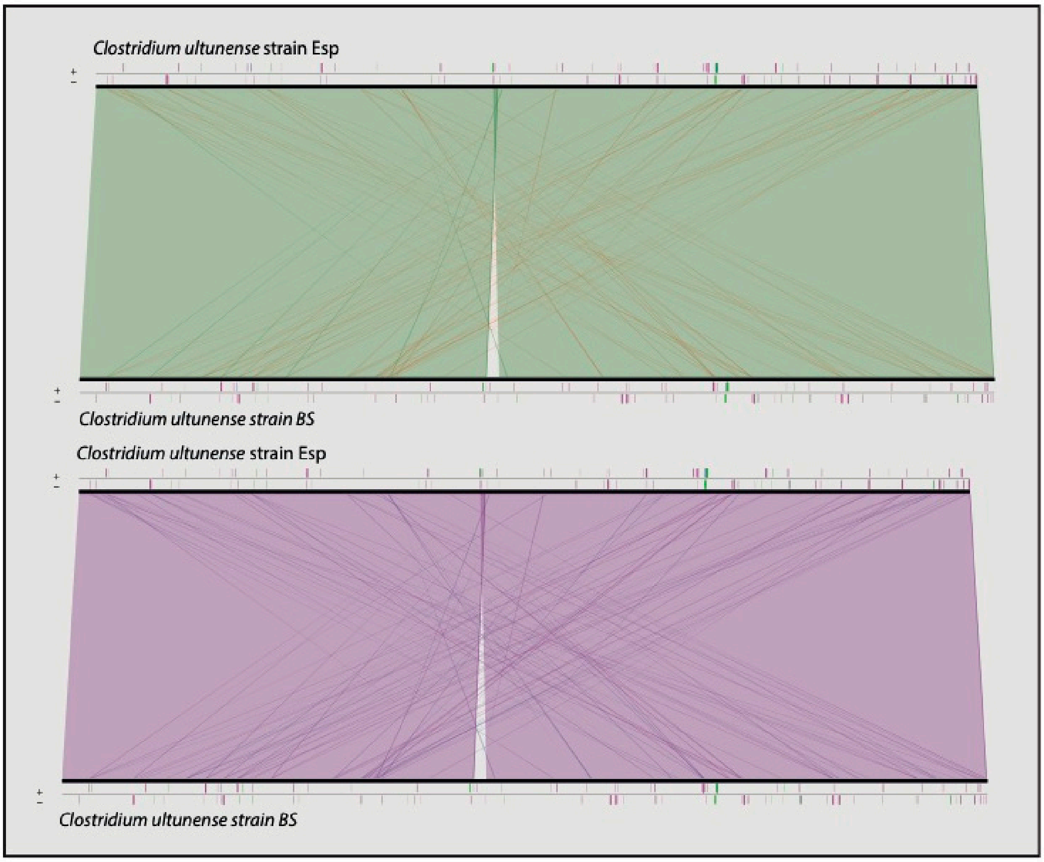

Figure S1. Synteny comparison of *Clostridium ultunense strain Esp* genome with the genome of the type strain *Clostridium ultunense strain BS*^{T}. The lines indicate syntons between two genomes. Red lines show inversions around the origin of replication. Vertical bars on the border line indicate different elements in genomes, where pink = transposases or insertion sequences, blue = rRNA and green = tRNA.

