

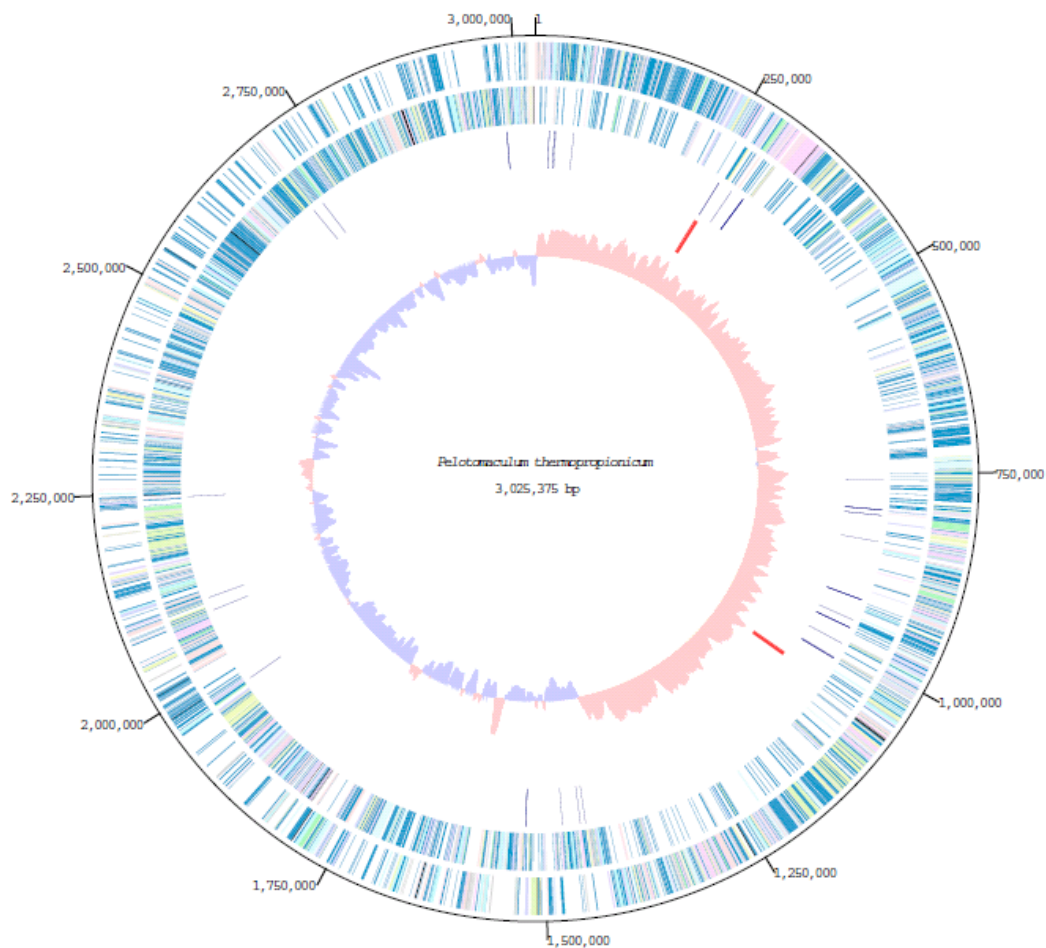


Fig. S1. Schematic circular diagram of the *P. thermopropionicum* genome. The outermost circle, predicted protein-coding regions on the plus strand (colors represent functional categories according to the COG database [<http://www.ncbi.nlm.nih.gov/COG>]). The second circle, predicted protein-coding regions on the minus strands. The third circle, tRNAs. The forth circle, rRNAs. The fifth circle, GC skew (red, positive; blue negative).

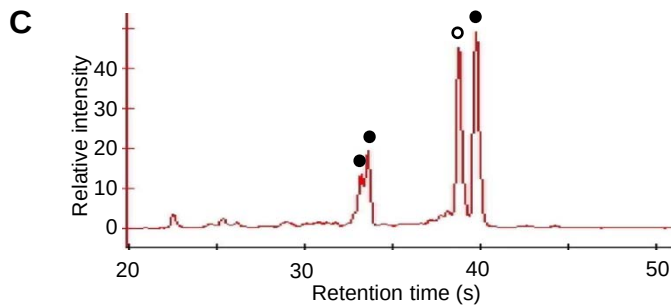
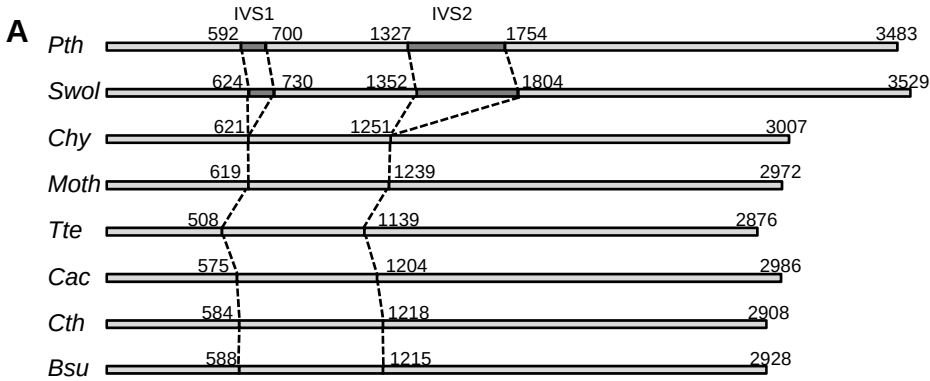
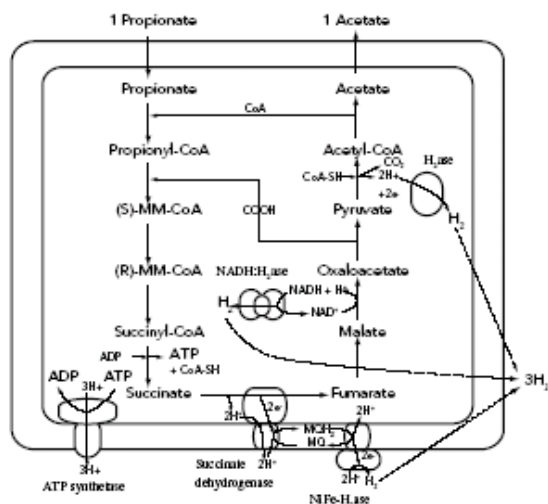
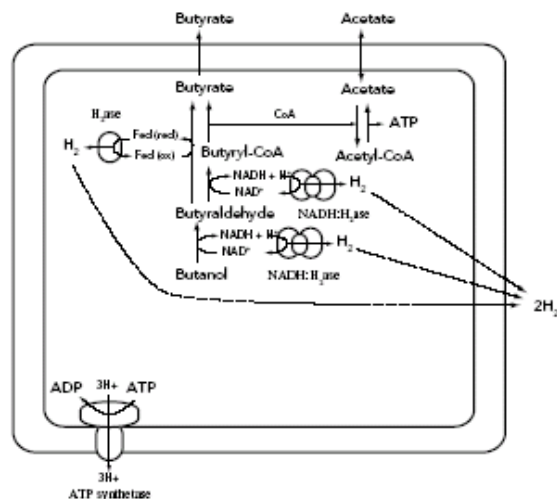


Fig. S2. The structure of 23S rRNA. A, a comparative schematic presentation of 23S rRNAs in *Firmicutes* bacteria. For organism names, refer to Table 1. B, alignments of IVS1 and IVS2 of *P. thermopropionicum* and *S. wolfei*. Red letters indicate inverting sequences. C, an electrophoretic pattern of a *P. thermopropionicum* RNA fraction analyzed by the Bioanalyzer (Agilent). Black circles indicate 23S rRNA peaks, while a white circle indicates a 16S rRNA peak.

