
Environment
🟦 Freshwater
🟫 Soil
🟨 Sediment
🟥 Gut
⬛ Oil
⬜ Biofilm
🟦 Marine
🟩 Sludge
Tree scale: 0.1
Environment
Clades
Phylum6
Phylum5
Phylum4-1
Phylum4
Phylum3
Phylum2.1
Phylum2.2
Lineage I
Endomicrobia
Phylum1.class5
Phylum2
Lineage IIc
Lineage IId
Lineage IIb
Lineage IIa
Lineage VI
Lineage V
Lineage III
Elusimicrobiaceae
Lineage IV

Figure S1. Phylogenetic classification of 41 *Elusimicrobia*-related genomes based on their 16S rRNA gene sequences. Reference sequences from the SILVA database anchor the tree. The maximum likelihood phylogeny was inferred under the GTR model of evolution. For each *Elusimicrobia* genome, we indicated the lineage where the 16S sequence is nested in based on Herlemann *et al.* 2007; Geissinger *et al.* 2009 and Yarza *et al.* 2014. Scale bar indicates the average number of substitutions per site. The inner color bar indicates the environment of origin. Operational Taxonomic Unit (OTU) names colored in blue correspond to 16S from genome outgroups used in this study whereas OTUs colored in red correspond to the 16S from the Elusimicrobia genomes used in this study. OTUs colored in black were downloaded from the SILVA database.

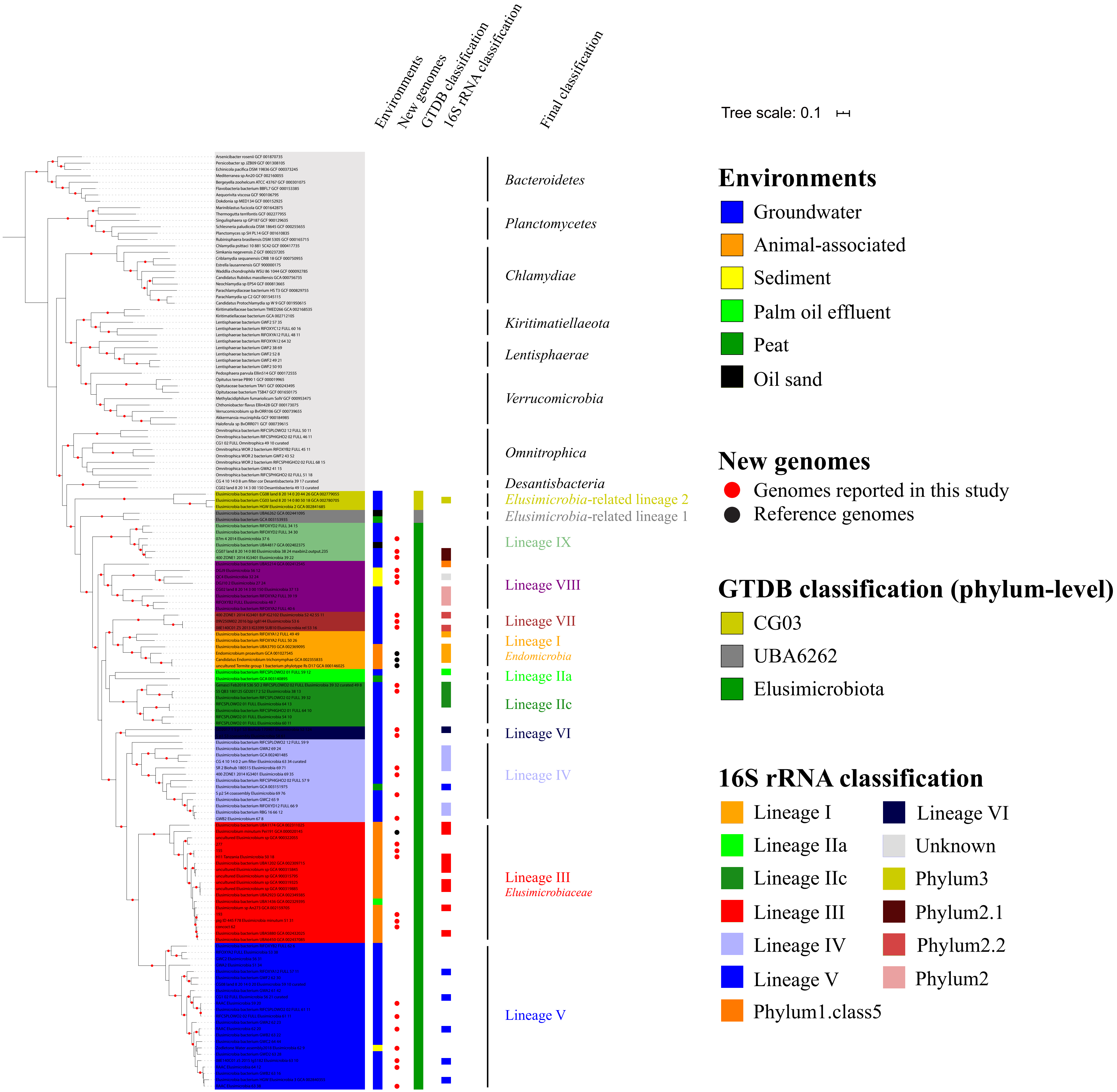
Environments
New genomes
GTDB classification
16S rRNA classification
Final classification
Tree scale: 0.1
Arsenicibacter rosenii GCF 001870735
Persicobacter sp JZB09 GCF 001308105
Echinicola pacifica DSM 19836 GCF 000373245
Mediterranea sp An20 GCF 002160055
Bergeyella zoohelcum ATCC 43767 GCF 000301075
Flavobacteria bacterium BBFL7 GCF 000153385
Aequorivita viscosa GCF 900106795
Dokdonia sp MED134 GCF 000152925
Marinilabilia fucicola GCF 001642875
Thermogutta terrifontis GCF 002277955
Singulisphaera sp GP187 GCF 900129635
Schlesneria paludicola DSM 18645 GCF 000255655
Planctomyces sp SH PL14 GCF 001610835
Rubinisphaera brasiliensis DSM 5305 GCF 000165715
Chlamydia psittaci 10 881 SC42 GCF 000417735
Simkania negevensis Z GCF 000237205
Criblamydia sequanensis CRIB 18 GCF 000750955
Estrella lausannensis GCF 900000175
Waddlia chondrophila WSU 86 1044 GCF 000092785
Candidatus Rubidus massiliensis GCA 000756735
Neochlamydia sp EPS4 GCF 000813665
Parachlamydiaceae bacterium HS T3 GCF 000829755
Parachlamydia sp C2 GCF 001545115
Candidatus Protochlamydia sp W 9 GCF 001950615
Kiritimatiellaceae bacterium TMED266 GCA 002168535
Kiritimatiellaceae bacterium GCA 002712105
Lentisphaerae bacterium GWF2 57 35
Lentisphaerae bacterium RIFOXYC12 FULL 60 16
Lentisphaerae bacterium RIFOXYA12 FULL 48 11
Lentisphaerae bacterium RIFOXYA12 64 32
Lentisphaerae bacterium GWF2 38 69
Lentisphaerae bacterium GWF2 52 8
Lentisphaerae bacterium GWF2 49 21
Lentisphaerae bacterium GWF2 50 93
Pedosphaera parvula Ellin514 GCF 000172555
Opitutus terrae PB90 1 GCF 000019965
Opitutaceae bacterium TAV1 GCF 000243495
Opitutaceae bacterium TSB47 GCF 001650175
Methylacidiphilum fumariolicum SolV GCF 000953475
Chthoniobacter flavus Ellin428 GCF 000173075
Verrucomicrobium sp BvORR106 GCF 000739655
Akkermansia muciniphila GCF 900184985
Haloferula sp BvORR071 GCF 000739615
Omnitrophica bacterium RIFCSPLOWO2 12 FULL 50 11
Omnitrophica bacterium RIFCSPHIGHO2 02 FULL 46 11
CG1 02 FULL Omnitrophica 49 10 curated
Omnitrophica WOR 2 bacterium RIFOXYB2 FULL 45 11
Omnitrophica WOR 2 bacterium GWF2 43 52
Omnitrophica WOR 2 bacterium RIFCSPHIGHO2 02 FULL 68 15
Omnitrophica bacterium GWA2 41 15
Omnitrophica bacterium RIFCSPHIGHO2 02 FULL 51 18
CG 4 10 14 0 8 um filter cor Desantisbacteria 39 17 curated
CG02 land 8 20 14 3 00 150 Desantisbacteria 49 13 curated
Elusimicrobia bacterium CG08 land 8 20 14 0 20 44 26 GCA 002779055
Elusimicrobia bacterium CG03 land 8 20 14 0 80 50 18 GCA 002780705
Elusimicrobia bacterium HGW Elusimicrobia 2 GCA 002841685
Elusimicrobia bacterium UBA6262 GCA 002441095
Elusimicrobia bacterium GCA 003153935
Elusimicrobia bacterium RIFOXYD2 FULL 34 15
Elusimicrobia bacterium RIFOXYD2 FULL 34 30
07m 4 2014 Elusimicrobia 37 6
Elusimicrobia bacterium UBA4817 GCA 002402375
CG07 land 8 20 14 0 80 Elusimicrobia 38 24 maxbin2.output.235
400 ZONE1 2014 IG3401 Elusimicrobia 39 22
400 ZONE1 2014 IG3401 BJP IG2102 Elusimicrobia 52 42 55 11
Elusimicrobia bacterium RIFOXYA12 FULL 49 49
Elusimicrobia bacterium RIFOXYA2 FULL 50 26
Elusimicrobia bacterium UBA3793 GCA 002369095
Endomicrobium proavitum GCA 001027545
Candidatus Endomicrobium trichonymphae GCA 002355835
uncultured Termite group 1 bacterium phylotype Rs D17 GCA 000146025
Elusimicrobia bacterium RIFCSPLOWO2 01 FULL 59 12
Elusimicrobia bacterium GCA 003140895
Elusimicrobia bacterium RIFCSPLOWO2 02 FULL 39 32
Elusimicrobia bacterium RIFCSPHIGHO2 01 FULL 64 10
RIFCSPLOWO2 01 FULL Elusimicrobia 54 10
RIFCSPLOWO2 01 FULL Elusimicrobia 60 11
Elusimicrobia bacterium RIFCSPLOWO2 12 FULL 59 9
Elusimicrobia bacterium GWA2 69 24
Elusimicrobia bacterium GCA 002401485
CG 4 10 14 0 2 um filter Elusimicrobia 63 34 curated
SR 2 Biohub 180515 Elusimicrobia 69 71
400 ZONE1 2014 IG3401 Elusimicrobia 69 35
Elusimicrobia bacterium RIFCSPHIGHO2 02 FULL 57 9
Elusimicrobia bacterium GCA 003151975
S p2 S4 coassembly Elusimicrobia 69 76
Elusimicrobia bacterium GWC2 65 9
Elusimicrobia bacterium RIFOXYD12 FULL 66 9
Elusimicrobia bacterium RBG 16 66 12
GWB2 Elusimicrobium 67 8
Bacteroidetes
Planctomycetes
Chlamydiae
Kiritimatiellaeota
Lentisphaerae
Verrucomicrobia
Omnitrophica
Desantisbacteria
Elusimicrobia-related lineage 2
Elusimicrobia-related lineage 1
Lineage IX
Lineage VIII
Lineage VII
Lineage I
Endomicrobia
Lineage IIa
Lineage IIc
Lineage VI
Lineage IV
Lineage III
Elusimicrobiaceae
Lineage V
Environments
🟦 Groundwater
🟧 Animal-associated
🟨 Sediment
🟩 Palm oil effluent
🟩 Peat
⬛ Oil sand
New genomes
● Genomes reported in this study
● Reference genomes
GTDB classification (phylum-level)
🟨 CG03
▨ UBA6262
🟩 Elusimicrobiota
16S rRNA classification
🟧 Lineage I
🟩 Lineage IIa
🟩 Lineage IIc
🟥 Lineage III
🟦 Lineage IV
🟦 Lineage V
🟧 Phylum1.class5
⬛ Lineage VI
⬜ Unknown
🟨 Phylum3
🟫 Phylum2.1
🟥 Phylum2.2
🟥 Phylum2

Figure S2. Placement of the 94 genomes related to the *Elusimicrobia* phylum. The maximum likelihood tree was constructed based on a concatenated alignment of 16 ribosomal proteins under an LG+gamma model of evolution. The inner color bar indicates the environment of origin. Black circles represent the four genomes described in previous studies whereas red circles represent the 30 new genomes added in this study. The remaining genomes come from the NCBI genome database. The two classifications based on 16S rRNA sequences and the GTDB are also indicated. Scale bars indicate the mean number of substitutions per site. The lineages of genomes are indicated by colored ranges and roman numbers. The bootstraps are indicated by red circles when ≥ 85.

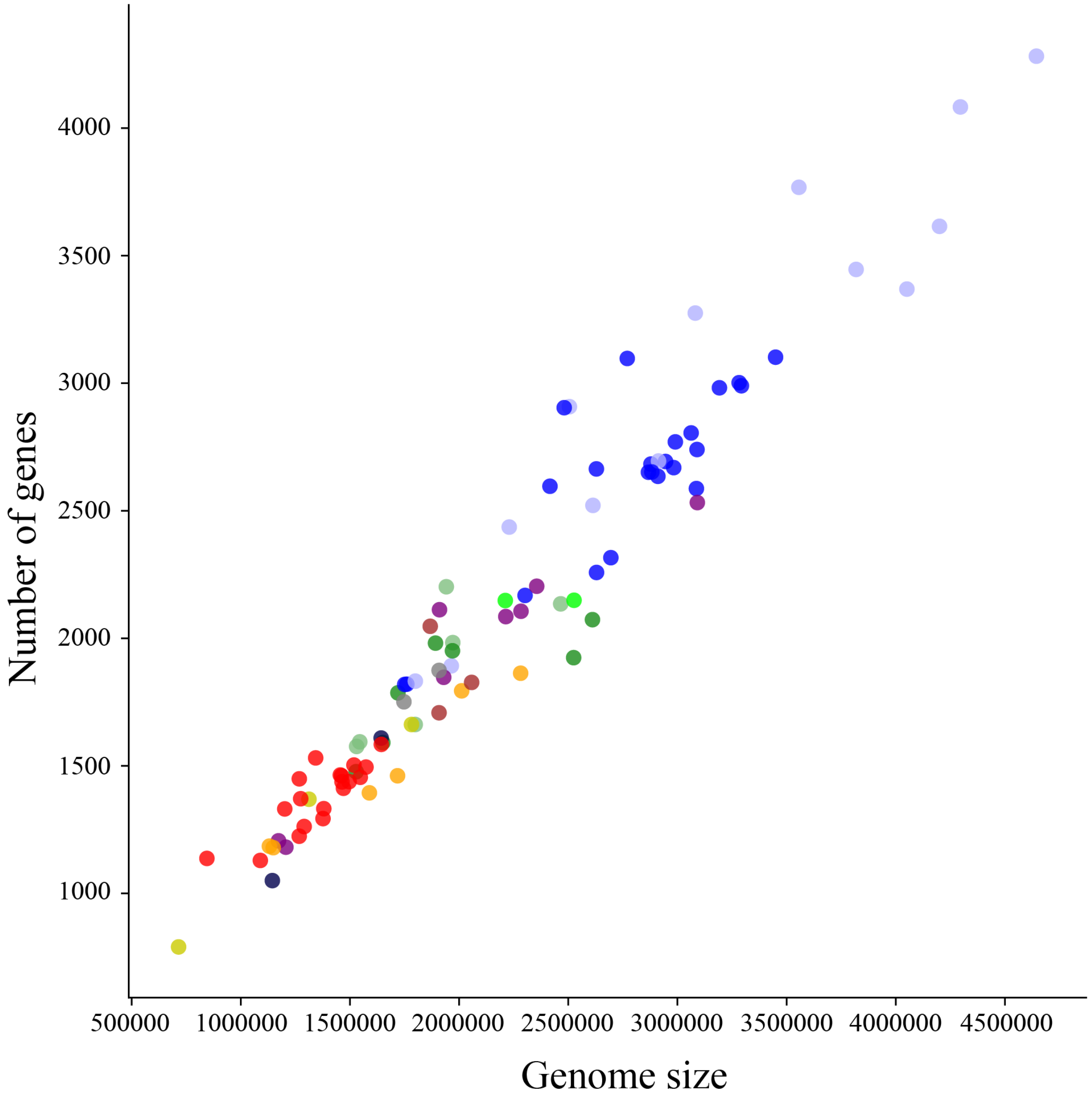

Figure S3. Number of genes and size (in base pairs) of the 94 *Elusimicrobia* genomes. Each genome is represented by a dot of the color of the lineage it has been classified to (see Figure 1 for color scheme).

