrogenase subunit D (HdD)	Swol_0398-0399	97.1	4E-47	Slip_2072	74.7	1E-34						
SWMB_01716	Hydrogenase subunit B (HdB)	Swol_0400	98.3	0	Slip_2071	61.2	2E-143						
SWMB_01715	Flavoprotein oxidoreductase subunit A (FloxA)	Swol_0401	97.6	0	Slip_2070	55.5	2E-134						
SWMB_01714	Flavoprotein oxidoreductase subunit B (FloxB)	Swol_0402	98.2	0	Slip_2069	76.4	5E-162						
Fix system (+AD)													
SWMB_01042	acyl-CoA dehydrogenase	Swol_2126	98.7	0	Slip_0874	38.6	3E-87						
SWMB_01043	ETF-ubiquinone oxidoreductase (FixC)	Swol_2124	98.4	0	Slip_0877	47.9	3E-127						
SWMB_01044	Ferredoxin (FixX)	Swol_2123	95.7	2E-63	Slip_0878	42.4	4E-16						
SWMB_01045	Electron transfer flavoprotein β subunit (FixA)	Swol_2122	94.4	2E-148	Slip_0875	35.5	2E-38						
SWMB_01046	Electron transfer flavoprotein α subunit (FixB)	Swol_2121	96.5	0	Slip_0876	36.6	4E-58						
Fix system (+AD/EH/CT)													
								Slip_0455	acyl-CoA dehydrogenase	<i>S. wolfei</i> subsp. <i>meritlithytratica</i> JCM14075			
								Slip_0456	acyl-CoA dehydrogenase	SWMB_01042	63.1	2E-178	
								Slip_0457	ETF-ubiquinone oxidoreductase (FixC)	SWMB_01043	64.9	0	
								Slip_0458	Ferredoxin (FixX)	SWMB_01044	64.9	4E-41	
								Slip_0459	Electron transfer flavoprotein β subunit (FixA)	SWMB_01045	59.3	1E-96	
								Slip_0460	Electron transfer flavoprotein α subunit (FixB)	SWMB_01046	51.1	3E-101	
								Slip_0461	enoyl-CoA hydratase				
								Slip_0462	butyryl-CoA:acetate CoA-transferase				
Acyl-CoA dehydrogenase linked to ETF													
SWMB_00118	Acyl-CoA dehydrogenase	Swol_0268	99.2	0	Slip_2109	40.1	1E-85						
SWMB_00119	fixA, eTfB electron transfer flavoprotein beta subunit	Swol_0267	96.5	0	Slip_2110	33.0	6E-36						
SWMB_00120	fixB, eTfA electron transfer flavoprotein alpha subunit	Swol_0266	95.6	0	Slip_2111	33.9	5E-43						
Iron-sulfur-binding reductase linked to ETF													
SWMB_02180	Electron transfer flavoprotein small subunit	Swol_0696	97.2	2E-158	Slip_1418	74.8	2E-121						
SWMB_02181	Electron transfer flavoprotein large subunit	Swol_0697	99.7	0	Slip_1417	79.8	3E-176						
SWMB_02182	Fe-S oxidoreductase	Swol_0698	97.1	0	Slip_1416	72.6	0						
ATP synthase													
SWMB_00535	Putative F ₀ F ₁ -ATPase subunit (ATPase_gene1)	Swol_2389	98.9	4E-58	Slip_2290	51.6	2E-15						
SWMB_00536	F ₁ -ATPase subunit 6	Swol_2388	98.7	3E-162	Slip_2288	57.3	1E-93						
SWMB_00537	Lipid-binding protein	Swol_2387	98.6	3E-41	Slip_2287	77.1	1E-23						
SWMB_00538	F ₁ -type ATPase subunit b	Swol_2386	98.8	4E-122	Slip_2286	60.8	1E-83						
SWMB_00539	F ₁ -type ATPase subunit delta	Swol_2385	97.3	1E-128	Slip_2285	51.1	4E-64						
SWMB_00540	ATP synthase subunit alpha	Swol_2384	99.6	0	Slip_2284	81.3	0						
SWMB_00541	F ₁ -ATPase gamma subunit	Swol_2383	97.0	0	Slip_2283	69.9	6E-147						
SWMB_00542	ATP synthase subunit beta	Swol_2382	100.0	0	Slip_2282	81.7	0						
SWMB_00543	F ₁ -ATPase epsilon subunit	Swol_2381	100.0	1E-96	Slip_2281	71.6	1E-67						

