Supplementary Information:

Microbial aerotrophy enables continuous primary production in diverse cave ecosystems

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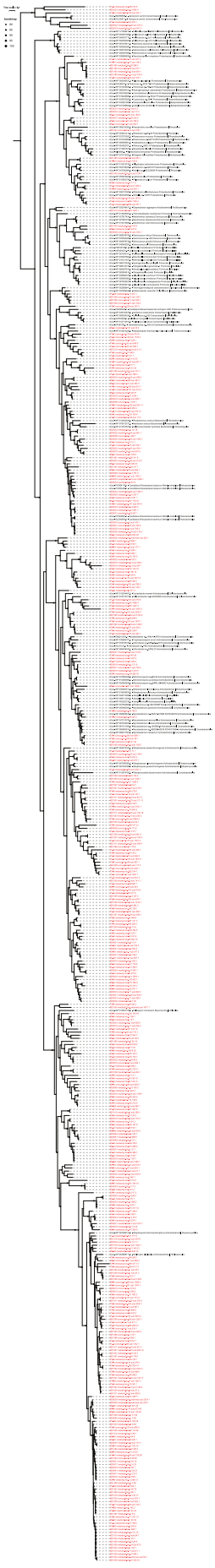
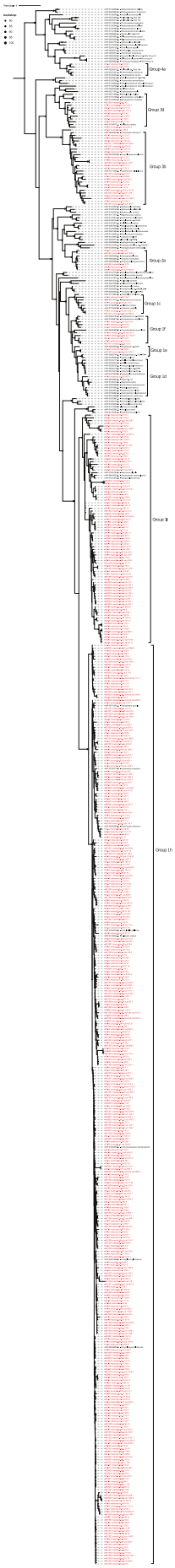
Supplementary Figures

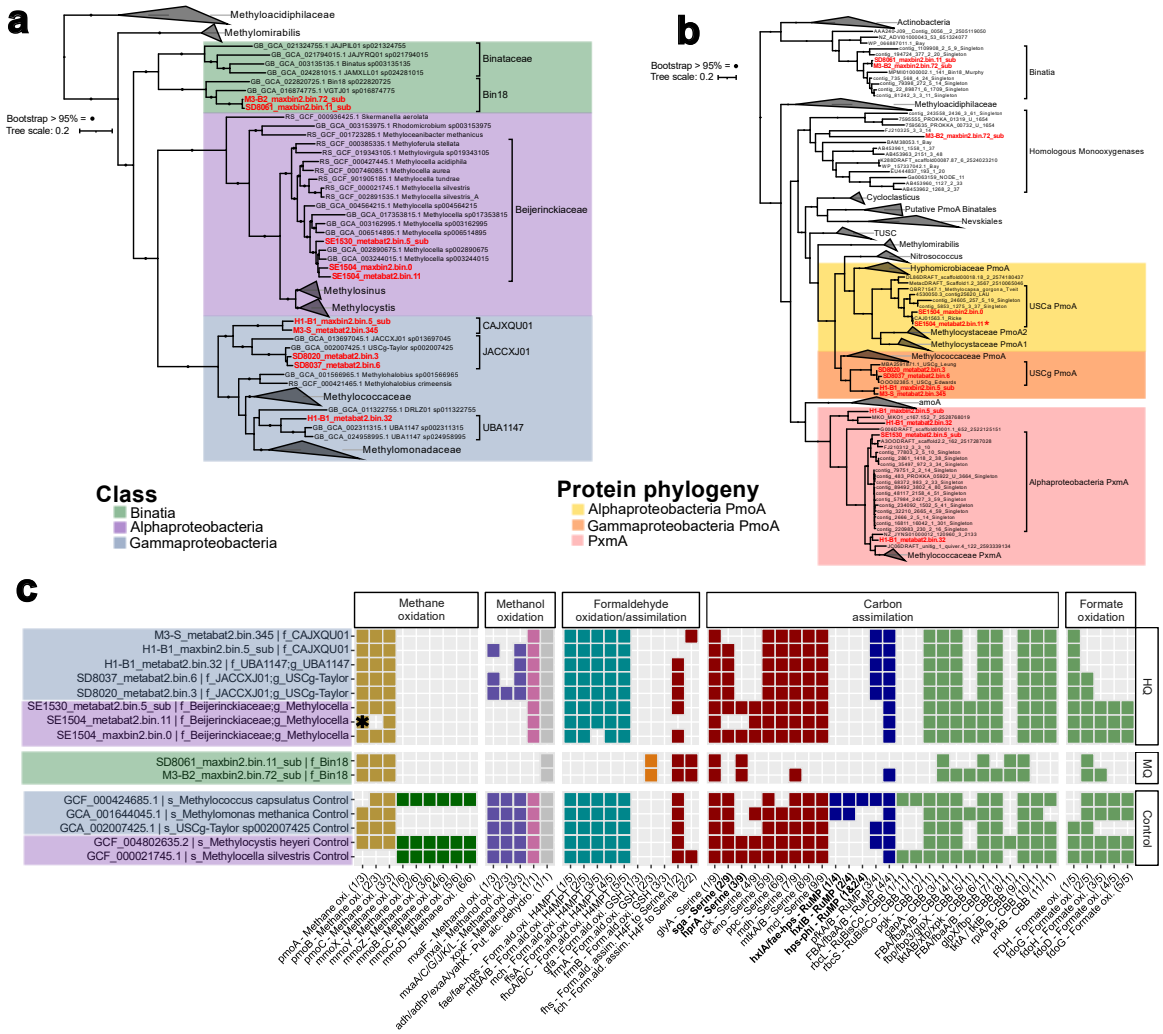
Supplementary Figure 1. Maximum-likelihood phylogenetic tree of carbon monoxide dehydrogenase large subuit (CoxL) amino acid sequences, rooted at midpoint. The tree shows sequences from this study's MAGs alongside (red) representative reference sequences (black). The tree was inferred using LG+F+I model post selection, used all sites, and was bootstrapped with 1000 replicates.



