

Table S1. List of *Dehalobacteriia* genomes used in the analysis (in green rows)

Types of the genomes provided in this table are *isolate*, *mixed culture* and MAG  
 Cmpl. : CheckM completion rate  
 Cntmn: ChecM contamination rate

Order	Genome	Genome Assembly ID	Size (Mb)	Cmpl. (%)	Cntmn (%)	GC (%)	CD (%)	Protein Count	16S	Ref.
o__Dehalobacteriales	<i>D.farmicoaceticum</i>	GCF_002224645.1	3.8	95.6	2.6	43.2	86.1	3,620	Yes	9
	<i>Ca. F. warabiya</i>	GCF_002777255.1	6.4	98.9	2.7	46.4	87.5	5,804	Yes	11
	DUPU01	GCA_012838175.1	2.4	91.9	2.0	42.1	88.8	2,447	No	38
	HGM13862	GCF_900760825.1	1.7	79.9	2.7	47.6	87.1	1,878	No	N/A
	AS06rmzACSIP_243	GCA_012515255.1	1.3	71.2	2.0	55.4	88.6	1,371	No	38
	UBA5752	GCA_002419055.1	2.1	91.9	0.7	42.7	88.8	1,965	No	36
o__UBA4068	UBA4068	GCA_002382665.1	2.0	91.2	0.3	43.2	89.0	1,966	No	36
	UBA5757	GCA_002418965.1	1.9	89.1	0.9	43.8	86.2	1,808	Yes	36
	Lab288P3bin203	GCA_009783495.1	1.1	59.6	1.8	55.7	87.6	1,315	No	38
	Nt197P3bin103	GCA_009783415.1	2.8	64.2	2.5	46.6	86.8	2,197	No	38
	Nt197P4bin8	GCA_009778255.1	2.2	70.8	1.7	42.9	90.0	2,024	No	38
	Nt197P3bin19	GCA_009782975.1	0.9	57.8	0.9	52.2	90.0	968	No	38
	UBA4997	GCA_002398485.1	1.7	78.5	0.8	40.5	74.9	1,568	Yes	39
	UBA5755	GCA_002419005.1	1.5	90.9	0.5	42.2	89.7	1,456	No	36
	UBA7702	GCA_002482535.1	2.6	93.1	0.9	49.5	88.8	2,402	No	40
	o__UBA7702	RUG14212	GCA_902796855.1	2.1	84.8	2.6	57.4	88.8	1,936	No
RUG11176		GCA_902766525.1	1.5	80.5	0.9	49.9	90.4	1,649	No	37

**Table S2. List of primer sequences matched against 16S sequences from *Dehalobacteriia***

a. Primer sequences from Engelbrekston et al., ISMEJ 2010, representative of commonly used 16S rRNA gene primers

b. Metacharacters: K=GT, M=AC, R=AG, S=CG, W=AG, Y=CT

c. matches, mismatches

16S rRNA primer (a)	5'-3' sequence (b)	Dehalobacteriia sequence (c)	Variants	Comments
27F	AGAGTTTGATCMTGGCTCAG	AGAGTTTGATCCTGGCTCAG	f__UBA5755: AGAGTTTGATCCTGGATCAG	Should amplify, with exception of variant
357F	CTCTACGGGAGGCAGCAG	CTCTACGGGAGGCAGCAG	none	Should amplify
530F	GTGCCAGCMGCCGCGG	GTGCCAGCAGCCGCGG	none	Should amplify
803F	ATTAGATACCTGGTAGTC	ATTAGATACCCGGTAATC	none	Probably won't amplify with mismatches near 3' end
926F	AAACTYAAAKGAATTGACGG	AAACTCAAAGGAATTGACGG	none	Should amplify
1114F	GCAACGAGCGCAACCC	GCAACGAGCGCAACCC	none	Should amplify
342R	CTGCTGCSYCCGTAG	CTGCTGCCTCCGTAG	none	Should amplify
519R	GWATTACCGCGGCKGCTG	GTATTACCGCGGCTGCTG	none	Should amplify even with mismatch at 5' end
787R	CTACCGGGTATCTAAT	TTACCGGGTATCTAAT	none	May amplify, noting mismatches closer to 5' end
907R	CCGTCAATTCMTTRAGTTT	CCGTCAATTCCTTTGAGTTT	none	Should amplify
1100R	GGGTTGCGCTCGTTG	GGGTTGCGCTCGTTG	none	Should amplify
1392R	ACGGGCGGTGTGTRC	ACGGGCGGTGTGTAC	none	Should amplify

**Table S3. List of 16S rRNA gene amplicon datasets associated with the identified *Dehalobacteriia* sequences**

5% raw num: raw number of sequences that share 95% or higher similarity to *Dehalobacteriia* sequences

5% perc: proportion of the "5% raw num" sequences out of total downloaded sequences from each study

Isolation Source	Reference	Total Downloaded Sequences	5% raw num	5% perc
Mouse cecum	41	7223	7	0.10
Cecal contents from <i>Mus musculus</i> strain C57BL/6J; sample lean_donor, leptin genotype +/-	42	4157	6	0.14
Cecum of mother 1 mouse offspring with genotype ob/ob	43	Offspring: 3998	Offspring: 5	0.13
Cecum of mother 1 mouse offspring with genotype ob/ob	43	Mother: 1120	Mother: 2	0.18
Human feces; subj10; 12 weeks; carb-r diet	44	6909	1	0.01
Insect gut	45	623	3	0.48
Push core sediment sample from the vadose zone of a hydrocarbon contaminated aquifer	46	486	3	0.62
Mud volcano	47	185	2	1.08









