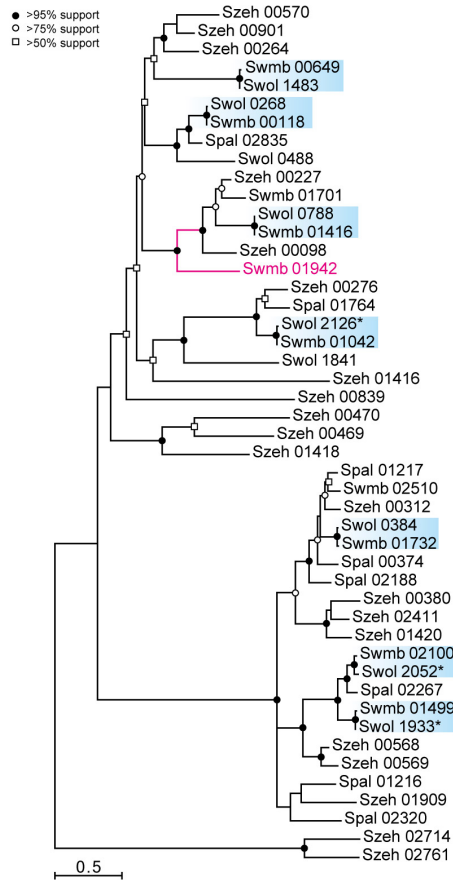
The gray bars indicate that there are no corresponding genes with significant similarity (<20%).

Table S7. *Syntrophothermus lipocalidus* strain TGB-C1^T genes encoding nitrogenase complex

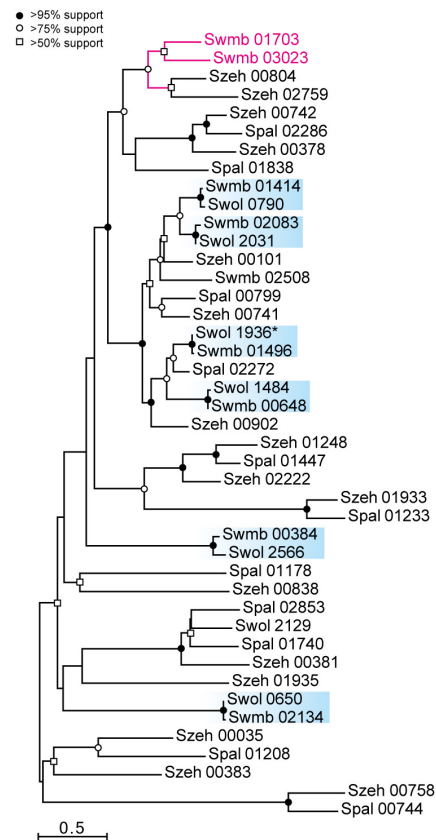
Locus tag in TGB-C1	Predicted product	<i>Thermacetogenium phaeum</i> PB			<i>Clostridium butyricum</i> CWB11009			<i>Syntrophobacter fumaroxidans</i> MPOB		
		Locus Tag	%ID	e-value	Locus Tag	%ID	e-value	Locus Tag	%ID	e-value
Slip_2118	nitrogen regulatory protein P-II family	Tph_c08760	81.3	2E-50	Ga0077125_11736	41.1	1E-26	Sfum_0726	42.0	1E-25
Slip_2119	ammonium transporter	Tph_c08750	88.8	0	Ga0077125_11735	44.7	8E-132	Sfum_0727	35.1	3E-58
Slip_2120	glutamine amidotransferase class-I	Tph_c08740	81.4	7E-146	Ga0077125_10774	28.9	3.E-08	Sfum_0596	41.6	2E-39
Slip_2121	modC molybdate transport system ATP-binding protein	Tph_c26420	50.9	2E-64	Ga0077125_115825	44.6	3E-53	Sfum_3696	47.8	5E-54
Slip_2122	modB molybdate transport system permease protein	Tph_c26410	57.8	5E-87	Ga0077125_115824	48.6	2E-65	Sfum_3698	46.4	1E-63
Slip_2123	modA molybdate transport system substrate-binding protein	Tph_c26400	49.8	5E-74	Ga0077125_115823	42.0	1E-56	Sfum_3697	40.9	2E-53
	nifV homocitrate synthase	Tph_c08720								
Slip_2124	nifB nitrogen fixation protein NifB	Tph_c08710	82.6	5E-167	Ga0077125_115813	41.0	2E-66	Sfum_1011	42.8	4E-69
	Nitrogenase FeMo-cofactor scaffold and assembly protein NifN							Sfum_1012		
Slip_2125	nifE nitrogenase molybdenum-cofactor synthesis protein	Tph_c08700	93.3	0	Ga0077125_115814	36.7	2E-91	Sfum_1013	37.3	4E-84
	ferredoxin, 2Fe-2s							Sfum_1014		
Slip_2126	nifK nitrogenase molybdenum-iron protein beta chain	Tph_c08690	95.1	0	Ga0077125_115815	38.5	2E-101	Sfum_1015	39.5	4E-105
Slip_2127	nifD nitrogenase molybdenum-iron protein alpha chain	Tph_c08680	94.2	0	Ga0077125_115816	34.7	6E-97	Sfum_1016	36.3	3E-103
Slip_2128	nifl2 nitrogen regulatory protein PII 2	Tph_c08670	95.9	1E-81	Ga0077125_115817	39.5	1E-24	Sfum_1017	44.0	2E-23
Slip_2129	nifl1 nitrogen regulatory protein PII 1	Tph_c08660	96.2	2E-70	Ga0077125_115818	55.1	5E-34	Sfum_1018	54.7	2E-34
Slip_2130	nifH nitrogenase iron protein NifH	Tph_c08650	98.2	0	Ga0077125_115819	68.1	5E-139	Sfum_1019	67.8	5E-136