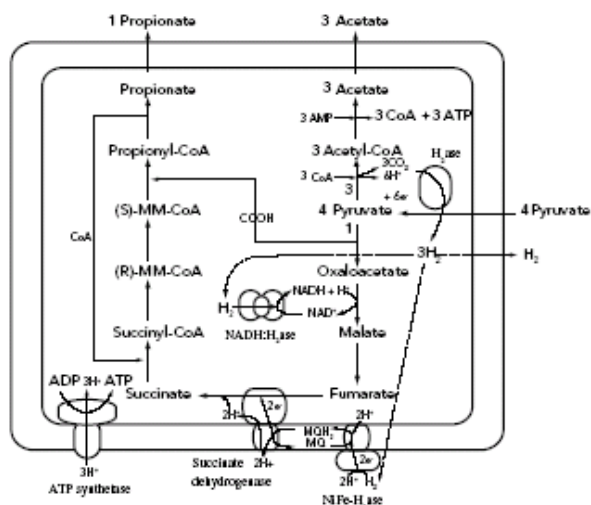
A. Propionate



B. Butanol



C. Pyruvate



D. Fumarate

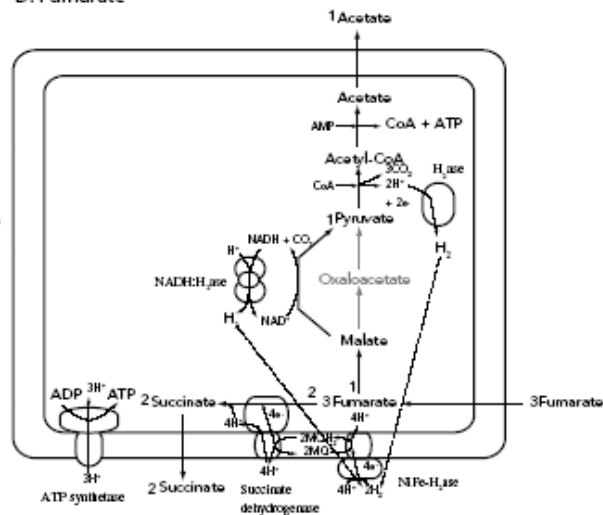


Fig. S3. Carbon and electron flows in *P. thermopropionicum* growing on four different substrates. A, propionate; B, 1-butanol; C, pyruvate; D, fumarate. H₂ase, hydrogenase; NADH:H₂ase, NADH-utilizing hydrogenase; MQ, menaquinone; MQH₂, menaquinol.

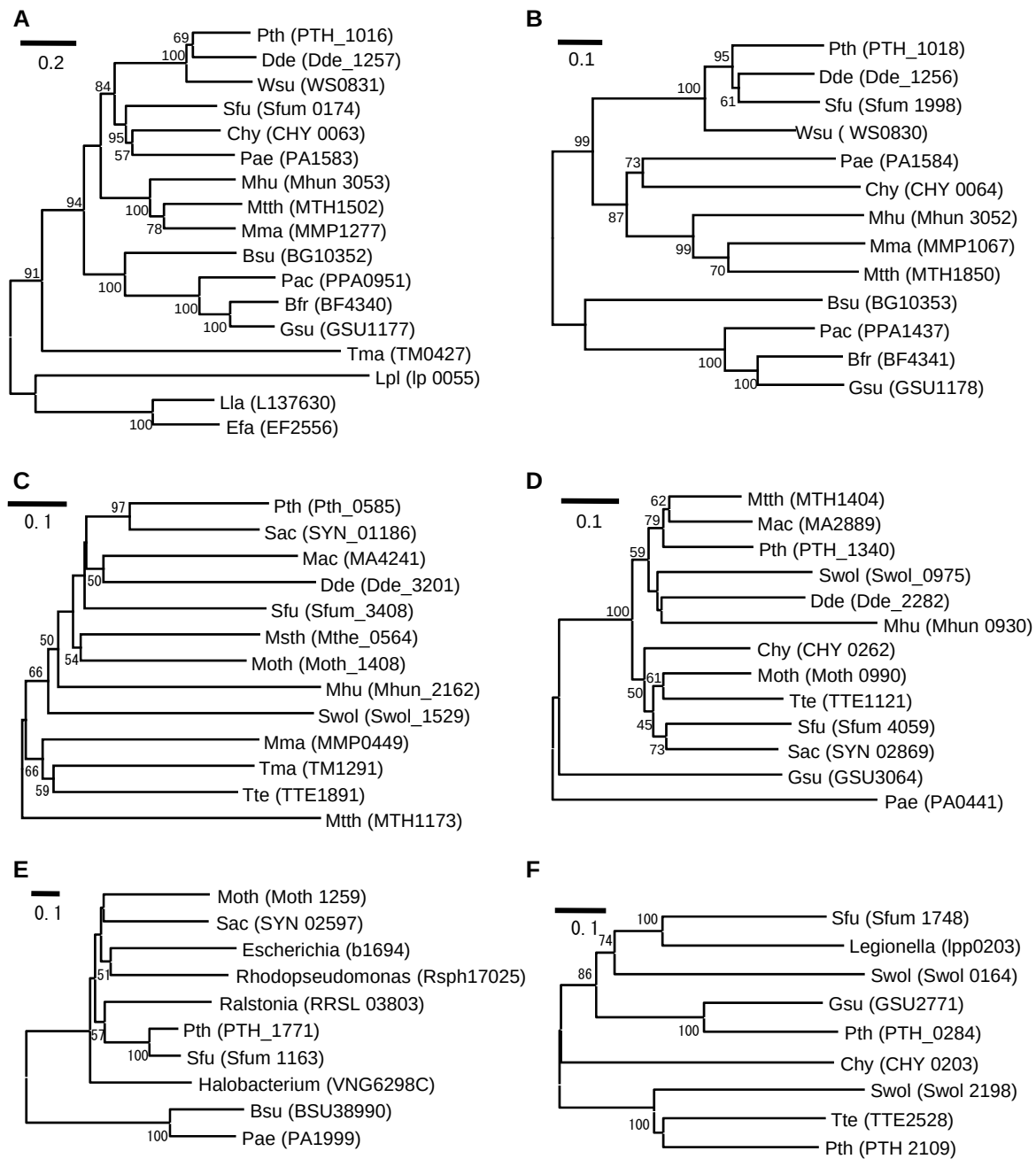


Fig. S4. Neighbor-joining trees showing phylogenetic relationships of CDSs in *P. thermopropionicum* showing atypical codon usages with corresponding genes in other organisms. (A) COG2009, succinate dehydrogenase cytochrome subunit; (B) COG0479, succinate dehydrogenase FeS subunit; (C) COG1149, ATPase containing a ferredoxin domain; (D) COG0145 acetone carboxylase, beta subunit; (E) COG4670 acyl CoA:acetate/3-ketoacid CoA transferase; (F) COG1943 transposase. CDSs are shown with organism names (see Table S1) and locus tags in parentheses. The numbers at the branch nodes are bootstrap values (per 100 trials); only values greater than 50 are shown. A scale bar indicates substitution per site.

