Table S1 Comparison of genome properties for 10 distinct bins identified from two metagenomes. The mean coverage is calculated by dividing total read counts with read length. ORF, open reading frame. Nearest neighbors are determined in the RAST v4.0. ND, not determined.

| Metagenome ID | Bin ID | Sequence size (bp) | Number of contigs | # of marker proteins (%) | Mean coverage | GC (%) | # of ORFs | ORFs, unknown function | # of RNA | copy of 16S rRNA gene detected | Nearest neighbor in RAST |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **Fen-75cm** | **Fn1** | **1716974** | **90** | **95 (91)** | **38.2** | **56.3** | **1931** | **632** | **27** | **1** | **Nitrosopumilus maritimus** |
| **Fen-75cm** | Fn2 | 3105568 | 576 | 24 (77) | 10.5 | 65.2 | 2939 | ND | 31 | 0 | Syntrophobacter fumaroxidans |
| **Fen-75cm** | Fn3 | 1706685 | 482 | 14 (45) | 6.5 | 57.8 | 1655 | ND | 11 | 0 | Syntrophobacter fumaroxidans |
| **Fen-75cm** | Fn4 | 2334861 | 529 | 11 (35) | 7.0 | 46.9 | 2272 | ND | 17 | 0 | Ignavibacterium album |
| **Fen-75cm** | Fn5 | 4008418 | 1082 | 21 (68) | 7.5 | 47.7 | 4452 | ND | 13 | 0 | Desulfuromonas acetoxidans |
| **Fen-75cm** | Fn6 | 1692800 | 324 | 20 (65) | 9.9 | 52.4 | 1652 | ND | 25 | 1 | Dehalococcoides sp. |
| **T3M75** | **Bg1** | **1781977** | **74** | **102 (98)** | **205** | **67.5** | **1754** | **514** | **61** | **1** | **Aciduliprofundum boonei** |
| **T3M75** | Bg2 | 2715205 | 631 | 22 (71) | 7.5 | 56.1 | 2780 | ND | 30 | 0 | Desulfuromonas acetoxidans |
| **T3M75** | Bg3 | 1912896 | 241 | 70 (67) | 9.7 | 42.5 | 2286 | ND | 31 | 1 | Thermococcus onnurineus |
| **T3M75** | Bg4 | 2596749 | 566 | 66 (63) | 12.8 | 51.0 | 3431 | ND | 12 | 0 | Methanosarcina acetivorans |

# Table S2 Name and EC number of enzymes present in Figure 2 of metabolic reconstruction.

| Enzyme# | Enzyme name | EC# | Enzyme# | Enzyme name | EC# |
|---|---|---|---|---|---|
| 1 | phosphoglucomutase | 5.4.2.2 | 23 | malate dehydrogenase | 1.1.1.37 |
| 2 | glucokinase | 2.7.1.2 | 24 | acetyl-CoA C-acetyltransferase | 2.3.1.9 |
| 3 | glucose-6-phosphate isomerase | 5.3.1.9 | 25 | aldehyde dehydrogenase (NAD+) | 1.2.1.3 |
| 4 | fructose-1,6-bisphosphatase | 3.1.3.11 | 26 | alcohol dehydrogenase | 1.1.1.1 |
| 5 | 6-phosphofructokinase | 2.7.1.11 | 27 | transketolase | 2.2.1.1 |
| 6 | fructose-bisphosphate aldolase, class I | 4.1.2.13 | 28 | ribulose-phosphate 3-epimerase | 5.1.3.1 |
| 7 | glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) | 1.2.1.59 | 29 | ribose 5-phosphate isomerase | 5.3.1.6 |
| 8 | phosphoglycerate kinase | 2.7.2.3 | 30 | ribose-phosphate pyrophosphokinase | 2.7.6.1 |
| 9 | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase | 5.4.2.12 | 31 | long-chain acyl-CoA synthetase | 6.2.1.3 |
| 10 | enolase | 4.2.1.11 | 32 | acyl-coA dehydrogenase | 1.3.8.7 |
| 11 | pyruvate kinase | 2.7.1.40 | 33 | Enoyl-CoA hydratase | 4.2.1.17 |
| 12 | pyruvate ferredoxin oxidoreductase, alpha subunit | 1.2.7.1 | 34 | 3-hydroxyacyl-CoA dehydrogenase | 1.1.1.35 |
| 13 | AMP-type acetyl-CoA synthetase | 6.2.11 | 35 | 3-ketoacyl-CoA thiolase | 2.3.1.16 |
| 14 | phosphoenolpyruvate carboxykinase | 4.1.1.32 | 36 | NADH-quinone oxidoreductase | 1.6.5.3 |
| 15 | pyruvate carboxylase | 6.4.1.1 | 37 | Succinate dehydrogenase/fumarate reductase | 1.3.5.1 |
| 16 | citrate synthase | 2.3.3.1 | 38 | ubiquinol-cytochrome c reductase | 1.10.2.2 |
| 17 | aconitate hydratase | 4.2.1.3 | 39 | F-type H+-transporting ATPase | 3.6.3.14 |
| 18 | isocitrate dehydrogenase (NAD+) | 1.1.1.41 | 40 | inorganic pyrophosphatase | 3.6.1.1 |
| 19 | 2-oxoglutarate ferredoxin oxidoreductase subunit alpha | 1.2.7.3 | 41 | sulfate adenylyltransferase | 2.7.7.4 |
| 20 | succinyl-CoA synthetase alpha subunit | 6.2.1.5 | 42 | thiosulfate sulfurtransferase | 2.8.1.1 |
| 21 | succinate dehydrogenase (ubiquinone) flavoprotein subunit | 1.3.5.1 | 43 | sulfur:oxygen oxidoreductase | 1.13.11.18 |
| 22 | fumarate hydratase | 4.2.1.2 | 44 | dissimilatory sulfite reductase | 1.8.99.3 |