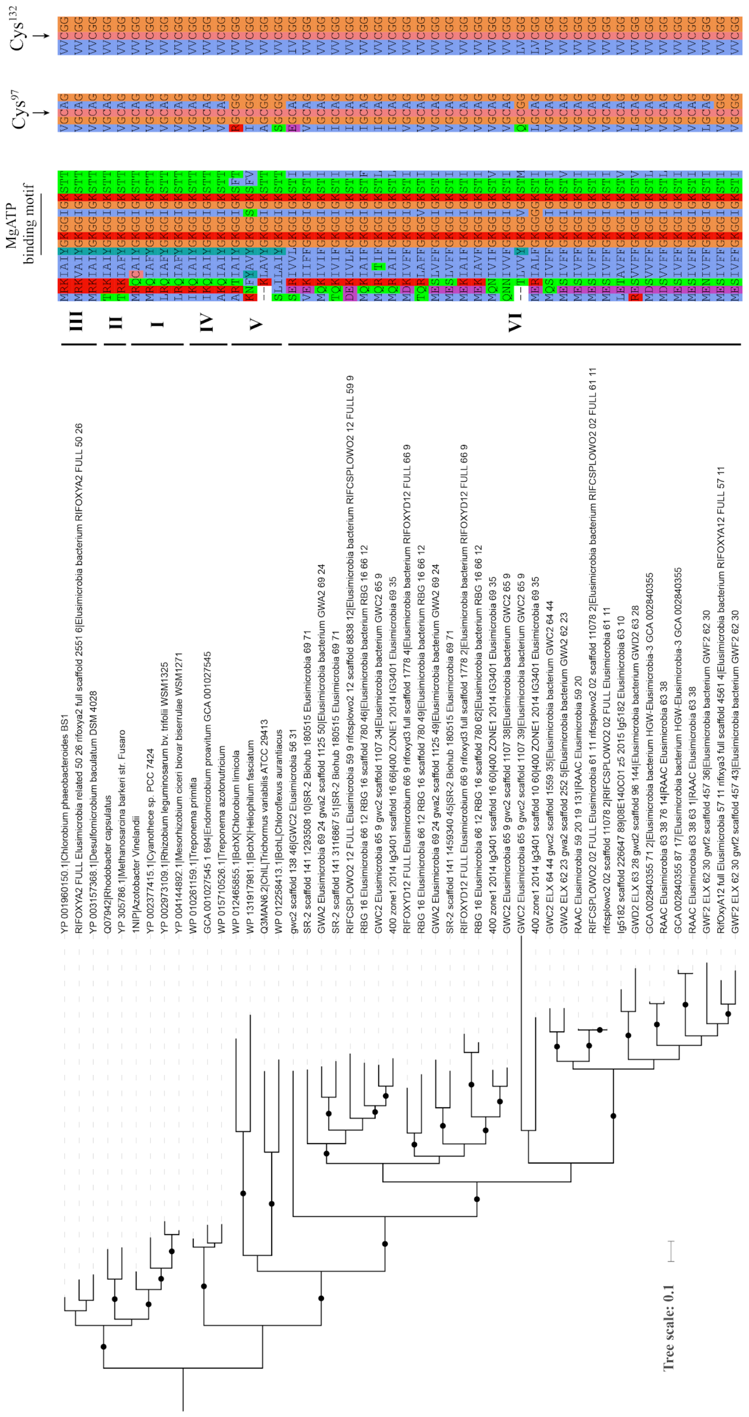

Figure S4. Phylogenetic tree of the nifH genes of *Elusimicrobia* and the nitrogenases of other bacterial species, and the conserved amino acids around the two crucial cysteine residues that coordinate the [Fe_4S_4] ligands in the Fe protein and for the binding of MgATP (GXGXXG). The cysteine residues, based on *A. vinelandii* numbering, are indicated with vertical arrows. Scale bar indicates substitutions per site.

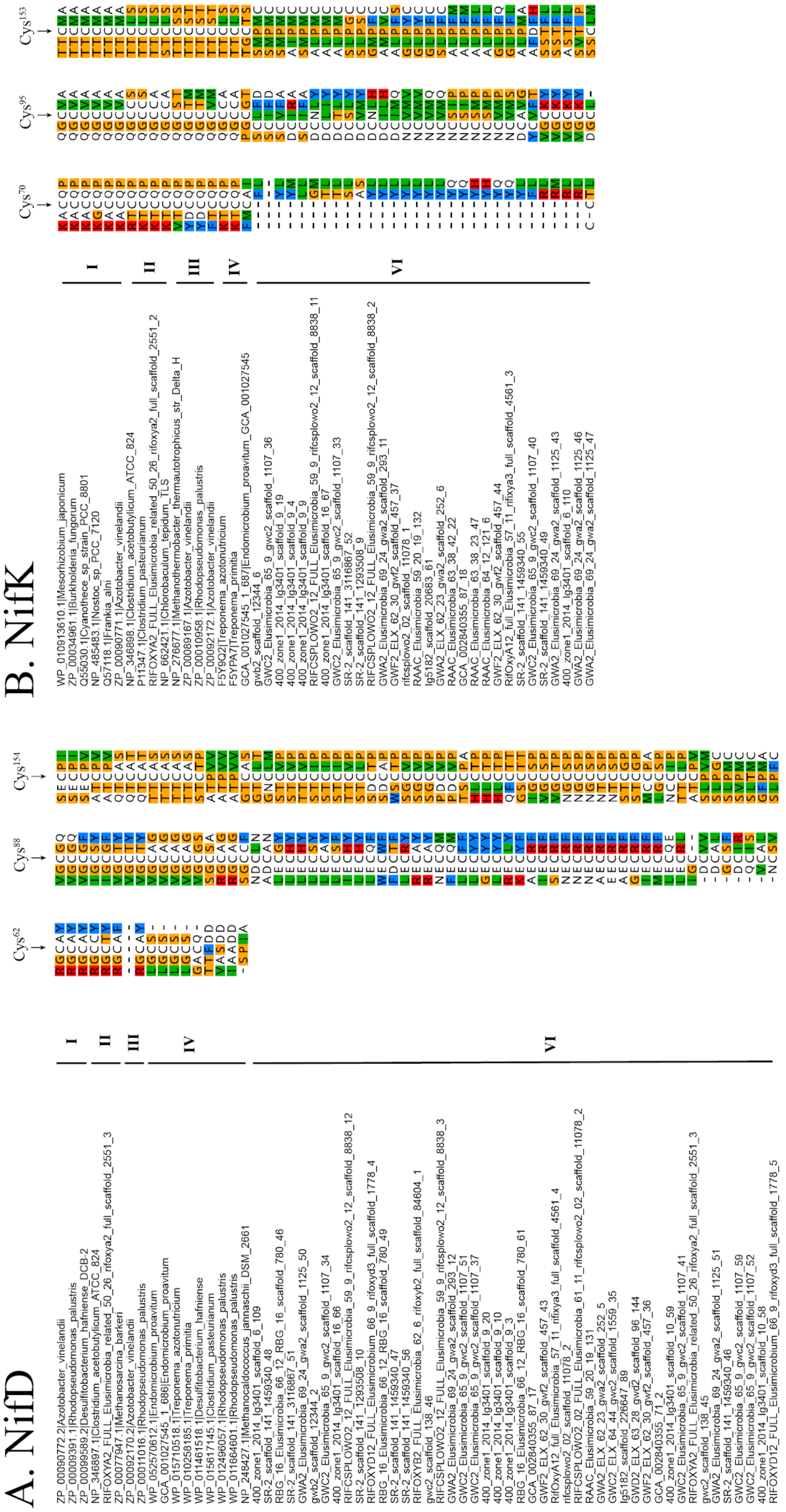

Figure S5. Conservation of the three crucial cysteine residues that coordinate the P-cluster in NifD (alpha) and NifK (beta) in *Elusimicrobia* and homologs in groups I, II, III and VI. The cysteine residues, based on *A vinelandii* numbering, are indicated with vertical arrows.

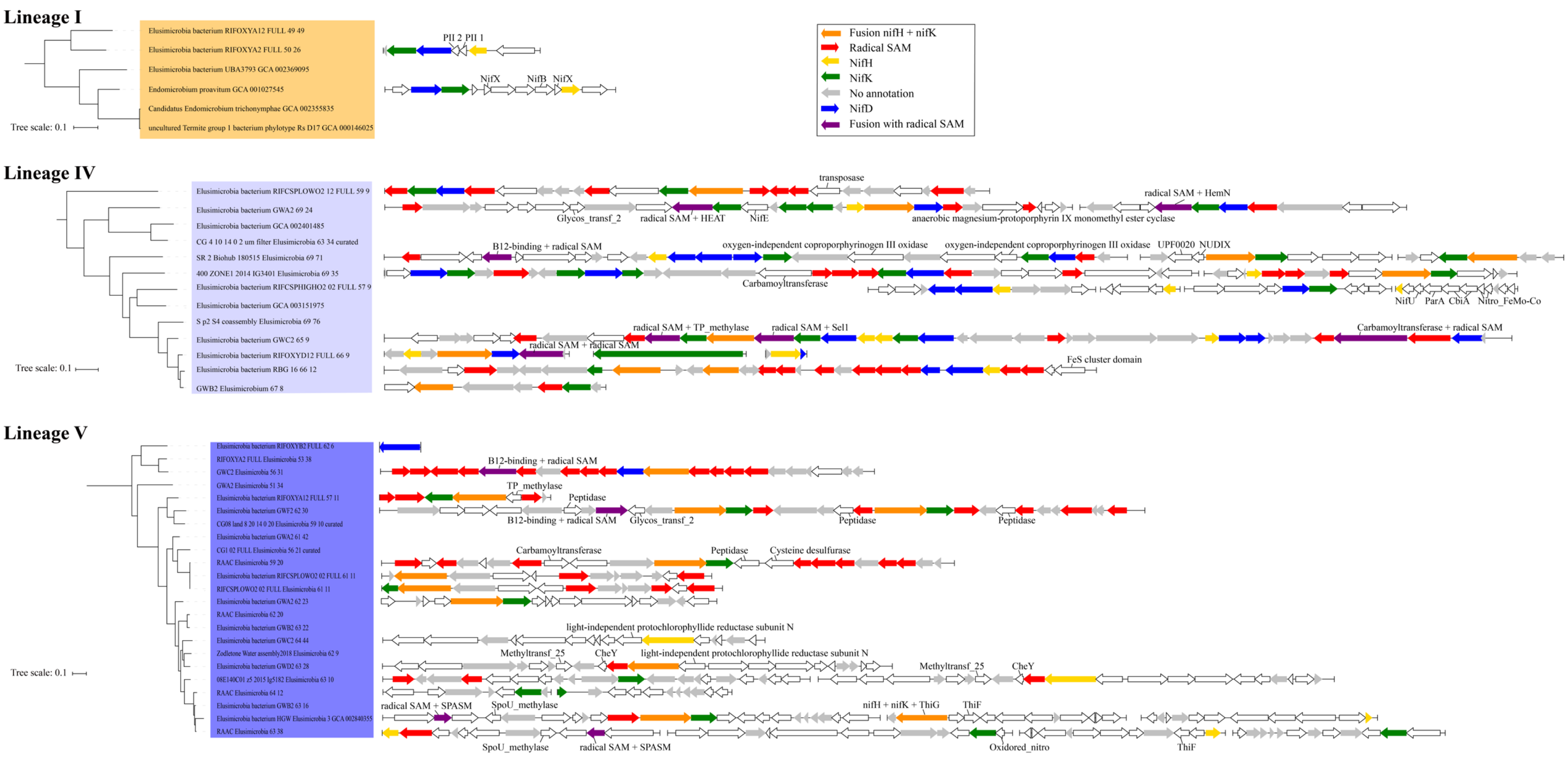Lineage I
Elusimicrobia bacterium RIFOXYA12 FULL 49 49
Elusimicrobia bacterium RIFOXYA2 FULL 50 26
Elusimicrobia bacterium UBA3793 GCA 002369095
Endomicrobium proavitum GCA 001027545
Candidatus Endomicrobium trichonymphae GCA 002355835
uncultured Termite group 1 bacterium phylotype Rs D17 GCA 000146025
Tree scale: 0.1
PII 2 PII 1
NifX
NifB
NifX
Fusion nifH + nifK
Radical SAM
NifH
NifK
No annotation
NifD
Fusion with radical SAM
Lineage IV
Elusimicrobia bacterium RIFCSPLOWO2 12 FULL 59 9
Elusimicrobia bacterium GWA2 69 24
Elusimicrobia bacterium GCA 002401485
CG 4 10 14 0 2 um filter Elusimicrobia 63 34 curated
SR 2 Biohub 180515 Elusimicrobia 69 71
400 ZONE1 2014 IG3401 Elusimicrobia 69 35
Elusimicrobia bacterium RIFCSPHIGHO2 02 FULL 57 9
Elusimicrobia bacterium GCA 003151975
S p2 S4 coassembly Elusimicrobia 69 76
Elusimicrobia bacterium GWC2 65 9
Elusimicrobia bacterium RIFOXYD12 FULL 66 9
Elusimicrobia bacterium RBG 16 66 12
GWB2 Elusimicrobium 67 8
Tree scale: 0.1
transposase
Glycos_transf_2
radical SAM + HEAT
NifE
anaerobic magnesium-protoporphyrin IX monomethyl ester cyclase
radical SAM + HemN
B12-binding + radical SAM
oxygen-independent coproporphyrinogen III oxidase
oxygen-independent coproporphyrinogen III oxidase
UPF0020
NUDIX
Carbamoyltransferase
NifU
ParA
CbiA
Nitro_FeMo-Co
radical SAM + TP_methylase
radical SAM + Sel1
Carbamoyltransferase + radical SAM
radical SAM + radical SAM
FeS cluster domain
Lineage V
Elusimicrobia bacterium RIFOXYB2 FULL 62 6
RIFOXYA2 FULL Elusimicrobia 53 38
GWC2 Elusimicrobia 56 31
GWA2 Elusimicrobia 51 34
Elusimicrobia bacterium RIFOXYA12 FULL 57 11
Elusimicrobia bacterium GWF2 62 30
CG08 land 8 20 14 0 20 Elusimicrobia 59 10 curated
Elusimicrobia bacterium GWA2 61 42
CG1 02 FULL Elusimicrobia 56 21 curated
RAAC Elusimicrobia 59 20
Elusimicrobia bacterium RIFCSPLOWO2 02 FULL 61 11
RIFCSPLOWO2 02 FULL Elusimicrobia 61 11
Elusimicrobia bacterium GWA2 62 23
RAAC Elusimicrobia 62 20
Elusimicrobia bacterium GWB2 63 22
Elusimicrobia bacterium GWC2 64 44
Zodletone Water assembly2018 Elusimicrobia 62 9
Elusimicrobia bacterium GWD2 63 28
08E140C01 z5 2015 Ig5182 Elusimicrobia 63 10
RAAC Elusimicrobia 64 12
Elusimicrobia bacterium GWB2 63 16
Elusimicrobia bacterium HGW Elusimicrobia 3 GCA 002840355
RAAC Elusimicrobia 63 38
Tree scale: 0.1
B12-binding + radical SAM
TP_methylase
Peptidase
B12-binding + radical SAM
Glycos_transf_2
Peptidase
Peptidase
Carbamoyltransferase
Peptidase
Cysteine desulfurase
light-independent protochlorophyllide reductase subunit N
Methyltransf_25
CheY
light-independent protochlorophyllide reductase subunit N
Methyltransf_25
CheY
radical SAM + SPASM
SpoU_methylase
nifH + nifK + ThiG
ThiF
SpoU_methylase
radical SAM + SPASM
Oxidored_nitro
ThiF

Figure S6. Genomic neighborhood of nitrogenase in genomes from lineages I, IV and V. The 20 genes before and after the *nifH* genes are displayed when possible. Genes are colored according to their annotations. The maximum likelihood tree was constructed based on a concatenated alignment of 16 ribosomal proteins under an LG+gamma model of evolution (Figure 1). Scale bars indicate substitutions per site.

