

## SUPPLEMENTARY INFORMATION

**Supplementary Table 1** | General genome properties.

Characteristic	Value
Size (bp)	2,752,854
GC content (%)	58.58
Coding density (%)	89.24
rRNAs	3
tRNAs	47
miscRNAs	4
Repeat content (%)	2.97

**Supplementary Table 2** | 16S and 23S rDNA-containing contigs from 454 pyrosequencing demonstrating the diverse bacterial side community in enrichment culture “Twente”.

Contig no.	Length (nt)	no. reads	Best BLAST hit (accession no.) <sup>*</sup>	E-value	% id	Phylum affiliation
00002	153	5	Uncultured <i>Acidobacterium</i> clone 16S rDNA (AM936563.1)	$1 \times 10^{-64}$	96	<i>Acidobacteria</i>
			<i>Lewinella lutea</i> FYK2402M69 16S rDNA (AB301494.1)	$5 \times 10^{-38}$	85	<i>Bacteroidetes</i>
00158	151	3	Uncultured <i>Hyphomicrobium</i> clone 16S rDNA (EU634808.1)	$1 \times 10^{-64}$	97	<i>Proteobacteria</i>
			<i>Hyphomicrobium sulfonivorans</i> 25S 16S rDNA (AY305006.1)	$7 \times 10^{-62}$	96	<i>Proteobacteria</i>
05954	127 (293) <sup>†</sup>	4	Uncultured bacterium clone 23S rDNA (EU686587.1)	$1 \times 10^{-39}$	90	Unclassified

			<i>Gemmata obscuriglobus</i> DSM 5831T 23S rDNA (AF245369.1)	$1 \times 10^{-39}$	88	<i>Planctomycetes</i>
08725	156	3	Uncultured bacterium clone 23S rDNA (EU917532.1)	$1 \times 10^{-24}$	90	Unclassified
			<i>Geobacter uraniireducens</i> Rf4 23S rDNA (CP000698.1)	$2 \times 10^{-22}$	84	<i>Proteobacteria</i>
11380	282	2	Uncultured <i>Myxococcales</i> clone 16S rDNA (EU193072.1)	$3 \times 10^{-134}$	98	<i>Proteobacteria</i>
			<i>Desulfuromonas svalbardensis</i> 103 16S rDNA (AY835391.1)	$8 \times 10^{-103}$	92	<i>Proteobacteria</i>
12461	281	3	Uncultured bacterium clone 16S rDNA (EU703011.1)	$3 \times 10^{-127}$	96	Unclassified
			<i>Dehalococcoides</i> sp. BHI80-52 16S rDNA (AJ431247.1)	$3 \times 10^{-114}$	93	<i>Chloroflexi</i>
12631	498	9	Uncultured bacterium clone 16S rDNA (EF522841.1)	0.0	99	Unclassified
			<i>Planctomycete</i> str. GMD14H10 16S rDNA (AY162122.1)	$4 \times 10^{-116}$	80	<i>Planctomycetes</i>
13213	158	2	<i>Acidithiobacillus thiooxidans</i> 8930P 23S rDNA (AF362021.1)	$2 \times 10^{-36}$	83	<i>Proteobacteria</i>
			<i>Acidithiobacillus thiooxidans</i> 8930P 23S rDNA (AF362021.1)	$2 \times 10^{-36}$	83	<i>Proteobacteria</i>
14774	305	3	Uncultured bacterium clone 16S rDNA (FJ478657.1)	$5 \times 10^{-137}$	97	Unclassified
			<i>Desulfonatronum</i> sp. ASO4-2 16S rDNA (FJ469578.1)	$8 \times 10^{-84}$	87	<i>Proteobacteria</i>
18707	244	3	Uncultured bacterium clone 16S rDNA (AY741700.1)	$2 \times 10^{-104}$	95	Unclassified
			<i>Chlorobi</i> bacterium str. Mat9-16 16S rDNA (AB478415.1)	$3 \times 10^{-88}$	90	<i>Chlorobi</i>
18822	288	7	Uncultured <i>Acidobacteria</i> clone 23S rDNA (DQ139446.1)	$3 \times 10^{-45}$	78	<i>Acidobacteria</i>
			<i>Symbiobacterium thermophilum</i> IAM 14836 23S rDNA (AP006840.1)	$1 \times 10^{-42}$	77	<i>Firmicutes</i>
20833	249	2	Uncultured bacterium clone 16S rDNA (AY741703.1)	$3 \times 10^{-119}$	98	Unclassified
			<i>Chlorobi</i> bacterium str. Mat9-16 16S rDNA (AB478415.1)	$4 \times 10^{-99}$	92	<i>Chlorobi</i>
20858	102 (283) <sup>†</sup>	2	Uncultured bacterium clone 16S rDNA (FM206266.1)	$4 \times 10^{-37}$	96	Unclassified
			<i>Anaeromyxobacter dehalogenans</i> 2CP-1 16S rDNA (CP001359.1)	$7 \times 10^{-34}$	94	<i>Proteobacteria</i>

20939	297	3	Uncultured bacterium clone 23S rDNA (AY705482.1)	$2 \times 10^{-103}$	89	Unclassified
			<i>Solibacter usitatus</i> Ellin6067 23S rDNA (CP000473.1)	$3 \times 10^{-76}$	82	<i>Acidobacteria</i>
26016	180	7	Uncultured bacterium clone 16S rDNA (EF522841.1)	$7 \times 10^{-82}$	98	Unclassified
			<i>Chrysiogenes arsenatis</i> BAL-1 16S rDNA (X81319.1)	$7 \times 10^{-63}$	90	<i>Chrysiogenetes</i>
26218	341	4	Uncultured <i>Acidobacteria</i> clone 16S rDNA (AM936563.1)	$4 \times 10^{-146}$	94	<i>Acidobacteria</i>
			<i>Holophaga foetida</i> 16S rDNA (X77215.1)	$2 \times 10^{-91}$	88	<i>Acidobacteria</i>
26241	112	7	Uncultured <i>Acidobacteria</i> clone 16S rDNA (AM935977.1)	$3 \times 10^{-38}$	93	<i>Acidobacteria</i>
			Gamma proteobacterium MH179 16S rDNA (EU052733.1)	$1 \times 10^{-36}$	92	<i>Proteobacteria</i>
26319	62/145 (548) <sup>†</sup>	7	Uncultured bacterium clone 16S rDNA (EU795193.1)/ <i>Mycoplasma genitalium</i> ATCC 33530 23S rDNA (AY816341.1)	$2 \times 10^{-18}/ 1 \times 10^{-27}$	96/85	Unclassified/ <i>Tenericutes</i>
			<i>Methylobacterium radiotolerans</i> JCM 2831 16S rDNA (CP001001.1)/ <i>Mycoplasma genitalium</i> ATCC 33530 23S rDNA (AY816341.1)	$2 \times 10^{-18}/ 1 \times 10^{-27}$	96/85	<i>Proteobacterial</i> / <i>Tenericutes</i>
26321	131	2	Uncultured bacterium clone 16S rDNA (AJ296615.1)	$7 \times 10^{-48}$	94	Unclassified
			<i>Rhizobium</i> sp. 29953 16S rDNA (AB456645)	$3 \times 10^{-33}$	87	<i>Proteobacteria</i>
00003	24667	1949				
00151	32435	2412				
26131	1841	164				
26320	175	30				
<i>M. oxyfera</i> 16S and 23S rRNA gene-containing contigs						

\*For each sequence the best overall BLASTn match and the best cultured organism BLASTn match are listed. †Contig only partially consists of rDNA sequence. ‡Contig contains both 16S rDNA and 23S rDNA sequence.

