Supplementary Information

Comparative genomic analysis reveals metabolic flexibility of Woesearchaeota

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Supplementary Note 1

Subgroup definition from the reference paper was consequently updated[1], as follows: (1) Woese-5 were found to encompass sequences belonging to Pacearchaeota; (2) Woese-22 were removed as the 16S rRNA gene sequences did not cluster within Woesearchaeota; and (3) Woese-14 and Woese-21 were further split into two sister groups (Supplementary Fig. 5).

Supplementary Note 2

Subgroups in different trees.

In the phylogenetic analyses, the tree based on the 50% top-ranked orthologs (UFBOOT: 91% and SH-aLRT: 94%, on average) is more statistically supported than the tree based on 15 ribosomal proteins (rps) (UFBOOT: 88% and SH-aLRT: 89%, on average). They have a Robinson-Foulds distance of 96.

Subgroup A, B, C, G and J are monophyletic in the orthologs tree and 15rps tree (Supplementary Fig. 44). The rest subgroups D, E, F, H and I are paraphyletic in the 15rps tree and formed some contradicting groupings. However, the grouping is not statistically well-supported (UFBOOT < 95%; SH-aLRT < 80%). For example, in 15 rp tree, MP5_1_678 and YT1_142 of subgroup H form sister to the subgroup C with weak support (56% UFBOOT and 71% SH-aLRT) and, the clade formed by T1Sed10_208R1, CG10_big_fil_rev_8_21_14_0_10_34_8 and subgroup G also has poor support (73.4% UFBOOT and 68% SH-aLRT). Similarly, the sisterhood of UBA10107, YT2_062, UBA10192, CG10_big_fil_rev_8_21_14_0_10_44_13 and MP5_7_64 to subgroup H and J in the 15 rp tree is not strongly supported (96% UFBOOT and 77% SH-aLRT). Considering that the trimmed alignments of the 15 ribosomal proteins were relatively short (2734 amino acids) and have only 2488 parsimony-informative sites, they likely harbor insufficient information to resolve groupings in the Woesearchaeota as indicated by the low support.

The sequence clusters based on 16S rRNA gene phylogenetic analysis agree well with the tree based on the 50% top-ranked orthologs. Taking advantage of 16S rRNA gene sequence recovered from genomes, several previous defined sequence clusters are able to link with genome-based subgroups. Woese-3, Woese-4, Woese-21a, Woese-24, Woese-14a and Woese-14b correspond to subgroup A, C, J, I, H and E respectively. In addition, subgroup G could be linked with a monophyletic clade in 16S rRNA gene tree including Woese-8, Woese-10, Woese-9, Woese-6, Woese-18 and Woese-20, indicating that a large part of subgroup G diversity remains unexplored. Subgroup D was paraphyletic in the 16S rRNA gene tree, whose sequence representatives were found in Woese-21b and Woese-14a. However, it should be noted that more 16S rRNA gene sequences retrieved from genomes are required to accurately describe their relationship.

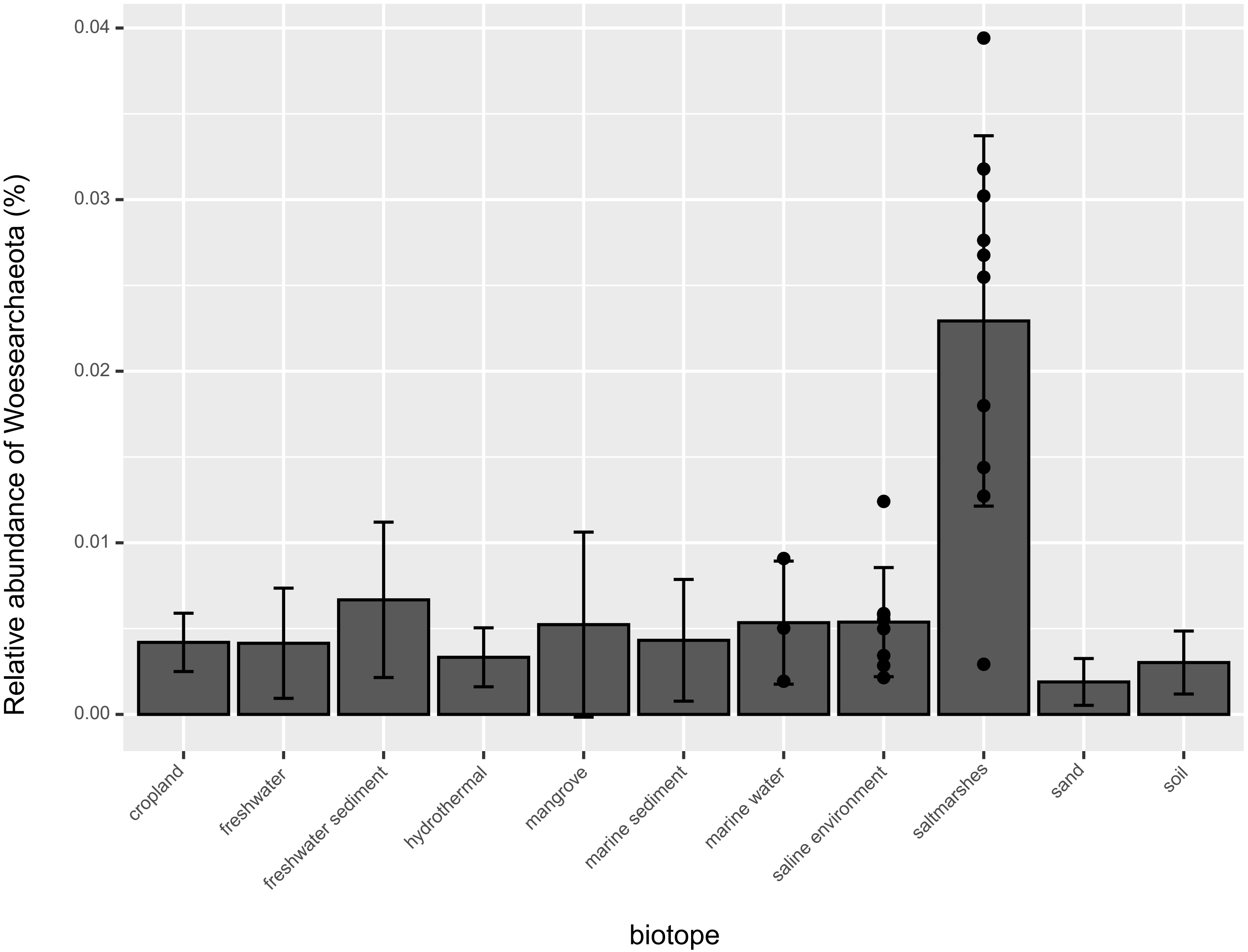
Supplementary Tables

Supplementary Table 1. Mantel test between Euclidean distance matrix of available physiochemical parameters in metadata of EMP datasets and unweighted UniFrac matrix of corresponding Woesearchaeota community. The test was done using “mantel” function in vegan package in R (3.6.0). Pearson correlation was used and significance level was obtained from 999 permutations. Number of libraries indicates the number of libraries with parameters available for the correlation test. Mantel statistic r, ranging for -1 (negative) to 0 (no effect) to 1 (positive), measures the strength of the relationship.

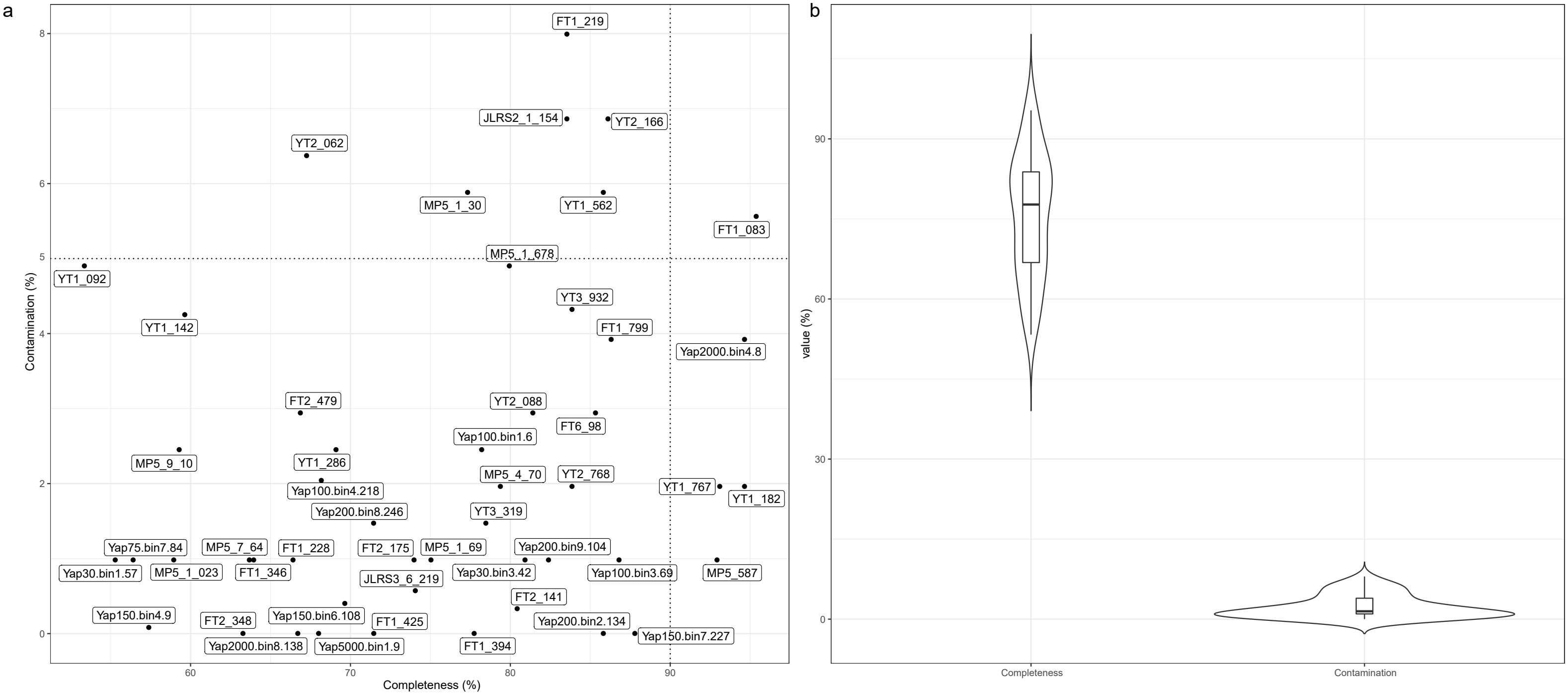
Parameter	Mantel statistic (r)	Significance	Number of libraries
temperature (°C)	0.167461	0.001	726
pH	0.1245451	0.001	593
salinity (psu)	0.2956271	0.001	167
oxygen (mg/L)	0.2113615	0.021	37
phosphate (μmol/L)	0.3474911	0.001	226
ammonium (μumol/L)	0.2128725	0.001	63
nitrate (μmol/L)	0.4036696	0.001	457
sulfate (μmol/L)	0.011915	0.356	152

Supplementary Table 2. The linkage of 16S rRNA gene sequence clusters and genome-based subgroups.

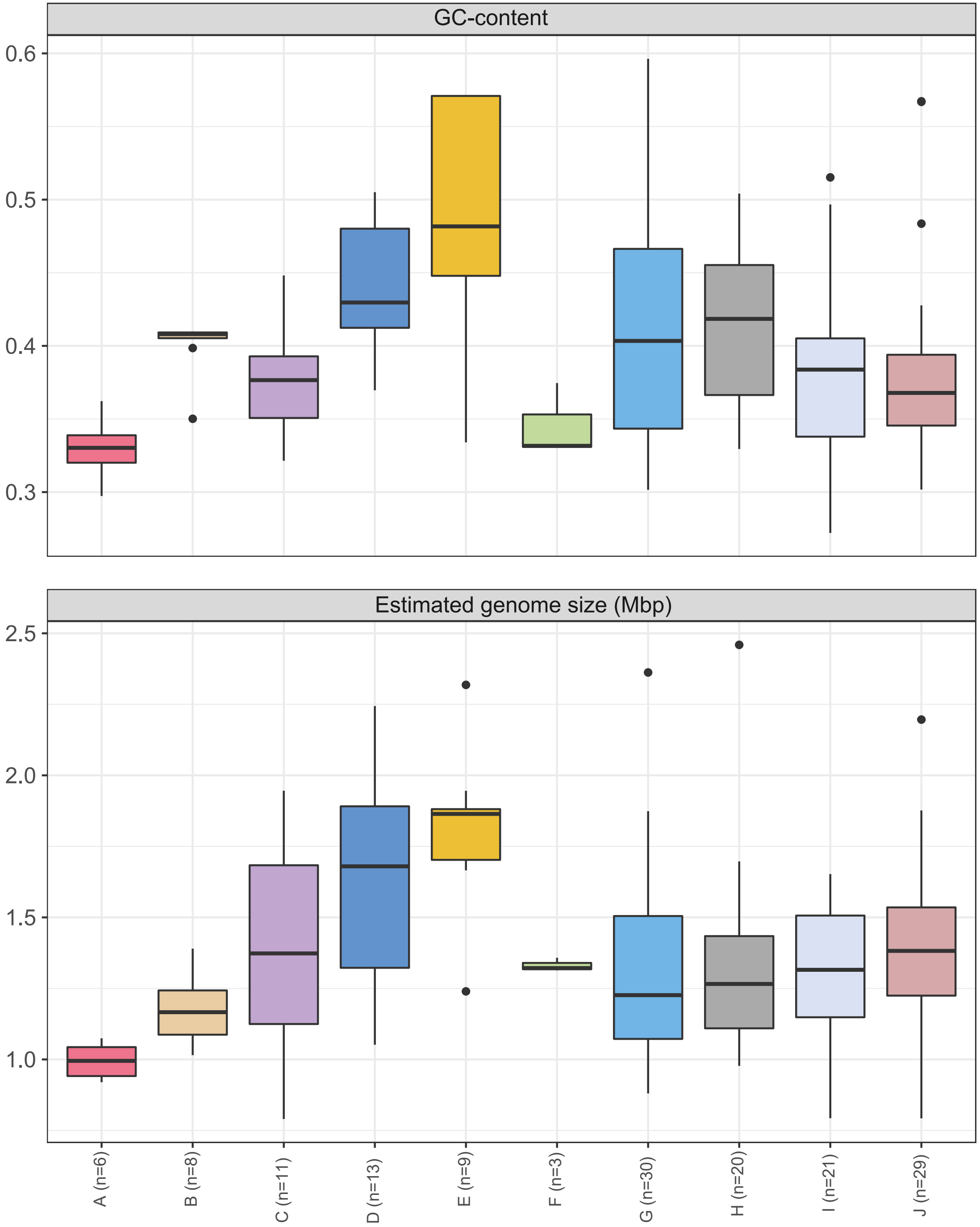
Genome-based subgroups	16S rRNA gene sequence clusters	Monophyly of gene sequence clusters
Subgroup A	Woese-3	Yes
Subgroup C	Woese-4	Yes
Subgroup D	Woese-21b, Woese-23b	No
Subgroup E	Woese-14b	Yes
Subgroup G	Woese-8, Woese-10, Woese-9, Woese-6, Woese-18, Woese-20	Yes
Subgroup H	Woese-14a	Yes
Subgroup I	Woese-24	Yes
Subgroup J	Woese-21a	Yes



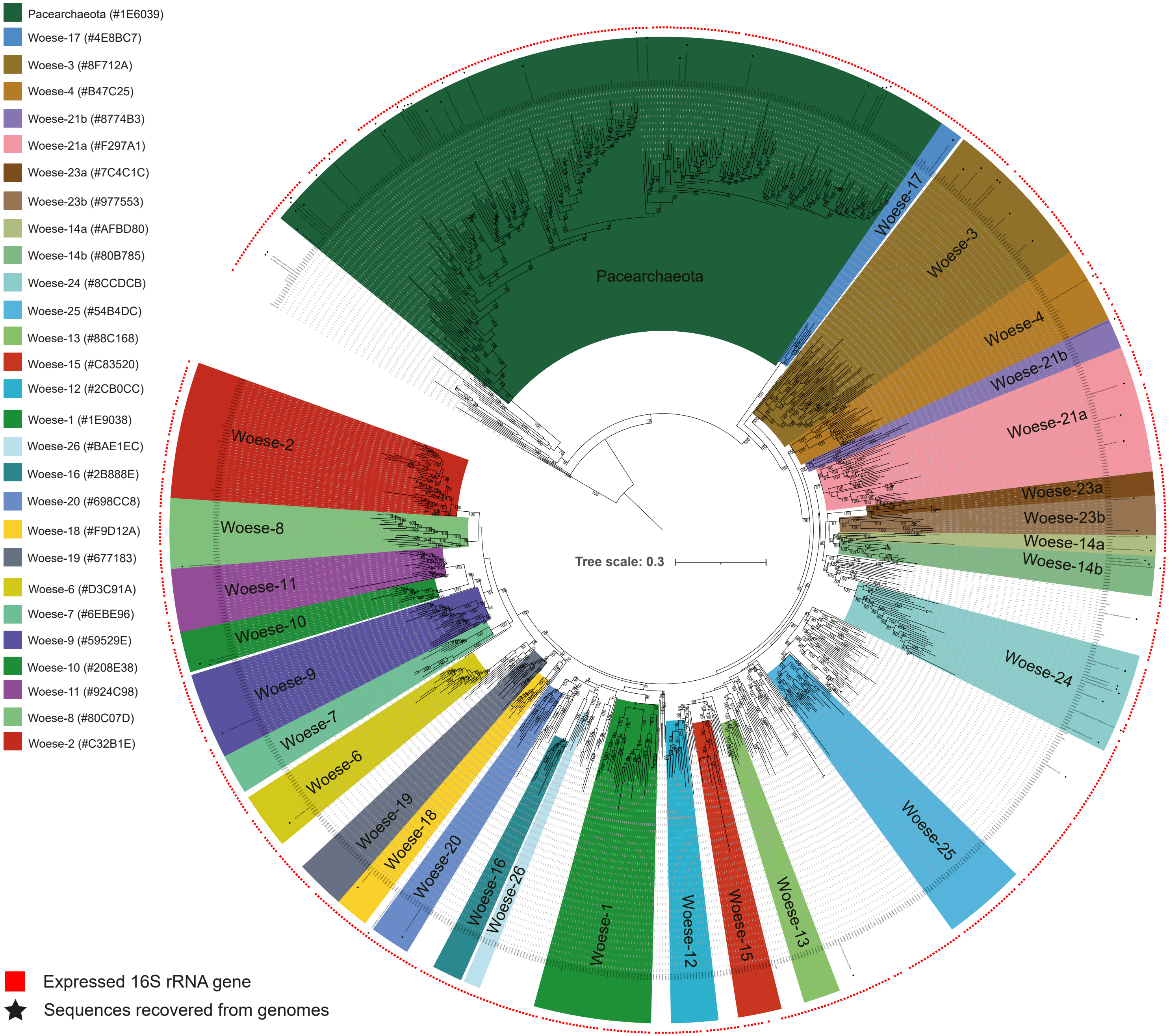
Supplementary Fig. 1: The average relative abundance of Woesearchaeota based on 2163 16S rRNA gene amplicon dataset. Data are presented as mean + / - SD. The number of replicates used for different biotopes are as follows: freshwater: 629, cropland: 590, freshwater sediment: 365, marine sediment: 293, sand: 174, mangrove: 46, soil: 30, hydrothermal: 15, saltmarshes: 10, saline environment: 8, marine water: 3. Source data are provided as a Source Data file.



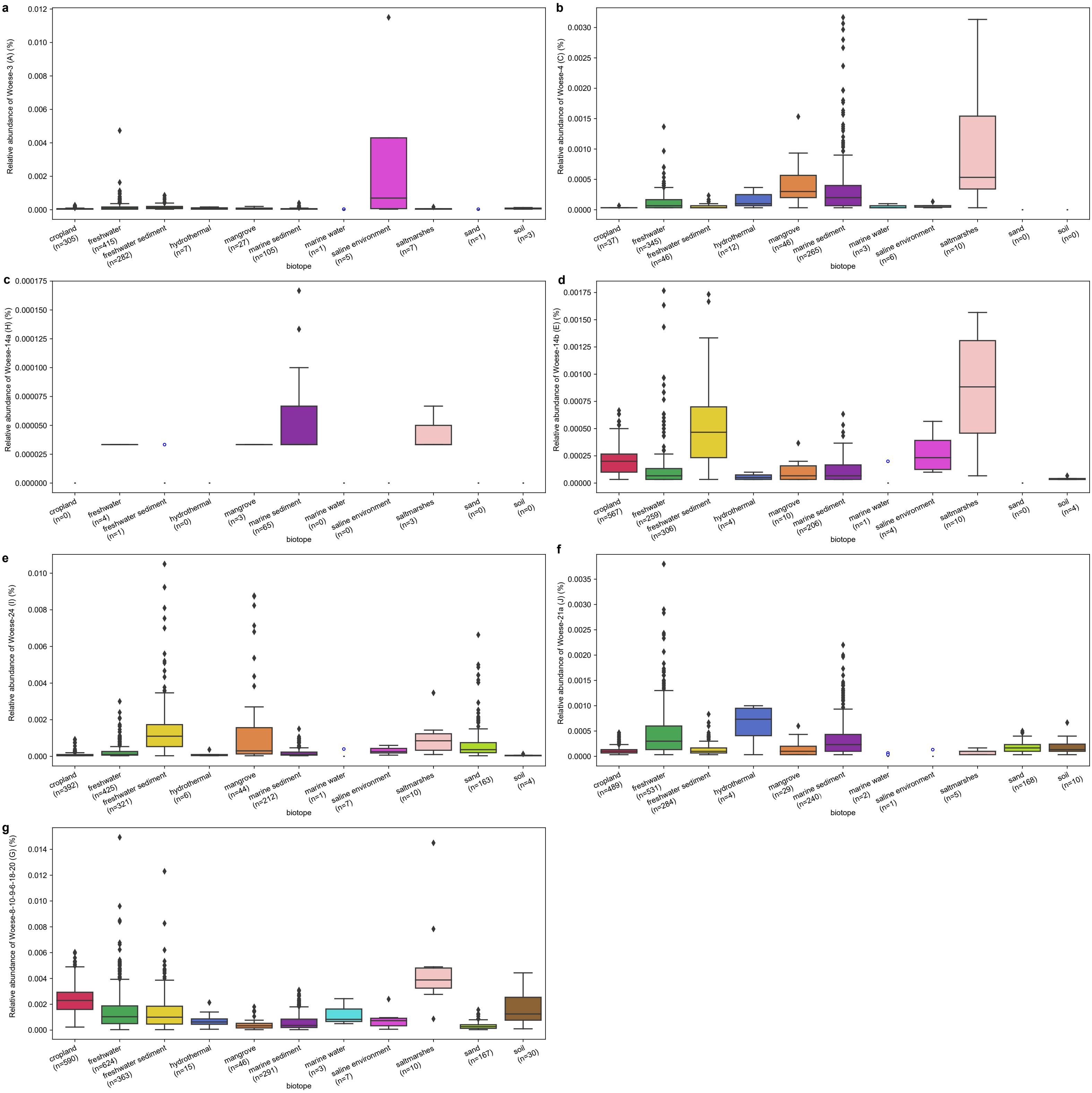
Supplementary Fig. 2: Estimated quality statistics of 49 Woesearchaeota metagenome-assembled genomes (MAGs). Completeness and contamination were estimated with CheckM (v 1.0.12) as described in the method section and raw values could be found in Supplementary Data 2. (**a**) Plot of estimated contamination versus estimated completeness. Each point denotes a MAG and its name is labeled alongside. Dashed line shows the completeness threshold of 90% and contamination threshold of 5%. (**b**) Violin plot and box plot of estimated genome quality metrics. The shape of violin plot represents a kernel density estimation to show probabilistic distribution of the data (n=49). Median of the estimated completeness (77.7 %) and contamination (1.47 %) are shown as the thick black bar. The upper and lower hinges of the box plot indicate the first and third quartile respectively. The upper/lower whiskers stretch out of the hinge to the largest/smallest value less than 1.5 * interquartile range. Source data are provided as a Source Data file.



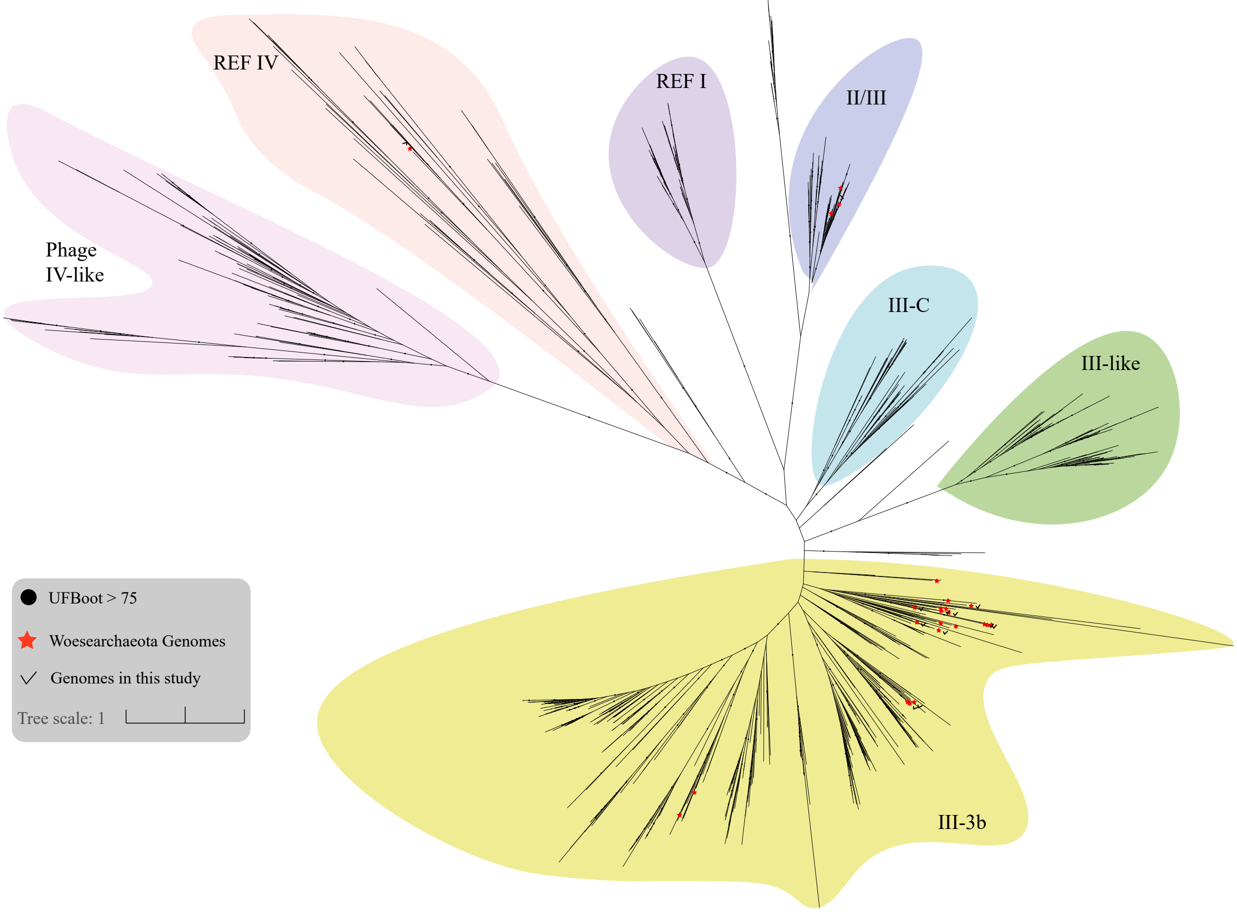
Supplementary Fig. 3: Box plot of general genomic features (GC-content and estimated genome size) of Woesearchaeota MAGs (n=150) of different subgroups. The number of MAGs in each subgroup is shown in parenthesis. GC-content was calculated by CheckM (v 1.0.12). Estimated genome size is calculated by dividing the MAG size by the estimated completeness and then multiplying 100. Thick black bar shows the median value. The upper and lower hinges of the boxplot indicate the first and third quartile respectively. The upper/lower whiskers stretch out of the hinge to the largest/smallest value less than the 1.5 * interquartile range. Colors were used to distinguish different subgroups according to the Fig. 2. The black points correspond to the values great than the 1.5 * interquartile range. Source data are provided as a Source Data file.



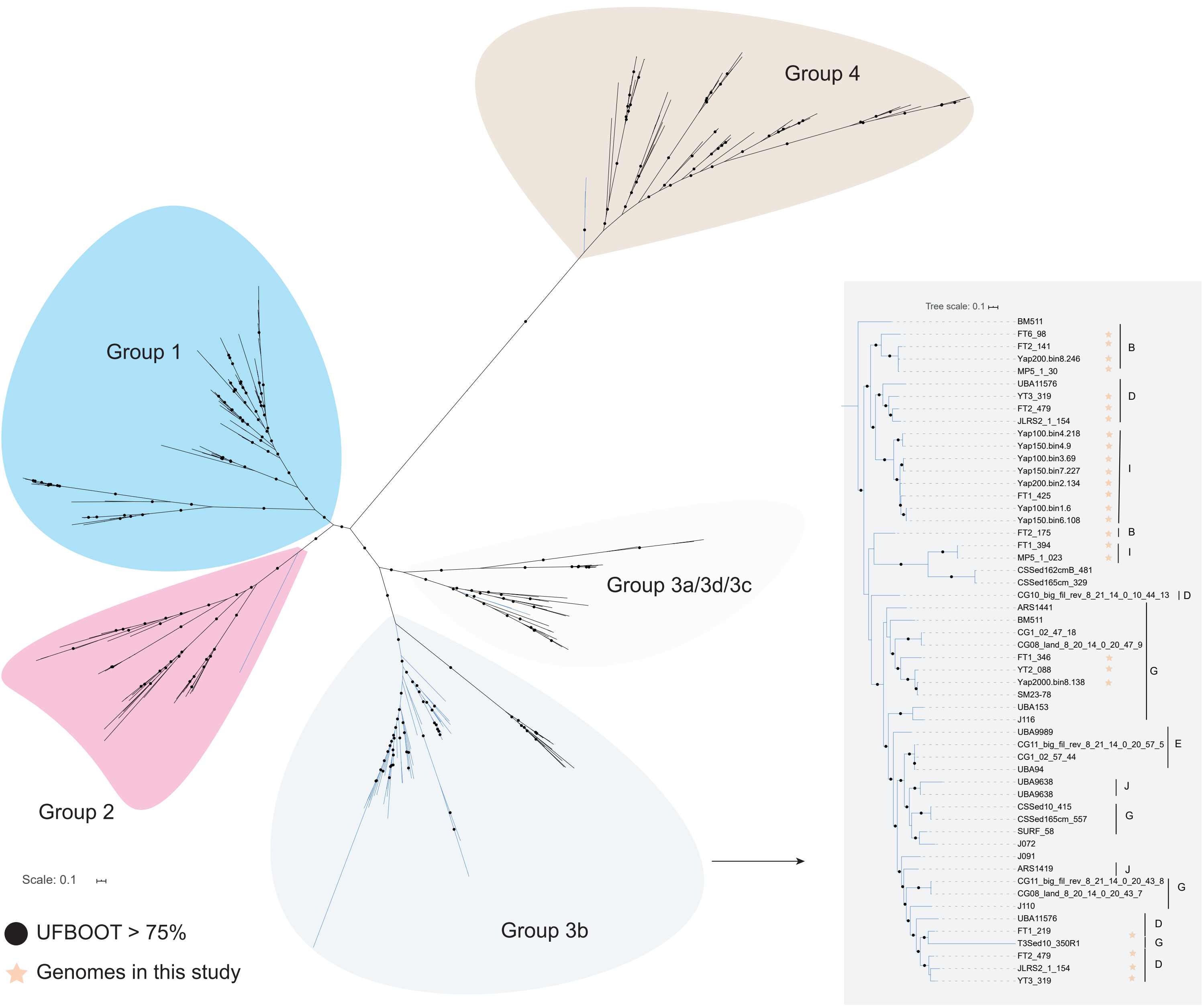
Supplementary Fig. 4: Phylogenetic analysis based on 16S rRNA gene sequences using IQ-Tree (v 1.6.8) based on the TIM+F+G model. The tree includes 891 16S rRNA gene sequences (35 from Woesearchaeota MAGs, 28 from Pacearchaeota MAGs, and three from unclassified MAGs, 823 from SILVA SSU 132 database or Liu et al.[1]) and was rooted using two sequences from Nanoarchaeota. The ultrafast bootstrap values are shown at the nodes. The hex code for the color of each sequence cluster was shown at the legend. Stars denote 16S rRNA gene sequences retrieved from genome and red rectangles indicate a shared sequence identity (>97%) with sequences in an expressed 16S rRNA gene dataset[2]. Scale bar shows the average nucleotide substitutions per site. Source data are provided as a Source Data file.