K19118	csd2, cas7; CRISPR-associated protein Csd2	0	1	0	0	1	0	0	2	0	0
K19119	cas5d; CRISPR-associated protein Cas5d	0	0	0	0	1	0	0	1	0	0
K19134	csx10; CRISPR-associated protein Csx10	1	0	0	0	0	0	0	0	0	0
K19137	csn2; CRISPR-associated protein Csn2	1	0	0	0	0	0	0	0	0	0
K19138	csm2; CRISPR-associated protein Csm2	0	1	0	0	0	0	0	0	0	0
K19139	csm4; CRISPR-associated protein Csm4	0	1	0	0	0	0	0	0	0	0
K19140	csm5; CRISPR-associated protein Csm5	0	1	0	0	0	0	0	0	0	0
K19141	cmr5; CRISPR-associated protein Cmr5	1	0	0	0	0	0	0	0	0	0
K19147	mcrC; 5-methylcytosine-specific restriction enzyme subunit McrC	1	0	0	0	0	0	0	1	0	1
K19157	yafQ; mRNA interferase YafQ [EC:3.1.-.]	2	0	1	0	0	0	0	0	0	0
K19158	yoeB; toxin YoeB [EC:3.1.-.]	1	0	1	0	0	0	0	0	0	0
K19159	yefM; antitoxin YefM	1	0	0	0	0	0	0	0	0	0
K19171	dndD; DNA sulfox modification protein DndD	0	0	1	0	0	0	0	0	0	0
K19200	IAI; isopenicillin-N N-acyltransferase like protein	0	0	1	0	0	0	0	0	0	0
K19221	cobA, btuR; cob(II)alamin adenosyltransferase [EC:2.5.1.17]	1	0	4	1	1	1	1	1	1	1
K19222	menI, DHNAT; 1,4-dihydroxy-2-naphthoyl-CoA hydrolase [EC:3.1.2.28]	0	0	0	0	0	0	0	0	1	0
K19224	lye; cwfF; peptidoglycan O1-endopeptidase lytE [EC:3.4.-.]	1	1	1	0	0	0	0	0	0	0
K19239	spz2; predicted membrane protein	1	1	1	0	0	0	0	0	0	0
K19244	ala; alanine dehydrogenase [EC:1.4.1.1]	0	0	1	0	0	0	0	0	0	0
K19270	hxpA; mannitol-1-/sugar-/sorbitol-6-phosphatase [EC:3.1.3.22 3.1.3.23 3.1.3.50]	1	0	0	0	0	0	0	1	0	0
K19294	algI; alginate O-acetyltransferase complex protein AlgI	1	0	1	0	1	0	0	1	1	1
K19302	bcrC; undecaprenyl-diphosphatase [EC:3.6.1.27]	2	1	3	1	1	1	1	0	1	1
K19333	kdgR; Icr family transcriptional regulator, KDG regulon repressor	0	0	2	0	1	0	0	0	0	0
K19350	lsa; lincosamide and streptogramin A transport system ATP-binding/permease protein	0	0	1	0	1	0	0	0	0	1
K19405	mcsB; protein arginine kinase [EC:2.7.14.1]	1	1	1	1	1	1	1	1	0	0
K19411	mcsA; protein arginine kinase activator	1	1	1	1	1	1	1	1	0	0
K19421	epsC; polysaccharide biosynthesis protein EpsC	1	1	1	1	1	1	0	1	0	0
K19422	epsD; glycosyltransferase EpsD [EC:2.4.-.]	1	0	2	0	1	1	0	0	0	0
K19423	epsE; glycosyltransferase EpsE [EC:2.4.-.]	1	0	0	0	1	1	0	0	0	0
K19424	epsF; glycosyltransferase EpsF [EC:2.4.-.]	0	0	0	0	0	1	0	0	0	0
K19425	epsH; glycosyltransferase EpsH [EC:2.4.-.]	1	0	0	0	0	0	0	0	0	0
K19427	epsI; glycosyltransferase EpsI [EC:2.4.-.]	1	0	0	0	1	0	0	0	0	0
K19428	epsJ; sugar transferase EpsJ [EC:2.-.-.]	0	0	1	0	1	0	0	0	0	0
K19430	epsN; pyridoxal phosphate-dependent aminotransferase EpsN [EC:2.6.1.-.]	1	0	1	0	1	1	0	0	0	0
K19545	lnuA_C_D_E; lin; lincosamide nucleotidyltransferase A/C/D/E	0	0	0	0	1	0	0	0	0	0
K19689	ampS, pepS, ampT; aminopeptidase [EC:3.4.11.-.]	1	1	1	1	1	1	1	1	1	1
K19709	ydfI; acetate CoA-transferase [EC:2.8.3.8]	0	0	1	0	0	0	0	0	0	0
K19736	aeR; TetR/Acr family transcriptional regulator, regulator of autoinduction and epiphytic fitness	0	0	0	0	0	0	0	1	0	0
K19784	chrR; NOR; chromate reductase, NAD(P)H dehydrogenase (quinone)	1	0	1	0	1	0	0	0	0	0
K19802	ycjG, ykfb; L-Ala-D/L-Glu epimerase [EC:5.1.1.20]	0	0	1	0	0	0	0	0	0	0
K19814	eam; glutamate 2,3-aminomutase [EC:5.4.3.9]	2	1	0	0	0	0	0	0	0	0
K19955	adh2; alcohol dehydrogenase [EC:1.1.1.-.]	1	0	0	0	0	1	1	1	0	0
K19960	chnA; cyclohexanol dehydrogenase [EC:1.1.1.245]	1	0	0	0	0	0	0	0	0	0
K20038	cutC; choline trimethylamine-lyase [EC:4.3.99.4]	1	1	1	0	0	0	0	0	0	0
K20074	prpC, phpP; PPM family protein phosphatase [EC:3.1.3.16]	1	1	1	1	2	1	1	1	1	1
K20156	sgc5; 2-amino-4-deoxychorismate dehydrogenase [EC:1.3.8.16]	0	0	0	0	0	0	0	0	0	0
K20265	gadC; glutamate:GABA antiporter	0	0	0	2	2	0	0	0	0	0
K20429	vioA; dTDP-4-amino-4,6-dideoxy-D-glucose transaminase [EC:2.6.1.33]	1	0	1	0	0	0	0	0	0	0
K20445	ndhF; nicotinate dehydrogenase FAD-subunit [EC:1.17.1.5]	0	1	4	0	0	1	0	0	0	0
K20446	ndhS; nicotinate dehydrogenase small FeS subunit [EC:1.17.1.5]	0	0	1	0	0	0	0	0	0	0
K20447	ndhL; nicotinate dehydrogenase large molybdopterin subunit [EC:1.17.1.5]	2	3	9	0	0	1	1	3	0	0
K20448	ndhM; nicotinate dehydrogenase medium molybdopterin subunit [EC:1.17.1.5]	0	0	1	0	0	0	0	1	0	0
K20449	hnr; 6-hydroxynicotinate reductase [EC:1.3.7.1]	0	0	1	0	0	0	0	0	0	0
K20451	rmj; methylitaconate Delta-isomerase [EC:5.3.3.6]	0	0	4	0	0	0	0	0	0	0
K20454	dmi; 2,3-dimethylmalate lyase [EC:4.1.3.32]	0	0	0	0	0	0	0	1	0	0
K20459	nukF, mcdF, sbdF; lantibiotic transport system ATP-binding protein	0	0	0	0	0	0	0	0	1	0
K20460	nukE, mcdE, sbdE; lantibiotic transport system permease protein	0	0	0	0	0	0	0	0	1	0
K20487	nisK, spaK; two-component system, OmpR family, lantibiotic biosynthesis sensor histidine kinase NisK/SpaK [EC:2.7.13.3]	1	0	0	0	0	0	0	0	1	1
K20488	nisR, spaR; two-component system, OmpR family, lantibiotic biosynthesis response regulator NisR/SpaR	1	0	0	0	1	0	0	0	1	1
K20609	sgcX; putative aminopeptidase [EC:3.4.11.-.]	0	0	1	0	0	0	0	0	0	0
K20625	ahy; acetylene hydratase [EC:4.2.1.112]	0	0	3	0	0	0	0	0	0	0
K20680	fttB; dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase [EC:2.6.1.90]	0	0	1	0	0	0	0	0	0	0
K20763	naa; 5-nitroanthranilic acid aminohydrolase [EC:3.5.99.8]	0	0	1	0	0	0	0	0	0	0
K20859	phnPP; phosphoribosyl 1,2-cyclic phosphate 1,2-diphosphodiesterase [EC:3.1.4.57]	0	0	1	0	0	0	0	0	0	0
K20882	hadA; (R)-2-hydroxy-4-methylpentanoate CoA-transferase [EC:2.8.3.24]	1	0	0	0	0	0	0	0	0	0
K20922	vpsJ; polysaccharide biosynthesis protein VpsJ	1	0	0	0	0	0	0	0	0	0
K21020	siaD; diguanylate cyclase [EC:2.7.7.65]	0	0	1	0	0	0	0	0	0	0
K21022	roeA; diguanylate cyclase [EC:2.7.7.65]	0	0	0	0	0	0	0	1	0	0
K21028	ynjE; molybdopterin synthase sulfurtransferase [EC:2.8.1.11]	0	0	1	0	0	0	0	0	0	0
K21029	moeB; molybdopterin-synthase adenylyltransferase [EC:2.7.7.80]	0	1	1	0	0	0	0	0	1	2
K21030	tari; D-ribitol-5-phosphate cytidyltransferase [EC:2.7.7.40]	0	0	0	1	1	0	0	0	0	0