**Supplementary Table 3** | Number of metaproteomic peptides obtained from culture "Ooij" that could be mapped to potential consensus genomes of *M. oxyfera* "Ooij" assembled with different algorithms for short read mapping. The optimum assembly was achieved with 7 or more iterations of Blast with word length 8, as this assembly led to the highest number of peptides identified.

Iteration	Reference "Twente"	peptides mapped				
		Blast (WL 8)	Blast (WL 12)	MegaBlast (WL 8)	MegaBlast (WL 12)	Maq
1	1959	2516	2210	2506	2210	634
2		2975	2669		2665	680
3		3124	2863		2855	739
4		3188	2964		2949	794
5		3213	3014		2996	833
6		3226	3037		3017	871
7		3229	3044		3027	889
8		3229	3042		3027	906
9		3228	3044		3029	925
10		3229	3047		3031	934
11		3229	3047		3033	934
12			3048		3032	945

(WL = word length)

Supplementary Table 4 | Genes encoding denitrification enzymes from *M. oxyfera*.

Enzyme	Gene	Best BLASTP hit NCBI (BLASTP search against <i>Paracoccus denitrificans</i> between brackets)				Transcript -ome coverage	No. of peptides detected	ORF identifier	Enrichment culture "Ooij" sequences	
		% Identity	% Similarity	Expected (E)-value	GenBank identifier				Average coverage/ % identity	no. of peptides detected
Nitrate reductase	narG	67 (46)	80 (62)	0.0 (0.0)	EAR23355 <i>Nitrococcus mobilis</i> Nb-231 (Pden_4236)	2	ND	DAMO_0778	34.9/96.8	14
	narH	65 (50)	80 (66)	0.0 ( $4 \times 10^{-126}$ )	EAR23356 <i>Nitrococcus mobilis</i> Nb-231 (Pden_4235)	1	ND	DAMO_0776	34.7/97.5	ND
	narI	57 (38)	71 (56)	$8 \times 10^{-64}$ ( $3 \times 10^{-27}$ )	Nwi_0778 <i>Nitrobacter winogradski</i> Nb-255 (Pden_4233)	1	ND	DAMO_0774	37.3/99.1	ND
	narJ	35 (31)	52 (43)	$1 \times 10^{-18}$ (0.002)	EAR23357 <i>Nitrococcus mobilis</i> Nb-231 (Pden_4234)	1	ND	DAMO_0775	41.3/99.3	ND
	narX	Not present in <i>M. oxyfera</i> *								
Periplasmic nitrate reductase	napA	55 (51)	72 (63)	0.0 (0.0)	Glov_1056 <i>Geobacter lovleyi</i> SZ (Pden_4721)	1	11	DAMO_2411	33.9/88.2	23
	napB	44 (26)	55 (36)	$7 \times 10^{-6}$ (1.2)	EDO26469 <i>Nematostella vectensis</i> (Pden_4722)	1	ND	DAMO_2410	29.9/89.0	ND
	napD	Not present in <i>M. oxyfera</i>								
	napE	Not present in <i>M. oxyfera</i>								
Nitrite reductase	napC	Not present in <i>M. oxyfera</i>								
	nirS	58 (54)	72 (70)	0.0 ( $8 \times 10^{-158}$ )	Rcas_3430 <i>Roseiflexus castenholzii</i> DSM 13941 (Pden_2487)	18	96	DAMO_2415	35.0/90.8	192
	nirJ	46 (48)	69 (63)	$4 \times 10^{-111}$ ( $4 \times 10^{-90}$ )	MA3035 <i>Methanosarcina acetivorans</i> C2A (Pden_2494)	2	ND	DAMO_2413	25.0/88.0	ND
	nirF	45 (37)	64 (59)	$5 \times 10^{-95}$ ( $2 \times 10^{-74}$ )	EDN67735 <i>Beggiatoa</i> sp. PS (Pden_2490)	1	19	DAMO_2412	27.2/88.7	29
	fused nirD/G & nirH/L	46 (29)	64 (46)	$5 \times 10^{-87}$ ( $5 \times 10^{-29}$ )	Rxyl_0505 <i>Rubrobacter xylanophilus</i> DSM 9941 (Pden_2491)	1	ND	DAMO_2409	15.4/88.7	ND
Nitric oxide reductase	norZ1	65 (29)	77 (47)	0.0 ( $5 \times 10^{-24}$ )	Gmet_3493 <i>Geobacter metallireducens</i> GS-15 (Pden_2483)	1	ND	DAMO_1889	34.1/94.0	ND
	norZ2	34 (26)	52 (46)	$2 \times 10^{-121}$ ( $6 \times 10^{-29}$ )	Gmet_3493 <i>Geobacter metallireducens</i> GS-15 (Pden_2483)	78	ND	DAMO_2434	42.1/91.2	7
	norZ3	34 (26)	53 (46)	$4 \times 10^{-121}$ ( $2 \times 10^{-27}$ )	Gmet_3493 <i>Geobacter metallireducens</i> GS-15 (Pden_2483)	352	4	DAMO_2437	53.5/91.7	67
	norB norC	Not present in <i>M. oxyfera</i>								
Nitrous oxide reductase	nosZ	Not present in <i>M. oxyfera</i>								
	nosD	Not present in <i>M. oxyfera</i>								
	nosF	Not present in <i>M. oxyfera</i>								
	nosY	Not present in <i>M. oxyfera</i>								
	nosL	50 (23)	69 (44)	$6 \times 10^{-43}$ ( $7 \times 10^{-4}$ )	Gsu1258 <i>Geobacter sulfurreducens</i> PCA (Pden_4215)	0	ND	DAMO_1959	17.6/88.9	ND

Genes encoding denitrification enzymes were identified by BLASTP search of translated ORFs against the NCBI NR database. Similarity to *P. denitrificans* homologs was determined by BLASTP search at the Genome Project of *P. denitrificans* within NCBI. \*In the *M. oxyfera* nar operon, which is organized like that of *N. winogradski*, a different gene with no sequence similarity is present at the position of narX; its best BLASTP hit is to kusc0320 (*Candidatus* Kueneria stuttgartiensis, unknown protein). ND, not detected.