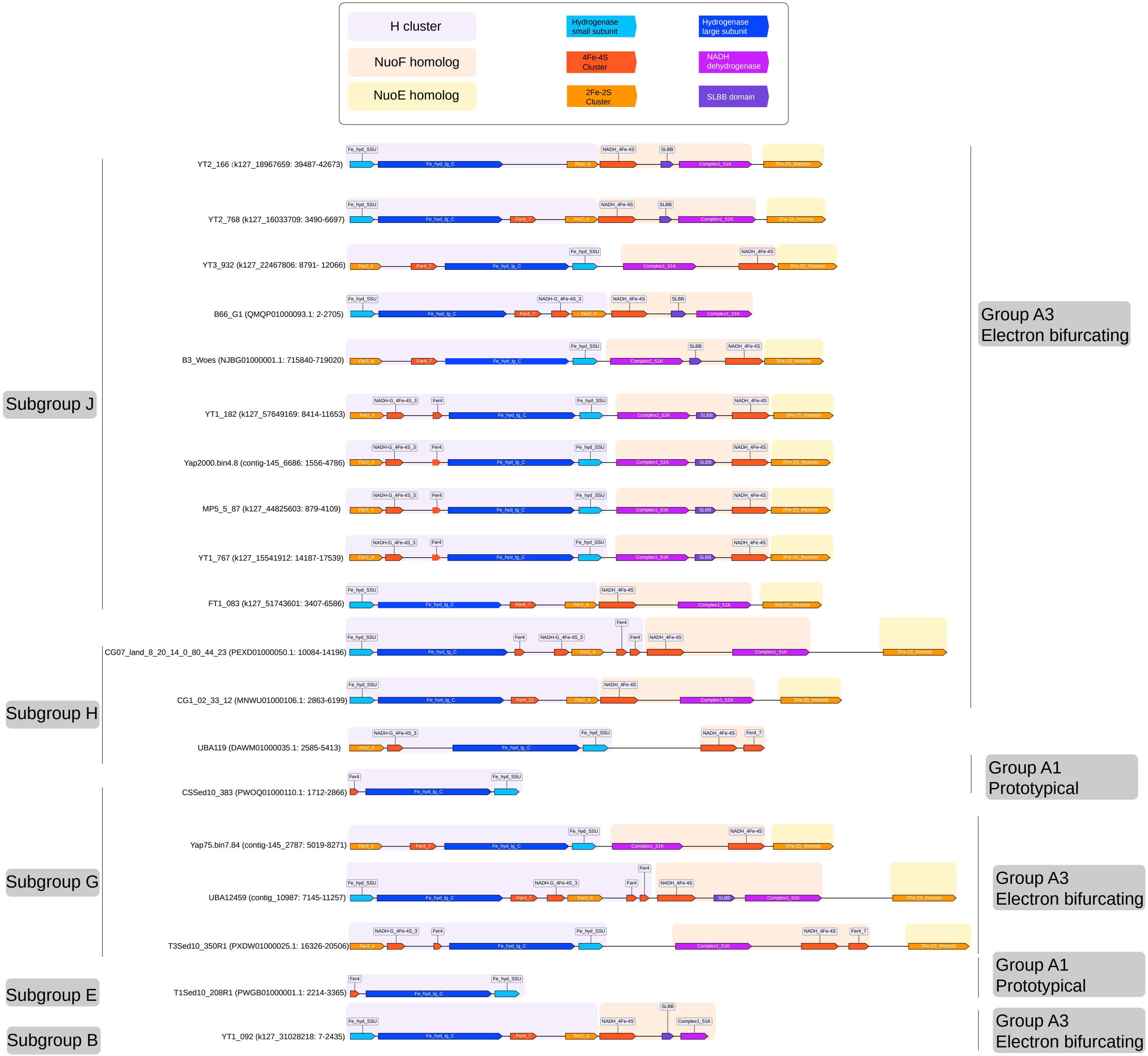
Supplementary Fig. 5: Distribution of Woesearchaeota subgroups in the studied biotopes. a-g, Distribution of Woese-3 that is linked with subgroup A (**a**), Woese-4 that is linked with subgroup C (**b**), Woese-14a that is linked with subgroup H (**c**), Woese-14b that is linked with subgroup E (**d**), Woese-24 that is linked with subgroup I (**e**), Woese-21a that is linked with subgroup J (**f**) and the aggregate of Woese-8, Woese-10, Woese-9, Woese-6, Woese-18 and Woese-20 that are linked with subgroup G (**g**) in the 2163 investigated libraries. Colors were used to distinguish different biotopes according to the Fig. 1. Thick black bar shows the median value. The upper and lower hinges of the boxplot indicate the first and third quartile respectively. The upper/lower whiskers stretch out of the hinge to the largest/smallest value less than 1.5 * interquartile range. The black points correspond to the values great than the 1.5 * interquartile range. Data less than 3 are shown as hollow blue points. The number of datasets for each biotope used in each panel are as follows: cropland: (a: 305, b: 37, c: 0, d: 567, e: 392, f: 489, g: 590), freshwater: (a: 415, b: 345, c:4, d: 259, e: 425, f: 531, g: 624), freshwater sediment: (a: 282, b: 46, c:1, d: 306, e: 321, f: 284, g: 363), hydrothermal: (a: 7, b: 12, c:0, d: 4, e: 6, f: 4, g: 15), mangrove: (a: 27, b: 46, c:3, d: 10, e: 44, f: 29, g: 46), marine sediment: (a: 105, b: 265, c: 65, d: 206, e: 212, f: 240, g: 291), marine water: (a: 1, b: 3, c: 0, d: 1, e: 1, f: 2, g: 3), saline environment (a: 5, b: 6, c: 0, d: 4, e: 7, f: 1, g: 7), saltmarshes (a: 7, b: 10, c: 3, d: 10, e: 10, f: 5, g: 10), sand (a: 1, b: 0, c: 0, d: 0, e: 163, f: 168, g: 167), and soil (a: 3, b: 0, c: 0, d: 4, e: 4, f: 10, g: 30). Source data are provided as a Source Data file.



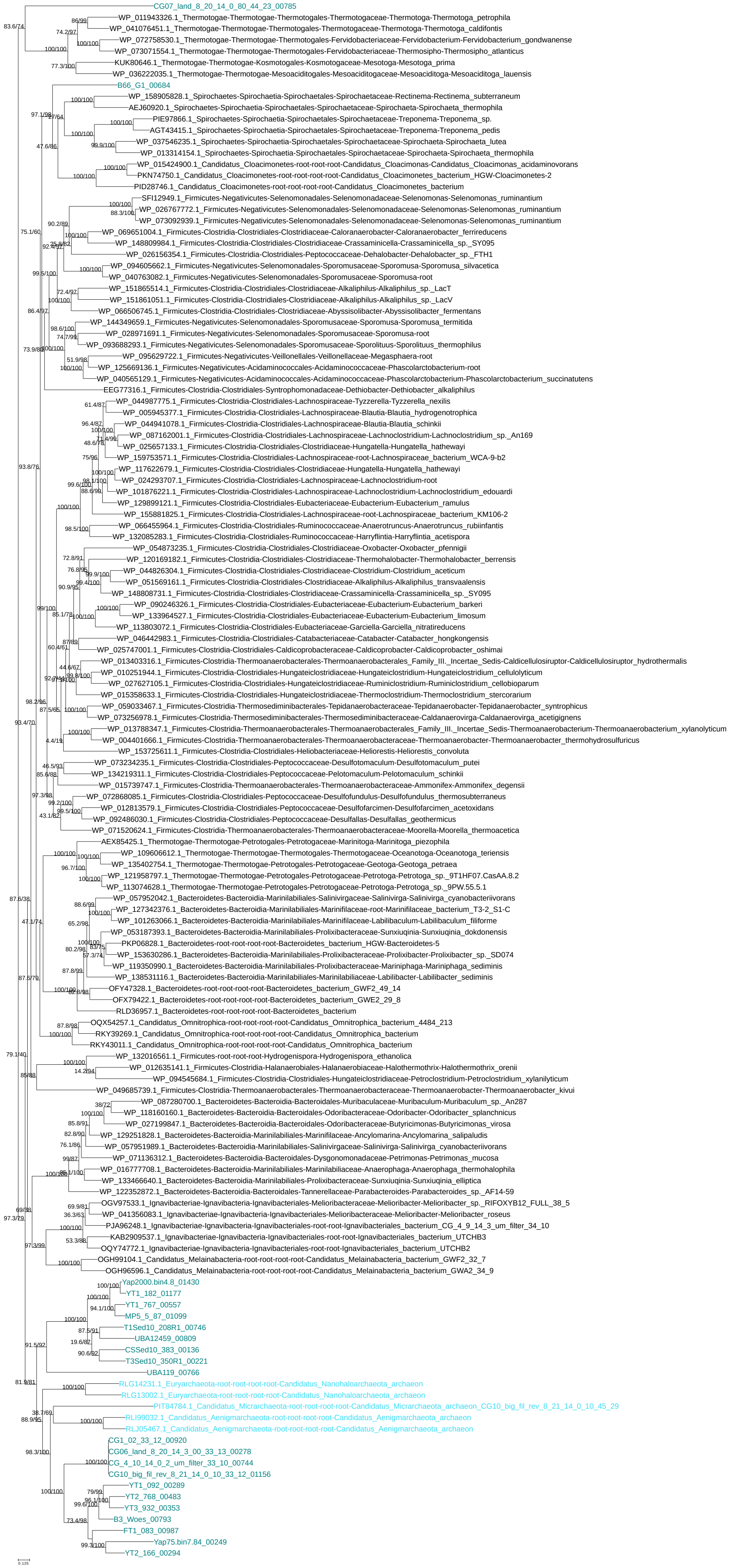
Supplementary Fig. 6: Phylogenetic analysis of ribulose 1,5-bisphosphate carboxylase large subunit (*rbcL)* based on LG+G model using IQ-Tree. The tree is unrooted and includes an alignment of 776 sequences of 163 sites. Scale bar shows the average number of substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).



Supplementary Fig. 7: Phylogenetic analysis of [NiFe] hydrogenase based on LG+G model. The tree is unrooted and includes an alignment of 277 sequences of 169 sites. Scale bar shows the average number of substitutions per site. Inset shows phylogenetic clades of [NiFe] hydrogenase group 3b of Woesearchaeota. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).


H cluster
NuoF homolog
NuoE homolog
Hydrogenase small subunit
Hydrogenase large subunit
4Fe-4S Cluster
NADH dehydrogenase
2Fe-2S Cluster
SLBB domain
YT2_166 (k127_18967659: 39487-42673)
YT2_768 (k127_16033709: 3490-6697)
YT3_932 (k127_22467806: 8791- 12066)
B66_G1 (QMQP01000093.1: 2-2705)
B3_Woes (NJBG01000001.1: 715840-719020)
YT1_182 (k127_57649169: 8414-11653)
Yap2000.bin4.8 (contig-145_6686: 1556-4786)
MP5_5_87 (k127_44825603: 879-4109)
YT1_767 (k127_15541912: 14187-17539)
FT1_083 (k127_51743601: 3407-6586)
CG07_land_8_20_14_0_80_44_23 (PEXD01000050.1: 10084-14196)
CG1_02_33_12 (MNWU01000106.1: 2863-6199)
UBA119 (DAWM01000035.1: 2585-5413)
CSSed10_383 (PWOQ01000110.1: 1712-2866)
Yap75.bin7.84 (contig-145_2787: 5019-8271)
UBA12459 (contig_10987: 7145-11257)
T3Sed10_350R1 (PXDW01000025.1: 16326-20506)
T1Sed10_208R1 (PWGB01000001.1: 2214-3365)
YT1_092 (k127_31028218: 7-2435)
Fe_hyd_SSU
Fe_hyd_lg_C
Fer2_4
Fer4_7
Fer4
Fer4_21
NADH-G_4Fe-4S_3
NADH_4Fe-4S
SLBB
Complex1_51K
2Fe-2S_thioredx
Subgroup J
Subgroup H
Subgroup G
Subgroup E
Subgroup B
Group A3 Electron bifurcating
Group A1 Prototypical
Group A3 Electron bifurcating
Group A1 Prototypical
Group A3 Electron bifurcating

Supplementary Fig. 8: Genomic regions encoding [FeFe] hydrogenase complex in Woesearchaeota MAGs. All genes are drawn to scale. Detailed location of [FeFe] hydrogenase is shown in the parenthesis by the format (contig name: starting bases - ending bases). Most [FeFe] hydrogenase in Woesearchaeota is trimeric, containing a H cluster, NuoF homologue and NuoE homologue. [FeFe] hydrogenase large subunit and small subunit, consisting of the catalytic domains, are respectively marked in dark and light blue. Dark orange and light orange correspond to 4Fe-4S cluster and 2Fe-2S cluster respectively. NADH dehydrogenase domain and soluble ligand binding domain are colored in respectively in dark and light purple. Domains were annotated by Pfam (v 32.0) by InterProScan (v 5.38-76.0, client version). The corresponding domain names and Pfam accessions are shown as below: Fe_hyd_SSU: PF02256, Fe_hyd_lg_C: PF02906, Fer2_4: PF13510, NADH-G_4Fe-4S_3: PF00037, Fer4: PF02906, Complex1_51K: PF01512, SLBB: PF10531, NADH_4Fe-4S: PF10589, 2Fe-2S_thioredx: PF01257, Fer4_7: PF12838, Fer4_21: PF14697.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WP_015739747.1_Firmicutes-Clostridia-Thermoanaerobacterales-Thermoanaerobacteraceae-Ammonifex-Ammonifex_degensii
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RLJ05467.1_Candidatus_Aenigmarchaeota-root-root-root-root-Candidatus_Aenigmarchaeota_archaeon
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CG10_big_fil_rev_8_21_14_0_10_33_12_01156
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YT3_932_00353
B3_Woes_00793
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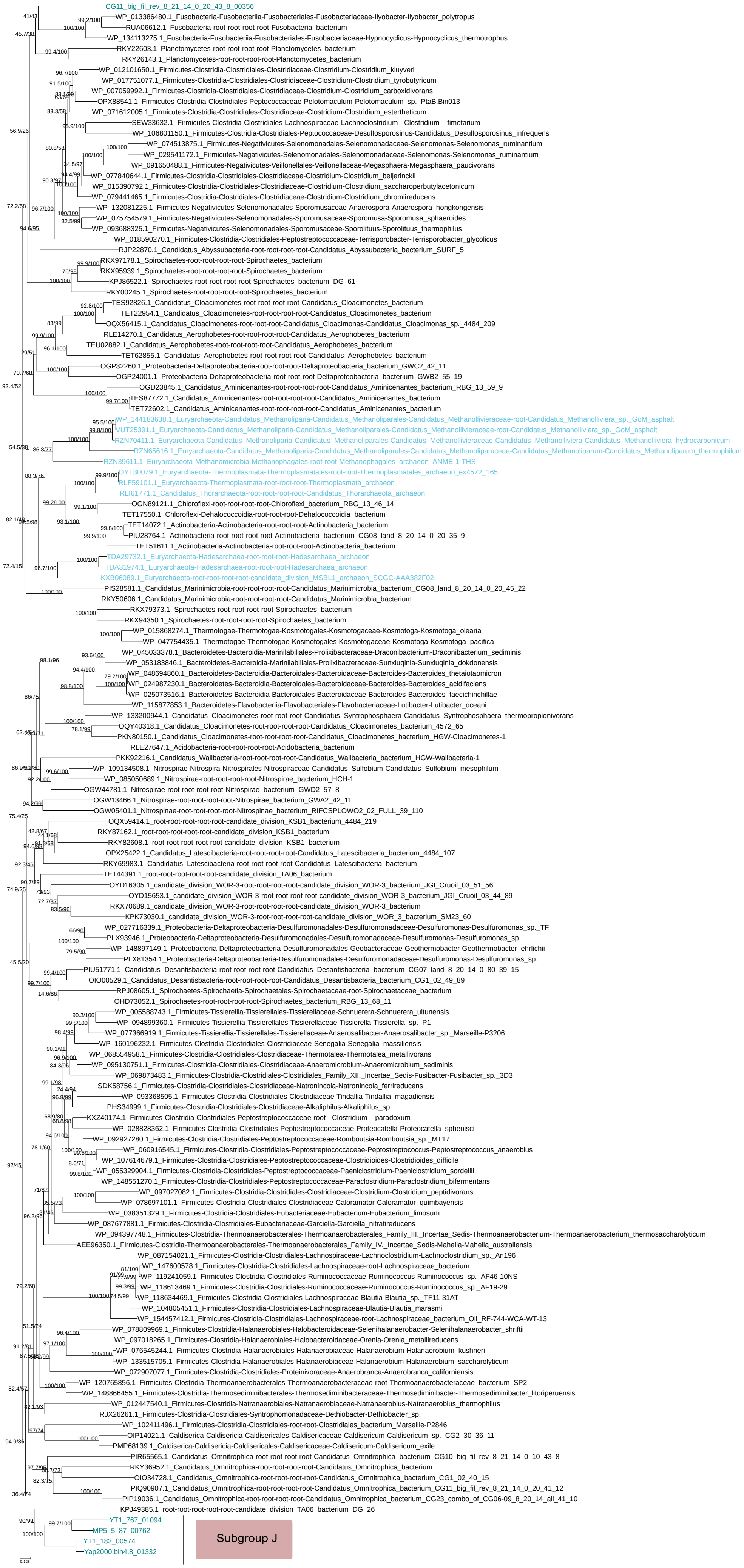
YT2_166_00294
0.125

Supplementary Fig. 9: Phylogenetic analysis of catalytic subunit of [FeFe] hydrogenase in Woesearchaeota. The tree was unrooted and inferred using IQ-Tree LG+G+C20 model on an alignment of 216 taxa and 598 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan and green respectively. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).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RKY26143.1_Planctomycetes-root-root-root-root-Planctomycetes_bacterium
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WP_038351329.1_Firmicutes-Clostridia-Clostridiales-Eubacteriaceae-Eubacterium-Eubacterium_limosum
WP_087677881.1_Firmicutes-Clostridia-Clostridiales-Eubacteriaceae-Garciella-Garciella_nitratireducens
WP_094397748.1_Firmicutes-Clostridia-Thermoanaerobacterales-Thermoanaerobacterales_Family_III._Incertae_Sedis-Thermoanaerobacterium-Thermoanaerobacterium_thermosaccharolyticum
AEE96350.1_Firmicutes-Clostridia-Thermoanaerobacterales-Thermoanaerobacterales_Family_IV._Incertae_Sedis-Mahella-Mahella_australiensis
WP_087154021.1_Firmicutes-Clostridia-Clostridiales-Lachnospiraceae-Lachnoclostridium-Lachnoclostridium_sp._An196
WP_147600578.1_Firmicutes-Clostridia-Clostridiales-Lachnospiraceae-root-Lachnospiraceae_bacterium
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WP_118613469.1_Firmicutes-Clostridia-Clostridiales-Ruminococcaceae-Ruminococcus-Ruminococcus_sp._AF19-29
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WP_154457412.1_Firmicutes-Clostridia-Clostridiales-Lachnospiraceae-root-Lachnospiraceae_bacterium_Oil_RF-744-WCA-WT-13
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WP_097018265.1_Firmicutes-Clostridia-Halanaerobiales-Halobacteroidaceae-Orenia-Orenia_metallireducens
WP_076545244.1_Firmicutes-Clostridia-Halanaerobiales-Halanaerobiaceae-Halanaerobium-Halanaerobium_kushneri
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OIP14021.1_Caldiserica-Caldisericia-Caldisericales-Caldisericaceae-Caldisericum-Caldisericum_sp._CG2_30_36_11
PMP68139.1_Caldiserica-Caldisericia-Caldisericales-Caldisericaceae-Caldisericum-Caldisericum_exile
PIR65565.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium_CG10_big_fil_rev_8_21_14_0_10_43_8
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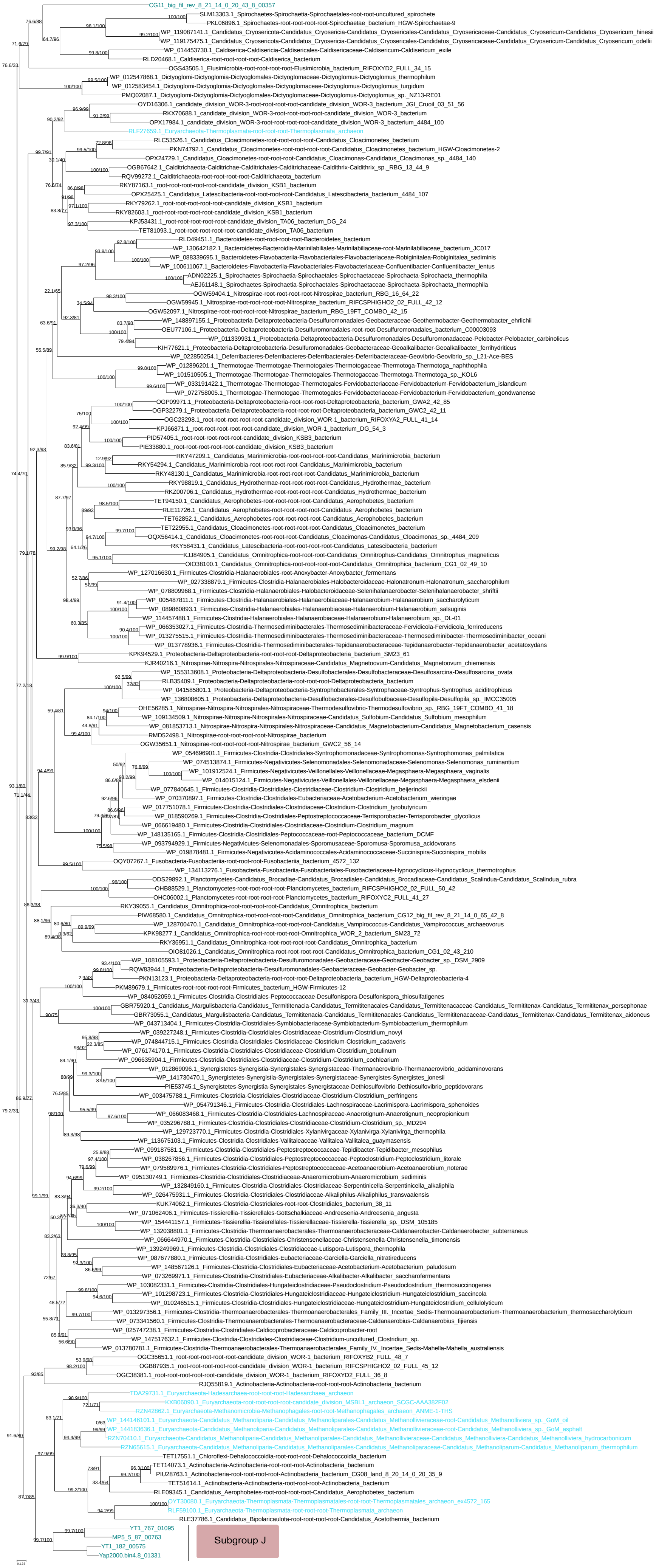
PIP19036.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium_CG23_combo_of_CG06-09_8_20_14_all_41_10
KPJ49385.1_root-root-root-root-root-candidate_division_TA06_bacterium_DG_26
YT1_767_01094
MP5_5_87_00762
YT1_182_00574
Yap2000.bin4.8_01332
Subgroup J
0.125

Supplementary Fig. 10: Phylogenetic analysis of *rnfC* gene (*Rhodobacter* nitrogen fixation complex subunit C). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 147 taxa and 440 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea, and Woesearchaeota are colored in black, cyan, and green, respectively. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).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WP_119175475.1_Candidatus_Cryosericota-Candidatus_Cryosericia-Candidatus_Cryosericales-Candidatus_Cryosericaceae-Candidatus_Cryosericum-Candidatus_Cryosericum_odellii
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OGS43505.1_Elusimicrobia-root-root-root-Elusimicrobia_bacterium_RIFOXYD2_FULL_34_15
WP_012547868.1_Dictyoglomi-Dictyoglomia-Dictyoglomales-Dictyoglomaceae-Dictyoglomus-Dictyoglomus_thermophilum
WP_012583454.1_Dictyoglomi-Dictyoglomia-Dictyoglomales-Dictyoglomaceae-Dictyoglomus-Dictyoglomus_turgidum
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OPX17984.1_candidate_division_WOR-3-root-root-root-candidate_division_WOR-3_bacterium_4484_100
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RLC53526.1_Candidatus_Cloacimonetes-root-root-root-Candidatus_Cloacimonetes_bacterium
PKN74792.1_Candidatus_Cloacimonetes-root-root-root-Candidatus_Cloacimonetes_bacterium_HGW-Cloacimonetes-2
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RKY82603.1_root-root-root-root-candidate_division_KSB1_bacterium
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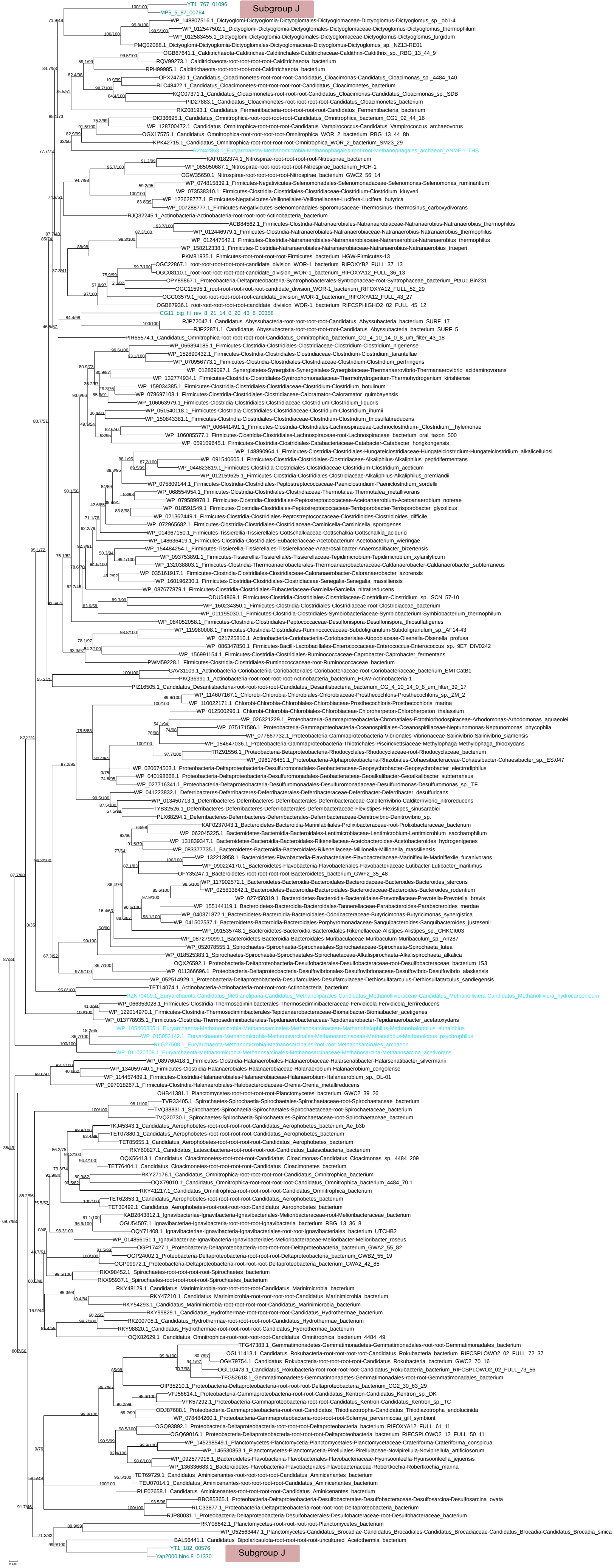
WP_087677880.1_Firmicutes-Clostridia-Clostridiales-Eubacteriaceae-Garciella-Garciella_nitratireducens
WP_148567126.1_Firmicutes-Clostridia-Clostridiales-Eubacteriaceae-Acetobacterium-Acetobacterium_paludosum
WP_073269971.1_Firmicutes-Clostridia-Clostridiales-Eubacteriaceae-Alkalibacter-Alkalibacter_saccharofermentans
WP_103082331.1_Firmicutes-Clostridia-Clostridiales-Hungateiclostridiaceae-Pseudoclostridium-Pseudoclostridium_thermosuccinogenes
WP_101298723.1_Firmicutes-Clostridia-Clostridiales-Hungateiclostridiaceae-Hungateiclostridium-Hungateiclostridium_saccincola
WP_010246515.1_Firmicutes-Clostridia-Clostridiales-Hungateiclostridiaceae-Hungateiclostridium-Hungateiclostridium_cellulolyticum
WP_013297356.1_Firmicutes-Clostridia-Thermoanaerobacterales-Thermoanaerobacterales_Family_III._Incertae_Sedis-Thermoanaerobacterium-Thermoanaerobacterium_thermosaccharolyticum
WP_073341560.1_Firmicutes-Clostridia-Thermoanaerobacterales-Thermoanaerobacteraceae-Caldanaerobius-Caldanaerobius_fijiensis
WP_025747238.1_Firmicutes-Clostridia-Clostridiales-Caldicoprobacteraceae-Caldicoprobacter-root
WP_147517632.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Clostridium-uncultured_Clostridium_sp.
WP_013780781.1_Firmicutes-Clostridia-Thermoanaerobacterales-Thermoanaerobacterales_Family_IV._Incertae_Sedis-Mahella-Mahella_australiensis
OGC35651.1_root-root-root-root-candidate_division_WOR-1_bacterium_RIFOXYB2_FULL_48_7
OGB87935.1_root-root-root-root-candidate_division_WOR-1_bacterium_RIFCSPHIGHO2_02_FULL_45_12
OGC38381.1_root-root-root-root-candidate_division_WOR-1_bacterium_RIFOXYD2_FULL_36_8
RJQ55819.1_Actinobacteria-Actinobacteria-root-root-root-Actinobacteria_bacterium
TDA29731.1_Euryarchaeota-Hadesarchaea-root-root-root-Hadesarchaea_archaeon
KXB06090.1_Euryarchaeota-root-root-root-root-candidate_division_MSBL1_archaeon_SCGC-AAA382F02
RZN42862.1_Euryarchaeota-Methanomicrobia-Methanophagales-root-root-Methanophagales_archaeon_ANME-1-THS
WP_144146101.1_Euryarchaeota-Candidatus_Methanoliparia-Candidatus_Methanoliparales-Candidatus_Methanoliviceraceae-root-Candidatus_Methanoliviera_sp._GoM_oil
WP_144183636.1_Euryarchaeota-Candidatus_Methanoliparia-Candidatus_Methanoliparales-Candidatus_Methanoliviceraceae-root-Candidatus_Methanoliviera_sp._GoM_asphalt
RZN70410.1_Euryarchaeota-Candidatus_Methanoliparia-Candidatus_Methanoliparales-Candidatus_Methanoliviceraceae-Candidatus_Methanoliviera-Candidatus_Methanoliviera_hydrocarbonicum
RZN65615.1_Euryarchaeota-Candidatus_Methanoliparia-Candidatus_Methanoliparales-Candidatus_Methanoliparaceae-Candidatus_Methanoliparum-Candidatus_Methanoliparum_thermophilum
TET17551.1_Chloroflexi-Dehalococcoidia-root-root-root-Dehalococcoidia_bacterium
TET14073.1_Actinobacteria-Actinobacteria-root-root-root-Actinobacteria_bacterium
PIU28763.1_Actinobacteria-root-root-root-Actinobacteria_bacterium_CG08_land_8_20_14_0_20_35_9
TET51614.1_Actinobacteria-Actinobacteria-root-root-root-Actinobacteria_bacterium
RLE09345.1_Candidatus_Aerophobetes-root-root-root-Candidatus_Aerophobetes_bacterium
OYT30080.1_Euryarchaeota-Thermoplasmata-Thermoplasmatales-root-root-Thermoplasmatales_archaeon_ex4572_165
RLF59100.1_Euryarchaeota-Thermoplasmata-root-root-root-Thermoplasmata_archaeon
RLE37786.1_Candidatus_Bipolaricaulota-root-root-root-Candidatus_Acetothermia_bacterium
YT1_767_01095
MP5_5_87_00763
YT1_182_00575
Yap2000.bin4.8_01331
Subgroup J
0.125

Supplementary Fig. 11: Phylogenetic analysis of *rnfD* gene (*Rhodobacter* nitrogen fixation complex subunit D). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 173 taxa and 339 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan, and green, respectively. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).