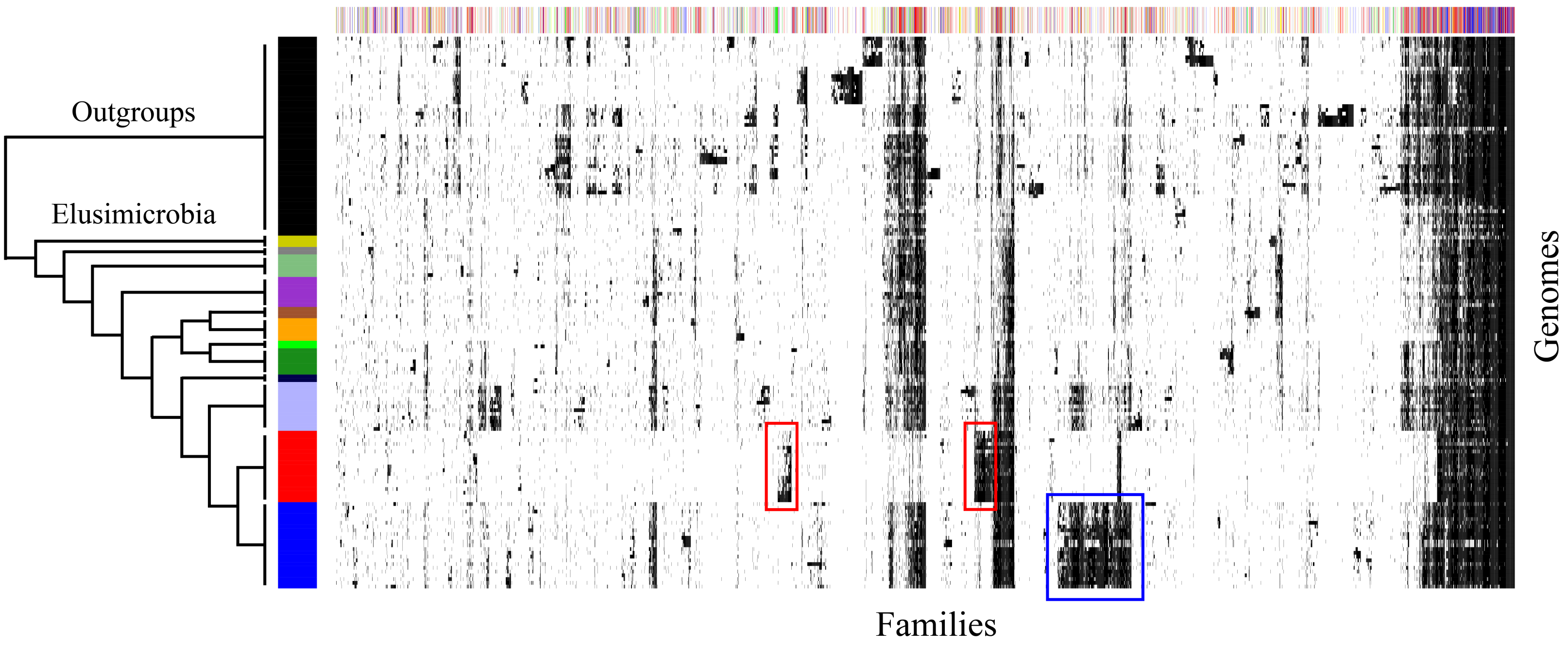
Outgroups
Elusimicrobia
Genomes
Families

Figure S7. The distribution of 6,608 protein families across the 110 genomes. The distribution of 6,608 protein families (columns) in 110 genomes (rows). Genomes were sorted according to the phylogeny in Figure 1. Families are clustered based on the presence (black) / absence (white) profiles (using Jaccard distance and complete-linkage method). The colored top bar corresponds to the functional category of families (Metabolism: red, Genetic Information Processing: blue, Cellular Processes: green, Environmental Information Processing: yellow, Organismal systems: orange, Unclassified: grey, Unknown: white). Specific clusters of interest are highlighted with colored boxes, discussed in the main text.


Tree scale: 0.1
group C
group B
group A
WP_014163756.1|Thermovirga lienii
WP_014357055.1|Acetobacterium woodii
WP_006521135.1|Desulfotomaculum gibsoniae
WP_009016131.1|Acidaminococcus
WP_028308072.1|Desulfitibacter alkalitolerans
WP_015327627.1|Halobacteroides halobius
WP_015358348.1|Clostridium stercorarium
WP_003512576.1|Ruminiclostridium thermocellum
WP_010251919.1|Hungateiclostridium cellulolyticum
WP_013780872.1|Mahella_australiensis
WP_015907773.1|Caldicellulosiruptor bescii
WP_013432575.1|Caldicellulosiruptor
WP_013403323.1|Caldicellulosiruptor hydrothermalis
WP_013788354.1|Thermoanaerobacterium xylanolyticum
WP_014062652.1|Thermoanaerobacter
WP_012543804.1|Coprothermobacter proteolyticus
WP_006573282.1|Pseudoflavonifractor capillosus
WP_015558596.1|Ruminococcus_champanellensis
WP_027642172.1|Clostridium clostridioforme
WP_015513457.1|Coprococcus catus
WP_014186009.1|Desulfosporosinus orientis
AET69947.1|Desulfosporosinus_orientis_DSM_765
AEJ20518.1|Treponema_caldarium_DSM_7334
WP_014625284.1|Spirochaeta_thermophila
WP_014043230.1|Caldicellulosiruptor_lactoaceticus
WP_027626440.1|Clostridium lundense
WP_014184511.1|Desulfosporosinus_orientis
WP_014903221.1|Desulfosporosinus_meridiei
WP_010251391.1|Hungateiclostridium cellulolyticum
WP_014186347.1|Desulfosporosinus_orientis
WP_009618950.1|Desulfosporosinus sp. OT
WP_023161685.1|Clostridium_autoethanogenum
WP_004064152.1|Eubacterium plexicaudatum
CBL09217.1|Roseburia_intestinalis_M50/1
CBL12146.1|Roseburia_intestinalis_XB6B4
WP_013810321.1|Desulfotomaculum_nigrificans
EEG77321.1|Dethiobacter_alkaliphilus_AHT_1
WP_011393215.1|Moorella thermoacetica
WP_013406267.1|Halanaerobium hydrogeniformans
WP_004514179.1|Geobacter metallireducens
WP_010943974.1|Geobacter_sulfurreducens
WP_014552161.1|Geobacter sulfurreducens
WP_012645645.1|Geobacter daltonii
WP_015839082.1|Geobacter sp. M21
WP_015722465.1|Geobacter sp. M18
WP_014857143.1|Melioribacter_roseus
RAAC_Elusimicrobia_62_20_4_13|RAAC_Elusimicrobia_62_20
400_zone1_2014_lg3401_scaffold_47_78|400_ZONE1_2014_IG3401_Elusimicrobia_69_35
RifOxyA12_full_Elusimicrobia_57_11_rifixya3_full_scaffold_2248_8|Elusimicrobia_bacterium_RIFOXYA12_FULL_57_11
GWA2_ELX_62_23_gwa2_scaffold_1737_42|Elusimicrobia_bacterium_GWA2_62_23
GWF2_ELX_62_30_gwf2_scaffold_10218_6|Elusimicrobia_bacterium_GWF2_62_30
GWA2_ELX_61_42_gwa2_scaffold_179_53|Elusimicrobia_bacterium_GWA2_61_42
RAAC_Elusimicrobia_62_20_18_26|RAAC_Elusimicrobia_62_20
GWB2_ELX_63_22_gwb2_scaffold_493_43|Elusimicrobia_bacterium_GWB2_63_22
GWD2_ELX_63_28_gwd2_scaffold_1239_19|Elusimicrobia_bacterium_GWD2_63_28
k141_965371_1|Zodletone_Water_assembly2018_Elusimicrobia_62_9
GWC2_ELX_64_44_gwc2_scaffold_288_55|Elusimicrobia_bacterium_GWC2_64_44
lg5182_scaffold_8058_35|08E140C01_z5_2015_lg5182_Elusimicrobia_63_10
GWB2_ELX_63_16_gwb2_scaffold_353_25|Elusimicrobia_bacterium_GWB2_63_16
RAAC_Elusimicrobia_63_38_7_35|RAAC_Elusimicrobia_63_38
RAAC_Elusimicrobia_64_12_179_21|RAAC_Elusimicrobia_64_12
GCA_002840355_9_22|Elusimicrobia_bacterium_HGW-Elusimicrobia-3_GCA_002840355
WP_017873317.1
WP_013823945.1
WP_013809975.1|Desulfotomaculum nigrificans
WP_011877929.1|Desulfotomaculum reducens
WP_013842496.1|Desulfotomaculum ruminis
WP_027202827.1|Butyricimonas virosa
WP_009137123.1|Odoribacter laneus
WP_014624881.1|Spirochaeta_thermophila
WP_013759422.1|Treponema brennaborense
WP_015724298.1
WP_005996231.1|Desulfovibrio fructosivorans
WP_005659983.1|Dethiosulfovibrio peptidovorans
WP_012996079.1
WP_012268929.1
WP_013298247.1|Thermoanaerobacterium thermosaccharolyticum
WP_006784034.1|Turicibacter sanguinis
WP_013387666.1|Ilyobacter polytropus
WP_003493657.1|Clostridium
WP_003493654.1|Clostridium
WP_026894719.1|Clostridiisalibacter paucivorans
WP_012065100.1|Alkaliphilus metalliredigens
GCA_000020145_1_747|Elusimicrobium_minutum_Pei191_GCA_000020145
WP_010250208.1|Hungateiclostridium cellulolyticum
WP_027627041.1|Ruminiclostridium cellobioparum
WP_004629692.1|Ruminiclostridium cellobioparum
WP_012582931.1|Dictyoglomus turgidum
WP_015513468.1|Coprococcus catus
WP_029502581.1|Lachnoclostridium phytofermentans
WP_006778911.1|Hungatella hathewayi
WP_026892185.1|Clostridium aerotolerans
WP_015757276.1|Desulfofarcimen acetoxidans
WP_007953762.1|Pelosinus fermentans
WP_012635236.1|Halothermothrix orenii
WP_015326565.1|Halobacteroides_halobius
WP_015360284.1|[Clostridium]_stercorarium
WP_009906363.1|Clostridioides_difficile
WP_021388284.1|Clostridioides_difficile
WP_009891715.1|Clostridiales
WP_014792620.1|Desulfitobacterium
WP_014904712.1|Desulfosporosinus_meridiei
WP_013809931.1|Desulfotomaculum nigrificans
WP_006520976.1|Desulfallas gibsoniae
WP_009015959.1|Acidaminococcus
WP_014079355.1
WP_013274254.1|Clostridium saccharolyticum
WP_006190671.1|Selenomonas_sputigena
WP_003532170.1
WP_011721124.1|Firmicutes
WP_023436998.1|Clostridium tetani
WP_010966505.1|Clostridium_acetobutylicum
WP_027639106.1|Clostridium cadaveris
WP_013238683.1|Clostridium
WP_017414827.1|Clostridium tunisiense
WP_015617566.1|Clostridium_pasteurianum
WP_014522006.1|Clostridium_botulinum
WP_012048389.1|Clostridium_botulinum
WP_012099524.1|Clostridium_botulinum
WP_014553922.1|Halanaerobium_praevalens
WP_004817153.1|Anaerococcus hydrogenalis
WP_008392956.1|Clostridium_sp._SS2/1
WP_009202817.1|Anaerostipes hadrus
CBL19415.1|Ruminococcus_sp._SR1/5
CBL24113.1|Blautia_obeum_A2-162
WP_004840268.1
WP_028085756.1|Dorea longicatena
WP_015536912.1|Faecalibacterium_prausnitzii
CBK97939.1|Faecalibacterium_prausnitzii_L2-6
WP_005944276.1|Faecalibacterium
WP_014115957.1|Oscillibacter_valericigenes
CBK89222.1|Faecalitalea_cylindroides_T2-87
WP_019893070.1|Allobaculum stercoricanis
WP_008705182.1|Ruminococcus_sp._5_1_39BFAA
WP_027207458.1|Butyrivibrio fibrisolvens
WP_013708979.1|Coriobacterium glomerans
WP_003148188.1|Atopobium_rimae
WP_021724994.1|Olsenella profusa
CBK90768.1|Eubacterium_rectale_DSM_17629
WP_015568820.1|Eubacterium_rectale
WP_008753040.1|Lachnoanaerobaculum saburreum
CBK78614.1|Clostridium_cf._saccharolyticum_K10
CBL41863.1|butyrate-producing_bacterium_SS3/4
WP_009016297.1|Acidaminococcus
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WP_014553742.1|Halanaerobium_praevalens
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WP_021393206.1|Clostridioides_difficile
WP_009888725.1|Clostridiales
WP_032511600.1|Clostridioides_difficile
WP_014063301.1|Thermoanaerobacter_wiegelii
WP_014758430.1|Thermoanaerobacterium_aotearoense
WP_013788347.1|Thermoanaerobacterium xylanolyticum
WP_027637669.1|Clostridium cadaveris
WP_026894721.1|Clostridiisalibacter paucivorans
GCA_000020145_1_745|Elusimicrobium_minutum_Pei191_GCA_000020145
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CBL26524.1|Ruminococcus_torques_L2-14
WP_002848990.1|Ruminococcus albus
WP_015359535.1|Clostridium_stercorarium
WP_015558166.1|Ruminococcus_champanellensis
WP_012283632.1|Heliobacterium modesticaldum
WP_004800637.1|Absiella dolichum
WP_006352873.1
CBK81749.1|Coprococcus_catus_GD/7
WP_029502583.1|Lachnoclostridium phytofermentans
WP_015534570.1|Coprococcus_eutactus
WP_012739633.1|Eubacterium eligens
CBL40039.1|butyrate-producing_bacterium_SS3/4
CBK75094.1|Butyrivibrio_fibrisolvens_16/4
WP_002568888.1|Clostridium bolteae
WP_008393326.1|Clostridiales
WP_005600915.1|Butyrivibrio crossotus
WP_012743215.1|Eubacterium_rectale
CBK92742.1|Eubacterium_rectale_M104/1
WP_015560436.1|Roseburia_intestinalis
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WP_014624879.1|Spirochaeta_thermophila
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WP_027202830.1|Butyricimonas virosa
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WP_005798358.1|Bacteroides
WP_014299406.1|Bacteroides fragilis
WP_028726954.1|Parabacteroides gordonii
WP_009126776.1|Bacteroides fluxus
WP_005929426.1|Bacteroides salyersiae
WP_004314012.1|Bacteroides
WP_005679640.1|Bacteroides caccae
WP_011108013.1|Bacteroides_thetaiotaomicron
WP_007748547.1|Bacteroides
WP_014270720.1|Sphaerochaeta_pleomorpha
WP_013967702.1|Treponema_caldarium
WP_002678778.1|Treponema_denticola
WP_013700376.1|Treponema succinifaciens
WP_014487517.1|Brachyspira intermedia
WP_014935965.1|Brachyspira_pilosicoli
WP_013243002.1|Brachyspira pilosicoli
WP_006009278.1|Desulfovibrio piger
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pig_ID_2176_F64_scaffold_170_31|155
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GCA_900315845_7_242|uncultured_Elusimicrobium_sp_GCA_900315845
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GCA_002437085_48_38|Elusimicrobia_bacterium_UBA6450_GCA_002437085
pig_ID_445_F78_scaffold_0_93|pig_ID_445_F78_Elusimicrobia_minutum_51_31
pig_ID_2176_F64_scaffold_17318_8|193
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WP_023162310.1|Clostridium_autoethanogenum
WP 012060267.1|Clostridium beijerinckii
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WP 012548684.1|Dictyoglomus thermophilum
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WP 012579795.1|Thermosipho africanus
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WP_028027642.1|Enterorhabdus mucosicola
WP_009146318.1|Phascolarctobacterium succinatutens
WP_009165839.1|Pyramidobacter piscolens
WP_007156182.1
WP_033162999.1|Sharpea azabuensis
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WP_013708694.1|Coriobacterium glomerans
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WP_002846126.1|Peptostreptococcus anaerobius
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WP_019225315.1|Dehalobacter
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WP_014825387.1|Desulfosporosinus_acidiphilus
WP_014829295.1|Desulfosporosinus_acidiphilus
WP_014187542.1|Desulfosporosinus_orientis
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WP 012200078.1|Lachnoclostridium phytofermentans
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WP 011025272.1|Caldanaerobacter subterraneus
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WP 011917383.1|Caldicellulosiruptor saccharolyticus
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WP 012201800.1|Lachnoclostridium phytofermentans
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WP_027356557.1|Desulfofundulus thermocisternus
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WP 013253085.1|Sediminispirochaeta smaragdinae
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WP 073168671.1|Tangfeifania diversioriginum
SHE46849.1|Mariniphaga anaerophila
OFX31211.1|Bacteroidetes bacterium GWA2 42 15
WP 093921738.1|Sunxiuqinia elliptica
WP 053187393.1|Sunxiuqinia dokdonensis
WP_014553773.1|Halanaerobium_praevalens
WP_015327873.1|Halobacteroides_halobius
WP_014296497.1|Marinitoga_piezophila
WP_013607267.1|Sphaerochaeta_globosa
WP_014268912.1|Sphaerochaeta_pleomorpha
WP 010935952.1|Dehalococcoides mccartyi
WP_015406793.1|Dehalococcoides_mccartyi
WP_015407397.1|Dehalococcoides_mccartyi
WP_023651831.1|Dehalococcoides
WP 012881504.1|Dehalococcoides mccartyi
WP 013907122.1|Thermodesulfatator indicus
WP_014902186.1|Desulfosporosinus_meridiei
WP_014827653.1|Desulfosporosinus_acidiphilus
WP_014187152.1|Desulfosporosinus_orientis
WP_014795695.1|Desulfitobacterium_dehalogenans
WP_028893679.1|Syntrophorhabdus aromaticivorans
WP_013809932.1|Desulfotomaculum_nigrificans
WP_003540305.1|Desulfotomaculum nigrificans
WP_013810744.1|Desulfotomaculum_nigrificans
WP_006521126.1|Desulfotomaculum_gibsoniae
WP_012031839.1
WP_006571360.1
WP_028256896.1|Veillonella montpellierensis
WP_006556240.1|Veillonella seminalis
WP_028255372.1|Veillonella magna
WP_004607406.1|Clostridium scindens
WP 015617234.1|Clostridium pasteurianum
WP_002607524.1|Firmicutes
WP_005884626.1|Fusobacterium mortiferum
WP_005436344.1|Sutterella wadsworthensis
WP_011591981.1|Clostridium perfringens
WP_027128738.1|Fusobacterium perfoetens
WP_010939057.1|Desulfovibrio_vulgaris
WP_012625129.1|Desulfovibrio
WP_027722058.1|Desulfovibrio zosterae
WP_011368163.1|Desulfovibrio alaskensis
WP_011697718.1|Syntrophobacter fumaroxidans
WP_013175699.1|Syntrophothermus lipocalidus
WP_018703705.1|Anaeromusa acidaminophila
WP_011073665.1|Shewanella_oneidensis
WP_012276514.1|Shewanella halifaxensis
WP_022854720.1|Thermodesulfobacterium thermophilum
WP_012545114.1|Thermodesulfovibrio_yellowstonii
WP_028842274.1|Thermodesulfovibrio
WP_022852507.1|Thermodesulfatator atlanticus
WP_013756852.1|Thermodesulfobium_narugense
WP_018712282.1|Campylobacter ureolyticus
WP_022372326.1|Duodenibacillus massiliensis
WP_013275594.1|Thermosediminibacter oceani
WP_011393383.1|Moorella thermoacetica
WP_021432325.1|Paraclostridium bifermentans
WP_014355220.1|Acetobacterium woodii
WP_015707165.1|Treponema primitia
WP_011861902.1|Clostridiales
WP_007285433.1|Intestinibacter bartlettii
WP_018591881.1|Terrisporobacter glycolicus
WP_010295100.1|Clostridium senegalense
WP_023975234.1|Clostridium beijerinckii
WP_026885750.1|Clostridium beijerinckii
WP_007063270.1
WP_011989407.1|Clostridium kluyveri
WP_023162857.1|Clostridium autoethanogenum
WP 013237377.1|Clostridium
WP_013237377.1|Clostridium
WP_007960496.1|Pelosinus fermentans
WP_023163434.1|Clostridium_autoethanogenum
WP_013238388.1|Clostridium ljungdahlii
WP_014282026.1
WP_010345843.1
CCC85802.1|Paenibacillus_polymyxa_M1
WP_016822145.1
WP_028591227.1
WP_018884458.1|Paenibacillus massiliensis
WP_025700928.1
WP_025688954.1
WP_012662530.1|Desulfobacterium autotrophicum
WP_011187724.1
WP_015337360.1|Desulfovibrio hydrothermalis
WP_011366599.1|Desulfovibrio alaskensis
WP_024825939.1|Desulfovibrio magneticus
WP_027186285.1|Desulfovibrio inopinatus
WP_027721164.1|Desulfovibrio zosterae
WP_012765956.1