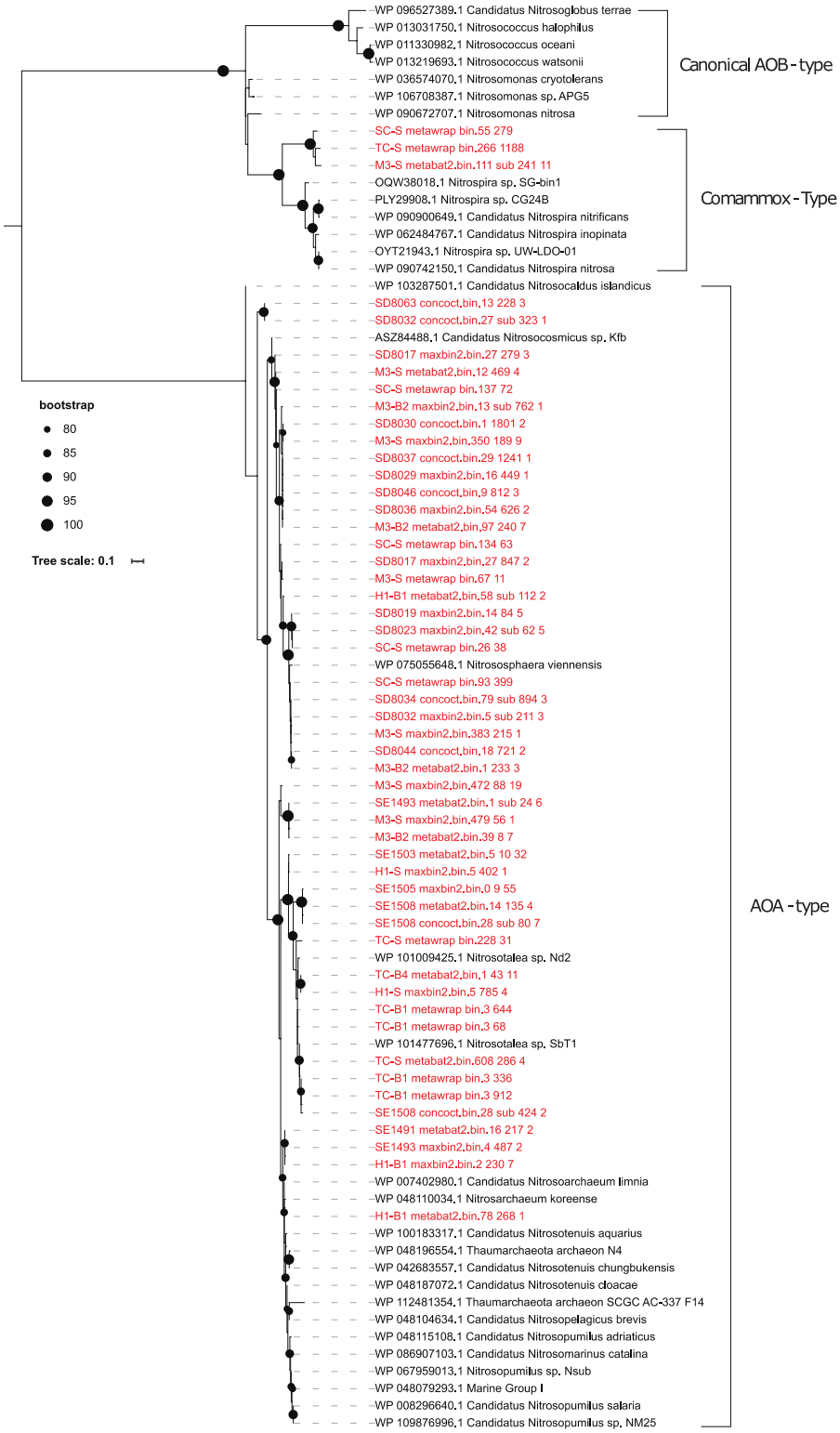
Supplementary Figure 2. Maximum-likelihood phylogenetic tree of [NiFe] hydrogenase amino acid sequences, rooted at midpoint. The tree shows sequences from this study's MAGs alongside (red) representative reference sequences (black). The tree was inferred using Q.pfam+I+ G4 model post selection, used all sites, and was bootstrapped with 1000 replicates.


Tree scale: 1
bootstrap
80
85
90
95
100
Group 4a
Group 3d
Group 3b
Group 2a
Group 1c
Group 1f
Group 1e
Group 1d
Group 3
Group 1h

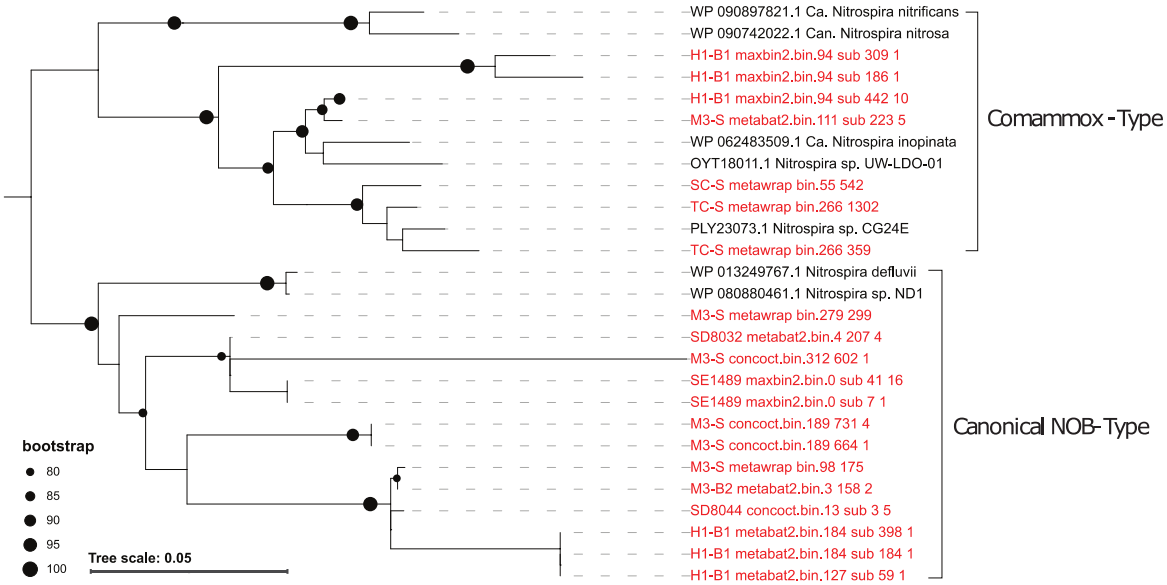
Supplementary Figure 3. **Methanotroph phylogeny and metabolic potential.** **a**, Phylogenetic tree of high-quality MAGs (completion >90% and contamination <5%) encoding metabolic potential for aerobic methane oxidation and known methanotrophs. **b**, protein phylogeny of Proteobacterial PmoA and PxmA. Tree was generated with the ultrafast bootstrap approximation option using 1000 iterations and enabling the ModelFinder option (Best-fit model: LG+F+R6). **c**, Methanotroph MAG annotation to identify metabolic pathways and potential for methane carbon assimilation using DRAM and KEGG database.