YT1_767_01096
MP5_5_87_00764
Subgroup J
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WP_012547502.1_Dictyoglomi-Dictyoglomia-Dictyoglomales-Dictyoglomaceae-Dictyoglomus-Dictyoglomus_thermophilum
WP_012583455.1_Dictyoglomi-Dictyoglomia-Dictyoglomales-Dictyoglomaceae-Dictyoglomus-Dictyoglomus_turgidum
PMQ02088.1_Dictyoglomi-Dictyoglomia-Dictyoglomales-Dictyoglomaceae-Dictyoglomus-Dictyoglomus_sp._NZ13-RE01
OGB67641.1_Calditrichaeota-Calditrichae-Calditrichales-Calditrichaceae-Caldithrix-Caldithrix_sp._RBG_13_44_9
RQV99273.1_Calditrichaeota-root-root-root-root-Calditrichaeota_bacterium
RPH99985.1_Calditrichaeota-root-root-root-root-Calditrichaeota_bacterium
OPX24730.1_Candidatus_Cloacimonetes-root-root-root-Candidatus_Cloacimonas-Candidatus_Cloacimonas_sp._4484_140
RLC48422.1_Candidatus_Cloacimonetes-root-root-root-root-Candidatus_Cloacimonetes_bacterium
KQC07371.1_Candidatus_Cloacimonetes-root-root-root-Candidatus_Cloacimonas-Candidatus_Cloacimonas_sp._SDB
PID27883.1_Candidatus_Cloacimonetes-root-root-root-root-Candidatus_Cloacimonetes_bacterium
RKZ08193.1_Candidatus_Fermentibacteria-root-root-root-root-Candidatus_Fermentibacteria_bacterium
OIO36695.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium_CG1_02_44_16
WP_128700472.1_Candidatus_Omnitrophica-root-root-root-Candidatus_Vampirococcus-Candidatus_Vampirococcus_archaeovorus
OGX17575.1_Candidatus_Omnitrophica-root-root-root-root-Omnitrophica_WOR_2_bacterium_RBG_13_44_8b
KPK42715.1_Candidatus_Omnitrophica-root-root-root-root-Omnitrophica_WOR_2_bacterium_SM23_29
RZN42863.1_Euryarchaeota-Methanomicrobia-Methanophagales-root-root-Methanophagales_archaeon_ANME-1-THS
KAF0182374.1_Nitrospirae-root-root-root-root-Nitrospirae_bacterium
WP_085050687.1_Nitrospirae-root-root-root-root-Nitrospirae_bacterium_HCH-1
OGW35650.1_Nitrospirae-root-root-root-root-Nitrospirae_bacterium_GWC2_56_14
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WP_122628777.1_Firmicutes-Negativicutes-Veillonellales-Veillonellaceae-Lucifera-Lucifera_butyrica
WP_007288777.1_Firmicutes-Negativicutes-Selenomonadales-Sporomusaceae-Thermosinus-Thermosinus_carboxydivorans
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ACB84562.1_Firmicutes-Clostridia-Natranaerobiales-Natranaerobiaceae-Natranaerobius-Natranaerobius_thermophilus
WP_012446979.1_Firmicutes-Clostridia-Natranaerobiales-Natranaerobiaceae-Natranaerobius-Natranaerobius_thermophilus
WP_012447542.1_Firmicutes-Clostridia-Natranaerobiales-Natranaerobiaceae-Natranaerobius-Natranaerobius_thermophilus
WP_158212338.1_Firmicutes-Clostridia-Natranaerobiales-Natranaerobiaceae-Natranaerobius-Natranaerobius_trueperi
PKM81935.1_Firmicutes-root-root-root-root-Firmicutes_bacterium_HGW-Firmicutes-13
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OGC08110.1_root-root-root-root-root-candidate_division_WOR-1_bacterium_RIFOXYA12_FULL_36_13
OPY89867.1_Proteobacteria-Deltaproteobacteria-Syntrophobacterales-Syntrophaceae-root-Syntrophaceae_bacterium_PtaU1.Bin231
OGC11595.1_root-root-root-root-root-candidate_division_WOR-1_bacterium_RIFOXYA12_FULL_52_29
OGC03579.1_root-root-root-root-root-candidate_division_WOR-1_bacterium_RIFOXYA12_FULL_43_27
OGB87936.1_root-root-root-root-root-candidate_division_WOR-1_bacterium_RIFCSPHIGHO2_02_FULL_45_12
CG11_big_fil_rev_8_21_14_0_20_43_8_00358
RJP72042.1_Candidatus_Abyssubacteria-root-root-root-root-Candidatus_Abyssubacteria_bacterium_SURF_17
RJP22871.1_Candidatus_Abyssubacteria-root-root-root-root-Candidatus_Abyssubacteria_bacterium_SURF_5
PIR65574.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium_CG_4_10_14_0_8_um_filter_43_18
WP_066894185.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Clostridium-Clostridium_nigeriense
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WP_070956773.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Clostridium-Clostridium_perfringens
WP_012869097.1_Synergistetes-Synergistia-Synergistales-Synergistaceae-Thermanaerovibrio-Thermanaerovibrio_acidaminovorans
WP_132774934.1_Firmicutes-Clostridia-Clostridiales-Syntrophomonadaceae-Thermohydrogenium-Thermohydrogenium_kirishiense
WP_159034385.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Clostridium-Clostridium_botulinum
WP_078697103.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Caloramator-Caloramator_quimbayensis
WP_106063979.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Clostridium-Clostridium_liquoris
WP_051540118.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Clostridium-Clostridium_ihumii
WP_150843381.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Clostridium-Clostridium_thiosulfatireducens
WP_006441491.1_Firmicutes-Clostridia-Clostridiales-Lachnospiraceae-Lachnoclostridium-_Clostridium__hylemonae
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WP_075171586.1_Proteobacteria-Gammaproteobacteria-Oceanospirillales-Oceanospirillaceae-Neptunomonas-Neptunomonas_phycophila
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WP_090224170.1_Bacteroidetes-Flavobacteriia-Flavobacteriales-Flavobacteriaceae-Lutibacter-Lutibacter_maritimus
OFY35247.1_Bacteroidetes-root-root-root-root-Bacteroidetes_bacterium_GWF2_35_48
WP_117902572.1_Bacteroidetes-Bacteroidia-Bacteroidales-Bacteroidaceae-Bacteroides-Bacteroides_stercoris
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TET14074.1_Actinobacteria-Actinobacteria-root-root-root-Actinobacteria_bacterium
RZN70409.1_Euryarchaeota-Candidatus_Methanoliparia-Candidatus_Methanoliparales-Candidatus_Methanollivieraceae-Candidatus_Methanolliviera-Candidatus_Methanolliviera_hydrocarbonicum
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TVQ20730.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-root-Spirochaetaceae_bacterium
TKJ45343.1_Candidatus_Aerophobetes-root-root-root-root-Candidatus_Aerophobetes_bacterium_Ae_b3b
TET07880.1_Candidatus_Aerophobetes-root-root-root-root-Candidatus_Aerophobetes_bacterium
TET85655.1_Candidatus_Aerophobetes-root-root-root-root-Candidatus_Aerophobetes_bacterium
RKY60827.1_Candidatus_Latescibacteria-root-root-root-root-Candidatus_Latescibacteria_bacterium
OQX56413.1_Candidatus_Cloacimonetes-root-root-root-Candidatus_Cloacimonas-Candidatus_Cloacimonas_sp._4484_209
TET76404.1_Candidatus_Cloacimonetes-root-root-root-root-Candidatus_Cloacimonetes_bacterium
RKY27176.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium
OQX79010.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium_4484_70.1
RKY41217.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium
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TET30492.1_Candidatus_Aerophobetes-root-root-root-root-Candidatus_Aerophobetes_bacterium
KAB2843812.1_Ignavibacteriae-Ignavibacteria-Ignavibacteriales-Melioribacteraceae-root-Melioribacteraceae_bacterium
OGU54507.1_Ignavibacteriae-Ignavibacteria-root-root-root-Ignavibacteria_bacterium_RBG_13_36_8
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OGP24002.1_Proteobacteria-Deltaproteobacteria-root-root-root-Deltaproteobacteria_bacterium_GWB2_55_19
OGP09972.1_Proteobacteria-Deltaproteobacteria-root-root-root-Deltaproteobacteria_bacterium_GWA2_42_85
RKX98452.1_Spirochaetes-root-root-root-root-Spirochaetes_bacterium
RKX95937.1_Spirochaetes-root-root-root-root-Spirochaetes_bacterium
RKY48129.1_Candidatus_Marinimicrobia-root-root-root-root-Candidatus_Marinimicrobia_bacterium
RKY47210.1_Candidatus_Marinimicrobia-root-root-root-root-Candidatus_Marinimicrobia_bacterium
RKY54293.1_Candidatus_Marinimicrobia-root-root-root-root-Candidatus_Marinimicrobia_bacterium
RKY99829.1_Candidatus_Hydrothermae-root-root-root-root-Candidatus_Hydrothermae_bacterium
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RKY98820.1_Candidatus_Hydrothermae-root-root-root-root-Candidatus_Hydrothermae_bacterium
OQX82629.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium_4484_49
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OGL11413.1_Candidatus_Rokubacteria-root-root-root-root-Candidatus_Rokubacteria_bacterium_RIFCSPLOWO2_02_FULL_72_37
OGK79754.1_Candidatus_Rokubacteria-root-root-root-root-Candidatus_Rokubacteria_bacterium_GWC2_70_16
OGL10473.1_Candidatus_Rokubacteria-root-root-root-root-Candidatus_Rokubacteria_bacterium_RIFCSPLOWO2_02_FULL_73_56
TFG52618.1_Gemmatimonadetes-Gemmatimonadetes-Gemmatimonadales-root-root-Gemmatimonadales_bacterium
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OGQ69016.1_Proteobacteria-Deltaproteobacteria-root-root-root-Deltaproteobacteria_bacterium_RIFCSPLOWO2_12_FULL_50_11
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WP_146530853.1_Planctomycetes-Planctomycetia-Pirellulales-Pirellulaceae-Novipirellula-Novipirellula_artificiosorum
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BBO85365.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-Desulfosarcina-Desulfosarcina_ovata
RLC33877.1_Proteobacteria-Deltaproteobacteria-root-root-root-Deltaproteobacteria_bacterium
RJP80031.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-root-Desulfobacteraceae_bacterium
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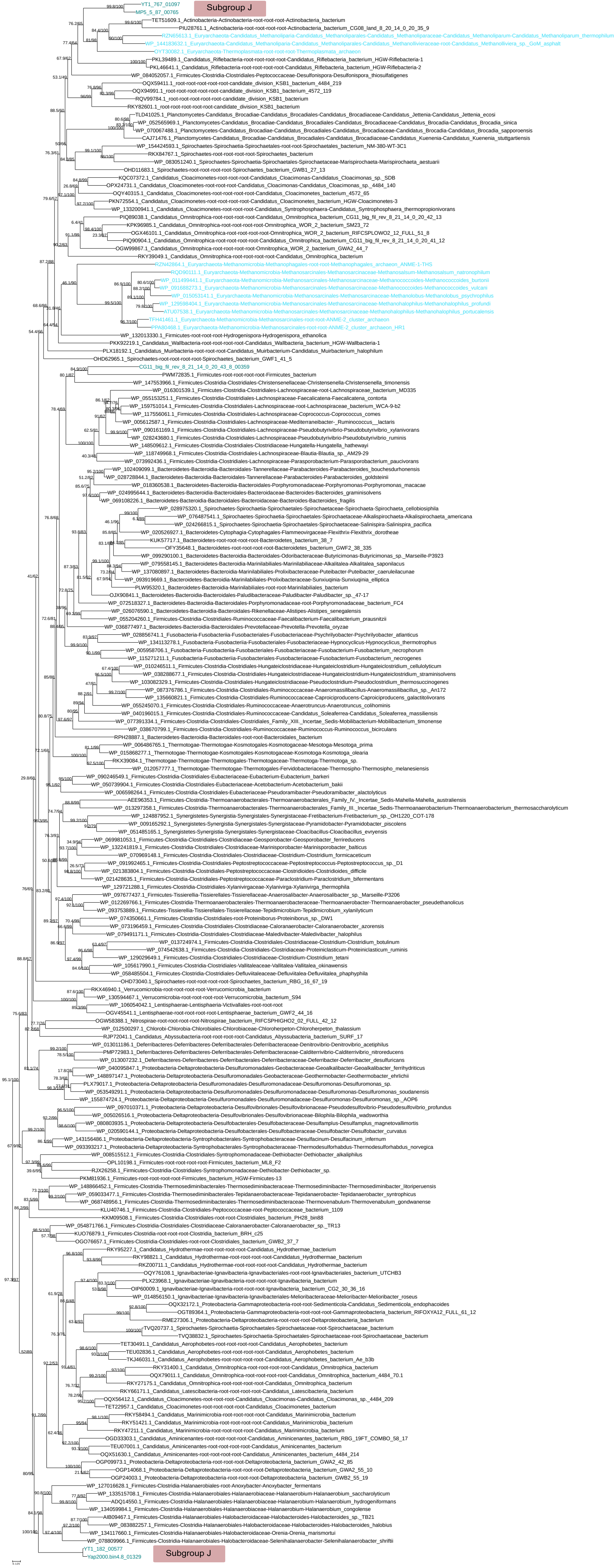
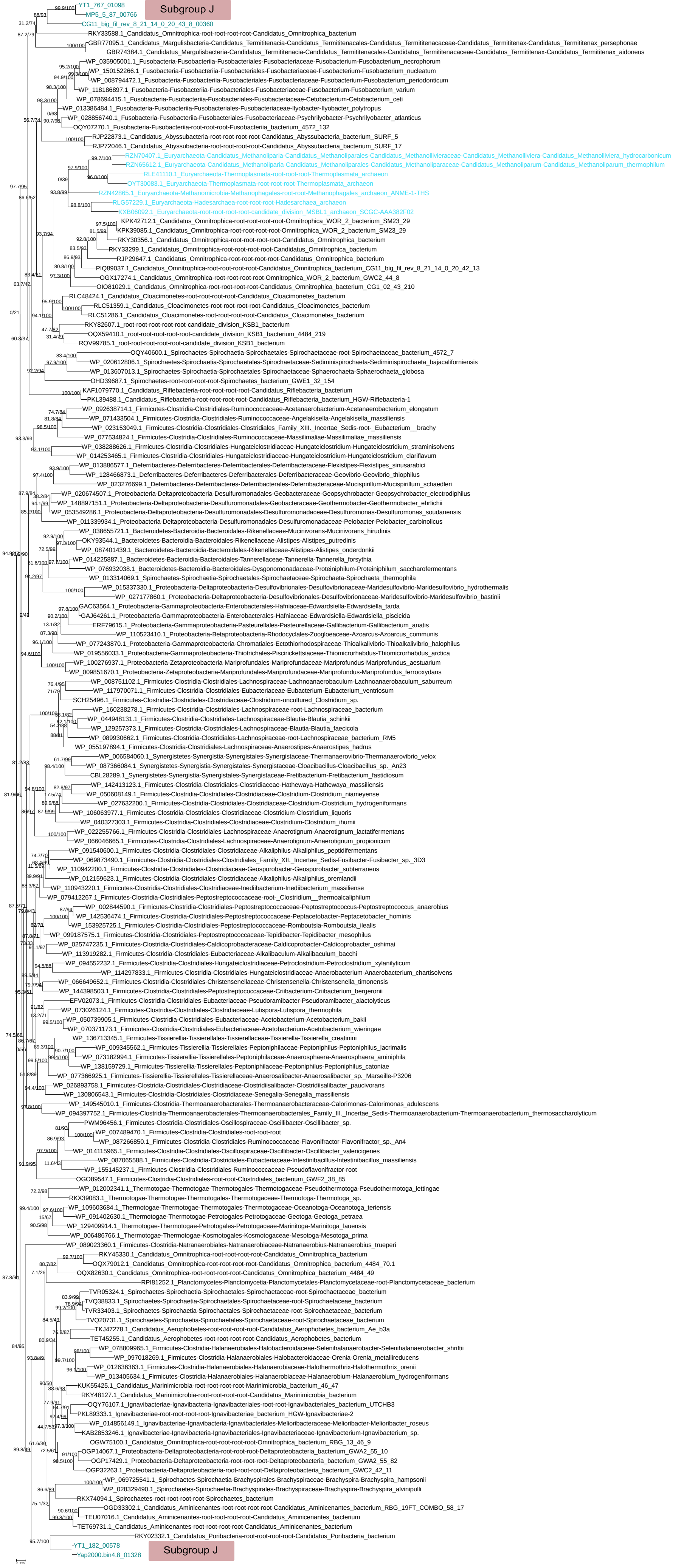
WP_052563447.1_Planctomycetes-Candidatus_Brocadiae-Candidatus_Brocadiales-Candidatus_Brocadiaceae-Candidatus_Brocadia-Candidatus_Brocadia_sinica
BAL56441.1_Candidatus_Bipolaricaulota-root-root-root-root-uncultured_Acetothermia_bacterium
YT1_182_00576
Yap2000.bin4.8_01330
Subgroup J
0.125

Supplementary Fig. 12: Phylogenetic analysis of *rnfG* gene (*Rhodobacter* nitrogen fixation complex subunit G). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 192 taxa and 231 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan, and green, respectively. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).



Supplementary Fig. 13: Phylogenetic analysis of *rnfE* gene (*Rhodobacter* nitrogen fixation complex subunit E). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 198 taxa and 233 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan, and green, respectively. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).


Subgroup J
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CG11_big_fil_rev_8_21_14_0_20_43_8_00360
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GBR77095.1_Candidatus_Margulisbacteria-Candidatus_Termitenicacia-Candidatus_Termitenicales-Candidatus_Termitenicaceae-Candidatus_Termitenitenax-Candidatus_Termitenitenax_persephonae
GBR74384.1_Candidatus_Margulisbacteria-Candidatus_Termitenicacia-Candidatus_Termitenicales-Candidatus_Termitenicaceae-Candidatus_Termitenitenax-Candidatus_Termitenitenax_aidoneus
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WP_150152266.1_Fusobacteria-Fusobacteriia-Fusobacteriales-Fusobacteriaceae-Fusobacterium-Fusobacterium_nucleatum
WP_008794472.1_Fusobacteria-Fusobacteriia-Fusobacteriales-Fusobacteriaceae-Fusobacterium-Fusobacterium_periodonticum
WP_118186897.1_Fusobacteria-Fusobacteriia-Fusobacteriales-Fusobacteriaceae-Fusobacterium-Fusobacterium_varium
WP_078694415.1_Fusobacteria-Fusobacteriia-Fusobacteriales-Fusobacteriaceae-Cetobacterium-Cetobacterium_ceti
WP_013386484.1_Fusobacteria-Fusobacteriia-Fusobacteriales-Fusobacteriaceae-Ilyobacter-Ilyobacter_polytropus
WP_028856740.1_Fusobacteria-Fusobacteriia-Fusobacteriales-Fusobacteriaceae-Psychrilyobacter-Psychrilyobacter_atlanticus
OQY07270.1_Fusobacteria-Fusobacteriia-root-root-root-Fusobacteriia_bacterium_4572_132
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RJP72046.1_Candidatus_Abyssubacteria-root-root-root-root-Candidatus_Abyssubacteria_bacterium_SURF_17
RZN70407.1_Euryarchaeota-Candidatus_Methanoliparia-Candidatus_Methanoliparales-Candidatus_Methanolivieraceae-Candidatus_Methanoliviera-Candidatus_Methanoliviera_hydrocarbonicum
RZN65612.1_Euryarchaeota-Candidatus_Methanoliparia-Candidatus_Methanoliparales-Candidatus_Methanoliparaceae-Candidatus_Methanoliparum-Candidatus_Methanoliparum_thermophilum
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OYT30083.1_Euryarchaeota-Thermoplasmata-root-root-root-Thermoplasmata_archaeon
RZN42865.1_Euryarchaeota-Methanomicrobia-Methanophagales-root-root-Methanophagales_archaeon_ANME-1-THS
RLG57229.1_Euryarchaeota-Hadesarchaea-root-root-root-Hadesarchaea_archaeon
KXB06092.1_Euryarchaeota-root-root-root-root-candidate_division_MSBL1_archaeon_SCGC-AAA382F02
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KPK39085.1_Candidatus_Omnitrophica-root-root-root-root-Omnitrophica_WOR_2_bacterium_SM23_29
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RKY33299.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium
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RLC51286.1_Candidatus_Cloacimonetes-root-root-root-root-Candidatus_Cloacimonetes_bacterium
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OQX59410.1_root-root-root-root-root-candidate_division_KSB1_bacterium_4484_219
RQV99785.1_root-root-root-root-root-candidate_division_KSB1_bacterium
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WP_013607013.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-Sphaerochaeta-Sphaerochaeta_globosa
OHD39687.1_Spirochaetes-root-root-root-root-Spirochaetes_bacterium_GWE1_32_154
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WP_130806543.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Senegalia-Senegalia_massiliensis
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OQX82630.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium_4484_49
RPI81252.1_Planctomycetes-Planctomycetia-Planctomycetales-Planctomycetaceae-root-Planctomycetaceae_bacterium
TVR05324.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-root-Spirochaetaceae_bacterium
TVQ38833.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-root-Spirochaetaceae_bacterium
TVR33403.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-root-Spirochaetaceae_bacterium
TVQ20731.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-root-Spirochaetaceae_bacterium
TKJ47278.1_Candidatus_Aerophobetes-root-root-root-root-Candidatus_Aerophobetes_bacterium_Ae_b3a
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OGP14067.1_Proteobacteria-Deltaproteobacteria-root-root-root-Deltaproteobacteria_bacterium_GWA2_55_10
OGP17429.1_Proteobacteria-Deltaproteobacteria-root-root-root-Deltaproteobacteria_bacterium_GWA2_55_82
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OGD33302.1_Candidatus_Aminicenantes-root-root-root-root-Candidatus_Aminicenantes_bacterium_RBG_19FT_COMBO_58_17
TEU07016.1_Candidatus_Aminicenantes-root-root-root-root-Candidatus_Aminicenantes_bacterium
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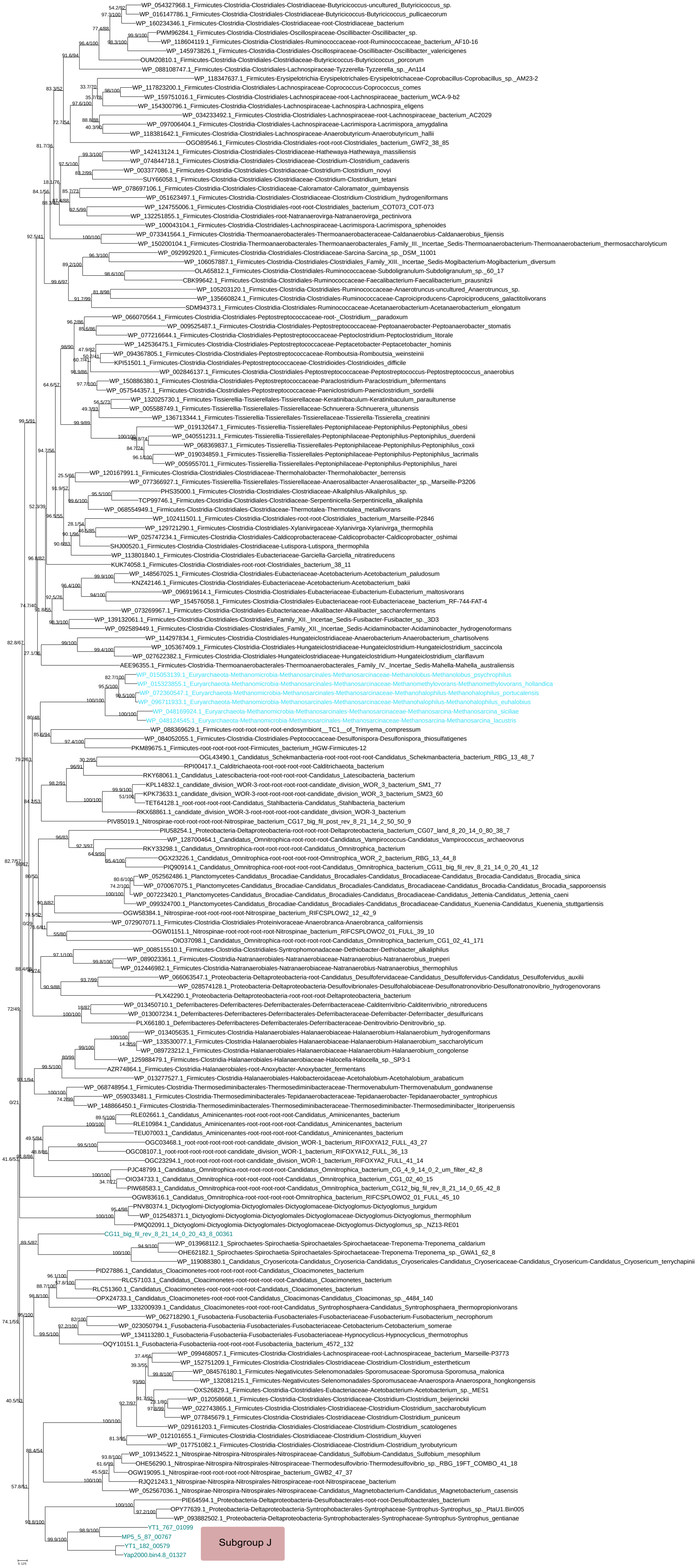
RKY02332.1_Candidatus_Poribacteria-root-root-root-root-Candidatus_Poribacteria_bacterium
YT1_182_00578
Yap2000.bin4.8_01328
Subgroup J
0.125

Supplementary Fig. 14: Phylogenetic analysis of *rnfA* gene (*Rhodobacter* nitrogen fixation complex subunit A). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 166 taxa and 186 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan, and green, respectively. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).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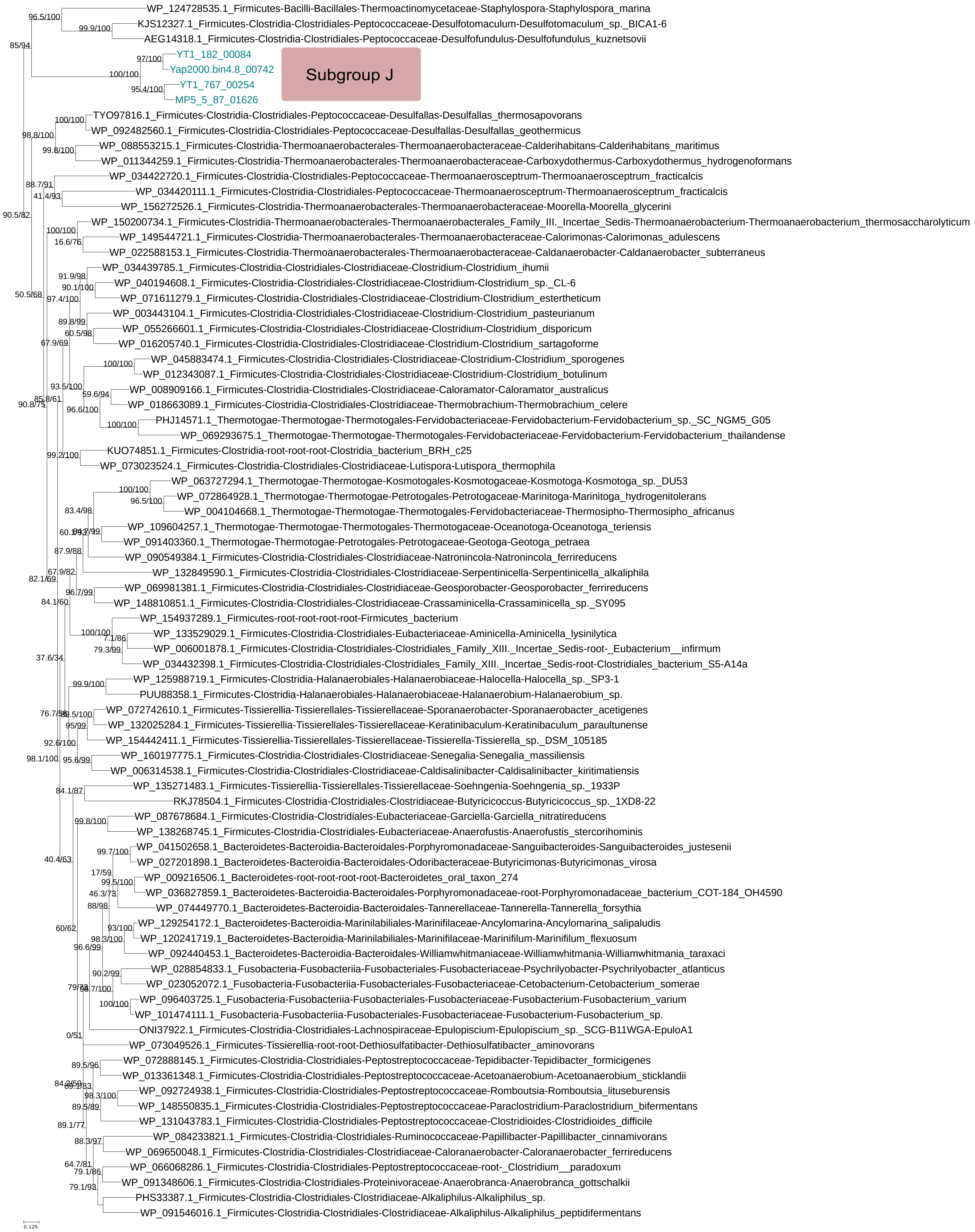
YT1_767_01099
MP5_5_87_00767
YT1_182_00579
Yap2000.bin4.8_01327
Subgroup J
0.125

Supplementary Fig. 15: Phylogenetic analysis of *rnfB* gene (*Rhodobacter* nitrogen fixation complex subunit B). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 170 taxa and 330 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan, and green, respectively. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).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97/100
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100/100
Subgroup J
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98.8/100
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90.5/82
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85.8/61
90.8/75
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83.4/98
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94.7/99
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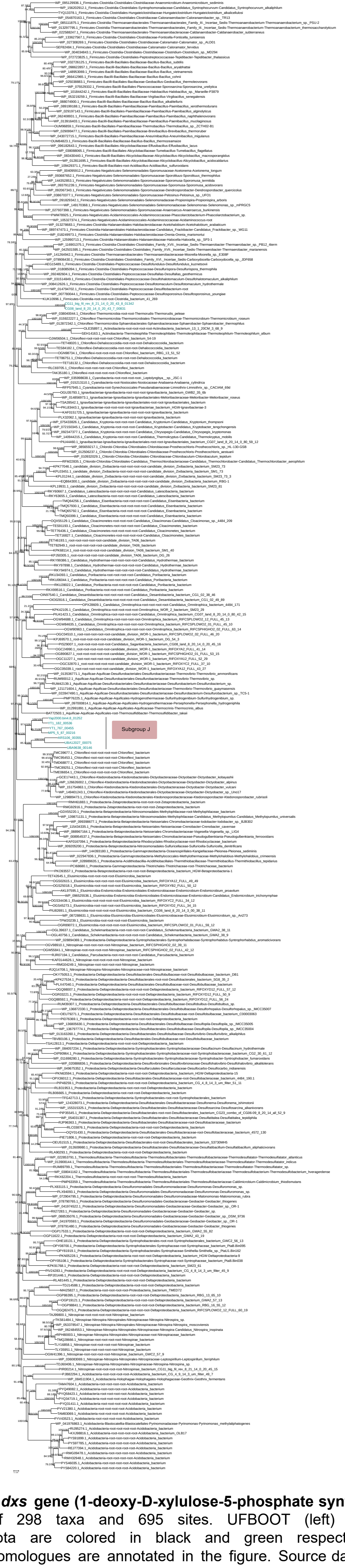
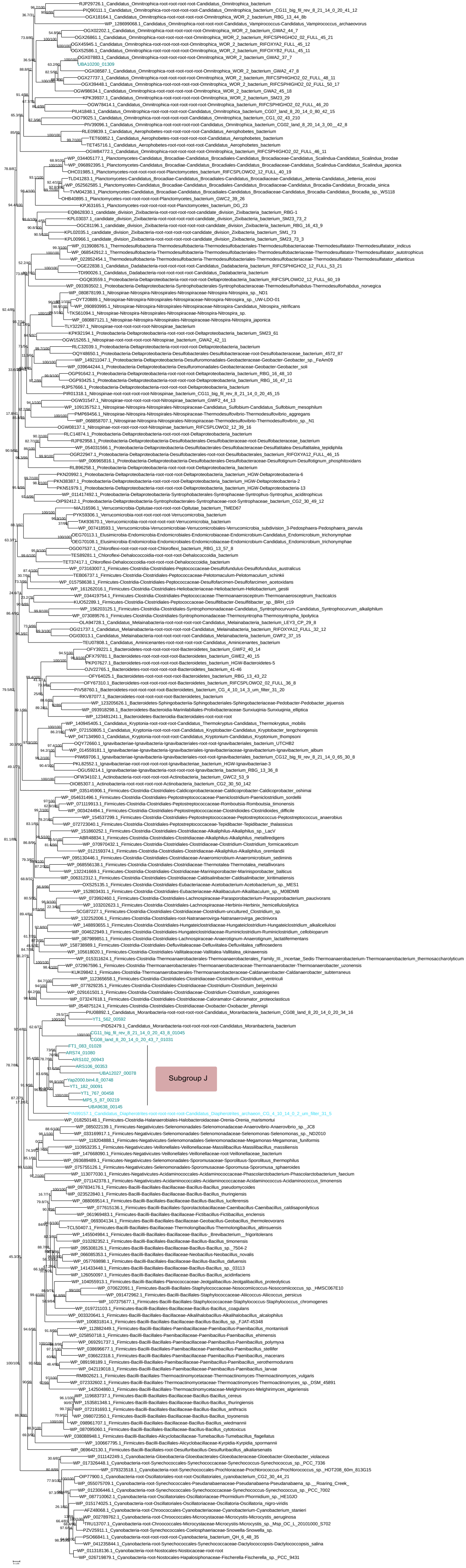
0.125

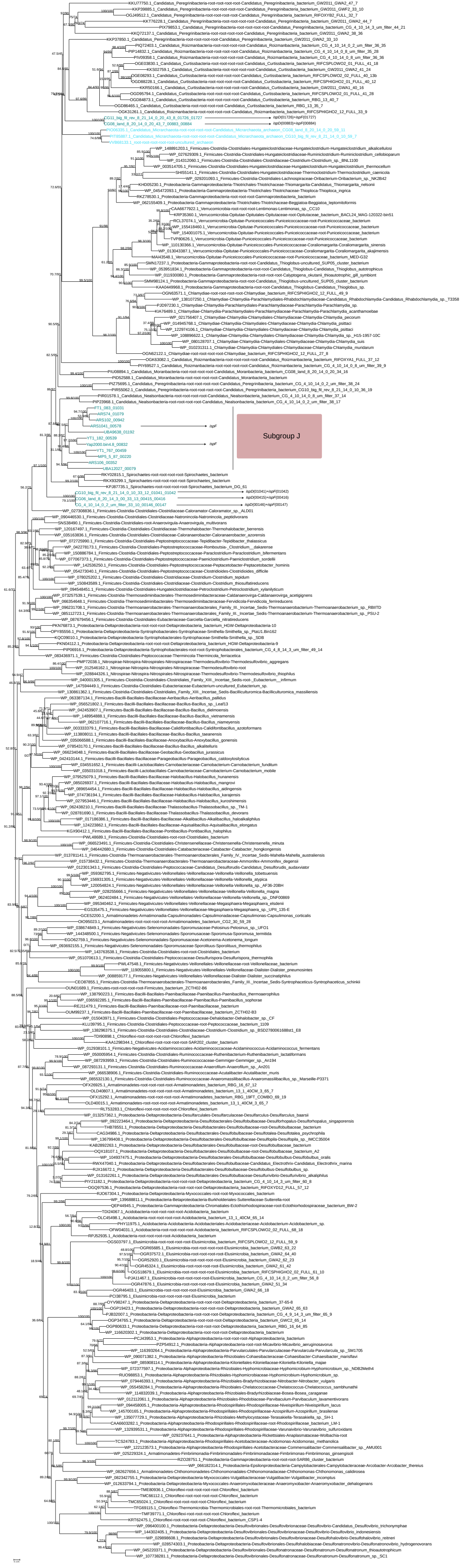
Supplementary Fig. 16: Phylogenetic analysis of *bcd* gene (butyryl-CoA dehydrogenase). The tree was unrooted and inferred using IQ-Tree LG +C20+G model on an alignment of 80 taxa and 356 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, and Woesearchaeota are colored in black and green respectively. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).



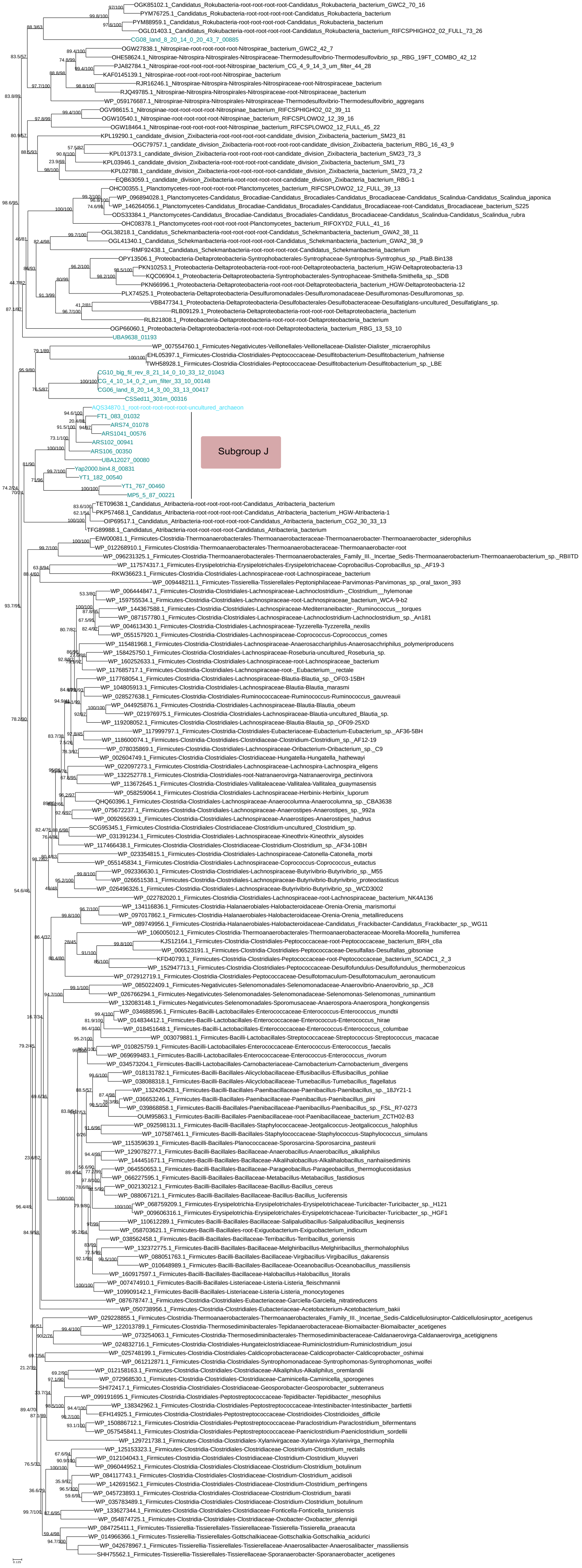
Supplementary Fig. 17: Phylogenetic analysis of *dxs* gene (1-deoxy-D-xylulose-5-phosphate synthase). The tree was unrooted and inferred using IQ-Tree LG+C50+F+I+G model on an alignment of 298 taxa and 695 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria and Woesearchaeota are colored in black and green respectively. Scale bar shows the number of average substitutions per site. Woesearchaeota subgroup J homologues are annotated in the figure. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).



Supplementary Fig. 18: Phylogenetic analysis of *dxr* gene (1-deoxy-D-xylulose 5-phosphate reductoisomerase). The tree was unrooted and inferred using IQ-Tree LG+C60+F+I+G model on an alignment of 232 taxa and 403 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Scale bar shows the number of average substitutions per site. Bacteria, Archaea and Woesearchaeota are colored in black, cyan andgreen respectively. Woesearchaeota subgroup J is annotated in the figure. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).



Supplementary Fig. 19: Phylogenetic analysis of *ispD/F* gene (2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase/2-C-methyl-D-erythritol 2,4 cyclodiphosphate synthase). The tree was unrooted and inferred using IQ-Tree LG+C20+F+G model on an alignment of 258 taxa and 465 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan and green respectively. Scale bar shows the number of average substitutions per site. Woesearchaeota subgroup J homologues are annotated in the figure. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).