# Table S3 Counts of genes representing each fermentation pathway.

| End product | Pathway | KEGG for genes in pathway | Fen75 Fn1 | T3M75 Bg1 |
|---|---|---|---|---|
| Lactate | 1 | K00016, L-lactate dehydrogenase [EC:1.1.1.27] | 0 | 0 |
| H2 | 1 | K06281, hydrogenase large subunit [EC:1.12.99.6] | 0 | 0 |
| | | K06282, hydrogenase small subunit [EC:1.12.99.6] | 0 | 0 |
| | 2 | K05586, bidirectional [NiFe] hydrogenase diaphorase subunit [EC:1.6.5.3] | 0 | 9 |
| | | K05587, bidirectional [NiFe] hydrogenase diaphorase subunit [EC:1.6.5.3] | 0 | 0 |
| | 3 | K00532, ferredoxin hydrogenase [EC:1.12.7.2] | 0 | 0 |
| | | K00533, ferredoxin hydrogenase large subunit [EC:1.12.7.2] | 0 | 0 |
| | | K06441, ferredoxin hydrogenase gamma subunit [EC:1.12.7.2] | 0 | 0 |
| Ethanol | 1 | K00128, aldehyde dehydrogenase (NAD+) [EC:1.2.1.3] | 0 | 1 |
| | 2 | K01568, pyruvate decarboxylase [EC:4.1.1.1] | 0 | 0 |
| | | K13953, alcohol dehydrogenase, propanol-preferring [EC:1.1.1.1] | 0 | 0 |
| | | K13954, alcohol dehydrogenase [EC:1.1.1.1] | 0 | 0 |
| | 3 | K00001, alcohol dehydrogenase [EC:1.1.1.1] | 0 | 0 |
| | | K00121, S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase [EC:1.1.1.284 1.1.1.1] | 0 | 0 |
| | | K04072, acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10 1.1.1.1] | 0 | 0 |
| Propionate | 1 | K00932, propionate kinase [EC:2.7.2.15] | 0 | 0 |
| | | K01026, propionate CoA-transferase [EC:2.8.3.1] | 0 | 0 |
| | | K13923, phosphotransacylase | 0 | 0 |
| | 2 | K01905, acetyl-CoA synthetase (ADP-forming) [EC:6.2.1.13] | 0 | 0 |
| | 3 | K01908, propionyl-CoA synthetase [EC:6.2.1.17] | 0 | 0 |
| CO2 | 1 | K00656, formate C-acetyltransferase [EC:2.3.1.54] | 1 | 1 |
| | 2 | K00123, formate dehydrogenase, alpha subunit [EC:1.2.1.2] | 0 | 0 |
| | 3 | K15827-32, formate hydrogenlyase subunit 2 | 0 | 0 |
| Acetate | 1 | K00625, phosphate acetyltransferase [EC:2.3.1.8] | 0 | 0 |
| | 2 | K00925, acetate kinase [EC:2.7.2.1] | 0 | 0 |
| Butyrate | 1 | K00248, butyryl-CoA dehydrogenase [EC:1.3.8.1] | 0 | 0 |
| | | K00634, phosphate butyryltransferase [EC:2.3.1.19] | 0 | 0 |
| | | K00929, butyrate kinase [EC:2.7.2.7] | 0 | 0 |

Table S4 Counts of genes encoding glycoside hydrolases and other carbohydrate active enzymes.