**Table S5.** Recipe for trace element solution A, 500 mL solution

Description	Volume (mg, unless stated)
HCl	10 mL
FeCl <sub>2</sub> ·4H <sub>2</sub> O	750
CoCl <sub>2</sub> ·6H <sub>2</sub> O	95
MnCl <sub>2</sub> ·4H <sub>2</sub> O	50
ZnCl <sub>2</sub>	35
H <sub>3</sub> BO <sub>3</sub>	3
Na <sub>2</sub> MoO <sub>4</sub> ·H <sub>2</sub> O	18
NiCl <sub>2</sub> ·6H <sub>2</sub> O	12
CuCl <sub>2</sub> ·2H <sub>2</sub> O	1
Water (MilliQ)	500 mL

**Table S6.** Recipe for trace element solution B, 500 mL solution

Description	Volume (mg, unless stated)
Na <sub>2</sub> SeO <sub>3</sub> ·5H <sub>2</sub> O	3
NaWO <sub>4</sub> ·2H <sub>2</sub> O	4
NaOH	250
Water (MilliQ)	500 mL

**Table S7.** Recipe for 1000X vitamin, 1L solution. After dissolving all the reagents in the water, the solution water was filter-sterilized three times into serum bottles and capped with sterile septa. The solution was then purged with sterile N<sub>2</sub> for 30 minutes.

Description	Volume (mg, unless stated)
p-aminobenzoate	20
Biotin	5
Nicotinic acid	50
Pantothenic acid	25
Pyridoxine	75
Thiamine	50
Cyanocobalamin	50
Water (MilliQ)	1 L

## FASP Protocol

All centrifugation steps were done at 14,000 rcf for 10 minutes unless indicated otherwise.