OGK85102.1_Candidatus_Rokubacteria-root-root-root-root-Candidatus_Rokubacteria_bacterium_GWC2_70_16
PYM76725.1_Candidatus_Rokubacteria-root-root-root-root-Candidatus_Rokubacteria_bacterium
PYM88959.1_Candidatus_Rokubacteria-root-root-root-root-Candidatus_Rokubacteria_bacterium
OGL01403.1_Candidatus_Rokubacteria-root-root-root-root-Candidatus_Rokubacteria_bacterium_RIFCSPHIGHO2_02_FULL_73_26
CG08_land_8_20_14_0_20_43_7_00885
OGW27838.1_Nitrospirae-root-root-root-root-Nitrospirae_bacterium_GWC2_42_7
OHE58624.1_Nitrospirae-Nitrospira-Nitrospirales-Nitrospiraceae-Thermodesulfovibrio-Thermodesulfovibrio_sp._RBG_19FT_COMBO_42_12
PJA82784.1_Nitrospirae-root-root-root-root-Nitrospirae_bacterium_CG_4_9_14_3_um_filter_44_28
KAF0145139.1_Nitrospirae-root-root-root-root-Nitrospirae_bacterium
RJR16246.1_Nitrospirae-Nitrospira-Nitrospirales-Nitrospiraceae-root-Nitrospiraceae_bacterium
RJQ49785.1_Nitrospirae-Nitrospira-Nitrospirales-Nitrospiraceae-root-Nitrospiraceae_bacterium
WP_059176687.1_Nitrospirae-Nitrospira-Nitrospirales-Nitrospiraceae-Thermodesulfovibrio-Thermodesulfovibrio_aggregans
OGV98615.1_Nitrospinae-root-root-root-root-Nitrospinae_bacterium_RIFCSPHIGHO2_02_39_11
OGW10540.1_Nitrospinae-root-root-root-root-Nitrospinae_bacterium_RIFCSPLOWO2_12_39_16
OGW18464.1_Nitrospinae-root-root-root-root-Nitrospinae_bacterium_RIFCSPLOWO2_12_FULL_45_22
KPL19290.1_candidate_division_Zixibacteria-root-root-root-root-candidate_division_Zixibacteria_bacterium_SM23_81
OGC79757.1_candidate_division_Zixibacteria-root-root-root-root-candidate_division_Zixibacteria_bacterium_RBG_16_43_9
KPL01373.1_candidate_division_Zixibacteria-root-root-root-root-candidate_division_Zixibacteria_bacterium_SM23_73_3
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KPL02788.1_candidate_division_Zixibacteria-root-root-root-root-candidate_division_Zixibacteria_bacterium_SM23_73_2
EQB63059.1_candidate_division_Zixibacteria-root-root-root-root-candidate_division_Zixibacteria_bacterium_RBG-1
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TWH58928.1_Firmicutes-Clostridia-Clostridiales-Peptococcaceae-Desulfitobacterium-Desulfitobacterium_sp._LBE
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CSSed11_301m_00316
AQS34870.1_root-root-root-root-root-uncultured_archaeon
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ARS74_01078
ARS1041_00576
ARS102_00941
ARS106_00350
UBA12027_00080
Yap2000.bin4.8_00831
YT1_182_00540
YT1_767_00460
MP5_5_87_00221
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WP_064550653.1_Firmicutes-Bacilli-Bacillales-Bacillaceae-Parageobacillus-Parageobacillus_thermoglucosidasius
WP_066227595.1_Firmicutes-Bacilli-Bacillales-Bacillaceae-Metabacillus-Metabacillus_fastidiosus
WP_002130212.1_Firmicutes-Bacilli-Bacillales-Bacillaceae-Bacillus-Bacillus_cereus
WP_088067121.1_Firmicutes-Bacilli-Bacillales-Bacillaceae-Bacillus-Bacillus_luciferensis
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WP_073254063.1_Firmicutes-Clostridia-Thermosediminibacterales-Thermosediminibacteraceae-Caldanaerovirga-Caldanaerovirga_acetigignens
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WP_012158163.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Alkaliphilus-Alkaliphilus_oremlandii
WP_072968530.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Caminicella-Caminicella_sporogenes
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WP_138342962.1_Firmicutes-Clostridia-Clostridiales-Peptostreptococcaceae-Intestinibacter-Intestinibacter_bartlettii
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WP_125153323.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Clostridium-Clostridium_rectalis
WP_012104043.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Clostridium-Clostridium_kluyveri
WP_096044952.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Clostridium-Clostridium_botulinum
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WP_084725411.1_Firmicutes-Tissierellia-Tissierellales-Tissierellaceae-Tissierella-Tissierella_praeacuta
WP_014966366.1_Firmicutes-Tissierellia-Tissierellales-Gottschalkiaceae-Gottschalkia-Gottschalkia_acidurici
WP_042678967.1_Firmicutes-Tissierellia-Tissierellales-Tissierellaceae-Anaerosalibacter-Anaerosalibacter_massiliensis
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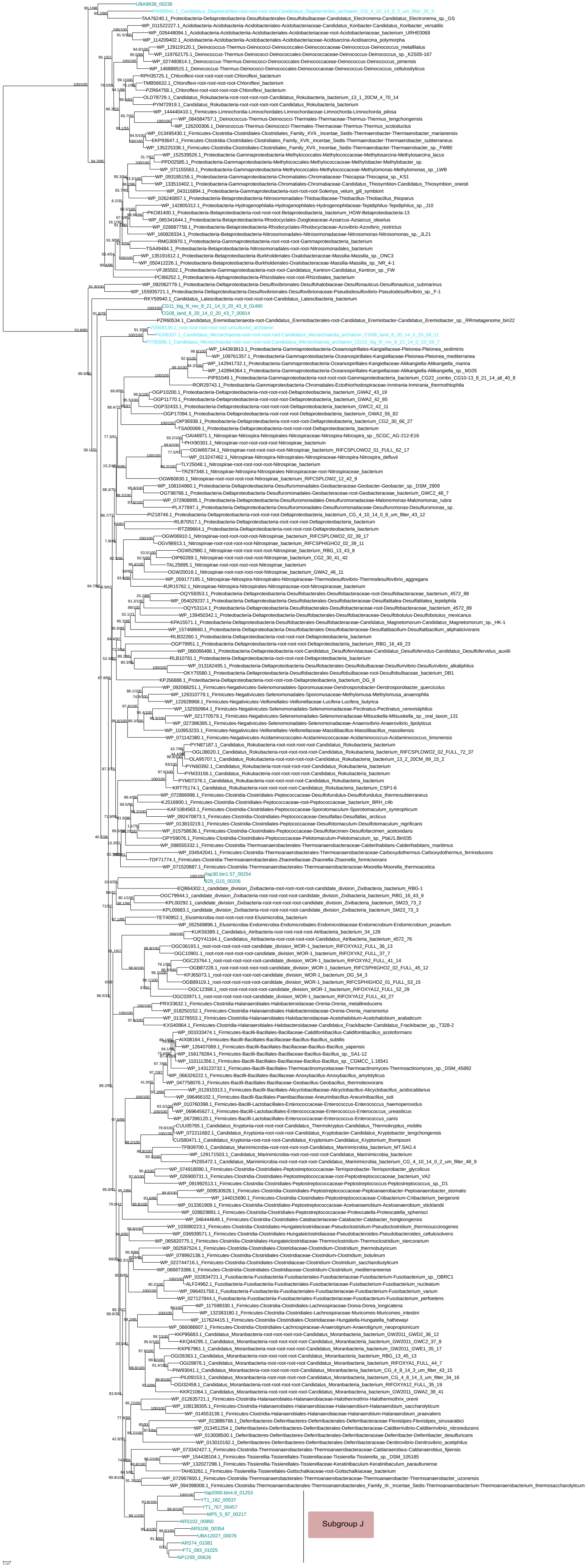
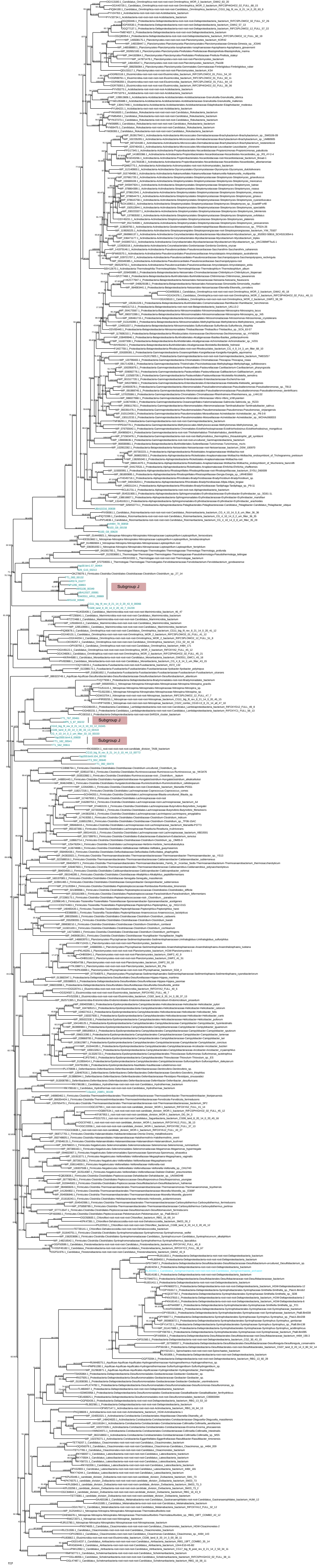
0.125

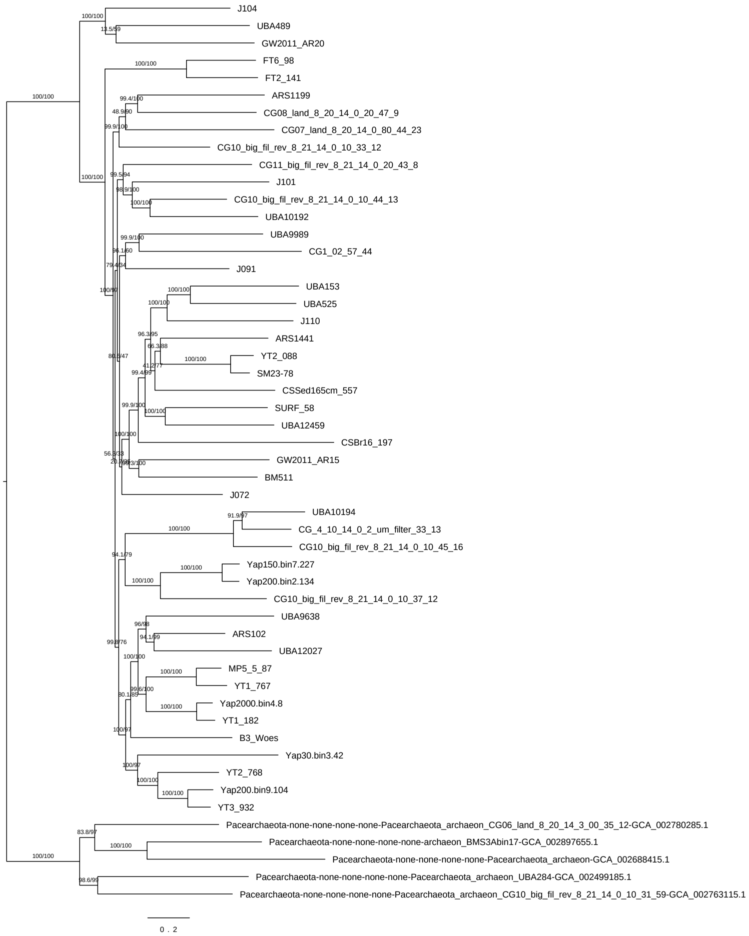
Supplementary Fig. 20: Phylogenetic analysis of *ispE* gene (4-diphosphocytidyl-2-C-methyl-D-erythritol kinase). The tree was unrooted and inferred using IQ-Tree LG+C60+F+I+G model on an alignment of 178 taxa and 322 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan and green respectively. Scale bar shows the number of average substitutions per site. Woesearchaeota subgroup J homologues are annotated in the figure. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).



Supplementary Fig. 21: Phylogenetic analysis of *ispG* gene (4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase). The tree was unrooted and inferred using IQ-Tree LG+C20+F+G model on an alignment of 217 taxa and 445 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan and green respectively. Woesearchaeota subgroup J homologues are annotated in the figure. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).



Supplementary Fig. 22: Phylogenetic analysis of *ispH* gene (4-hydroxy-3-methylbut-2-enyl diphosphate reductase). The tree was unrooted and inferred using IQ-Tree LG+C60+F+I+G model on an alignment of 410 taxa and 856 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan and green, respectively. Scale bar shows the number of average substitutions per site. Woesearchaeota subgroup J homologues are annotated in the figure. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).


J104
100/100
13.5/59
UBA489
GW2011_AR20
FT6_98
100/100
FT2_141
100/100
ARS1199
99.4/100
48.9/90
CG08_land_8_20_14_0_20_47_9
99.9/100
CG07_land_8_20_14_0_80_44_23
CG10_big_fil_rev_8_21_14_0_10_33_12
CG11_big_fil_rev_8_21_14_0_20_43_8
99.5/94
100/100
J101
98.9/100
CG10_big_fil_rev_8_21_14_0_10_44_13
100/100
UBA10192
UBA9989
99.9/100
CG1_02_57_44
96.1/60
79.4/34
J091
UBA153
100/100
100/97
100/100
UBA525
J110
ARS1441
96.3/95
66.3/88
YT2_088
100/100
80.6/47
41.2/77
SM23-78
99.4/99
CSSed165cm_557
SURF_58
99.9/100
100/100
UBA12459
100/100
CSBr16_197
56.3/33
GW2011_AR15
20.7/35
99.3/100
BM511
J072
UBA10194
91.9/97
CG_4_10_14_0_2_um_filter_33_13
100/100
CG10_big_fil_rev_8_21_14_0_10_45_16
94.1/79
Yap150.bin7.227
100/100
Yap200.bin2.134
100/100
CG10_big_fil_rev_8_21_14_0_10_37_12
UBA9638
96/98
ARS102
94.1/99
99.8/76
UBA12027
100/100
MP5_5_87
100/100
YT1_767
99.6/100
80.1/85
Yap2000.bin4.8
100/100
YT1_182
100/97
B3_Woes
Yap30.bin3.42
100/97
YT2_768
100/100
Yap200.bin9.104
100/100
YT3_932
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83.8/97
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100/100
100/100
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98.6/99
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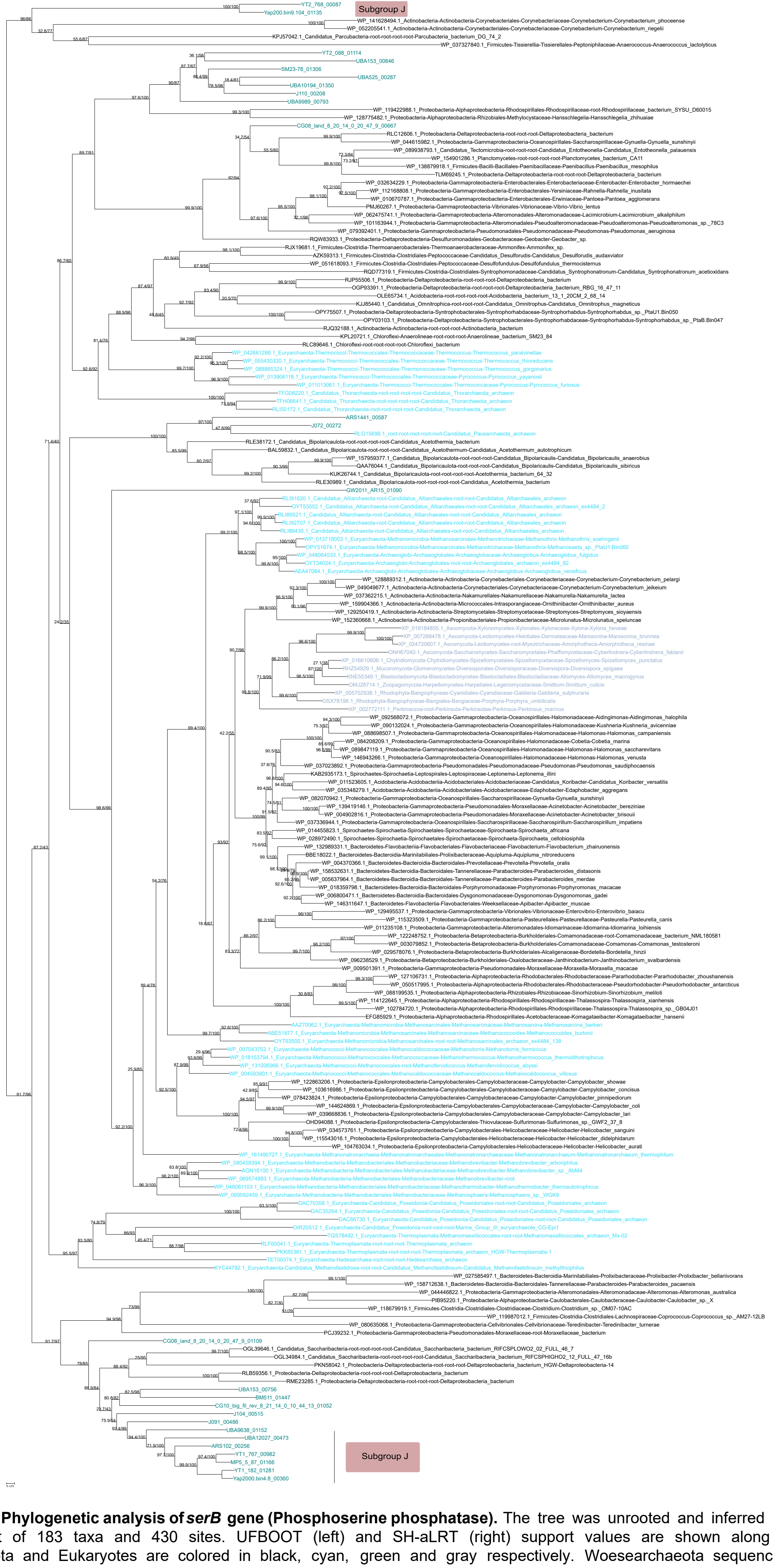
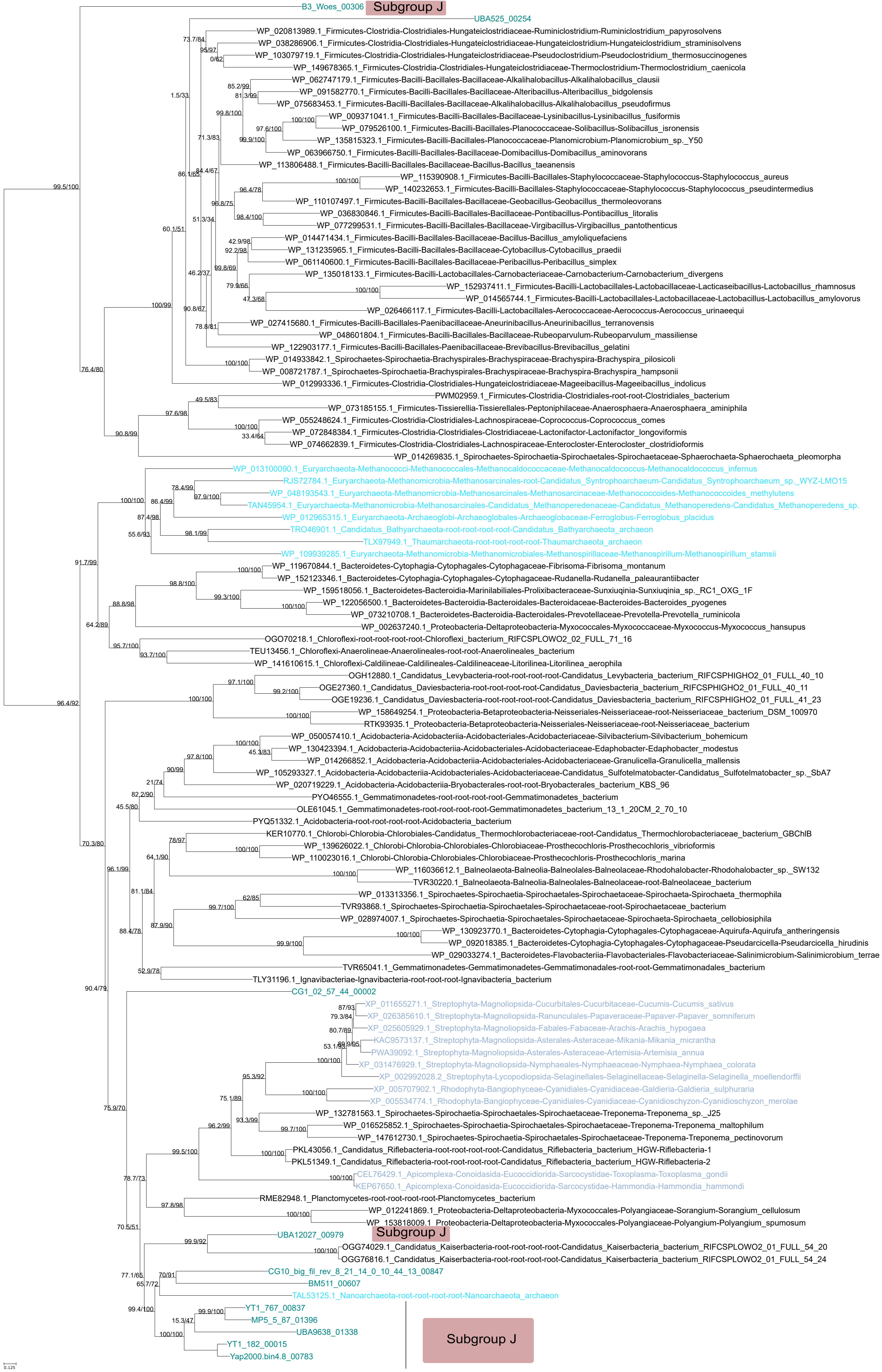
0 . 2

Supplementary Fig. 23: Full tree used in Fig. 5a. The tree is rooted using Pacearchaeota and based on an alignment of 52 taxa and 10896 sites. Raw data are available via figshare (see Data availability for more details). Scale bar shows the number of average substitutions per site.



Supplementary Fig. 24: Phylogenetic analysis of *serB* gene (Phosphoserine phosphatase). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 183 taxa and 430 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea, Woesearchaeota and Eukaryotes are colored in black, cyan, green and gray respectively. Woesearchaeota sequences are selected from 47 MAGs used in the inference of proteome content change history. Woesearchaeota subgroup J homologues are annotated in the figure. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).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WP_075683453.1_Firmicutes-Bacilli-Bacillales-Bacillaceae-Alkalihalobacillus-Alkalihalobacillus_pseudofirmus
WP_009371041.1_Firmicutes-Bacilli-Bacillales-Bacillaceae-Lysinibacillus-Lysinibacillus_fusiformis
WP_079526100.1_Firmicutes-Bacilli-Bacillales-Planococcaceae-Solibacillus-Solibacillus_isronensis
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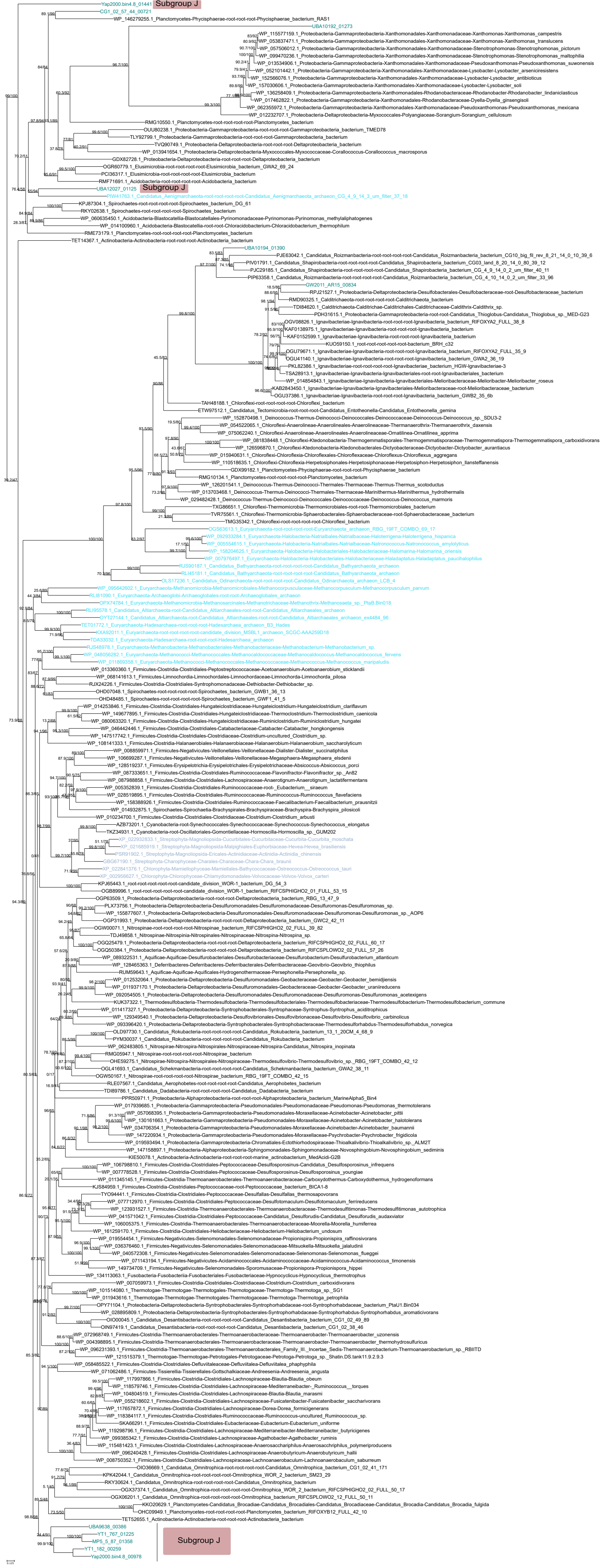
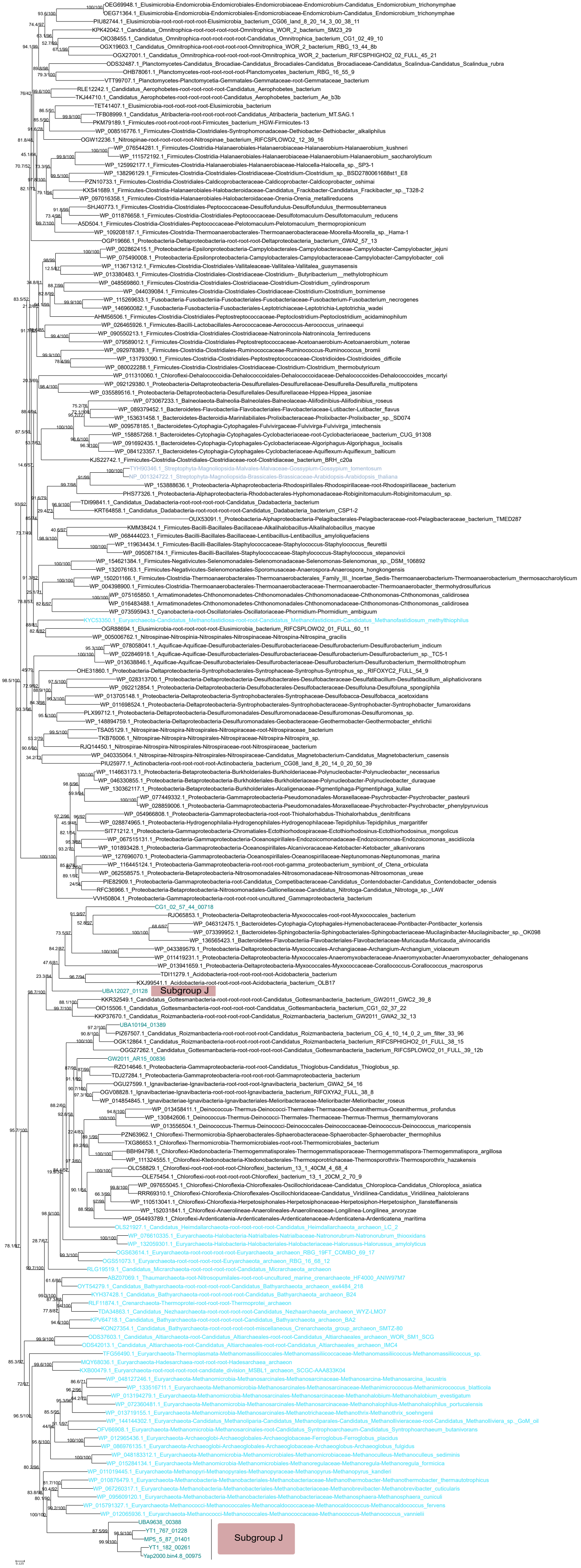
Subgroup J
0.125

Supplementary Fig. 25: Phylogenetic analysis of *lysC* gene (aspartokinase). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 112 taxa and 507 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea, Woesearchaeota and Eukaryotes are colored in black, cyan, green and grey respectively. Woesearchaeota sequences are selected from 47 MAGs used in the inference of proteome content change history. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).