| Pfam access# | GH# | Enzyme name | Fn1 | Bg1 |
|---|---|---|---|---|
| PF00144.19 | Other 10 | Beta-lactamase | 0 | 1 |
| PF00206.15 | Other 55 | Fumarate lyase | 2 | 2 |
| PF00534.15 | Other 51 | Glycosyl transferases group 1 | 2 | 6 |
| PF00535.21 | Other 52 | Glycosyl transferases group 2 | 4 | 5 |
| PF00723.16 | GH15 | Glycoside hydrolase family 15 | 0 | 1 |
| PF03065.10 | GH57 | Glycoside hydrolase family 57 | 0 | 1 |

Fig S1 Emerging self-organizing map (ESOM) for two metagenomes (A. Fen-75cm, B. T3M-75cm) and distinct taxonomic bins identified. The closest relatives for each bin are: Fn1-Thaumarchaeota, Fn2-Syntrophobacteraceae, Fn3-Syntrophobacter, Fn4-Ignavibacteriae, Fn5-Desulfuromonas, Fn6-Dehalococcoides; Bg1-Thermoplasmata TMEG, Bg2-Syntrophobacterales, Bg3-Crenarchaeota C2, Bg4-Methanosarcinales.

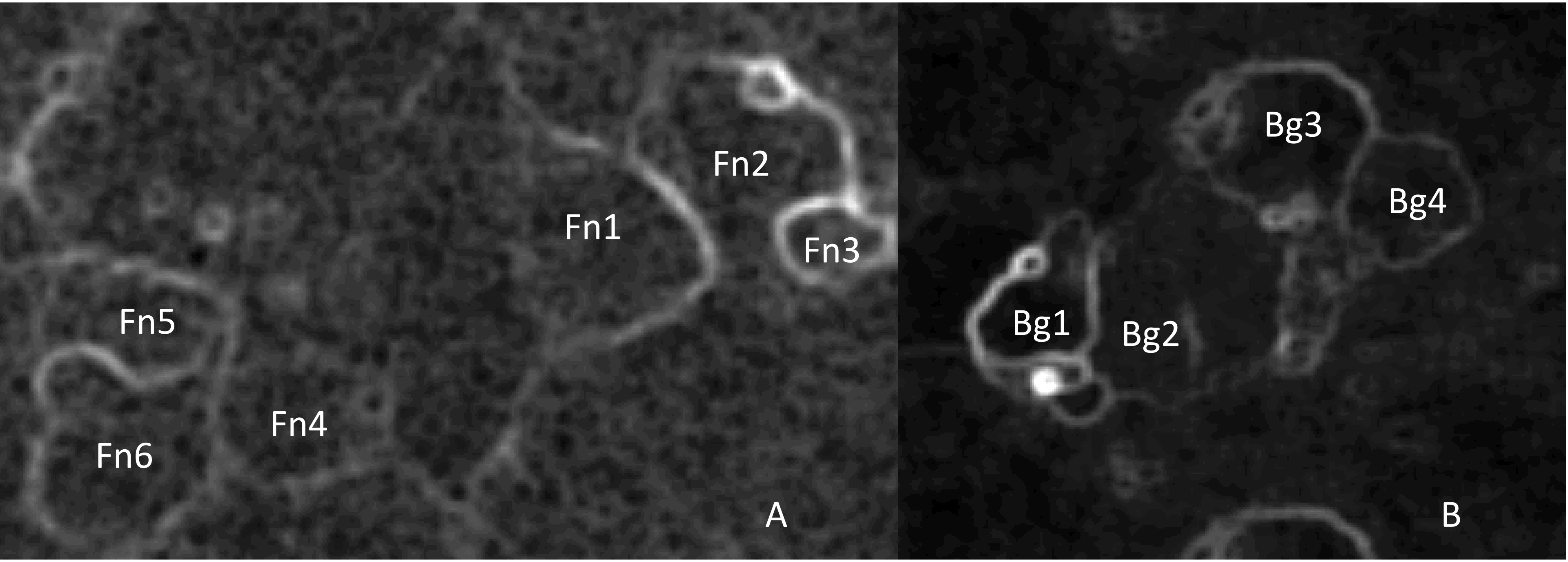
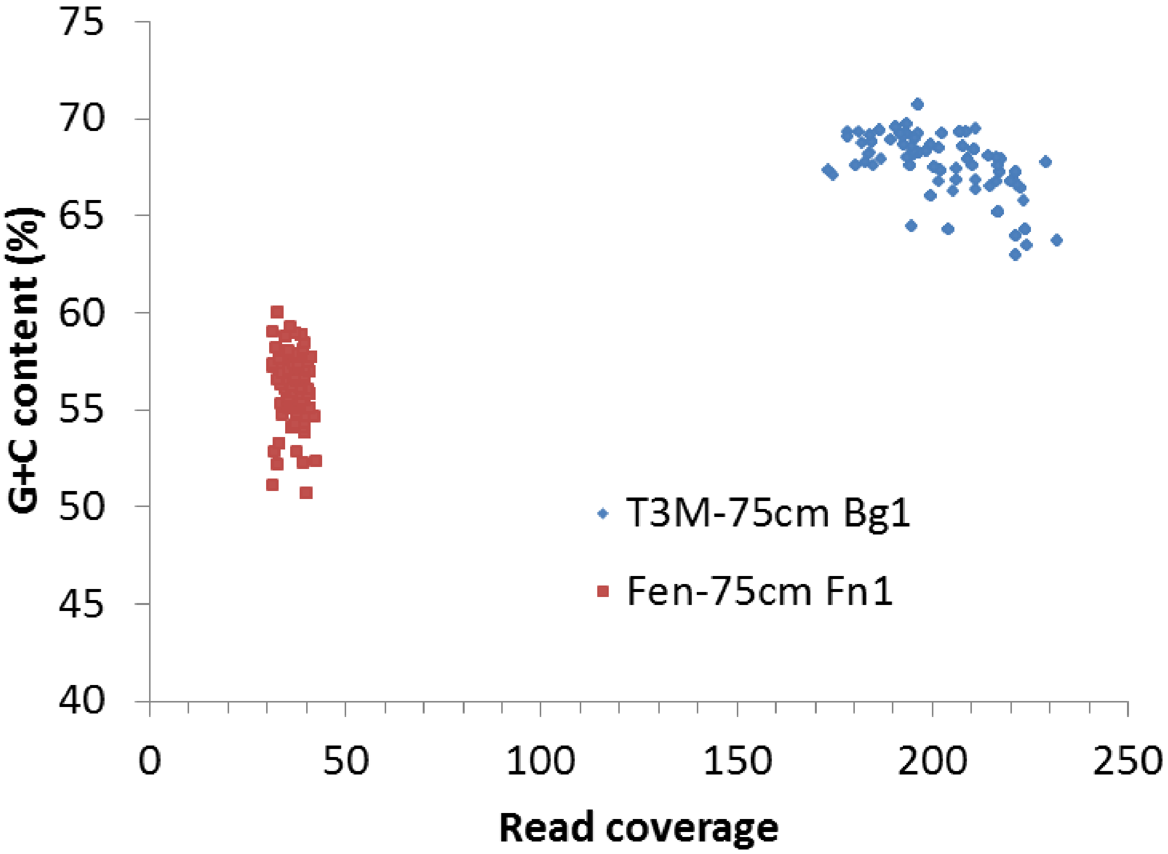