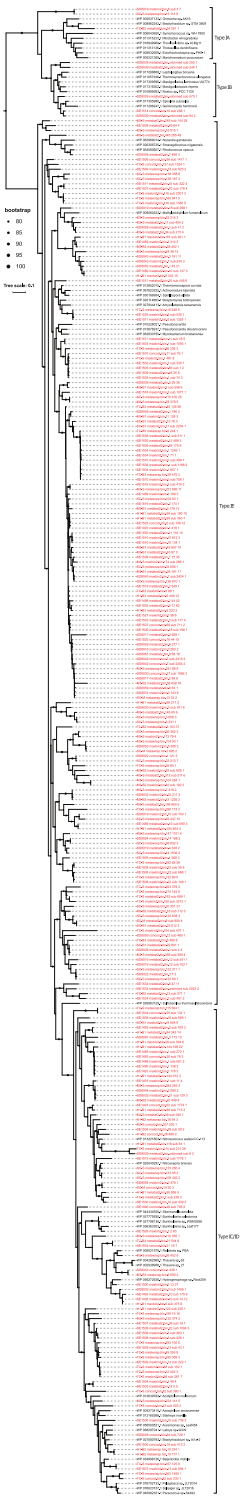
Supplementary Figure 4. Maximum-likelihood phylogenetic tree of ammonia monooxygenase subunit A (AmoA) amino acid sequences, rooted at midpoint. The tree shows sequences from this study's MAGs alongside (red) representative reference sequences (black) from both ammonia oxidising bacteria (AOB) and archaea (AOA). The tree was inferred using Q.yeast+F+G4 model post selection, used all sites, and was bootstrapped with 1000 replicates.


WP 096527389.1 Candidatus Nitrosoglobus terrae
WP 013031750.1 Nitrosococcus halophilus
WP 011330982.1 Nitrosococcus oceani
WP 013219693.1 Nitrosococcus watsonii
WP 036574070.1 Nitrosomonas cryotolerans
WP 106708387.1 Nitrosomonas sp. APG5
WP 090672707.1 Nitrosomonas nitrosa
SC-S metawrap bin.55 279
TC-S metawrap bin.266 1188
M3-S metabat2.bin.111 sub 241 11
OQW38018.1 Nitrospira sp. SG-bin1
PLY29908.1 Nitrospira sp. CG24B
WP 090900649.1 Candidatus Nitrospira nitrificans
WP 062484767.1 Candidatus Nitrospira inopinata
OYT21943.1 Nitrospira sp. UW-LDO-01
WP 090742150.1 Candidatus Nitrospira nitrosa
WP 103287501.1 Candidatus Nitrosocaldus islandicus
SD8063 concoct.bin.13 228 3
SD8032 concoct.bin.27 sub 323 1
ASZ84488.1 Candidatus Nitrosocosmicus sp. Kfb
SD8017 maxbin2.bin.27 279 3
M3-S metabat2.bin.12 469 4
SC-S metawrap bin.137 72
M3-B2 maxbin2.bin.13 sub 762 1
SD8030 concoct.bin.1 1801 2
M3-S maxbin2.bin.350 189 9
SD8037 concoct.bin.29 1241 1
SD8029 maxbin2.bin.16 449 1
SD8046 concoct.bin.9 812 3
SD8036 maxbin2.bin.54 626 2
M3-B2 metabat2.bin.97 240 7
SC-S metawrap bin.134 63
SD8017 maxbin2.bin.27 847 2
M3-S metawrap bin.67 11
H1-B1 metabat2.bin.58 sub 112 2
SD8019 maxbin2.bin.14 84 5
SD8023 maxbin2.bin.42 sub 62 5
SC-S metawrap bin.26 38
WP 075055648.1 Nitrososphaera viennensis
SC-S metawrap bin.93 399
SD8034 concoct.bin.79 sub 894 3
SD8032 maxbin2.bin.5 sub 211 3
M3-S maxbin2.bin.383 215 1
SD8044 concoct.bin.18 721 2
M3-B2 metabat2.bin.1 233 3
M3-S maxbin2.bin.472 88 19
SE1493 metabat2.bin.1 sub 24 6
M3-S maxbin2.bin.479 56 1
M3-B2 metabat2.bin.39 8 7
SE1503 metabat2.bin.5 10 32
H1-S maxbin2.bin.5 402 1
SE1505 maxbin2.bin.0 9 55
SE1508 metabat2.bin.14 135 4
SE1508 concoct.bin.28 sub 80 7
TC-S metawrap bin.228 31
WP 101009425.1 Nitrosotalea sp. Nd2
TC-B4 metabat2.bin.1 43 11
H1-S maxbin2.bin.5 785 4
TC-B1 metawrap bin.3 644
TC-B1 metawrap bin.3 68
WP 101477696.1 Nitrosotalea sp. SbT1
TC-S metabat2.bin.608 286 4
TC-B1 metawrap bin.3 336
TC-B1 metawrap bin.3 912
SE1508 concoct.bin.28 sub 424 2
SE1491 metabat2.bin.16 217 2
SE1493 maxbin2.bin.4 487 2
H1-B1 maxbin2.bin.2 230 7
WP 007402980.1 Candidatus Nitrosoarchaeum limnia
WP 048110034.1 Nitrosarchaeum koreense
H1-B1 metabat2.bin.78 268 1
WP 100183317.1 Candidatus Nitrosotenuis aquarius
WP 048196554.1 Thaumarchaeota archaeon N4
WP 042683557.1 Candidatus Nitrosotenuis chungbukensis
WP 048187072.1 Candidatus Nitrosotenuis cloacae
WP 112481354.1 Thaumarchaeota archaeon SCGC AC-337 F14
WP 048104634.1 Candidatus Nitrosopelagicus brevis
WP 048115108.1 Candidatus Nitrosopumilus adriaticus
WP 086907103.1 Candidatus Nitrosomarinus catalina
WP 067959013.1 Nitrosopumilus sp. Nsub
WP 048079293.1 Marine Group I
WP 008296640.1 Candidatus Nitrosopumilus salaria
WP 109876996.1 Candidatus Nitrosopumilus sp. NM25
Canonical AOB-type
Comammox-Type
AOA-type
bootstrap
80
85
90
95
100
Tree scale: 0.1