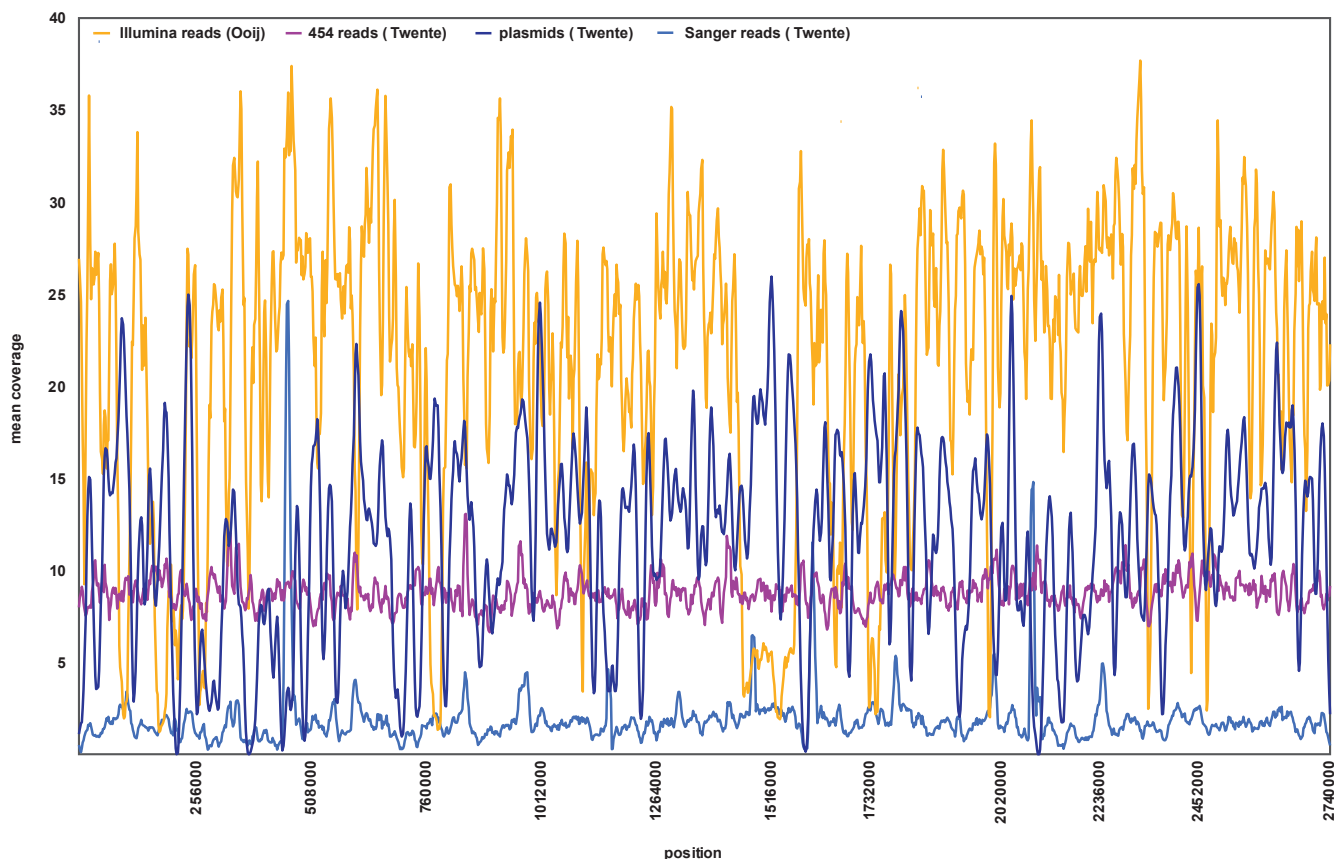
Supplementary Table 5 | Genes encoding selected carbon metabolism enzymes from *M. oxyfera*.

Enzyme	Gene	Best BLASTP hit NCBI (BLASTP against <i>Methylococcus capsulatus</i> between brackets)				Transcript -ome coverage	No. of peptides detected	ORF identifier	Enrichment culture "Ooij" sequences	
		% Identity	% Similarity	Expected (E)-value	GenBank identifier				Average coverage/ % identity	no. of peptides detected
Methane monooxygenase	pmoA1	= (53)	= (73)	= ( $1 \times 10^{-76}$ )	= (mca2854)	45	1	DAMO_2450	35.3/ 89.9	38
	pmoB1	= (40)	= (60)	= ( $1 \times 10^{-84}$ )	= (mca2853)	55	8	DAMO_2448	34.0/ 88.4	74
	pmoC1	53 (59)	68 (75)	$3 \times 10^{-73}$ ( $3 \times 10^{-71}$ )	CAE48351 <i>Methylocystis</i> sp. SC2 (mca2855)			DAMO_2451	63.7/ 90.8	30
	pmoC2	53 (59)	68 (75)	$3 \times 10^{-73}$ ( $3 \times 10^{-71}$ )	CAE48351 <i>Methylocystis</i> sp. SC2 (mca2855)	36	3	DAMO_2339		
	mmoX	Not present in <i>M. oxyfera</i>								
Methanol dehydrogenase	mxaf1	= (74)	= (88)	= (0.0)	= (mca0779)	62	69	DAMO_0112	2.4/ 89.7	ND
	mxaf2	68 (40)	80 (59)	0.0 ( $3 \times 10^{-126}$ )	Msil_3149 <i>Methylocella silvestris</i> BL2 (mca0779)	14	108	DAMO_0124	2.4/ 88.6	ND
	mxaf3	62 (49)	74 (63)	0.0 ( $3 \times 10^{-154}$ )	Minf_0992 <i>Methylacidiphilum inferorum</i> V4 (mca0299)	6	38	DAMO_0134	22.3/ 88.5	145
	mxaj1	54 (61)	72 (76)	$2 \times 10^{-84}$ ( $3 \times 10^{-60}$ )	ABE77337 <i>Methylomicrobium</i> sp. HG-1 (mca0780)	29	5	DAMO_0113	1.9/ 89.3	ND
	mxaj2	46 (29)	62 (52)	$2 \times 10^{-118}$ ( $7 \times 10^{-30}$ )	Msil_3148 <i>Methylocella silvestris</i> BL2 (mca0300)	8	ND	DAMO_0125	3.2/ 89.9	ND