Fig. S2 Plot of read coverage vs. G+C content for two metagenomes: Fen-75cm and T3M-75cm.



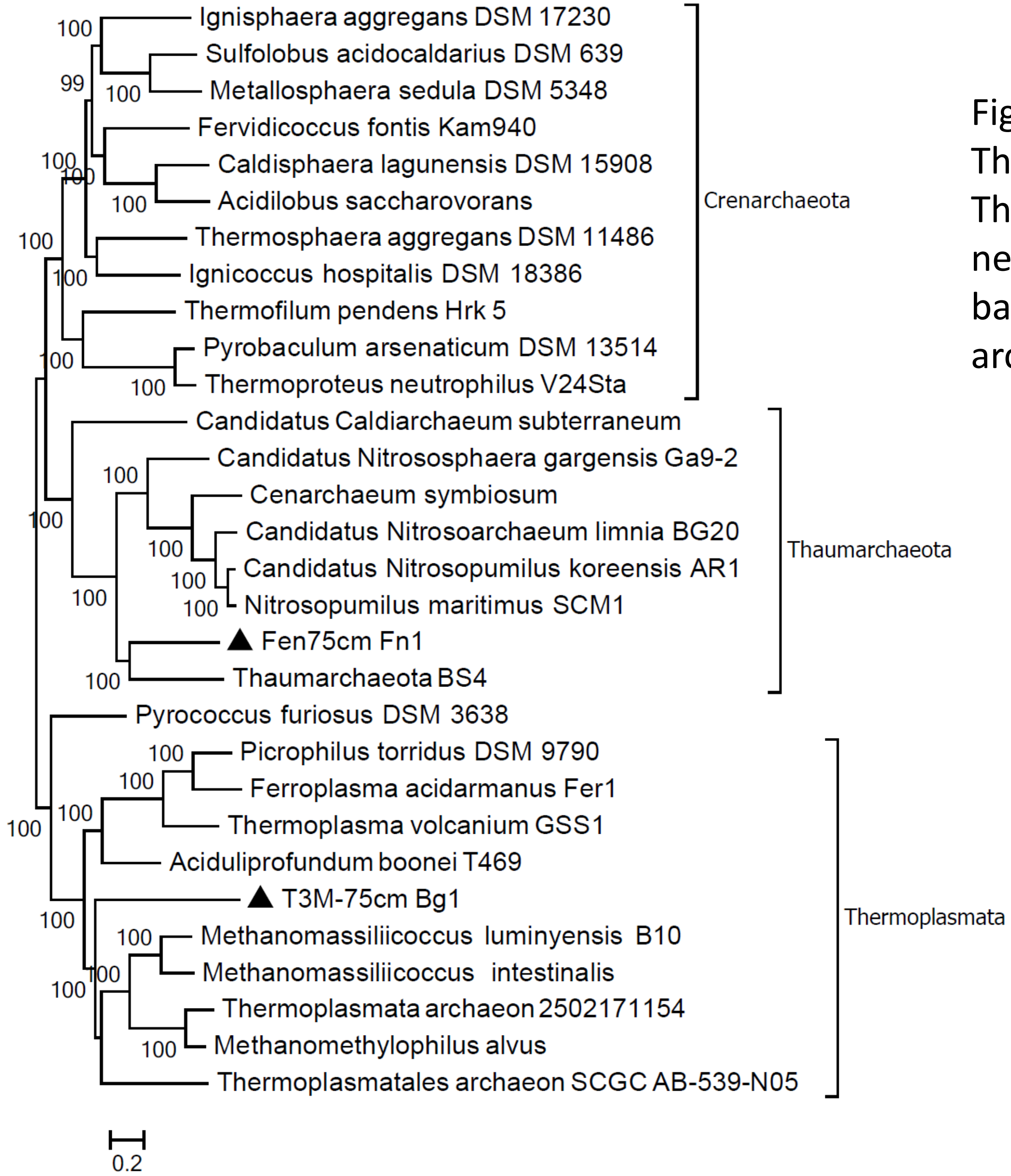


Fig. S3 Genome tree of Thaumarchaeota Fn1 and Thermoplasmata Bg1 and their nearest neighbors, calculated based on >90 concatenated archaeal marker genes.