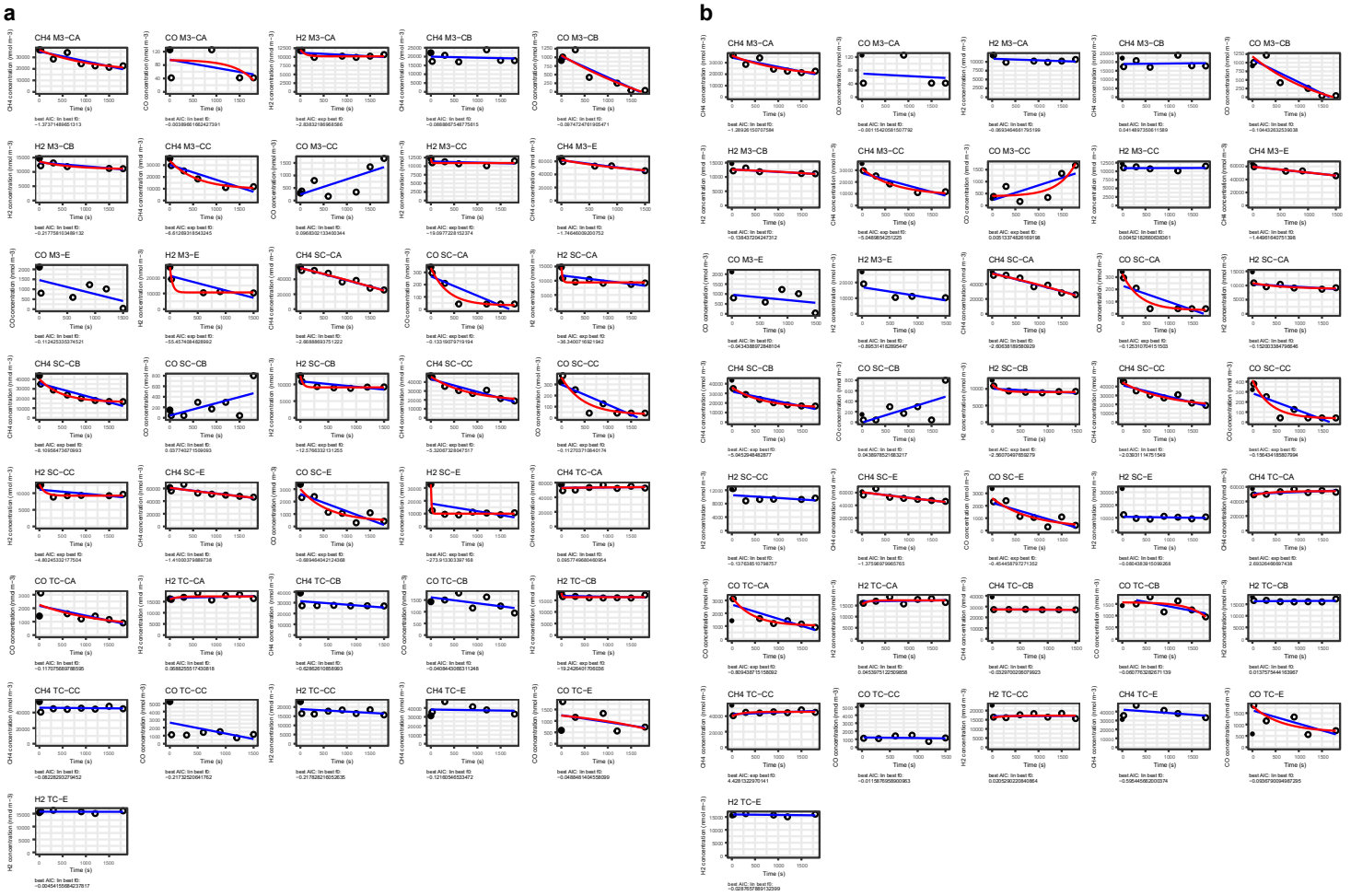
Supplementary Figure 5. Maximum-likelihood phylogenetic tree of nitrite oxidoreductase subunit A (NxrA) amino acid sequences, rooted at midpoint. The tree shows sequences from this study's MAGs alongside (red) representative reference sequences (black). The tree was inferred using the LG+I+G4 model post selection, used all sites, and was bootstrapped with 1000 replicates.



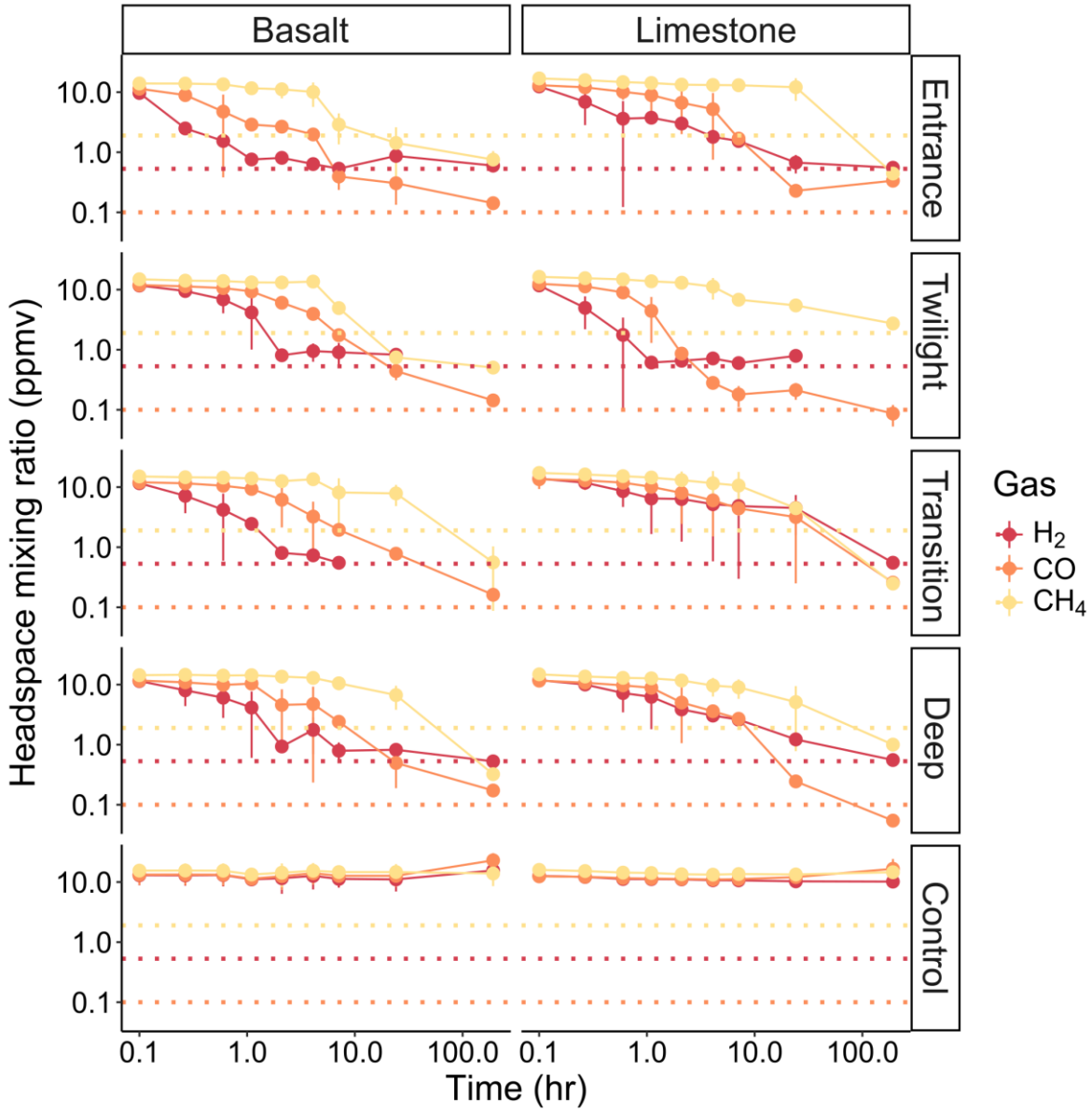
Supplementary Figure 6. Maximum-likelihood phylogenetic tree of Ribulose-1,5-bisphosphate carboxylase/oxygenase (RubisCo) large subunit (RbcL) amino acid sequences, rooted using type II RubisCO sequences (not shown). The tree shows sequences from this study's MAGs alongside (red) representative reference sequences (black). The tree was inferred using the LG+I+G4 model post selection, used all sites, and was bootstrapped with 1000 replicates.