The gray bars indicate that there are no corresponding genes with significant similarity (<20%).

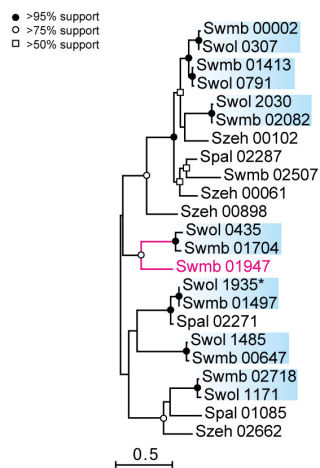
(A) Acyl-CoA dehydrogenase-related



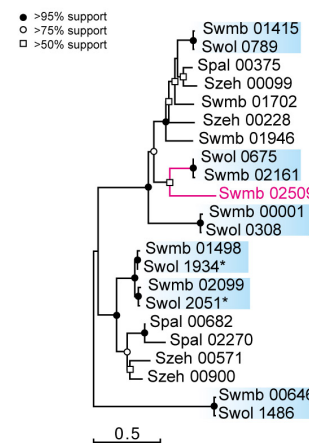
(B) Enoyl-CoA hydratase-related



(C) 3-hydroxyacyl-CoA dehydrogenase-related



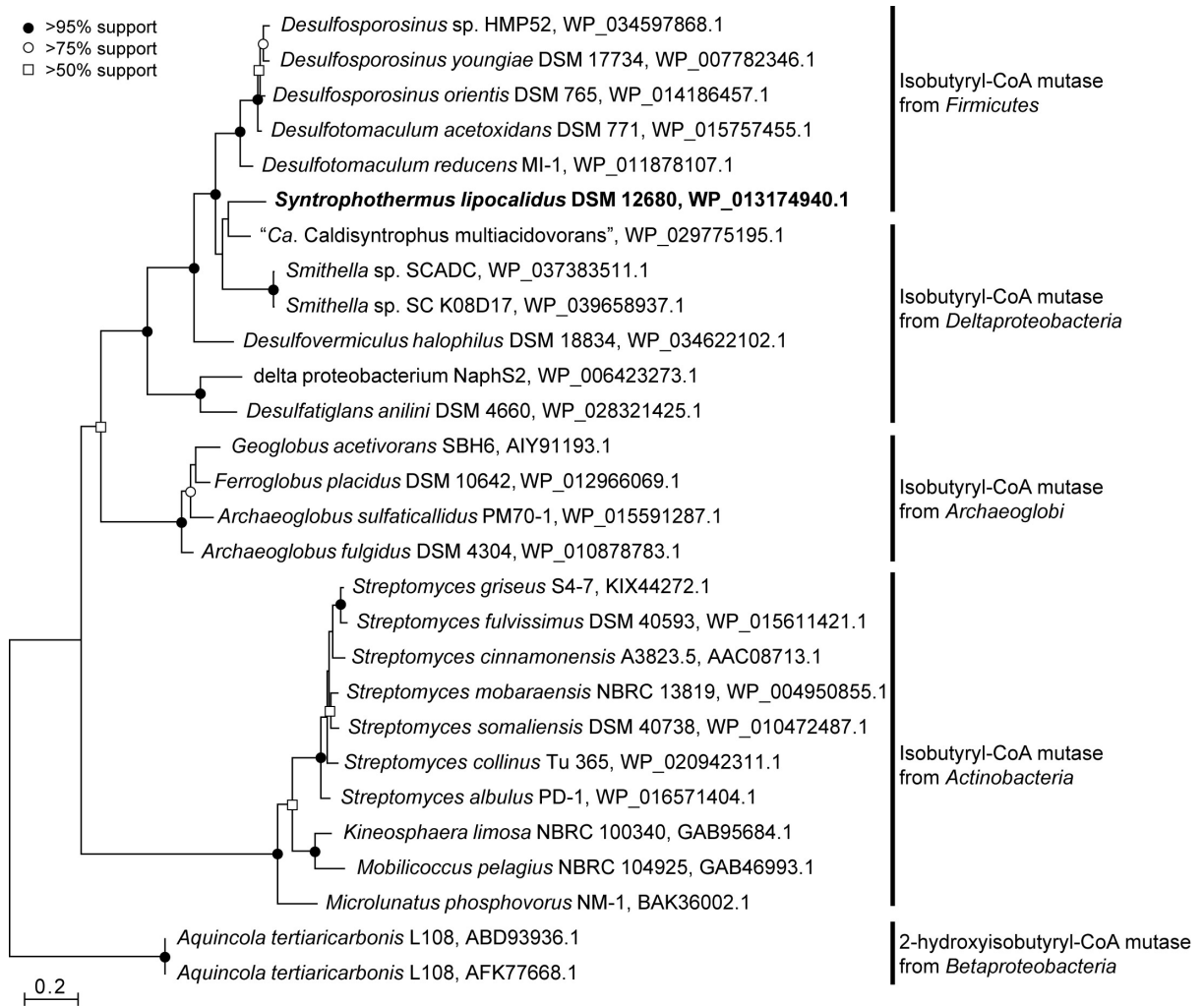
(D) Acetyl-CoA acetyltransferase-related