1. Each extract sample was diluted to a final concentration of 0.8  $\mu\text{g}/\mu\text{l}$  using ammonium bicarbonate buffer (ABC, 0.05 M stock, pH 9.0). The proteins in the diluted sample were denatured by adding dithioereitol to a final concentration of 5 mM and incubating the mixture at 30° C for 30 minutes.
2. The samples were mixed with 200  $\mu\text{l}$  of urea solution (UA, 8 M stock) and the filter units were centrifugated twice. The flow-through from each filter unit was discarded from the collection tube after each centrifugation step.
3. 100  $\mu\text{l}$  of iodoacetamide solution (IAA, 0.05 M) was added to the filter units and was mixed using a thermomixer temperature at 600 rpm. The filter unites were incubated for 20 minutes in the dark before being centrifugated.
4. 100  $\mu\text{l}$  of UA was added to the filter units which were then centrifugated twice.
5. 100  $\mu\text{l}$  of ABC was added to the filter units which were then centrifugated twice.
6. 40  $\mu\text{l}$  of ABC and 0.9  $\mu\text{l}$  of trypsin stock solution (0.4 ng/ $\mu\text{l}$ ) were added to the filter units and were mixed at 600 rpm in thermomixer for 1 minute. The flow-through from each filter unit was then discarded from the collection tube.
7. 500  $\mu\text{l}$  of MilliQ H<sub>2</sub>O was added to the filter units, which were incubated at 37° C in dark for 12 hours.
8. The filter component from each unit was relocated to a new container tube and was centrifugated.
9. 20  $\mu\text{l}$  of ABC was added to the filter units, which were then centrifugated twice. The flow-through containing peptides were transferred to 1.5 mL tubes and were stored at -20° C until proteomics analysis.

















WP\_089612429.1 hypothetical protein  
WP\_089612433.1 Protein LemA

3.9	1.2	0.3	3.3	0.9	0.3	27.2	7.3	0.3
7.0	1.4	0.2	5.0	0.8	0.2	26.0	7.6	0.3

Table S9. Protein assignments to 22 KEGG categories using BlastKOALA

KEGG Functional Category	Category Code	Raw number	% out of total annotated (702)	% out of proteins in proteome (1,012)
Genetic information processing	9120	115	16.4	11.4
Amino acid metabolism	9105	97	13.8	9.6
Energy metabolism	9102	90	12.8	8.9
Metabolism of cofactors and vitamins	9108	84	12.0	8.3
Carbohydrate metabolism	9101	80	11.4	7.9
Protein families: genetic information processing	9182	58	8.3	5.7
Environmental information processing	9130	49	7.0	4.8
Unclassified: metabolism	9191	38	5.4	3.8
Nucleotide metabolism	9104	36	5.1	3.6
Human diseases	9160	34	4.8	3.4
Protein families: signalling and cellular processing	9183	33	4.7	3.3
Cellular processes	9140	33	4.7	3.3
Metabolism of other amino acids	9106	23	3.3	2.3
Glycan biosynthesis and metabolism	9107	22	3.1	2.2
Xenobiotics degradation and metabolism	9111	22	3.1	2.2
Organismal systems	9150	20	2.8	2.0
Unclassified		19	2.7	1.9
Protein families: metabolism	9181	18	2.6	1.8
Unclassified: genetic information processing	9192	12	1.7	1.2
Unclassified: signalling and cellular processing	9193	11	1.6	1.1
Lipid metabolism	9103	10	1.4	1.0
Metabolism of terpenoids and polyketides	9109	4	0.6	0.4