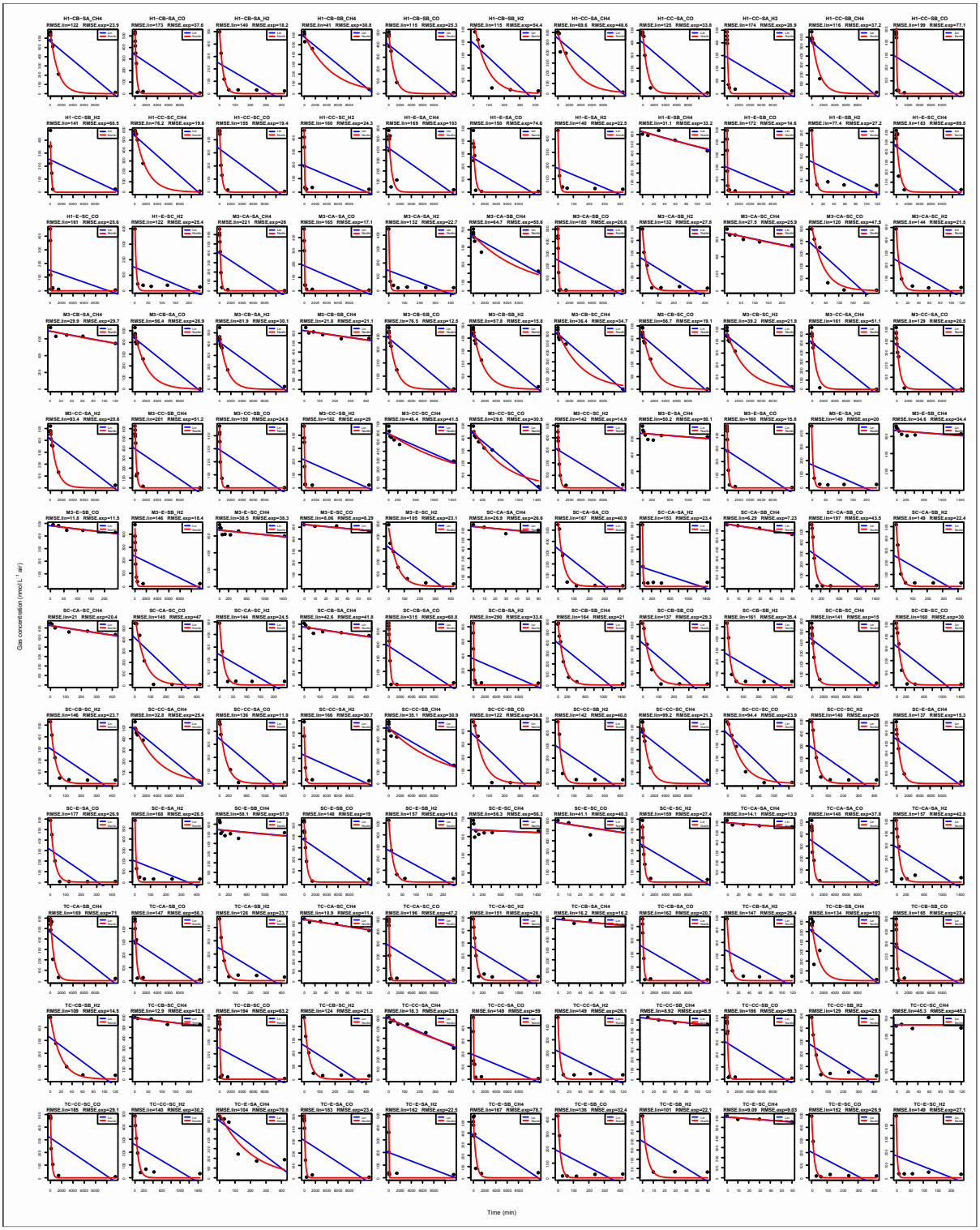
Supplementary Figure 7. Plots showing linear and non linear models of in situ flux measurements for H_2, CO and CH_4 across transient and equilibrium flux phases shown in panel **a** and **b** respectively. Best model fits, according to AIC for linear (lin) and non liner (exp) are given along with the flux value (nmol m^2 sec^{-1}).



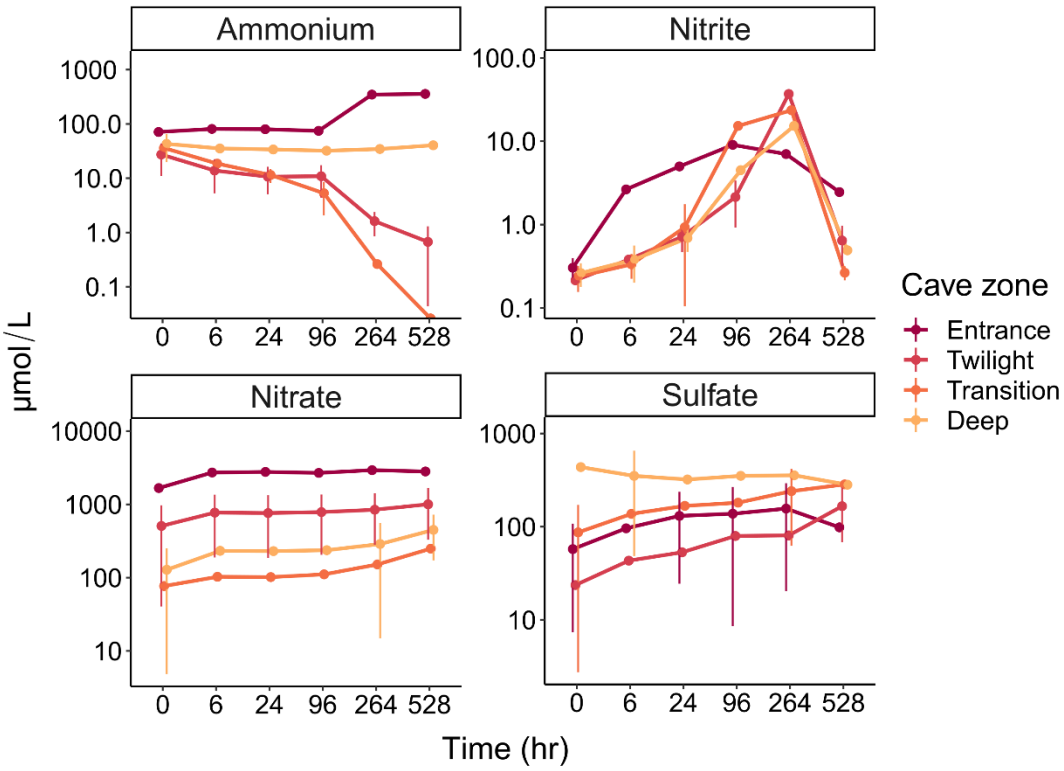
Supplementary Figure 8. The average measurements and standard deviation (n=44) of gas chromatography traces for bulk soil incubations and controls are shown, indicating uptake from ~10 ppmv to below average atmospheric levels for each gas (dashed line).