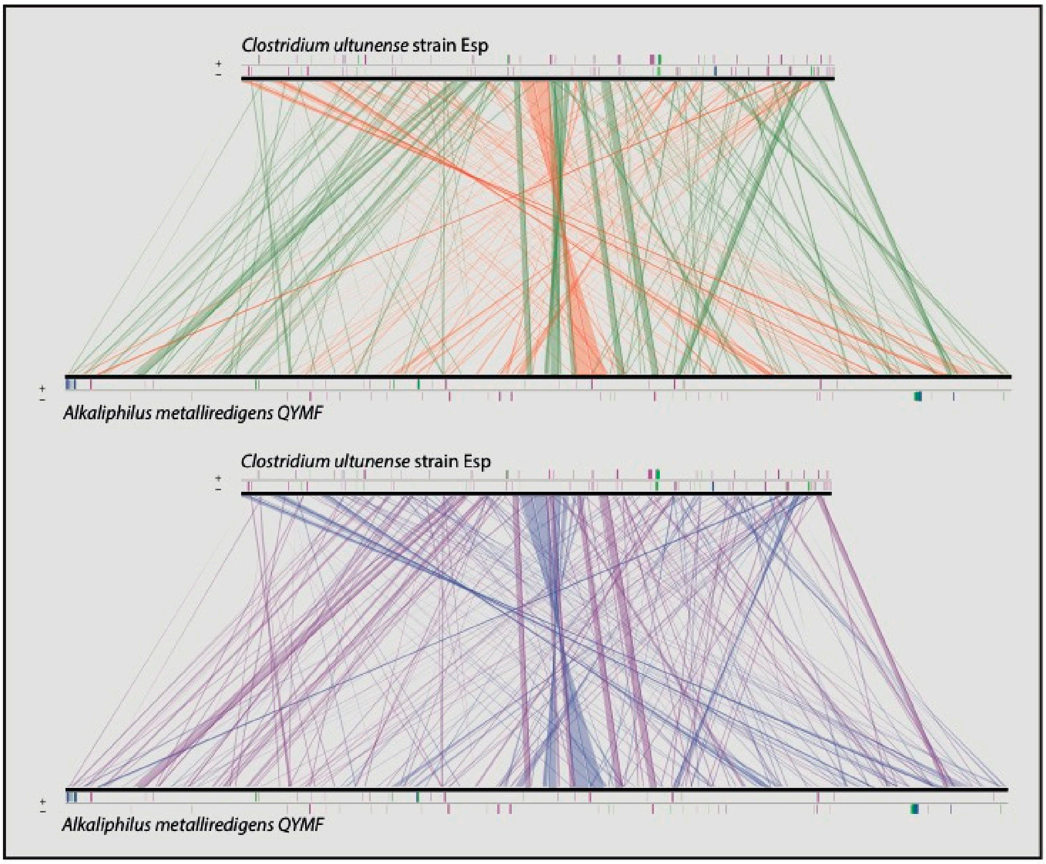

Figure S2. Synteny comparison of *Clostridium ultunense strain Esp* genome with the genome of *Alkaliphilus metalliredigens QYMF.* The lines indicate syntons between two genomes. Red lines show inversions around the origin of replication. Vertical bars on the border line indicate different elements in genomes, where pink = transposases or insertion sequences, blue = rRNA and green = tRNA.

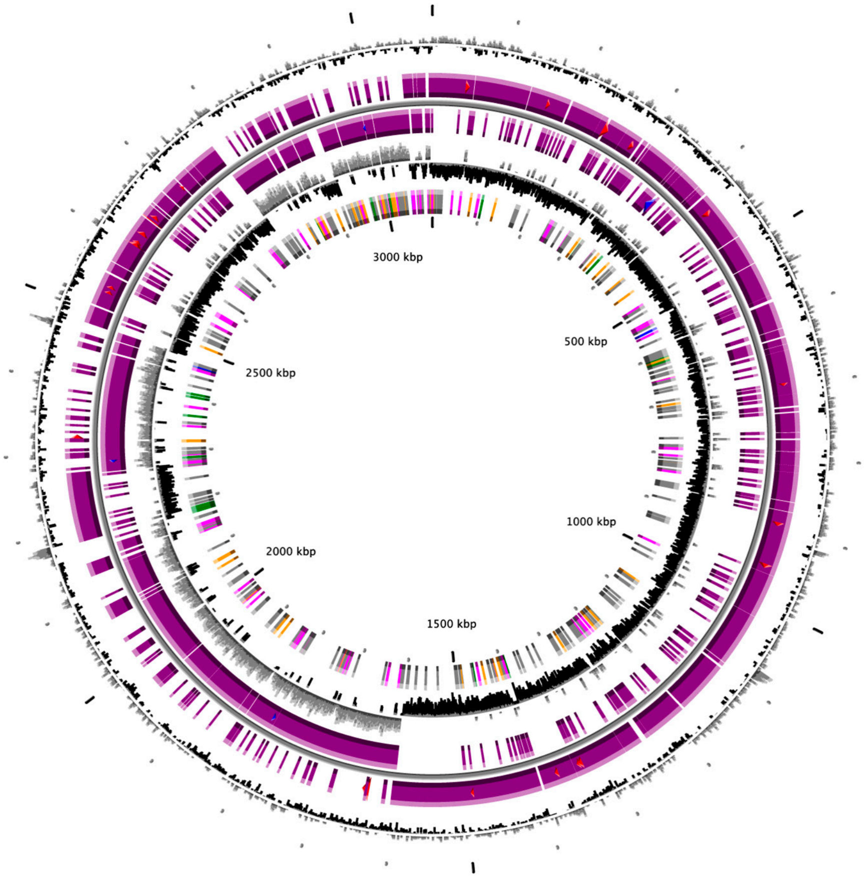

Figure S3. Circular map of the genome of *Clostridium ultunense* strain Esp. From outside to centre: (1) GC percent deviation (GC window - mean GC) in a 1000-bp window; (2) predicted CDSs transcribed in a clockwise direction; (3) predicted CDSs transcribed in a counter-clockwise direction; (4) GC skew (G+C/G-C) in a 1000-bp window; (5) rRNA (blue), tRNA (green), misc_RNA (orange), transposable elements (pink) and pseudogenes (grey). For more details see Table S1.

Table S1. Genome statistics for *Clostridium ultunense Esp.*

Attribute	Value	% of total
Genome size (bp)	3,093,245	100.00
DNA coding (bp)	2,629,258	85.00
DNA G+C content (bp)	9,89,838	32.40
Number of scaffolds	1	-
Total genes	3,303	100.00
Protein coding genes	3,236	97.97
RNA genes	66	1.25
Pseudo gene	57	1.99
Genes in internal clusters	1,580	45.00
Genes with function prediction	1,472	43.00
Genes assigned to COGs	2,623	79.41
Genes with Pfam domains	2,675	81.84
Genes with signal peptides	213	6.44
Genes with transmembrane helices	759	22.97
CRISPR repeats	8	0.24

Table S2. Presences of phages and phage remnants in *Clostridium ultunense* ESP, *Clostridium ultunense* BS^{T}, *Pseudothermotoga lettingae* TMO, Syntrophaceticus schinkii Sp3 and *Tepidanaerobacter acetatoxydans* Re1 genomes at time point of DNA isolation[1-3]. % of the genome which is predicted to encode prophage related genes are given in parenthesis.