	mxaj3	50 (35)	67 (53)	$4 \times 10^{-76}$ ( $8 \times 10^{-39}$ )	AAy96668 uncultured bacterium BAC10-4 (mca0300)	3	ND	DAMO_0136	23.9/ 87.3	5
	mxag1	59 (52)	67 (66)	$5 \times 10^{-49}$ ( $6 \times 10^{-43}$ )	Veis_1827 <i>Verminephrobacter eiseniae</i> EF01-2 (mca0781)	16	3	DAMO_0114	1.3/ 88.6	ND
	mxag2	50 (35)	68 (53)	$1 \times 10^{-20}$ ( $2 \times 10^{-7}$ )	Msil_3147 <i>Methylocella silvestris</i> BL2 (mca0781)	6	2	DAMO_0127	2.7/ 89.3	ND
	mxag3	43 (28)	56 (41)	$5 \times 10^{-18}$ ( $4 \times 10^{-9}$ )	AAy96667 uncultured bacterium BAC10-4 (mca0781)	5	6	DAMO_0138	30.6/ 87.2	13
	mxal	62 (63)	80 (78)	$4 \times 10^{-25}$ ( $4 \times 10^{-22}$ )	ACB32199 uncultured bacterium 16A2 (mca0782)	27	ND	DAMO_0115	0.8/ 88.2	ND
	mxar	62 (62)	80 (82)	$4 \times 10^{-125}$ ( $5 \times 10^{-128}$ )	Mfia_1895 <i>Methylobacillus flagellatus</i> KT (mca1525)	5	ND	DAMO_0116	1.7/ 89.1	ND
	mxas	44 (45)	58 (56)	$1 \times 10^{-60}$ ( $4 \times 10^{-56}$ )	Mfia_1896 <i>Methylobacillus flagellatus</i> KT (mca0784)	2	ND	DAMO_0117	1.8/ 89.9	ND
	mxaa	= (33)	= (48)	= ( $7 \times 10^{-31}$ )	= (mca0785)	1	ND	DAMO_0118	2.4/ 89.4	ND
	mxac	43 (46)	63 (60)	$1 \times 10^{-67}$ ( $3 \times 10^{-59}$ )	MDMS009_1430 <i>Methylophaga</i> sp DMS010 (mca1528)	1	ND	DAMO_0119	1.8/ 88.1	ND
	mxak	37 (31)	52 (48)	$2 \times 10^{-16}$ ( $3 \times 10^{-13}$ )	Mfia_2036 <i>Methylobacillus flagellatus</i> KT (mca1529)	1	ND	DAMO_0120	3.2/ 89.6	ND
	mxal	41 (44)	58 (56)	$2 \times 10^{-50}$ ( $1 \times 10^{-40}$ )	Mfia_2035 <i>Methylobacillus flagellatus</i> KT (mca1530)	1	2	DAMO_0121 <sup>†</sup>	1.4/ 89.4	ND
	mxad	53 (47)	65 (65)	$2 \times 10^{-40}$ ( $9 \times 10^{-41}$ )	ABS82778 uncultured <i>Methylophaga</i> sp. (mca0789)	1	2	DAMO_0121 <sup>†</sup>	1.4/ 89.4	ND
	mxae1	42 (-)	66 (-)	$4 \times 10^{-75}$ (-)	MDMS009_1396 <i>Methylophaga</i> sp DMS010 (-)	1	ND	DAMO_0122	2.8/ 89.1	ND
	mxae2	44 (-)	63 (-)	$8 \times 10^{-67}$ (-)	AAy96670 uncultured bacterium BAC10-4 (-)	4	2	DAMO_0128	3.1/ 90.0	ND
Formaldehyde dehydrogenase	adhP	Not present in <i>M. oxyfera</i>								
Formaldehyde activating enzyme	fae	70 (57)	80 (72)	$7 \times 10^{-60}$ ( $2 \times 10^{-37}$ )	EDL60092 <i>Planctomyces maris</i> DSM 8797 (mca2866)	19	13	DAMO_0454	44.6/ 95.2	44
Methylene H <sub>4</sub> MPT dehydrogenase	mtdB	40 (42)	55 (58)	$5 \times 10^{-46}$ ( $1 \times 10^{-45}$ )	Bphy_6482 <i>Burkholderia phymatum</i> STM815 (mca3019)	4	3	DAMO_0455	32.3/ 93.6	40
Methenyl H <sub>4</sub> MPT cyclohydrolase	mch	53 (37)	68 (57)	$5 \times 10^{-84}$ ( $3 \times 10^{-60}$ )	AAy96682 uncultured bacterium BAC10-4 (mca2863)	3	18	DAMO_0461	21.1/ 87.5	19
Formyltransferase/hydrolase complex	fhcA	55 (48)	70 (65)	$6 \times 10^{-162}$ ( $8 \times 10^{-145}$ )	AAy96680 uncultured bacterium BAC10-4 (mca2859)	5	2	DAMO_0458	39.3/ 93.6	39
	fhcB1	47 (25)	65 (44)	$6 \times 10^{-119}$ ( $5 \times 10^{-30}$ )	MK0259 <i>Methanopyrus kandleri</i> AV19 (mca2860)	4	4	DAMO_0457	39.6/ 92.0	40
	fhcB2	46 (25)	63 (45)	$4 \times 10^{-108}$ ( $3 \times 10^{-29}$ )	AAy96679 uncultured bacterium BAC10-4 (mca2860)	0/0	ND	DAMO_1135/ DAMO_1136	33.7/ 97.1	ND
	fhcC	50 (34)	66 (56)	$2 \times 10^{-88}$ ( $7 \times 10^{-38}$ )	AAy96681 uncultured bacterium BAC10-4 (mca2857)	5	ND	DAMO_0460	36.0/ 90.8	5
	fhcD	= (55)	= (71)	= ( $5 \times 10^{-81}$ )	= (mca2858)	4	ND	DAMO_0459	35.1/ 91.6	34
Methylene H <sub>4</sub> F dehydrogenase/Methenyl H <sub>4</sub> F cyclohydrolase	foiD	58 (-)	74 (-)	$1 \times 10^{-87}$ (-)	Moth_1516 <i>Moorella thermoacetica</i> ATCC 39073 (-)	1	ND	DAMO_1852	31.2/ 88.4	ND
5-formyl H <sub>4</sub> F cycloligase	mthfs	Not present in <i>M. oxyfera</i>								
Formate H <sub>4</sub> F ligase	fhs	Not present in <i>M. oxyfera</i>								
Formyl H <sub>4</sub> F deformylase	purU	64 (-)	80 (-)	$3 \times 10^{-106}$ (-)	EDT34736 <i>Geobacillus</i> sp. WCH70 (-)	1	ND	DAMO_2586	36.3/ 91.1	ND
Formate dehydrogenase	fdhA1	57 (40)	72 (56)	0.0 (0.0)	EEG07387 <i>Lutiella nitroferum</i> 2002 (mca1391)	0	2	DAMO_1138	2.3/ 89.4	ND
	fdhA2	43 (40)	62 (56)	0.0 (0.0)	Nither_0100 <i>Natranaerobius thermophilus</i> JW/NM-WN-LF (mca2576)	1	27	DAMO_0853	26.8/ 90.3	19
	fdhB1	54 (43)	68 (59)	$5 \times 10^{-125}$ ( $1 \times 10^{-67}$ )	ACD29487 <i>Ralstonia pickettii</i> 12J (mca1392)	0	2	DAMO_1137	3.2/ 87.6	ND
	fdhB/C2	40 (36)	59 (54)	$2 \times 10^{-107}$ ( $2 \times 10^{-79}$ )	Csac_0620 <i>Caldicellulosiruptor saccharolyticus</i> DSM 8903 (mca1392)	1	29.4/30	DAMO_0854	21.3/ 89.7	5
	fdhD	Not present in <i>M. oxyfera</i>								
Serine glyoxylate aminotransferase	sga	53 (34)	71 (53)	$5 \times 10^{-113}$ ( $7 \times 10^{-53}$ )	EAY55805 <i>Leptospirillum</i> sp. Group II UBA (mca1406)	3	13	DAMO_3099	27.1/ 88.1	10
Hydroxypyruvate dehydrogenase	hprA	Not present in <i>M. oxyfera</i>								
Serine hydroxymethyltransferase	glyA	68 (56)	80 (71)	$7 \times 10^{-170}$ ( $4 \times 10^{-119}$ )	SYN_02367 <i>Syntrophus aciditrophicus</i> SB (mca1660)	3	18	DAMO_1077	28.4/ 89.7	8
Glycerate kinase	gckA	Not present in <i>M. oxyfera</i>								
Phosphoenolpyruvate carboxylase	ppc	54 (-)	70 (-)	$1 \times 10^{-151}$ (-)	Daud_0773 <i>Candidatus "Desulfuridis audaxviator"</i> MP104C (-)	0	ND	DAMO_2168	33.0/ 97.5	12
Malyl-CoA lyase	mcl	Not present in <i>M. oxyfera</i>								