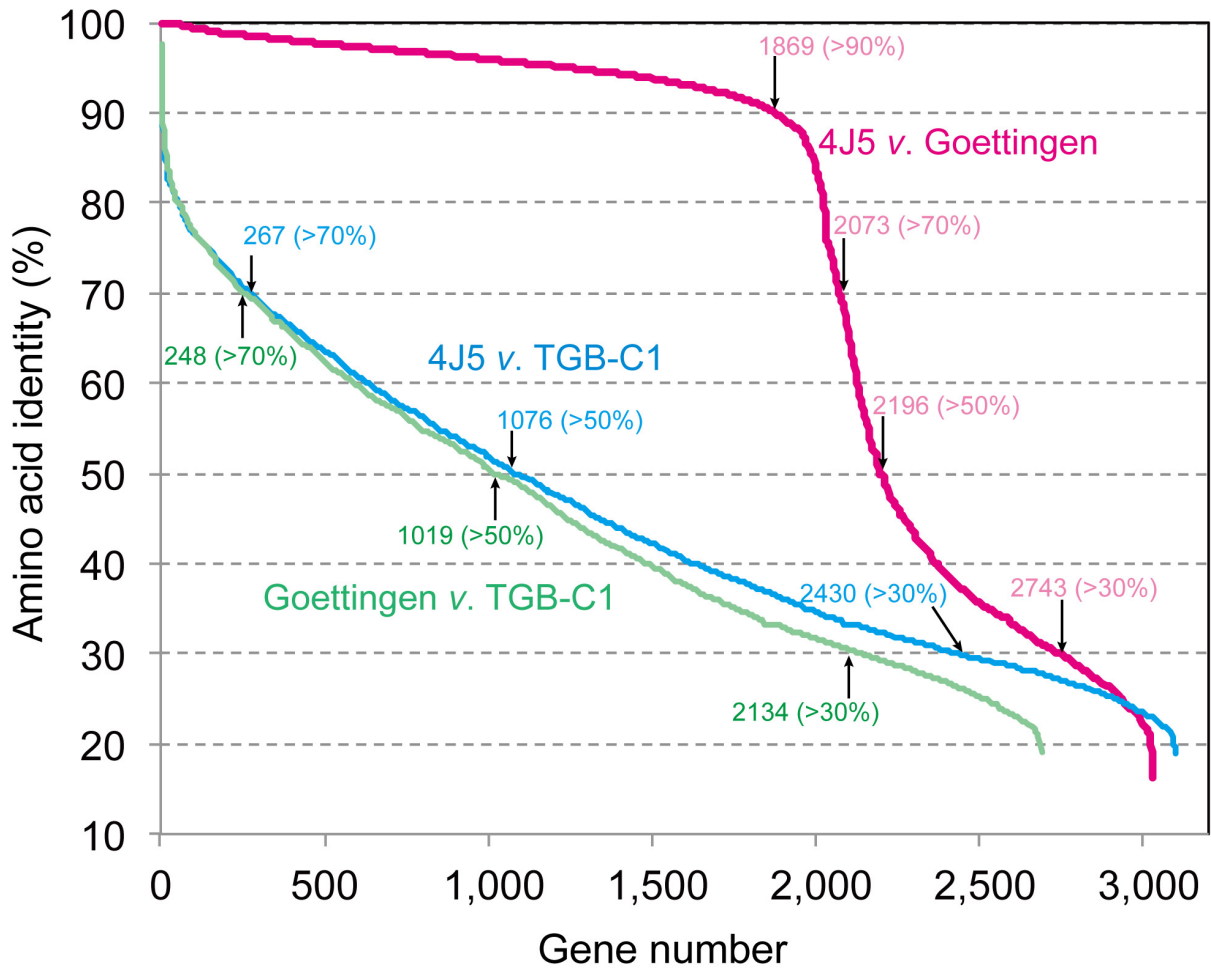
79 **Fig. S1.** Maximum likelihood trees of (A) acyl-CoA dehydrogenase, (B) enoyl-CoA
80 dehydratase, (C) 3-hydroxyacyl-CoA dehydrogenase, and (D) acetyl-CoA acetyltransferase of
81 genome-sequenced mesophilic *Syntrophomonadaceae* strains: *Syntrophomonas wolfei* subsp.

82 *methylbutyratica* strain 4J5 (locus tag: Swmb), *Syntrophomonas wolfei* subsp. *wolfei* strain
83 Göttingen (Swol), *Syntrophomonas palmitatica* strain JCM 14374 (Spal), and
84 *Syntrophomonas zehnderi* strain OL-4 (Szeh). The topology of the tree was estimated by
85 bootstrap analysis with 1,000 replicates. Bars indicate the change per amino acid site. Locus
86 tags of *Syntrophomonas wolfei* subsp. *wolfei* strain Göttingen with asterisk indicate
87 significant expressed enzymes based on proteomic study (9). Cluster with blue color indicates
88 a set of homologous gene of the strain 4J5 and Göttingen that has amino acid sequence
89 identity range 87.4%–99.7%.

90