Region	Region Length	Completeness	Total Proteins	Region position	Most Common Phage	GC%
Clostridium ultunense ESP (3,33%)						
1	7.7kb	Incomplete	9	86131-93902	PHAGE_Bacill_SP (NC_031245)	32.93%
2	24.4kb	Incomplete	21	1717007-1741436	PHAGE_Synech_ACG (NC_026927)	30.63%
3	29kb	Questionable	21	1813843-1842869	PHAGE_Mycoba_Panchino (NC_031281)	31.06%
4	6.8kb	Incomplete	9	2943158-2950029	PHAGE_Staphy_SPbeta (NC_029119)	32.17%
5	35.2kb	Intact	21	3051263-3086475	PHAGE_Stx2_c_1717 (NC_011357)	32.38%
Clostridium ultunense BS^{T} (1,13%)						
1	36.4kb	Intact	24	3172444-3208864	PHAGE_Stx2_c_1717 (NC_011357)	31.03%
Pseudothermotoga lettingae TMO (1,7%)						
1	11kb	Incomplete	14	999988-1010999	PHAGE_Plankt_LD (NC_016564)	37.88%
2	8kb	Incomplete	9	1115311-1123336	PHAGE_Synech_S_CAM7 (NC_031927)	39.22%
3	7.5kb	Incomplete	9	1465825-1473383	PHAGE_Geobac_E3 (NC_29073)	35.79%
4	10.3kb	Incomplete	10	1881355-1991711	PHAGE_Prochl_P_SSM2 (NC_006883)	39.65%
Syntrophaceticus schinkii SP3 (1,8%)						
1	4.7kb	Incomplete	7	88-4845	PHAGE_pSEUDO_JG004 (NC_019450)	48.97%
2	17.2kb	Incomplete	11	101385-118628	PHAGE_Bacill_Blue (NC_031056)	49.71%
3	8.1kb	Incomplete	9	2560898-2569090	PHAGE_Prochl_P_SSM2 (NC_006883)	51.39%
4	26.9kb	Incomplete	9	2846491-2873463	PHAGE_Plankt_PaV_LD (NC_016564)	43.36%
***Thermacetogenium phaeum* PB (1.45%)**						
1	42.8	Intact	41	2330541-2373372	PHAGE_Lactoc_28201 NC_031013	44.95%

1. Manzoor S, Bongcam-Rudloff E, Schnurer A, Muller B. Genome-Guided Analysis and Whole Transcriptome Profiling of the Mesophilic Syntrophic Acetate Oxidising Bacterium Syntrophaceticus schinkii. PLoS ONE. 2016;11(11):e0166520. Epub 2016/11/17. doi: 10.1371/journal.pone.0166520. PubMed PMID: 27851830; PubMed Central PMCID: PMCPMC5113046.

2. Müller B, Manzoor S, Niazi A, Bongcam-Rudloff E, Schnürer A. Genome-guided analysis of physiological capacities of Tepidanaerobacter acetatoxydans provides insights into environmental adaptations and syntrophic acetate oxidation. PLoS ONE. 2015;10(3):e0121237. doi: 10.1371/journal.pone.0121237.

3. Oehler D, Poehlein A, Leimbach A, Müller N, Daniel R, Gottschalk G, et al. Genome-guided analysis of physiological and morphological traits of the fermentative acetate oxidizer Thermacetogenium phaeum. BMC Genomics. 2012;13(1):723. doi: 10.1186/1471-2164-13-723.

Table S3. ABC transporter related genes found in *Clostridium ultunense strain ESP.*