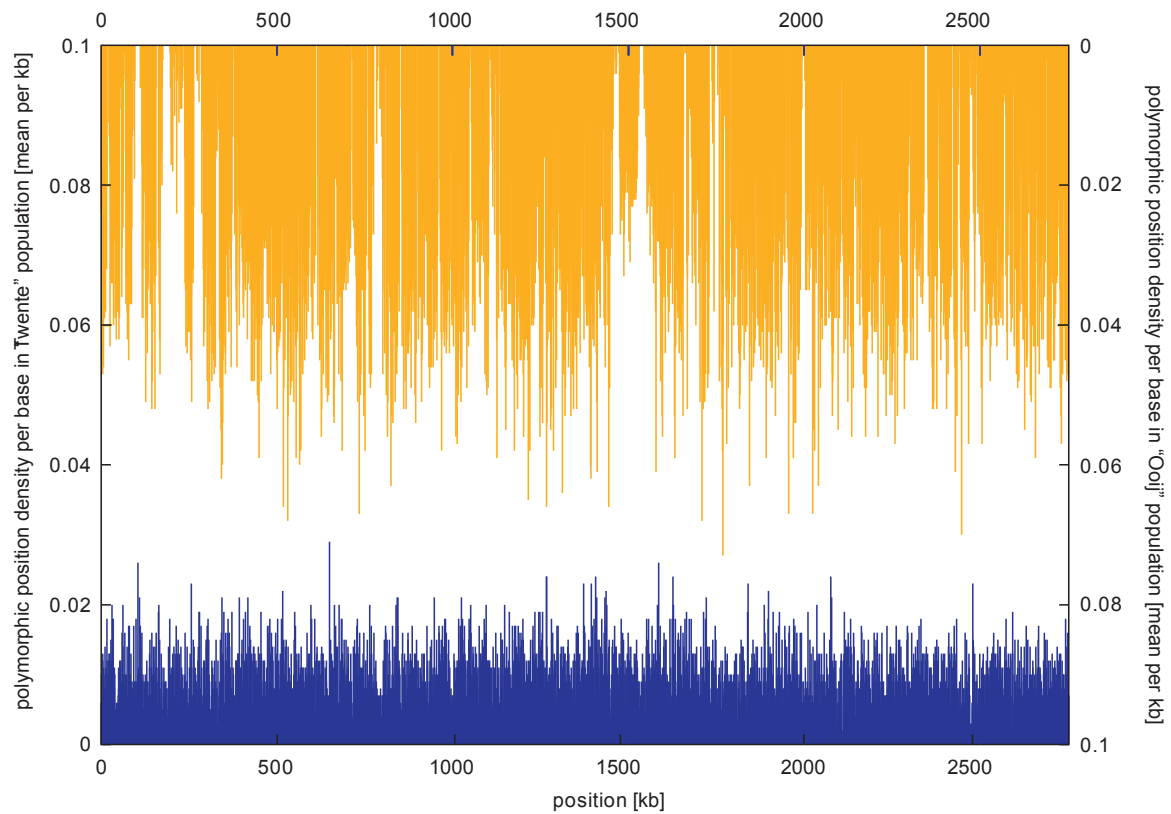
Hexulose-6-phosphate synthase	hspA	Not present in <i>M. oxyfera</i>								
Hexulose-6-phosphate isomerase	sbgU	Not present in <i>M. oxyfera</i>								
Ribulose bisphosphate carboxylase	cbbL	83 (58)	91 (72)	0.0 ( $1 \times 10^{-147}$ )	RC1_4061 <i>Rhodospirillum centenum</i> SW (mca2743)	1	12	DAMO_2165	35.1/ 97.5	47
	cbbS	68 (33)	86 (63)	$2 \times 10^{-54}$ ( $5 \times 10^{-15}$ )	Q09125 <i>Porphyridium aeruginum</i> (mca2744)	2	4	DAMO_2166	39.9/ 99.3	5
Phosphoribulosekinase	cbbP1	67 (55)	78 (69)	$9 \times 10^{-112}$ ( $5 \times 10^{-93}$ )	Tbd_2447 <i>Thiobacillus denitrificans</i> ATCC 25259 (mca3051)	1	3	DAMO_2116	12.9/ 93.4	ND
	cbbP2	42 (34)	59 (45)	$2 \times 10^{-67}$ ( $9 \times 10^{-5}$ )	Minf_1261 <i>Methylacidiphilum inferorum</i> V4 (mca3051)	3	ND	DAMO_2653	39.4/ 88.1	4
Fructose 1,6-bisphosphatase/ Sedoheptulose 1,7-bisphosphatase	cbbF-I	49 (-)	67 (-)	$2 \times 10^{-91}$ (-)	gvip434 <i>Gloeobacter violaceus</i> PCC 7421 (-)	1	5	DAMO_2163	28.3/ 89.4	2
	cbbF-II1	58 (-)	78 (-)	$4 \times 10^{-103}$ (-)	Rcas_1213 <i>Roseiflexus castenholzii</i> DSM 13941 (-)	2	17	DAMO_2650	29.7/ 90.7	10
	cbbF-II2	58 (-)	76 (-)	$1 \times 10^{-102}$ (-)	MXAN_4455 <i>Myxococcus xanthus</i> DK 1622 (-)	2	3	DAMO_2986	34.7/ 89.5	ND
	cbbF-II3	58 (-)	75 (-)	$1 \times 10^{-104}$ (-)	EEB33574 <i>Desulfovibrio piger</i> ATCC 29098 (-)	3	22	DAMO_0174	23.7/ 89.6	2

Genes encoding enzymes of carbon metabolism were identified by BLASTP search of translated ORFs against the NCBI NR database. Similarity to *M. capsulatus* was determined by BLASTP search at the Genome Project of *M. capsulatus* within NCBI. = indicates that *M. capsulatus* has the best BLASTP hit. (-) indicates that the gene is not present in *M. capsulatus*. ‡ DAMO\_0121 is a fused ORF of two proteins. ND, not detected.