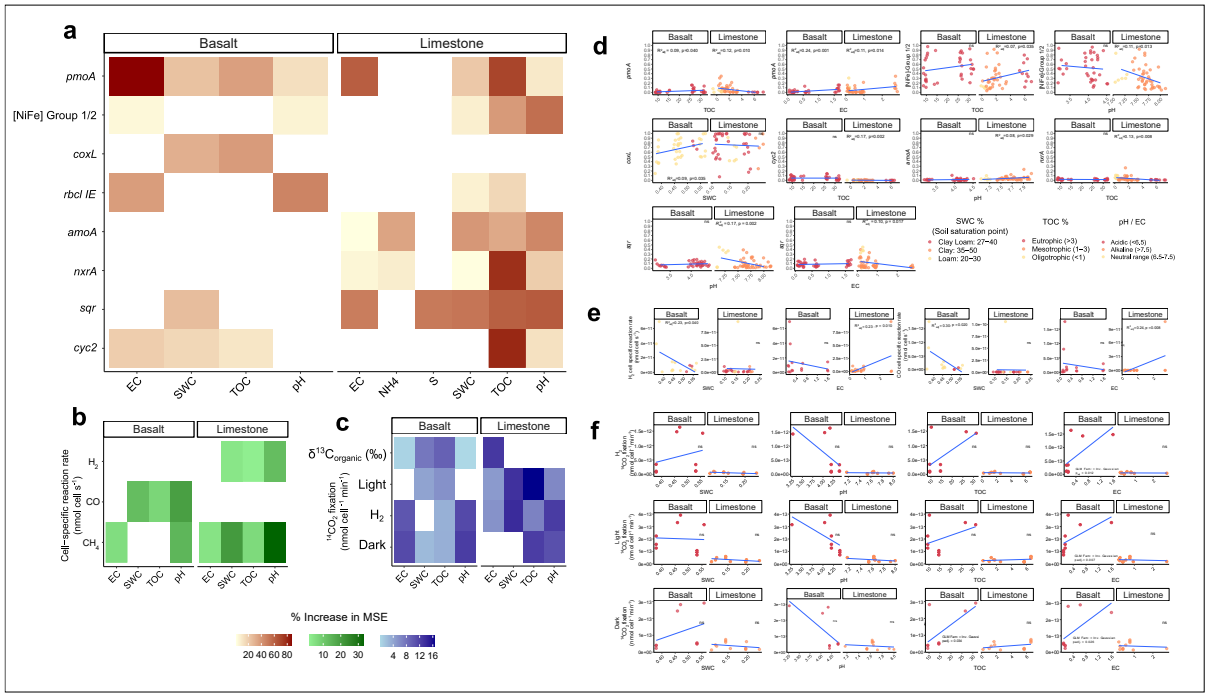
Supplementary Figure 9. Plots showing linear and nonlinear models fitted to trace gas oxidation for each sample. Root Mean Squared Error (RMSE) values are used to assess predictive accuracy. RMSE measures the average magnitude of prediction errors, with lower values indicating better fit.



Supplementary Figure 10. The average measurements and standard deviation (n=17) of oxic slurry incubations are shown for four nitrogen species and sulfur, representing biological replicates from all caves except biofilm in Harman 1.



Supplementary Figure 11. Lithology level driver analysis combining Random Forest and linear models. Random forest % increase in Mean Squared Error (MSE) provides a measure of the importance of predictor variables. Blank tiles in the heatmaps indicate that no stable model could be established. **a**, Random Forest analysis of soil physicochemical drivers influencing the average gene copies per organism involved in trace gas metabolism (*pmoA*, [NiFe] group 1 / 2, *coxL*), ammonium and nitrite oxidation (*amoA*, *nxrA*), sulfide oxidation (*sqr*) and iron oxidation (*cyc2*) and soil physicochemical drivers. **b**, Random Forest analysis of soil physicochemical drivers influencing the cell specific reaction rates of H_2, CO and CH_4. **c**, Random Forest analysis of soil physicochemical drivers influencing the ^{13}C signatures and ^{14}C carbon fixation. **d**, Linear relationship between the average gene copies per organism (n=85) involved in trace gas metabolism (*pmoA*, [NiFe] group 1 / 2, *coxL*), ammonium and nitrite oxidation (*amoA*, *nxrA*), sulfide oxidation (*sqr*) and iron oxidation (*cyc2*) and soil physicochemical drivers with p values derived from two-sided tests in linear models. **e**, linear relationship between the cell specific reaction rates of H_2, CO and CH_4 (n=39) and soil physicochemical drivers with p values derived from two-sided tests in linear models. **f**, Linear relationships between ^{14}C carbon fixation (n=21) and soil physicochemical drivers, with p values derived from two-sided tests in generalized linear models.



Supplementary notes

Supplementary Note 1. Phylogeny and physiology of cave methanotrophs.

Phylogeny of the PmoA sequences, encoded by the commonly used *pmoA* marker gene, indicated that several of the MAGs belong to the atmospheric methane oxidising groups USCα (Supplementary Figure 3b) and USCγ (Supplementary Figure 3). For the gammaproteobacterial MAGs, two MAGs, M3-S_metabat2.bin.345 and H1-B1_maxbin2.bin.5_sub, were classified as novel genera within the order CAJXQU01 (Figure S7a). Only one other genome within this order is in GTDB r214 (GCA_913058255.1, *CAJXQU01 sp913058255,* recovered from a marine metagenome), and does not encode *pmoCAB*. Potentially these genomes are the first representatives of a new methanotrophic order in the Gammaproteobacteria. In both MAGs, PmoA sequences grouped with other gammaproteobacterial PmoA sequences (Supplementary Figure 3b), however not within the well-defined isolate methanotrophs of the Methylococcaceae and Methylomonadaceae families. H1-B1_maxbin2.bin.5_sub also encoded PxmAB of the *pxmABC* operon, a homologue of the *pmoCAB.* While *pxmABC* is found in many methanotrophs, the function is currently unknown[1,2]. Both MAGs encode *pmoCAB* operon, *xoxF*-type methanol oxidation, and formaldehyde oxidation through the tetrahydromethanopterin (H_4MPT)-pathway (Supplementary Figure 3c).

MAG H1-B1_metabat2.bin.32 was classified as a novel species within the gammaproteobacterial family and genus UBA1147 (Supplementary Figure 3b). Three genomes, of which two encode *pmoCAB*, are present within this family in GTDB r214, (*UBA1147 sp002311315* recovered from a hydrothermal vent metagenome, and *UBA1147 sp024958995,* recovered from a marine metagenome). H1-B1_metabat2.bin.32 encoded a PmoA sequence clustering with Methylococcaceae PmoA sequences, along with two copies of PxmA sequences (Supplementary Figure 3b). A complete *pmoCAB* operon, along with *xoxF*-type methanol oxidation, and formaldehyde oxidation through the H_4MPT-pathway was encoded (Supplementary Figure 3c). SD8037_metabat2.bin.6 and SD8020_metabat2.bin.3 were classified as novel species within the gammaproteobacterial genus USCγ-Taylor (Figure S7b), both encoding PmoA sequences clustering with other USCγ sequences (Supplementary Figure 3b). Both encode full *pmoCAB* operons along with *xoxF*-type methanol oxidation and formaldehyde oxidation through the H_4MPT-pathway (Supplementary Figure 3c). Calcium-dependent methanol oxidation was encoded by *mxaFI* in SD8020_metabat2.bin.3, and partially in SD8037_metabat2.bin.6 (*mxaF*). All gammaproteobacterial MAGs lacked complete

metabolic potential to assimilate carbon. Canonical gammaproteobacterial methanotrophs usually utilise the RuMP cycle. While all MAGs encoded *pfkA/B* and *FBA*, the key genes hexulosephosphate synthase (*hxlA/fae-hps*) and hexulosephosphate isomerase (*hxlB*) were not encoded. Reasons for absence of detection could be genome incompleteness, or the gene is divergent enough from the KO database representatives to not be correctly assigned. An incomplete serine cycle is present, missing the key gene HPR[3].