C. ultunense	**Product**
CUESP__0051	energizing coupling factor of ABC influx transporter (ATP-binding protein)
CUESP__0052	energizing coupling factor of ABC influx transporter (ATP-binding protein)
CUESP__0069	ABC transporter, substrate-binding lipoprotein
CUESP__0070	ABC transporter, permease protein
CUESP__0071	Nitrate ABC transporter
CUESP__0120	Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein OppA (TC 3.A.1.5.1)
CUESP__0121	oligopeptide ABC transporter (permease)
CUESP__0122	oligopeptide ABC transporter (permease)
CUESP__0123	oligopeptide ABC transporter (ATP-binding protein)
CUESP__0124	oligopeptide ABC transporter (ATP-binding protein)
CUESP__0138	ABC transporter related protein
CUESP__0154	ABC transporter related
CUESP__0204	cell-division ABC transporter (ATP-binding protein)
CUESP__0281	bacitracin ABC efflux transporter (ATP-binding protein)
CUESP__0282	Efflux ABC transporter, permease protein
CUESP__0283	putative ABC efflux transporter (ATP-binding protein)
CUESP__0284	putative ABC-2 type transport system permease protein
CUESP__0303	putative peptide ABC transporter permease protein y4tP
CUESP__0304	putative peptide transporter permease subunit: membrane component of ABC superfamily
CUESP__0305	oligopeptide ABC transporter (ATP-binding protein)
CUESP__0306	oligopeptide ABC transporter (ATP-binding protein)
CUESP__0322	Phosphate ABC transporter ATP-binding protein
CUESP__0323	ABC transporter protein
CUESP__0365	ribose ABC transporter (ATP-binding protein)
CUESP__0366	D-ribose transporter subunit ; membrane component of ABC superfamily
CUESP__0399	ABC transporter related
CUESP__0404	putative ABC transporter permease protein
CUESP__0405	putative ABC transporter permease protein
CUESP__0406	ABC transporter, ATP-binding protein
CUESP__0437	putative permease of ABC transporter
CUESP__0438	putative ABC transporter component, ATP-binding
CUESP__0443	ABC transporter related protein (fragment)
CUESP__0468	sulfur mobilizing ABC protein, ATPase
CUESP__0493	guanosine ABC transporter (ATP-binding protein)
CUESP__0495	permease of ABC guanosine transporter
CUESP__0635	phosphate ABC transporter (ATP-binding protein)
CUESP__0636	ABC transporter membrane-spanning permease-phosphate transport
CUESP__0637	putative ABC transporter permease protein
CUESP__0686	fragment of guanosine ABC transporter (ATP-binding protein) (part 1)

CUESP__0687	fragment of guanosine ABC transporter (ATP-binding protein) (part 2)
CUESP__0731	putative iron-siderophore ABC transporter (ATP-binding protein) (fragment)
CUESP__0816	putative high-affinity branched-chain amino acid ABC transporter, permease protein LivH
CUESP__0817	Branched-chain amino acid ABC transporter, permease protein
CUESP__0818	leucine/isoleucine/valine transporter subunit ; ATP-binding component of ABC superfamily
CUESP__0819	leucine/isoleucine/valine transporter subunit ; ATP-binding component of ABC superfamily
CUESP__0922	Antibiotic ABC superfamily ATP binding cassette transporter
CUESP__0928	ABC transporter related
CUESP__0935	guanosine ABC transporter (ATP-binding protein) (fragment)
CUESP__0936	ribose ABC transporter (ATP-binding protein) (fragment)
CUESP__0941	ribose ABC transporter (ATP-binding protein)
CUESP__0942	fragment of ribose ABC transporter (permease) (part 1)
CUESP__0943	fragment of ribose ABC transporter (permease) (part 2)
CUESP__1009	putative ABC transporter permease protein HI_1471
CUESP__1011	ABC-type transporter, periplasmic subunit
CUESP__1037	leucine/isoleucine/valine transporter subunit ; membrane component of ABC superfamily
CUESP__1039	leucine/isoleucine/valine transporter subunit ; ATP-binding component of ABC superfamily
CUESP__1040	leucine/isoleucine/valine transporter subunit ; ATP-binding component of ABC superfamily
CUESP__1053	ribose ABC transporter (ATP-binding protein)
CUESP__1054	D-ribose transporter subunit membrane component of ABC superfamily
CUESP__1055	ABC-type sugar transport system periplasmic component-like protein
CUESP__1091	putative ABC-type transport system, periplasmic component/surface lipoprotein
CUESP__1092	Uncharacterized ABC transporter ATP-binding protein YufO
CUESP__1093	ABC-type uncharacterized transport system,permease component
CUESP__1094	putative ABC-type transport system, permease component
CUESP__1109	oligopeptide ABC transporter (ATP-binding protein)
CUESP__1110	putative cell wall oligopeptide ABC transporter (ATP binding protein)
CUESP__1135	Oligopeptide/dipeptide ABC transporter
CUESP__1136	Oligopeptide/dipeptide ABC transporter,permease protein
CUESP__1137	oligopeptide ABC transporter (ATP-binding protein)
CUESP__1138	putative cell wall oligopeptide ABC transporter (ATP binding protein)
CUESP__1139	Oligopeptide/dipeptide ABC transporter
CUESP__1334	ABC transporter-like protein
CUESP__1381	putative ABC transporter (ATP-binding protein)