Table S1. Microbial genomes analyzed in this study.

Organism name	Genome size (Mb) (Accession no.)	Taxon*	Niche**	Description
<i>Pth Pelotomaculum thermopropionicum</i>	3.0 (AP009389)	F	SB	Thermophile
<i>Chy Carboxydotherrmus hydrogenoformans</i>	2.4 (CP000141)	F		Thermophile
<i>Moth Moorella thermoacetica</i>	2.6 (CP000232)	F	HA***	Thermophile
<i>Tte Thermoanaerobacter tengcongensis</i>	2.7 (AE008691)	F	FB	Thermophile
<i>Swol Syntrophomonas wolfei</i>	2.9 (CP000252)	F	SB	
<i>Cth Clostridium thermocellum</i>	3.8 (CP000568)	F	FB	Thermophile
<i>Cac Clostridium acetobutylicum</i>	4.1 (AE001437)	F	FB	
<i>Lla Lactococcus lactis</i>	2.5 (AE005176)	F		
<i>Lpl Lactobacillus plantarum</i>	3.3 (AL935263)	F		
<i>Efa Enterococcus faecalis</i>	3.4 (AE016830)	F		
<i>Bsu Bacillus subtilis</i>	4.2 (AL009126)	F		
<i>Wsu Wolinella succinogenes</i>	2.1 (BX571656)	EP		
<i>Sac Syntrophus aciditrophicus</i>	3.2 (CP000252)	DP	SB	
<i>Sfu Syntrophobacter fumaroxidans</i>	5.0 (CP000478)	DP	SB	
<i>Dde Desulfovibrio desulfuricans</i>	3.7 (CP000112)	DP	SRB	
<i>Gsu Geobacter sulfurreducens</i>	3.8 (AE017180)	DP		
<i>Zmo Zymomonas mobilis</i>	2.1 (AE008692)	AP		
<i>Pae Pseudomonas aeruginosa</i>	6.3 (AE004091)	GP		
<i>Tde Treponema denticola</i>	2.8 (AE017226)	S	FB	
<i>Pac Propionibacterium acnes</i>	2.6 (AE017283)	A	FB	
<i>Bfr Bacteroides fragilis</i>	5.2 (CR626927)	B	FB	
<i>Tma Thermotoga maritima</i>	1.9 (AE000512)	T		Hyperthermophile
<i>Msth Methanosaeta thermophila</i>	1.9 (CP000477)	EA	MA	Thermophile
<i>Mtth Methanothermobacter thermautotrophicus</i>	1.8 (AE000666)	EA	MA	Thermophile
<i>Mhu Methanospirillum hungatei</i>	3.5 (CP000254)	EA	MA	
<i>Mma Methanococcus maripaludis</i>	1.7 (BX950229)	EA	MA	Marine organism
<i>Mac Methanosarcina acetivorans</i>	5.8 (AE010299)	EA	MA	

*F, Firmicutes; EB, Epsilonproteobacteria; DP, Deltaproteobacteria; AP, Alphaproteobacteria; GP, Gammaproteobacteria; S, Spirochaeta; A, Actinobacteria; T, Thermotoga; EA, Euryarchaeota.

**SB, syntrophic bacteria; HA, homoacetogen; FB, fermentative bacteria; SRB, sulfate-reducing bacteria; MA, methanogenic archaea. Niches were indicated for organisms whose close relatives have been detected in anaerobic biodegradation processes (e.g., references 1-3).

****Moth* is a homoacetogen converting CO₂ plus H₂ to acetate and vice versa (4), and closely related organisms have been detected in methanogenic digesters (3). Production of CO₂ plus H₂ suggests that this organism is capable of forming syntrophic interaction with methanogens.

References

1. Sekiguchi Y, Kamagata Y, Syutsubo K, Ohashi A, Harada H, Nakamura K (1998) *Microbiology* 144:2655-2665
2. Godon JJ, Zumstein E, Dabert P, Habouzit F, Moletta R. (1997) *Appl Environ Microbiol* 63:2802-2813
3. Roest K, Altinbas M, Paulo PL, Heilig HG, Akkermans AD, Smidt H, de Vos WM, Stams AJ (2005) *Microb Ecol* 50:440-446
4. Drake HL, Daniel SL (2004) *Res Microbiol* 155:869-883

Table S2. General features of the *P. thermopropionicum* SI genome.

General features	
Length of sequence	3025375
G + C ratio (%)	53.0
Protein-coding sequences (CDS)	2920
No. similar to known genes	1637
No. similar to genes of general function (R)	227
No. similar to genes of unknown function (S)	170
No. of genes not in COG database	886
Coding density (%)	86.3
Average CDS size (bp)	894
No. of 5S-16S-23S	2
No. of tRNAs	51

Table S3. Distribution of CDSs in the functional categories of the COG database presented as percentages to total CDS numbers.*