NZ_CP022121.1_211	JBMCNGCN_00213	K01926	Protein families: genetic information and processing	9182	rex; redox-sensing transcriptional repressor	138
NZ_CP022121.1_1110	JBMCNGCN_01151	K02355	Protein families: genetic information and processing	9182	fusa, GFM, EFG; elongation factor G	558
NZ_CP022121.1_2892	JBMCNGCN_02968	K02355	Protein families: genetic information and processing	9182	fusa, GFM, EFG; elongation factor G	426
NZ_CP022121.1_2636	JBMCNGCN_02701	K02356	Protein families: genetic information and processing	9182	efp; elongation factor P	138
NZ_CP022121.1_1942	JBMCNGCN_01999	K02357	Protein families: genetic information and processing	9182	tsf, TSM; elongation factor Ts	200
NZ_CP022121.1_682	JBMCNGCN_00703	K02469	Protein families: genetic information and processing	9182	gyrA; DNA gyrase subunit A [EC:5.6.2.2]	561
NZ_CP022121.1_683	JBMCNGCN_00704	K02470	Protein families: genetic information and processing	9182	gyrB; DNA gyrase subunit B [EC:5.6.2.2]	465
NZ_CP022121.1_1008	JBMCNGCN_01036	K02499	Protein families: genetic information and processing	9182	yabN; tetrapyrrole methylase family protein / MazG family protein	89
NZ_CP022121.1_1137	JBMCNGCN_01178	K02518	Protein families: genetic information and processing	9182	infA; translation initiation factor IF-1	66
NZ_CP022121.1_2561	JBMCNGCN_02626	K02519	Protein families: genetic information and processing	9182	infB, MTIF2; translation initiation factor IF-2	384
NZ_CP022121.1_2732	JBMCNGCN_02799	K02520	Protein families: genetic information and processing	9182	infC, MTIF3; translation initiation factor IF-3	101
NZ_CP022121.1_2558	JBMCNGCN_02623	K02600	Protein families: genetic information and processing	9182	nusA; transcription termination/antitermination protein NusA	238
NZ_CP022121.1_1100	JBMCNGCN_01141	K02601	Protein families: genetic information and processing	9182	nusG; transcription termination/antitermination protein NusG	136
NZ_CP022121.1_58	JBMCNGCN_00059	K02687	Protein families: genetic information and processing	9182	prmA; ribosomal protein L11 methyltransferase [EC:2.1.1.]	144
NZ_CP022121.1_2562	JBMCNGCN_02627	K02834	Protein families: genetic information and processing	9182	rfa; ribosome-binding factor A	57
NZ_CP022121.1_896	JBMCNGCN_00923	K02835	Protein families: genetic information and processing	9182	prfA, MTRF1, MRF1; peptide chain release factor 1	261
NZ_CP022121.1_1944	JBMCNGCN_02001	K02838	Protein families: genetic information and processing	9182	rrf, MRRF, RRF; ribosome recycling factor	132
NZ_CP022121.1_1933	JBMCNGCN_01990	K03168	Protein families: genetic information and processing	9182	topA; DNA topoisomerase I [EC:5.6.2.1]	424
NZ_CP022121.1_1094	JBMCNGCN_01130	K03218	Protein families: genetic information and processing	9182	rimB; 23S rRNA [guanosine2251'-O-] methyltransferase [EC:2.1.1.185]	94
NZ_CP022121.1_2729	JBMCNGCN_02796	K03437	Protein families: genetic information and processing	9182	spou; RNA methyltransferase, TrmH family	124
NZ_CP022121.1_695	JBMCNGCN_00716	K03497	Protein families: genetic information and processing	9182	parB, spo0I; ParB family transcriptional regulator, chromosome partitioning protein	123
NZ_CP022121.1_1009	JBMCNGCN_01037	K03530	Protein families: genetic information and processing	9182	hubB; DNA-binding protein HU-beta	64
NZ_CP022121.1_209	JBMCNGCN_00211	K03569	Protein families: genetic information and processing	9182	mreB; rod shape-determining protein MreB and related proteins	256
NZ_CP022121.1_927	JBMCNGCN_00954	K03569	Protein families: genetic information and processing	9182	mreB; rod shape-determining protein MreB and related proteins	253
NZ_CP022121.1_1203	JBMCNGCN_01243	K03595	Protein families: genetic information and processing	9182	era, ERAL1; GTPase	176
NZ_CP022121.1_204	JBMCNGCN_00206	K03609	Protein families: genetic information and processing	9182	mind; septum site-determining protein Mind	321
NZ_CP022121.1_1065	JBMCNGCN_01095	K03624	Protein families: genetic information and processing	9182	groA; transcription elongation factor GroA	106
NZ_CP022121.1_2469	JBMCNGCN_02533	K03631	Protein families: genetic information and processing	9182	recN; DNA repair protein RecN (Recombination protein N)	144
NZ_CP022121.1_1937	JBMCNGCN_01994	K03667	Protein families: genetic information and processing	9182	hslU; ATP-dependent HslU protease ATP-binding subunit HslU	303
NZ_CP022121.1_59	JBMCNGCN_00060	K03686	Protein families: genetic information and processing	9182	dnaj; molecular chaperone DnaJ	216
NZ_CP022121.1_61	JBMCNGCN_00062	K03687	Protein families: genetic information and processing	9182	grpE; molecular chaperone GrpE	62
NZ_CP022121.1_1081	JBMCNGCN_01117	K03696	Protein families: genetic information and processing	9182	clpC; ATP-dependent Clp protease ATP-binding subunit ClpC	539
NZ_CP022121.1_3893	JBMCNGCN_03480	K03698	Protein families: genetic information and processing	9182	cbf, cbf1; 3'-5' exoribonuclease [EC:3.1.-.]	166
NZ_CP022121.1_2599	JBMCNGCN_02664	K03706	Protein families: genetic information and processing	9182	codY; transcriptional pleiotropic repressor	164
NZ_CP022121.1_1024	JBMCNGCN_01052	K03788	Protein families: genetic information and processing	9182	PP1B, pplb; peptidyl-prolyl cis-trans isomerase B (cyclophilin B) [EC:5.2.1.8]	151
NZ_CP022121.1_702	JBMCNGCN_00723	K03833	Protein families: genetic information and processing	9182	selB, EEFSec; selenocysteine-specific elongation factor	321
NZ_CP022121.1_2546	JBMCNGCN_02610	K03977	Protein families: genetic information and processing	9182	engA, der; GTPase	301
NZ_CP022121.1_246	JBMCNGCN_00254	K04078	Protein families: genetic information and processing	9182	groES, HSP61; chaperonin GroES	68
NZ_CP022121.1_1632	JBMCNGCN_01685	K04083	Protein families: genetic information and processing	9182	hslO; molecular chaperone Hsp33	208