CUESP__1382	putative Uncharacterized ABC transporter permease YvcS
CUESP__1398	aliphatic sulfonate ABC transporter (ATP-binding protein)
CUESP__1419	ABC-type transport system, permease component
CUESP__1420	ABC transporter permease
CUESP__1434	ABC transporter related (fragment)
CUESP__1499	high affinity arginine ABC transporter (permease)
CUESP__1500	high affinity arginine ABC transporter (ATP-binding protein)
CUESP__1977	ABC transporter, permease protein
CUESP__1978	ABC transporter, substrate-binding protein
CUESP__2110	putative ABC-type cobalt transport system permease component CbiQ and related transporters-like protein
CUESP__2111	ABC transporter related
CUESP__2112	ABC transporter, ATP-binding protein
CUESP__2242	Cobalt ABC transporter, inner membrane subunit CbiQ
CUESP__2249	ABC transporter related
CUESP__2251	putative Iron compound ABC transporter,periplasmic iron compound-binding protein
CUESP__2252	Abc-2 transporter, permease protein
CUESP__2254	iron-dicitrate ABC transporter (permease)
CUESP__2260	ABC transporter related protein
CUESP__2289	Uncharacterized ABC transporter ATP-binding protein YwjA
CUESP__2391	fructose-amino acid ABC transporter (ATP-binding subunit) (fragment)
CUESP__2393	polyamine transporter subunit ; membrane component of ABC superfamily
CUESP__2394	Spermidine/putrescine ABC transporter, permease protein 2
CUESP__2447	ABC-type transporter, periplasmic subunit
CUESP__2448	ABC-type transporter, integral membrane subunit
CUESP__2449	ABC-type transporter, integral membrane subunit
CUESP__2450	oligopeptide ABC transporter (ATP-binding protein)
CUESP__2451	oligopeptide ABC transporter (ATP-binding protein)
CUESP__2521	methionine ABC transporter (ATP-binding protein)
CUESP__2522	methionine ABC transporter, permease component
CUESP__2523	methionine ABC transporter, substrate binding lipoprotein
CUESP__2635	ABC transporter, ATP-binding protein
CUESP__2761	Efflux ABC transporter, permease protein
CUESP__2804	ABC transporter related protein
CUESP__2814	Uncharacterized ABC transporter ATP-binding protein YvcR
CUESP__2830	putative ABC transporter (ATP-binding protein)
CUESP__2831	ABC transport system permease protein
CUESP__2836	putative ABC transporter, ATP-binding protein SagG
CUESP__2838	putative ABC-2 type transporter
CUESP__2857	putative ABC transporter anion-binding protein HVO_1888
CUESP__2858	Permease component of tungstate ABC transporter
CUESP__2859	ATPase component of tungstate ABC transporter (fragment)
CUESP__2879	ABC transporter related protein
CUESP__2880	putative ABC transporter (ATP-binding protein)
CUESP__2884	putative ABC transporter (ATP-binding protein)
CUESP__2887	ABC transporter related

CUESP__2917	ABC transporter substrate binding protein
CUESP__2918	Amino acid or sugar ABC transport system,permease protein
CUESP__2919	ABC transporter, ATP-binding protein
CUESP__2944	ABC transporter, ATP-binding protein (fragment)
CUESP__2945	ABC transporter, ATP-binding protein (fragment)
CUESP__2970	ABC transporter, ATP-binding protein
CUESP__3106	putative Antibiotic ABC transporter, permease protein
CUESP__3127	ABC-type multidrug transport system, ATPase component
CUESP__3228	oligopeptide ABC transporter (ATP-binding protein)
CUESP__3229	oligopeptide ABC transporter (ATP-binding protein)
CUESP__3230	oligopeptide ABC transporter (permease)
CUESP__3231	oligopeptide ABC transporter (permease)
CUESP__3232	ABC-type transporter, periplasmic subunit
CUESP__3256	fragment of putative ABC transporter component (part 1)
CUESP__3259	fragment of putative ABC transporter component (part 2)
CUESP__3335	putative ABC transporter permease protein HI_1471
CUESP__3337	ABC-type transporter, periplasmic subunit

Table S4. ABC transporter related genes found in *Pseudothermotoga lettingae* TMO*.*

T. lettingae	**Product**
Tlet_0021	ABC transporter-like protein
Tlet_0022	polar amino acid ABC transporter inner membrane subunit
Tlet_0023	polar amino acid ABC transporter inner membrane subunit
Tlet_0075	oligopeptide/dipeptide ABC transporter ATPase
Tlet_0076	oligopeptide/dipeptide ABC transporter ATPase
Tlet_0086	ABC transporter-like protein
Tlet_0137	ABC transporter-like protein
Tlet_0184	ABC transporter-like protein
Tlet_0198	oligopeptide/dipeptide ABC transporter ATPase
Tlet_0199	oligopeptide/dipeptide ABC transporter ATPase
Tlet_0211	ABC transporter-like protein
Tlet_0212	ABC transporter-like protein
Tlet_0296	ABC transporter-like protein
Tlet_0337	ABC transporter-like protein
Tlet_0353	oligopeptide/dipeptide ABC transporter ATPase
Tlet_0354	oligopeptide/dipeptide ABC transporter ATPase
Tlet_0360	ABC transporter-like protein
Tlet_0391	ABC transporter-like protein
Tlet_0463	ABC transporter
Tlet_0483	polar amino acid ABC transporter inner membrane subunit
Tlet_0484	ABC transporter-like protein
Tlet_0485	ABC transporter-like protein
Tlet_0550	ABC transporter-like protein
Tlet_0551	ABC transporter
Tlet_0552	ABC transporter
Tlet_0644	oligopeptide/dipeptide ABC transporter ATPase
Tlet_0645	oligopeptide/dipeptide ABC transporter ATPase
Tlet_0647	oligopeptide/dipeptide ABC transporter ATPase
Tlet_0648	oligopeptide/dipeptide ABC transporter ATPase
Tlet_0677	ABC transporter-like protein
Tlet_0721	ABC transporter-like protein
Tlet_0737	ABC transporter-like protein
Tlet_0802	ABC transporter-like protein
Tlet_0803	ABC transporter-like protein
Tlet_0808	ABC transporter-like protein
Tlet_0837	ABC transporter-like protein
Tlet_0839	anion ABC transporter anion-binding protein
Tlet_0856	oligopeptide/dipeptide ABC transporter ATPase
Tlet_0857	oligopeptide/dipeptide ABC transporter ATPase
Tlet_0861	polar amino acid ABC transporter inner membrane subunit
Tlet_0862	ABC transporter-like protein
Tlet_0863	polar amino acid ABC transporter inner membrane subunit
Tlet_0982	ABC transporter-like protein
Tlet_1020	ABC transporter-like protein
Tlet_1041	ABC transporter
Tlet_1042	ABC transporter-like protein
Tlet_1045	ABC transporter-like protein
Tlet_1062	ABC transporter-like protein