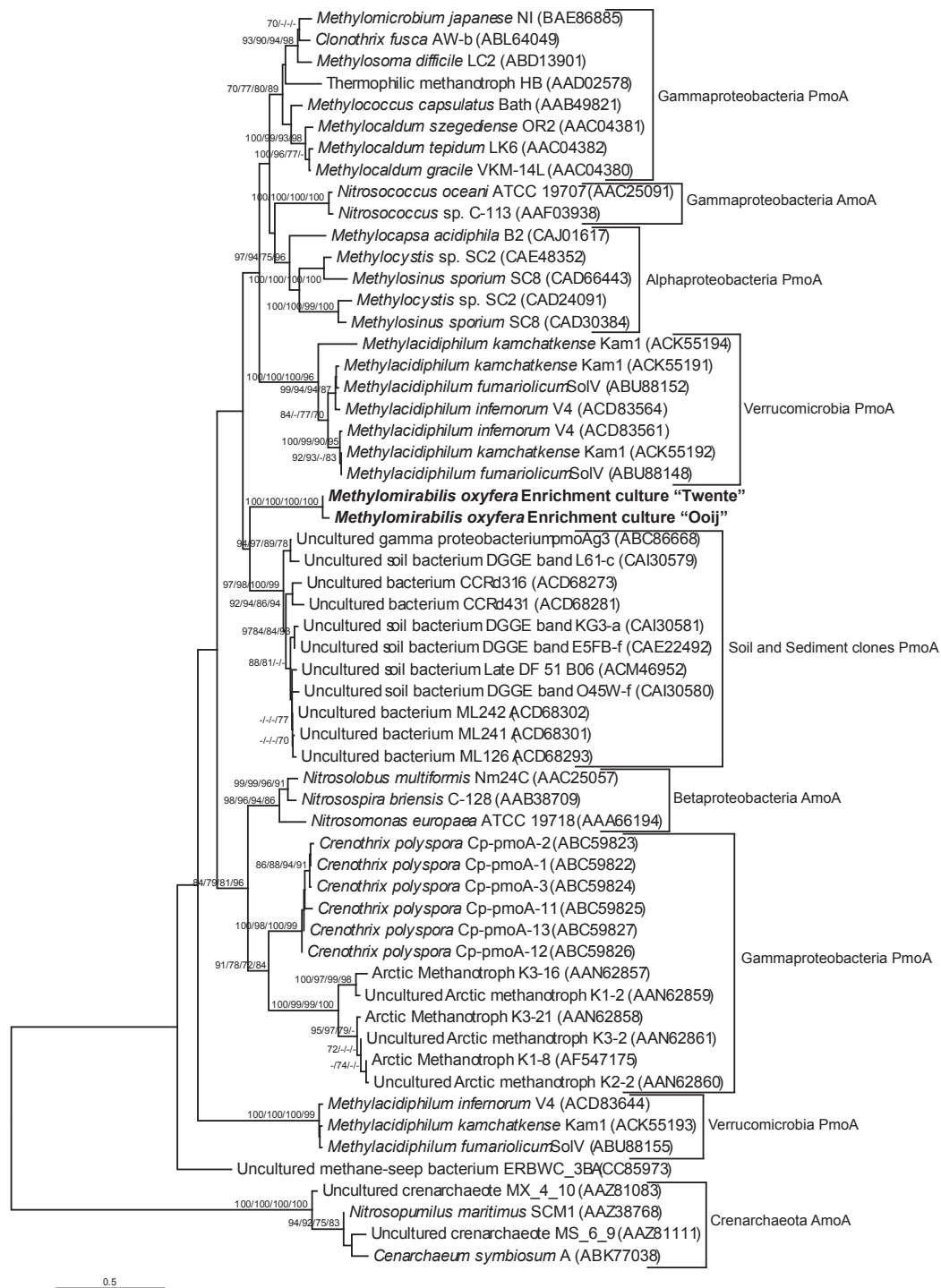


**Supplementary Figure 1** Coverage of the *Methylobacterium oxyfera* genome by different sets of sequences and clones. Sanger (light blue) and 454 pyrosequencing (purple) reads from the "Twente" enrichment culture were compared with the finished *M. oxyfera* genome using the blastn algorithm. Reads mapping uniquely on the genome, with at least 95 percent identity over at least 95 percent of their length were kept. For the plasmid (dark blue) coverage, clones having both their ends mapped with the previously described criteria, and separated by 7 to 13 kb (mean library insert size of 10 kb) were considered as localised on the *M. oxyfera* genome, and taken into account for the coverage computation. Illumina reads from the "Ooij" sample (orange) were mapped as described in the method section. For the visualization, a sliding window of 10 kb with a step size of 2 kb was used.





**Supplementary Figure 2** Single nucleotide polymorphism frequency in the two enrichment cultures ("Twente" blue, "Ooij" orange, from top) identified by mapping the DNA Illumina reads to their respective genomes using Maq (default settings). Sites with a polymorphic consensus were called as SNP sites.



**Supplementary Figure 3** | Phylogenetic relationship among PmoA and AmoA proteins. The distance tree was computed using the Dayhoff matrix method. Bootstrap values (>70%, 100 replicates) calculated within the Neighbor-Joining, Minimum-Evolution, Maximum-Parsimony and Maximum-Likelihood evolutionary methods are shown at branch points from left to right. The scale bar represents 0.5 changes per amino acid.