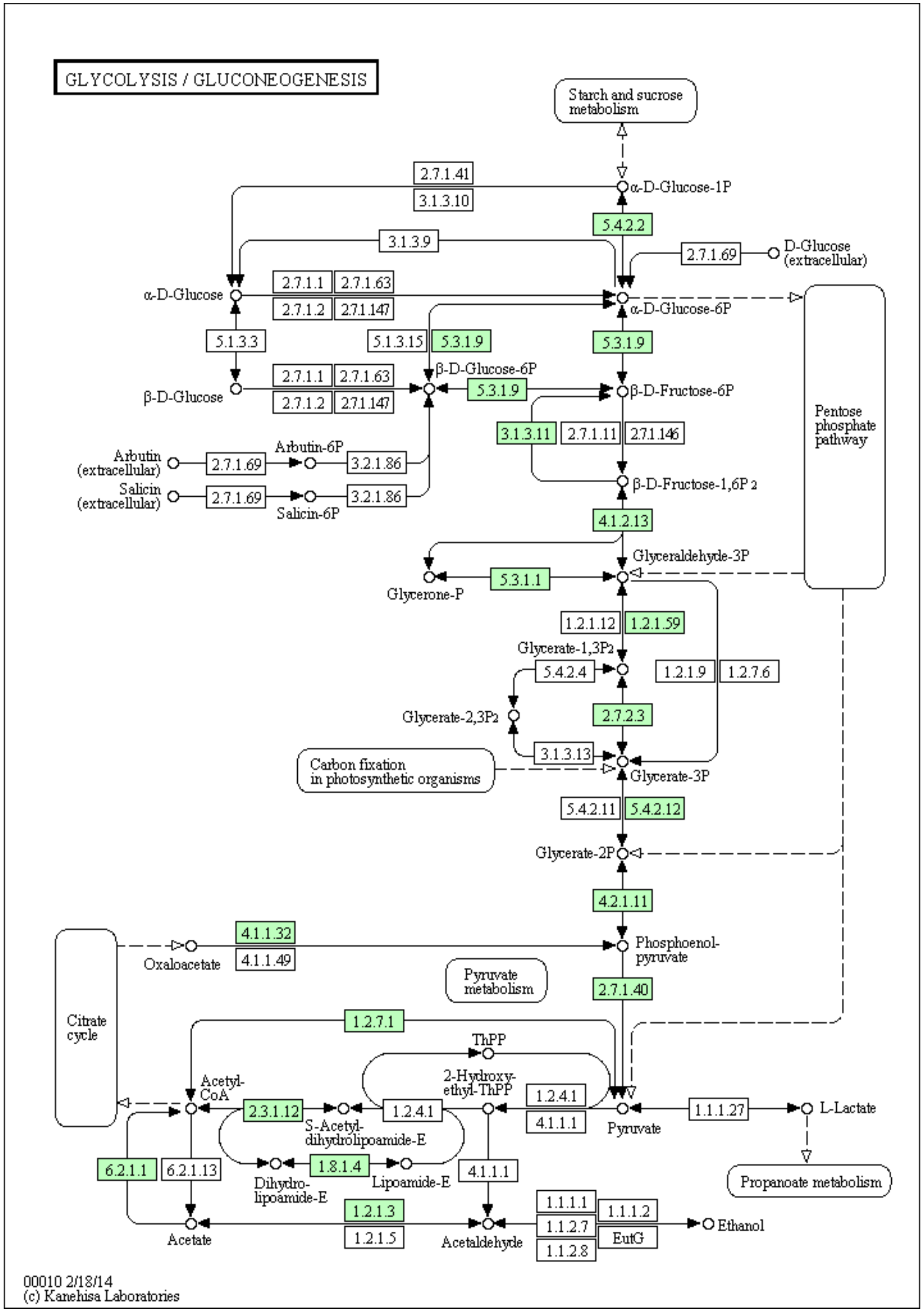


Fig. S4 Glycolysis/gluconeogenesis pathway detected in Fn1 genome. Green boxes indicate enzyme commission number of those detected in Fn1.

Fig. S5a Carbon fixation pathways for Thaumarchaeota Fn1. Green boxes indicate those detected in Fn1.