Figure S8. Phylogenetic tree of the [FeFe] hydrogenase (Maximum likelihood tree under an LG+I+G4 model of evolution). *Elusimicrobia* have group A, B and C [FeFe] hydrogenases. *Elusimicrobia* sequences are indicated with colored font. Scale bar indicates substitutions per site. The bootstraps are indicated by red circles when ≥ 85. The tree was made using sequences from (Greening et al. 2016; Matheus Carnevali et al. 2019). The sequences and tree are available with full bootstrap values in Fasta and Newick formats in Supplementary Data.


GCA_002412545_15_24|Elusimicrobia_bacterium_UBA5214_GCA_002412545
CG02_land_8_20_14_3.00_150_scaffold_3651_8|CG02_land_8_20_14_3_00_150_Elusimicrobia_37_13
CG07_land_8_20_14_0.80_scaffold_9378_6|CG07_land_8_20_14_0_80_Elusimicrobia_38_24__maxbin2.output.235
400_zone1_2014_Ig3401_scaffold_1000_19|400_ZONE1_2014_IG3401_Elusimicrobia_39_22
WP 012611421.1|Desulfovibrio vulgaris
WP 005996860.1|Desulfovibrio fructosivorans
WP 011937803.1|Geobacter uraniireducens
WP 011187820.1|Desulfotalea psychrophila
AAC38282.1|Thiocapsa roseopersicina
WP 010880393.1|Aquifex aeolicus
WP 000107403.1|Escherichia coli
WP 011153927.1|Cupriavidus necator
WP 051920814.1|Thermodesulfobacterium hydrogeniphilum
OHE57429.1|Thermodesulfovibrio sp. RBG 19FT COMBO 42 12
WP 011089681.1|Bradyrhizobium diazoefficiens
WP 028717756.1|Paracoccus yeei
AAX40740.1|Thiocapsa roseopersicina
WP 005626347.1|Mycolicibacterium hassiacum
AAC16277.1|Nostoc punctiforme PCC 73102
WP 014474618.1|Arcobacter sp. L
AFV98241.1|Candidatus Sulfuricurvum sp. RIFRC-1
WP 012083424.1|Sulfurovum sp. NBC37-1
WP 008339288.1|Sulfurimonas gotlandica
WP 013553042.1|Nitratifractor salsuginis
WP 013905833.1|Pyrococcus yayanosii
ACS32570.1|Thermococcus gammatolerans EJ3
WP 013537869.1|Thermovibrio ammonificans
WP 022846160.1|Desulfurobacterium sp. TC5-1
WP 012616797.1|Methanosphaerula palustris
WP 011170764.1|Methanococcus maripaludis
WP 011406878.1|Methanosphaera
WP 004029354.1|Methanobacterium formicicum
WP 016359193.1|Methanobrevibacter
WP 004032005.1|Methanobacterium formicicum
Q00404.1|Methanococcus voltae
AAM01483.1|Methanopyrus kandleri AV19
WP 013413806.1|Methanothermus fervidus
WP 011405926.1|Methanosphaera
WP 010876758.1|Methanothermobacter thermautotrophicus
WP 012548375.1|Dictyoglomus thermophilum
GCA_003140895_92_4|Elusimicrobia_bacterium_GCA_003140895
WP 011189453.1|Desulfotalea psychrophila
WP 011699561.1|Syntrophobacter fumaroxidans
WP 012305837.1|Synechococcus
WP 010872716.1|Synechocystis
WP 017305034.1|Spirulina subsalsa
WP 011958239.1|Roseiflexus sp. RS-1
WP 015153897.1|Cyanobacteria
WP 015216232.1|Anabaena cylindrica
WP 022948170.1|Methylohalobius crimeensis
AAD38065.1|Rhodobacter capsulatus
WP 040123534.1|Paraburkholderia xenovorans
WP 011385756.1|Magnetospirillum magneticum
WP 008616907.1|Magnetospirillum caucaseum
OFY50271.1|Bacteroidetes bacterium GWF2 41 31
OQX77629.1|Bacteroidetes bacterium 4484 249
GWF2 RBX1 related 35 9 gwf2 scaffold 2828 27 Margulisbacteria GW2A scaffold 2828 27
OGV54071.1|Lentisphaerae bacterium GWF2 50 93
OFY24680.1|Bacteroidetes bacterium GWF2 33 38
OFY08065.1|Bacteroidetes bacterium GWE2 42 42
OFY34865.1|Bacteroidetes bacterium GWF2 38 335
OHD67168.1|Spirochaetes bacterium RBG 16 49 21
OHD66423.1|Spirochaetes bacterium RBG 13 51 14
KPK81374.1|Bacteroides sp. SM23 62 1
KPL20536.1|Bacteroides sp. SM1 62
WP 011699072.1|Syntrophobacter fumaroxidans
WP 010936390.1|Dehalococcoides mccartyi
GWA2_Elusimicrobia_69_24_gwa2_scaffold_1021_8|Elusimicrobia_bacterium_GWA2_69_24
SR-2_scaffold_141_304462_82|SR-2_Biohub_180515_Elusimicrobia_69_71
ABK19623.1|Syntrophobacter fumaroxidans MPOB
CAG35742.1|Desulfotalea psychrophila LSv54
ADW17894.1|Desulfobulbus propionicus DSM 2032
WP 012545782.1|Thermodesulfovibrio yellowstonii
WP 013637988.1|Desulfurobacterium thermolithotrophum
400_zone1_2014_Ig3401_scaffold_3228_3|400_ZONE1_2014_IG3401_Elusimicrobia_39_22
WP 012302733.1|Candidatus Desulforudis audaxviator
RIFOXYA2_FULL_Elusimicrobia_related_50_26_rifoxya2_full_scaffold_959_8|Elusimicrobia_bacterium_RIFOXYA2_FULL_50_26
RIFOXYA12_FULL_Elusimicrobium-like_49_49_rifixya3_full_scaffold_20_107|Elusimicrobia_bacterium_RIFOXYA12_FULL_49_49
WP 022775381.1|Candidatus Symbiobacter mobilis
OGO60218.1|Chloroflexi bacterium RBG 19FT COMBO 49 13
KPK03429.1 |Anaerolineae bacterium SG8 19
OQY35418.1 |Anaerolineaceae bacterium 4572 5.1
WP 041970854.1 |Geobacter sp. OR-1
OGU06519.1 |Geobacteraceae bacterium GWC2 58 44
OGI09537.1|Margulisbacteria GW2A scaffold 2737 42
OFZ01736.1|Bdellovibrionales bacterium GWB1 52 6
OQW98730.1|Desulfobacteraceae bacterium A6
OGW22261.1|Nitrospirae bacterium GWA2 46 11
OGW19754.1|Nitrospirae bacterium GWC2 46 6
OGB98279.1|candidate division KSB1 bacterium RBG 16 48 16
OGD74736.1|Candidatus Coatesbacteria bacterium RBG 13 66 14
OGH97085.1 Margulisbacteria GW1C scaffold 764 21
RAAC 38 40 1 20 Margulisbacteria RA1A scaffold 1 20
WP 038049430.1|Thermoanaerobaculum aquaticum
WP 006930005.1|Caldithrix abyssi
WP 012376486.1|Opitutus terrae
SR-2_scaffold_141_1566148_2|SR-2_Biohub_180515_Elusimicrobia_69_71
400_zone1_2014_Ig3401_scaffold_33_83|400_ZONE1_2014_IG3401_Elusimicrobia_69_35
RIFOXYB2_FULL_Elusimicrobia_62_6_rifoxyb2_full_scaffold_8049_1|Elusimicrobia_bacterium_RIFOXYB2_FULL_62_6
gwa2_scaffold_188_133|GWA2_Elusimicrobia_51_34
rifoxya2_full_scaffold_183_46|RIFOXYA2_FULL_Elusimicrobia_53_38
rifcsplowo2_02_scaffold_80435_5|RIFCSPLOWO2_02_FULL_Elusimicrobia_61_11
RAAC_Elusimicrobia_59_20_43_13|RAAC_Elusimicrobia_59_20
RIFCSPLOWO2_02_FULL_Elusimicrobia_61_11_rifcsplowo2_02_scaffold_80435_5|Elusimicrobia_bacterium_RIFCSPLOWO2_02_FULL_61_11
bjp ig3402 sc 8 133 Melainabacteria BJ4A scaffold 8 133
OLS17582.1|Candidatus Odinarchaeota archaeon LCB 4
KYH40863.1|Candidatus Bathyarchaeota archaeon B63
KPJ59686.1|Latescibacteria bacterium DG 63
WP 010867988.1|Pyrococcus abyssi
WP 011012478.1|Pyrococcus furiosus
WP 053335021.1|Thermoanaerobaculum aquaticum
OIP41460.1|Candidatus Desantisbacteria bacterium CG2 30 40 21
OFW64375.1|Actinobacteria bacterium RBG 19FT COMBO 36 27
KPK70092.1|candidate division TA06 bacterium SM23 40
KPK75731.1|Phycisphaerae bacterium SM23 30
KPK45893.1|Nitrospira bacterium SM23 35
WP 008515176.1|Dethiobacter alkaliphilus
rifcsplowo2_01_scaffold_13047_26|RIFCSPLOWO2_01_FULL_Elusimicrobia_64_13
WP 008098529.1|Verrucomicrobiae bacterium DG1235
OGW31332.1|Nitrospirae bacterium GWF2 44 13
OHE59661.1|Thermodesulfovibrio sp. RBG 19FT COMBO 42 12
OGW47531.1|Nitrospirae bacterium GWC2 57 9
OGH97725.1 Margulisbacteria GW1B scaffold 641 8
OHB68269.1|Planctomycetes bacterium RBG 13 62 9
KPK67554.1|candidate division TA06 bacterium SM23 40
WP 006926982.1|Caldithrix abyssi
GWA2_Elusimicrobia_69_24_gwa2_scaffold_2292_40|Elusimicrobia_bacterium_GWA2_69_24
400_zone1_2014_Ig3401_scaffold_30_90|400_ZONE1_2014_IG3401_Elusimicrobia_69_35
WP 015790329.1|Halorhabdus utahensis
AKG53857.1|Dehalogenimonas sp. WBC-2
KUO41221.1|Hadesarchaea archaeon YNP 45
OGB89834.1 Saganbacteria HO1B scaffold 53 26
RIFCSPHIGHO2 01 FULL CP 53 15 rifcsphigho2 01 scaffold 383 32 Saganbacteria HO1A scaffold 383 32
OQY25179.1|Anaerolineaceae bacterium 4572 32.1
OGO66084.1|Chloroflexi bacterium RBG 19FT COMBO 55 16
OGO15058.1|Chloroflexi bacterium RBG 13 68 17
Rifle contig 669065 4 Sericytochromatia RAAC 196 scaffold 669065 4
WP 012544964.1|Thermodesulfovibrio yellowstonii
OHD14270.1|Spirochaetes bacterium GWB1 27 13
WP 048088262.1|Candidatus Methanoperedens nitroreducens
OGW22162.1|Nitrospirae bacterium GWA2 46 11
OGX29320.1|Omnitrophica WOR 2 bacterium RIFCSPHIGHO2 01 FULL 49 10
GCA_003153935_12_105|Elusimicrobia_bacterium_GCA_003153935
GCA_002441095_26_2|Elusimicrobia_bacterium_UBA6262_GCA_002441095
OGB88127.1|Candidatus Falkowbacteria bacterium RIFCSPLOWO2 12 FULL 45 13
OHD57608.1|Spirochaetes bacterium GWF1 51 8
OHD55674.1|Spirochaetes bacterium GWF1 49 6
OGX14137.1|Omnitrophica bacterium RIFOXYB12 FULL 50 7
OGC08307.1|Saganbacteria RX7D scaffold 1964 3
RIFOXYA2 FULL CP 36 21 rifoxya2 full scaffold 1302 12 Saganbacteria RX7A scaffold 411 11
RIFOXYA2 FULL CP 46 56 rifoxya2 full scaffold 0 616 Saganbacteria RX3A scaffold 0 616
OGC04278.1|Saganbacteria RX3D scaffold 27 112
OGC22319.1|Saganbacteria RX4D scaffold 616 7
RIFOXYB2 FULL CP 42 35 rifoxyb2 full scaffold 224 19 Saganbacteria RX4A scaffold 224 19
rifoxya2_full_scaffold_373_23|RIFOXYA2_FULL_Elusimicrobia_53_38
gwc2_scaffold_23_100|GWC2_Elusimicrobia_56_31
gwa2_scaffold_495_15|GWA2_Elusimicrobia_51_34
cg1_0.2_scaffold_248_c_33|CG1_02_FULL_Elusimicrobia_56_21_curated
RAAC_Elusimicrobia_59_20_11_31|RAAC_Elusimicrobia_59_20
RIFCSPLOWO2_02_FULL_Elusimicrobia_61_11_rifcsplowo2_02_scaffold_29872_4|Elusimicrobia_bacterium_RIFCSPLOWO2_02_FULL_61_11
rifcsplowo2_02_scaffold_29872_4|RIFCSPLOWO2_02_FULL_Elusimicrobia_61_11
RifOxyA12_full_Elusimicrobia_57_11_rifixya3_full_scaffold_1777_1|Elusimicrobia_bacterium_RIFOXYA12_FULL_57_11
CG08_land_8_20_14_0.20_scaffold_2706_c_12|CG08_land_8_20_14_0_20_Elusimicrobia_59_10_curated
k141_284623_1|Zodletone_Water_assembly2018_Elusimicrobia_62_9
GWF2_ELX_62_30_gwf2_scaffold_2464_7|Elusimicrobia_bacterium_GWF2_62_30
GWD2_ELX_63_28_gwd2_scaffold_595_2|Elusimicrobia_bacterium_GWD2_63_28
Ig5182_scaffold_8903_112|08E140C01_z5_2015_Ig5182_Elusimicrobia_63_10
GWC2_ELX_64_44_gwc2_scaffold_3479_25|Elusimicrobia_bacterium_GWC2_64_44
GWA2_ELX_62_23_gwa2_scaffold_118_187|Elusimicrobia_bacterium_GWA2_62_23
GWB2_ELX_63_22_gwb2_scaffold_21_70|Elusimicrobia_bacterium_GWB2_63_22
RAAC_Elusimicrobia_62_20_2_55|RAAC_Elusimicrobia_62_20
GWA2_ELX_61_42_gwa2_scaffold_61_28|Elusimicrobia_bacterium_GWA2_61_42
GCA_002840355_8_117|Elusimicrobia_bacterium_HGW-Elusimicrobia-3_GCA_002840355
GWB2_ELX_63_16_gwb2_scaffold_520_27|Elusimicrobia_bacterium_GWB2_63_16
RAAC_Elusimicrobia_63_38_98_3|RAAC_Elusimicrobia_63_38
Tree scale: 0.1
🟥 group1
🟩 group 3d
group 3c
group 3b