Supplementary Fig. 26: Phylogenetic analysis of *argB* gene (acetylglutamate kinase). The tree was unrooted and inferred using IQ-Tree LG+C20 +G model on an alignment of 211 taxa and 319 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea, Woesearchaeota and Eukaryotes are colored in black, cyan, green and grey, respectively. Woesearchaeota sequences are selected from 47 MAGs used in the inference of proteome content change history. Scale bar shows the number of average substitutions per site. Woesearchaeota subgroup J homologues are annotated in the figure. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).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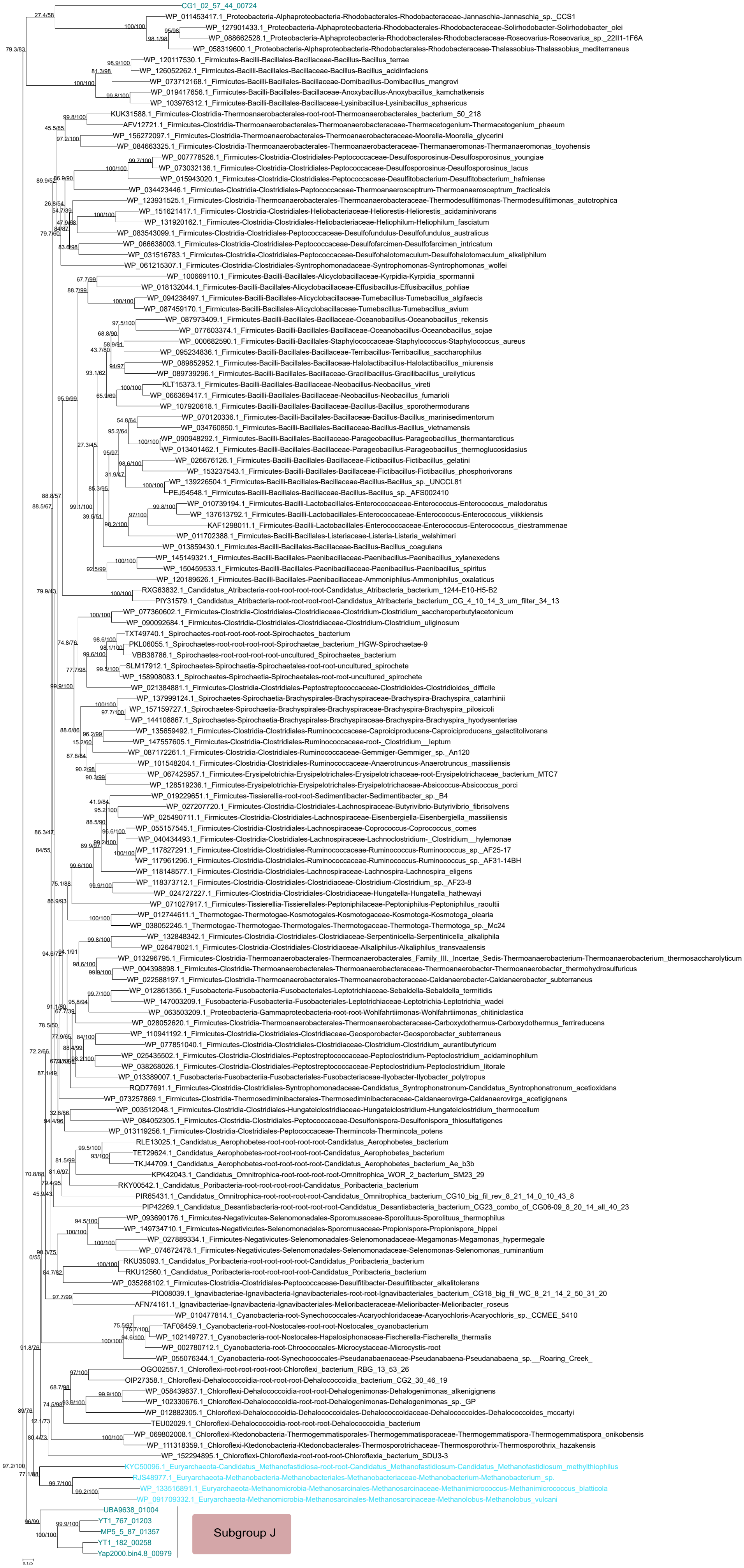
RLE12242.1_Candidatus_Aerophobetes-root-root-root-root-Candidatus_Aerophobetes_bacterium
TKJ44710.1_Candidatus_Aerophobetes-root-root-root-root-Candidatus_Aerophobetes_bacterium_Ae_b3b
TET41407.1_Elusimicrobia-root-root-root-root-Elusimicrobia_bacterium
TFB08999.1_Candidatus_Atribacteria-root-root-root-root-Candidatus_Atribacteria_bacterium_MT.SAG.1
PKM79189.1_Firmicutes-root-root-root-root-Firmicutes_bacterium_HGW-Firmicutes-13
WP_008516776.1_Firmicutes-Clostridia-Syntrophomonadaceae-Dethiobacter-Dethiobacter_alkaliphilus
OGW12236.1_Nitrospinae-root-root-root-root-Nitrospinae_bacterium_RIFCSPLOWO2_12_39_16
WP_076544281.1_Firmicutes-Clostridia-Halanaerobiales-Halanaerobiaceae-Halanaerobium-Halanaerobium_kushneri
WP_111572192.1_Firmicutes-Clostridia-Halanaerobiales-Halanaerobiaceae-Halanaerobium-Halanaerobium_saccharolyticum
WP_125992177.1_Firmicutes-Clostridia-Halanaerobiales-Halanaerobiaceae-Halocella-Halocella_sp._SP3-1
WP_138296129.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Clostridium-Clostridium_sp._BSD2780061688st1_E8
PZN10733.1_Firmicutes-Clostridia-Clostridiales-Caldicoprobacteraceae-Caldicoprobacter-Caldicoprobacter_oshimai
KXS41689.1_Firmicutes-Clostridia-Halanaerobiales-Halobacteroidaceae-Candidatus_Frackibacter-Candidatus_Frackibacter_sp._T328-2
WP_097016358.1_Firmicutes-Clostridia-Halanaerobiales-Halobacteroidaceae-Orenia-Orenia_metallireducens
SHJ40773.1_Firmicutes-Clostridia-Clostridiales-Peptococcaceae-Desulfofundulus-Desulfofundulus_thermosubterraneus
WP_011876658.1_Firmicutes-Clostridia-Clostridiales-Peptococcaceae-Desulfotomaculum-Desulfotomaculum_reducens
A5D504.1_Firmicutes-Clostridia-Clostridiales-Peptococcaceae-Pelotomaculum-Pelotomaculum_thermopropionicum
WP_109208187.1_Firmicutes-Clostridia-Thermoanaerobacterales-Thermoanaerobacteraceae-Moorella-Moorella_sp._Hama-1
OGP19666.1_Proteobacteria-Deltaproteobacteria-root-root-root-Deltaproteobacteria_bacterium_GWA2_57_13
WP_002862415.1_Proteobacteria-Epsilonproteobacteria-Campylobacterales-Campylobacteraceae-Campylobacter-Campylobacter_jejuni
WP_075490008.1_Proteobacteria-Epsilonproteobacteria-Campylobacterales-Campylobacteraceae-Campylobacter-Campylobacter_coli
WP_113671312.1_Firmicutes-Clostridia-Clostridiales-Vallitaleaceae-Vallitalea-Vallitalea_guaymasensis
WP_013380483.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Clostridium-_Butyribacterium__methylotrophicum
WP_048569860.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Clostridium-Clostridium_cylindrosporum
WP_044039084.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Clostridium-Clostridium_bornimense
WP_115269633.1_Fusobacteria-Fusobacteriia-Fusobacteriales-Fusobacteriaceae-Fusobacterium-Fusobacterium_necrogenes
WP_146960082.1_Fusobacteria-Fusobacteriia-Fusobacteriales-Leptotrichiaceae-Leptotrichia-Leptotrichia_wadei
AHM56506.1_Firmicutes-Clostridia-Clostridiales-Peptostreptococcaceae-Peptoclostridium-Peptoclostridium_acidaminophilum
WP_026465926.1_Firmicutes-Bacilli-Lactobacillales-Aerococcaceae-Aerococcus-Aerococcus_urinaeequi
WP_090550213.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Natronincola-Natronincola_ferrireducens
WP_079589012.1_Firmicutes-Clostridia-Clostridiales-Peptostreptococcaceae-Acetoanaerobium-Acetoanaerobium_noterae
WP_092978389.1_Firmicutes-Clostridia-Clostridiales-Ruminococcaceae-Ruminococcus-Ruminococcus_bromii
WP_131793090.1_Firmicutes-Clostridia-Clostridiales-Peptostreptococcaceae-Clostridioides-Clostridioides_difficile
WP_080022288.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Clostridium-Clostridium_thermobutyricum
WP_011310060.1_Chloroflexi-Dehalococcoidia-Dehalococcoidales-Dehalococcoidaceae-Dehalococcoides-Dehalococcoides_mccartyi
WP_092129380.1_Proteobacteria-Deltaproteobacteria-Desulfurellales-Desulfurellaceae-Desulfurella-Desulfurella_multipotens
WP_035589516.1_Proteobacteria-Deltaproteobacteria-Desulfurellales-Desulfurellaceae-Hippea-Hippea_jasoniae
WP_073067233.1_Balneolaeota-Balneolia-Balneolales-Balneolaceae-Aliifodinibius-Aliifodinibius_roseus
WP_089379452.1_Bacteroidetes-Flavobacteriia-Flavobacteriales-Flavobacteriaceae-Lutibacter-Lutibacter_flavus
WP_153631458.1_Bacteroidetes-Bacteroidia-Marinilabiliales-Prolixibacteraceae-Prolixibacter-Prolixibacter_sp._SD074
WP_009578185.1_Bacteroidetes-Cytophagia-Cytophagales-Fulvivirgaceae-Fulvivirga-Fulvivirga_imtechensis
WP_158857268.1_Bacteroidetes-Cytophagia-Cytophagales-Cyclobacteriaceae-root-Cyclobacteriaceae_bacterium_CUG_91308
WP_091692435.1_Bacteroidetes-Cytophagia-Cytophagales-Cyclobacteriaceae-Algoriphagus-Algoriphagus_locisalis
WP_084123357.1_Bacteroidetes-Cytophagia-Cytophagales-Cyclobacteriaceae-Aquiflexum-Aquiflexum_balticum
KJS22742.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-root-Clostridiaceae_bacterium_BRH_c20a
TYH90346.1_Streptophyta-Magnoliopsida-Malvales-Malvaceae-Gossypium-Gossypium_tomentosum
NP_001324722.1_Streptophyta-Magnoliopsida-Brassicales-Brassicaceae-Arabidopsis-Arabidopsis_thaliana
WP_153888636.1_Proteobacteria-Alphaproteobacteria-Rhodospirillales-Rhodospirillaceae-root-Rhodospirillaceae_bacterium
PHS77326.1_Proteobacteria-Alphaproteobacteria-Rhodobacterales-Hyphomonadaceae-Robiginitomaculum-Robiginitomaculum_sp.
TDI99841.1_Candidatus_Dadabacteria-root-root-root-root-Candidatus_Dadabacteria_bacterium
KRT64858.1_Candidatus_Dadabacteria-root-root-root-root-Candidatus_Dadabacteria_bacterium_CSP1-2
OUX53091.1_Proteobacteria-Alphaproteobacteria-Pelagibacterales-Pelagibacteraceae-root-Pelagibacteraceae_bacterium_TMED287
KMM38424.1_Firmicutes-Bacilli-Bacillales-Bacillaceae-Alkalihalobacillus-Alkalihalobacillus_macyae
WP_068444023.1_Firmicutes-Bacilli-Bacillales-Bacillaceae-Lentibacillus-Lentibacillus_amyloliquefaciens
WP_119634434.1_Firmicutes-Bacilli-Bacillales-Staphylococcaceae-Staphylococcus-Staphylococcus_fleurettii
WP_095087184.1_Firmicutes-Bacilli-Bacillales-Staphylococcaceae-Staphylococcus-Staphylococcus_stepanovicii
WP_154621384.1_Firmicutes-Negativicutes-Selenomonadales-Selenomonadaceae-Selenomonas-Selenomonas_sp._DSM_106892
WP_132076163.1_Firmicutes-Negativicutes-Selenomonadales-Sporomusaceae-Anaerospora-Anaerospora_hongkongensis
WP_150201166.1_Firmicutes-Clostridia-Thermoanaerobacterales-Thermoanaerobacterales_Family_III._Incertae_Sedis-Thermoanaerobacterium-Thermoanaerobacterium_thermosaccharolyticum
WP_004398900.1_Firmicutes-Clostridia-Thermoanaerobacterales-Thermoanaerobacteraceae-Thermoanaerobacter-Thermoanaerobacter_thermohydrosulfuricus
WP_075165850.1_Armatimonadetes-Chthonomonadetes-Chthonomonadales-Chthonomonadaceae-Chthonomonas-Chthonomonas_calidirosea
WP_016483488.1_Armatimonadetes-Chthonomonadetes-Chthonomonadales-Chthonomonadaceae-Chthonomonas-Chthonomonas_calidirosea
WP_073595943.1_Cyanobacteria-root-Oscillatoriales-Oscillatoriaceae-Phormidium-Phormidium_ambiguum
KYC53350.1_Euryarchaeota-Candidatus_Methanofastidiosa-root-root-Candidatus_Methanofastidiosum-Candidatus_Methanofastidiosum_methylthiophilus
OGR88694.1_Elusimicrobia-root-root-root-root-Elusimicrobia_bacterium_RIFCSPLOWO2_01_FULL_60_11
WP_005006762.1_Nitrospinae-Nitrospinia-Nitrospinales-Nitrospinaceae-Nitrospina-Nitrospina_gracilis
WP_078058041.1_Aquificae-Aquificae-Desulfurobacteriales-Desulfurobacteriaceae-Desulfurobacterium-Desulfurobacterium_indicum
WP_022846918.1_Aquificae-Aquificae-Desulfurobacteriales-Desulfurobacteriaceae-Desulfurobacterium-Desulfurobacterium_sp._TC5-1
WP_013638846.1_Aquificae-Aquificae-Desulfurobacteriales-Desulfurobacteriaceae-Desulfurobacterium-Desulfurobacterium_thermolithotrophum
OHE31860.1_Proteobacteria-Deltaproteobacteria-Syntrophobacterales-Syntrophaceae-Syntrophus-Syntrophus_sp._RIFOXYC2_FULL_54_9
WP_028313700.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-Desulfatibacillum-Desulfatibacillum_aliphaticivorans
WP_092212854.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-Desulfoluna-Desulfoluna_spongiiphila
WP_013705148.1_Proteobacteria-Deltaproteobacteria-Syntrophobacterales-Syntrophaceae-Desulfobacca-Desulfobacca_acetoxidans
WP_011698524.1_Proteobacteria-Deltaproteobacteria-Syntrophobacterales-Syntrophobacteraceae-Syntrophobacter-Syntrophobacter_fumaroxidans
PLX99712.1_Proteobacteria-Deltaproteobacteria-Desulfuromonadales-Desulfuromonadaceae-Desulfuromonas-Desulfuromonas_sp.
WP_148894759.1_Proteobacteria-Deltaproteobacteria-Desulfuromonadales-Geobacteraceae-Geothermobacter-Geothermobacter_ehrlichii
TSA05129.1_Nitrospirae-Nitrospira-Nitrospirales-Nitrospiraceae-root-Nitrospiraceae_bacterium
TKB76006.1_Nitrospirae-Nitrospira-Nitrospirales-Nitrospiraceae-Nitrospira-Nitrospira_sp.
RJQ14450.1_Nitrospirae-Nitrospira-Nitrospirales-Nitrospiraceae-root-Nitrospiraceae_bacterium
WP_040335064.1_Nitrospirae-Nitrospira-Nitrospirales-Nitrospiraceae-Candidatus_Magnetobacterium-Candidatus_Magnetobacterium_casensis
PIU25977.1_Actinobacteria-root-root-root-root-Actinobacteria_bacterium_CG08_land_8_20_14_0_20_50_39
WP_114663173.1_Proteobacteria-Betaproteobacteria-Burkholderiales-Burkholderiaceae-Polynucleobacter-Polynucleobacter_necessarius
WP_046330855.1_Proteobacteria-Betaproteobacteria-Burkholderiales-Burkholderiaceae-Polynucleobacter-Polynucleobacter_duraquae
WP_130362117.1_Proteobacteria-Betaproteobacteria-Burkholderiales-Alcaligenaceae-Pigmentiphaga-Pigmentiphaga_kullae
WP_077449332.1_Proteobacteria-Gammaproteobacteria-Pseudomonadales-Moraxellaceae-Psychrobacter-Psychrobacter_pasteurii
WP_028859006.1_Proteobacteria-Gammaproteobacteria-Pseudomonadales-Moraxellaceae-Psychrobacter-Psychrobacter_phenylpyruvicus
WP_054966808.1_Proteobacteria-Gammaproteobacteria-root-root-Thiohalorhabdus-Thiohalorhabdus_denitrificans
WP_028874965.1_Proteobacteria-Hydrogenophilalia-Hydrogenophilales-Hydrogenophilaceae-Tepidiphilus-Tepidiphilus_margaritifer
SIT71212.1_Proteobacteria-Gammaproteobacteria-Chromatiales-Ectothiorhodospiraceae-Ectothiorhodosinus-Ectothiorhodosinus_mongolicus
WP_067515131.1_Proteobacteria-Gammaproteobacteria-Oceanospirillales-Endozoicomonadaceae-Endozoicomonas-Endozoicomonas_ascidiicola
WP_101893428.1_Proteobacteria-Gammaproteobacteria-Oceanospirillales-Alcanivoracaceae-Ketobacter-Ketobacter_alkanivorans
WP_127696070.1_Proteobacteria-Gammaproteobacteria-Oceanospirillales-Oceanospirillaceae-Neptunomonas-Neptunomonas_marina
WP_116445124.1_Proteobacteria-Gammaproteobacteria-root-root-root-gamma_proteobacterium_symbiont_of_Ctena_orbiculata
WP_062558575.1_Proteobacteria-Betaproteobacteria-Nitrosomonadales-Nitrosomonadaceae-Nitrosomonas-Nitrosomonas_ureae
PIE82909.1_Proteobacteria-Gammaproteobacteria-root-Candidatus_Competibacteraceae-Candidatus_Contendobacter-Candidatus_Contendobacter_odensis
RFC36966.1_Proteobacteria-Betaproteobacteria-Nitrosomonadales-Gallionellaceae-Candidatus_Nitrotoga-Candidatus_Nitrotoga_sp._LAW
VVH50804.1_Proteobacteria-Gammaproteobacteria-root-root-root-uncultured_Gammaproteobacteria_bacterium
CG1_02_57_44_00718
RJO65853.1_Proteobacteria-Deltaproteobacteria-Myxococcales-root-root-Myxococcales_bacterium
WP_046312475.1_Bacteroidetes-Cytophagia-Cytophagales-Hymenobacteraceae-Pontibacter-Pontibacter_korlensis
WP_073399952.1_Bacteroidetes-Sphingobacteriia-Sphingobacteriales-Sphingobacteriaceae-Mucilaginibacter-Mucilaginibacter_sp._OK098
WP_136565423.1_Bacteroidetes-Flavobacteriia-Flavobacteriales-Flavobacteriaceae-Muricauda-Muricauda_alvinocaridis
WP_043389579.1_Proteobacteria-Deltaproteobacteria-Myxococcales-Archangiaceae-Archangium-Archangium_violaceum
WP_011419231.1_Proteobacteria-Deltaproteobacteria-Myxococcales-Anaeromyxobacteraceae-Anaeromyxobacter-Anaeromyxobacter_dehalogenans
WP_013941659.1_Proteobacteria-Deltaproteobacteria-Myxococcales-Myxococcaceae-Corallococcus-Corallococcus_macrosporus
TDI11279.1_Acidobacteria-root-root-root-root-Acidobacteria_bacterium
KXJ99541.1_Acidobacteria-root-root-root-root-Acidobacteria_bacterium_OLB17
UBA12027_01128
Subgroup J
KKR32549.1_Candidatus_Gottesmanbacteria-root-root-root-root-Candidatus_Gottesmanbacteria_bacterium_GW2011_GWC2_39_8
OIO15506.1_Candidatus_Gottesmanbacteria-root-root-root-root-Candidatus_Gottesmanbacteria_bacterium_CG1_02_37_22
KKP37670.1_Candidatus_Roizmanbacteria-root-root-root-root-Candidatus_Roizmanbacteria_bacterium_GW2011_GWA2_32_13
UBA10194_01389
PIZ67507.1_Candidatus_Roizmanbacteria-root-root-root-root-Candidatus_Roizmanbacteria_bacterium_CG_4_10_14_0_2_um_filter_33_96
OGK12864.1_Candidatus_Roizmanbacteria-root-root-root-root-Candidatus_Roizmanbacteria_bacterium_RIFCSPHIGHO2_01_FULL_38_15
OGG27262.1_Candidatus_Gottesmanbacteria-root-root-root-root-Candidatus_Gottesmanbacteria_bacterium_RIFCSPLOWO2_01_FULL_39_12b
GW2011_AR15_00836
RZO14646.1_Proteobacteria-Gammaproteobacteria-root-root-Candidatus_Thioglobus-Candidatus_Thioglobus_sp.
TDJ27284.1_Proteobacteria-Gammaproteobacteria-root-root-root-Gammaproteobacteria_bacterium
OGU27599.1_Ignavibacteriae-Ignavibacteria-root-root-root-Ignavibacteria_bacterium_GWA2_54_16
OGV08828.1_Ignavibacteriae-Ignavibacteria-root-root-root-Ignavibacteria_bacterium_RIFOXYA2_FULL_38_8
WP_014854845.1_Ignavibacteriae-Ignavibacteria-Ignavibacteriales-Melioribacteraceae-Melioribacter-Melioribacter_roseus
WP_013458411.1_Deinococcus-Thermus-Deinococci-Thermales-Thermaceae-Oceanithermus-Oceanithermus_profundus
WP_130842606.1_Deinococcus-Thermus-Deinococci-Thermales-Thermaceae-Thermus-Thermus_thermamylovorans
WP_013556504.1_Deinococcus-Thermus-Deinococci-Deinococcales-Deinococcaceae-Deinococcus-Deinococcus_maricopensis
PZN63962.1_Chloroflexi-Thermomicrobia-Sphaerobacterales-Sphaerobacteraceae-Sphaerobacter-Sphaerobacter_thermophilus
TXG86653.1_Chloroflexi-Thermomicrobia-Thermomicrobiales-root-root-Thermomicrobiales_bacterium
BBH94798.1_Chloroflexi-Ktedonobacteria-Thermogemmatisporales-Thermogemmatisporaceae-Thermogemmatispora-Thermogemmatispora_argillosa
WP_111324555.1_Chloroflexi-Ktedonobacteria-Ktedonobacterales-Thermosporotrichaceae-Thermosporothrix-Thermosporothrix_hazakensis
OLC58829.1_Chloroflexi-root-root-root-root-Chloroflexi_bacterium_13_1_40CM_4_68_4
OLE75454.1_Chloroflexi-root-root-root-root-Chloroflexi_bacterium_13_1_20CM_2_70_9
WP_097655045.1_Chloroflexi-Chloroflexia-Chloroflexales-Oscillochloridaceae-Candidatus_Chloroploca-Candidatus_Chloroploca_asiatica
RRR69310.1_Chloroflexi-Chloroflexia-Chloroflexales-Oscillochloridaceae-Candidatus_Viridilinea-Candidatus_Viridilinea_halotolerans
WP_110513041.1_Chloroflexi-Chloroflexia-Herpetosiphonales-Herpetosiphonaceae-Herpetosiphon-Herpetosiphon_llansteffanensis
WP_152031841.1_Chloroflexi-Anaerolineae-Anaerolineales-Anaerolineaceae-Longilinea-Longilinea_arvoryzae
WP_054493789.1_Chloroflexi-Ardenticatenia-Ardenticatenales-Ardenticatenaceae-Ardenticatena-Ardenticatena_maritima
OLS21927.1_Candidatus_Heimdallarchaeota-root-root-root-root-Candidatus_Heimdallarchaeota_archaeon_LC_2
WP_076610335.1_Euryarchaeota-Halobacteria-Natrialbales-Natrialbaceae-Natronorubrum-Natronorubrum_thiooxidans
WP_132059301.1_Euryarchaeota-Halobacteria-Halobacteriales-Halobacteriaceae-Halorussus-Halorussus_amylolyticus
OGS63614.1_Euryarchaeota-root-root-root-root-Euryarchaeota_archaeon_RBG_19FT_COMBO_69_17
OGS51073.1_Euryarchaeota-root-root-root-root-Euryarchaeota_archaeon_RBG_16_68_12
RLG19519.1_Candidatus_Micrarchaeota-root-root-root-root-Candidatus_Micrarchaeota_archaeon
ABZ07069.1_Thaumarchaeota-root-Nitrosopumilales-root-root-uncultured_marine_crenarchaeote_HF4000_ANIW97M7
OYT54279.1_Candidatus_Bathyarchaeota-root-root-root-root-Candidatus_Bathyarchaeota_archaeon_ex4484_218
KYH37428.1_Candidatus_Bathyarchaeota-root-root-root-root-Candidatus_Bathyarchaeota_archaeon_B24
BLF11874.1_Crenarchaeota-Thermoprotei-root-root-root-Thermoprotei_archaeon
TDA34863.1_Candidatus_Nezhaarchaeota-root-root-root-root-Candidatus_Nezhaarchaeota_archaeon_WYZ-LMO7
KPV64718.1_Candidatus_Bathyarchaeota-root-root-root-root-Candidatus_Bathyarchaeota_archaeon_BA2
KON27354.1_Candidatus_Bathyarchaeota-root-root-root-root-miscellaneous_Crenarchaeota_group_archaeon_SMTZ-80
ODS37603.1_Candidatus_Altiarchaeota-root-Candidatus_Altiarchaeales-root-root-Candidatus_Altiarchaeales_archaeon_WOR_SM1_SCG
ODS42013.1_Candidatus_Altiarchaeota-root-Candidatus_Altiarchaeales-root-root-Candidatus_Altiarchaeales_archaeon_IMC4
TFG58490.1_Euryarchaeota-Thermoplasmata-Methanomassiliicoccales-Methanomassiliicoccaceae-Methanomassiliicoccus-Methanomassiliicoccus_sp.
MQY66036.1_Euryarchaeota-Hadesarchaea-root-root-root-Hadesarchaea_archaeon
KXB00479.1_Euryarchaeota-root-root-root-candidate_division_MSBL1-candidate_division_MSBL1_archaeon_SCGC-AAA833K04
WP_048127246.1_Euryarchaeota-Methanomicrobia-Methanosarcinales-Methanosarcinaceae-Methanosarcina-Methanosarcina_lacustris
WP_133516711.1_Euryarchaeota-Methanomicrobia-Methanosarcinales-Methanosarcinaceae-Methanimicrococcus-Methanimicrococcus_blatticola
WP_013194279.1_Euryarchaeota-Methanomicrobia-Methanosarcinales-Methanosarcinaceae-Methanohalobium-Methanohalobium_evestigatum
WP_072360481.1_Euryarchaeota-Methanomicrobia-Methanosarcinales-Methanosarcinaceae-Methanohalophilus-Methanohalophilus_portucalensis
WP_013719155.1_Euryarchaeota-Methanomicrobia-Methanosarcinales-Methanotrichaceae-Methanothrix-Methanothrix_soehngenii
WP_144144302.1_Euryarchaeota-Candidatus_Methanoliparia-Candidatus_Methanoliparales-Candidatus_Methanoliparaceae-root-Candidatus_Methanoliparia_sp._GoM_oil
OFV66908.1_Euryarchaeota-Methanomicrobia-Methanosarcinales-root-Candidatus_Syntrophoarchaeum-Candidatus_Syntrophoarchaeum_butanivorans
WP_012965436.1_Euryarchaeota-Archaeoglobi-Archaeoglobales-Archaeoglobaceae-Ferroglobus-Ferroglobus_placidus
WP_080976135.1_Euryarchaeota-Archaeoglobi-Archaeoglobales-Archaeoglobaceae-Archaeoglobus-Archaeoglobus_fulgidus
WP_048183312.1_Euryarchaeota-Methanomicrobia-Methanomicrobiales-Methanomicrobiaceae-Methanoculleus-Methanoculleus_sediminis
WP_015284134.1_Euryarchaeota-Methanomicrobia-Methanomicrobiales-Methanoregulaceae-Methanoregula-Methanoregula_formicica
WP_011019445.1_Euryarchaeota-Methanopyri-Methanopyrales-Methanopyraceae-Methanopyrus-Methanopyrus_kandleri
WP_013876479.1_Euryarchaeota-Methanobacteria-Methanobacteriales-Methanothermaceae-Methanothermococcus-Methanothermobacter_thermautotrophicus
WP_067260317.1_Euryarchaeota-Methanobacteria-Methanobacteriales-Methanobacteriaceae-Methanobrevibacter-Methanobrevibacter_cuticularis
WP_095609120.1_Euryarchaeota-Methanobacteria-Methanobacteriales-Methanobacteriaceae-Methanosphaera-Methanosphaera_cuniculi
WP_015791327.1_Euryarchaeota-Methanococci-Methanococcales-Methanocaldococcaceae-Methanocaldococcus-Methanocaldococcus_fervens
WP_012065936.1_Euryarchaeota-Methanococci-Methanococcales-Methanococcaceae-Methanococcus-Methanococcus_vannielii
UBA9638_00388
YT1_767_01228
MP5_5_87_01401
YT1_182_00261
Yap2000.bin4.8_00975
Subgroup J
0.03

Supplementary Fig. 27: Phylogenetic analysis of *argC* gene (N-acetyl-gamma-glutamyl-phosphate reductase). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 185 taxa and 351 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea, Woesearchaeota and Eukaryotes are colored in black, cyan, green and grey respectively. Woesearchaeota sequences are selected from 47 MAGs used in the inference of proteome content change history. Scale bar shows the number of average substitutions per site. Woesearchaeota subgroup J homologues are annotated in the figure. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).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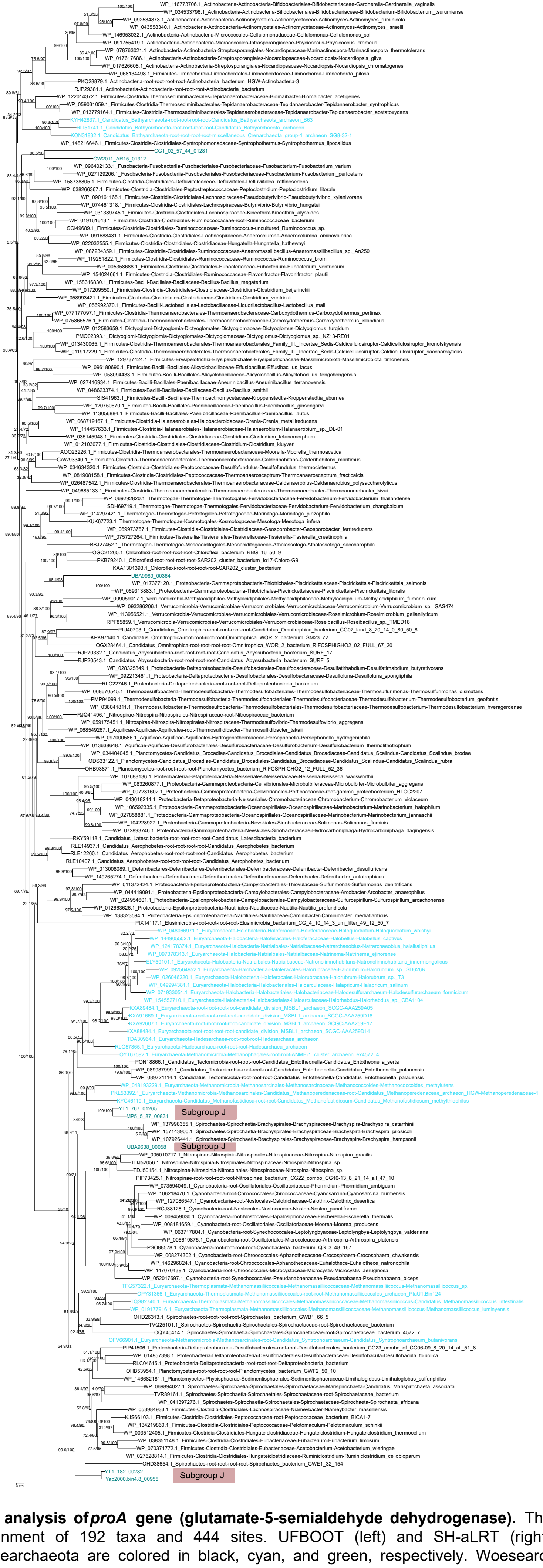
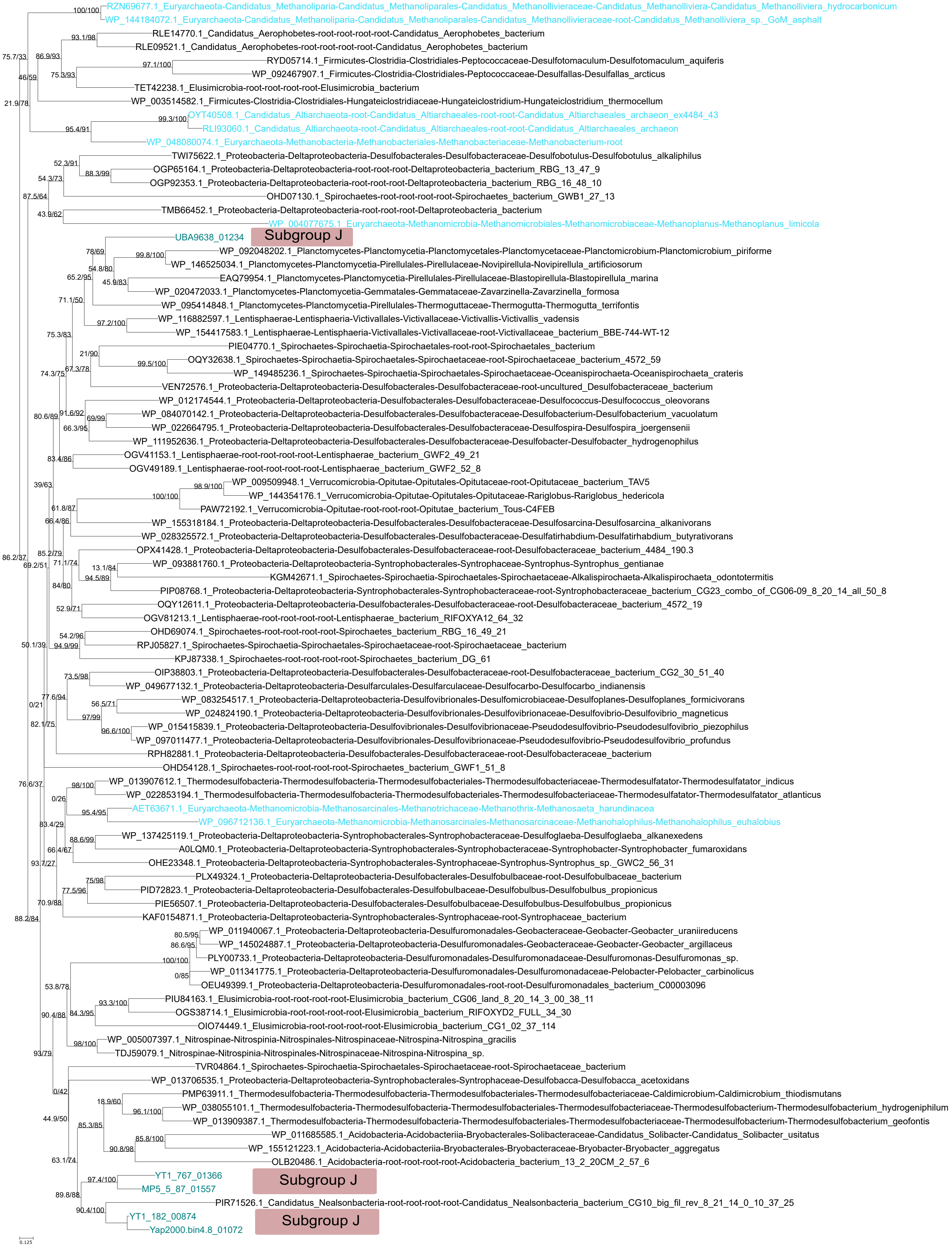
Subgroup J
0.125

Supplementary Fig. 28: Phylogenetic analysis of*argJ* gene (glutamate N-acetyltransferase/amino-acid acetyltransferase). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 144 taxa and 402 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan and green, respectively. Woesearchaeota sequences are selected from 47 MAGs used in the inference of proteome content change history. Woesearchaeota subgroup J homologues are annotated in the figure. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).



