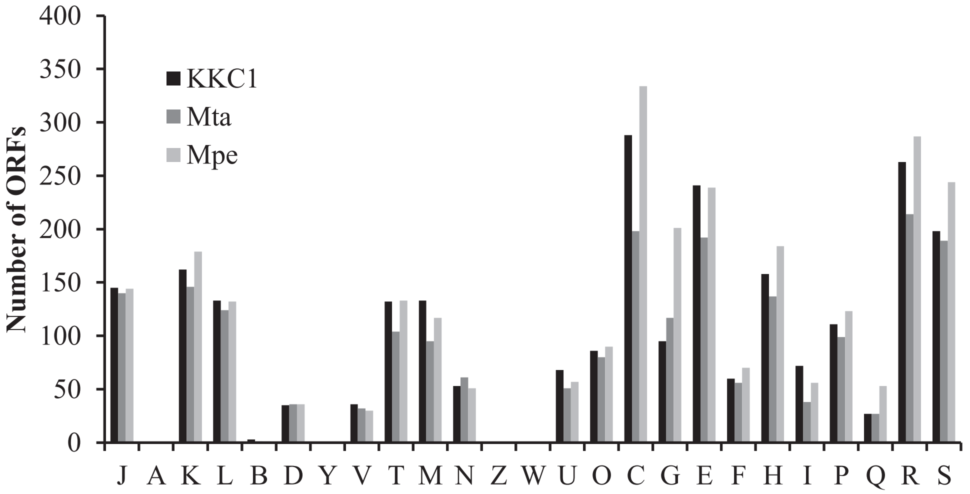
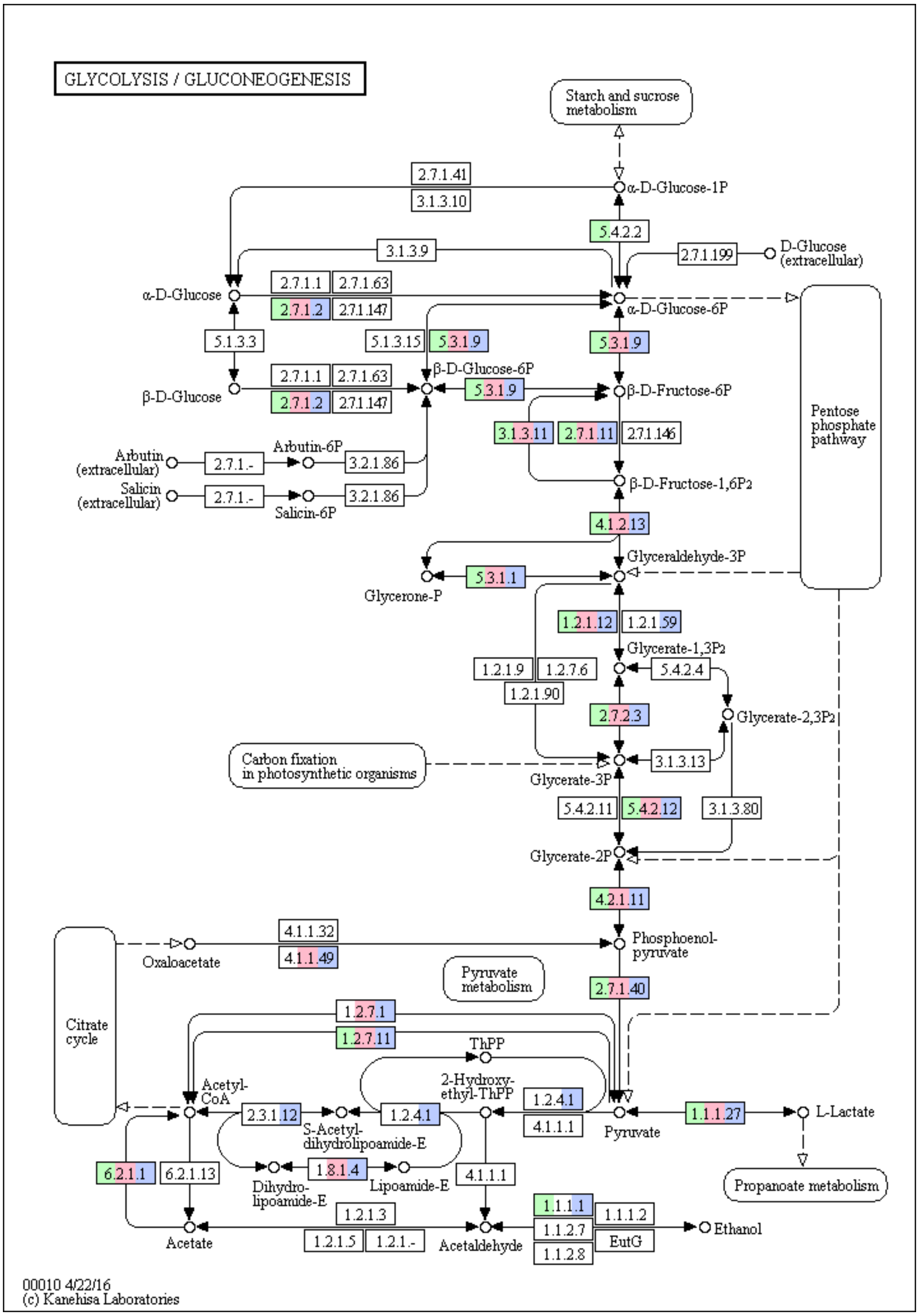


Fig. S1. Numbers of ORFs associated with the general Clusters of Orthologous Groups (COG) functional categories.