Category			Archaea**	Bacteria**	<i>Pth</i>	<i>Chy</i>	<i>Moth</i>	<i>Tte</i>	<i>Swol</i>	<i>Cth</i>	<i>Cac</i>	<i>Lla</i>	<i>Lpl</i>	<i>Efa</i>	<i>Bsu</i>	<i>Wsu</i>	<i>Sac</i>	<i>Sfu</i>	<i>Dde</i>	<i>Gsu</i>	<i>Zmo</i>	<i>Pae</i>	<i>Tde</i>	<i>Pac</i>	<i>Bfr</i>	<i>Tma</i>	<i>Msth</i>	<i>Mth</i>	<i>Mhu</i>	<i>Mma</i>	<i>Mac</i>
J	Translation	4.98	3.66	4.83	4.03	4.19	4.36	5.94	5.25	3.47	4.64	3.70	3.51	3.00	4.20	3.70	4.09	3.06	3.54	5.13	2.60	4.07	4.65	2.79	5.21	8.71	5.86	4.76	6.64	2.91	
A	RNA processing and modification	0.03	0.01	0.00	0.00	0.00	0.00	0.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.02	0.00	0.04	0.00	0.00	0.06	0.05	0.03	0.05	0.02	
K	Transcription	3.50	4.95	4.18	3.89	5.64	5.24	5.51	5.68	6.40	5.40	8.14	6.27	6.34	3.58	2.89	3.83	3.52	3.60	3.48	6.74	3.36	5.45	3.52	3.89	4.04	3.21	4.14	3.59	3.16	
L	Replication, recombination and repair	4.71	4.43	5.82	3.96	4.71	5.53	7.80	8.59	3.37	6.72	4.22	4.53	3.03	3.49	4.52	3.49	3.35	3.52	3.66	2.15	3.25	4.17	3.19	4.38	4.56	3.72	5.50	3.00	5.75	
B	Chromatin structure and dynamics	0.10	0.00	0.10	0.00	0.00	0.04	0.12	0.03	0.02	0.00	0.00	0.00	0.00	0.00	0.03	0.10	0.02	0.03	0.00	0.00	0.00	0.00	0.05	0.40	0.20	0.25	0.22	0.04		
D	Cell cycle control, mitosis and meiosis	0.68	0.69	1.06	1.17	1.52	1.30	1.63	1.36	0.87	0.60	0.61	0.60	0.71	0.88	0.70	0.85	0.70	0.85	0.87	0.48	0.68	0.52	0.67	1.17	0.63	0.56	0.74	0.87	0.61	
V	Defense mechanisms	1.02	1.15	0.89	0.88	0.93	1.55	2.10	0.96	2.38	1.56	1.59	1.47	1.16	1.19	1.22	1.44	1.14	0.98	1.05	1.08	3.32	1.60	2.32	1.51	0.87	0.71	1.30	0.71	1.52	
T	Signal transduction mechanisms	1.92	3.45	2.88	3.57	3.60	4.26	5.04	5.50	4.51	1.88	2.66	2.70	3.47	6.94	3.85	6.70	6.13	7.54	2.47	4.80	3.05	2.28	3.68	2.87	1.85	1.94	8.06	1.58	2.19	
M	Cell wall/membrane biogenesis	2.34	4.11	4.52	3.11	3.67	3.94	4.46	5.56	4.81	3.96	4.44	3.63	4.23	4.77	5.48	5.53	4.69	5.00	5.08	3.98	3.83	2.85	6.82	3.41	3.40	3.01	3.00	1.80	2.13	
N	Cell motility	0.83	1.38	2.53	2.05	2.12	2.15	2.99	3.00	2.60	0.28	0.15	0.36	1.22	3.85	2.24	0.95	2.38	3.39	1.97	2.39	2.27	0.00	0.02	2.68	0.35	0.10	2.81	1.14	0.79	
Z	Cytoskeleton	0.00	0.01	0.00	0.00	0.00	0.00	0.04	0.03	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
W	Extracellular structures	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	
U	Intracellular trafficking and secretion	0.85	1.72	0.79	1.45	1.71	1.41	1.71	1.88	1.02	0.92	0.64	0.93	0.93	2.48	2.24	2.32	1.29	2.22	2.01	2.55	1.05	0.76	1.49	1.75	1.15	0.76	1.64	0.93	0.97	
O	Posttranslational modification, protein turnover, chaperones	2.62	2.62	2.29	2.69	2.86	2.43	3.34	2.97	1.83	1.64	1.56	1.41	2.16	3.54	2.74	3.58	2.72	3.12	3.30	2.86	2.17	2.44	1.72	2.48	3.69	2.80	3.37	2.51	2.25	
C	Energy production and conversion	5.68	4.37	6.13	6.89	7.20	4.26	5.24	3.37	2.90	2.80	3.33	2.91	3.98	7.03	5.57	9.16	5.25	6.27	3.48	4.99	2.31	4.85	3.23	5.21	7.21	7.69	6.52	7.95	5.33	
G	Carbohydrate transport and metabolism	2.25	3.49	2.12	1.45	3.30	4.58	2.60	4.42	4.41	4.60	6.06	5.37	4.58	1.55	2.42	3.49	2.53	1.93	2.43	2.36	2.65	7.29	4.30	7.06	3.23	2.14	2.29	2.34	1.56	
E	Amino acid transport and metabolism	5.57	5.91	5.79	6.43	6.75	6.97	5.70	5.25	5.40	6.49	6.12	5.16	6.52	6.37	4.31	6.63	6.03	4.81	6.32	7.22	4.27	6.41	3.97	8.47	6.52	5.04	5.56	6.21	5.08	
F	Nucleotide transport and metabolism	1.89	1.63	2.09	1.84	1.89	1.87	2.10	1.98	1.61	2.72	2.39	2.55	1.67	2.08	1.60	1.63	1.19	1.35	2.15	1.57	1.53	2.65	1.36	2.39	2.89	2.50	1.85	2.50	1.24	
H	Coenzyme transport and metabolism	3.40	2.65	3.84	3.85	4.34	2.11	4.23	3.15	2.78	2.56	2.45	1.92	2.54	3.63	2.77	4.22	2.77	2.70	3.80	2.58	1.87	4.13	2.65	2.53	6.75	4.38	5.10	5.83	2.89	
I	Lipid transport and metabolism	1.67	2.66	2.47	2.61	1.34	1.80	2.60	1.14	1.78	2.32	2.26	1.80	2.54	1.50	1.95	2.17	1.09	1.64	2.34	3.79	1.39	2.00	1.40	1.31	1.27	1.27	0.93	0.87	0.77	
P	Inorganic ion transport and metabolism	3.56	3.63	2.84	2.65	3.45	3.24	3.22	2.87	2.80	3.56	3.46	3.45	3.80	5.31	2.89	3.73	2.99	3.17	3.53	4.57	3.66	4.05	4.61	5.06	5.65	3.41	4.63	4.19	5.33	
Q	Secondary metabolites synthesis, transport and catabolism	1.10	1.79	0.79	1.41	0.96	1.09	0.93	0.71	1.04	1.12	1.10	0.96	2.22	0.97	1.11	1.17	0.88	1.06	1.37	2.74	0.37	0.96	0.65	0.83	0.63	0.25	0.22	0.44	1.92	
R	General function prediction only	11.30	8.19	7.81	7.81	7.98	8.48	8.65	9.02	8.80	9.13	9.51	8.07	8.65	7.65	7.87	10.33	6.98	7.75	8.47	9.27	7.22	7.69	6.91	10.03	11.19	12.33	11.80	11.06	11.68	
S	Function unknown	6.43	4.81	5.89	5.16	5.86	4.54	9.00	6.70	5.88	5.52	4.83	5.13	5.54	4.02	4.34	5.48	3.82	4.52	3.57	5.87	5.12	3.77	3.23	4.72	10.33	9.37	9.54	9.69	6.94	
-	Not categorized	33.56	32.69	30.34	33.11	25.97	28.86	23.90	20.57	31.28	31.55	30.77	37.28	31.70	24.98	35.56	24.49	37.46	30.97	33.52	25.38	42.56	31.42	41.49	22.98	24.93	28.68	16.00	25.87	34.89	

*Refer to Table 1 for organism names.

**Average values for 34 bacteria and 12 archaea cited from reference 10 in the main text.

Table S4. Genes encoding hydrogenases and formate dehydrogenases in *P. thermopropionicum*