Supplementary Fig. 29: Phylogenetic analysis of *proA* gene (glutamate-5-semialdehyde dehydrogenase). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 192 taxa and 444 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan, and green, respectively. Woesearchaeota sequences are selected from 47 MAGs used in the inference of proteome content change history. Woesearchaeota subgroup J homologues are annotated in the figure. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).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75.7/33
86.9/93
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46/59
75.3/93
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21.9/78
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43.9/62
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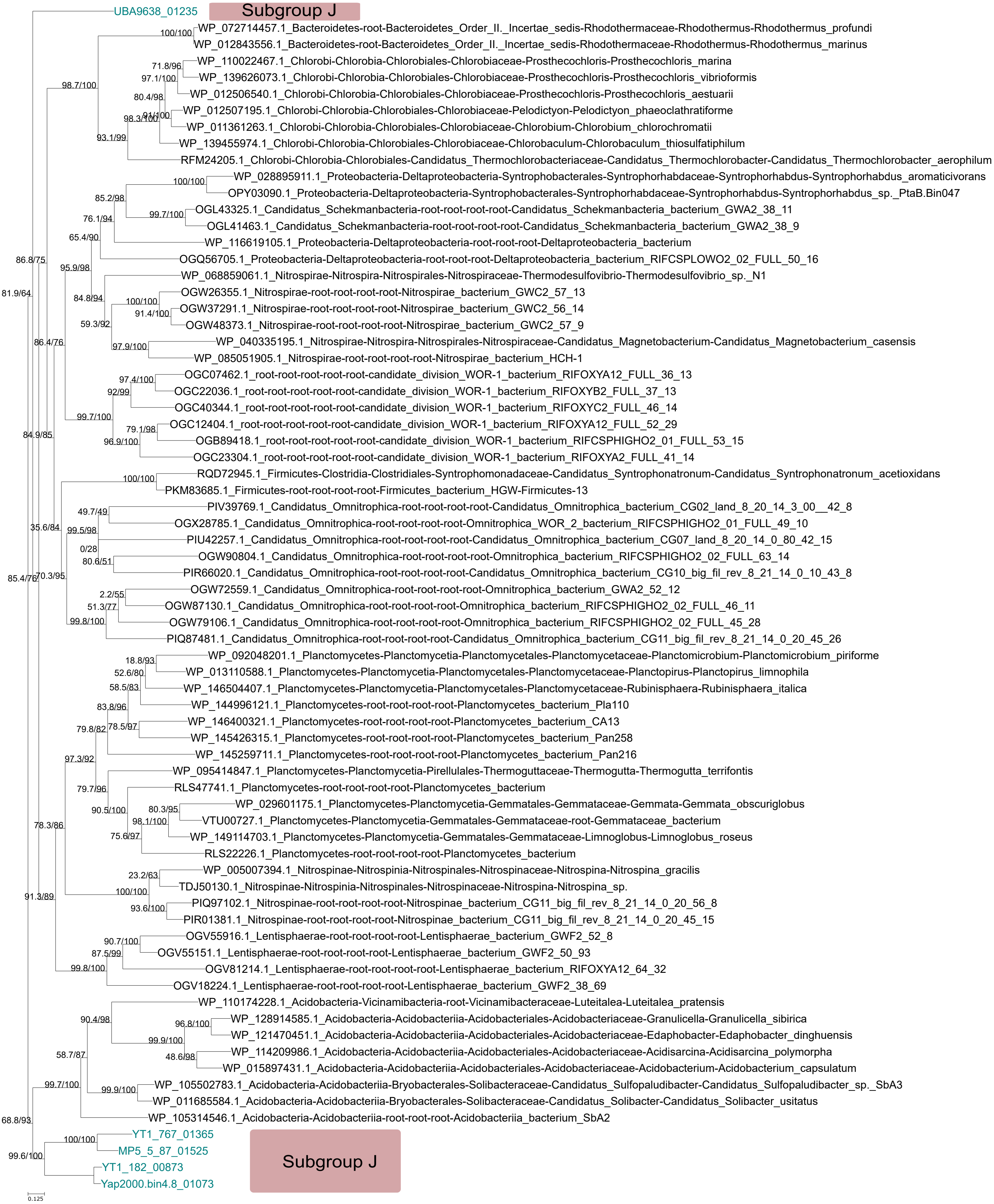
WP_004077675.1_Euryarchaeota-Methanomicrobia-Methanomicrobiales-Methanomicrobiaceae-Methanoplanus-Methanoplanus_limicola
UBA9638_01234
Subgroup J
78/69
WP_092048202.1_Planctomycetes-Planctomycetia-Planctomycetales-Planctomycetaceae-Planctomicrobium-Planctomicrobium_piriforme
99.8/100
54.8/80
WP_146525034.1_Planctomycetes-Planctomycetia-Pirellulales-Pirellulaceae-Novipirellula-Novipirellula_artificiosorum
65.2/95
45.9/83
EAQ79954.1_Planctomycetes-Planctomycetia-Pirellulales-Pirellulaceae-Blastopirellula-Blastopirellula_marina
WP_020472033.1_Planctomycetes-Planctomycetia-Gemmatales-Gemmataceae-Zavarzinella-Zavarzinella_formosa
71.1/50
WP_095414848.1_Planctomycetes-Planctomycetia-Pirellulales-Thermoguttaceae-Thermogutta-Thermogutta_terrifontis
WP_116882597.1_Lentisphaerae-Lentisphaeria-Victivallales-Victivallaceae-Victivallis-Victivallis_vadensis
97.2/100
WP_154417583.1_Lentisphaerae-Lentisphaeria-Victivallales-Victivallaceae-root-Victivallaceae_bacterium_BBE-744-WT-12
75.3/83
PIE04770.1_Spirochaetes-Spirochaetia-Spirochaetales-root-root-Spirochaetales_bacterium
21/90
99.5/100
OQY32638.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-root-Spirochaetaceae_bacterium_4572_59
74.3/75
67.3/78
WP_149485236.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-Oceanispirochaeta-Oceanispirochaeta_crateris
VEN72576.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-root-uncultured_Desulfobacteraceae_bacterium
WP_012174544.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-Desulfococcus-Desulfococcus_oleovorans
80.6/89
91.6/92
69/99
WP_084070142.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-Desulfobacterium-Desulfobacterium_vacuolatum
66.3/95
WP_022664795.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-Desulfospira-Desulfospira_joergensenii
WP_111952636.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-Desulfobacter-Desulfobacter_hydrogenophilus
OGV41153.1_Lentisphaerae-root-root-root-root-Lentisphaerae_bacterium_GWF2_49_21
83.4/86
OGV49189.1_Lentisphaerae-root-root-root-root-Lentisphaerae_bacterium_GWF2_52_8
39/63
98.9/100
WP_009509948.1_Verrucomicrobia-Opitutae-Opitutales-Opitutaceae-root-Opitutaceae_bacterium_TAV5
100/100
WP_144354176.1_Verrucomicrobia-Opitutae-Opitutales-Opitutaceae-Rariglobus-Rariglobus_hedericola
61.8/87
PAW72192.1_Verrucomicrobia-Opitutae-root-root-root-Opitutae_bacterium_Tous-C4FEB
66.4/86
WP_155318184.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-Desulfosarcina-Desulfosarcina_alkanivorans
WP_028325572.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-Desulfatirhabdium-Desulfatirhabdium_butyrativorans
86.2/37
85.2/79
OPX41428.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-root-Desulfobacteraceae_bacterium_4484_190.3
69.2/51
71.1/74
13.1/84
WP_093881760.1_Proteobacteria-Deltaproteobacteria-Syntrophobacterales-Syntrophaceae-Syntrophus-Syntrophus_gentianae
94.5/89
KGM42671.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-Alkalispirochaeta-Alkalispirochaeta_odontotermitis
84/80
PIP08768.1_Proteobacteria-Deltaproteobacteria-Syntrophobacterales-Syntrophobacteraceae-root-Syntrophobacteraceae_bacterium_CG23_combo_of_CG06-09_8_20_14_all_50_8
52.9/71
OQY12611.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-root-Desulfobacteraceae_bacterium_4572_19
OGV81213.1_Lentisphaerae-root-root-root-root-Lentisphaerae_bacterium_RIFOXYA12_64_32
54.2/96
OHD69074.1_Spirochaetes-root-root-root-root-Spirochaetes_bacterium_RBG_16_49_21
50.1/39
94.9/99
RPJ05827.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-root-Spirochaetaceae_bacterium
KPJ87338.1_Spirochaetes-root-root-root-root-Spirochaetes_bacterium_DG_61
73.5/98
OIP38803.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-root-Desulfobacteraceae_bacterium_CG2_30_51_40
77.6/94
WP_049677132.1_Proteobacteria-Deltaproteobacteria-Desulfarculales-Desulfarculaceae-Desulfocarbo-Desulfocarbo_indianensis
0/21
56.5/71
WP_083254517.1_Proteobacteria-Deltaproteobacteria-Desulfovibrionales-Desulfomicrobiaceae-Desulfoplanes-Desulfoplanes_formicivorans
97/99
WP_024824190.1_Proteobacteria-Deltaproteobacteria-Desulfovibrionales-Desulfovibrionaceae-Desulfovibrio-Desulfovibrio_magneticus
82.1/75
96.6/100
WP_015415839.1_Proteobacteria-Deltaproteobacteria-Desulfovibrionales-Desulfovibrionaceae-Pseudodesulfovibrio-Pseudodesulfovibrio_piezophilus
WP_097011477.1_Proteobacteria-Deltaproteobacteria-Desulfovibrionales-Desulfovibrionaceae-Pseudodesulfovibrio-Pseudodesulfovibrio_profundus
RPH82881.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-root-Desulfobacteraceae_bacterium
OHD54128.1_Spirochaetes-root-root-root-root-Spirochaetes_bacterium_GWF1_51_8
76.6/37
98/100
WP_013907612.1_Thermodesulfobacteria-Thermodesulfobacteria-Thermodesulfobacteriales-Thermodesulfobacteriaceae-Thermodesulfatator-Thermodesulfatator_indicus
0/26
WP_022853194.1_Thermodesulfobacteria-Thermodesulfobacteria-Thermodesulfobacteriales-Thermodesulfobacteriaceae-Thermodesulfatator-Thermodesulfatator_atlanticus
95.4/95
AET63671.1_Euryarchaeota-Methanomicrobia-Methanosarcinales-Methanotrichaceae-Methanothrix-Methanosaeta_harundinacea
83.4/29
WP_096712136.1_Euryarchaeota-Methanomicrobia-Methanosarcinales-Methanosarcinaceae-Methanohalophilus-Methanohalophilus_euhalobius
88.6/99
WP_137425119.1_Proteobacteria-Deltaproteobacteria-Syntrophobacterales-Syntrophobacteraceae-Desulfoglaeba-Desulfoglaeba_alkanexedens
66.4/67
A0LQM0.1_Proteobacteria-Deltaproteobacteria-Syntrophobacterales-Syntrophobacteraceae-Syntrophobacter-Syntrophobacter_fumaroxidans
93.7/27
OHE23348.1_Proteobacteria-Deltaproteobacteria-Syntrophobacterales-Syntrophaceae-Syntrophus-Syntrophus_sp._GWC2_56_31
75/98
PLX49324.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobulbaceae-root-Desulfobulbaceae_bacterium
77.5/96
PID72823.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobulbaceae-Desulfobulbus-Desulfobulbus_propionicus
70.9/88
PIE56507.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobulbaceae-Desulfobulbus-Desulfobulbus_propionicus
88.2/84
KAF0154871.1_Proteobacteria-Deltaproteobacteria-Syntrophobacterales-Syntrophaceae-root-Syntrophaceae_bacterium
80.5/95
WP_011940067.1_Proteobacteria-Deltaproteobacteria-Desulfuromonadales-Geobacteraceae-Geobacter-Geobacter_uraniireducens
86.6/95
WP_145024887.1_Proteobacteria-Deltaproteobacteria-Desulfuromonadales-Geobacteraceae-Geobacter-Geobacter_argillaceus
100/100
PLY00733.1_Proteobacteria-Deltaproteobacteria-Desulfuromonadales-Desulfuromonadaceae-Desulfuromonas-Desulfuromonas_sp.
0/85
WP_011341775.1_Proteobacteria-Deltaproteobacteria-Desulfuromonadales-Desulfuromonadaceae-Pelobacter-Pelobacter_carbinolicus
53.8/78
OEU49399.1_Proteobacteria-Deltaproteobacteria-Desulfuromonadales-root-root-Desulfuromonadales_bacterium_C00003096
93.3/100
PIU84163.1_Elusimicrobia-root-root-root-root-Elusimicrobia_bacterium_CG06_land_8_20_14_3_00_38_11
90.4/88
84.3/95
OGS38714.1_Elusimicrobia-root-root-root-root-Elusimicrobia_bacterium_RIFOXYD2_FULL_34_30
OIO74449.1_Elusimicrobia-root-root-root-root-Elusimicrobia_bacterium_CG1_02_37_114
98/100
WP_005007397.1_Nitrospinae-Nitrospinia-Nitrospinales-Nitrospinaceae-Nitrospina-Nitrospina_gracilis
93/79
TDJ59079.1_Nitrospinae-Nitrospinia-Nitrospinales-Nitrospinaceae-Nitrospina-Nitrospina_sp.
TVR04864.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-root-Spirochaetaceae_bacterium
0/42
WP_013706535.1_Proteobacteria-Deltaproteobacteria-Syntrophobacterales-Syntrophaceae-Desulfobacca-Desulfobacca_acetoxidans
18.9/60
PMP63911.1_Thermodesulfobacteria-Thermodesulfobacteria-Thermodesulfobacteriales-Thermodesulfobacteriaceae-Caldimicrobium-Caldimicrobium_thiodismutans
96.1/100
WP_038055101.1_Thermodesulfobacteria-Thermodesulfobacteria-Thermodesulfobacteriales-Thermodesulfobacteriaceae-Thermodesulfobacterium-Thermodesulfobacterium_hydrogeniphilum
44.9/50
WP_013909387.1_Thermodesulfobacteria-Thermodesulfobacteria-Thermodesulfobacteriales-Thermodesulfobacteriaceae-Thermodesulfobacterium-Thermodesulfobacterium_geofontis
85.3/85
85.8/100
WP_011685585.1_Acidobacteria-Acidobacteriia-Bryobacterales-Solibacteraceae-Candidatus_Solibacter-Candidatus_Solibacter_usitatus
90.8/98
WP_155121223.1_Acidobacteria-Acidobacteriia-Bryobacterales-Bryobacteraceae-Bryobacter-Bryobacter_aggregatus
63.1/74
OLB20486.1_Acidobacteria-root-root-root-root-Acidobacteria_bacterium_13_2_20CM_2_57_6
97.4/100
YT1_767_01366
Subgroup J
MP5_5_87_01557
89.8/88
PIR71526.1_Candidatus_Nealsonbacteria-root-root-root-root-Candidatus_Nealsonbacteria_bacterium_CG10_big_fil_rev_8_21_14_0_10_37_25
90.4/100
YT1_182_00874
Subgroup J
Yap2000.bin4.8_01072
0.125

Supplementary Fig. 30: Phylogenetic analysis *of hisI* gene (Phosphoribosyl-AMP cyclohydrolase). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 91 taxa and 128 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan and green, respectively. Woesearchaeota sequences are selected from 47 MAGs used in the inference of proteome content change history. Scale bar shows the number of average substitutions per site. Woesearchaeota subgroup J homologues are annotated in the figure. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).


UBA9638_01235
Subgroup J
100/100
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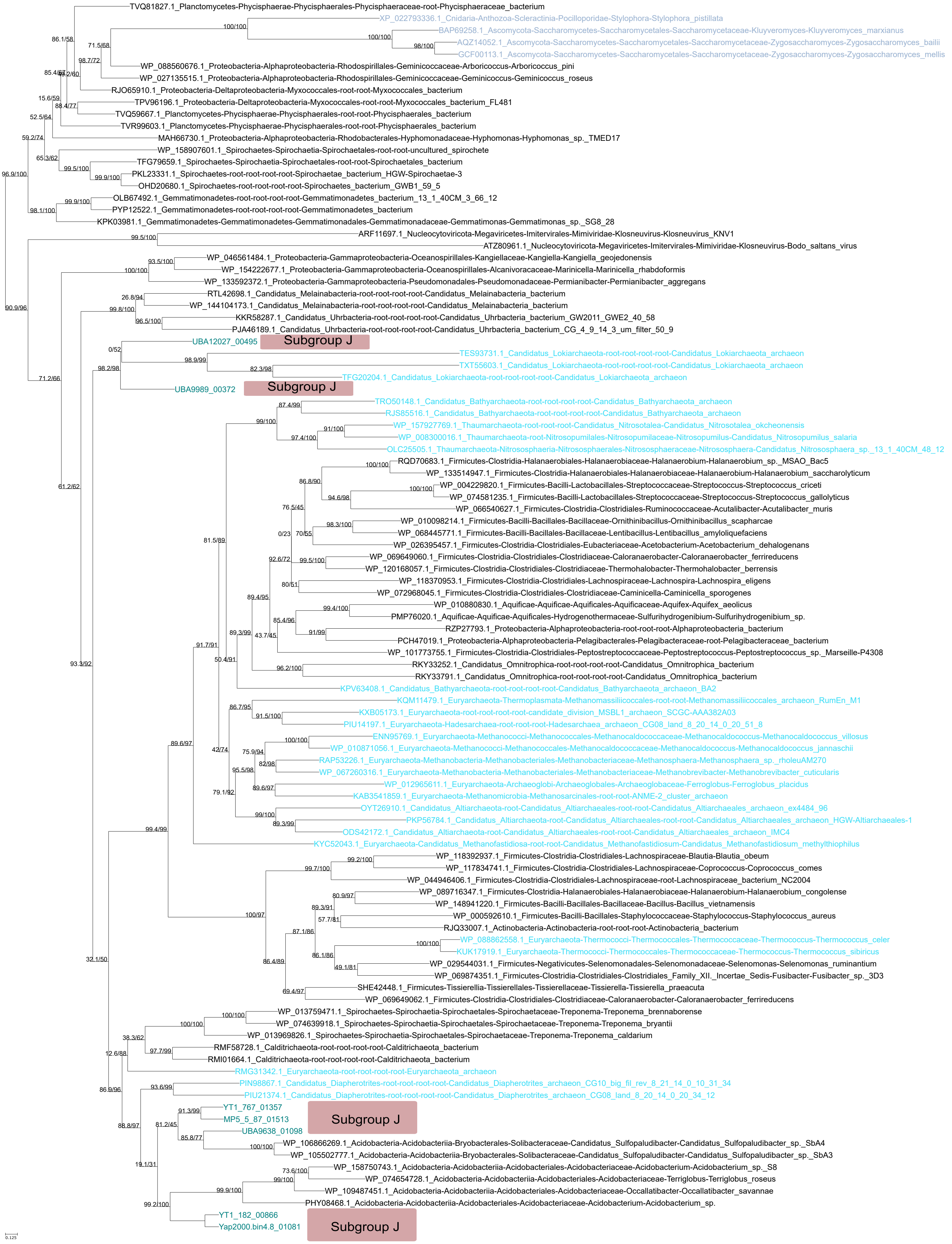
WP_012843556.1_Bacteroidetes-root-Bacteroidetes_Order_II._Incertae_sedis-Rhodothermaceae-Rhodothermus-Rhodothermus_marinus
71.8/96
WP_110022467.1_Chlorobi-Chlorobia-Chlorobiales-Chlorobiaceae-Prosthecochloris-Prosthecochloris_marina
97.1/100
WP_139626073.1_Chlorobi-Chlorobia-Chlorobiales-Chlorobiaceae-Prosthecochloris-Prosthecochloris_vibrioformis
98.7/100
WP_012506540.1_Chlorobi-Chlorobia-Chlorobiales-Chlorobiaceae-Prosthecochloris-Prosthecochloris_aestuarii
80.4/98
WP_012507195.1_Chlorobi-Chlorobia-Chlorobiales-Chlorobiaceae-Pelodictyon-Pelodictyon_phaeoclathratiforme
98.3/100
91/100
WP_011361263.1_Chlorobi-Chlorobia-Chlorobiales-Chlorobiaceae-Chlorobium-Chlorobium_chlorochromatii
93.1/99
WP_139455974.1_Chlorobi-Chlorobia-Chlorobiales-Chlorobiaceae-Chlorobaculum-Chlorobaculum_thiosulfatiphilum
RFM24205.1_Chlorobi-Chlorobia-Chlorobiales-Candidatus_Thermochlorobacteriaceae-Candidatus_Thermochlorobacter-Candidatus_Thermochlorobacter_aerophilum
100/100
WP_028895911.1_Proteobacteria-Deltaproteobacteria-Syntrophobacterales-Syntrophorhabdaceae-Syntrophorhabdus-Syntrophorhabdus_aromaticivorans
85.2/98
OPY03090.1_Proteobacteria-Deltaproteobacteria-Syntrophobacterales-Syntrophorhabdaceae-Syntrophorhabdus-Syntrophorhabdus_sp._PtaB.Bin047
99.7/100
OGL43325.1_Candidatus_Schekmanbacteria-root-root-root-root-Candidatus_Schekmanbacteria_bacterium_GWA2_38_11
76.1/94
OGL41463.1_Candidatus_Schekmanbacteria-root-root-root-root-Candidatus_Schekmanbacteria_bacterium_GWA2_38_9
65.4/90
WP_116619105.1_Proteobacteria-Deltaproteobacteria-root-root-root-Deltaproteobacteria_bacterium
86.8/75
OGQ56705.1_Proteobacteria-Deltaproteobacteria-root-root-root-Deltaproteobacteria_bacterium_RIFCSPLOWO2_02_FULL_50_16
95.9/98
WP_068859061.1_Nitrospirae-Nitrospira-Nitrospirales-Nitrospiraceae-Thermodesulfovibrio-Thermodesulfovibrio_sp._N1
81.9/64
100/100
OGW26355.1_Nitrospirae-root-root-root-root-Nitrospirae_bacterium_GWC2_57_13
84.8/94
91.4/100
OGW37291.1_Nitrospirae-root-root-root-root-Nitrospirae_bacterium_GWC2_56_14
59.3/92
OGW48373.1_Nitrospirae-root-root-root-root-Nitrospirae_bacterium_GWC2_57_9
86.4/76
97.9/100
WP_040335195.1_Nitrospirae-Nitrospira-Nitrospirales-Nitrospiraceae-Candidatus_Magnetobacterium-Candidatus_Magnetobacterium_casensis
WP_085051905.1_Nitrospirae-root-root-root-root-Nitrospirae_bacterium_HCH-1
97.4/100
OGC07462.1_root-root-root-root-root-candidate_division_WOR-1_bacterium_RIFOXYA12_FULL_36_13
92/99
OGC22036.1_root-root-root-root-root-candidate_division_WOR-1_bacterium_RIFOXYB2_FULL_37_13
OGC40344.1_root-root-root-root-root-candidate_division_WOR-1_bacterium_RIFOXYC2_FULL_46_14
99.7/100
79.1/98
OGC12404.1_root-root-root-root-root-candidate_division_WOR-1_bacterium_RIFOXYA12_FULL_52_29
84.9/85
96.9/100
OGB89418.1_root-root-root-root-root-candidate_division_WOR-1_bacterium_RIFCSPHIGHO2_01_FULL_53_15
OGC23304.1_root-root-root-root-root-candidate_division_WOR-1_bacterium_RIFOXYA2_FULL_41_14
100/100
RQD72945.1_Firmicutes-Clostridia-Clostridiales-Syntrophomonadaceae-Candidatus_Syntrophonatronum-Candidatus_Syntrophonatronum_acetioxidans
PKM83685.1_Firmicutes-root-root-root-root-Firmicutes_bacterium_HGW-Firmicutes-13
49.7/49
PIV39769.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium_CG02_land_8_20_14_3_00__42_8
35.6/84
99.5/98
OGX28785.1_Candidatus_Omnitrophica-root-root-root-root-Omnitrophica_WOR_2_bacterium_RIFCSPHIGHO2_01_FULL_49_10
PIU42257.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium_CG07_land_8_20_14_0_80_42_15
0/28
OGW90804.1_Candidatus_Omnitrophica-root-root-root-root-Omnitrophica_bacterium_RIFCSPHIGHO2_02_FULL_63_14
80.6/51
PIR66020.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium_CG10_big_fil_rev_8_21_14_0_10_43_8
85.4/76
70.3/95
2.2/55
OGW72559.1_Candidatus_Omnitrophica-root-root-root-root-Omnitrophica_bacterium_GWA2_52_12
51.3/77
OGW87130.1_Candidatus_Omnitrophica-root-root-root-root-Omnitrophica_bacterium_RIFCSPHIGHO2_02_FULL_46_11
99.8/100
OGW79106.1_Candidatus_Omnitrophica-root-root-root-root-Omnitrophica_bacterium_RIFCSPHIGHO2_02_FULL_45_28
PIQ87481.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium_CG11_big_fil_rev_8_21_14_0_20_45_26
18.8/93
WP_092048201.1_Planctomycetes-Planctomycetia-Planctomycetales-Planctomycetaceae-Planctomicrobium-Planctomicrobium_piriforme
52.6/80
WP_013110588.1_Planctomycetes-Planctomycetia-Planctomycetales-Planctomycetaceae-Planctopirus-Planctopirus_limnophila
58.5/83
WP_146504407.1_Planctomycetes-Planctomycetia-Planctomycetales-Planctomycetaceae-Rubinisphaera-Rubinisphaera_italica
83.8/96
WP_144996121.1_Planctomycetes-root-root-root-root-Planctomycetes_bacterium_Pla110
79.8/82
78.5/97
WP_146400321.1_Planctomycetes-root-root-root-root-Planctomycetes_bacterium_CA13
WP_145426315.1_Planctomycetes-root-root-root-root-Planctomycetes_bacterium_Pan258
97.3/92
WP_145259711.1_Planctomycetes-root-root-root-root-Planctomycetes_bacterium_Pan216
WP_095414847.1_Planctomycetes-Planctomycetia-Pirellulales-Thermoguttaceae-Thermogutta-Thermogutta_terrifontis
79.7/96
RLS47741.1_Planctomycetes-root-root-root-root-Planctomycetes_bacterium
80.3/95
WP_029601175.1_Planctomycetes-Planctomycetia-Gemmatales-Gemmataceae-Gemmata-Gemmata_obscuriglobus
90.5/100
98.1/100
VTU00727.1_Planctomycetes-Planctomycetia-Gemmatales-Gemmataceae-root-Gemmataceae_bacterium
78.3/86
75.6/97
WP_149114703.1_Planctomycetes-Planctomycetia-Gemmatales-Gemmataceae-Limnoglobus-Limnoglobus_roseus
RLS22226.1_Planctomycetes-root-root-root-root-Planctomycetes_bacterium
23.2/63
WP_005007394.1_Nitrospinae-Nitrospinia-Nitrospinales-Nitrospinaceae-Nitrospina-Nitrospina_gracilis
100/100
TDJ50130.1_Nitrospinae-Nitrospinia-Nitrospinales-Nitrospinaceae-Nitrospina-Nitrospina_sp.
91.3/89
93.6/100
PIQ97102.1_Nitrospinae-root-root-root-root-Nitrospinae_bacterium_CG11_big_fil_rev_8_21_14_0_20_56_8
PIR01381.1_Nitrospinae-root-root-root-root-Nitrospinae_bacterium_CG11_big_fil_rev_8_21_14_0_20_45_15
90.7/100
OGV55916.1_Lentisphaerae-root-root-root-root-Lentisphaerae_bacterium_GWF2_52_8
87.5/99
OGV55151.1_Lentisphaerae-root-root-root-root-Lentisphaerae_bacterium_GWF2_50_93
99.8/100
OGV81214.1_Lentisphaerae-root-root-root-root-Lentisphaerae_bacterium_RIFOXYA12_64_32
OGV18224.1_Lentisphaerae-root-root-root-root-Lentisphaerae_bacterium_GWF2_38_69
WP_110174228.1_Acidobacteria-Vicinamibacteria-root-Vicinamibacteraceae-Luteitalea-Luteitalea_pratensis
90.4/98
96.8/100
WP_128914585.1_Acidobacteria-Acidobacteriia-Acidobacteriales-Acidobacteriaceae-Granulicella-Granulicella_sibirica
99.9/100
WP_121470451.1_Acidobacteria-Acidobacteriia-Acidobacteriales-Acidobacteriaceae-Edaphobacter-Edaphobacter_dinghuensis
58.7/87
48.6/98
WP_114209986.1_Acidobacteria-Acidobacteriia-Acidobacteriales-Acidobacteriaceae-Acidisarcina-Acidisarcina_polymorpha
WP_015897431.1_Acidobacteria-Acidobacteriia-Acidobacteriales-Acidobacteriaceae-Acidobacterium-Acidobacterium_capsulatum
99.7/100
99.9/100
WP_105502783.1_Acidobacteria-Acidobacteriia-Bryobacterales-Solibacteraceae-Candidatus_Sulfopaludibacter-Candidatus_Sulfopaludibacter_sp._SbA3
WP_011685584.1_Acidobacteria-Acidobacteriia-Bryobacterales-Solibacteraceae-Candidatus_Solibacter-Candidatus_Solibacter_usitatus
68.8/93
WP_105314546.1_Acidobacteria-Acidobacteriia-root-root-root-Acidobacteriia_bacterium_SbA2
100/100
YT1_767_01365
MP5_5_87_01525
99.6/100
YT1_182_00873
Yap2000.bin4.8_01073
Subgroup J
0.125

Supplementary Fig. 31: Phylogenetic analysis of *hisG* gene (ATP phosphoribosyltransferase). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 72 taxa and 279 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria and Woesearchaeota are colored in black and green, respectively. Woesearchaeota sequences are selected from 47 MAGs used in the inference of proteome content change history. Woesearchaeota subgroup J homologues are annotated in the figure. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).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100/100
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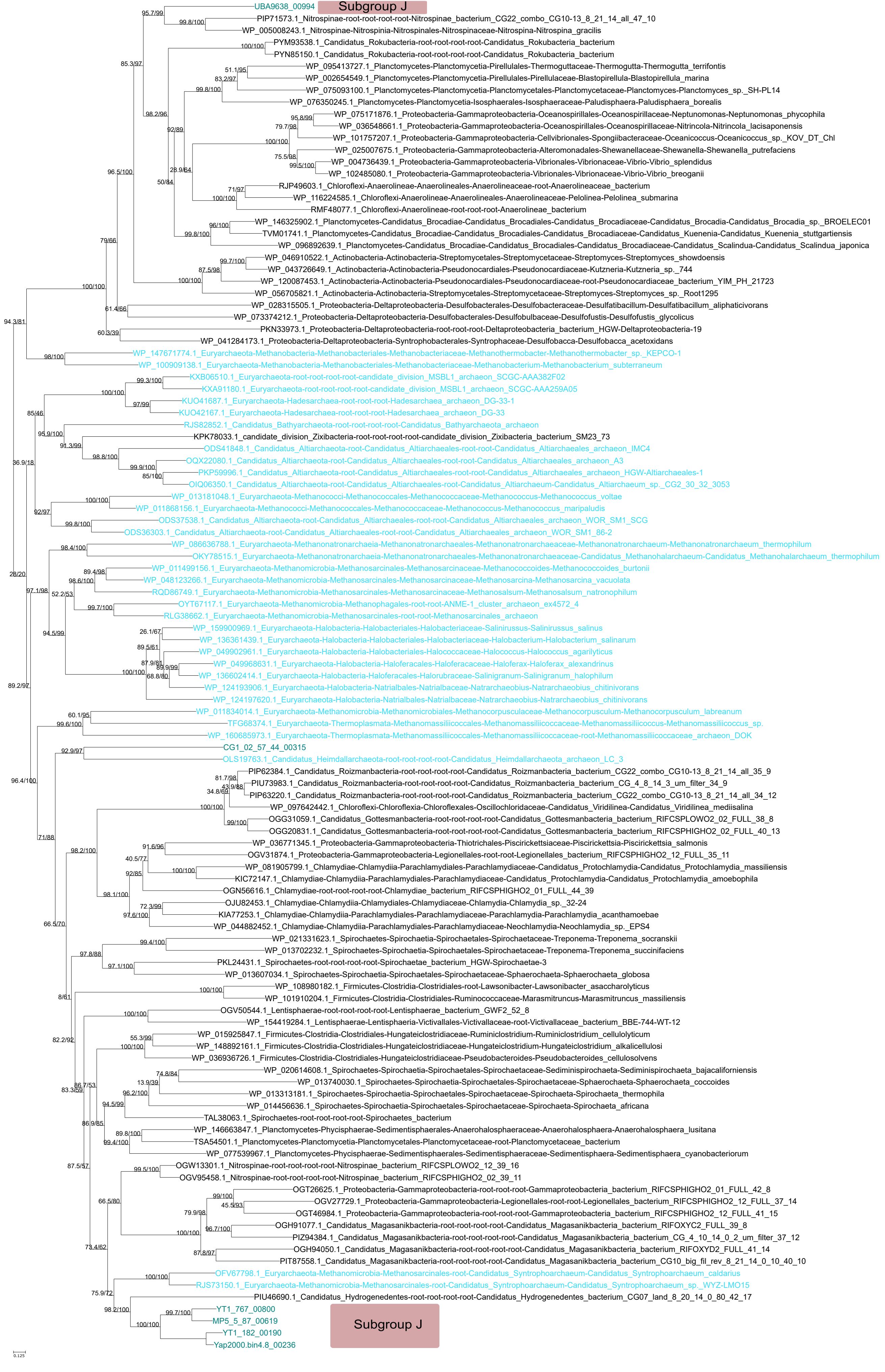
86.1/58
100/100
BAP69258.1_Ascomycota-Saccharomycetes-Saccharomycetales-Saccharomycetaceae-Kluyveromyces-Kluyveromyces_marxianus
71.5/68
98/100
AQZ14052.1_Ascomycota-Saccharomycetes-Saccharomycetales-Saccharomycetaceae-Zygosaccharomyces-Zygosaccharomyces_bailii
GCF00113.1_Ascomycota-Saccharomycetes-Saccharomycetales-Saccharomycetaceae-Zygosaccharomyces-Zygosaccharomyces_mellis
98.7/72
WP_088560676.1_Proteobacteria-Alphaproteobacteria-Rhodospirillales-Geminicoccaceae-Arboricoccus-Arboricoccus_pini
85.4/67
49.2/60
WP_027135515.1_Proteobacteria-Alphaproteobacteria-Rhodospirillales-Geminicoccaceae-Geminicoccus-Geminicoccus_roseus
RJO65910.1_Proteobacteria-Deltaproteobacteria-Myxococcales-root-root-Myxococcales_bacterium
15.6/59
TPV96196.1_Proteobacteria-Deltaproteobacteria-Myxococcales-root-root-Myxococcales_bacterium_FL481
88.4/77
TVQ59667.1_Planctomycetes-Phycisphaerae-Phycisphaerales-root-root-Phycisphaerales_bacterium
52.5/64
TVR99603.1_Planctomycetes-Phycisphaerae-Phycisphaerales-root-root-Phycisphaerales_bacterium
MAH66730.1_Proteobacteria-Alphaproteobacteria-Rhodobacterales-Hyphomonadaceae-Hyphomonas-Hyphomonas_sp._TMED17
59.2/74
WP_158907601.1_Spirochaetes-Spirochaetia-Spirochaetales-root-root-uncultured_spirochete
65.3/62
TFG79659.1_Spirochaetes-Spirochaetia-Spirochaetales-root-root-Spirochaetales_bacterium
99.5/100
96.9/100
PKL23331.1_Spirochaetes-root-root-root-root-Spirochaetae_bacterium_HGW-Spirochaetae-3
99.9/100
OHD20680.1_Spirochaetes-root-root-root-root-Spirochaetes_bacterium_GWB1_59_5
99.9/100
OLB67492.1_Gemmatimonadetes-root-root-root-root-Gemmatimonadetes_bacterium_13_1_40CM_3_66_12
98.1/100
PYP12522.1_Gemmatimonadetes-root-root-root-root-Gemmatimonadetes_bacterium
KPK03981.1_Gemmatimonadetes-Gemmatimonadetes-Gemmatimonadales-Gemmatimonadaceae-Gemmatimonas-Gemmatimonas_sp._SG8_28
99.5/100
ARF11697.1_Nucleocytoviricota-Megaviricetes-Imitervirales-Mimiviridae-Klosneuvirus-Klosneuvirus_KNV1
ATZ80961.1_Nucleocytoviricota-Megaviricetes-Imitervirales-Mimiviridae-Klosneuvirus-Bodo_saltans_virus
93.5/100
WP_046561484.1_Proteobacteria-Gammaproteobacteria-Oceanospirillales-Kangiellaceae-Kangiella-Kangiella_geojedonensis
100/100
WP_154222677.1_Proteobacteria-Gammaproteobacteria-Oceanospirillales-Alcanivoracaceae-Marinicella-Marinicella_rhabdoformis
WP_133592372.1_Proteobacteria-Gammaproteobacteria-Pseudomonadales-Pseudomonadaceae-Permianibacter-Permianibacter_aggregans
26.8/94
RTL42698.1_Candidatus_Melainabacteria-root-root-root-root-Candidatus_Melainabacteria_bacterium
90.9/96
99.8/100
WP_144104173.1_Candidatus_Melainabacteria-root-root-root-root-Candidatus_Melainabacteria_bacterium
96.5/100
KKR58287.1_Candidatus_Uhrbacteria-root-root-root-root-Candidatus_Uhrbacteria_bacterium_GW2011_GWE2_40_58
PJA46189.1_Candidatus_Uhrbacteria-root-root-root-root-Candidatus_Uhrbacteria_bacterium_CG_4_9_14_3_um_filter_50_9
UBA12027_00495
Subgroup J
0/52
TES93731.1_Candidatus_Lokiarchaeota-root-root-root-root-Candidatus_Lokiarchaeota_archaeon
98.9/99
TXT55603.1_Candidatus_Lokiarchaeota-root-root-root-root-Candidatus_Lokiarchaeota_archaeon
98.2/98
82.3/98
TFG20204.1_Candidatus_Lokiarchaeota-root-root-root-root-Candidatus_Lokiarchaeota_archaeon
71.2/66
UBA9989_00372
Subgroup J
87.4/99
TRO50148.1_Candidatus_Bathyarchaeota-root-root-root-root-Candidatus_Bathyarchaeota_archaeon
99/100
RJS85516.1_Candidatus_Bathyarchaeota-root-root-root-root-Candidatus_Bathyarchaeota_archaeon
91/100
WP_157927769.1_Thaumarchaeota-root-root-root-Candidatus_Nitrosotalea-Candidatus_Nitrosotalea_okcheonensis
97.4/100
WP_008300016.1_Thaumarchaeota-root-Nitrosopumilales-Nitrosopumilaceae-Nitrosopumilus-Candidatus_Nitrosopumilus_salaria
OLC25505.1_Thaumarchaeota-Nitrososphaeria-Nitrososphaerales-Nitrososphaeraceae-Nitrososphaera-Candidatus_Nitrososphaera_sp._13_1_40CM_48_12
100/100
RQD70683.1_Firmicutes-Clostridia-Halanaerobiales-Halanaerobiaceae-Halanaerobium-Halanaerobium_sp._MSAO_Bac5
WP_133514947.1_Firmicutes-Clostridia-Halanaerobiales-Halanaerobiaceae-Halanaerobium-Halanaerobium_saccharolyticum
86.8/90
100/100
WP_004229820.1_Firmicutes-Bacilli-Lactobacillales-Streptococcaceae-Streptococcus-Streptococcus_criceti
61.2/62
94.6/98
WP_074581235.1_Firmicutes-Bacilli-Lactobacillales-Streptococcaceae-Streptococcus-Streptococcus_gallolyticus
76.5/45
WP_066540627.1_Firmicutes-Clostridia-Clostridiales-Ruminococcaceae-Acutalibacter-Acutalibacter_muris
98.3/100
WP_010098214.1_Firmicutes-Bacilli-Bacillales-Bacillaceae-Ornithinibacillus-Ornithinibacillus_scapharcae
0/23
70/55
WP_068445771.1_Firmicutes-Bacilli-Bacillales-Bacillaceae-Lentibacillus-Lentibacillus_amyloliquefaciens
81.5/89
WP_026395457.1_Firmicutes-Clostridia-Clostridiales-Eubacteriaceae-Acetobacterium-Acetobacterium_dehalogenans
92.6/72
99.5/100
WP_069649060.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Caloranaerobacter-Caloranaerobacter_ferrireducens
WP_120168057.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Thermohalobacter-Thermohalobacter_berrensis
80/51
WP_118370953.1_Firmicutes-Clostridia-Clostridiales-Lachnospiraceae-Lachnospira-Lachnospira_eligens
89.4/95
WP_072968045.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Caminicella-Caminicella_sporogenes
99.4/100
WP_010880830.1_Aquificae-Aquificae-Aquificales-Aquificaceae-Aquifex-Aquifex_aeolicus
85.4/96
PMP76020.1_Aquificae-Aquificae-Aquificales-Hydrogenothermaceae-Sulfurihydrogenibium-Sulfurihydrogenibium_sp.
91/99
RZP27793.1_Proteobacteria-Alphaproteobacteria-root-root-root-Alphaproteobacteria_bacterium
89.3/99
43.7/45
PCH47019.1_Proteobacteria-Alphaproteobacteria-Pelagibacterales-Pelagibacteraceae-root-Pelagibacteraceae_bacterium
91.7/91
WP_101773755.1_Firmicutes-Clostridia-Clostridiales-Peptostreptococcaceae-Peptostreptococcus-Peptostreptococcus_sp._Marseille-P4308
50.4/91
RKY33252.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium
93.3/92
96.2/100
RKY33791.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium
KPV63408.1_Candidatus_Bathyarchaeota-root-root-root-root-Candidatus_Bathyarchaeota_archaeon_BA2
KQM11479.1_Euryarchaeota-Thermoplasmata-Methanomassiliicoccales-root-root-Methanomassiliicoccales_archaeon_RumEn_M1
86.7/95
KXB05173.1_Euryarchaeota-root-root-root-root-candidate_division_MSBL1_archaeon_SCGC-AAA382A03
91.5/100
PIU14197.1_Euryarchaeota-Hadesarchaea-root-root-root-Hadesarchaea_archaeon_CG08_land_8_20_14_0_20_51_8
89.6/97
100/100
ENN95769.1_Euryarchaeota-Methanococci-Methanococcales-Methanocaldococcaceae-Methanocaldococcus-Methanocaldococcus_villosus
42/74
75.9/94
WP_010871056.1_Euryarchaeota-Methanococci-Methanococcales-Methanocaldococcaceae-Methanocaldococcus-Methanocaldococcus_jannaschii
82/98
RAP53226.1_Euryarchaeota-Methanobacteria-Methanobacteriales-Methanobacteriaceae-Methanosphaera-Methanosphaera_sp._rholeuAM270
95.5/98
WP_067260316.1_Euryarchaeota-Methanobacteria-Methanobacteriales-Methanobacteriaceae-Methanobrevibacter-Methanobrevibacter_cuticularis
89.6/97
WP_012965611.1_Euryarchaeota-Archaeoglobi-Archaeoglobales-Archaeoglobaceae-Ferroglobus-Ferroglobus_placidus
79.1/92
KAB3541859.1_Euryarchaeota-Methanomicrobia-Methanosarcinales-root-root-ANME-2_cluster_archaeon
OYT26910.1_Candidatus_Altiarchaeota-root-Candidatus_Altiarchaeales-root-Candidatus_Altiarchaeales-root-Candidatus_Altiarchaeales_archaeon_ex4484_96
99/100
PKP56784.1_Candidatus_Altiarchaeota-root-Candidatus_Altiarchaeales-root-Candidatus_Altiarchaeales_archaeon_HGW-Altiarchaeales-1
89.3/99
99.4/99
ODS42172.1_Candidatus_Altiarchaeota-root-Candidatus_Altiarchaeales-root-Candidatus_Altiarchaeales_archaeon_IMC4
KYC52043.1_Euryarchaeota-Candidatus_Methanofastidiosa-root-root-Candidatus_Methanofastidiosum-Candidatus_Methanofastidiosum_methylthiophilus
99.2/100
WP_118392937.1_Firmicutes-Clostridia-Clostridiales-Lachnospiraceae-Blautia-Blautia_obeum
99.7/100
WP_117834741.1_Firmicutes-Clostridia-Clostridiales-Lachnospiraceae-Coprococcus-Coprococcus_comes
WP_044946406.1_Firmicutes-Clostridia-Clostridiales-Lachnospiraceae-root-Lachnospiraceae_bacterium_NC2004
80.9/97
WP_089716347.1_Firmicutes-Clostridia-Halanaerobiales-Halanaerobiaceae-Halanaerobium-Halanaerobium_congolense
100/97
89.3/91
WP_148941220.1_Firmicutes-Bacilli-Bacillales-Bacillaceae-Bacillus-Bacillus_vietnamensis
57.7/81
WP_000592610.1_Firmicutes-Bacilli-Bacillales-Staphylococcaceae-Staphylococcus-Staphylococcus_aureus
87.1/86
RJQ33007.1_Actinobacteria-Actinobacteria-root-root-root-Actinobacteria_bacterium
100/100
WP_088862558.1_Euryarchaeota-Thermococci-Thermococcales-Thermococcaceae-Thermococcus-Thermococcus_celer
32.1/50
86.1/86
KUK17919.1_Euryarchaeota-Thermococci-Thermococcales-Thermococcaceae-Thermococcus-Thermococcus_sibiricus
86.4/89
WP_029544031.1_Firmicutes-Negativicutes-Selenomonadales-Selenomonadaceae-Selenomonas-Selenomonas_ruminantium
49.1/81
WP_069874351.1_Firmicutes-Clostridia-Clostridiales-Clostridiales_Family_XII._Incertae_Sedis-Fusibacter-Fusibacter_sp._3D3
SHE42448.1_Firmicutes-Tissierellia-Tissierellales-Tissierellaceae-Tissierella-Tissierella_praeacuta
69.4/97
WP_069649062.1_Firmicutes-Clostridia-Clostridiales-Clostridiaceae-Caloranaerobacter-Caloranaerobacter_ferrireducens
100/100
WP_013759471.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-Treponema-Treponema_brennaborense
100/100
WP_074639918.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-Treponema-Treponema_bryantii
38.3/62
WP_013969826.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-Treponema-Treponema_caldarium
RMF58728.1_Calditrichaeota-root-root-root-root-Calditrichaeota_bacterium
12.6/88
97.7/99
RMI01664.1_Calditrichaeota-root-root-root-root-Calditrichaeota_bacterium
RMG31342.1_Euryarchaeota-root-root-root-root-Euryarchaeota_archaeon
93.6/99
PIN98867.1_Candidatus_Diapherotrites-root-root-root-root-Candidatus_Diapherotrites_archaeon_CG10_big_fil_rev_8_21_14_0_10_31_34
86.9/96
PIU21374.1_Candidatus_Diapherotrites-root-root-root-root-Candidatus_Diapherotrites_archaeon_CG08_land_8_20_14_0_20_34_12
YT1_767_01357
91.3/99
Subgroup J
MP5_5_87_01513
88.8/97
81.2/45
UBA9638_01098
85.8/77
WP_106866269.1_Acidobacteria-Acidobacteriia-Bryobacterales-Solibacteraceae-Candidatus_Sulfopaludibacter-Candidatus_Sulfopaludibacter_sp._SbA4
100/100
WP_105502777.1_Acidobacteria-Acidobacteriia-Bryobacterales-Solibacteraceae-Candidatus_Sulfopaludibacter-Candidatus_Sulfopaludibacter_sp._SbA3
19.1/31
73.6/100
WP_158750743.1_Acidobacteria-Acidobacteriia-Acidobacteriales-Acidobacteriaceae-Acidobacterium-Acidobacterium_sp._S8
99/100
WP_074654728.1_Acidobacteria-Acidobacteriia-Acidobacteriales-Acidobacteriaceae-Terriglobus-Terriglobus_roseus
99.9/100
WP_109487451.1_Acidobacteria-Acidobacteriia-Acidobacteriales-Acidobacteriaceae-Occallatibacter-Occallatibacter_savannae
99.2/100
PHY08468.1_Acidobacteria-Acidobacteriia-Acidobacteriales-Acidobacteriaceae-Acidobacterium-Acidobacterium_sp.
YT1_182_00866
Subgroup J
Yap2000.bin4.8_01081
0.125