KKC1, *Calderihabitans maritimus* KKC1 (3,509 ORFs); Mta, *Moorella thermoacetica* (2,463 ORFs); Mpe, *Moorella perchloratireducens* (3,349 ORFs). Functional categories: A, RNA processing and modification; B, chromatin structure and dynamics; C, energy production and conversion; D, cell cycle control, cell division, and chromosome partitioning; E, amino acid transport and metabolism; F, nucleotide transport and metabolism; G, carbohydrate transport and metabolism; H, coenzyme transport and metabolism; I, lipid transport and metabolism; J, translation, ribosomal structure, and biogenesis; K, transcription; L, replication, recombination, and repair; M, cell wall/membrane/envelope biogenesis; N, cell motility; O, posttranslational modification, protein turnover, chaperones; P, inorganic ion transport and metabolism; Q, secondary metabolites biosynthesis, transport and catabolism; R, general function prediction only; S, function unknown; T, signal transduction mechanisms; U, intracellular trafficking, secretion, and vesicular transport; V, defense mechanisms; W, extracellular structures; Y, nuclear structure; and Z, cytoskeleton.

A


GLYCOLYSIS / GLUCONEOGENESIS
Starch and sucrose metabolism
α-D-Glucose-1P
2.7.1.41
3.1.3.10
5.4.2.2
3.1.3.9
2.7.1.199
D-Glucose (extracellular)
α-D-Glucose
2.7.1.1
2.7.1.63
2.7.1.2
2.7.1.147
α-D-Glucose-6P
5.1.3.3
5.1.3.15
5.3.1.9
5.3.1.9
β-D-Glucose
2.7.1.1
2.7.1.63
2.7.1.2
2.7.1.147
β-D-Glucose-6P
5.3.1.9
β-D-Fructose-6P
3.1.3.11
2.7.1.11
2.7.1.146
Pentose phosphate pathway
Arbutin (extracellular)
2.7.1.-
Arbutin-6P
3.2.1.86
Salicin (extracellular)
2.7.1.-
Salicin-6P
3.2.1.86
β-D-Fructose-1,6P2
4.1.2.13
Glyceraldehyde-3P
Glycerone-P
5.3.1.1
1.2.1.12
1.2.1.59
Glycerate-1,3P2
1.2.1.9
1.2.7.6
1.2.1.90
5.4.2.4
2.7.2.3
Glycerate-2,3P2
Carbon fixation in photosynthetic organisms
Glycerate-3P
3.1.3.13
5.4.2.11
5.4.2.12
3.1.3.80
Glycerate-2P
4.2.1.11
Citrate cycle
Oxaloacetate
4.1.1.32
4.1.1.49
Phosphoenol-pyruvate
Pyruvate metabolism
2.7.1.40
1.2.7.1
1.2.7.11
ThPP
2-Hydroxy-ethyl-ThPP
Acetyl-CoA
2.3.1.12
S-Acetyl-dihydrolipoamide-E
1.2.4.1
1.2.4.1
4.1.1.1
Pyruvate
1.1.1.27
L-Lactate
6.2.1.1
6.2.1.13
Dihydro-lipoamide-E
1.8.1.4
Lipoamide-E
4.1.1.1
Propanoate metabolism
1.1.1.1
1.1.1.2
1.2.1.3
1.1.2.7
EutG
Ethanol
1.2.1.5
1.2.1.-
1.1.2.8
Acetate
Acetaldehyde
00010 4/22/16
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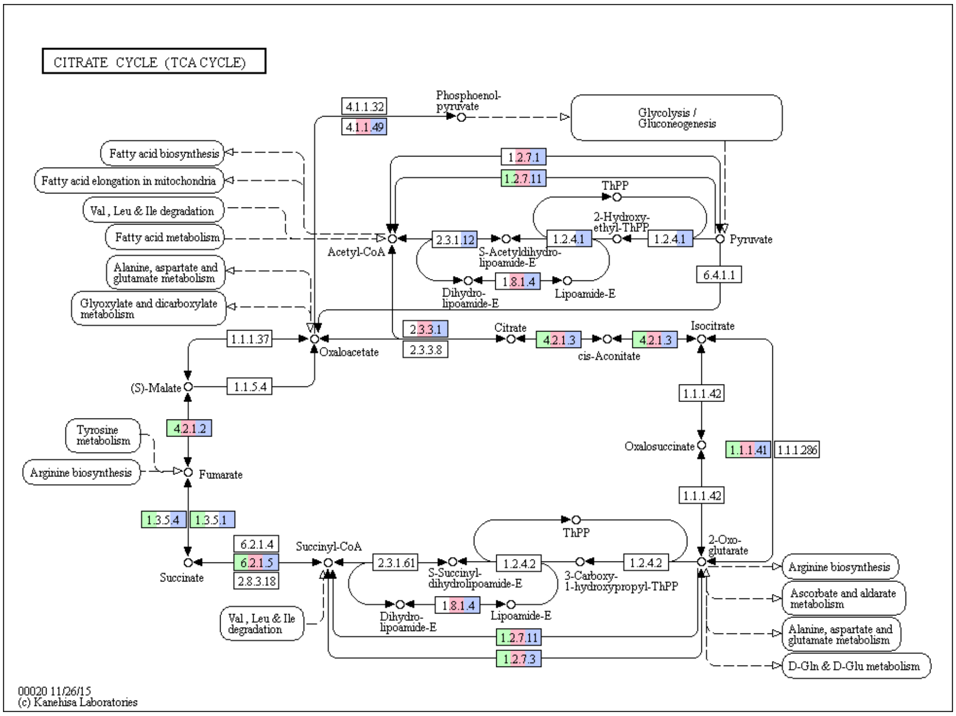
B