NZ_CP022121.1_1934	JBMCNGCN_01991	K04094	Protein families: genetic information and processing	9182	mFO, gid; methylenetetrahydrofolate--RNA-(araci1-5)-methyltransferase [EC:2.1.1.7]	248
NZ_CP022121.1_424	JBMCNGCN_00434	K05516	Protein families: genetic information and processing	9182	cbpC; curved DNA-binding protein	145
NZ_CP022121.1_954	JBMCNGCN_00981	K05808	Protein families: genetic information and processing	9182	yhbH; putative sigma-54 modulation protein	112
NZ_CP022121.1_468	JBMCNGCN_00479	K06284	Protein families: genetic information and processing	9182	rB family transcriptional regulator, transcriptional pleiotropic regulator of transition st:	64
NZ_CP022121.1_755	JBMCNGCN_00777	K06942	Protein families: genetic information and processing	9182	yehF; ribosome-binding ATPase	230
NZ_CP022121.1_2860	JBMCNGCN_02994	K07040	Protein families: genetic information and processing	9182	ycdO, ylnB; DUF177 domain-containing protein	66
NZ_CP022121.1_1679	JBMCNGCN_01443	K07447	Protein families: genetic information and processing	9182	ruvX; putative prokaryotic-16S rRNA nucleoside transferase	45
NZ_CP022121.1_1006	JBMCNGCN_01034	K07533	Protein families: genetic information and processing	9182	psrA; foldase protein PsrA [EC:5.2.1.8]	24
NZ_CP022121.1_192	JBMCNGCN_00194	K07574	Protein families: genetic information and processing	9182	yhbY; RNA-binding protein	70
NZ_CP022121.1_1084	JBMCNGCN_01120	K07736	Protein families: genetic information and processing	9182	carD; CarD family transcriptional regulator	140
NZ_CP022121.1_197	JBMCNGCN_00199	K08301	Protein families: genetic information and processing	9182	rng, cfaA; ribonuclease G [EC:3.1.26.-]	329
NZ_CP022121.1_999	JBMCNGCN_01027	K09685	Protein families: genetic information and processing	9182	purI; purine operon repressor	140
NZ_CP022121.1_57	JBMCNGCN_00058	K09761	Protein families: genetic information and processing	9182	rsmE; 16S rRNA (aracil498-N3)-methyltransferase [EC:2.1.1.193]	115
NZ_CP022121.1_1653	JBMCNGCN_01706	K09825	Protein families: genetic information and processing	9182	perR; Fur family transcriptional regulator, peroxide stress response regulator	65
NZ_CP022121.1_2395	JBMCNGCN_02458	K13628	Protein families: genetic information and processing	9182	isca; iron-sulfur cluster assembly protein	10
NZ_CP022121.1_775	JBMCNGCN_00797	K18979	Protein families: genetic information and processing	9182	queG; epoyoxyquinone reductase [EC:1.17.9.6]	82
NZ_CP022121.1_62	JBMCNGCN_00063	K22447	Protein families: genetic information and processing	9182	ccr, tbc; archael chaperonin	391
NZ_CP022121.1_1316	JBMCNGCN_01367	K02666	Protein families: metabolism	9181	K06666; fatty-acyl-CoA synthase [EC:6.2.1.-]	617
NZ_CP022121.1_2766	JBMCNGCN_02834	K09093	Protein families: metabolism	9181	eps8b, capB; protein-tyrosine kinase [EC:2.7.10.3]	87
NZ_CP022121.1_1567	JBMCNGCN_01620	K01262	Protein families: metabolism	9181	pepP; Xaa-Pro aminopeptidase [EC:3.4.11.9]	158
NZ_CP022121.1_1135	JBMCNGCN_01176	K01265	Protein families: metabolism	9181	map; methionyl aminopeptidase [EC:3.4.11.18]	216
NZ_CP022121.1_1936	JBMCNGCN_01993	K01419	Protein families: metabolism	9181	hslV, clpQ; ATP-dependent HslUV protease, peptidase subunit HslV [EC:3.4.25.2]	132
NZ_CP022121.1_2639	JBMCNGCN_02704	K03568	Protein families: metabolism	9181	tdlD; TldD protein	287
NZ_CP022121.1_2638	JBMCNGCN_02703	K03592	Protein families: metabolism	9181	pmbA; PmbA protein	239
NZ_CP022121.1_971	JBMCNGCN_00998	K03797	Protein families: metabolism	9181	E3.4.21.102, prc, ctpA; carboxyl-terminal processing protease [EC:3.4.21.102]	161
NZ_CP022121.1_1298	JBMCNGCN_01343	K03797	Protein families: metabolism	9181	E3.4.21.102, prc, ctpA; carboxyl-terminal processing protease [EC:3.4.21.102]	90
NZ_CP022121.1_1438	JBMCNGCN_01482	K03798	Protein families: metabolism	9181	ftsH, hlyB; cell division protease FtsH [EC:3.4.24.-]	413
NZ_CP022121.1_1037	JBMCNGCN_01067	K03798	Protein families: metabolism	9181	ftsH, hlyB; cell division protease FtsH [EC:3.4.24.-]	399
NZ_CP022121.1_13	JBMCNGCN_00014	K06894	Protein families: metabolism	9181	yfmM; alpha-2-macroglobulin	475
NZ_CP022121.1_725	JBMCNGCN_00747	K08602	Protein families: metabolism	9181	pepP, pepB; oligonucleotide phosphatase [EC:3.4.24.-]	376
NZ_CP022121.1_1886	JBMCNGCN_01943	K12132	Protein families: metabolism	9181	prkC, stkP; eukaryotic-like serine/threonine-protein kinase [EC:2.7.11.1]	245
NZ_CP022121.1_3891	JBMCNGCN_03478	K19224	Protein families: metabolism	9181	lytE, cwfF; peptidoglycan DL-endopeptidase LytE [EC:3.4.-.]	19
NZ_CP022121.1_734	JBMCNGCN_00756	K19689	Protein families: metabolism	9181	ampS, pepS, ampT; aminopeptidase [EC:3.4.11.1]	294
NZ_CP022121.1_1885	JBMCNGCN_01942	K20074	Protein families: metabolism	9181	pprC, phpP; PPM family protein phosphatase [EC:3.1.3.16]	91
NZ_CP022121.1_3579	JBMCNGCN_03667	K01552	Protein families: signal and cellular processes	9182	ecfA; energy-coupling factor transport system ATP-binding protein [EC:7.-.-.]	301
NZ_CP022121.1_756	JBMCNGCN_00778	K01552	Protein families: signal and cellular processes	9182	ecfA; energy-coupling factor transport system ATP-binding protein [EC:7.-.-.]	168
NZ_CP022121.1_2908	JBMCNGCN_02982	K16104	Protein families: signal and cellular processes	9183	mmdA; methylenecylo-CoxB biosynthesis subunit alpha [EC:7.2.4.3]	501
NZ_CP022121.1_2423	JBMCNGCN_02486	K01989	Protein families: signal and cellular processes	9183	K01989; putative tryptophan/lysine transport system substrate-binding protein	173
NZ_CP022121.1_334	JBMCNGCN_00342	K02003	Protein families: signal and cellular processes	9183	ABC.CD.A; putative ABC transport system ATP-binding protein	104
NZ_CP022121.1_2100	JBMCNGCN_02164	K02016	Protein families: signal and cellular processes	9183	ABC.FE.V.S; iron complex transport system substrate-binding protein	124