Enzyme	Locus tag	Annotation	Gene	COG category	Size (aa)*	Orientation	Subunit	Putative function	SP**	MP**	TAT**
Hydrogenase 1	PTH_0668	Iron only hydrogenase large subunit containig		COG4624	530	+	Fe-hydrogenase	MQ** ↔ H ₂			+
	PTH_0669	Fe-S-cluster-containing hydrogenase components 1	HybA	COG0437	271	+	Fe-S protein				
	PTH_0670	Hypothetical protein			89	+	NrfD (e ⁻ ↔ MQ)		+	+	
Hydrogenase 2	PTH_1377	Hypothetical hydrogenase subunit			624	-	Fe-hydrogenase	NADH ↔ H ₂			
	PTH_1378	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit	NuoF	COG1894	650	-	NADH binding protein				
	PTH_1379	NADH:ubiquinone oxidoreductase 24 kD subunit	NuoE	COG1905	192	-	Fe-S protein				
Hydrogenase 3	PTH_2010	Hypothetical hydrogenase subunit			574	-	Fe-hydrogenase	Fd** ↔ H ₂			
	PTH_2011	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit	NuoF	COG1894	551	-	NADH binding protein				
	PTH_2012	NADH:ubiquinone oxidoreductase 24 kD subunit	NuoE	COG1905	162	-	Fe-S protein				
Hydrogenase 4	PTH_1701	Ni,Fe-hydrogenase I small subunit	HyaA	COG1740	332	+	NiFe-hydrogenase	MQ ↔ H ₂	+		+
	PTH_1702	Ni,Fe-hydrogenase I large subunit	HyaB	COG0374	482	+	NiFe-hydrogenase				
	PTH_1703	Fe-S-cluster-containing hydrogenase components 1	HybA	COG0437	277	+	Fe-S protein				
	PTH_1704	NrfD participates in the transfer of electrons from quinone pool into the terminal complemts			389	+	NrfD (e ⁻ ↔ MQ)		+	+	
Formate dehydrogenase 1	PTH_2645	Hypothetical formate dehydrogenase, containing partial COG3383			526	-	Formate dehydrogenase	Formate ↔ NADH			
	PTH_2646	Hypothetical formate dehydrogenase, containing partial COG3383			354	-	Formate dehydrogenase				
	PTH_2647	Putative NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit containing partial NuoG			309	-	ferredoxin				
	PTH_2648	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit	NuoF	COG1894	617	-	NADH binding protein				
	PTH_2649	NADH:ubiquinone oxidoreductase 24 kD subunit	NuoE	COG1905	162	-	Fe-S protein				
Formate dehydrogenase 2	PTH_1711	Hypothetical formate dehydrogenase, containing partial COG3383, Uncharacterized anaerobic dehydrogenase			208	+	Formate dehydrogenase	Formate ↔ MQ			+
	PTH_1712	Selenocysteine-containing anaerobic dehydrogenase	BisC	COG0243	799	+	Formate dehydrogenase				
	PTH_1713	Fe-S-cluster-containing hydrogenase components 1	HybA	COG0437	274	+	Fe-S protein				
	PTH_1714	Transmembrane electron transfer subunit, NrfD			389	+	NrfD (e ⁻ ↔ MQ)		+	+	

* amino acids.

**SP, signal peptide; MP, membrane binding region; TAT, twin-arginine translocation signature; MQ, menaquinone; Fd, ferredoxin.

Table S5. Genes related to sulfate reduction in *P. thermopropionicum*

Locus_tag	Annotation	Genes	COG	note
PTH_0235	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic compo	TauA	COG0715	
PTH_0236	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	TauB	COG1116	
PTH_0237	ABC-type nitrate/sulfonate/bicarbonate transport systemM permease compone	TauC	COG0600	
PTH_0238	Adenylylsulfate kinase and related kinases	CysC	COG0529	
PTH_0239	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit	SdhA	COG1055	Adenylylsulfate reductase alpha
PTH_0240	Ferredoxin	-	COG1146	Adenylylsulfate reductase beta
PTH_0241	ATP sulfurylase (sulfate adenylyltransferase)	MET3	COG2046	
PTH_0242	Dissimilatory sulfite reductase (desulfovirdin), alpha and beta subunits	DsrA	COG2221	

Table S6. Input and output domains of signal transduction systems found in the *P. thermopropionicum* genome.

Domain	Number		
	One component	Two component	Total
Input domain	165	22	187
PAS	12	7	19
GAF	11	4	15
LysR_substrate	5	1	6
PASTA	4		4
Cache	4		4
TOBE	3		3
Chase2	3		3
Chase3	2	1	3
Output domain	165	30	195
HTH_3	17		17
HD	15	1	16
AraC	10	3	13
LysR(HTH_1)	10	1	11
GGDEF	9	1	10
pkinase	9		9
GntR	7		7
MarR	3	4	7
MCP	5		5
GerE	3	2	5
HTH_11	3	2	5

Table S7. PAS domain-containing CDSs in the *P. thermopropionicum* genome.

Locus tag	Output domain*	Description	Proteins encoded by physically linked genes
One component system			
PTH0508	HTH_3	AAA-type ATPase	Aldehyde:ferredoxin oxidoreductase
PTH0546	GGDEF		MoxR-like ATPases COG0714
PTH0752	GntR		Hypothetical protein COG1719
PTH0844	LysR	AAA-type ATPase, RocR-like	Pyruvate:ferredoxin oxidoreductase
PTH0850	AraC	AAA-type ATPase, RocR-like	Class IV alcohol dehydrogenase
PTH1192	HTH_8		Acetyl-CoA carboxylase
PTH1355	HTH_11	AAA-type ATPase, RocR-like	Methylmalonyl-CoA pathway enzymes
PTH1663	GGDEF		Pyruvate:ferredoxin oxidoreductase
PTH1772	HTH_3	AAA-type ATPase, RocR-like	Acyl CoA:acetate/3-ketoacid CoA transferase
PTH2004	GGDEF		Arginine/lysine/ornithine decarboxylases
PTH2615	HD		Molybdopterin biosynthesis enzyme
PTH2869	CBF/NF-Y	AAA-type ATPase	Hypothetical protein
Two component system			
PTH0100	LytR		Uncharacterized dehydrogenase
PTH1349	HTH_3		TRAP C4-dicarboxylate transporter
PTH1422	No RR		
PTH1778	No RR		
PTH1830	MarR		Predicted enzyme COG0325
PTH2257	AraC		Predicted permeases COG0730
PTH2684	LuxR		Tas alcohol dehydrogenase

*According to the pfam database. In two-component systems, those in neighboring response regulators are presented. No RR, no response regulator physically linked.

Table S8. CDSs in *P. thermopropionicum* exhibiting atypical codon usages and predicted donor organisms.