Supplementary Fig. 32: Phylogenetic analysis of *hisA* gene (phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 103 taxa and 449 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branch. Bacteria, Archaea, Woesearchaeota and Eukaryotes are colored in black, cyan, green and grey, respectively. Woesearchaeota sequences are selected from 47 MAGs used in the inference of proteome content change history. Scale bar shows the number of average substitutions per site. Woesearchaeota subgroup J homologues are annotated in the figure. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).


UBA9638_00994
Subgroup J
PIP71573.1_Nitrospinae-root-root-root-root-Nitrospinae_bacterium_CG22_combo_CG10-13_8_21_14_all_47_10
WP_005008243.1_Nitrospinae-Nitrospinia-Nitrospinales-Nitrospinaceae-Nitrospina-Nitrospina_gracilis
PYM93538.1_Candidatus_Rokubacteria-root-root-root-root-Candidatus_Rokubacteria_bacterium
PYN85150.1_Candidatus_Rokubacteria-root-root-root-root-Candidatus_Rokubacteria_bacterium
WP_095413727.1_Planctomycetes-Planctomycetia-Pirellulales-Thermoguttaceae-Thermogutta-Thermogutta_terrifontis
WP_002654549.1_Planctomycetes-Planctomycetia-Pirellulales-Pirellulaceae-Blastopirellula-Blastopirellula_marina
WP_075093100.1_Planctomycetes-Planctomycetia-Planctomycetales-Planctomycetaceae-Planctomyces-Planctomyces_sp._SH-PL14
WP_076350245.1_Planctomycetes-Planctomycetia-Isosphaerales-Isosphaeraceae-Paludisphaera-Paludisphaera_borealis
WP_075171876.1_Proteobacteria-Gammaproteobacteria-Oceanospirillales-Oceanospirillaceae-Neptunomonas-Neptunomonas_phycophila
WP_036548661.1_Proteobacteria-Gammaproteobacteria-Oceanospirillales-Oceanospirillaceae-Nitrincola-Nitrincola_lacisaponensis
WP_101757207.1_Proteobacteria-Gammaproteobacteria-Cellvibrionales-Spongiibacteraceae-Oceanicoccus-Oceanicoccus_sp._KOV_DT_Chl
WP_025007675.1_Proteobacteria-Gammaproteobacteria-Alteromonadales-Shewanellaceae-Shewanella-Shewanella_putrefaciens
WP_004736439.1_Proteobacteria-Gammaproteobacteria-Vibrionales-Vibrionaceae-Vibrio-Vibrio_splendidus
WP_102485080.1_Proteobacteria-Gammaproteobacteria-Vibrionales-Vibrionaceae-Vibrio-Vibrio_breoganii
RJP49603.1_Chloroflexi-Anaerolineae-Anaerolineales-Anaerolineaceae-root-Anaerolineaceae_bacterium
WP_116224585.1_Chloroflexi-Anaerolineae-Anaerolineales-Anaerolineaceae-Pelolinea-Pelolinea_submarina
RMF48077.1_Chloroflexi-Anaerolineae-root-root-root-Anaerolineae_bacterium
WP_146325902.1_Planctomycetes-Candidatus_Brocadiae-Candidatus_Brocadiales-Candidatus_Brocadiaceae-Candidatus_Brocadia-Candidatus_Brocadia_sp._BROELEC01
TVM01741.1_Planctomycetes-Candidatus_Brocadiae-Candidatus_Brocadiales-Candidatus_Brocadiaceae-Candidatus_Kuenenia-Candidatus_Kuenenia_stuttgartiensis
WP_096892639.1_Planctomycetes-Candidatus_Brocadiae-Candidatus_Brocadiales-Candidatus_Brocadiaceae-Candidatus_Scalindua-Candidatus_Scalindua_japonica
WP_046910522.1_Actinobacteria-Actinobacteria-Streptomycetales-Streptomycetaceae-Streptomyces-Streptomyces_showdoensis
WP_043726649.1_Actinobacteria-Actinobacteria-Pseudonocardiales-Pseudonocardiaceae-Kutzneria-Kutzneria_sp._744
WP_120087453.1_Actinobacteria-Actinobacteria-Pseudonocardiales-Pseudonocardiaceae-root-Pseudonocardiaceae_bacterium_YIM_PH_21723
WP_056705821.1_Actinobacteria-Actinobacteria-Streptomycetales-Streptomycetaceae-Streptomyces-Streptomyces_sp._Root1295
WP_028315505.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobacteraceae-Desulfatibacillum-Desulfatibacillum_aliphaticivorans
WP_073374212.1_Proteobacteria-Deltaproteobacteria-Desulfobacterales-Desulfobulbaceae-Desulfofustis-Desulfofustis_glycolicus
PKN33973.1_Proteobacteria-Deltaproteobacteria-root-root-root-Deltaproteobacteria_bacterium_HGW-Deltaproteobacteria-19
WP_041284173.1_Proteobacteria-Deltaproteobacteria-Syntrophobacterales-Syntrophaceae-Desulfobacca-Desulfobacca_acetoxidans
WP_147671774.1_Euryarchaeota-Methanobacteria-Methanobacteriales-Methanobacteriaceae-Methanothermobacter-Methanothermobacter_sp._KEPCO-1
WP_100909138.1_Euryarchaeota-Methanobacteria-Methanobacteriales-Methanobacteriaceae-Methanobacterium-Methanobacterium_subterraneum
KXB06510.1_Euryarchaeota-root-root-root-root-candidate_division_MSBL1_archaeon_SCGC-AAA382F02
KXA91180.1_Euryarchaeota-root-root-root-root-candidate_division_MSBL1_archaeon_SCGC-AAA259A05
KUO41687.1_Euryarchaeota-Hadesarchaea-root-root-root-Hadesarchaea_archaeon_DG-33-1
KUO42167.1_Euryarchaeota-Hadesarchaea-root-root-root-Hadesarchaea_archaeon_DG-33
RJS82852.1_Candidatus_Bathyarchaeota-root-root-root-Candidatus_Bathyarchaeota_archaeon
KPK78033.1_candidate_division_Zixibacteria-root-root-root-candidate_division_Zixibacteria_bacterium_SM23_73
ODS41848.1_Candidatus_Altiarchaeota-root-Candidatus_Altiarchaeales-root-root-Candidatus_Altiarchaeales_archaeon_IMC4
OQX22080.1_Candidatus_Altiarchaeota-root-Candidatus_Altiarchaeales-root-root-Candidatus_Altiarchaeales_archaeon_A3
PKP59996.1_Candidatus_Altiarchaeota-root-Candidatus_Altiarchaeales-root-root-Candidatus_Altiarchaeales_archaeon_HGW-Altiarchaeales-1
OIQ06350.1_Candidatus_Altiarchaeota-root-Candidatus_Altiarchaeales-root-Candidatus_Altiarchaeum-Candidatus_Altiarchaeum_sp._CG2_30_32_3053
WP_013181048.1_Euryarchaeota-Methanococci-Methanococcales-Methanococcaceae-Methanococcus-Methanococcus_voltae
WP_011868156.1_Euryarchaeota-Methanococci-Methanococcales-Methanococcaceae-Methanococcus-Methanococcus_maripaludis
ODS37538.1_Candidatus_Altiarchaeota-root-Candidatus_Altiarchaeales-root-root-Candidatus_Altiarchaeales_archaeon_WOR_SM1_SCG
ODS36303.1_Candidatus_Altiarchaeota-root-Candidatus_Altiarchaeales-root-root-Candidatus_Altiarchaeales_archaeon_WOR_SM1_86-2
WP_086636788.1_Euryarchaeota-Methanonatronarchaeia-Methanonatronarchaeales-Methanonatronarchaeaceae-Methanonatronarchaeum-Methanonatronarchaeum_thermophilum
OKY78515.1_Euryarchaeota-Methanonatronarchaeia-Methanonatronarchaeales-Methanonatronarchaeaceae-Candidatus_Methanohalarchaeum-Candidatus_Methanohalarchaeum_thermophilum
WP_011499156.1_Euryarchaeota-Methanomicrobia-Methanosarcinales-Methanosarcinaceae-Methanococcoides-Methanococcoides_burtonii
WP_048123266.1_Euryarchaeota-Methanomicrobia-Methanosarcinales-Methanosarcinaceae-Methanosarcina-Methanosarcina_vacuolata
RQD86749.1_Euryarchaeota-Methanomicrobia-Methanosarcinales-Methanosarcinaceae-Methanosalsum-Methanosalsum_natronophilum
OYT67117.1_Euryarchaeota-Methanomicrobia-Methanophagales-root-root-ANME-1_cluster_archaeon_ex4572_4
RLG38662.1_Euryarchaeota-Methanomicrobia-Methanosarcinales-root-root-Methanosarcinales_archaeon
WP_159900969.1_Euryarchaeota-Halobacteria-Halobacteriales-Halobacteriaceae-Salinirussus-Salinirussus_salinus
WP_136361439.1_Euryarchaeota-Halobacteria-Halobacteriales-Halobacteriaceae-Halobacterium-Halobacterium_salinarum
WP_049902961.1_Euryarchaeota-Halobacteria-Halobacteriales-Halococcaceae-Halococcus-Halococcus_agarilyticus
WP_049968631.1_Euryarchaeota-Halobacteria-Haloferacales-Haloferacaceae-Haloferax-Haloferax_alexandrinus
WP_136602414.1_Euryarchaeota-Halobacteria-Haloferacales-Halorubraceae-Salinigranum-Salinigranum_halophilum
WP_124193906.1_Euryarchaeota-Halobacteria-Natrialbales-Natrialbaceae-Natrarchaeobius-Natrarchaeobius_chitinivorans
WP_124197620.1_Euryarchaeota-Halobacteria-Natrialbales-Natrialbaceae-Natrarchaeobius-Natrarchaeobius_chitinivorans
WP_011834014.1_Euryarchaeota-Methanomicrobia-Methanomicrobiales-Methanocorpusculaceae-Methanocorpusculum-Methanocorpusculum_labreanum
TFG68374.1_Euryarchaeota-Thermoplasmata-Methanomassiliicoccales-Methanomassiliicoccaceae-Methanomassiliicoccus-Methanomassiliicoccus_sp.
WP_160685973.1_Euryarchaeota-Thermoplasmata-Methanomassiliicoccales-Methanomassiliicoccaceae-root-Methanomassiliicoccaceae_archaeon_DOK
CG1_02_57_44_00315
OLS19763.1_Candidatus_Heimdallarchaeota-root-root-root-Candidatus_Heimdallarchaeota_archaeon_LC_3
PIP62384.1_Candidatus_Roizmanbacteria-root-root-root-root-Candidatus_Roizmanbacteria_bacterium_CG22_combo_CG10-13_8_21_14_all_35_9
PIU73983.1_Candidatus_Roizmanbacteria-root-root-root-root-Candidatus_Roizmanbacteria_bacterium_CG_4_8_14_3_um_filter_34_9
PIP63220.1_Candidatus_Roizmanbacteria-root-root-root-root-Candidatus_Roizmanbacteria_bacterium_CG22_combo_CG10-13_8_21_14_all_34_12
WP_097642442.1_Chloroflexi-Chloroflexia-Chloroflexales-Oscillochloridaceae-Candidatus_Viridilinea-Candidatus_Viridilinea_mediisalina
OGG31059.1_Candidatus_Gottesmanbacteria-root-root-root-root-Candidatus_Gottesmanbacteria_bacterium_RIFCSPLOWO2_02_FULL_38_8
OGG20831.1_Candidatus_Gottesmanbacteria-root-root-root-root-Candidatus_Gottesmanbacteria_bacterium_RIFCSPHIGHO2_02_FULL_40_13
WP_036771345.1_Proteobacteria-Gammaproteobacteria-Thiotrichales-Piscirickettsiaceae-Piscirickettsia-Piscirickettsia_salmonis
OGV31874.1_Proteobacteria-Gammaproteobacteria-Legionellales-root-root-Legionellales_bacterium_RIFCSPHIGHO2_12_FULL_35_11
WP_081905799.1_Chlamydiae-Chlamydiia-Parachlamydiales-Parachlamydiaceae-Candidatus_Protochlamydia-Candidatus_Protochlamydia_massiliensis
KIC72147.1_Chlamydiae-Chlamydiia-Parachlamydiales-Parachlamydiaceae-Candidatus_Protochlamydia-Candidatus_Protochlamydia_amoebophila
OGN56616.1_Chlamydiae-root-root-root-root-Chlamydiae_bacterium_RIFCSPHIGHO2_01_FULL_44_39
OJU82453.1_Chlamydiae-Chlamydiia-Chlamydiales-Chlamydiaceae-Chlamydia-Chlamydia_sp._32-24
KIA77253.1_Chlamydiae-Chlamydiia-Parachlamydiales-Parachlamydiaceae-Parachlamydia-Parachlamydia_acanthamoebae
WP_044882452.1_Chlamydiae-Chlamydiia-Parachlamydiales-Parachlamydiaceae-Neochlamydia-Neochlamydia_sp._EPS4
WP_021331623.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-Treponema-Treponema_socranskii
WP_013702232.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-Treponema-Treponema_succinifaciens
PKL24431.1_Spirochaetes-root-root-root-Spirochaetae_bacterium_HGW-Spirochaetae-3
WP_013607034.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-Sphaerochaeta-Sphaerochaeta_globosa
WP_108980182.1_Firmicutes-Clostridia-Clostridiales-root-Lawsonibacter-Lawsonibacter_asaccharolyticus
WP_101910204.1_Firmicutes-Clostridia-Clostridiales-Ruminococcaceae-Marasmitruncus-Marasmitruncus_massiliensis
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WP_015925847.1_Firmicutes-Clostridia-Clostridiales-Hungateiclostridiaceae-Ruminiclostridium-Ruminiclostridium_cellulolyticum
WP_148892161.1_Firmicutes-Clostridia-Clostridiales-Hungateiclostridiaceae-Hungateiclostridium-Hungateiclostridium_alkalicellulosi
WP_036936726.1_Firmicutes-Clostridia-Clostridiales-Hungateiclostridiaceae-Pseudobacteroides-Pseudobacteroides_cellulosolvens
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WP_013313181.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-Spirochaeta-Spirochaeta_thermophila
WP_014456636.1_Spirochaetes-Spirochaetia-Spirochaetales-Spirochaetaceae-Spirochaeta-Spirochaeta_africana
TAL38063.1_Spirochaetes-root-root-root-root-Spirochaetes_bacterium
WP_146663847.1_Planctomycetes-Phycisphaerae-Sedimentisphaerales-Anaerohalosphaeraceae-Anaerohalosphaera-Anaerohalosphaera_lusitana
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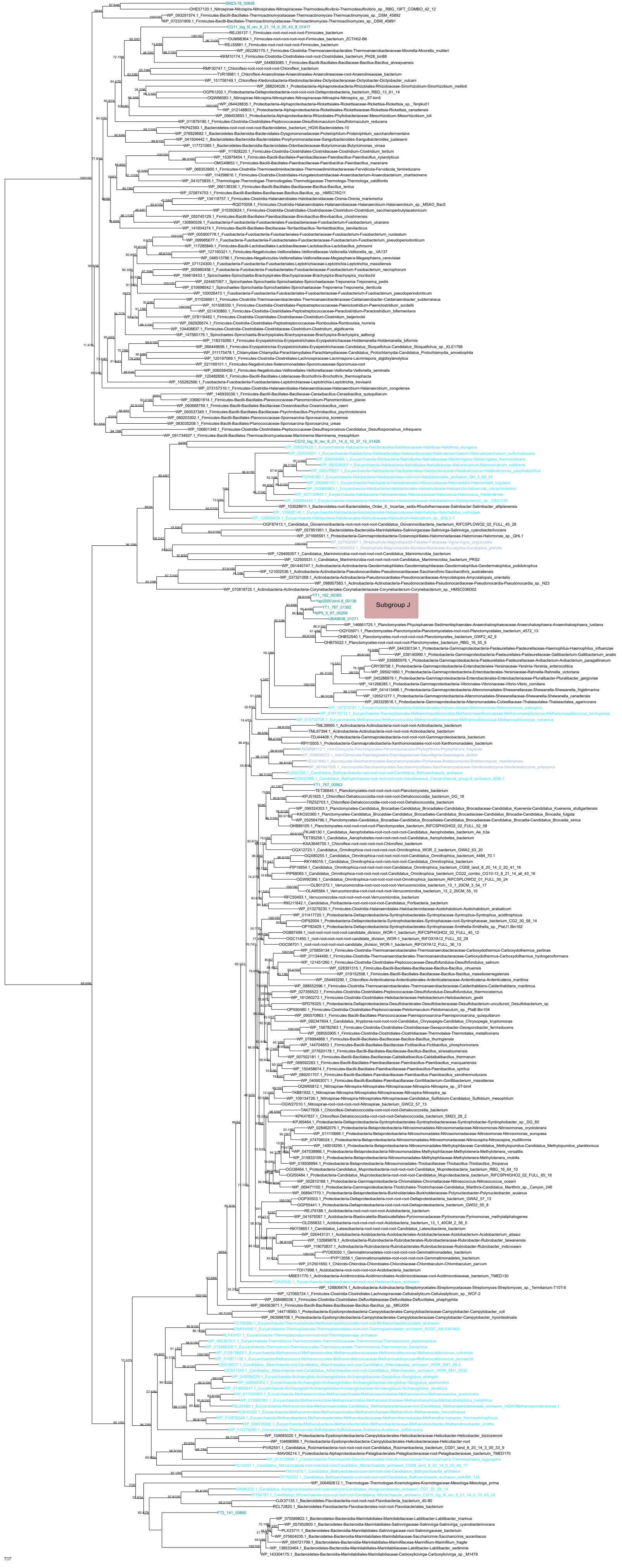
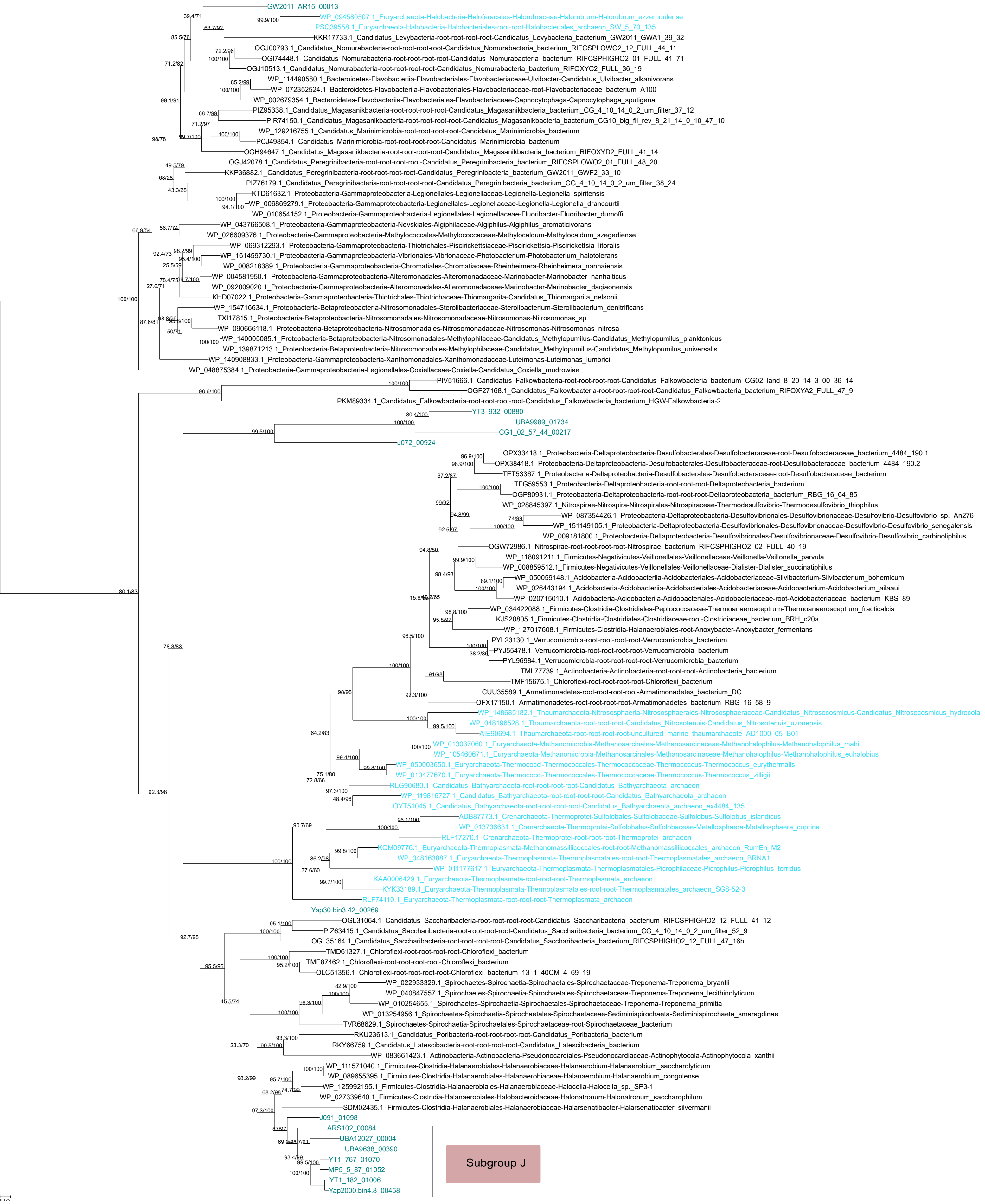
OGV95458.1_Nitrospinae-root-root-root-root-Nitrospinae_bacterium_RIFCSPHIGHO2_02_39_11
OGT26625.1_Proteobacteria-Gammaproteobacteria-root-root-root-Gammaproteobacteria_bacterium_RIFCSPHIGHO2_01_FULL_42_8
OGV27729.1_Proteobacteria-Gammaproteobacteria-Legionellales-root-root-Legionellales_bacterium_RIFCSPHIGHO2_12_FULL_37_14
OGT46984.1_Proteobacteria-Gammaproteobacteria-root-root-root-Gammaproteobacteria_bacterium_RIFCSPHIGHO2_12_FULL_41_15
OGH91077.1_Candidatus_Magasanikbacteria-root-root-root-root-Candidatus_Magasanikbacteria_bacterium_RIFOXYC2_FULL_39_8
PIZ94384.1_Candidatus_Magasanikbacteria-root-root-root-root-Candidatus_Magasanikbacteria_bacterium_CG_4_10_14_0_2_um_filter_37_12
OGH94050.1_Candidatus_Magasanikbacteria-root-root-root-root-Candidatus_Magasanikbacteria_bacterium_RIFOXYD2_FULL_41_14
PIT87558.1_Candidatus_Magasanikbacteria-root-root-root-root-Candidatus_Magasanikbacteria_bacterium_CG10_big_fil_rev_8_21_14_0_10_40_10
OFV67798.1_Euryarchaeota-Methanomicrobia-Methanosarcinales-root-Candidatus_Syntrophoarchaeum-Candidatus_Syntrophoarchaeum_caldarius
RJS73150.1_Euryarchaeota-Methanomicrobia-Methanosarcinales-root-Candidatus_Syntrophoarchaeum-Candidatus_Syntrophoarchaeum_sp._WYZ-LMO15
PIU46690.1_Candidatus_Hydrogenedentes-root-root-root-root-Candidatus_Hydrogenedentes_bacterium_CG07_land_8_20_14_0_80_42_17
YT1_767_00800
MP5_5_87_00619
YT1_182_00190
Yap2000.bin4.8_00236
Subgroup J
0.125

Supplementary Fig. 33: Phylogenetic analysis of *aroA* gene (3-phosphoshikimate 1-carboxyvinyltransferase). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 113 taxa and 437 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan and green, respectively. Woesearchaeota sequences are selected from 47 MAGs used in the inference of proteome content change history. Woesearchaeota subgroup J homologues are annotated in the figure. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).