NZ_CP022121.1_1532	JBMCNGCN_01585	K02016	Protein families: signal and cellular processes	9183	ABC.FE.V.S; iron complex transport system substrate-binding protein	74
NZ_CP022121.1_1273	JBMCNGCN_01316	K02028	Protein families: signal and cellular processes	9183	ABC.PA.A; polar amino acid transport system ATP-binding protein [EC:7.4.2.1]	131
NZ_CP022121.1_1209	JBMCNGCN_01249	K02051	Protein families: signal and cellular processes	9183	ABC.SN.S; NiT/Tau family transport system substrate-binding protein	141
NZ_CP022121.1_2770	JBMCNGCN_02838	K02238	Protein families: signal and cellular processes	9183	comEC; competence protein ComEC	78
NZ_CP022121.1_55	JBMCNGCN_00056	K02503	Protein families: signal and cellular processes	9183	HINT1, hint1; histidine triad (HTI) family protein	61
NZ_CP022121.1_888	JBMCNGCN_00398	K03282	Protein families: signal and cellular processes	9183	mscL; large conductance mechanosensitive channel	91
NZ_CP022121.1_1792	JBMCNGCN_01846	K03284	Protein families: signal and cellular processes	9183	yhbE; phosphatase subunit alpha	225
NZ_CP022121.1_102	JBMCNGCN_00103	K03427	Protein families: signal and cellular processes	9183	hsdM; type II restriction enzyme M protein [EC:2.1.1.72]	408
NZ_CP022121.1_2357	JBMCNGCN_02426	K03522	Protein families: signal and cellular processes	9183	fixB, eHfA; electron transfer flavoprotein alpha subunit	207
NZ_CP022121.1_77	JBMCNGCN_00078	K03699	Protein families: signal and cellular processes	9183	tylC; magnesium and cobalt exporter, CNM family	225
NZ_CP022121.1_1154	JBMCNGCN_01195	K06990	Protein families: signal and cellular processes	9183	MEMO1; MEMO1 family protein	224
NZ_CP022121.1_562	JBMCNGCN_00576	K07316	Protein families: signal and cellular processes	9183	mod; adenine-specific DNA-methyltransferase [EC:2.1.1.72]	211
NZ_CP022121.1_3348	JBMCNGCN_03431	K07316	Protein families: signal and cellular processes	9183	mod; adenine-specific DNA-methyltransferase [EC:2.1.1.72]	208
NZ_CP022121.1_1218	JBMCNGCN_01258	K07473	Protein families: signal and cellular processes	9183	dinJ; DNA-damage-inducible protein J	42
NZ_CP022121.1_2960	JBMCNGCN_03040	K08369	Protein families: signal and cellular processes	9183	ydjE; MFS transporter, putative metabolite:H+ symporter	269
NZ_CP022121.1_493	JBMCNGCN_00505	K08369	Protein families: signal and cellular processes	9183	ydjE; MFS transporter, putative metabolite:H+ symporter	178
NZ_CP022121.1_870	JBMCNGCN_00897	K09013	Protein families: signal and cellular processes	9183	suFC; Fe-S cluster assembly ATP-binding protein	163
NZ_CP022121.1_80	JBMCNGCN_00081	K14392	Protein families: signal and cellular processes	9182	panF; sodium/garothenate symporter	101
NZ_CP022121.1_406	JBMCNGCN_00416	K15987	Protein families: signal and cellular processes	9183	hpaA; K(+)-stimulated pyrophosphate-energized sodium pump [EC:7.1.3.2]	792
NZ_CP022121.1_354	JBMCNGCN_00362	K15987	Protein families: signal and cellular processes	9183	hpaA; K(+)-stimulated pyrophosphate-energized sodium pump [EC:7.1.3.2]	418
NZ_CP022121.1_2368	JBMCNGCN_02437	K19091	Protein families: signal and cellular processes	9183	casG; CRISPR-associated endoribonuclease CasG [EC:3.1.-.]	29
NZ_CP022121.1_3443	JBMCNGCN_03529	K19115	Protein families: signal and cellular processes	2913	chz2; CRISPR-associated protein Chz2	237
NZ_CP022121.1_2983	JBMCNGCN_03064	K19156	Protein families: signal and cellular processes	9186	prf, sohA; antitoxin Prf	12
NZ_CP022121.1_2767	JBMCNGCN_02835	K19420	Protein families: signal and cellular processes	9183	epsA, capA; protein tyrosine kinase modulator	48
NZ_CP022121.1_1247	JBMCNGCN_01288	K25034	Protein families: signal and cellular processes	9183	btuB; cobalamin transport system substrate-binding protein	114
NZ_CP022121.1_721	JBMCNGCN_00743	K00179	Unclassified		iorA; indolepyruvate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.8]	409
NZ_CP022121.1_722	JBMCNGCN_00744	K00180	Unclassified		iorB; indolepyruvate ferredoxin oxidoreductase, beta subunit [EC:1.2.7.8]	119
NZ_CP022121.1_2358	JBMCNGCN_02427	K00313	Unclassified		fixC; electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]	248
NZ_CP022121.1_2935	JBMCNGCN_03015	K00573	Unclassified		E2.1.1.77, pcm; protein-L-isoaspartate(D-aspartate)-O-methyltransferase [EC:2.1.1.77]	81
NZ_CP022121.1_1486	JBMCNGCN_01540	K01023	Unclassified		astT; arylsulfate sulfotransferase [EC:2.8.2.22]	287
NZ_CP022121.1_1879	JBMCNGCN_01936	K01462	Unclassified		PDF, def; peptide deformylase [EC:3.5.1.88]	46
NZ_CP022121.1_2842	JBMCNGCN_02915	K01463	Unclassified		bshB1; N-acetylglucosamine malate decarboxylase I [EC:3.5.5.-]	288
NZ_CP022121.1_3213	JBMCNGCN_03293	K01533	Unclassified		copB; P-type Cu2+ transporter [EC:7.2.2.9]	38
NZ_CP022121.1_1389	JBMCNGCN_01440	K01537	Unclassified		ATP2C; P-type Ca2+ transporter type 2C [EC:7.2.2.10]	653
NZ_CP022121.1_978	JBMCNGCN_01005	K01993	Unclassified		ABC-2.TX; HlyD family secretion protein	101
NZ_CP022121.1_1462	JBMCNGCN_01516	K03744	Unclassified		lemA; LemA protein	103
NZ_CP022121.1_3619	JBMCNGCN_03707	K03744	Unclassified		lemA; LemA protein	62
NZ_CP022121.1_3412	JBMCNGCN_03499	K03753	Unclassified		mobB; molybdopterine-guanine dinucleotide biosynthesis adapter protein	81
NZ_CP022121.1_90	JBMCNGCN_00091	K03969	Unclassified		pspA; phage shock protein A	139
NZ_CP022121.1_3246	JBMCNGCN_03327	K04750	Unclassified		phnB; PhnB protein	103
NZ_CP022121.1_2254	JBMCNGCN_02323	K05937	Unclassified		K05937; uncharacterized protein	52
NZ_CP022121.1_715	JBMCNGCN_00737	K06207	Unclassified		tpa, bpa; GTP-binding protein	418
NZ_CP022121.1_1629	JBMCNGCN_01682	K06923	Unclassified		K06923; uncharacterized protein	162
NZ_CP022121.1_601	JBMCNGCN_00615	K06926	Unclassified		K06926; uncharacterized protein	43
NZ_CP022121.1_818	JBMCNGCN_00844	K06929	Unclassified		K06929; uncharacterized protein	47
NZ_CP022121.1_1047	JBMCNGCN_01077	K06950				