Figure S9. Phylogenetic tree of the groups 1, 2 and 3 of [NiFe] hydrogenase (Maximum likelihood tree under a LG+G4 model of evolution). *Elusimicrobia* have group 1, group 3b, 3c and 3d [NiFe] hydrogenases. *Elusimicrobia* sequences are indicated with colored font. Scale bar indicates substitutions per site. The bootstraps are indicated by red circles when ≥ 85. The tree was made using sequences from (Matheus Carnevali et al. 2019). The sequences and tree are available with full bootstrap values in Fasta and Newick format in Supplementary Data.


Tree scale: 1
Mbh-Mrp-Oxidoreductase
Mbh-Mrp
Ech
NADH dehydrogenase
Hydrogenase-related complex
WP 023992909.1|Methanobacterium sp. MB1
BAP63347.1|Methanococcus maripaludis OS7
Q58433.1|Methanocaldococcus jannaschii DSM 2661
WP 004076146.1|Methanoplanus limicola
WP 012956197.1|Methanobrevibacter ruminantium
WP 011171406.1|Methanococcus maripaludis
Q57935.1|Methanocaldococcus jannaschii DSM 2661
WP 007045054.1|Methanotorris formicicus
WP 012543586.1|Coprothermobacter proteolyticus
WP 062282954.1|Flexilinea flocculi
WP 061918525.1|Bellilinea caldifistulae
WP 013560598.1|Anaerolinea thermophila
WP 062417842.1|Levilinea saccharolytica
KPL71028.1|Leptolinea tardivitalis
OQY81639.1|Anaerolineae bacterium UTCFX3
WP 095041790.1|Candidatus Promineofilum breve
OGO20034.1|Chloroflexi bacterium RBG 16 48 8
WP 008528233.1|Halorhabdus tiamatea
OGS50808.1|Euryarchaeota archaeon RBG 16 68 12
WP 015284192.1|Methanoregula formicica
OGS45312.1|Euryarchaeota archaeon RBG 16 67 27
RIFOXYA12_FULL_Elusimicrobium-like_49_49_rifixya3_full_scaffold_22_33|Elusimicrobia_bacterium_RIFOXYA12_FULL_49_49
RIFOXYA2_FULL_Elusimicrobia_related_50_26_rifoxya2_full_scaffold_692_24|Elusimicrobia_bacterium_RIFOXYA2_FULL_50_26
OGS17601.1|Elusimicrobia bacterium RIFOXYA2 FULL 50 26
OGF05053.1|Candidatus Edwardsbacteria bacterium RifOxyC12 full 54 24
RIFOXYA2_FULL_Elusimicrobia_rel_39_19_rifoxya2_full_scaffold_791_10|Elusimicrobia_bacterium_RIFOXYA2_FULL_39_19
OGS20111.1|Elusimicrobia bacterium RIFOXYA2 FULL 39 19
OJU09134.1|Clostridiales bacterium 43-6
DGJ9_scaffold_20613_3|DGJ9_Elusimicrobia_56_12
OGV40124.1|Lentisphaerae bacterium GWF2 49 21
GCA_001027545_1_38|Endomicrobium_proavitum_GCA_001027545
WP 052569507.1|Endomicrobium proavitum
WP 011737331.1|Pelobacter propionicus
RIFOXYD2_FULL_Elusimicrobia_34_15_rifoxyd2_full_scaffold_431_5|Elusimicrobia_bacterium_RIFOXYD2_FULL_34_15
OGV58663.1|Lentisphaerae bacterium RIFOXYA12 FULL 48 11
GCA_003153935_9_10|Elusimicrobia_bacterium_GCA_003153935
OGC36805.1|Saganbacteria RX6A scaffold 1178 17
GCA_000020145_1_1122|Elusimicrobium_minutum_Pei191_GCA_000020145
WP 012415297.1|Elusimicrobium minutum
gwa2_scaffold_188_115|GWA2_Elusimicrobia_51_34
CG08_land_8_20_14_0.20_scaffold_72847_c_2|CG08_land_8_20_14_0_20_Elusimicrobia_59_10_curated
k141_849172_2|Zodletone_Water_assembly2018_Elusimicrobia_62_9
gwc2_scaffold_3720_14|GWC2_Elusimicrobia_56_31
rifoxya2_full_scaffold_74_63|RIFOXYA2_FULL_Elusimicrobia_53_38
RIFOXYB2_FULL_Elusimicrobia_62_6_rifoxyb2_full_scaffold_11724_4|Elusimicrobia_bacterium_RIFOXYB2_FULL_62_6
RifOxyA12_full_Elusimicrobia_57_11_rifixya3_full_scaffold_4256_7|Elusimicrobia_bacterium_RIFOXYA12_FULL_57_11
GWA2_ELX_61_42_gwa2_scaffold_550_52|Elusimicrobia_bacterium_GWA2_61_42
RAAC_Elusimicrobia_62_20_36_13|RAAC_Elusimicrobia_62_20
GWB2_ELX_63_22_gwb2_scaffold_1732_13|Elusimicrobia_bacterium_GWB2_63_22
GWA2_ELX_62_23_gwa2_scaffold_899_12|Elusimicrobia_bacterium_GWA2_62_23
RAAC_Elusimicrobia_63_38_45_9|RAAC_Elusimicrobia_63_38
GWD2_ELX_63_28_gwd2_scaffold_420_17|Elusimicrobia_bacterium_GWD2_63_28
Ig5182_scaffold_153296_51|08E140C01_z5_2015_Ig5182_Elusimicrobia_63_10
GWB2_ELX_63_16_gwb2_scaffold_551_16|Elusimicrobia_bacterium_GWB2_63_16
OGR38599.1|Elusimicrobia bacterium GWA2 64 40
GCA_002840355_27_8|Elusimicrobia_bacterium_HGW-Elusimicrobia-3_GCA_002840355
RAAC_Elusimicrobia_64_12_134_14|RAAC_Elusimicrobia_64_12
Rifle contig 47474 22 Sericytochromatia RAAC 196 scaffold 47474 22
WP 011929095.1|Dehalococcoides mccartyi
WP 021758533.1|Desulfovibrio gigas
WP 011024634.1|Caldanaerobacter subterraneus
CAA76121.1|Methanosarcina barkeri
WP 011448732.1|Methanospirillum hungatei
OGV56416.1|Lentisphaerae bacterium GWF2 50 93
RAAC_Elusimicrobia_62_20_4_20|RAAC_Elusimicrobia_62_20
EKY27035.1|Clostridium celatum DSM 1785
WP 012199760.1|Lachnoclostridium phytofermentans
WP 010251151.1|Acetivibrio cellulolyticus
WP 014254276.1|Clostridium clariflavum
WP 027622667.1|Clostridium clariflavum
KJJ85970.1|Candidatus Omnitrophus magneticus
EKD26902.1|uncultured bacterium
OGH94446.1|Margulisbacteria GW1B scaffold 5446 11
OGI06409.1|Margulisbacteria GW1C scaffold 764 21
WP 013129492.1|Thermosphaera aggregans
ADL18787.1|Acidilobus saccharovorans 345-15
WP 011821374.1|Hyperthermus butylicus
WP 013562528.1|Desulfurococcus mucosus
WP 003869954.1|Thermoanaerobacter
WP 015869371.1|Kosmotoga olearia
WP 011994862.1|Fervidobacterium nodosum
WP 012057434.1|Thermosipho melanesiensis
WP 004102511.1|Thermosipho africanus
WP 004080082.1|Thermotoga
WP 015919825.1|Thermotoga neapolitana
WP 008084560.1|Aciduliprofundum boonei
WP 011012589.1|Pyrococcus furiosus
WP 013467129.1|Thermococcus barophilus
WP 012571445.1|Thermococcus onnurineus
BAA30554.1|Pyrococcus horikoshii OT3
CAB49628.1|Pyrococcus abyssi GE5
WP 014121212.1|Thermococcus sp. AM4
WP 015858334.1|Thermococcus gammatolerans
GCA_002412545_11_285|Elusimicrobia_bacterium_UBA5214_GCA_002412545
RIFOXYA12_FULL_Elusimicrobium-like_49_49_rifixya3_full_scaffold_53_17|Elusimicrobia_bacterium_RIFOXYA12_FULL_49_49
WP 011309368.1|Dehalococcoides mccartyi
WP 000621450.1|Bacillus cereus group
WP 000621456.1|Bacillus
RIFCSPLOWO2_01_FULL_Elusimicrobia_59_12_rifcsplowo2_01_scaffold_11183_20|Elusimicrobia_bacterium_RIFCSPLOWO2_01_FULL_59_12
GCA_003140895_83_61|Elusimicrobia_bacterium_GCA_003140895
S36_SO-2_scaffold_197726_16|Genasci_Feb2018_S36_SO-2_RIFCSPLOWO2_02_FULL_Elusimicrobia_39_32_curated_49_8
S5_GD2017_2_S2_scaffold_31_21|S5_QB3_180125_GD2017-2_S2_Elusimicrobia_38_13
RIFCSPLOWO2_02_FULL_Elusimicrobia_39_32_rifcsplowo2_02_scaffold_826_23|Elusimicrobia_bacterium_RIFCSPLOWO2_02_FULL_39_32
rifcsplowo2_01_scaffold_18537_8|RIFCSPLOWO2_01_FULL_Elusimicrobia_64_13
rifcsplowo2_01_scaffold_37047_7|RIFCSPLOWO2_01_FULL_Elusimicrobia_60_11
rifcsplowo2_01_scaffold_24568_20|RIFCSPLOWO2_01_FULL_Elusimicrobia_54_10
cg1_0.2_scaffold_119_c_22|CG1_02_FULL_Elusimicrobia_56_21_curated
RAAC_Elusimicrobia_59_20_37_100|RAAC_Elusimicrobia_59_20
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S_p1_S3_170907_scaffold_1605228_22|GD2017-1_S_p1_S3_Biohub_170907_Elusimicrobia_52_124
GWA2_Elusimicrobia_69_24_gwa2_scaffold_5333_17|Elusimicrobia_bacterium_GWA2_69_24
CG_4_10_14_0.2_scaffold_1295_c_16|CG_4_10_14_0_2_um_filter_Elusimicrobia_63_34_curated
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GWC2_Elusimicrobia_65_9_gwc2_scaffold_4834_26|Elusimicrobia_bacterium_GWC2_65_9
RBG_16_Elusimicrobia_66_12_RBG_16_scaffold_1611_26|Elusimicrobia_bacterium_RBG_16_66_12
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WP 002210277.1|Yersinia
WP 011097562.1|Xylella fastidiosa
WP 008570969.1|Xanthomonas
Q0C1E4.1|Hyphomonas neptunium ATCC 15444
XP 001596735.1|Sclerotinia sclerotiorum 1980 UF-70
XP 002487339.1|Talaromyces stipitatus ATCC 10500
XP 001275783.1|Aspergillus clavatus NRRL 1
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GCA_003151975_21_30|Elusimicrobia_bacterium_GCA_003151975
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RBG_16_Elusimicrobia_66_12_RBG_16_scaffold_11811_18|Elusimicrobia_bacterium_RBG_16_66_12
GWC2_Elusimicrobia_65_9_gwc2_scaffold_10434_11|Elusimicrobia_bacterium_GWC2_65_9
gwb2_scaffold_6981_6|GWB2_Elusimicrobium_67_8
gwc2_scaffold_1804_39|GWC2_Elusimicrobia_56_31
cg1_0.2_scaffold_392_c_11|CG1_02_FULL_Elusimicrobia_56_21_curated
RIFCSPLOWO2_02_FULL_Elusimicrobia_61_11_rifcsplowo2_02_scaffold_63229_2|Elusimicrobia_bacterium_RIFCSPLOWO2_02_FULL_61_11
rifcsplowo2_02_scaffold_63229_2|RIFCSPLOWO2_02_FULL_Elusimicrobia_61_11
RAAC_Elusimicrobia_59_20_35_81|RAAC_Elusimicrobia_59_20
GWF2_ELX_62_30_gwf2_scaffold_216_69|Elusimicrobia_bacterium_GWF2_62_30
Ig5182_scaffold_26230_38|08E140C01_z5_2015_Ig5182_Elusimicrobia_63_10
GWB2_ELX_63_16_gwb2_scaffold_274_38|Elusimicrobia_bacterium_GWB2_63_16
RAAC_Elusimicrobia_63_38_19_31|RAAC_Elusimicrobia_63_38
GCA_002840355_78_49|Elusimicrobia_bacterium_HGW-Elusimicrobia-3_GCA_002840355
RAAC_Elusimicrobia_64_12_19_7|RAAC_Elusimicrobia_64_12
GWC2_ELX_64_44_gwc2_scaffold_288_125|Elusimicrobia_bacterium_GWC2_64_44
GWD2_ELX_63_28_gwd2_scaffold_421_56|Elusimicrobia_bacterium_GWD2_63_28
GWA2_ELX_62_23_gwa2_scaffold_483_22|Elusimicrobia_bacterium_GWA2_62_23
GWA2_ELX_61_42_gwa2_scaffold_179_119|Elusimicrobia_bacterium_GWA2_61_42
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WP 022856172.1|Thermodesulfobacterium thermophilum
WP 027187553.1|Desulfovibrio cuneatus
WP 009368261.1|Bilophila sp. 4 1 30
WP 005028008.1|Bilophila wadsworthia
WP 013809561.1|Desulfotomaculum nigrificans
WP 011344721.1|Carboxydothermus hydrogenoformans
WP 011474902.1|Rhodopseudomonas palustris
WP011389179.1|Rhodospirillumrubrum
WP 008388614.1|Rhodovulum sp. PH10
WP 018606884.1|Uliginosibacterium gangwonense
WP 028535106.1|Paludibacterium yongneupense
WP 012745069.1|Kosmotoga
KPJ69723.1|Candidate division WOR 1 bacterium DG 54 3
OGC11840.1|Saganbacteria RX5A CDS 991
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KPK39519.1|Omnitrophica WOR 2 bacterium SM23 29
KPL19793.1|candidate division Zixibacteria bacterium SM23 81
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OIO80949.1|Candidatus Omnitrophica bacterium CG1 02 43 210