Tlet_1071	ABC transporter-like protein
Tlet_1072	ABC transporter-like protein
Tlet_1122	ABC transporter-like protein
Tlet_1123	ABC transporter-like protein
Tlet_1210	ABC transporter-like protein
Tlet_1211	ABC transporter-like protein
Tlet_1212	ABC transporter-like protein
Tlet_1217	ABC transporter-like protein
Tlet_1218	ABC transporter-like protein
Tlet_1234	multidrug ABC transporter ATPase-like protein
Tlet_1234	multidrug ABC transporter ATPase-like protein
Tlet_1235	ABC transporter
Tlet_1249	ABC transporter-like protein
Tlet_1266	ABC transporter-like protein
Tlet_1273	ABC transporter-like protein
Tlet_1280	ABC transporter-like protein
Tlet_1299	ABC transporter substrate-binding protein
Tlet_1309	oligopeptide/dipeptide ABC transporter ATPase
Tlet_1310	oligopeptide/dipeptide ABC transporter ATPase
Tlet_1320	ABC transporter-like protein
Tlet_1327	ABC transporter-like protein
Tlet_1342	ABC transporter-like protein
Tlet_1353	ABC transporter-like protein
Tlet_1372	ABC transporter-like protein
Tlet_1415	ABC transporter-like protein
Tlet_1416	ABC transporter-like protein
Tlet_1419	ABC transporter-like protein
Tlet_1441	oligopeptide/dipeptide ABC transporter ATPase
Tlet_1442	oligopeptide/dipeptide ABC transporter ATPase
Tlet_1471	ABC transporter-like protein
Tlet_1503	oligopeptide/dipeptide ABC transporter ATPase
Tlet_1504	oligopeptide/dipeptide ABC transporter ATPase
Tlet_1527	oligopeptide/dipeptide ABC transporter ATPase
Tlet_1528	oligopeptide/dipeptide ABC transporter ATPase
Tlet_1560	ABC transporter-like protein
Tlet_1561	putative ABC-2 type transport system permease
Tlet_1608	ABC transporter-like protein
Tlet_1609	ABC transporter-like protein
Tlet_1641	ABC transporter-like protein
Tlet_1678	ABC transporter-like protein
Tlet_1699	phosphate ABC transporter ATPase
Tlet_1791	ABC transporter
Tlet_1792	ABC transporter-like protein
Tlet_1834	ABC transporter
Tlet_1835	ABC transporter-like protein
Tlet_1861	putative ABC-2 type transport system permease
Tlet_1862	ABC transporter-like protein
Tlet_1933	oligopeptide/dipeptide ABC transporter ATPase
Tlet_1934	oligopeptide/dipeptide ABC transporter ATPase
Tlet_1937	ABC transporter-like protein
Tlet_1938	ABC transporter-like protein
Tlet_2004	oligopeptide/dipeptide ABC transporter ATPase

Tlet_2005	oligopeptide/dipeptide ABC transporter ATPase
Tlet_2022	oligopeptide/dipeptide ABC transporter ATPase
Tlet_2023	oligopeptide/dipeptide ABC transporter ATPase

Table S5. ABC transporter related genes found in *Thermacetogenium phaeum* and *Syntrophaceticus schinkii* genomes [1].