Table S11. Similarity of electron bifurcation proteins identified from *D. formicoaceticum* proteome against proteins described in previous studies

S. ovata		Sporomusa ovata		S. fructosivorans JJ		Solidisulfobivibrio fructosivorans JJ		O. alaskensis G20		Oleidesulfobivibrio alaskensis G20	
Query	Prokka ID	Query	NCBI ID	Query Description	Subject	Subject Description	Coverage	Identity	E-value	Score	
StnA	JBMCGNCK_01549	WP_089609810.1		NADH-quinone oxidoreductase subunit E	WP_021167189.1	StnA ( <i>S. ovata</i> )	84.0%	41.3%	3.00E-39	119	
StnB	JBMCGNCK_01550	WP_242965405.1		NAD(P)H-quinone oxidoreductase subunit E	WP_021167190.1	StnB ( <i>S. ovata</i> )	94.0%	57.3%	0	583	
StnC	JBMCGNCK_01551	WP_089609812.1		FAD-dependent oxidoreductase	WP_021167191.1	StnC ( <i>S. ovata</i> )	88.0%	40.7%	0	833	
HndA	JBMCGNCK_01556	WP_089609814.1		NuoE-like protein	EFL52768.1	NADH dehydrogenase (ubiquinone) 24 dKa subunit ( <i>S. fructosivorans JJ</i> )	91%	40.4%	1.00E-45	134	
HndB	JBMCGNCK_01557	WP_157677371.1		(2Fe-2S) ferredoxin domain-containing protein	EFL52769.1	Putative NAD-reducing hydrogenase subunit ( <i>S. fructosivorans JJ</i> )	90.0%	36.1%	4.00E-23	73.9	
HndC	JBMCGNCK_01558	WP_242965405.1		NADH-quinone oxidoreductase subunit NuoF	EFL52770.1	NADH dehydrogenase (quinone) [ <i>S. fructosivorans JJ</i> ]	75.0%	62.0%	0	567	
HndD	JBMCGNCK_01559	WP_089609815.1		[FeFe] hydrogenase, group A	EFL52771.1	Hydrogenase, Fe-only ( <i>S. fructosivorans JJ</i> )	100.0%	54.3%	0	610	
FloxA	JBMCGNCK_01698	WP_157677380.1		Hydrogenase iron-sulfur subunit	ABB38011.2	methyl-viologen-reducing hydrogenase delta subunit ( <i>O. alaskensis G20</i> )	100.0%	52.2%	1.00E-26	85.5	
FloxB	JBMCGNCK_01699	WP_089609931.1		4Fe-4S binding protein	ABB38012.1	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein ( <i>O. alaskensis G20</i> )	91%	32.67%	1.00E-55	172	
FloxC	JBMCGNCK_01700	WP_198306669.1		4Fe-4S dicluster domain-containing protein	ABB38013.1	Putative hydrogenase ( <i>O. alaskensis G20</i> )	96%	33.73%	1.00E-65	201	
FloxD	JBMCGNCK_01701	WP_089609932.1		FAD/NAD(P)-binding protein	ABB38014.1	Dihydroorotate dehydrogenase, electron transfer subunit ( <i>O. alaskensis G20</i> )	97%	47.5	1.00E-99	283	
HdrA	JBMCGNCK_01696	WP_089609930.1		CoB--CoM heterodisulfide reductase iron-sulfur subunit A family protein	ABB38010.1	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein ( <i>O. alaskensis G20</i> )	99%	53.80%	2.00E-176	499	
HdrA	JBMCGNCK_01697	WP_089609930.1		CoB--CoM heterodisulfide reductase iron-sulfur subunit A family protein	ABB38010.1	4Fe-4S ferredoxin iron-sulfur binding domain-containing protein ( <i>O. alaskensis G20</i> )	98%	60.20%	7.00E-80	240	
HdrB	JBMCGNCK_01695	WP_089609929.1		CoB--CoM heterodisulfide reductase iron-sulfur subunit B family protein	ABB38009.1	CoB--CoM heterodisulfide reductase subunit B ( <i>O. alaskensis G20</i> )	92%	42.91%	1.00E-86	251	
HdrC	JBMCGNCK_01694	WP_198306668.1		4Fe-4S dicluster domain-containing protein	ABB38018.1	Heterodisulfide reductase C subunit ( <i>O. alaskensis G20</i> )	91%	37.90%	2.00E-49	149	

**Figure S1.** Distribution of genes encoding TCA cycle in the *Dehalobacteriia*