a

```

ABK77038_Cenarchaeum_symbiosum      : GDYIFYTDWANTSF--TVFSTISQTLMLVVGATYYTFTGVPGTATYYALI
ABY89139_Nitrosopumilus_maritimus    : GDYIFYTDWANTSY--TVFSTISQTLMLVVGATYYTFTGVPGTATYYALI
AAZ81111_Uncultured_crenarchaeote    : GDYIFYTDWANTSY--TVFSTIGNILVSVGATYYLFTGVPGTATYYGLI
AAU92182_Methylococcus_capsulatus    : GDWDFWSDWKDRRLWVTTPVIVLVTTPAAVQSYLWERYRPLPWGATVCVLG
BAE86885_Methylomicrobium_japanese   : GDWDFWTDWKDRRLWVTVAPIVSITTPAAVQAVLWRYRILWAGATLCVLG
AAA87217_Methylomicrobium_album_BG8_pmo1: -----TDWKDRRLWVTVLPVIGITTPAAVQAVVWYRWRPLPGAMLAVLG
ACE95888_Methylomicrobium_album_BG8_pmo2: -----XDKDRQWVPLVTPVIGITTPAAVQAVLWVKFRPLPGATLCVAA
CAE47800_Methylocystis_sp_SC2_pmoA1  : GDWDFWVDWKDRRMWPTVVPVILGVTCAAQAQFVWVNFRLPFGAVFAALG
CAE48352_Methylocystis_sp_SC2_pmoA2  : GDWDFWLDKDRRMWPTVTPVIVMCAAAAQSFVTRFRPLPIGATTVVLA
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CAD66447_Methylosinus_trichosporium_SM6: -----RMWPTVAPVIVMCAAAAQVQSFVWOKFRPLPIGATVACLA
CAD30381_Methylosinus_trichosporium_SM6: -----VDWKDRRMWPTVVPVILGVTAAATQAFVWENFKLPPGATFVAVLG
AAB70518_Methylobacter_sp_BB5_1_pmoA1 : GDWDFWTDWKDRRLWVTVAPIVSITTPAAVQAVLWRYRPLPWGAVVCVLG
ACE95886_Methylobacter_sp_BB5_1_pmoA2 : -----VDWKDRQWVPLVTPVIGITTPAAVQAVLWVKFRPLPGATLCVTA
ACE95894_Methylomonas_methanica_S1_pmoA1: GDWDFWTDWKDRRLWVTVAPIVSITTPAAVQAVLWRYRPLPWGATLSVVA
ACE95893_Methylomonas_methanica_S1_pmoA2: -----VDWKDRQWVPLVTPVIGITTPAAVQAVLWVKFRPLPGATLCVAA
AAF08214_Methylomonas_sp_LW13_pmoA1  : GDWDFWTDWKDRRLWVTVAPIVSITTPAAVQAVLWRYRPLPWGATLSVVA
ACE95890_Methylomonas_sp_LW13_pmoA2  : -----VDWKDRQWVPLVTPVIGITTPAAVQAVLWVKFRPLPGATLCVAA
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ABC59827_Crenothrix_polyspora       : GDWDFWLDWKDRQWVPLVTPVILITTPCAAIQYVWVNYRQPPGATLCILA
ABU88148_M_fumariolicum_solV_pmoA1   : GDWSFWTDWKDRMWPVVPVAPVMDITTPAACQAILWTKFKAPITGATFSCAG
ABU88152_M_fumariolicum_solV_pmoA2   : GDWSFWTDWKDRMWPVVPVAPVADITTPAAVQVILWTKFKMPIGATFCTVG
ABU88155_M_fumariolicum_solV_pmoA3   : GDWSFWTDWKDRRYFPVIGVTSYMLVSVQAAQWIKARLPMGLTLCVAG
ACC85973_ERBWC_3B                   : GDWDFWVDWKDRQYVVTTPVIMMIVAAIQAVFAHFRLPIGATLCGVV
ACD68273_Uncultured_ha_bacterium_CCRd316: GDWDFWTDWKDRRWLVTPVIVLITTPAAIQYLLWVKRPLPGATVCCVVG
ACD68281_Uncultured_haw_bact_CCRd431 : GDWDFWVDWKDRRWLVTPVIVLITTPAAIQYLLWVKRPRVPGATVCCVVG
ACD68293_ML126_uncultured_bacterium  : GDWDFWTDWKDRRFWLVTPVIVLITTPAAIQYVLDWVKRPLPGATVCCVVG
ABA58955_Nitrosococcus_oceani_ATCC_19707: GDWDFWVDWKDRRFWVTVPVIVSVVTPAAAQAFVWVKFRPLPWGATLVTLG
ABI60300_Nitrosomonas_eutropha_C91   : GDWDFWMDWKDRQWVVPVTPVIGITVCSAIMYVWVNYRQPPGATLCVVC
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AAB86881_Nitrosospira_sp_NpAV_pmoA1  : GDWDFWLDWKDRQWVVPVTPVIGITVCSAIMYVWVNYRPLPWGATLCIVC
Methylomirabilis_oxyfera_Twente_pmoA : GDWDFWLDWKDRRWVTPVIVLITTPAATQVFMWVKRMLPPIGATFCVMT
Methylomirabilis_oxyfera_Ooij_pmoA   : GDWDFWLDWKDRRWVTPVIVLITTPAATQVFMWVKRMLPPIGATFCVMT

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AAZ81111_Uncultured_crenarchaeote    : MQVWVIK--GAFALGYPPYDFIVTP-MWIPSCMLLDLAYWATKRNKHS
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BAE86885_Methylomicrobium_japanese   : LLLGEWINRYNFFGWTYFFPINF-VFPSNLMPGAIVLDVILMLSN-SMTL
AAA87217_Methylomicrobium_album_BG8_pmo1: LLLGEWINRYNFFGWTYFFPINF-VFPSQFAPGAIVLDVILMLSN-SMQL
ACE95888_Methylomicrobium_album_BG8_pmo2: LLLGEWINRYNFFGWTYFFPINF-VLPAATMLPGAIVLDAILMLSN-SFTI
CAE47800_Methylocystis_sp_SC2_pmoA1  : LLLGEWINRYNFFGWTYFFPINF-VFPAVSLVPGAILDITVLMMSG-SYLF
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ACD68281_Uncultured_haw_bact_CCRd431 : LLLGEWINRYNFFGWTYFFPINF-VFPAVSLVPGAILDITVLMMSG-SYLF
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ABA58955_Nitrosococcus_oceani_ATCC_19707: LLLGEWINRYNFFGWTYFFPINF-VFPAVSLVPGAILDITVLMMSG-SYLF
ABI60300_Nitrosomonas_eutropha_C91   : LLLGEWINRYNFFGWTYFFPINF-VFPAVSLVPGAILDITVLMMSG-SYLF
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Methylomirabilis_oxyfera_Twente_pmoA : LLLGEWINRYNFFGWTYFFPINF-VFPAVSLVPGAILDITVLMMSG-SYLF
Methylomirabilis_oxyfera_Ooij_pmoA   : LLLGEWINRYNFFGWTYFFPINF-VFPAVSLVPGAILDITVLMMSG-SYLF

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ABY89139_Nitrosopumilus_maritimus   : LILFGGVLVGSLSLPLFMVLLITVA-D--LETA--FKYRPT
AAZ81111_Uncultured_crenarchaeote    : LILFGGVLVGSLSLPLFMVLLITVA-D--LETA--FKYRPT
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ACE95893_Methylomonas_methanica_S1_pmoA2: TSIFGGAAFLLFYFPTNWPIIPLHVPVEY-ANQLTADLFGFOYIRTG
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ACE95890_Methylomonas_sp_LW13_pmoA2  : TSIFGGAAFLLFYFPTNWPIIPLHVPVEY-ANQLTADLFGFOYIRTG
CAJ01617_Methylocapsa_acidiphila     : TAVVGAMGWGLLFYFSPNWPIIPLHVPVEY-NGMLMSIADLQGYHYVRTG
ABC59827_Crenothrix_polyspora       : TAVVGSGLGWGLLFYFSPNWPIIPLHVPVEY-NGMMLTADLQGYHYVRTG
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ABU88152_M_fumariolicum_solV_pmoA2   : TAVVGSGLGWGLLFYFIPNWPIIPLHVPVEY-NGMMLTADLQGYHYVRTG
ABU88155_M_fumariolicum_solV_pmoA3   : TYLFGAYAFLLTFYFANWVMIPLHVPVEY-NGMLMSIADLQGYHYVRTG
ACC85973_ERBWC_3B                   : TAALGAIAGLIMFPTSNWPIIPLHVPVEY-NGMLMSIADLQGYHYVRTG
ACD68273_Uncultured_ha_bacterium_CCRd316: TGIFGGLLWGLVFYFPGNWPIIPLHVPVEY-NGMLMSIADLQGYHYVRTG
ACD68281_Uncultured_haw_bact_CCRd431 : TGIFGGLLWGLVFYFPGNWPIIPLHVPVEY-NGMLMSIADLQGYHYVRTG