Locus tag	Annotation	Donor relative	P value*
PTH 2	COG0592 DNA polymerase sliding clamp subunit	<i>Cth</i>	6.5
PTH 57	COG1013 2-oxoacid:ferredoxin oxidoreductases beta subunit	<i>Bfr</i>	12.5
PTH 69	COG0143 methionyl-tRNA synthetase	<i>Dde</i>	18.0
PTH 74	COG0411 ABC-type transporter, ATPase component	<i>Moth</i>	10.0
PTH 90	COG0718 uncharacterized conserved protein	<i>Moth</i>	4.3
PTH 102	COG1171 threonine dehydratase	<i>Chy</i>	54.4
PTH 142	Hypothetical protein	<i>Chy</i>	9.5
PTH 144	Hypothetical protein	<i>Swol</i>	9.7
PTH 166	Hypothetical protein	<i>Sfu</i>	21.1
PTH 176	Hypothetical protein	<i>Moth</i>	10.2
PTH 177	Hypothetical protein	<i>Swol</i>	12.9
PTH 185	Hypothetical membrane protein	<i>Dde</i>	42.3
PTH 189	COG1098 predicted RNA binding protein	<i>Moth</i>	4.8
PTH 190	Hypothetical protein	<i>Dde</i>	23.3
PTH 227	Hypothetical protein	<i>Sac</i>	3.0
PTH 228	COG1104 cysteine sulfinate desulfinate	<i>Sac</i>	4.0
PTH 251	Hypothetical protein	<i>Moth</i>	28.9
PTH 279	COG1725 predicted transcriptional regulator	<i>Moth</i>	110.1
PTH 280	COG4463 transcriptional repressor of stress genes	<i>Moth</i>	4.9
PTH 284	COG1943 transposase	<i>Dde</i>	40.3
PTH 302	COG0050 GTPase	<i>Pae</i>	52.3
PTH 304	Hypothetical membrane protein	<i>Sfu</i>	7.2
PTH 320	COG0087 ribosomal protein L3	<i>Moth</i>	19.9
PTH 332	COG0094 ribosomal protein L5	<i>Pae</i>	46.2
PTH 340	COG0201 preprotein translocase subunit	<i>Tte</i>	30.4
PTH 341	COG0024 methionine aminopeptidase	<i>Gsu</i>	50.0
PTH 348	Hypothetical protein	<i>Chy</i>	11.5
PTH 352	COG1122 ABC-type transporter, ATPase component	<i>Gsu</i>	6.7
PTH 363	Hypothetical protein	<i>Mac</i>	9.1
PTH 385	Hypothetical protein	<i>Pae</i>	5.6
PTH 482	COG4569 acetaldehyde dehydrogenase	<i>Bsu</i>	17.8
PTH 500	COG2002 regulator of stationary/spore expression	<i>Mhu</i>	8.5
PTH 520	Hypothetical protein	<i>Dde</i>	14.3
PTH 576	COG1116 ABC-type transporter, ATPase component	<i>Swol</i>	23.1
PTH 580	Hypothetical protein	<i>Moth</i>	43.1
PTH 585	COG1149 ATPase containing an inserted ferredoxin domain	<i>Sac</i>	7.5
PTH 592	COG1028 short-chain alcohol dehydrogenase	<i>Gsu</i>	21.4
PTH 607	Hypothetical regulator protein	<i>Pae</i>	5.8
PTH 610	COG2414 aldehyde:ferredoxin oxidoreductase	<i>Dde</i>	4.0
PTH 612	COG0476 dinucleotide-utilizing enzyme	<i>Moth</i>	9.1
PTH 616	COG1509 lysine 2,3-aminomutase	<i>Chy</i>	40.3
PTH 620	Hypothetical protein	<i>Chy</i>	40.3
PTH 627	Hypothetical protein	<i>Sac</i>	14.7
PTH 632	Hypothetical protein	<i>Sfu</i>	24.5
PTH 633	Hypothetical membrane protein	<i>Dde</i>	16.3
PTH 634	Hypothetical protein	<i>Moth</i>	10.0
PTH 656	COG0736 phosphopantetheinyl transferase	<i>Bsu</i>	17.1
PTH 715	Hypothetical protein	<i>Bfr</i>	25.6
PTH 774	Hypothetical membrane protein	<i>Cth</i>	54.9
PTH 782	Hypothetical protein	<i>Mac</i>	34.4
PTH 795	COG0537 diadenosine tetraphosphate hydrolase	<i>Sac</i>	17.8
PTH 797	Hypothetical protein	<i>Moth</i>	7.7
PTH 799	Hypothetical signaling protein	<i>Moth</i>	18.3
PTH 804	COG0740 protease subunit of ATP-dependent Clp proteases	<i>Moth</i>	23.8
PTH 810	COG0715 ABC-type transporter, periplasmic component	<i>Mac</i>	8.5
PTH 818	COG1792 cell shape-determining protein	<i>Moth</i>	4.6
PTH 840	COG2005 N-terminal domain of molybdenum-binding protein	<i>Moth</i>	15.5
PTH 842	COG0555 ABC-type transporter, permease component	<i>Moth</i>	9.7
PTH 850	COG3829 RocR transcriptional regulator	<i>Moth</i>	9.0
PTH 875	COG1420 HrcA transcriptional regulator	<i>Sfu</i>	5.2
PTH 892	COG0319 predicted metal-dependent hydrolase	<i>Chy</i>	53.9
PTH 944	COG1945 uncharacterized conserved protein	<i>Mac</i>	30.4
PTH 988	COG3830 ACT domain-containing protein	<i>Mth</i>	4.7
PTH 1016	COG2009 succinate dehydrogenase, cytochrome b subunit	<i>Gsu</i>	13.5
PTH 1018	COG0479 succinate dehydrogenase, Fe-S protein subunit	<i>Dde</i>	42.3
PTH 1041	COG0053 predicted Co/Zn/Cd cation transporters	<i>Cth</i>	4.3
PTH 1048	COG0124 histidyl-tRNA synthetase	<i>Dde</i>	7.1
PTH 1057	Hypothetical protein	<i>Dde</i>	17.8
PTH 1071	Hypothetical transcriptional regulator	<i>Bfr</i>	21.8
PTH 1075	COG1086 predicted nucleoside-diphosphate sugar epimerase	<i>Moth</i>	6.5
PTH 1078	COG1209 dTDP-glucose pyrophosphorylase	<i>Sac</i>	4.5
PTH 1088	Hypothetical membrane protein	<i>Dde</i>	52.3
PTH 1123	Hypothetical protein	<i>Chy</i>	28.4

Table 8. Continued.