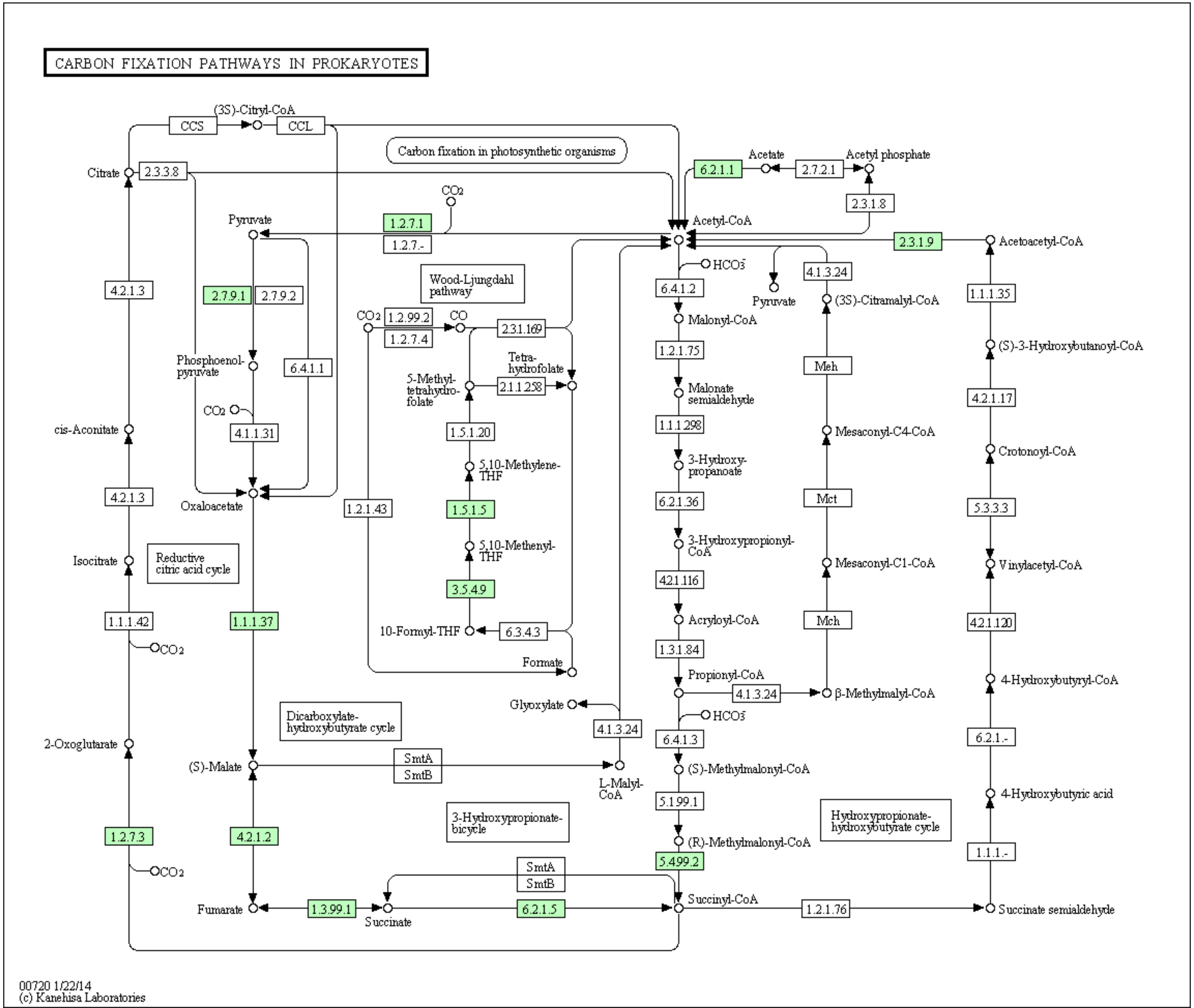
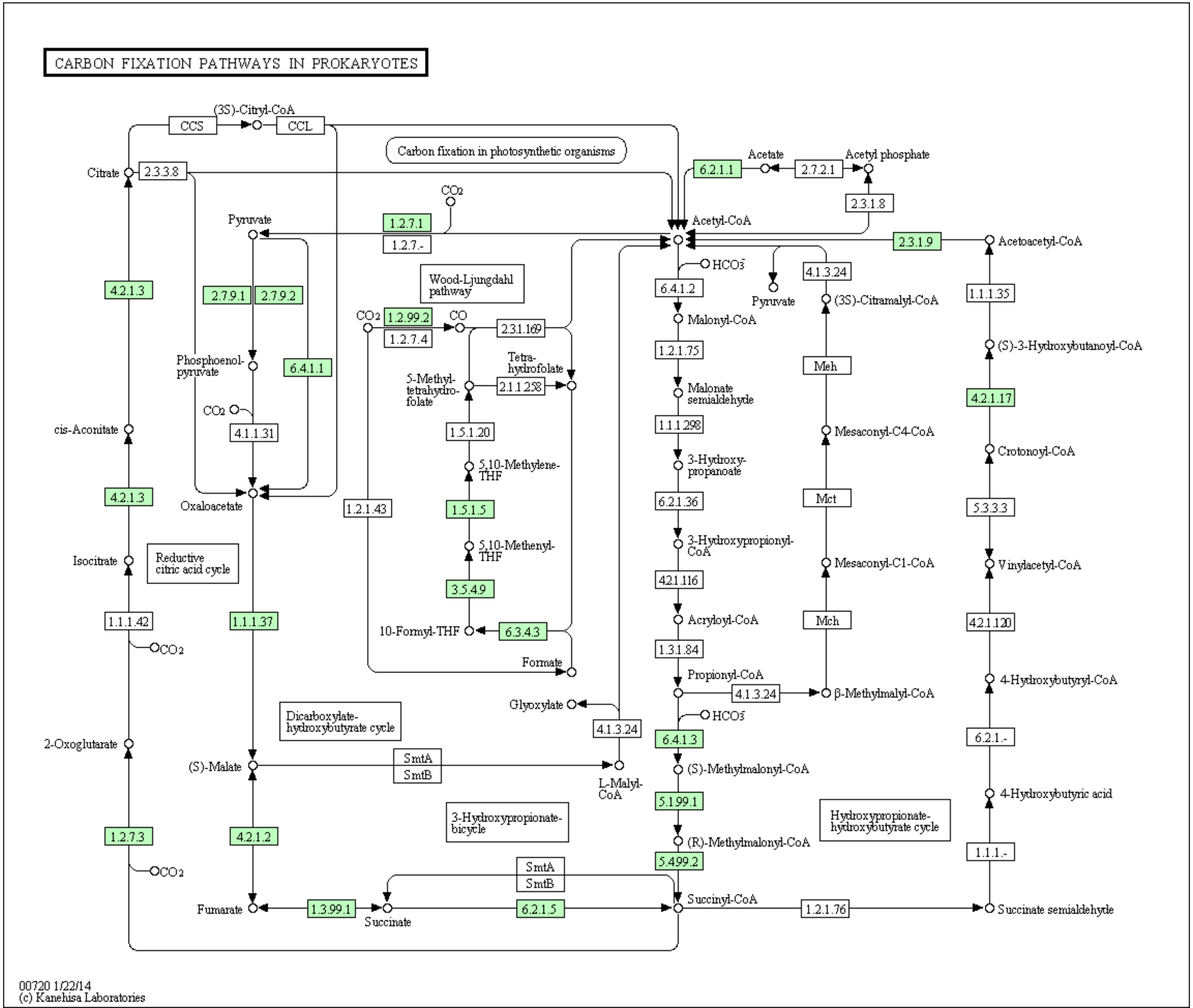


Fig. S5b Carbon fixation pathways for Thermoplasmata Bg1. Green boxes indicate those detected in Bg1.