CITRATE CYCLE (TCA CYCLE)
4.1.1.32
4.1.1.49
Phosphoenol-pyruvate
Glycolysis / Gluconeogenesis
Fatty acid biosynthesis
Fatty acid elongation in mitochondria
Val, Leu & Ile degradation
Fatty acid metabolism
Alanine, aspartate and glutamate metabolism
Glyoxylate and dicarboxylate metabolism
1.2.7.1
1.2.7.11
ThPP
2-Hydroxy-ethyl-ThPP
Acetyl-CoA
2.3.1.12
S-Acetyldihydro-lipoamide-E
1.2.4.1
1.2.4.1
Pyruvate
6.4.1.1
Dihydro-lipoamide-E
1.8.1.4
Lipoamide-E
2.3.3.1
2.3.3.8
Citrate
4.2.1.3
cis-Aconitate
4.2.1.3
Isocitrate
1.1.1.37
Oxaloacetate
(S)-Malate
1.1.5.4
1.1.1.42
Oxalosuccinate
1.1.1.41
1.1.1.286
1.1.1.42
Tyrosine metabolism
4.2.1.2
Arginine biosynthesis
Fumarate
1.3.5.4
1.3.5.1
ThPP
6.2.1.4
Succinyl-CoA
6.2.1.5
2.8.3.18
Succinate
2.3.1.61
S-Succinyl-dihydrolipoamide-E
1.2.4.2
3-Carboxy-1-hydroxypropyl-ThPP
1.2.4.2
2-Oxo-glutarate
Arginine biosynthesis
Ascorbate and aldarate metabolism
Alanine, aspartate and glutamate metabolism
D-Gln & D-Glu metabolism
Val, Leu & Ile degradation
Dihydro-lipoamide-E
1.8.1.4
Lipoamide-E
1.2.7.11
1.2.7.3
00020 11/26/15
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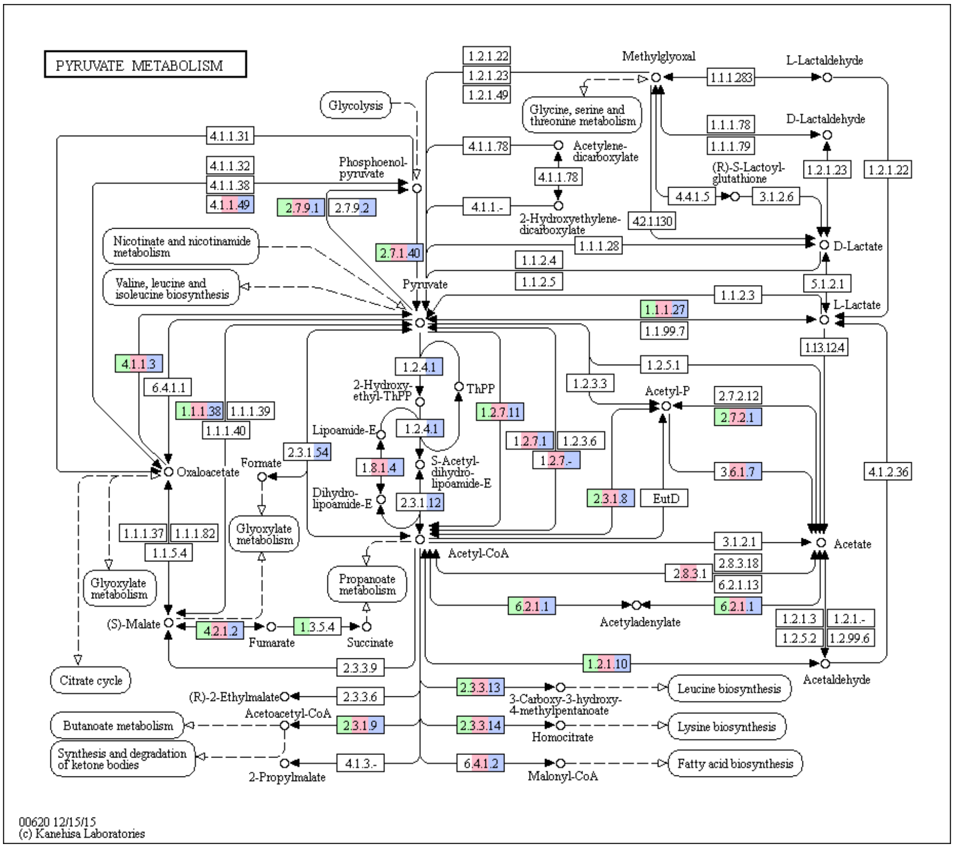
C