Cytochrome *c* oxidase was encoded in all gammaproteobacterial MAGs, and the cytochrome *bd* oxidase was also encoded in USCγ-Taylor and CAJXQU01 MAGs, both cytochromes are characterised by high oxygen affinity[4]. Dissimilatory nitrate reduction (*narGHJI*) was fully encoded in *USCγ-Taylor* and *UBA1147* MAGs, while partially encoded in *CAJXQU01* (*narGH* and *narGHJ*). Assimilatory sulphate reduction (*cysDCHJI*, lacking *cysN*) and partial dissimilatory sulphate reduction (*dsrCEF)*, though lacking the key genes *dsrAB*, was encoded in UBA1147. Three MAGs, SE1530_metabat2.bin.5_sub, SE1504_maxbin2.bin.0, and SE1504_metabat2.bin.11 were classified into three different species (<95% ANI) within the alphaproteobacterial *Methylocella* genus (Supplementary Figure 3b). This genus contains the well-studied isolate *Methylocella silvestris* and the recent upland soil cluster alpha atmospheric methane oxidising isolate *M. gorgona*. SE1504_maxbin2.bin.0 encoded a PmoA sequence clustering with USCα PmoA, while SE1504_metabat2.bin.11 encoded a partial USCα-clustering sequence (67 aa, denoted by * in Supplementary Figure 3b & c) located at the edge of a short contig (2890 bp). SE1530_metabat2.bin.5_sub encoded no USCα-PmoA sequence but contained a sequence clustering with alphaproteobacterial PxmA sequences (Supplementary Figure 3b). All MAGs encoded XoxF-type methanol oxidation, and formaldehyde oxidation through the H_4MPT-pathway. While SE1530_metabat2.bin.5_sub, SE1504_maxbin2.bin.0 had the genomic potential to assimilate formaldehyde through H_4F and serine cycle, bin.11 is missing two key serine cycle genes, *sga* and *hprA* (Supplementary Figure 3), and does not encode the H_4F pathway, perhaps due to genome incompleteness. Oxidation of formate to carbon dioxide was also encoded in all MAGs. Similar to the USCα isolate *M. gorgona* the CBB cycle was incomplete and missing the RuBisCo genes in all three MAGs in contrast to the USCα-encoding MAGs of [5] and other members of the *Methylocella* genus[6]. Control genome *M. silvestris* encodes the high oxygen affinity *cbb*$_3$-type and *bd*-type cytochromes, while the *Methylocella* MAGs obtained here encode low oxygen affinity type-*o* cytochromes [4].

CAJXQU01 MAGs were amongst the three most dominant predicted methanotrophic taxa in the cave system, along with JACCXJ01 and *Methylocella* (Supplementary Figure 3a). Carbon and energy acquisition pathways from each MAG in these taxonomic groups were

compiled, revealing broadly similar methylotrophic lifestyles (Supplementary Figure 3c). However, in contrast to CAJXQU01 and JACCXJ01, *Methylocella* MAGs from the caves encoded the complete tetrahydrofolate pathway and serine cycle to assimilate carbon from formate (Supplementary Figure 3c). Additionally, all three taxonomic groups encoded a complete TCA cycle and glyoxylate shunt, the core 3C glycolysis steps of the Embden-Meyerhof-Parnas pathway, and the pentose phosphate pathway, whilst only *Methylocella* MAGs additionally encoded the Entner-Doudoroff pathway.

In addition to the alpha and gammaproteobacterial likely new methanotrophs, copper membrane bound monooxygenases (CuMMOs), representing methane monooxygenase homologs, were identified in the MAGs SD8061_maxbin2.bin.11_sub and M3-B2_maxbin2.bin.72_sub and were classified as novel genera within the Bin18 family (Supplementary Figure 3c). Both MAGs contained PmoA-like sequences grouping with other PmoA-like sequences from the Binatia class (Figure S7b). M3-B2_maxbin2.bin.72_sub also contained an additional MMO-like sequence that grouped with other hydrocarbon monooxygenases. None of the members within Binatia have been experimentally confirmed to be able to carry out methanotrophy. Furthermore, genes for methanol and formaldehyde oxidation could not be identified, indicating that the Bin18 MAGs are most likely not capable of methanotrophy and may be oxidising other hydrocarbons.

Supplementary Note 2

Etymological Information

We propose renaming the Pseudonocardiaceae genus GCA-003244245 as '*Candidatus* Hydrogenomurus', based on the high-quality annotated genome SE1519_metabat2.bin.2 (completeness/contamination: 100%/2.79%) from Tunnel basalt caves (herein '*Candidatus* Hydrogenomurus basanatii')

Species: '*Candidatus* Hydrogenomurus basanatii' (ba.sa.na'tii. N.L. gen. n. *basanatii*, of the basalt cave (Tunnel Cave), where the bacterium was identified)

Genus: '*Candidatus* Hydrogenomurus' (Hy.dro.ge.no.mu.rus. N.L. neut. n. *hydrogenum*, hydrogen (that which produces water, so called because it forms water when exposed to oxygen); from Gr. neut. n. *hydôr*, water; from Gr. ind. v. *gennaô*, to produce; L. masc. n. *murus*, wall; N.L. masc. n. *Hydrogenomurus*, a hydrogen-using bacterium from cave wall)

Full Classification:

- Domain: Bacteria
- Phylum: Actinomycetota

- Class: Actinomycetia
- Order: Mycobacteriales
- Family: Pseudonocardiaceae
- Genus: GCA-003244245 (proposed as '*Candidatus* Hydrogenomurus')
- Species: '*Candidatus* Hydrogenomurus basanatii'

We propose renaming the Egibacteraceae genus JACCXR01 as '*Candidatus* Hydrogenocavus', based on the high-quality annotated genome M3-B2_metabat2.bin.58 (completeness/contamination: 96.56%/3.3%) from Shades of death limestone caves (herein '*Candidatus* Hydrogenocavus calcicola')

Species: '*Candidatus* Hydrogenocavus calcicola' (cal.ci'co.la. L. masc./fem. n. *calx* (gen. calcis), chalk; L. masc./fem. n. suff. -*cola*, an inhabitant; from L. masc./fem. n. *incola*, dweller; N.L. masc./fem. n. *calcicola*, of the limestone cave (Shades of death), where the bacterium was identified)