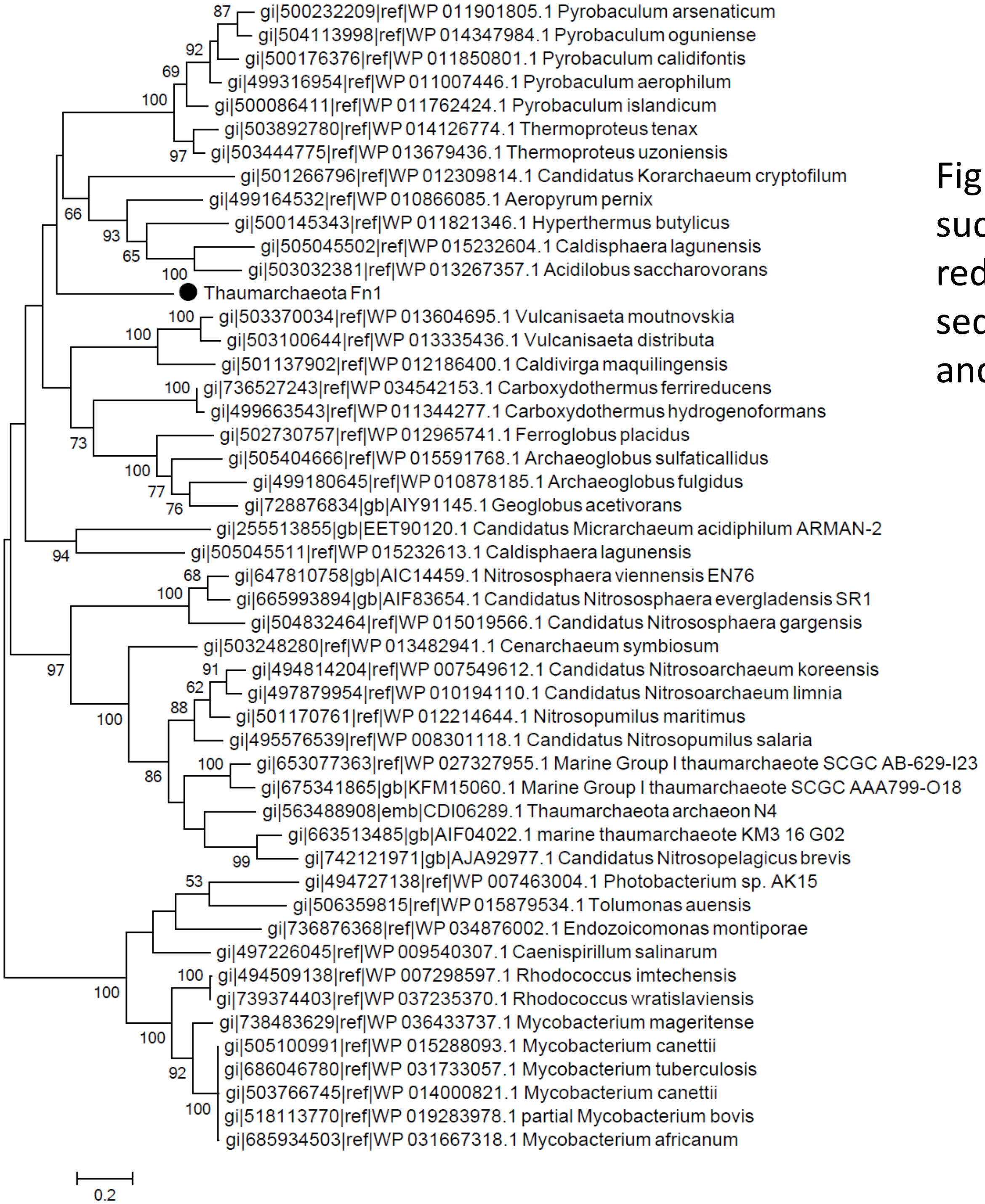


Fig. S6 Maximum likelihood tree of succinate dehydrogenase /fumarate reductase iron-sulfur protein sequences for Thaumarchaeota Fn1 and its closest relatives.

Fig. S7 Maximum likelihood tree of *dsrA* protein sequences for Thermoplasmata Bg1 and its closest relatives.