PYRUVATE METABOLISM
1.2.1.22
1.2.1.23
1.2.1.49
Methylglyoxal
1.1.1.283
L-Lactaldehyde
Glycolysis
Glycine, serine and threonine metabolism
4.1.1.31
1.1.1.78
D-Lactaldehyde
4.1.1.78
Acetylene-dicarboxylate
1.1.1.79
4.1.1.32
Phosphoenol-pyruvate
4.1.1.78
(R)-S-Lactoyl-glutathione
1.2.1.23
1.2.1.22
4.1.1.38
4.1.1.49
2.7.9.1
2.7.9.2
4.1.1.-
4.4.1.5
3.1.2.6
2-Hydroxyethylene-dicarboxylate
4.2.1.130
Nicotinate and nicotinamide metabolism
2.7.1.40
1.1.1.28
D-Lactate
1.1.2.4
Valine, leucine and isoleucine biosynthesis
Pyruvate
1.1.2.5
5.1.2.1
1.1.2.3
L-Lactate
1.1.1.27
1.1.99.7
4.1.1.3
1.13.12.4
1.2.4.1
1.2.5.1
6.4.1.1
2-Hydroxy-ethyl-ThPP
ThPP
1.2.3.3
Acetyl-P
2.7.2.12
1.1.1.38
1.1.1.39
1.2.7.11
2.7.2.1
1.1.1.40
Lipoamide-E
1.2.4.1
1.2.7.1
1.2.3.6
2.3.1.54
1.2.7.-
Oxaloacetate
Formate
1.8.1.4
S-Acetyl-dihydro-lipoamide-E
3.6.1.7
4.1.2.36
Dihydro-lipoamide-E
2.3.1.12
2.3.1.8
EutD
1.1.1.37
1.1.1.82
Glyoxylate metabolism
3.1.2.1
Acetate
1.1.5.4
Acetyl-CoA
2.8.3.18
2.8.3.1
Glyoxylate metabolism
Propanoate metabolism
6.2.1.13
6.2.1.1
6.2.1.1
Acetyladenylate
1.2.1.3
1.2.1.-
(S)-Malate
4.2.1.2
Fumarate
1.3.5.4
Succinate
1.2.5.2
1.2.99.6
2.3.3.9
1.2.1.10
Acetaldehyde
Citrate cycle
2.3.3.13
3-Carboxy-3-hydroxy-4-methylpentanoate
Leucine biosynthesis
(R)-2-Ethylmalate
2.3.3.6
Acetoacetyl-CoA
Butanoate metabolism
2.3.1.9
2.3.3.14
Homocitrate
Lysine biosynthesis
Synthesis and degradation of ketone bodies
2-Propylmalate
4.1.3.-
6.4.1.2
Malonyl-CoA
Fatty acid biosynthesis
00620 12/15/15
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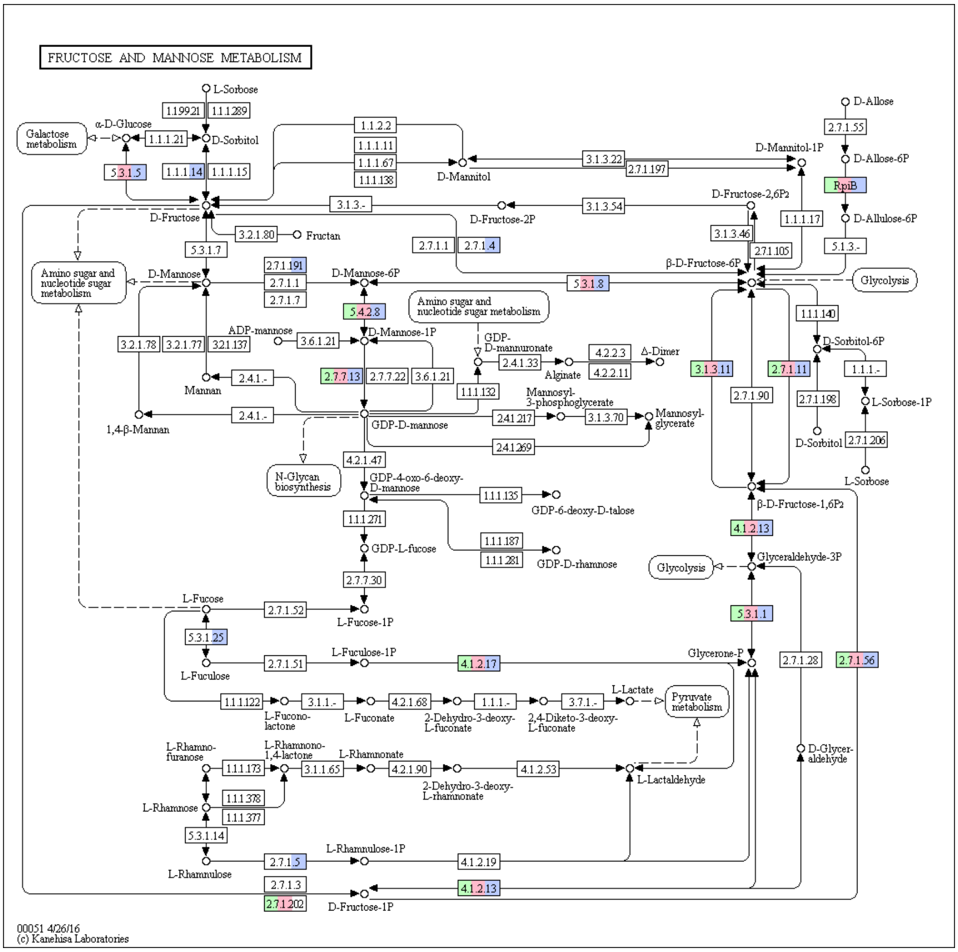
D