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Ig8144_scaffold_10101_3|09V250M02_2016_bjp_ig8144_Elusimicrobia_53_6
08E140C01_z5_2013_Ig3399_sub10_scaffold_166_8|08E140C01_Z5_2013_IG3399_SUB10_Elusimicrobia_rel_53_16
RIFOXYA2_FULL_Elusimicrobia_related_50_26_rifoxya2_full_scaffold_1172_19|Elusimicrobia_bacterium_RIFOXYA2_FULL_50_26
RIFOXYA12_FULL_Elusimicrobium-like_49_49_rifixya3_full_scaffold_23_129|Elusimicrobia_bacterium_RIFOXYA12_FULL_49_49
OGS11810.1|Elusimicrobia bacterium RIFOXYB1 FULL 48 9
DGJ9_scaffold_3528_3|DGJ9_Elusimicrobia_56_12
DGJ10_2_scaffold_287_28|DGJ10_2_Elusimicrobia_27_24
QC4_scaffold_253_8|QC4_Elusimicrobia_32_24
RIFOXYD2_FULL_Elusimicrobia_34_15_rifoxyd2_full_scaffold_556_12|Elusimicrobia_bacterium_RIFOXYD2_FULL_34_15
RIFOXYD2_FULL_Elusimicrobia_34_30_rifoxyd2_full_scaffold_1250_13|Elusimicrobia_bacterium_RIFOXYD2_FULL_34_30
CG07_land_8_20_14_0.80_scaffold_24307_1|CG07_land_8_20_14_0_80_Elusimicrobia_38_24__maxbin2.output.235
GCA_002402375_14_25|Elusimicrobia_bacterium_UBA4817_GCA_002402375
07M_4_2014_scaffold_153_26|07m_4_2014_Elusimicrobia_37_6
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RIFOXYA2_FULL_Elusimicrobia_rel_39_19_rifoxya2_full_scaffold_121_30|Elusimicrobia_bacterium_RIFOXYA2_FULL_39_19
RIFOXYA2_FULL_Elusimicrobium_40_6_rifoxya2_full_scaffold_3318_1|Elusimicrobia_bacterium_RIFOXYA2_FULL_40_6
rifoxyb2_full_scaffold_6941_5|RIFOXYB2_FULL_Elusimicrobia_48_7
CG02_land_8_20_14_3.00_150_scaffold_9524_1|CG02_land_8_20_14_3_00_150_Elusimicrobia_37_13
GCA_002779055_85_1|Elusimicrobia_bacterium_CG08_land_8_20_14_0_20_44_26_GCA_002779055
GCA_002841685_55_27|Elusimicrobia_bacterium_HGW-Elusimicrobia-2_GCA_002841685
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WP 014013072.1|Thermococcus sp. 4557
WP 011449544.1|Methanospirillum hungatei
WP 008083483.1|Aciduliprofundum boonei
WP 009164181.1|Pyramidobacter piscolens
WP 013048648.1|Aminobacterium colombiense
WP 014163350.1|Thermovirga lienii
WP 013467760.1|Thermococcus barophilus
WP 004066458.1|Thermococcus litoralis
WP 011012581.1|Pyrococcus furiosus
WP 013905871.1|Pyrococcus yayanosii
WP 010867842.1|Pyrococcus abyssi
WP 010885519.1|Pyrococcus horikoshii
WP 011388069.1|Rhodospirillum rubrum
WP 014123101.1|Thermococcus sp. AM4
WP 011839350.1|Staphylothermus marinus
WP 014767907.1|Desulfurococcus amylolyticus
WP 004068373.1|Thermococcus litoralis
WP 014122941.1|Thermococcus sp. AM4
WP 012571234.1|Thermococcus onnurineus
WP 011139635.1|Wolinella succinogenes
WP 025345477.1|Sulfurospirillum multivorans
WP 025773400.1|Moorella thermoacetica
WP 022587809.1|Caldanaerobacter subterraneus
WP 006234109.1|Collinsella aerofaciens
WP 022739022.1|Adlercreutzia equolifaciens
WP 011474970.1|Rhodopseudomonas palustris
WP 002440707.1|Shimwellia blattae
WP 001288122.1|Proteobacteria
WP 005366168.1|Photobacterium
WP 001102279.1|Escherichia
WP 004699424.1|Yersinia aldovae
CAJ72523.1|Candidatus Kuenenia stuttgartiensis
KKM10693.1|Clostridiales bacterium PH28 bin88
KUO60464.1|Gracilibacter sp. BRH c7a
WP 015756422.1|Desulfotomaculum acetoxidans
WP 013843216.1|Desulfotomaculum ruminis
WP 013623369.1|Syntrophobotulus glycolicus
WP 014183752.1|Desulfosporosinus orientis
WP 007780611.1|Desulfosporosinus youngiae
KJS50016.1|Peptococcaceae bacterium BRH c23
OGI19952.1 Melainabacteria HO7A scaffold 2189 39
WP 019553945.1|Propionispira raffinosivorans
WP 028986298.1|Thermicanus aegyptius
CCQ93003.1|Clostridium ultunense Esp
WP 018133527.1|Effusibacillus pohliae
WP 035046311.1|Anoxybacillus
WP 006323220.1|Anoxybacillus flavithermus
WP 014902103.1|Desulfosporosinus meridiei
WP 009619272.1|Desulfosporosinus sp. OT
WP 015945149.1|Desulfitobacterium hafniense
WP 014795396.1|Desulfitobacterium dehalogenans
WP 019851221.1|Desulfitobacterium sp. PCE1
WP 027938372.1|Anaeroarcus burkinensis
WP 018702624.1|Anaeromusa acidaminophila
WP 004094701.1|Acetonema longum
WP 021167282.1|Sporomusa
WP 019880045.1|Succinispira mobilis
CDB46957.1|Phascolarctobacterium sp. CAG 207
WP 051533411.1|Anaerovibrio sp. RM50
WP 051555427.1|Anaerovibrio lipolyticus
WP 011941639.1|Acidiphilium cryptum
WP 011719564.1|Acidothermus cellulolyticus
WP 010917712.1|Thermoplasma volcanium
WP 009989217.1|Sulfolobus
RIFCSPLOWO2_12_FULL_Elusimicrobia_59_9_rifcsplowo2_12_scaffold_10334_2|Elusimicrobia_bacterium_RIFCSPLOWO2_12_FULL_59_9
RIFCSPLOWO2_02_FULL_Elusimicrobia_39_32_rifcsplowo2_02_scaffold_9_37|Elusimicrobia_bacterium_RIFCSPLOWO2_02_FULL_39_32
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WP 012035107.1|Methanocella arvoryzae
WP 011448802.1|Methanospirillum hungatei
AAM30759.1|Methanosarcina mazei Go1
WP 011024251.1 |Methanosarcina acetivorans
WP 010937244.1|Dehalococcoides mccartyi
WP 011310005.1|Dehalococcoides mccartyi
WP 012034226.1|Dehalococcoides mccartyi
WP 013250744.1|Nitrospira defluvii
DGJ9_scaffold_1389_7|DGJ9_Elusimicrobia_56_12
OIO35201.1|Candidatus Omnitrophica bacterium CG1 02 44 16
OGF47622.1|Candidatus Firestonebacteria bacterium RIFOXYD2 FULL 39 29
RIFOXYB2_FULL_Elusimicrobia_62_6_rifoxyb2_full_scaffold_1566_8|Elusimicrobia_bacterium_RIFOXYB2_FULL_62_6
OGS60071.1|Elusimicrobia bacterium RIFOXYB2 FULL 62 6
OGC10990.1|Saganbacteria RX5A CDS 79
OGC25124.1|Saganbacteria RX4D scaffold 616 7
RIFOXYA2 FULL CP 46 56 rifoxya2 full scaffold 3 157 Saganbacteria RX3A scaffold 3 157
OGC05255.1 Saganbacteria RX3D scaffold 14 124
rifoxyb2_full_scaffold_1222_2|RIFOXYB2_FULL_Elusimicrobia_48_7
OGS28126.1|Elusimicrobia bacterium RIFOXYB2 FULL 48 7
RIFOXYA2_FULL_Elusimicrobia_rel_39_19_rifoxya2_full_scaffold_350_21|Elusimicrobia_bacterium_RIFOXYA2_FULL_39_19
OGS21231.1|Elusimicrobia bacterium RIFOXYA2 FULL 39 19
OGC16152.1|Saganbacteria RX7A scaffold 3923 5
CG08_land_8_20_14_0.20_scaffold_18180_c_4|CG08_land_8_20_14_0_20_Elusimicrobia_59_10_curated
CG08_land_8_20_14_0.20_scaffold_25199_c_4|CG08_land_8_20_14_0_20_Elusimicrobia_59_10_curated
gwa2_scaffold_244_55|GWA2_Elusimicrobia_51_34
OGR48196.1|Elusimicrobia bacterium GWA2 51 34
CBE69905.1|Candidatus Methylomirabilis oxyfera
WP 041548276.1|Nocardioides
WP 003400663.1|Mycobacterium tuberculosis complex
WP 010950337.1|Mycobacterium
WP 041360899.1|Methylococcus capsulatus
WP 011089083.1|Bradyrhizobium diazoefficiens
WP 011471411.1|Rhodopseudomonas palustris
WP 011493360.1|Paraburkholderia xenovorans
WP 011492896.1|Paraburkholderia xenovorans
ABC35876.1|Burkholderia thailandensis E264
WP 080231407.1|Burkholderia pseudomallei
EDO87384.1|Burkholderia pseudomallei 406e
WP 001258168.1|Leptospira interrogans
WP 001258166.1|Leptospira interrogans
PWU03612.1|Melainabacteria BJ4A scaffold 8 168
OGV38448.1|Lentisphaerae bacterium GWF2 45 14
OHD16850.1|Spirochaetes bacterium GWB1 27 13
OGH98787.1|Margulisbacteria GW1B scaffold 5446 11
OGI03157.1|Melainabacteria GW9A scaffold 1992 25
OGV17826.1|Lentisphaerae bacterium GWF2 38 69
OLA74616.1|Acinetobacter sp. CAG 196 36 41
OGH95554.1|Melainabacteria GW8A scaffold 6287 29
EKE03926.1|uncultured bacterium
OGI19993.1|Melainabacteria RX6B scaffold 3033 7
EKD26756.1|uncultured bacterium
OGX52972.1|Omnitrophica WOR 2 bacterium RIFOXYA12 FULL 38 10
OGX38568.1|Omnitrophica WOR 2 bacterium RIFCSPHIGHO2 02 FULL 50 17
OGW68527.1|Omnitrophica bacterium GWA2 50 21
GCA_003140895_51_11|Elusimicrobia_bacterium_GCA_003140895
cg1_0.2_scaffold_353_c_36|CG1_02_FULL_Elusimicrobia_56_21_curated
CG_4_10_14_0.2_scaffold_2584_c_4|CG_4_10_14_0_2_um_filter_Elusimicrobia_63_34_curated
GWC2_Elusimicrobia_65_9_gwc2_scaffold_14082_5|Elusimicrobia_bacterium_GWC2_65_9
OGL64714.1|Candidatus Tectomicrobia bacterium RIFCSPLOWO2 02 FULL 70 19
400_zone1_2014_Ig3401_scaffold_1_431|400_ZONE1_2014_IG3401_Elusimicrobia_69_35
WP 004512343.1|Geobacter metallireducens
WP 004511864.1|Geobacter metallireducens
WP 010941403.1|Geobacter sulfurreducens
OFZ55604.1|Bdellovibrionales bacterium RIFOXYC1 FULL 54 43
GWA2_Elusimicrobia_69_24_gwa2_scaffold_2505_11|Elusimicrobia_bacterium_GWA2_69_24
OHB51406.1|Planctomycetes bacterium GWF2 41 51
OGV73492.1|Lentisphaerae bacterium RIFOXYA12 64 32
gwc2_scaffold_1322_37|GWC2_Elusimicrobia_56_31
rifoxya2_full_scaffold_49_156|RIFOXYA2_FULL_Elusimicrobia_53_38
RifOxyA12_full_Elusimicrobia_57_11_rifixya3_full_scaffold_1066_5|Elusimicrobia_bacterium_RIFOXYA12_FULL_57_11
GWA2_ELX_62_23_gwa2_scaffold_1737_17|Elusimicrobia_bacterium_GWA2_62_23
Ig5182_scaffold_8058_11|08E140C01_z5_2015_Ig5182_Elusimicrobia_63_10
RAAC_Elusimicrobia_62_20_18_52|RAAC_Elusimicrobia_62_20
GWB2_ELX_63_22_gwb2_scaffold_493_18|Elusimicrobia_bacterium_GWB2_63_22
GWF2_ELX_62_30_gwf2_scaffold_10545_4|Elusimicrobia_bacterium_GWF2_62_30
GWA2_ELX_61_42_gwa2_scaffold_179_28|Elusimicrobia_bacterium_GWA2_61_42
GWC2_ELX_64_44_gwc2_scaffold_288_30|Elusimicrobia_bacterium_GWC2_64_44
GWD2_ELX_63_28_gwd2_scaffold_696_22|Elusimicrobia_bacterium_GWD2_63_28
GCA_002840355_28_5|Elusimicrobia_bacterium_HGW-Elusimicrobia-3_GCA_002840355
RAAC_Elusimicrobia_64_12_182_5|RAAC_Elusimicrobia_64_12
GWB2_ELX_63_16_gwb2_scaffold_353_50|Elusimicrobia_bacterium_GWB2_63_16
RAAC_Elusimicrobia_63_38_66_5|RAAC_Elusimicrobia_63_38

Figure S10. Phylogenetic tree of the group 4 [NiFe] hydrogenase (Maximum likelihood tree under a LG+I+G4 model of evolution). *Elusimicrobia* have Mbh-Mrp, Mbh-Mrp-Oxidoreductase, Ech and Hydrogenase-related complex [NiFe] hydrogenases. They also have NADH dehydrogenase. *Elusimicrobia* sequences are indicated with colored font. Scale bar indicates substitutions per site. The bootstraps are indicated by red circles when ≥ 85. The tree was made using sequences from (Matheus Carnevali et al. 2019). The sequences and tree are available with full bootstrap values in Fasta and Newick format in Supplementary Data.