Supplementary Fig. 34: Phylogenetic analysis of *trpG* gene (glutamine amidotransferase of anthranilate synthase). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 263 taxa and 268 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan and green, respectively. Woesearchaeota sequences are selected from 47 MAGs used in the inference of proteome content change history. Woesearchaeota subgroup J homologues are annotated in the figure. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).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KKR17733.1_Candidatus_Levybacteria-root-root-root-root-Candidatus_Levybacteria_bacterium_GW2011_GWA1_39_32
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OGI74448.1_Candidatus_Nomurabacteria-root-root-root-root-Candidatus_Nomurabacteria_bacterium_RIFCSPHIGHO2_01_FULL_41_71
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WP_072352524.1_Bacteroidetes-Flavobacteriia-Flavobacteriales-Flavobacteriaceae-root-Flavobacteriaceae_bacterium_A100
WP_002679354.1_Bacteroidetes-Flavobacteriia-Flavobacteriales-Flavobacteriaceae-Capnocytophaga-Capnocytophaga_sputigena
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OGJ42078.1_Candidatus_Peregrinibacteria-root-root-root-root-Candidatus_Peregrinibacteria_bacterium_RIFCSPLOWO2_01_FULL_48_20
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PIZ76179.1_Candidatus_Peregrinibacteria-root-root-root-root-Candidatus_Peregrinibacteria_bacterium_CG_4_10_14_0_2_um_filter_38_24
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UBA9989_01734
CG1_02_57_44_00217
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WP_151149105.1_Proteobacteria-Deltaproteobacteria-Desulfovibrionales-Desulfovibrionaceae-Desulfovibrio-Desulfovibrio_senegalensis
WP_009181800.1_Proteobacteria-Deltaproteobacteria-Desulfovibrionales-Desulfovibrionaceae-Desulfovibrio-Desulfovibrio_carbinoliphilus
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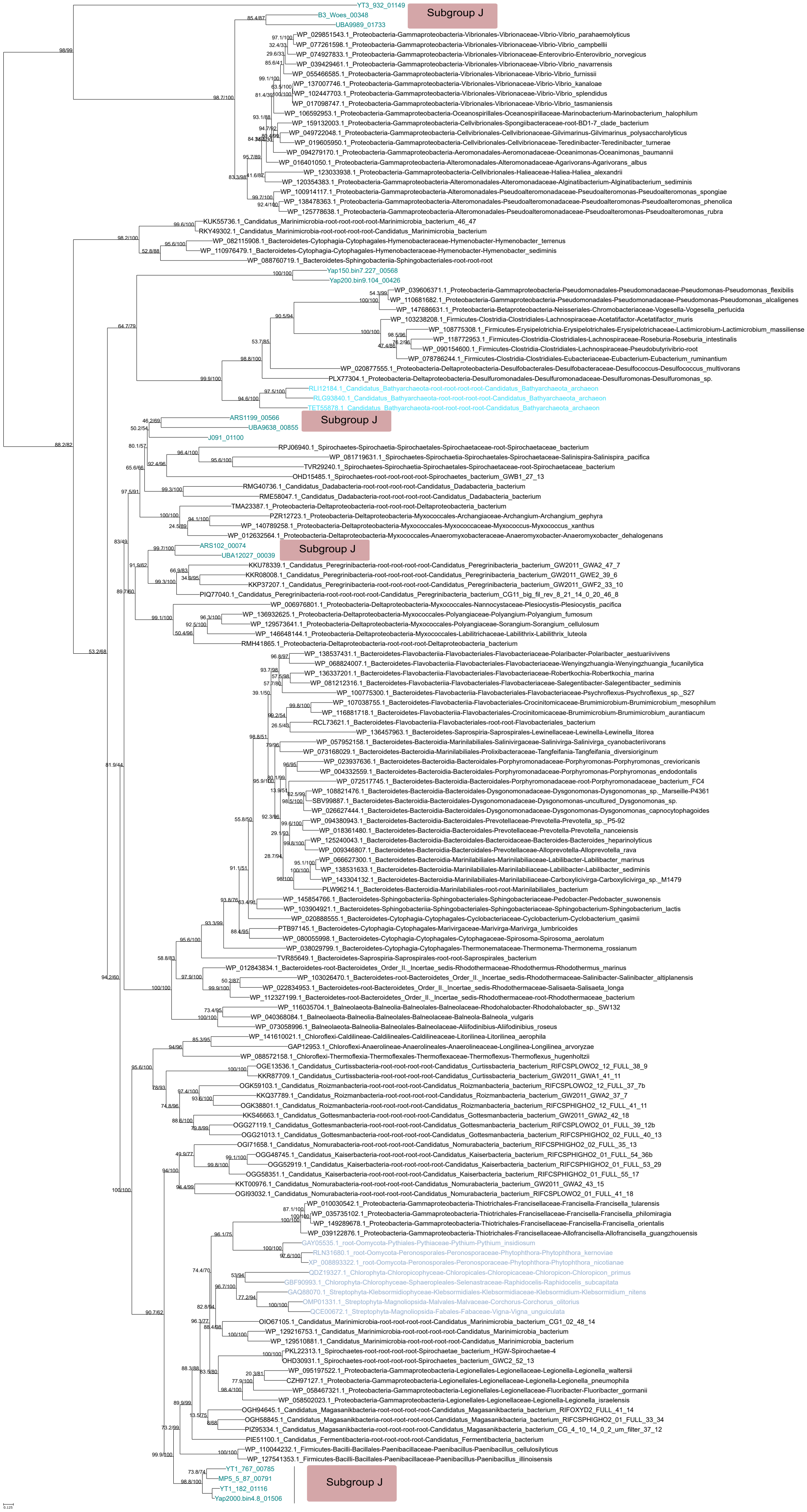
YT1_767_01070
MP5_5_87_01052
YT1_182_01006
Yap2000.bin4.8_00458
Subgroup J
0.125

Supplementary Fig. 35: Phylogenetic analysis of *purB* gene (adenylosuccinate lyase). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 115 taxa and 571 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan and green, respectively. Woesearchaeota sequences are selected from 47 MAGs used in the inference of proteome content change history. Scale bar shows the number of average substitutions per site. Woesearchaeota subgroup J homologues are annotated in the figure. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).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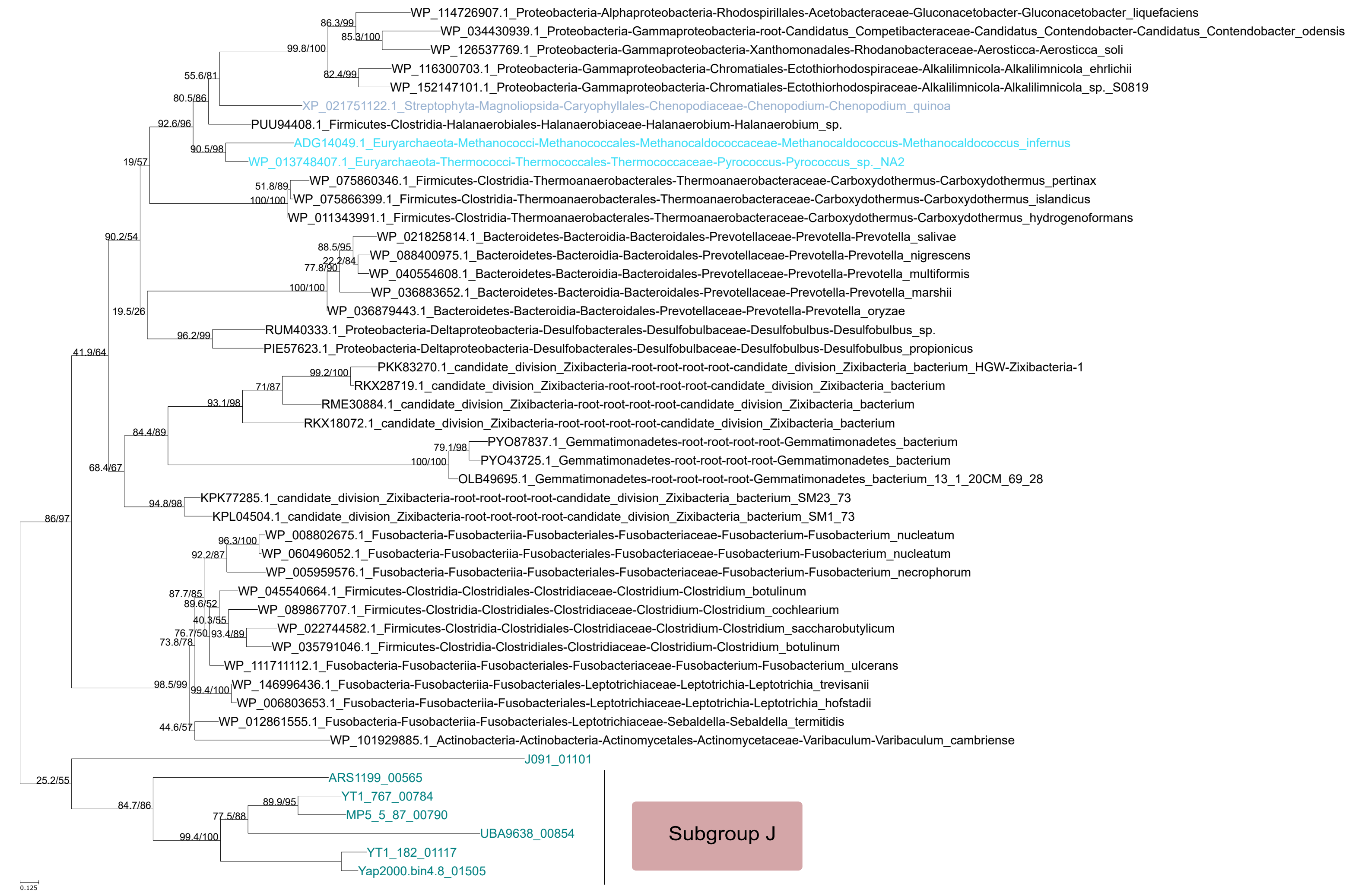
YT1_767_00785
MP5_5_87_00791
YT1_182_01116
Yap2000.bin4.8_01506
Subgroup J
0.125

Supplementary Fig. 36: Phylogenetic analysis of *purC* gene (SAICAR synthetase). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 153 taxa and 773 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea, Woesearchaeota and Eukaryotes are colored in black, cyan, green and grey, respectively. Woesearchaeota sequences are selected from 47 MAGs used in the inference of proteome content change history. Scale bar shows the number of average substitutions per site. Woesearchaeota subgroup J homologues are annotated in the figure. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).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19/57
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90.2/54
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22.2/84
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96.2/99
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41.9/64
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93.1/98
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79.1/98
100/100
PYO43725.1_Gemmatimonadetes-root-root-root-root-Gemmatimonadetes_bacterium
68.4/67
OLB49695.1_Gemmatimonadetes-root-root-root-root-Gemmatimonadetes_bacterium_13_1_20CM_69_28
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94.8/98
86/97
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96.3/100
92.2/87
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40.3/55
76.7/50
93.4/89
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89.9/95
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77.5/88
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99.4/100
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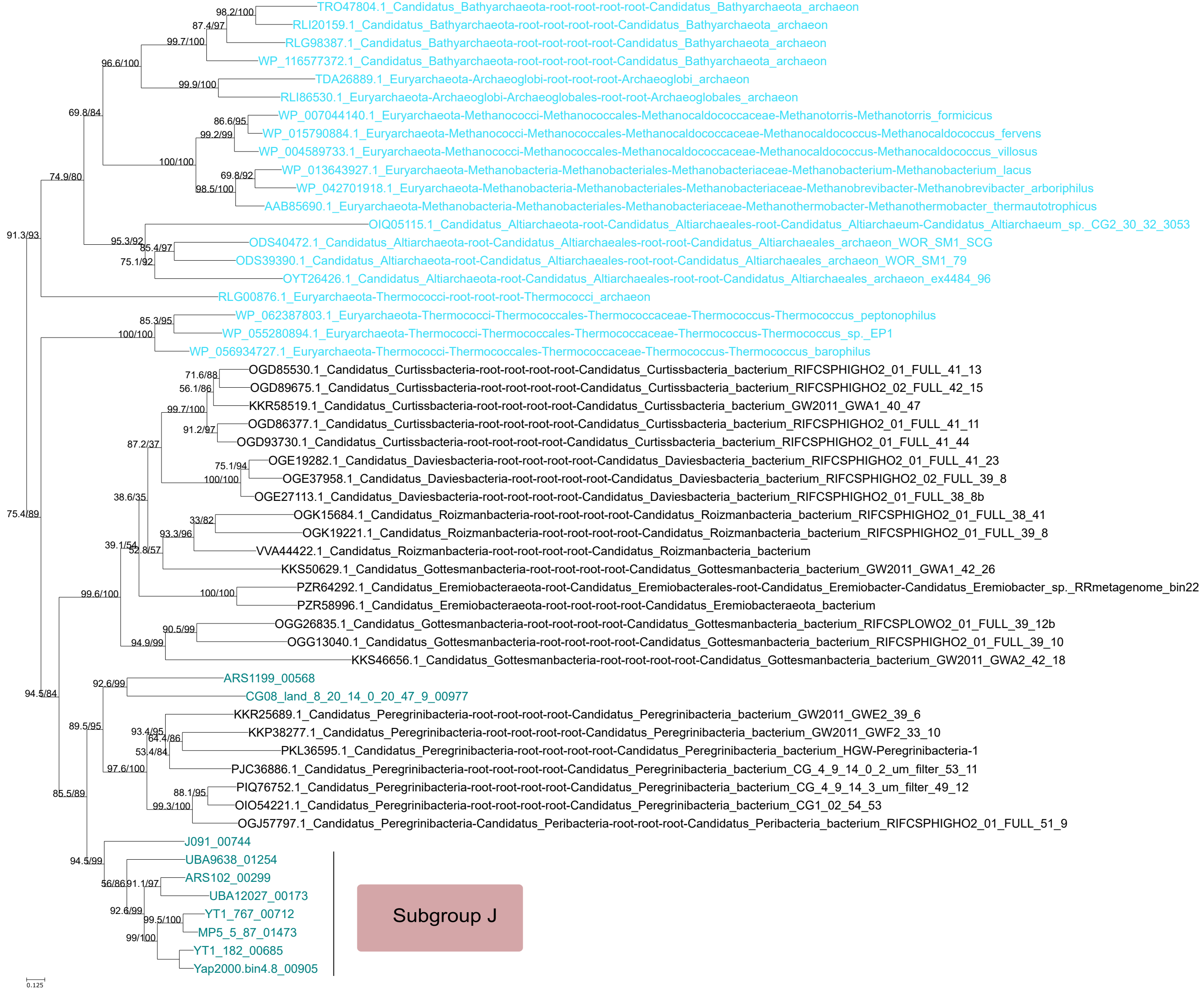
Subgroup J
0.125

Supplementary Fig. 37: Phylogenetic analysis of *purE* gene (AIR carboxylase). The tree was unrooted and inferred using IQ-Tree LG+C20+G model on an alignment of 47 taxa and 509 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea, Woesearchaeota and Eukaryotes are colored in black, cyan, green and grey, respectively. Woesearchaeota sequences are selected from 47 MAGs used in the inference of proteome content change history. Woesearchaeota subgroup J homologues are annotated in the figure. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).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86.6/95
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74.9/80
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69.8/92
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98.5/100
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56.1/86
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99.7/100
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75.1/94
OGE19282.1_Candidatus_Daviesbacteria-root-root-root-root-Candidatus_Daviesbacteria_bacterium_RIFCSPHIGHO2_01_FULL_41_23
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OGE37958.1_Candidatus_Daviesbacteria-root-root-root-root-Candidatus_Daviesbacteria_bacterium_RIFCSPHIGHO2_02_FULL_39_8
38.6/35
OGE27113.1_Candidatus_Daviesbacteria-root-root-root-root-Candidatus_Daviesbacteria_bacterium_RIFCSPHIGHO2_01_FULL_38_8b
75.4/89
33/82
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93.3/96
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39.1/54
52.8/57
VVA44422.1_Candidatus_Roizmanbacteria-root-root-root-root-Candidatus_Roizmanbacteria_bacterium
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64.4/86
53.4/84
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97.6/100
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99.3/100
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56/86
91.1/97
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92.6/99
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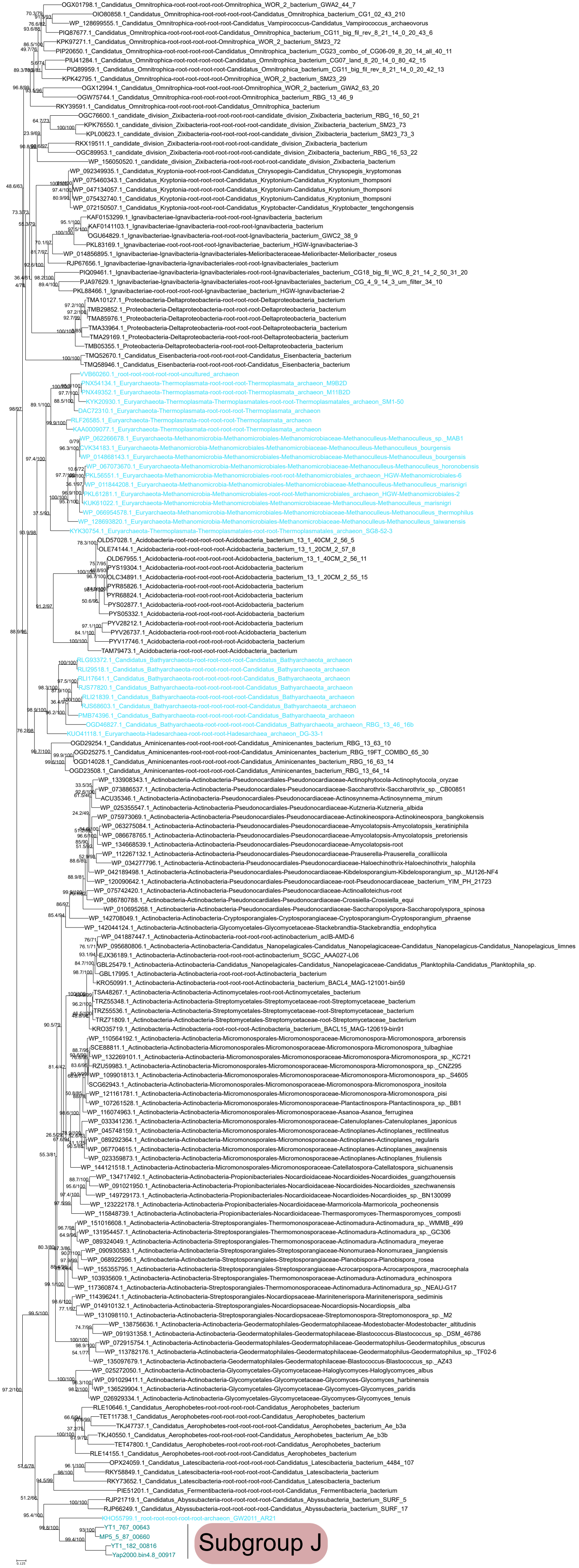
99.5/100
MP5_5_87_01473
99/100
YT1_182_00685
Yap2000.bin4.8_00905
Subgroup J
0.125

Supplementary Fig. 38: Phylogenetic analysis of *purP* gene (5-formaminoimidazole-4-carboxamide-1-(beta)-D-ribofuranosyl 5'-monophosphate synthetase). An unrooted phylogenetic tree was inferred using IQ-Tree LG+C20+G model on an alignment of 59 taxa and 544 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan and green, respectively. Woesearchaeota sequences are selected from 47 MAGs used in the inference of proteome content change history. Scale bar shows the number of average substitutions per site. Woesearchaeota subgroup J homologues are annotated in the figure. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).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TRZ55536.1_Actinobacteria-Actinobacteria-Streptomycetales-Streptomycetaceae-root-Streptomycetaceae_bacterium
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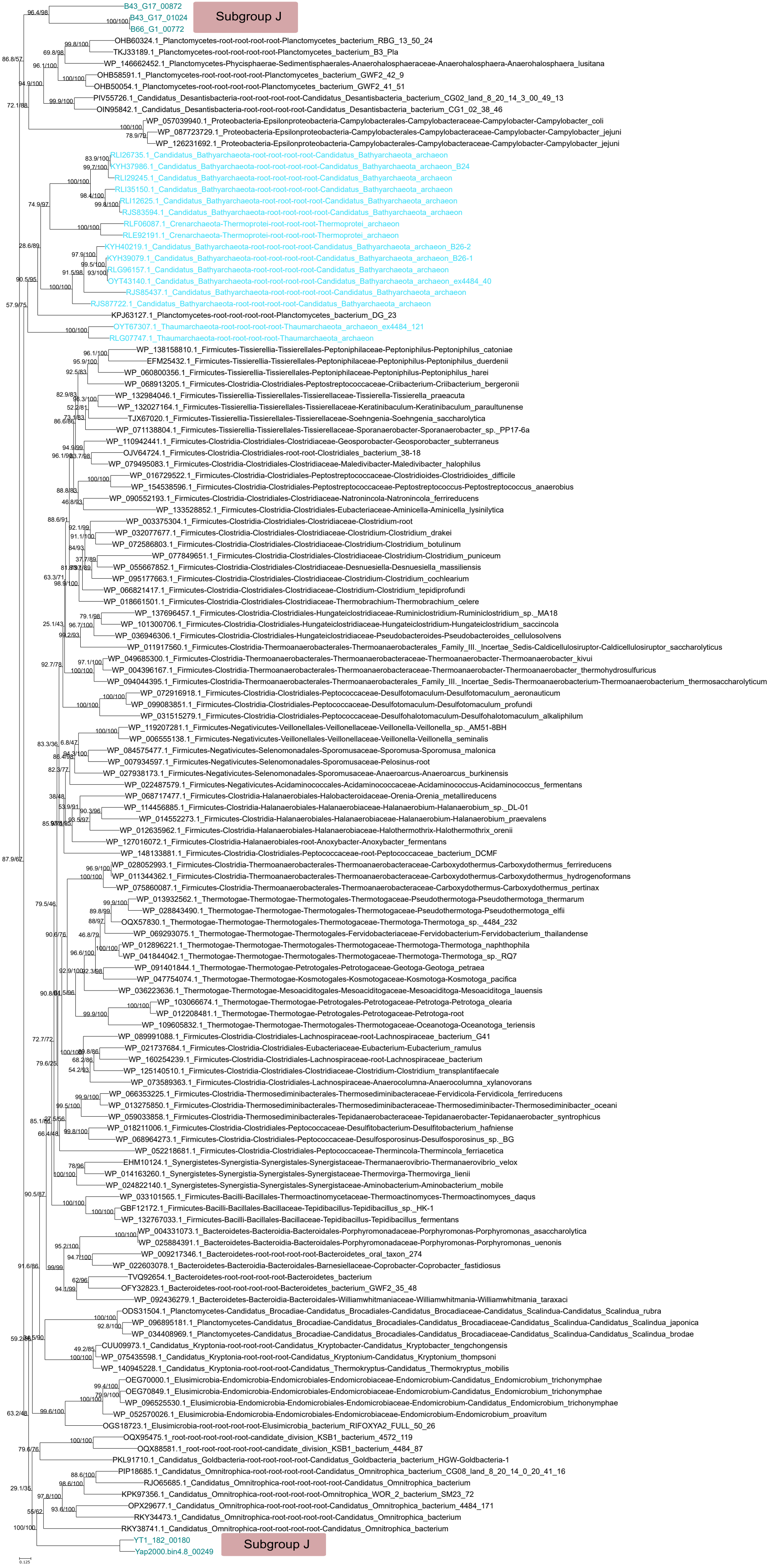
MP5_5_87_00660
YT1_182_00816
Yap2000.bin4.8_00917
Subgroup J
0.125

Supplementary Fig. 39: Phylogenetic analysis of *pfk* gene (phosphofrutokinase). The tree was unrooted and inferred using IQ-Tree LG+G+F+C20 model on an alignment of 169 taxa and 351 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan and green, respectively. Woesearchaeota sequences are selected from the subgroup J MAGs. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).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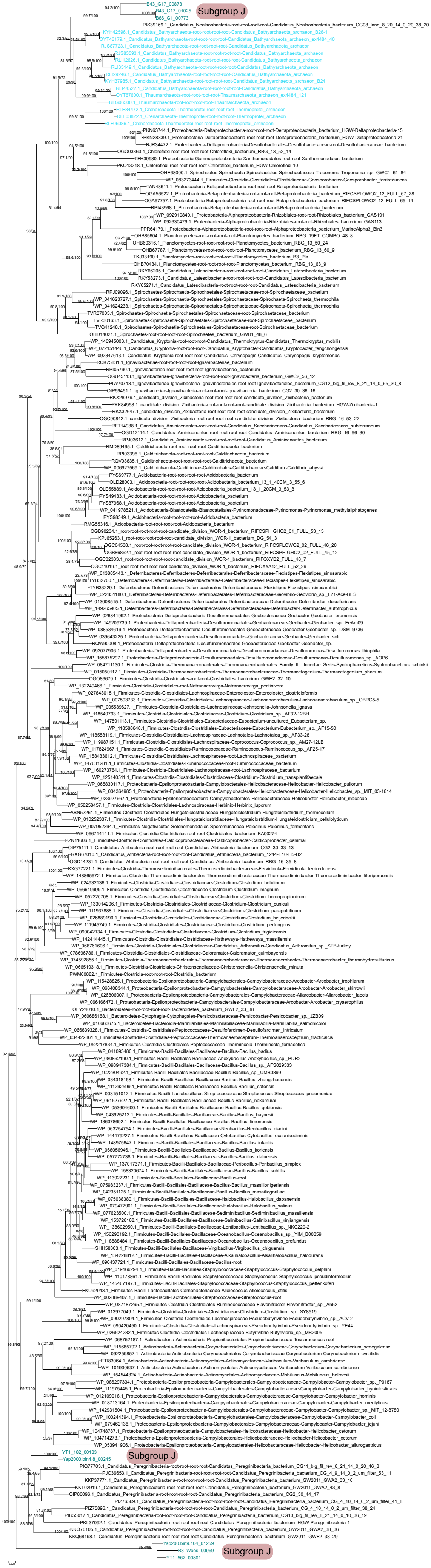
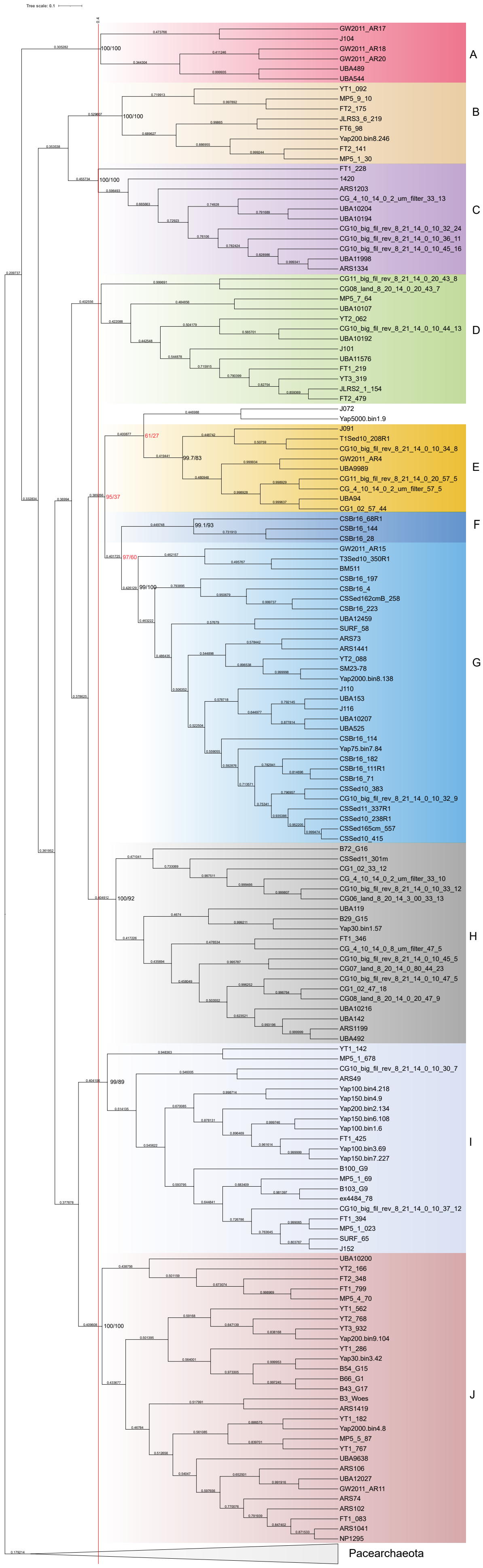
WP_073589363.1_Firmicutes-Clostridia-Clostridiales-Lachnospiraceae-Anaerocolumna-Anaerocolumna_xylanovorans
WP_066353225.1_Firmicutes-Clostridia-Thermosediminibacterales-Thermosediminibacteraceae-Fervidicola-Fervidicola_ferrireducens
WP_013275850.1_Firmicutes-Clostridia-Thermosediminibacterales-Thermosediminibacteraceae-Thermosediminibacter-Thermosediminibacter_oceani
WP_059033858.1_Firmicutes-Clostridia-Thermosediminibacterales-Tepidanaerobacteraceae-Tepidanaerobacter-Tepidanaerobacter_syntrophicus
WP_018211006.1_Firmicutes-Clostridia-Clostridiales-Peptococcaceae-Desulfitobacterium-Desulfitobacterium_hafniense
WP_068964273.1_Firmicutes-Clostridia-Clostridiales-Peptococcaceae-Desulfosporosinus-Desulfosporosinus_sp._BG
WP_052218681.1_Firmicutes-Clostridia-Clostridiales-Peptococcaceae-Thermincola-Thermincola_ferriacetica
EHM10124.1_Synergistetes-Synergistia-Synergistales-Synergistaceae-Thermanaerovibrio-Thermanaerovibrio_velox
WP_014163260.1_Synergistetes-Synergistia-Synergistales-Synergistaceae-Thermovirga-Thermovirga_lienii
WP_024822140.1_Synergistetes-Synergistia-Synergistales-Synergistaceae-Aminobacterium-Aminobacterium_mobile
WP_033101565.1_Firmicutes-Bacilli-Bacillales-Thermoactinomycetaceae-Thermoactinomyces-Thermoactinomyces_daqus
GBF12172.1_Firmicutes-Bacilli-Bacillales-Bacillaceae-Tepidibacillus-Tepidibacillus_sp._HK-1
WP_132767033.1_Firmicutes-Bacilli-Bacillales-Bacillaceae-Tepidibacillus-Tepidibacillus_fermentans
WP_004331073.1_Bacteroidetes-Bacteroidia-Bacteroidales-Porphyromonadaceae-Porphyromonas-Porphyromonas_asaccharolytica
WP_025884391.1_Bacteroidetes-Bacteroidia-Bacteroidales-Porphyromonadaceae-Porphyromonas-Porphyromonas_uenonis
WP_009217346.1_Bacteroidetes-root-root-root-root-Bacteroidetes_oral_taxon_274
WP_022603078.1_Bacteroidetes-Bacteroidia-Bacteroidales-Barnesiellaceae-Coprobacter-Coprobacter_fastidiosus
TVQ92654.1_Bacteroidetes-root-root-root-root-Bacteroidetes_bacterium
OFY32823.1_Bacteroidetes-root-root-root-root-Bacteroidetes_bacterium_GWF2_35_48
WP_092436279.1_Bacteroidetes-Bacteroidia-Bacteroidales-Williamwhitmaniaceae-Williamwhitmania-Williamwhitmania_taraxaci
ODS31504.1_Planctomycetes-Candidatus_Brocadiae-Candidatus_Brocadiales-Candidatus_Brocadiaceae-Candidatus_Scalindua-Candidatus_Scalindua_rubra
WP_096895181.1_Planctomycetes-Candidatus_Brocadiae-Candidatus_Brocadiales-Candidatus_Brocadiaceae-Candidatus_Scalindua-Candidatus_Scalindua_japonica
WP_034408969.1_Planctomycetes-Candidatus_Brocadiae-Candidatus_Brocadiales-Candidatus_Brocadiaceae-Candidatus_Scalindua-Candidatus_Scalindua_brodae
CUU09973.1_Candidatus_Kryptonia-root-root-root-Candidatus_Kryptobacter-Candidatus_Kryptobacter_tengchongensis
WP_075435598.1_Candidatus_Kryptonia-root-root-root-Candidatus_Kryptonium-Candidatus_Kryptonium_thompsoni
WP_140945228.1_Candidatus_Kryptonia-root-root-root-Candidatus_Thermokryptus-Candidatus_Thermokryptus_mobilis
OEG70000.1_Elusimicrobia-Endomicrobia-Endomicrobiales-Endomicrobiaceae-Endomicrobium-Candidatus_Endomicrobium_trichonymphae
OEG70849.1_Elusimicrobia-Endomicrobia-Endomicrobiales-Endomicrobiaceae-Endomicrobium-Candidatus_Endomicrobium_trichonymphae
WP_096525530.1_Elusimicrobia-Endomicrobia-Endomicrobiales-Endomicrobiaceae-Endomicrobium-Candidatus_Endomicrobium_trichonymphae
WP_052570026.1_Elusimicrobia-Endomicrobia-Endomicrobiales-Endomicrobiaceae-Endomicrobium-Endomicrobium_proavitum
OGS18723.1_Elusimicrobia-root-root-root-root-Elusimicrobia_bacterium_RIFOXYA2_FULL_50_26
OQX95475.1_root-root-root-root-root-candidate_division_KSB1_bacterium_4572_119
OQX88581.1_root-root-root-root-root-candidate_division_KSB1_bacterium_4484_87
PKL91710.1_Candidatus_Goldbacteria-root-root-root-root-Candidatus_Goldbacteria_bacterium_HGW-Goldbacteria-1
PIP18685.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium_CG08_land_8_20_14_0_20_41_16
RJO65685.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium
KPK97356.1_Candidatus_Omnitrophica-root-root-root-root-Omnitrophica_WOR_2_bacterium_SM23_72
OPX29677.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium_4484_171
RKY34473.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium
RKY38741.1_Candidatus_Omnitrophica-root-root-root-root-Candidatus_Omnitrophica_bacterium
YT1_182_00180
Yap2000.bin4.8_00249
Subgroup J
0.125

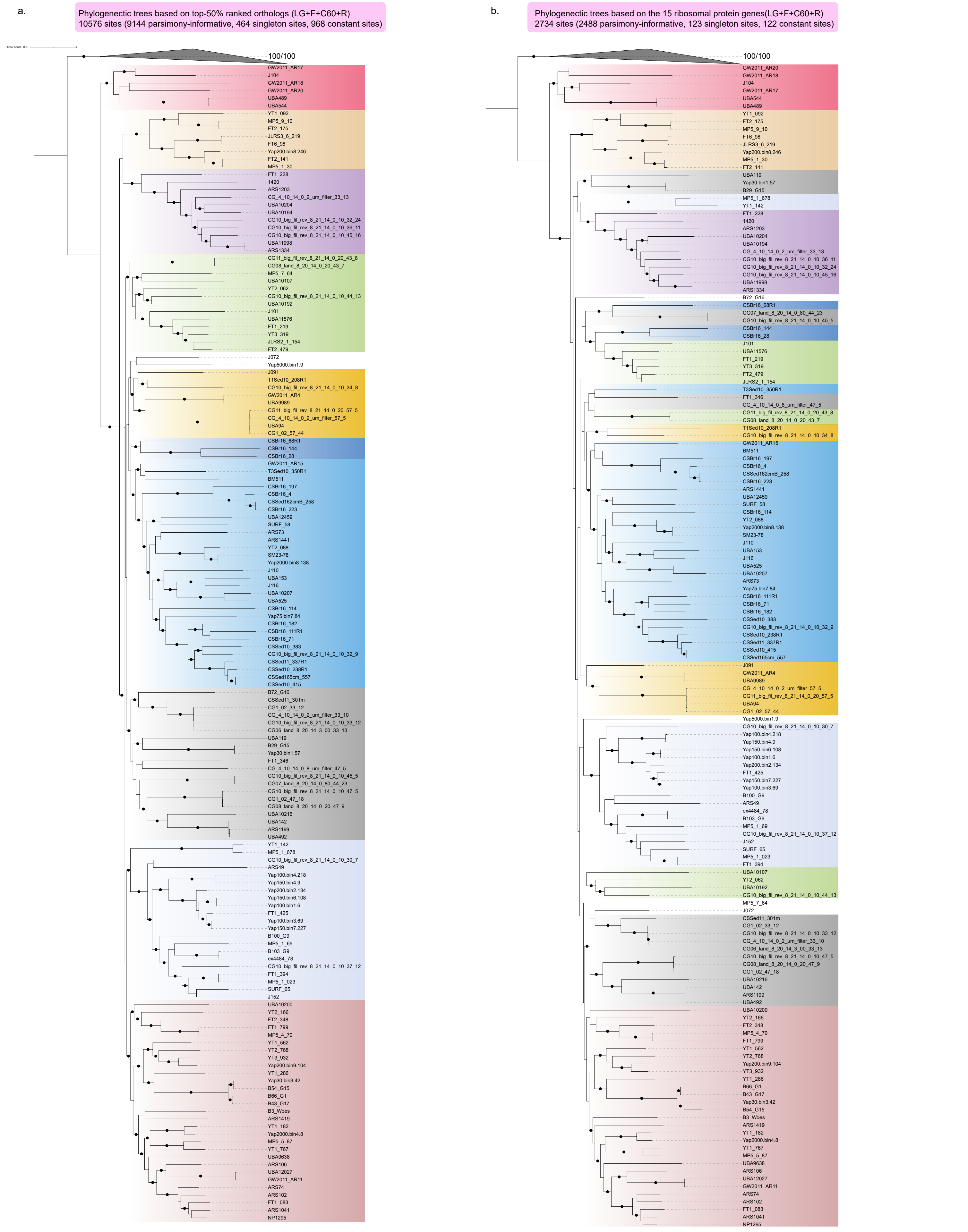
Supplementary Fig. 40: Phylogenetic analysis of *ackA* gene (Acetate kinase). The tree was unrooted and inferred using IQ-Tree LG+G+F+C20 model on an alignment of 136 taxa and 400 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan and green, respectively. Woesearchaeota sequences are selected from the subgroup J MAGs. Scale bar shows the number of average substitutions per site. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).



Supplementary Fig. 41: Phylogenetic analysis of *pta* gene (Phosphate acetyltransferase). The tree was unrooted and inferred using IQ-Tree LG+C50 +F+I+G model on an alignment of 222 taxa and 557 sites. UFBOOT (left) and SH-aLRT (right) support values are shown along the branches. Bacteria, Archaea and Woesearchaeota are colored in black, cyan and green, respectively. Scale bar shows the number of average substitutions per site. Woesearchaeota sequences are selected from the subgroup J MAGs. Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).



Supplementary Fig. 42: Ultrametric tree of the phylogenetic analysis of 152 woesearchaeotal MAGs using IQ-Tree (v 2.0.7) LG+F+R+C60 model on the concatenated 50% top-ranked marker proteins. Red line denotes a branch length of 0.4 of the ultrametric tree. The numbers at the middle of the branch are the relative evolutionary divergence value calculated from the original tree (the tree shown in Fig. 2). UFBOOT (left) and SH-aLRT (right) support values are shown behind the node for subgroup division. Support values colored in red indicates the reliability of the clade is not strongly supported and therefore subgroup was assigned at the next node whose UFBOOT >= 95% and SH-aLRT >= 80%.



Supplementary Fig. 43: Comparison of subgroup in the top-50% ranked orthologs trees and 15 ribosomal protein trees. a. Phylogenetic tree based on the top-50% ranked orthologs tree. **b**. Phylogenetic tree based on 15 ribosomal proteins. Genomes are colored according to the subgroup assigned using the top-50% ranked orthologs tree. Scale bar shows average substitution per site. Black dots indicate nodes with support value (UFBOOT >= 95% and SH-aLRT >= 80%). Source data are provided as a Source Data file and raw data are also available via figshare (See Data availability for more details).

References:

1. Liu, X. *et al.* Insights into the ecology, evolution, and metabolism of the widespread Woesearchaeotal lineages. *Microbiome* **6**, 102 (2018).

2. Karst, S. M. *et al.* Retrieval of a million high-quality, full-length microbial 16S and 18S rRNA gene sequences without primer bias. *Nature Biotechnology* **36**, 190–195 (2018).