FRUCTOSE AND MANNOSE METABOLISM
L-Sorbose
1.1.99.21
1.1.1.289
Galactose metabolism
α-D-Glucose
1.1.1.21
D-Sorbitol
5.3.1.5
1.1.1.14
1.1.1.15
1.1.2.2
1.1.1.11
1.1.1.67
1.1.1.138
D-Mannitol
3.1.3.22
2.7.1.197
D-Mannitol-1P
D-Allose
2.7.1.55
D-Allose-6P
RpiB
D-Allulose-6P
5.1.3.-
D-Fructose
3.1.3.-
D-Fructose-2P
3.1.3.54
D-Fructose-2,6P₂
3.1.3.46
2.7.1.105
1.1.1.17
3.2.1.80
Fructan
5.3.1.7
2.7.1.1
2.7.1.4
β-D-Fructose-6P
Glycolysis
Amino sugar and nucleotide sugar metabolism
D-Mannose
2.7.1.191
2.7.1.1
2.7.1.7
D-Mannose-6P
5.3.1.8
5.4.2.8
Amino sugar and nucleotide sugar metabolism
ADP-mannose
3.6.1.21
D-Mannose-1P
3.2.1.78
3.2.1.77
3.2.1.137
GDP-D-mannuronate
2.4.1.33
Alginate
4.2.2.3
4.2.2.11
Δ-Dimer
3.1.3.11
2.7.1.11
1.1.1.140
D-Sorbitol-6P
1.1.1.-
L-Sorbose-1P
Mannan
2.4.1.-
2.7.7.13
2.7.7.22
3.6.1.21
1.1.1.132
Mannosyl-3-phosphoglycerate
2.7.1.90
2.7.1.198
2.4.1.-
1,4-β-Mannan
GDP-D-mannose
2.4.1.217
3.1.3.70
Mannosyl-glycerate
D-Sorbitol
2.7.1.206
2.4.1.269
L-Sorbose
4.2.1.47
N-Glycan biosynthesis
GDP-4-oxo-6-deoxy-D-mannose
1.1.1.135
GDP-6-deoxy-D-talose
β-D-Fructose-1,6P₂
1.1.1.271
4.1.2.13
1.1.1.187
1.1.1.281
GDP-L-fucose
GDP-D-rhamnose
Glycolysis
Glyceraldehyde-3P
2.7.7.30
L-Fucose
2.7.1.52
L-Fucose-1P
5.3.1.1
5.3.1.25
L-Fuculose-1P
L-Fuculose
2.7.1.51
4.1.2.17
Glycerone-P
2.7.1.28
2.7.1.56
1.1.1.122
3.1.1.-
4.2.1.68
1.1.1.-
3.7.1.-
L-Lactate
Pyruvate metabolism
L-Fucono-lactone
L-Fuconate
2-Dehydro-3-deoxy-L-fuconate
2,4-Diketo-3-deoxy-L-fuconate
L-Rhamno-furanose
L-Rhamnono-1,4-lactone
L-Rhamnonate
1.1.1.173
3.1.1.65
4.2.1.90
4.1.2.53
D-Glycer-aldehyde
2-Dehydro-3-deoxy-L-rhamnonate
L-Lactaldehyde
1.1.1.378
L-Rhamnose
1.1.1.377
5.3.1.14
L-Rhamnulose-1P
L-Rhamnulose
2.7.1.5
4.1.2.19
2.7.1.3
4.1.2.13
2.7.1.202
D-Fructose-1P
00051 4/26/16
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E

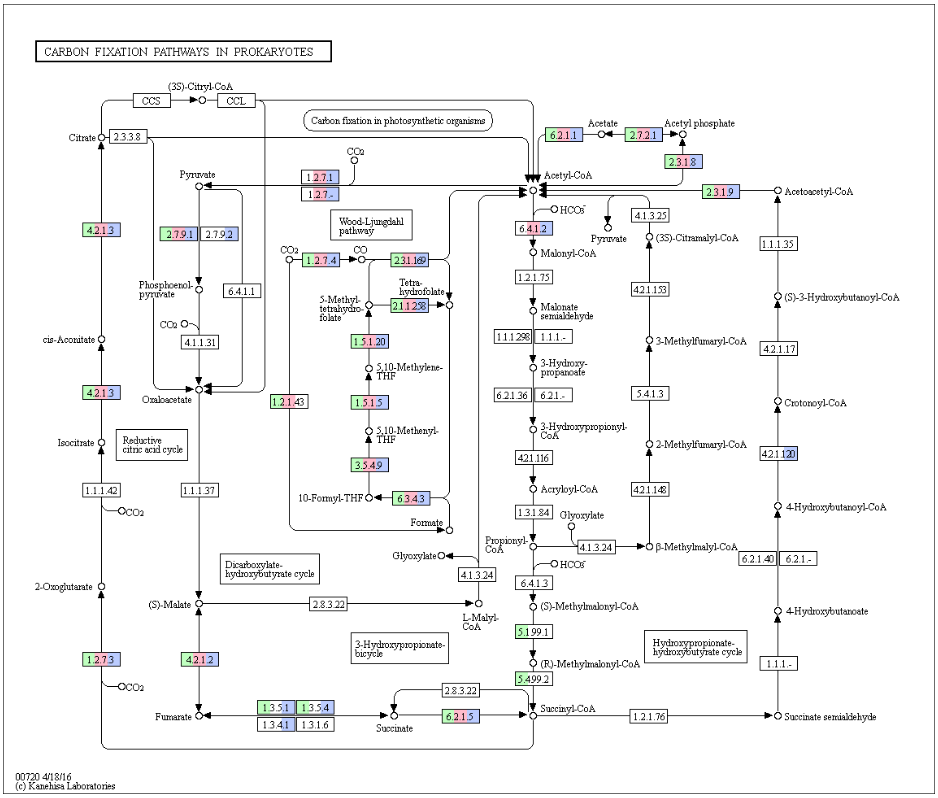
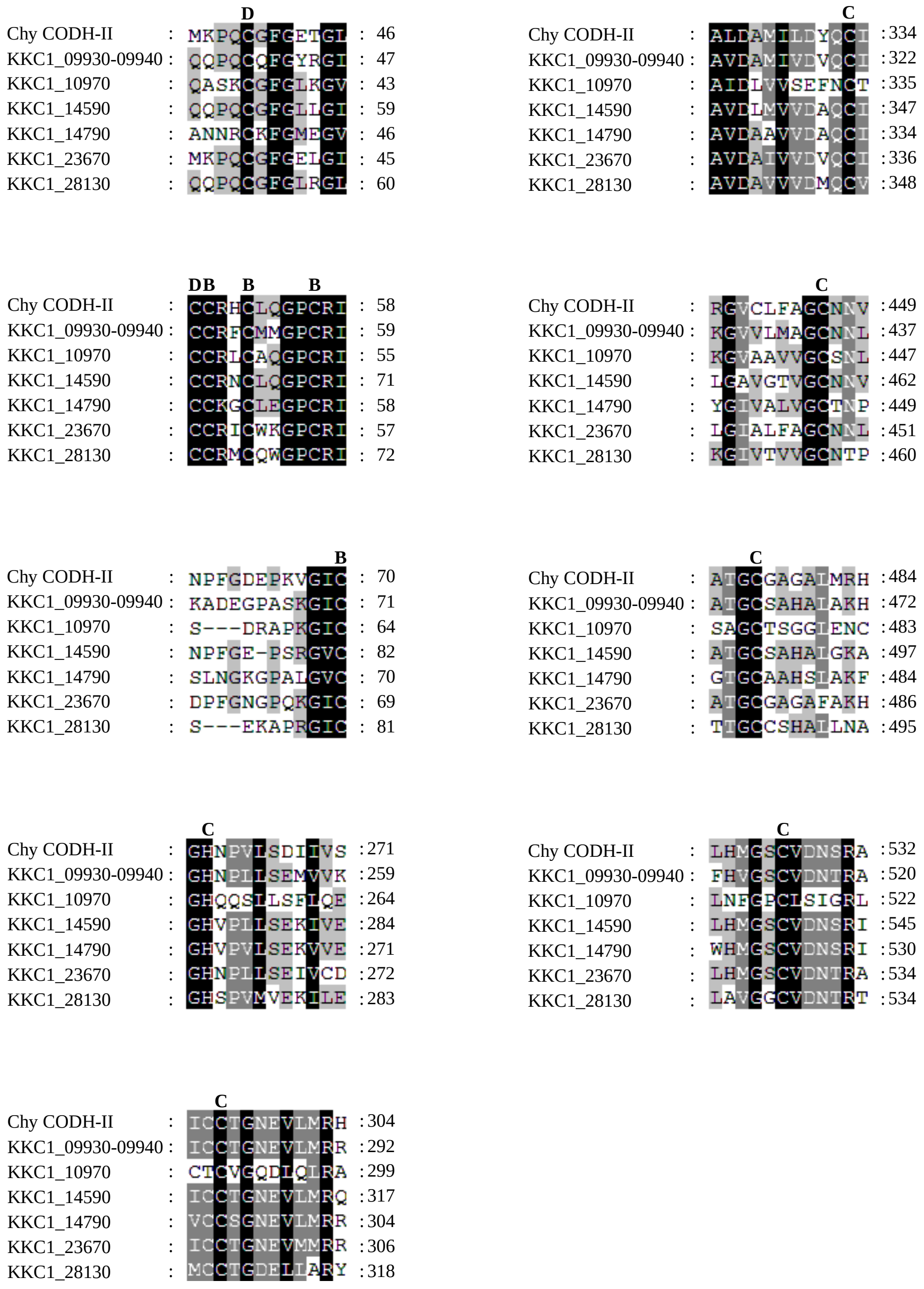