Locus tag	Annotation	Donor	P value
PTH 1129	COG0169 shikimate 5-dehydrogenase	<i>Swol</i>	6.4
PTH 1132	COG0337 3-dehydroquinate synthetase	<i>Bsu</i>	5.8
PTH 1134	COG2804 type II secretory pathway ATPase	<i>Moth</i>	19.6
PTH 1158	COG0312 predicted Zn-dependent protease	<i>Mac</i>	8.5
PTH 1197	COG1189 predicted rRNA methylase	<i>Cth</i>	15.5
PTH 1202	COG0750 predicted Zn-dependent protease	<i>Mac</i>	34.6
PTH 1220	Hypothetical protein	<i>Tde</i>	30.4
PTH 1228	Hypothetical membrane protein	<i>Chy</i>	10.3
PTH 1233	COG3581 uncharacterized conserved protein	<i>Swol</i>	9.8
PTH 1239	COG0730 predicted permease	<i>Swol</i>	10.5
PTH 1254	COG0528 uridylate kinase	<i>Dde</i>	4.0
PTH 1256	COG1146 ferredoxin	<i>Swol</i>	60.8
PTH 1263	COG0442 prolyl-tRNA synthetase	<i>Bsu</i>	9.5
PTH 1270	COG0858 ribosome-binding factor A	<i>Swol</i>	17.8
PTH 1284	Hypothetical protein	<i>Mac</i>	5.2
PTH 1287	COG0527 aspartokinases	<i>Swol</i>	5.2
PTH 1302	Hypothetical protein	<i>Dde</i>	13.1
PTH 1304	COG1692 Uncharacterized conserved protein	<i>Cth</i>	4.3
PTH 1309	COG0182 predicted translation initiation factor 2B subunit	<i>Dde</i>	41.1
PTH 1315	COG0406 fructose-2,6-bisphosphatase	<i>Swol</i>	7.0
PTH 1320	COG1842 phage shock protein A	<i>Moth</i>	39.2
PTH 1326	COG3581 uncharacterized conserved protein	<i>Bsu</i>	25.1
PTH 1334	COG1302 uncharacterized conserved protein	<i>Moth</i>	16.0
PTH 1335	COG2301 citrate lyase beta subunit	<i>Moth</i>	20.6
PTH 1340	COG0145 acetone carboxylase, beta subunit	<i>Dde</i>	18.0
PTH 1366	COG4770 Acetyl/propionyl-CoA carboxylase, alpha subunit	<i>Mhu</i>	11.5
PTH 1370	Hypothetical protein	<i>Bsu</i>	6.4
PTH 1386	COG0205 6-phosphofructokinase	<i>Chy</i>	28.6
PTH 1392	Hypothetical protein	<i>Tde</i>	5.9
PTH 1396	COG2244 membrane protein involved in protein export	<i>Moth</i>	23.5
PTH 1400	COG0602 organic radical activating enzymes	<i>Moth</i>	23.5
PTH 1404	Hypothetical membrane protein	<i>Swol</i>	34.1
PTH 1420	COG0017 aspartyl/asparaginyl-tRNA synthetase	<i>Swol</i>	9.7
PTH 1429	COG0046 phosphoribosylformylglycinamide synthase	<i>Mac</i>	8.0
PTH 1439	COG2226 methylase involved in menaquinone biosynthesis	<i>Dde</i>	5.2
PTH 1445	COG3847 F1p pilus assembly protein	<i>Swol</i>	23.7
PTH 1450	COG2197 response regulator containing a CheY-receiver domain	<i>Swol</i>	6.5
PTH 1460	COG4326 sporulation control protein	<i>Swol</i>	14.2
PTH 1462	COG1226 Kef-type K ⁺ transport system	<i>Tte</i>	5.8
PTH 1471	COG1974 SOS-response transcriptional repressor	<i>Moth</i>	7.7
PTH 1474	COG2122 Uncharacterized conserved protein	<i>Bfr</i>	5.2
PTH 1475	COG0842 ABC-type multidrug transporter, permease component	<i>Moth</i>	25.5
PTH 1510	COG1073 hydrolases of the alpha/beta superfamily	<i>Mac</i>	12.5
PTH 1535	COG1975 xanthine and CO dehydrogenases maturation factor	<i>Dde</i>	22.5
PTH 1537	COG0471 di and tricarboxylate transporters	<i>Swol</i>	39.2
PTH 1547	Hypothetical protein	<i>Cth</i>	32.7
PTH 1553	COG2025 electron transfer flavoprotein, alpha subunit	<i>Dde</i>	16.1
PTH 1582	Hypothetical protein	<i>Cth</i>	6.5
PTH 1640	COG0700 uncharacterized membrane protein	<i>Sac</i>	15.5
PTH 1641	COG2715 uncharacterized membrane protein	<i>Sac</i>	19.6
PTH 1652	COG1335, amidase	<i>Moth</i>	6.5
PTH 1665	COG3857 ATP-dependent nuclease, subunit B	<i>Dde</i>	36.4
PTH 1699	COG0309 hydrogenase maturation factor	<i>Moth</i>	5.8
PTH 1701	COG1740 Ni,Fe-hydrogenase I small subunit	<i>Moth</i>	24.9
PTH 1702	COG0374 Ni,Fe-hydrogenase I large subunit	<i>Moth</i>	6.6
PTH 1703	COG0437 FeS cluster-containing hydrogenase component	<i>Moth</i>	5.8
PTH 1705	COG1942 uncharacterized protein	<i>Moth</i>	24.9
PTH 1709	COG1826 protein secretion pathway component	<i>Dde</i>	19.6
PTH 1714	COG5557 polysulphide reductase	<i>Sac</i>	12.5
PTH 1715	COG1826 protein secretion pathway component	<i>Dde</i>	23.8
PTH 1752	Hypothetical protein	<i>Mac</i>	4.0
PTH 1753	COG0669 phosphopantetheine adenylyltransferase	<i>Swol</i>	23.1
PTH 1771	COG4670 acyl CoA:acetate/3-ketoacid CoA transferase	<i>Dde</i>	19.6
PTH 1795	COG0194 guanylate kinase	<i>Mac</i>	16.1
PTH 1805	COG0284 orotidine-5'-phosphate decarboxylase	<i>Moth</i>	10.0
PTH 1818	COG0564 pseudouridylate synthases	<i>Mac</i>	19.9
PTH 1829	Hypothetical protein	<i>Sac</i>	4.7
PTH 1838	Hypothetical membrane protein	<i>Moth</i>	6.5
PTH 1880	Hypothetical membrane protein	<i>Moth</i>	5.2
PTH 1900	Hypothetical protein	<i>Dde</i>	16.7
PTH 1908	COG3267 type II secretory pathway, component	<i>Moth</i>	24.9
PTH 1910	Hypothetical transcriptional regulator	<i>Moth</i>	5.8
PTH 1953	COG0292 ribosomal protein L20	<i>Dde</i>	4.5
PTH 1958	Hypothetical protein	<i>Moth</i>	7.7

Table 8. Continued.