Genus: '*Candidatus* Hydrogenocavus' (Hy.dro.ge.no.ca.vus. N.L. neut. n. *hydrogenum*, hydrogen (that which produces water, so called because it forms water when exposed to oxygen); from Gr. neut. n. *hydôr*, water; from Gr. ind. v. *gennaô*, to produce; L. n. cava, cave; N.L. masc. n. *Hydrogenocavus*, a hydrogen-using bacterium from caves)

Full Classification:

- Domain: Bacteria
- Phylum: Actinomycetota
- Class: Actinomycetia
- Order: Euzebyales
- Family: Egibacteraceae
- Genus: JACCXR01 (proposed as '*Candidatus* Hydrogenocavus')
- Species: '*Candidatus* Hydrogenocavus calcicola'

We propose renaming the Actinomycetota order JACCUZ01 as '*Candidatus* Hydrogenolapis', based on the high-quality annotated genome SD8021_metabat2.bin.4

(completeness/contamination: 84.11%/1.1%) from the limestone cave Scrubby Creek (herein '*Candidatus* Hydrogenolapis speleophilus').

Species: '*Candidatus* Hydrogenolapis speleophilus' (spe.le.o'phi.lus. N.L. masc. adj. speleophilus, cave-loving, referring to the cave environment where the MAG was identified)

Genus: '*Candidatus* Hydrogenolapis' (Hy.dro.ge.no.la'pis. N.L. neut. n. hydrogenum, hydrogen; L. n. lapis, stone; N.L. neut. n. Hydrogenolapis, a hydrogen-oxidizing bacterium)

Family: '*Candidatus* Hydrogenolapaceae' (Hy.dro.ge.no.la.pa'ce'ae. N.L. neut. n. Hydrogenolapis, a (Candidatus) bacterial genus; suff. -aceae ending to denote a family; N.L. fem. pl. n. Hydrogenolapaceae, family of the genus Hydrogenolapis)

Order: '*Candidatus* Hydrogenolapales' (Hy.dro.ge.no.la'pa.les. N.L. neut. n. Hydrogenolapis, a (Candidatus) bacterial genus; suff. -ales ending to denote an order; N.L. fem. pl. n. Hydrogenolapales, order of the family Hydrogenolapaceae)

Full Classification:

Domain: Bacteria

Phylum: Actinomycetota

Class: Actinomycetia

Order: JACCUZ01 (proposed as '*Candidatus* Hydrogenolapales')

Family: JACCUZ01 (proposed as '*Candidatus* Hydrogenolapaceae')

Genus: JACCUZ01 (proposed as '*Candidatus* Hydrogenolapis')

Species: '*Candidatus* Hydrogenolapis speleophilus

We propose renaming the Gammaproteobacterial order JACCXJ01 as '*Candidatus* Methyloligotrophales', based on the high-quality annotated genome SD8037_metabat2.bin.6 (completeness/contamination: 96.44%/0.56%) from Shades of death limestone caves (herein '*Candidatus* Methyloligotropha calcicola')

Species: '*Candidatus* Methyloligotropha calcicola' (cal.ci'co.la. L. masc./fem. n. *calx* (gen. calcis), chalk; L. masc./fem. n. suff. -*cola*, an inhabitant; from L. masc./fem. n. *incola*, dweller; N.L. masc./fem. n. *calcicola*, of the limestone cave (Shades of death), where the bacterium was identified)

Genus: '*Candidatus* Methyloligotropha' (Me.thy.lo.li.go.tro'pha. N.L. neut. n. *methylum*, from French *méthyle*, back-formation from *méthylène*, coined from Gr. n. *methu*, wine, and Gr. n. *hulê*, wood, referring to the methyl group; N.L. pref. methylo-, pertaining to the methyl radical; Gr. masc. adj. *oligos*, little, few; Gr. masc./fem. adj. *trophos*, feeder, rearer, that which nourishes; N.L. fem. n. *Methyloligotropha*, an oligotrophic methyl-using bacterium)

Family: '*Candidatus* Methyloligotrophaceae' (Me.thy.lo.li.go.tro'pha.ce'ae. N.L. neut. n. *Methyloligotropha* a (Candidatus) bacterial genus; suff. -aceae ending to denote a family; N.L. fem. pl. n. *Methyloligotrophaceae*, family of the genus *Methyloligotropha*)

Order: '*Candidatus* Methyloligotrophales' (Me.thy.lo.li.go.tro'pha'les. N.L. neut. n. *Methyloligotropha* a (Candidatus) bacterial genus; suff. -ales ending to denote an order; N.L. fem. pl. n. *Methyloligotrophales*, order of the family *Methyloligotrophaceae*)

Full Classification:

- Domain: Bacteria
- Phylum: Proteobacteria
- Class: Gammaproteobacteria
- Order: JACCXJ01 (proposed as '*Candidatus* Methyloligotrophales')
- Family: JACCXJ01 (proposed as '*Candidatus* Methyloligotrophaceae')
- Genus: USCg-Taylor (proposed as '*Candidatus* Methyloligotropha')
- Species: '*Candidatus* Methyloligotropha calcicola'

We propose renaming the Gammaproteobacterial order CAJXQU01 as '*Candidatus* Methylocavales', based on the high-quality annotated genome H1-B1_maxbin2.bin.5_sub

(completeness/contamination: 97.84%/2.43%) from Harman basalt caves (herein '*Candidatus* Methylocavus basanatii')

Species: '*Candidatus* Methylocavus basanatii' (ba.sa.na'tii. N.L. gen. n. *basanatii*, of the basalt cave (Harman 1), where the bacterium was identified)

Genus: '*Candidatus* Methylocavus' (Me.thy.lo.ca.vus. N.L. neut. n. *methylum*, from French *méthyle*, back-formation from *méthylène*, coined from Gr. n. *methu*, wine, and Gr. n. *hulê*, wood, referring to the methyl group; N.L. pref. methylo-, pertaining to the methyl radical; L. n. cava, cave; N.L. neut. n. *Methylocavus*, a methyl-using bacterium from caves)

Family: '*Candidatus* Methylocavaceae' (Me.thy.lo.ca.va.ce'ae. N.L. neut. n. *Methylocavus* a (Candidatus) bacterial genus; suff. -aceae ending to denote a family; N.L. fem. pl. n. *Methylocavaceae*, family of the genus *Methylocavus*)

Order: '*Candidatus* Methylocavales' (Me.thy.lo.ca.va'les. N.L. neut. n. *Methylocavus* a (Candidatus) bacterial genus; suff. -ales ending to denote an order; N.L. fem. pl. n. *Methylocavales*, order of the family Methylocavaceae)

Full Classification:

- Domain: Bacteria
- Phylum: Proteobacteria
- Class: Gammaproteobacteria
- Order: CAJXQU01 (proposed as '*Candidatus* Methylocavales')
- Family: CAJXQU01 (proposed as '*Candidatus* Methylocavaceae')
- Genus: CAJXQU01 (proposed as '*Candidatus* Methylocavus')
- Species: '*Candidatus* Methylocavus basanatii'

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