Type C (cbb3)
qNOR
Type B
New type?
Type A
cNOR
Tree scale: 1
NP_148062.1|Aeropyrum_pernix_K1
WP_008441349.1|Halorubrum_californiense
CAA71525.1|Natronomonas_pharaonis
WP_049928572.1|Halopiger_goleimassiliensis
WP_049888867.1|Natronococcus_occultus
WP_090309191.1|Natronorubrum_texcoconense
Aquifex_aeolicus_O67937|unknown
WP_018914608.1|Thiomonas_sp._FB-6
WP_091712936.1|Methylobacterium_phyllostachyos
WP_043201277.1|Paraburkholderia_acidipaludis
WP_042057359.1|Acidomonas_methanolica
WP_085091361.1|Azospirillum_oryzae
WP_013177985.1|Truepera_radiovictrix
WP_027483790.1|Deinococcus_pimensis
ALW90450.1|Deinococcus_actinosclerus
WP_013458307.1|Oceanithermus_profundus
WP_013703169.1|Marinithermus_hydrothermalis
WP_027891229.1|Meiothermus_chliarophilus
WP_038056548.1|Thermus_amyloliquefaciens
OGO10369.1|Chloroflexi_bacterium_RBG_13_66_10
OQY19783.1|Anaerolineaceae_bacterium_4572_32.1
CBE68178.1|Candidatus_Methylomirabilis_oxyfera
OGW14262.1|Nitrospirae_bacterium_GWA2_42_11
WP_029520322.1|Persephonella_sp._IF05-L8
WP_067330013.1|Sulfurovum_riftiae
OHE10778.1|Sulfurimonas_sp._RIFOXYD12_FULL_33_39
WP_072679966.1|Arcobacter_sp._LA11
OGU38604.1|Ignavibacteria_bacterium_GWA2_36_19
OHE00888.1|Sulfurimonas_sp._RIFCSPLOWO2_02_FULL_36_28
WP_092912870.1|Hydrogenimonas_thermophila
YP_003022821.1|Geobacter_sp._M21
CAA82229.1|Pseudomonas_stutzeri
AAG34384.1|Pseudomonas_fluorescens
BAB84303.1|Roseobacter_denitrificans
BAA90782.1|Alcaligenes_faecalis
NP_534866.1|Agrobacterium_tumefaciens_str._C58
WP_006871449.1|Legionella_drancourtii
WP_025987383.1|Burkholderia_thailandensis
WP_066556414.1|Sphingobium_sp._TKS
OJW29330.1|Rhodospirillales_bacterium_69-11
WP_008456294.1|Natrinema_gari
SDF02486.1|Halorientalis_regularis
SDZ77349.1|Haloplanus_vescus
SJM61259.1|Lactobacillus_fermentum
YP_001124768.1|Geobacillus_thermodenitrificans_NG80-2
WP_003331062.1|Bacillus_azotoformans
GWA2_Elusimicrobia_69_24_gwa2_scaffold_3589_27|Elusimicrobia_bacterium_GWA2_69_24
GWA2_ELX_62_23_gwa2_scaffold_5825_6|Elusimicrobia_bacterium_GWA2_62_23
cg1_0.2_scaffold_5851_c_6|CG1_02_FULL_Elusimicrobia_56_21_curated
RAAC_Elusimicrobia_59_20_25_206|RAAC_Elusimicrobia_59_20
CG_4_10_14_0.2_scaffold_2897_c_7|CG_4_10_14_0_2_um_filter_Elusimicrobia_63_34_curated
ERJ21813.1|Campylobacter_concisus_UNSW3
CRY99017.1|Neisseria_meningitidis_serogroup_B
CBW14123.1|Haemophilus_parainfluenzae_T3T1
ABD94720.1|Pseudomonas_aeruginosa
SJN17569.1|Pseudoalteromonas_sp._JB197
GAQ14115.1|Myroides_odoratimimus
AFH89980.2|Corynebacterium_pseudotuberculosis_31
GCA_003140895_14_16|Elusimicrobia_bacterium_GCA_003140895
CG_4_10_14_0.2_scaffold_34_c_21|CG_4_10_14_0_2_um_filter_Elusimicrobia_63_34_curated
gwb2_scaffold_3283_7|GWB2_Elusimicrobium_67_8
RIFOXYD12_FULL_Elusimicrobium_66_9_rifoxyd3_full_scaffold_3111_3|Elusimicrobia_bacterium_RIFOXYD12_FULL_66_9
WP_071313791.1|Anaerobacillus_arseniciselenatis
WP_027414870.1|Aneurinibacillus_terranovensis
WP_044390181.1|Bacillus_subterraneus
WP_079507272.1|Bacillus_jeotgali
WP_011197266.1|Symbiobacterium_thermophilum
AEQ75414.1|Leptospirillum_ferriphilum
BAM06481.1|Leptospirillum_ferrooxidans_C2-3
WP_029915749.1|Pelobacter_seleniigenes
AOY59322.1|Desulfococcus_multivorans
KOY52867.1|Polaribacter_dokdonensis_DSW-5
KIF31770.1|Hassallia_byssoidea_VB512170
WP_091516722.1|Flexibacter_flexilis
OUR97135.1|Halobacteriovorax_marinus
WP_102243045.1|Bacteriovorax_stolpii
PIQ28007.1|bacterium_(Candidatus_Blackallbacteria)_CG18_big_fil_WC_8_21_14_2_50_49_26
KHE90990.1|Candidatus_Scalindua_brodae
WP_015469929.1|Bdellovibrio_exovorus
WP_061835668.1|Bdellovibrio_bacteriovorus
OGE19126.1|Candidatus_Dadabacteria_bacterium_RIFCSPHIGHO2_12_FULL_53_21
PIT98784.1|Bdellovibrionales_bacterium_CG10_big_fil_rev_8_21_14_0_10_45_34
WP_082901917.1|Leptolyngbya_valderiana
WP_018981786.1|Salinimonas_chungwhensis
WP_039220109.1|Alteromonas_marina
WP_071951600.1|Alteromonas_mediterranea
WP_070176136.1|Alteromonas_lipolytica
WP_073324560.1|Aestuariibacter_aggregatus
AAC46108.1|Rhodobacter_capsulatus
ABF65277.1|Ruegeria_sp._TM1040
sp Q05572.1 FIXN RHIME
AHL30239.1|Sphingomonas_sp._NX-3
YP_002516840.1|Caulobacter_vibrioides_NA1000
sp Q03073.1 FIXN BRADU
SMX59739.1|Bradyrhizobium_sp._ORS_285
S_p2_S4_coassembly_k141_1278569_3|S_p2_S4_coassembly_Elusimicrobia_69_76
S_p1_S3_coassembly_k141_1616416_8|S_p1_S3_coassembly_Elusimicrobia_58_61
S5_GD2017_2_S2_scaffold_122_60|S5_QB3_180125_GD2017-2_S2_Elusimicrobia_38_13
RIFCSPLOWO2_02_FULL_Elusimicrobia_39_32_rifcsplowo2_02_scaffold_39_42|Elusimicrobia_bacterium_RIFCSPLOWO2_02_FULL_39_32
EDY39380.1|Cyanobium_sp._PCC_7001
WP_012407146.1|Nostoc_punctiforme
WP_017303448.1|Spirulina_subsalsa
WP_019499491.1|Pseudanabaena_sp._PCC_6802
WP_099883944.1|Synechococcus_sp._65AY6A5
WP_011243817.1|Synechococcus
WP_058995290.1|Leptolyngbya_sp._NIES-2104
WP_015150964.1|Oscillatoria_acuminata
WP_010469823.1|Acaryochloris_sp._CCMEE_5410
sp Q06473.2 COX1 SYNY3
WP_099702197.1|Chroococcales_cyanobacterium_IPPAS_B-1203
WP_035153422.1|Calothrix_sp._336/3
WP_073628984.1|Scytonema_sp._HK-05
NP_923686.1|Gloeobacter_violaceus_PCC_7421
WP_023174521.1|Gloeobacter_kilaueensis
WP_065716051.1|Synechococcus_sp._PCC_8807
WP_012409913.1|Nostoc_punctiforme
WP_094345093.1|Nostoc_sp._'Peltigera_membranacea_cyanobiont'_232
OBQ08035.1|Anabaena_sp._AL09
WP_028083358.1|Dolichospermum_circinale
OBQ43552.1|Aphanizomenon_flos-aquae_WA102
WP_096564280.1|Scytonema_sp._NIES-4073
KIF36896.1|Hassallia_byssoidea_VB512170
WP_089126893.1|Tolypothrix_sp._NIES-4075
WP_026720841.1|Fischerella_sp._PCC_9431
WP_053456453.1|Hapalosiphon_sp._MRB220
WP_096727993.1|Nostoc_carneum
WP_096590759.1|Calothrix_sp._NIES-2098
WP_013193309.1|Trichormus_azollae
WP_096578826.1|Nostocales
WP_035485457.1|Alicyclobacillus_contaminans
OGC78093.1|candidate_division_Zixibacteria_bacterium_RBG_16_50_21
sp P00396.1 COX1 BOVIN
ABA78027.1|Rhodobacter_sphaeroides_2.4.1
WP_072245353.1|Roseibaca_calidilacus
WP_066818473.1|Defluviimonas_alba
sp P08305.1 COX1A PARDE
WP_096431750.1|Thioclava_arenosa
WP_072899810.1|Cognatiyoonia_sediminum
WP_039018302.1|Halocynthiibacter_namhaensis
WP_085887363.1|Pseudooceanicola_marinus
WP_090028298.1|Lutimaribacter_saemankumensis
WP_013179238.1|Truepera_radiovictrix
sp Q9RR77 Q9RR77 DEIRA
sp P98005.1 COX13 THET8
WP_040779827.1|Meiothermus_timidus
WP_041658460.1|Marinithermus_hydrothermalis
GWC2_ELX_64_44_gwc2_scaffold_296_75|Elusimicrobia_bacterium_GWC2_64_44
SR-2_scaffold_141_1015313_157|SR-2_Biohub_180515_Elusimicrobia_69_71
GWA2_Elusimicrobia_69_24_gwa2_scaffold_16786_13|Elusimicrobia_bacterium_GWA2_69_24
GWC2_Elusimicrobia_65_9_gwc2_scaffold_6933_7|Elusimicrobia_bacterium_GWC2_65_9
RIFOXYD12_FULL_Elusimicrobium_66_9_rifoxyd3_full_scaffold_8618_3|Elusimicrobia_bacterium_RIFOXYD12_FULL_66_9
gwb2_scaffold_37434_2|GWB2_Elusimicrobium_67_8
PIR25656.1|Deltaproteobacteria_bacterium_CG11_big_fil_rev_8_21_14_0_20_42_23
CAC08532.1|Rhodothermus_marinus
WP_068121289.1|Rhodothermaceae_bacterium_RA
WP_094548366.1|Rubricoccus_marinus
KPP95186.1|Bacteroidetes_bacterium_HLUCCA01
WP_069133290.1|Rhodohalobacter_halophilus
WP_018127091.1|Balneola_vulgaris
WP_020401590.1|Gracilimonas_tropica
PIO47847.1|Chlorobium_sp._445
WP_031501002.1|Bryobacter_aggregatus
WP_053335001.1|Thermoanaerobaculum_aquaticum
OYW03066.1|Acidobacteria_bacterium_37-71-11
WP_013630949.1|Rubinisphaera_brasiliensis
WP_002653988.1|Blastopirellula_marina
WP_082846157.1|Planctomyces_sp._SH-PL14
OGC95752.1|candidate_division_Zixibacteria_bacterium_RBG_16_53_22
PJA26831.1|candidate_division_Zixibacteria_bacterium_CG_4_9_14_3_um_filter_46_8
OGC00951.1|candidate_division_KSB1_bacterium_RBG_16_48_16
AKF06459.1|Sandaracinus_amylolyticus
WP_050726922.1|Vulgatibacter_incomptus
WP_075276095.1|Pajaroellobacter_abortibovis
APR79665.1|Minicystis_rosea
WP_012240201.1|Sorangium_cellulosum
AKT43929.1|Chondromyces_crocatus
WP_015716040.1|Thermus_scotoductus
RIFCSPLOWO2_01_FULL_Elusimicrobia_59_12_rifcsplowo2_01_scaffold_8371_8|Elusimicrobia_bacterium_RIFCSPLOWO2_01_FULL_59_12
GCA_003151975_12_12|Elusimicrobia_bacterium_GCA_003151975
RIFCSPHIGHO2_02_FULL_Elusimicrobia_57_9_rifcsphigho2_02_scaffold_37722_12|Elusimicrobia_bacterium_RIFCSPHIGHO2_02_FULL_57_9
CG_4_10_14_0.2_scaffold_76_c_53|CG_4_10_14_0_2_um_filter_Elusimicrobia_63_34_curated
GCA_002401485_86_8|Elusimicrobia_bacterium_GCA_002401485
rifcsplowo2_01_scaffold_21348_6|RIFCSPLOWO2_01_FULL_Elusimicrobia_60_11
rifcsplowo2_01_scaffold_21348_5|RIFCSPLOWO2_01_FULL_Elusimicrobia_60_11
S5_GD2017_2_S2_scaffold_637_4|S5_QB3_180125_GD2017-2_S2_Elusimicrobia_38_13
RIFCSPLOWO2_02_FULL_Elusimicrobia_39_32_rifcsplowo2_02_scaffold_973_6|Elusimicrobia_bacterium_RIFCSPLOWO2_02_FULL_39_32
S36_SO-2_scaffold_379086_4|Genasci_Feb2018_S36_SO-2_RIFCSPLOWO2_02_FULL_Elusimicrobia_39_32_curated_49_8
RIFCSPHIGHO2_01_FULL_Elusimicrobia_64_10_rifcsphigho2_01_scaffold_19950_15|Elusimicrobia_bacterium_RIFCSPHIGHO2_01_FULL_64_10
rifcsplowo2_01_scaffold_19516_11|RIFCSPLOWO2_01_FULL_Elusimicrobia_64_13
sp O53290 COX1 MYCTU
WP_052891118.1|Thermogemmatispora_carboxidivorans
AHG87837.1|Gemmatirosa_kalamazoonesis
WP_052446190.1|Geoalkalibacter_ferrihydriticus
WP_096459593.1|Sulfurifustis_variabilis
WP_102073219.1|Pusillimonas_sp._JR1/69-3-13
WP_013220362.1|Nitrosococcus_watsonii
WP_021227406.1|Sphingobium_lactosutens
WP_055845124.1|Sphingomonas_sp._Leaf343
WP_084410344.1|Fulvimarina_manganoxydans
WP_099867643.1|Pararhizobium_haloflavum
WP_002646059.1|Gimesia_maris
WP_002650546.1|Blastopirellula_marina
WP_054492930.1|Ardenticatena_maritima
WP_088571408.1|Thermoflexus_hugenholtzii
WP_054536710.1|Herpetosiphon_geysericola
WP_012122029.1|Roseiflexus_castenholzii
WP_012871115.1|Sphaerobacter_thermophilus
WP_012872064.1|Sphaerobacter_thermophilus
AHG89945.1|Gemmatirosa_kalamazoonesis
KPJ89936.1|Gemmatimonas_sp._SG8_17
OGL18143.1|Candidatus_Rokubacteria_bacterium_RIFCSPLOWO2_12_FULL_69_21
WP_081793531.1|Paenibacillus_darwinianus
sp P24010.3 COX1 BACSU
WP_027094641.1|Cohnella_thermotolerans
PKB63209.1|SAR202_cluster_bacterium_Io17-Chloro-G1
WP_089722081.1|Candidatus_Entotheonella_palauensis
PIQ26723.1|bacterium_(Candidatus_Blackallbacteria)_CG18_big_fil_WC_8_21_14_2_50_49_26
WP_096056567.1|Verrucomicrobia_bacterium
WP_068631155.1|Cephaloticoccus_primus
WP_012374891.1|Opitutus_terrae
PAW73427.1|Opitutae_bacterium_Tous-C5TDCM

Figure S11. Phylogenetic tree of the catalytic subunit I of heme-copper oxygen reductases (Maximum likelihood tree under a LG+F+I+G4 model of evolution). *Elusimicrobia* have an aa_3-type heme-copper oxygen reductase (Type A) and nitric oxide reductase that uses quinol as the electron donor (qNOR). *Elusimicrobia* sequences are indicated with colored font. The bootstraps are indicated by red circles when ≥ 85. The tree was made using sequences from (Matheus Carnevali et al. 2019). Scale bar indicates substitutions per site. The sequences and tree are available with full bootstrap values in Fasta and Newick format in Supplementary Data.