Locus tag	Annotation	Donor	P value
PTH 1967	Hypothetical protein	<i>Mac</i>	10.8
PTH 1989	COG1343 Uncharacterized protein	<i>Dde</i>	16.3
PTH 2000	COG1960 acyl-CoA dehydrogenase	<i>Dde</i>	59.8
PTH 2001	COG2086 electron transfer flavoprotein, beta subunit	<i>Sfu</i>	19.7
PTH 2006	Hypothetical protein	<i>Gsu</i>	16.0
PTH 2007	COG0860 N-acetylmuramoyl-L-alanine amidase	<i>Gsu</i>	23.1
PTH 2011	COG1894 NADH oxidoreductase, NADH-binding subunit	<i>Moth</i>	5.6
PTH 2016	Hypothetical protein	<i>Moth</i>	7.1
PTH 2018	Hypothetical protein	<i>Moth</i>	42.3
PTH 2021	Hypothetical protein	<i>Moth</i>	9.0
PTH 2023	Hypothetical protein	<i>Sac</i>	10.7
PTH 2024	Hypothetical protein	<i>Sfu</i>	10.5
PTH 2031	COG1284 uncharacterized conserved protein	<i>Moth</i>	4.8
PTH 2041	COG2197 response regulator containing a CheY-receiver domain	<i>Moth</i>	9.0
PTH 2064	COG1352 methylase of chemotaxis methyl-accepting protein	<i>Sfu</i>	23.5
PTH 2065	COG1871 chemotaxis protein, methylation of MCP proteins	<i>Swol</i>	5.6
PTH 2068	COG1191 DNA-directed RNA polymerase sigma subunit	<i>Moth</i>	16.0
PTH 2072	COG1298 flagellar biosynthesis pathway, component FlhA	<i>Moth</i>	5.8
PTH 2082	COG1843 flagellar hook capping protein	<i>Moth</i>	6.9
PTH 2083	Hypothetical protein	<i>Swol</i>	17.1
PTH 2084	COG2882 flagellar biosynthesis chaperone	<i>Cth</i>	15.5
PTH 2085	COG1157 flagellar type III secretory pathway ATPase	<i>Moth</i>	4.9
PTH 2112	COG1256 flagellar hook-associated protein	<i>Sfu</i>	29.5
PTH 2119	COG1291 flagellar motor component	<i>Moth</i>	9.0
PTH 2141	Hypothetical protein	<i>Mac</i>	9.1
PTH 2148	Hypothetical protein	<i>Moth</i>	5.8
PTH 2150	COG1351 predicted alternative thymidylate synthase	<i>Moth</i>	24.9
PTH 2155	COG0602 organic radical activating enzyme	<i>Chy</i>	84.2
PTH 2163	Hypothetical protein	<i>Moth</i>	4.0
PTH 2169	Hypothetical protein	<i>Tma</i>	6.5
PTH 2180	Hypothetical protein	<i>Gsu</i>	20.3
PTH 2196	Hypothetical protein	<i>Swol</i>	21.9
PTH 2202	COG0840 methyl-accepting chemotaxis protein	<i>Dde</i>	42.3
PTH 2208	Hypothetical protein	<i>Sfu</i>	16.7
PTH 2226	COG0177 predicted EndoIII-related endonuclease	<i>Mac</i>	5.1
PTH 2227	COG3330 uncharacterized conserved protein	<i>Sfu</i>	19.9
PTH 2231	COG0247 Fe-S oxidoreductase	<i>Moth</i>	9.0
PTH 2232	COG2186 transcriptional regulator	<i>Moth</i>	4.8
PTH 2249	Hypothetical protein	<i>Swol</i>	9.8
PTH 2262	Hypothetical protein	<i>Swol</i>	23.5
PTH 2281	COG1472 beta-glucosidase-related glycosidases	<i>Moth</i>	4.9
PTH 2291	COG2984 ABC-type transporter, periplasmic component	<i>Moth</i>	4.8
PTH 2303	COG1848 predicted nucleic acid-binding protein	<i>Moth</i>	6.5
PTH 2327	Hypothetical protein	<i>Sfu</i>	5.2
PTH 2361	COG5513, Predicted secreted protein	<i>Moth</i>	4.8
PTH 2373	Hypothetical protein	<i>Moth</i>	28.8
PTH 2374	Hypothetical protein	<i>Moth</i>	43.1
PTH 2387	COG0745 response regulator consisting of a CheY-receiver domain	<i>Moth</i>	30.4
PTH 2395	COG3436 transposase and inactivated derivative	<i>Moth</i>	4.9
PTH 2415	Hypothetical protein	<i>Moth</i>	36.5
PTH 2441	Hypothetical protein	<i>Moth</i>	9.0
PTH 2444	Hypothetical transcriptional regulator	<i>Sfu</i>	5.6
PTH 2447	Hypothetical protein	<i>Swol</i>	49.3
PTH 2458	Hypothetical protein	<i>Moth</i>	9.6
PTH 2461	Hypothetical protein	<i>Moth</i>	29.4
PTH 2487	Hypothetical protein	<i>Moth</i>	4.9
PTH 2554	COG1694 predicted pyrophosphatase	<i>Moth</i>	16.0
PTH 2556	Hypothetical protein	<i>Moth</i>	39.2
PTH 2575	COG1134 ABC-type transporter, ATPase component	<i>Swol</i>	18.0
PTH 2578	COG1088 dTDP-D-glucose 4,6-dehydratase	<i>Dde</i>	87.3
PTH 2581	Hypothetical protein	<i>Chy</i>	14.0
PTH 2589	COG1396 predicted transcriptional regulator	<i>Bfr</i>	8.3
PTH 2592	COG0491 Zn-dependent hydrolase	<i>MstH</i>	33.3
PTH 2594	COG0014 gamma-glutamyl phosphate reductase	<i>Moth</i>	12.5
PTH 2627	COG1977 molybdopterin converting factor, small subunit	<i>Mac</i>	5.1
PTH 2628	Hypothetical protein	<i>Tde</i>	7.0
PTH 2629	COG1606 ATP-utilizing enzyme	<i>Chy</i>	16.1
PTH 2634	COG0451 nucleoside-diphosphate-sugar epimerase	<i>Chy</i>	76.7
PTH 2642	Hypothetical protein	<i>Mac</i>	13.1
PTH 2667	COG0863 DNA modification methylase	<i>Sfu</i>	35.7
PTH 2668	Hypothetical proteins	<i>Mac</i>	11.1
PTH 2694	Hypothetical proteins	<i>Swol</i>	31.4
PTH 2704	COG0789 predicted transcriptional regulator	<i>Dde</i>	76.4

Table 8. Continued.

Locus tag	Annotation	Donor	P value
PTH 2712	COG0691 tmRNA-binding protein	<i>Mac</i>	7.1
PTH 2715	Hypothetical proteins	<i>Bfr</i>	23.7
PTH 2719	Hypothetical proteins	<i>Swol</i>	21.4
PTH 2745	COG4942 membrane-bound metallopeptidase	<i>Dde</i>	21.8
PTH 2746	COG2177 cell division protein	<i>Sac</i>	11.7
PTH 2748	Hypothetical protein	<i>Bfr</i>	25.1
PTH 2750	COG3959 transketolase, N-terminal subunit	<i>Swol</i>	56.9
PTH 2752	COG1186 protein chain release factor B	<i>Mac</i>	48.3
PTH 2777	Hypothetical membrane protein	<i>Tde</i>	7.5
PTH 2779	Hypothetical proteins	<i>Chy</i>	83.4
PTH 2781	Hypothetical proteins	<i>Chy</i>	70.2
PTH 2797	Hypothetical proteins	<i>Mac</i>	4.0
PTH 2802	Hypothetical proteins	<i>Bsu</i>	4.0
PTH 2803	COG0842 ABC-type multidrug transporter, permease component	<i>Chy</i>	113.1
PTH 2804	COG0842 ABC-type multidrug transporter, permease component	<i>Chy</i>	80.7
PTH 2807	Hypothetical protein	<i>Mac</i>	29.5
PTH 2809	Hypothetical protein	<i>Moth</i>	4.3
PTH 2812	COG0055 F0F1-type ATP synthase, beta subunit	<i>Chy</i>	53.1
PTH 2815	COG0712 F0F1-type ATP synthase, delta subunit	<i>Moth</i>	14.2
PTH 2827	COG1971 predicted membrane protein	<i>Mtth</i>	10.5
PTH 2830	COG0216 protein chain release factor A	<i>Bsu</i>	28.9
PTH 2831	Hypothetical protein	<i>Mac</i>	5.8
PTH 2832	Hypothetical protein	<i>Swol</i>	43.6
PTH 2833	COG0254 ribosomal protein L31	<i>Tde</i>	19.6
PTH 2835	COG0739 membrane proteins related to metalloendopeptidase	<i>Moth</i>	4.3
PTH 2845	COG1014 2-oxoacid:ferredoxin oxidoreductases, gamma subunit	<i>Mac</i>	25.6
PTH 2849	COG0436 Aspartate/tyrosine/aromatic aminotransferase	<i>Chy</i>	10.9
PTH 2857	COG1576 uncharacterized conserved protein	<i>Tde</i>	5.1
PTH 2860	Hypothetical protein	<i>Swol</i>	16.5
PTH 2862	COG0739 membrane protein related to metalloendopeptidase	<i>Sfu</i>	9.1
PTH 2866	Hypothetical protein	<i>Sfu</i>	33.3
PTH 2875	Hypothetical protein	<i>Moth</i>	4.3
PTH 2881	Hypothetical protein	<i>Moth</i>	39.2

*P values represent confidence levels estimated by the chi-square test of the codon-usage data.