T. phaeum	**Product**
Tph_c00470	ABC transporter permease
Tph_c01060	ABC transporter substrate-binding protein
Tph_c01070	ABC transporter, permease protein, FecCD family
Tph_c01080	ABC transporter ATP-binding protein
Tph_c01190	ABC transporter permease
Tph_c01200	ABC transporter ATP-binding protein
Tph_c01210	ABC transporter substrate-binding protein
Tph_c01550	ABC transporter permease
Tph_c01560	ABC transporter ATP-binding protein
Tph_c01570	ABC transporter substrate-binding protein
Tph_c01600	molybdate ABC transporter substrate-binding protein ModA
Tph_c03230	ABC transporter ATP-binding protein
Tph_c03240	cobalt ABC transporter permease CbiQ
Tph_c03410	iron ABC transporter substrate binding protein
Tph_c03420	ABC transporter, permease protein FecCD
Tph_c03430	iron ABC transporter ATP-binding protein
Tph_c03500	ABC transporter
Tph_c03550	oligopeptide ABC transporter ATP-binding protein
Tph_c03560	oligopeptide ABC transporter ATP-binding protein
Tph_c03980	ABC-type tungstate transport system, permease component TupB
Tph_c04360	ABC transporter ATP-binding protein
Tph_c04370	ABC-type cobalt import system, permease component
Tph_c04860	phosphate ABC transporter ATP-binding protein PstB
Tph_c04880	phosphate ABC transporter permease
Tph_c04890	phosphate ABC transporter permease
Tph_c05200	cobalt ABC transporter permease
Tph_c05210	cobalt ABC transporter ATP-binding protein CbiO
Tph_c09780	cobalt ABC transporter permease CbiQ
Tph_c09790	cobalt ABC transporter ATP-binding protein CbiO
Tph_c10680	ABC transporter ATP-binding protein
Tph_c10690	ABC transport system permease
Tph_c13160	ABC transporter ATP-binding protein
Tph_c13800	taurine ABC transport system permease protein TauC
Tph_c13810	taurine ABC transporter ATP-binding protein TauB
Tph_c13820	bicarbonate ABC transporter substrate binding protein
Tph_c15200	ABC-1-like protein kinase
Tph_c15800	hemin ABC transporter ATP-binding protein HmuV
Tph_c15810	vitamin B12 ABC transport system permease protein BtuC
Tph_c15820	vitamin B12 ABC transporter substrate-binding protein BtuF
Tph_c17070	D,D-dipeptide ABC transporter ATP-binding protein DppF
Tph_c17080	D,D-dipeptide ABC transporter ATP-binding protein DppD
Tph_c17090	D,D-dipeptide ABC transport system permease protein DppC
Tph_c17100	D,D-dipeptide ABC transport system permease protein DdpB

Tph_c17110	D,D-dipeptide ABC transporter substrate binding protein DdpA
Tph_c17920	glutathione ABC transporter substrate protein GsiD
Tph_c17930	glutathione ABC transport system permease protein GsiC
Tph_c17940	glutathione ABC transport system permease protein GsiA
Tph_c17950	glutathione ABC transporter ATP-binding protein GsiA
Tph_c18310	cobalt import ABC transporter substrate-binding protein
Tph_c18320	cobalt import ABC transporter, permease protein
Tph_c19110	ABC transporter-like protein
Tph_c19120	ABC transporter ATP-binding protein YfiB
Tph_c20380	ABC-type glycine betaine transport system, substrate-binding domain-containing protein
Tph_c20470	ABC transporter permease protein YknZ
THEPHA_2236	ABC transporter related protein (fragment)
Tph_c22400	ABC-3 family transport protein
Tph_c23550	ABC transporter
Tph_c23560	ABC transporter
Tph_c23600	antimicrobial peptide ABC transporter ATPase
Tph_c23660	ABC transporter permease
Tph_c23750	branched chain amino acid ABC transporter permease
Tph_c24810	ABC transporter ATP-binding protein
Tph_c24820	ABC transporter ATP-binding protein
Tph_c25200	oligopeptide/dipeptide ABC transporter ATPase
Tph_c25210	ABC-2-like transporter, permease protein
Tph_c26400	molybdate/tungstate ABC transporter substrate binding protein ModA
Tph_c26410	molybdate/tungstate ABC transport system permease protein ModB
Tph_c26420	molybdate/tungstate ABC transporter ATP-binding protein ModC
Tph_c27340	phosphate ABC transporter permease
Tph_c28160	serine protease/ABC transporter B family protein TagC
Tph_c29150	ABC transporter ATP-binding protein

Label	Gene	Product
SSCH_20015	nasA	Nitrate transporter (MFS general substrate transporter)
SSCH_150019	fdhC	Formate / nitrite transporter
SSCH_220008	mgtE	Mg2+ transporter mgtE
SSCH_240022	_	putative cation transporter
SSCH_300016	_	Efflux transporter, RND family, MFP subunit
SSCH_350016	_	EamA-like transporter family
SSCH_350041	_	Na/Pi-cotransporter II-like protein
SSCH_620002	copA	fragment of copper transporter ATPase (part 1)
SSCH_620003	copA	fragment of copper transporter ATPase (part 2)
SSCH_680023	_	Cation diffusion facilitator family transporter (Part 2)
SSCH_680024	_	Cation diffusion facilitator family transporter (Part 1)
SSCH_710032	yloB	fragment of P-type calcium transport ATPase (part 1)

SSCH_710033	yloB	fragment of P-type calcium transport ATPase (part 2)
SSCH_800009	_	Major facilitator superfamily transporter
SSCH_800020	_	acetate transporter
SSCH_870009	ecfA	Energy-coupling factor transporter ATP-binding protein EcfA
SSCH_1110015	_	Major Facilitator Superfamily transporter
SSCH_1320004	_	Mg2 transporter protein CorA family protein
SSCH_1330022	_	predicted Permeases of the drug/metabolite transporter (DMT) superfamily
SSCH_1340016	_	Putative membrane transporter (fragment)
SSCH_1390006	_	Cation diffusion facilitator family transporter
SSCH_1420002	_	MgtC/SapB transporter
SSCH_1440003	_	Multidrug-efflux transporter
SSCH_1790001	_	Putative membrane transporter (fragment)
SSCH_1820001	_	Putative membrane transporter (fragment)
SSCH_2060005	_	Efflux transporter, RND family, MFP subunit (fragment)

1. Manzoor S, Bongcam-Rudloff E, Schnurer A, Muller B. Genome-Guided Analysis and Whole Transcriptome Profiling of the Mesophilic Syntrophic Acetate Oxidising Bacterium Syntrophaceticus schinkii. PLoS ONE. 2016;11(11):e0166520. Epub 2016/11/17. doi: 10.1371/journal.pone.0166520. PubMed PMID: 27851830; PubMed Central PMCID: PMCPMC5113046.