93 **Fig. S2.** A maximum likelihood tree of isobutyryl-CoA mutase. The topology of the tree was
 94 estimated by bootstrap analysis with 1,000 replicates. Bar indicates 0.2 change per amino
 95 acid site.



98 **Fig. S3.** Comparison of amino acid identities between the genome of “*Syntrophomonas*
 99 *wolfei* subsp. *methylbutyratica*” strain 4J5, *Syntrophomonas wolfei* subsp. *wolfei* strain
 100 Göttingen, and *Syntrophothermus lipocalidus* strain TGB-C1.

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103 **Supplemental material.** Amino acid sequences of annotated proteins within the genome of
 104 *Syntrophomonas wolfei* subsp. *methylbutyratica* strain 4J5.

105

106 **Supplemental references**

107

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MGEKNIPLVTFNAGYELQIPLYLKILKSAVYMSGSHETFLPSTLIDGSEVILDFDFTFSTNIVKIEFSTFVSNVKNPKMDVAGDQYEVATYVAVSNPNIAHFFHGQGL SOGGLDLSARHATKLSHIFHATNEVSNRBLKEEWFVAVGSTVFNEDVSTYFHELNDLNDLKKVLPITQHLITPTEQKADQKSKLQVLAJGQISPTVNDNSGEMK
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