Fig. S2. Comparison of metabolic pathways in *C. maritimus* KKC1, *M. thermoacetica*, *M. perchloratireducens*.

A. glycolysis and gluconeogenesis. B. TCA cycle. C. Pyruvate metabolism. D. fructose and mannose metabolism. E. Carbon fixation pathways in Prokaryotes. Green, *C. maritimus*; red, *M. thermoacetica*; blue, *M. perchloratireducens*. The empty box indicates that there are no ORFs assigned. Pathway maps were generated by KEGG.



```
                       D
Chy CODH-II      : MKPQCGFGETGI : 46
KKC1_09930-09940 : QQPQCQFGYRGI : 47
KKC1_10970       : QASKCGFGLKGV : 43
KKC1_14590       : QQPQCGFGLLGI : 59
KKC1_14790       : ANNRCKFGMEGV : 46
KKC1_23670       : MKPQCGFGELGI : 45
KKC1_28130       : QQPQCGFGLRGI : 60
```

```
                   DB  B    B
Chy CODH-II      : CCRHCLQGPCRI : 58
KKC1_09930-09940 : CCRFCMMGPCRI : 59
KKC1_10970       : CCRLCAQGPCRI : 55
KKC1_14590       : CCRNCLQGPCRI : 71
KKC1_14790       : CCKGCLEGPCRI : 58
KKC1_23670       : CCRICWKGPCRI : 57
KKC1_28130       : CCRMCQWGPCRI : 72
```

```
                              B
Chy CODH-II      : NPFGDEPKVGIC : 70
KKC1_09930-09940 : KADEGPASKGIC : 71
KKC1_10970       : S---DRAPKGIC : 64
KKC1_14590       : NPFGE-PSRGVC : 82
KKC1_14790       : SLNGKGPALGVC : 70
KKC1_23670       : DPFGNGPQKGIC : 69
KKC1_28130       : S---EKAPRGIC : 81
```

```
                    C
Chy CODH-II      : GHNPVLSDIIVS :271
KKC1_09930-09940 : GHNPLLSEMVVK :259
KKC1_10970       : GHQQSLLSFLQE :264
KKC1_14590       : GHVPLLSEKIVE :284
KKC1_14790       : GHVPVLSEKVVE :271
KKC1_23670       : GHNPLLSEIVCD :272
KKC1_28130       : GHSPVMVEKILE :283
```

```
                     C
Chy CODH-II      : ICCTGNEVLMRH :304
KKC1_09930-09940 : ICCTGNEVLMRR :292
KKC1_10970       : CTCVGQDLQLRA :299
KKC1_14590       : ICCTGNEVLMRQ :317
KKC1_14790       : VCCSGNEVLMRR :304
KKC1_23670       : ICCTGNEVMMRR :306
KKC1_28130       : MCCTGDELLARY :318
```

```
                             C
Chy CODH-II      : ALDAMILDYQCI :334
KKC1_09930-09940 : AVDAMIVDVQCI :322
KKC1_10970       : AIDLVVSEFNCT :335
KKC1_14590       : AVDLMVVDAQCI :347
KKC1_14790       : AVDAAVVDAQCI :334
KKC1_23670       : AVDAIVVDVQCI :336
KKC1_28130       : AVDAVVVDMQCV :348
```

```
                           C
Chy CODH-II      : RGVCLFAGCNNV :449
KKC1_09930-09940 : KGVVLMAGCNNL :437
KKC1_10970       : KGVAAVVGCSNL :447
KKC1_14590       : LGAVGTVGCNNV :462
KKC1_14790       : YGIVALVGCTNP :449
KKC1_23670       : LGIALFAGCNNL :451
KKC1_28130       : KGIVTVVGCNTP :460
```

```
                      C
Chy CODH-II      : ATGCGAGAIMRH :484
KKC1_09930-09940 : ATGCSAHAIAKH :472
KKC1_10970       : SAGCTSGGIENC :483
KKC1_14590       : ATGCSAHAIGKA :497
KKC1_14790       : GTGCAAHSIAKF :484
KKC1_23670       : ATGCGAGAFAKH :486
KKC1_28130       : TTGCCSHAILNA :495
```

```
                        C
Chy CODH-II      : LHMGSCVDNSRA :532
KKC1_09930-09940 : FHVGSCVDNTRA :520
KKC1_10970       : LNFGPCLSIGRL :522
KKC1_14590       : LHMGSCVDNSRI :545
KKC1_14790       : WHMGSCVDNSRI :530
KKC1_23670       : LHMGSCVDNTRA :534
KKC1_28130       : LAVGGCVDNTRT :534
```