Label	Gene	Product
SSCH_20015	nasA	Nitrate transporter (MFS general substrate transporter)
SSCH_150019	fdhC	Formate / nitrite transporter
SSCH_220008	mgtE	Mg2+ transporter mgtE
SSCH_240022	_	putative cation transporter
SSCH_300016	_	Efflux transporter, RND family, MFP subunit
SSCH_350016	_	EamA-like transporter family
SSCH_350041	_	Na/Pi-cotransporter II-like protein
SSCH_620002	copA	fragment of copper transporter ATPase (part 1)
SSCH_620003	copA	fragment of copper transporter ATPase (part 2)
SSCH_680023	_	Cation diffusion facilitator family transporter (Part 2)
SSCH_680024	_	Cation diffusion facilitator family transporter (Part 1)
SSCH_710032	yloB	fragment of P-type calcium transport ATPase (part 1)
SSCH_710033	yloB	fragment of P-type calcium transport ATPase (part 2)
SSCH_800009	_	Major facilitator superfamily transporter
SSCH_800020	_	acetate transporter
SSCH_870009	ecfA	Energy-coupling factor transporter ATP-binding protein EcfA
SSCH_1110015	_	Major Facilitator Superfamily transporter
SSCH_1320004	_	Mg2 transporter protein CorA family protein
SSCH_1330022	_	predicted Permeases of the drug/metabolite transporter (DMT) superfamily
SSCH_1340016	_	Putative membrane transporter (fragment)

SSCH_1390006	_	Cation diffusion facilitator family transporter
SSCH_1420002	_	MgtC/SapB transporter
SSCH_1440003	_	Multidrug-efflux transporter
SSCH_1790001	_	Putative membrane transporter (fragment)
SSCH_1820001	_	Putative membrane transporter (fragment)
SSCH_2060005	_	Efflux transporter, RND family, MFP subunit (fragment)

Table S6. Transporter genes in *Syntrophaceticus schinkii* and *Thermacetogenium phaeum* genomes [1, 2].

Thermacetogenium phaeum

Label	**Gene**	**Product**
Tph_c00620	_	EamA-like drug/metabolite transporter
Tph_c01450	_	MFS-1 transporter
Tph_c04110	_	acetate transporter
Tph_c04730	_	MFS-1 transporter
Tph_c06440	_	II-like Na/Pi co-transporter
Tph_c08750	amt	high affinity ammonium transporter Amt
Tph_c10870	_	magnesium transporter MgtE family
Tph_c11750	_	transporter MgtC/SapB family
Tph_c13530	_	transporter
Tph_c17800	cytX	hydroxymethylpyrimidine transporter CytX
Tph_c18840	feoA	ferrous iron transporter FeoA
Tph_c19760	_	multidrug-efflux transporter
Tph_c20360	_	EamA-like drug/metabolite transporter
Tph_c20490	_	RND-like efflux transporter
Tph_c20600	_	C4-dicarboxylate transporter/malic acid transport protein
Tph_c20980	azlD	branched-chain amino acid transporter AzlD
Tph_c21840	_	Bcr/CflA family multidrug resistance transporter
Tph_c22090	_	drug/metabolite transporter, EamA-like protein
THEPHA_2341	_	Drug resistance transporter EmrB/QacA subfamily (fragment)
Tph_c22900	_	drug resistance transporter, EmrB/QacA subfamily
Tph_c23590	_	RND-like efflux transporter
Tph_c23650	_	RND family efflux transporter MFP subunit
Tph_c23720	_	drug/metabolite transporter
Tph_c23890	_	drug/metabolite transporter
Tph_c24970	_	MFS transporter
Tph_c25070	_	MFS transporter
Tph_c27260	_	MFS-1 transporter

1. Manzoor S, Bongcam-Rudloff E, Schnurer A, Muller B. Genome-Guided Analysis and Whole Transcriptome Profiling of the Mesophilic Syntrophic Acetate Oxidising Bacterium Syntrophaceticus schinkii. PLoS ONE. 2016;11(11):e0166520. Epub 2016/11/17. doi: 10.1371/journal.pone.0166520. PubMed PMID: 27851830; PubMed Central PMCID: PMCPMC5113046.
2. Oehler D, Poehlein A, Leimbach A, Müller N, Daniel R, Gottschalk G, et al. Genome-guided analysis of physiological and morphological traits of the fermentative acetate oxidizer Thermacetogenium phaeum. BMC Genomics. 2012;13(1):723. doi: 10.1186/1471-2164-13-723.