Formate dehydrogenase
Nitrate reductases (NapA, NasA, and NarB)
Cytoplasmic nitrite oxidoreductase (NxrA)
Unknown Function
Thiosulfate/polysulphide reductases (PhsA and PsrA)
Tetrathionate reductase (TtrA)
Nitrate reductase (NarG)
Arsenate reductase (ArrA)
Trimethylamine N-oxide reductase (TorA)
Dimethyl sulphoxide reductase (DmsA)
Periplasmic nitrite oxidoreductase(NxrA)
Alternative Complex III
Quinone reductase complex (Qrcb)
Tree scale: 1
DmsA E coli sp P18775
DmsA Actinobacillus succinogenes 130Zgi 75429943 ref ZP 007325271
DmsA Haemophilus influenza sp P45004
TMAO Shewanella massilia CAA06851
TMAO Photobacterium profundum YP 129680
TMAO Vibrio vulnificus YP 004189064
TMAO Citrobacter youngae ZP 06352135
TMAO Salmonella enterica gb AEZ47489
TMAO E coli CAA52095
Natrinema pellirubrum
Hydrogenobaculum sp
Hydrogenobacter thermophilus
SR-2 scaffold 141 222437 26
Beggiatoa sp
BAL57377 uncultured Acetothermia bacterium
Candidatus Methanoperedens nitroreducens
rifcsplowo2 01 scaffold 16737 2
S p1 S3 170907 scaffold 633672 2
S p2 S4 coassembly k141 1496388 58
RIFCSPHIGHO2 02 FULL Elusimicrobia 57 9 rifcsphigho2 02 scaffold 24326 7
RBG1 11 267 Zixibacteria
NxrA1|Nitrospira defluvii
NxrA2|Nitrospira defluvii
RIFCSPLOWO2 12 FULL Elusimicrobia 59 9 rifcsplowo2 12 scaffold 3265 13
S p1 S3 coassembly k141 1467004 6
planctomycete KSU 1 ZP 10101005
CAJ72445|Candidatus K stuttgartiensis
OWY72777 1|cyanobacterium TDX16
RIFCSPLOWO2 01 FULL Elusimicrobia 59 12 rifcsplowo2 01 scaffold 9892 31
CG 4 10 14 0.2 scaffold 266 c 30
RIFCSPLOWO2 02 FULL Elusimicrobia 39 32 rifcsplowo2 02 scaffold 39 34
S5 GD2017 2 S2 scaffold 122 53
P42175.2|Bacillus subtilis (narG)
AAT47523|Halomonas maura
P09152.4|Escherichia coli
NarG Escherichia coli
1Q16
AAZ43099|Pseudomonas stutzeri (NarG)
AAZ430991|Pseudomonas stutzeri A1501
Pseudomonas fluorescens|AEV63780
Pseudomonas fluorescens|AAG34373.1
EAR23355|Nitrococcus mobilis
ZP_01048070|Nitrobacter
ABA05326|Nitrobacter winogradskyi
A Nitrobacter hamburgensis
YP 578186|Nitrobacter hamburgensis
KRT74986|Deltaproteobacteria bacterium CSP1 8
PIZ32461|Armatimonadetes bacterium CG 4 10 14 0 8 um filter 66 14
WP_072910116|Malonomonas rubra
WP_029917027|Pelobacter seleniigenes
WP_066727835|Desulfuromonas sp DDH964
WP_085011779|Geothermobacter sp EPR M
GWC2 Elusimicrobia 65 9 gwc2 scaffold 2849 37
RAAC Elusimicrobia 59 20 37 35
WP_094160975|Thiomonas delicata
WP_092728517|Algoriphagus alkaliphilus
TAL62315|Bacteriodetes bacterium
WP_031445324|Arenibacter algicola
PsrA PhsA Thermus thermophilus YP 004130
PsrA PhsA Geobacter lovleyi ZP 01593406
PsrA PhsA Acidiphilium cryptum YP 001233491
B Caldithrix abyssi ZP 09550397
PsrA PhsA Archaeoglobus fulgidus NP 071207
PsrA PhsA Moorella thermoacetica ATCC YP 429324
PsrA Carboxydothermus hydrogenoformans YP 361367
PhsA Wolinella succinogenes NP 906934
PsrA Wolinella succinogenes NP 906381
PsrA PhsA Thermosinus carboxydivorans ZP 01667237
SR-2 scaffold 141 222437 58
TtrA BAL59996 Candidatus Acetothermus autotrophicum
TtrA WP 015720697 Geobacter sp M18
TtrA WP 068515226 Caldimicrobium thiodismutans
TtrA KRT749781 Deltaproteobacteria bacterium CSP1 8
TtrA Aeropyrum pernix NP 148724
TtrA Pyrobaculum arsenaticum YP 001152643
TtrA Pyrobaculum aerophilum NP 559177
TtrA Photobacterium profundum YP 133039
TtrA Wolinella succinogenes NP 907142
TtrA Haemophilus somnus gb ABI25172
TtrA Yersinia enterocolitica YP 001005907
Alkalilimnicola ehrlichii ABI55571
ArxA Ectothiorhodospira sp PHS 1 ZP 09695308
Halorhodospira halophila YP 001001949
ArrA Chrysiogenes arsenatis gb AAU11839
ArrA Halarsenatibacter silvermanii gb ACF74513
ArrA Bacillus selenitireducens gb AAQ19491
ArrA Wolinella succinogenes NP 906980
ArrA Sulfurospirillum barnesii gb AAU11840
QrcB Syntrophobacter fumaroxidans YP 844744
QrcB delta proteobacterium NaphS2 ZP 07200609
QrcB Desulfatibacillum alkenivorans YP 002430439
QrcB Desulfococcus oleovorans YP 001530428
MFIc Desulfococcus oleovorans YP 001530428
QrcB Desulfomicrobium baculatum YP 003159879
MFic Desulfomicrobium baculatum YP 003159879
QrcB Desulfovibrio magneticus YP 002953179
MFic Desulfovibrio magneticus YP 002953179
QrcB Desulfovibrio vulgaris YP 967712
MFIc Desulfovibrio vulgaris YP 967712
WP 011939627 Geobacter uraniireducens
OHB25939 Desulfuromonadaceae bacterium GWB2 53 15
OFW15409 Acidobacteria bacterium RIFCSPLOWO2 02 FULL 67 21
SRR636581 qc 1 paired CBMW 12 contig 1069 89 Sericytochromatia CBMW 12
OGO37950 Chloroflexi bacterium RBG 16 57 11
MFIc Mariprofundus ferrooxydans ZP 01451016
ActB Leptospira interrogans serovar NP 713447
ActB Bdellovibrio bacteriovorus NP 96849
ActB Cytophaga hutchinsonii YP 678817
ActB Flavobacterium psychrophilum YP 001295304
CG 4 10 14 0.2 scaffold 761 c 9
GCA 003151975 33 69
RBG 16 Elusimicrobia 66 12 RBG 16 scaffold 11758 37
GWC2 Elusimicrobia 65 9 gwc2 scaffold 2849 44
RIFCSPHIGHO2 02 FULL Elusimicrobia 57 9 rifcsphigho2 02 scaffold 459734 1
RIFCSPHIGHO2 02 FULL Elusimicrobia 57 9 rifcsphigho2 02 scaffold 113297 3
RIFCSPHIGHO2 02 FULL Elusimicrobia 57 9 rifcsphigho2 02 scaffold 455579 1
GWA2 Elusimicrobia 69 24 gwa2 scaffold 6045 5
SR-2 scaffold 141 1015313 151
GWC2 Elusimicrobia 65 9 gwc2 scaffold 2125 2
RIFOXYD12 FULL Elusimicrobium 66 9 rifoxyd3 full scaffold 3755 8
PIQ24251 bacterium Candidatus Blackallbacteria CG18 big fil WC 8 21 14 2 50 49 26
LSPB 72 contig 19959 10 Sericytochromatia LSPB 72
OGU76910 Ignavibacteria bacterium RBG 16 34 14
WP 014560253 Ignavibacterium album
ActB Methylacidiphilum infernorum YP 001940612
ActB PJA26839 candidate division Zixibacteria bacterium CG 4 9 14 3 um filter 46 8
ActB Opitutus terrae gb ACB77208
ActB Salinibacter ruber emb CBH25246
ActB Rhodothermus marinus gb ABV55245
ActB Anaeromyxobacter dehalogenans YP 002491266
ActB Chloroflexus aggregans YP 002464666
ActB Candidatus Koribacter versatilis Ellin345 YP 592078
ActB Candidatus Solibacter usitatus YP 821785
ActB WP 036500289 Nitrosococcus oceani
ActB Nitrosococcus oceani YP 343269
ActB WP 007080924 Rhodanobacter fulvus
ActB Ralstonia eutropha YP 298623
ActB Methylobacterium sp 4 YP 001772545
ActB Gluconacetobacter diazotrophicus YP 001602862
ActB Thermus thermophilus BAD71587
GCA 002412545 24 51
FdhN Escherichia coli pdb 1KQG
WP 014770341 formate dehydrogenase Sulfurospirillum barnesii
WP 082946371 formate dehydrogenase Arcobacter skirrowii
WP 081666492 formate dehydrogenase Sulfurimonas hongkongensis
WP 095297644 formate dehydrogenase Helicobacter sp 12S0223210
CAA37989 formate dehydrogenase Wolinella succinogenes
FdhA Wolinella succinogenes NP 907333
bjp ig3402 Sc 21 5 0 2 B 69
WP 015250571 anaerobic dehydrogenase Singulisphaera acidiphila
WP 078058457 formate dehydrogenase Mycobacterium icosiumassiliensis
WP 083131745 formate dehydrogenase Mycobacterium branderi
WP 087139919 formate dehydrogenase Mycobacterium chimaera
WP 037370579 formate dehydrogenase Amycolatopsis orientalis
WP 081982073 formate dehydrogenase Streptacidiphilus albus
WP 030736623 formate dehydrogenase Streptomyces griseus
WP 030397252 formate dehydrogenase Kitasatospora purpeofusca
WP 051652582 formate dehydrogenase Kitasatospora cheerisanensis
WP 069801994 formate dehydrogenase Thermogemmatispora onikobensis
OGF56502 formate dehydrogenase Candidatus Fraserbacteria bacterium RBG 16 55 9
PMP74658 formate dehydrogenase Roseiflexus castenholzii
WP 066783325 formate dehydrogenase Chloroflexus islandicus
PMP83579 formate dehydrogenase Chloroflexus aggregans
LSPB 72 contig 19959 33 Sericytochromatia LSPB 72
WP 012593908 Cyanothece sp PCC 8801
WP 075904084 formate dehydrogenase Moorea bouillonii
WP 070395532 formate dehydrogenase Moorea producens
WP 038077715 formate dehydrogenase Tolypothrix bouteillei
KYC43517 formate dehydrogenase Scytonema hofmannii PCC 7110
WP 096555384 1 Nostoc sp NIES 4103
WP 073643293 formate dehydrogenase Nostoc calcicola
WP 067770818 Nostoc sp NIES 3756
ALF52373 formate dehydrogenase Nostoc piscinale CENA21
formateDH TIGR01591 AAL81645.1 Pyrococcus furiosus DSM 3638
formateDH TIGR01591 WP 009989210.1 Saccharolobus solfataricus
SR-2 scaffold 141 304462 63
cg1 0.2 scaffold 624 c 22
RAAC Elusimicrobia 59 20 43 5
formateDH TIGR01591 WP 009989018.1 Saccharolobus solfataricus
formateDH TIGR01591 2IV2
formateDH TIGR01591 P07658.2 ECOLI
GWC2 ELX 64 44 gwc2 scaffold 611 52
WP 114638720 Polynucleobacter necessarius
WP 011902950 Polynucleobacter asymbioticus
WP 108508770 Polynucleobacter acidiphobus
WP 055451629 Thiomonas bhubaneswarensis
WP 066702393 Curvibacter delicatus
WP 088955982 Variovorax sp HW608
WP 047786433 Variovorax paradoxus
DGJ9 scaffold 4331 9
RIFOXYB2 FULL WOR1 45 9 curatedcompleterepermuted 295
RifOxyA12 full CP 36 13 rifixya3 full scaffold 411 21
CG02 land 8 20 14 3.00 150 scaffold 3067 27
07M 4 2014 scaffold 2045 1
400 zone1 2014 lg3401 scaffold 1000 11
WP 078664599 formate dehydrogenase subunit alpha Carboxydocella sporoproducens
formateDH TIGR01591 WP 010913191.1 Mesorhizobium japonicum
WP 084663263 formate dehydrogenase subunit alpha Thermanaeromonas toyohensis
WP 081358555 formate dehydrogenase subunit alpha Moorella thermoacetica
GCA 002412545 5 20
RifOxyA12 full Melainabacteria 32 12 rifixya3 full scaffold 5076 5
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WP 083764070 formate dehydrogenase subunit alpha Syntrophobacter fumaroxidans
WP 083610934 formate dehydrogenase subunit alpha Desulfatibacillum alkenivorans
WP 092229420 formate dehydrogenase subunit alpha Desulfobacula phenolica
RIFOXYD2 FULL CP 41 8 rifoxyd2 full scaffold 3759 6
RIFOXYB2 FULL CP 42 35 rifoxyb2 full scaffold 224 34
WP 093395222 formate dehydrogenase subunit alpha Thermodesulforhabdus norvegica
WP 073248330 formate dehydrogenase subunit alpha Caloramator proteoclasticus
WP 091728478 formate dehydrogenase subunit alpha Proteiniborus ethanoligenes
WP 091546885 formate dehydrogenase subunit alpha Alkaliphilus peptidifermentans
WP 078060538 formate dehydrogenase subunit alpha Desulfotomaculum copahuensis
formateDH TIGR01591 P06131.1 FDHA METFO
WP 084219033 formate dehydrogenase subunit alpha Syntrophorhabdus aromaticivorans
WP 083756393 formate dehydrogenase subunit alpha Syntrophus aciditrophicus
RIFCSPLOWO2 01 FULL Elusimicrobia 59 12 rifcsplowo2 01 scaffold 19048 16
cd02754 YP 147719.1
cd02754 BAB04334.1
cd02754 sp P42434.2 NASC BACSU
WP 007086372 nitrate reductase Bacillus bataviensis
WP 045524506 Bacillus niacini
OLE52235 formate dehydrogenase subunit alpha Acidobacteria bacterium 13 1 20CM 3 53 8
WP 041975004 Pyrinomonas methylaliphatogenes
OJV90051 nitrite reductase Chloroflexi bacterium 54 19
WP 012876459 Thermobaculum terrenum
SRR636581 qc 1 paired CBMW 12 contig 2137 37 Sericytochromatia CBMW 12
cd02754 CAF19042.1
AAV47412.1
cd02754 BAA74791.1
cd02754 CAD71546.1
WP 002646572 Gimesia maris
WP 083732404 Fuerstia marisgermanicae
WP 129580475 Sorangium cellulosum
WP 007277256 Lentisphaera araneosa
WP 007415860 Pedosphaera parvula
S5 GD2017 2 S2 scaffold 122 26
RIFCSPLOWO2 02 FULL Elusimicrobia 39 32 rifcsplowo2 02 scaffold 39 12
CG 4 10 14 0.2 scaffold 266 c 29
cd02754 EAA64369.1
cd02754 NP 733731.1 NarB
cd02754 ZP 00330770.1
cd02754 ZP 00317362.1
cd02754 YP 075885.1
cd02754 pdb 2NAP A
cd02754 ZP 00100034.2
cd02754 YP 074746.1
CG 4 10 14 0.2 scaffold 622 c 26
napA WP 002852404.1 Campylobacter
CAD55547.1
NapA WP 000784576.1 Vibrio cholerae
NapA Aggregatibacter actinomycetemcomitansgi 18027860 gb AAL558911 AF321232 1
NapA WP 000778047.1 Escherichia
cd02754 sp P33937.3 NAPA ECOLI
NapA Pseudomonas stutzeri A15gi 76365559 gb ABA421731
NapA Q56350.1 NAPA PARPN
cd02754 pdb 1OGY A
NapA P39185.2 NAPA CUPNH
cd02754 sp P39185.2 NAPA CUPNH
cd02754 BAC70041.1
cd02754 ZP 00215255.1
cd02754 AAF74559.1
cd02754 NP 213150.1
WP 032520549 1 partial Prochlorococcus marinus
AII48079 nitrate reductase subunit alpha Synechococcus sp KORDI52
cd02754 CAE08979.1
NarB Synechococcus elongatus PCC 6301gi 56685283 dbj BAD785051
cd02754 P39458 NARB SYNP7
WP 017660777 1 Geitlerinema sp PCC 7105
WP 080807034 1 Halomicronema hongdechloris
cd02754 ZP 00309248.1
cd02754 ZP 00242118.1
cd02754 ZP 00265697.1
NarB Pseudomonas stutzeri A1501gi 146282752 ref YP 0011729051
NasA Azotobacter vinelandii AvOPgi 67153430 ref ZP 004151751
cd02754 NP 800575.1
cd02754 ZP 00314901.1
cd02754 ZP 00169754.1
cd02754 AAM73546.1
NasA Klebsiella oxytocagi 4755082 gb AAA251002
cd02754 Q06457.2 NASA KLEOX

Figure S12. Phylogenetic analysis of the dimethyl sulfoxide (DMSO) reductase superfamily (Maximum likelihood tree under a LG+F+G4 model of evolution). *Elusimicrobia* have an alternative complex III, a tetrathionate reductase (TtrA), cytoplasmic and periplasmic nitrite oxidoreductase (NXR), formate dehydrogenase and nitrate reductase (NapA and NasA). *Elusimicrobia* sequences are indicated with colored font. Scale bar indicates substitutions per site. The bootstraps are indicated by red circles when ≥ 85. The tree was made using sequences from (Castelle et al. 2013; Matheus Carnevali et al. 2019). The sequences and tree are available with full bootstrap values in Fasta and Newick format in Supplementary Data.

SUPPLEMENTARY DATASET

Supplementary Dataset 1. List of the 94 genomes used in this study. For each genome (column A), the NCBI genome accession, completeness and the contamination based on single copy genes are displayed in columns B, C and D respectively. Columns from E to J informs about the concatenated ribosomal proteins. Environments are provided in columns K and L, pubmed PMID in column M. The GTDB classification is shown in column N, classification based on 16S rRNA in column O. Final classification is shown in column P.

Supplementary Dataset 2. List of the 17 genomes from Myxococcales and Gracilibacteria genomes with the group VI nifH. Genome names and taxonomy are provided in columns A and C. When available, NCBI assembly accession is provided in column B.

Supplementary Dataset 3. Metabolic capacities across the 94 Elusimicrobia genomes. Genome names and environments are provided in columns A and B. Each metabolic feature is considered either complete (indicated by 1 and a red cell), partial (indicated by P and an orange cell) or absent (indicated by 0 and a white cell). Completeness of the pathways is based on literature and annotations (see the row 2 for partial information and the materials and methods for full details).