Figure S3. Alignment of amino acid sequences for CooSs from *C. hydrogenoformans* (CODH-II) and *C. maritimus* KKC1.

Conserved residues are indicated with a black background. Residues conserved in >80% and >60% of the proteins examined are indicated with a white type on a dark gray background and by a black type on a light gray background, respectively. Residues linking Clusters B, D, and C are indicated by black type on top.

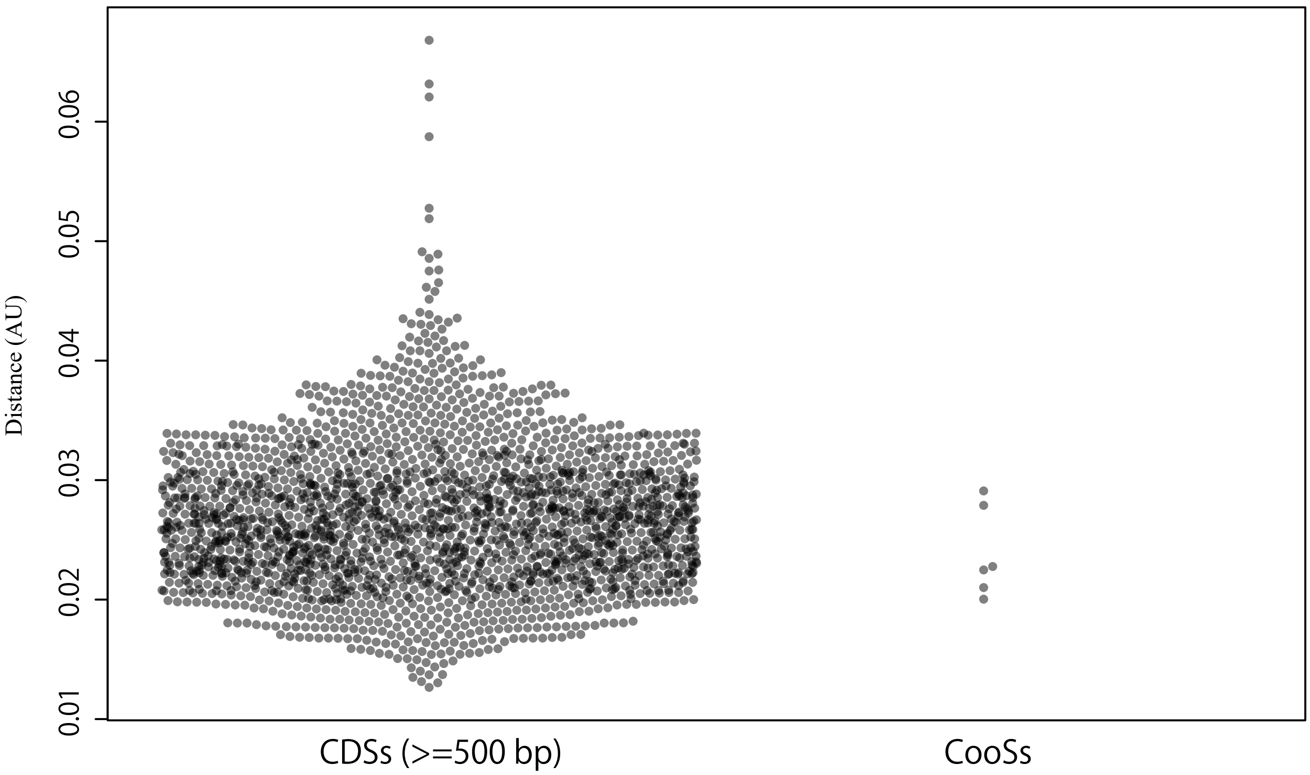


Fig. S4. Distances of CDS tetranucleotide frequency to that of the whole *C. maritimus* KKC1 genome. Left column: CDSs greater equal than 500 bp. Right column: six cooS genes (KKC1_09930-40, KKC1_10970, KKC1_14590, KKC1_14790, KKC1_23670, KKC1_28130). Distances are expressed in arbitrary units (AU).

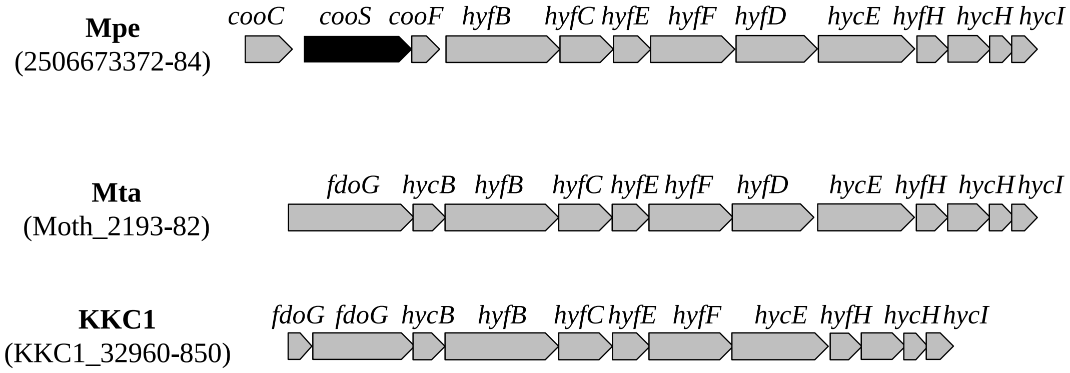


Figure S5. Schematic representation of *hyf*/*hyc*-type ECH gene clusters from *C. maritimus KKC1, Moorella thermoacetica* and *Moorella perchloratireducens*.
KKC1, *C. maritimus*; Mta, *M. thermoacetica*; Mpe, *M. perchloratireducens*. Black, *cooS*; gray, other functional protein.

Table S1. CDSs made up of COGs found in pyruvate:ferredoxin oxidoreductase.

KKC1[a]				Mta[a]				Mpe[a]			
Locus tag	COG	K number[b]	Subunit name[b]	Locus tag	COG	K number[b]	Subunit name[b]	Locus tag[c]	COG	K number[b]	Subunit name[b]
KKC1_06220	COG0674	K00174	korA	Moth_0033	COG0674	K00174	korA	2506673660	COG1146	K00176	korD
KKC1_06230	COG1013	K00175	korB	Moth_0034	COG1013	K00175	korB	2506673661	COG1014	K00177	korC
KKC1_06240	COG1014	K00177	korC	Moth_0035	COG1014	K00177	korC	2506673662	COG1013	K00175	korB
				Moth_0036	COG1149	K00176	korD	2506673663	COG0674	K00174	korA
KKC1_10900	COG1146	K00176	korD								
KKC1_10910	COG0674	K00174	korA	Moth_1983	COG1149	K00176	korD	2506674734	COG0674	K00174	korA
KKC1_10920	COG1013	K00175	korB	Moth_1984	COG0674	K00174	korA	2506674735	COG1013	K00175	korB
KKC1_10930	COG1014	K00177	korC	Moth_1985	COG1013	K00175	korB	2506674736	COG1146	K00176	korD
				Moth_1986	COG1014	K00177	korC	2506674737	COG1014	K00177	korC
KKC1_14030	COG0674	K00174	korA								
KKC1_14040	COG1013	K00175	korB					2506675637	COG2221	K00176	korD
KKC1_14050	COG1146	K00176	korD					2506675638	COG0674	K00174	korA
KKC1_14060	COG1014	K00177	korC					2506675639	COG1013	K00175	korB
								2506675640	COG1014	K00177	korC
KKC1_15100	COG1146	K00176	korD								
KKC1_15110	COG0674	K00174	korA								
KKC1_15120	COG1013	K00175	korB								
KKC1_15130	COG1014	K00177	korC								
KKC1_21110	COG0674	K00174	korA								
KKC1_21120	COG1013	K00175	korB								
KKC1_21130	COG1014	K00177	korC								
KKC1_21140	COG1146	K00176	korD								
KKC1_27530	COG1146	K00176	korD								
KKC1_27540	COG1014	K00177	korC								
KKC1_27550	COG1013	K00175	korB								
KKC1_27560	COG0674	K00174	korA								
				Moth_0064[d]	COG0674	K00169	porA	2506673623[e]	COG0674	K00169	porA
					COG1014	K00172	porG		COG1014	K00172	porG
					COG1013	K00170	porB		COG1013	K00170	porB
				Moth_0376	COG1014	K00172	porG	2506674258	COG1144	K00172	porG
				Moth_0377	COG1144	K00171	porD	2506674259	COG0674	K00169	porA
				Moth_0378	COG0674	K00169	porA	2506674260	COG1013	K00170	porB
				Moth_0379	COG1013	K00170	porB				
								2506674776	COG1014	K00172	porG
				Moth_1591	COG1013	K00170	porB	2506674777	COG1144	K00171	porD
				Moth_1592	COG0674	K00169	porA	2506674778	COG0674	K00169	porA
				Moth_1593	COG1014	K00172	porG	2506674779	COG1013	K00170	porB
				Moth_1921	COG1013	K00170	porB	2506675171	COG1014	K00172	porG
				Moth_1922	COG0674	K00169	porA	2506675172	COG1013	K00170	porB
				Moth_1923	COG1144	K00171	porD	2506675173	COG0674	K00169	porA
				Moth_1924	COG1014	K00172	porG	2506675174	COG1144	K00171	porD
KKC1_00050	COG1014	K00180	iorB	Moth_0934	COG1014	K00180	iorB	2506674290	COG1014	K00180	iorB
KKC1_16920	COG1014	K00180	iorB	Moth_2276	COG1014	K00180	iorB	2506675897	COG1014	K00180	iorB

[a] KKC1, *Calderihabitans maritimus* KKC1; Mta, *Moorella thermoacetica*; Mpe, *Moorella perchloratireducens*.

[b] Description of KEGG Orthology. Kor, 2-oxoglutarate (α-ketoglutarate):ferredoxin oxidoreductase; por, pyruvate:ferredoxin oxidoreductase; ior, indolepyruvate:ferredoxin oxidoreductase.

[c] Locus tag of M. perchloratireducens is represented by IMG Gene ID.

[d] Moth_0064 is a fusion of three COGs, COG0674, COG1014, COG1013 (E. Pierce1, G. Xie, R. D. Barabote, E. Saunders, C. S. Han, J. C. Detter, P. Richardson, T. S. Brettin, A. Das, L. G. Ljungdahl and S. W. Ragsdale. Environ Microbiol 10:2550–2573. 2008.)

[e] This CDS showed 89% similarlity with Moth_0064.