ACD68293_ML126_uncultured_bacterium  : TGIFGGMLWGLVFYFPGNWPIIPLHVPVEY-NGMLMSIADLQGYHYVRTG
ABA58955_Nitrosococcus_oceani_ATCC_19707: TAVVGSGLMYGLLMYFANWPIIPLHVPVEY-NGMVMTLADLQGYHYVRTG
ABI60300_Nitrosomonas_eutropha_C91   : TAVVGGGFFGLMFYFPGNWPIIPLHVPVEY-NGMLMSIADLQGYHYVRTG
ABB74106_Nitrosospira_multiformis_25196 : TAVVGGGAFGLLFYFPGNWPIIPLHVPVEY-NGMLMSIADLQGYHYVRTG
AAB86881_Nitrosospira_sp_NpAV_pmoA1  : TAVVGGGAFGLLFYFPGNWPIIPLHVPVEY-NGMLMSIADLQGYHYVRTG
Methylomirabilis_oxifera_Twente_pmoA : TALFGGMWGLLFYFANWPIIPLHVPVEY-NGMLMSIADLQGYHYVRTG
Methylomirabilis_oxifera_Ooij_pmoA  : TALFGGMWGLLFYFANWPIIPLHVPVEY-NGMLMSIADLQGYHYVRTG

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ABK77038_Cenarchaeum_symbiosum      : LPFYMTPIEPVVGKIFYN
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AAZ81111_Uncultured_crenarchaeote    : LPFYMTPIEPVVGKIFYN
AAU92182_Methylococcus_capsulatus   : TPEYIRMVEKGTTLRTFG
BAE86885_Methylomicrobium_japanese  : TPEYIRMVEKGTTLRTFG
AAA87217_Methylomicrobium_album_BG8_pmo1: TPEYIRMVEKGTTLRTFG
ACE95888_Methylomicrobium_album_BG8_pmo2: MPEYLRRIERGTLRTFG
CAE47800_Methylocystis_sp_SC2_pmoA1  : MPEYIRMVERGTTLRTFG
CAE48352_Methylocystis_sp_SC2_pmoA2  : TPEYIRMVERGTTLRTFG
BAF49660_Methylocaldum_sp_T025      : TPEYIRMVEKGTTLRTFG
AAA87220_Methylosinus_trichosporium_OB3b: MPEYIRMVERGTTLRTFG
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CAD30381_Methylosinus_trichosporium_SM6 : MPEYIRMVERGTTLRTFG
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ACE95886_Methylobacter_sp_BB5_1_pmoA2 : MPEYLRRIERGTLRTFG
ACE95894_Methylomonas_methanica_S1_pmoA1: TPEYIRMV-----
ACE95893_Methylomonas_methanica_S1_pmoA2: MPEYLRRIERGTLRTFG
AAF08214_Methylomonas_sp_LW13_pmoA1  : TPEYIRMVEKGTTLRTFG
ACE95890_Methylomonas_sp_LW13_pmoA2  : MPEYLRRIERGTLRTFG
CAJ01617_Methylocapsa_acidiphila     : MPEYLRRIERGTLRTFG
ABC59827_Crenothrix_polyspora       : TPEYIRMVEKGTTLRTFG
ABU88148_M_fumariolicum_solV_pmoA1   : TPEYIRMVEKGTTLRTFG
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ACC85973_ERBWC_3B                   : TPEYLRRIERGTLRTFG
ACD68273_Uncultured_ha_bacterium_CCRd316: TPEYIRRIERGTLRTFG
ACD68281_Uncultured_haw_bact_CCRd431 : TPEYIRRIERGTLRTFG
ACD68293_ML126_uncultured_bacterium  : TPEYIRRIERGTLRTFG
ABA58955_Nitrosococcus_oceani_ATCC_19707: TPEYIRMIEKGTTLRTFG
ABI60300_Nitrosomonas_eutropha_C91   : TPEYVRLIEQSLRTFG
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AAB86881_Nitrosospira_sp_NpAV_pmoA1  : TPEYVRLIEQSLRTFG
Methylomirabilis_oxifera_Twente_pmoA : TPEYIRIVERGTTLRTFG
Methylomirabilis_oxifera_Ooij_pmoA  : TPEYIRIVERGTTLRTFG

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b.

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%          +          *          +          *
ABK77030_Cenarchaeum_symbiosum_A : LPSAEAHGVQAQLQSRFRIEDEFN-----RQSLQTGETLCLAGS
ABY89142_Nitrosopumilus_maritimus_SCM1 : LPTADAHGVQAQLQSRFRIEDEFN-----RQSLQTGETLVLQGT
AAU92183_Methylococcus_capsulatus_Bath : ASAHGEKSQAAPFMRRTIHWYDLNWSKE---KVKINETVEIKGKPHVFEG
BAE86886_Methylococcobium_japanense_NI : ASAHGEKSQAAPFMRRTIHWYDLNWSK---MVSVNEMTMSISGKPHVFEG
ACE95889_Methylococcobium_album_BG8_pmb2 : ALAHGEKALEPFI RMRTIQWYDVQVWSK---QFKVNEEVTVSGRPHVFAED
CAE47801_Methylocystis_sp_SC2_pmoB1 : ASAHGEKSQAAPFMRRTLNWYDVQVWSKT---TVNVNEEMVLSGKIHFVSA
CAE48353_Methylocystis_sp_SC2_pmoB2 : AAHAGERSQAAPFMRRTLNWYDVQVWSKT---ELNVNDEMELTGVKPHVFSG
BAF49661_Methylocaldum_sp_T_025 : ASAHGEKSQAAPFMRRTIHWYDLNWSKE---KVKVNEEVEITGKPHVVFEG
AAF37894_Methylosinus_trichosporium_OB3b : AEAHGEKSQAAPFMRRTLNWYDVQVWSKT---SLNVNESMVLGSKVHFVSA
ACE95887_Methylobacter_sp_BB5_1_pmoB2 : AQAHGEKALEPFI RMRTIQWYDVQVWSKT---KFNVDDEVSVSGKPHVFAED
ACE95892_Methylomonas_methanica_S1_pmoB2 : AQAHGEKALEPFI RMRTIQWYDVQVWSKT---KFNVDDEVSVSGKPHVFAED
CAJ01618_Methylocapsa_acidiphila_B2 : ADAHGEKSQAAPFMRRTLNWYDVQVWSKT---SLNVNEEMEITGKLIHMADA
ABU88156_M_fumariolicum_SolV_pmoB1 : ASGIGERAQEAAILRMRTAQFYDVRFSN---HLKVGEDLVVTVGKVMILPI
ABU88149_M_fumariolicum_SolV_pmoB2 : VQGMGAKSQAAPFMRRTVFFDTRFSFTPNRNVKVGDEFCTGKVMMLMPT
ABU88153_M_fumariolicum_SolV_pmoB3 : VQGMGAKSQAAPFMRRTVFFYDTQFSFAPTNRNVKVGEEFSTGKVMMLMPT
ABA58954_Nitrosococcus_oceani_ATCC19707 : VAAHGEKQAAPFMRRTIHWYDMVWSK---TIAVNETYITGKPHVVFED
ABI60299_Nitrosomonas_eutropha_C91 : VAAHGEKSQEPFLRMRTVQWYDVQVWSKPE---VTKVNEAQITGKPHLAED
ABB74107_Nitrosospira_multiformis_25196 : AAHAGERSQEPFLRMRTIQWYDMKWSKPE---TTKVNDIATMTGKPHLAED
AAB86882_Nitrosospira_sp_NpAV_amoB1 : AAHAGERSQEPFLRMRTIQWYDMKWSKPD---TTKVNDFATMTGKPHLAED
Methylomirabilis_oxifyfera_Twente_pmoB : AAHAGERSQEPFLRMRTITFYDTKWSKA---RVQPGETMDLTGKPHTFSE
Methylomirabilis_oxifyfera_Ooij_pmoB : AWAHAGERSQEPFLRMRTITFYDTKWSKA---RVQPGETMDLTGKPHTFSE

60          *          80          *          100
ABK77030_Cenarchaeum_symbiosum_A : FVSLVERDLRGWNSIFSESTNAGNRWEILSRD---PPGNVFDIPGNSEI
ABY89142_Nitrosopumilus_maritimus_SCM1 : LVSLVERDLRGWISIFSESTNAGNRWEMLSRD---PPGNVFDIPGNVVV
AAU92183_Methylococcus_capsulatus_Bath : WPETVDEPDVAFLNVGMPGPVPIRKESYIGGQ---LVPRSVRLEIGKTY
BAE86886_Methylococcobium_japanense_NI : WPETVDEPDVAFLNIGIPGPVPIRAGSWIGGQ---LVPRSVRLEIGKTY
ACE95889_Methylococcobium_album_BG8_pmb2 : WPVSVKPDAAFLNVSTPGPVLIRTERWLNK---PWNSVALQPPGGDY
CAE47801_Methylocystis_sp_SC2_pmoB1 : WPQAVANPRVSLNAGEPGPVLIRKSAFVGEV---FAPRSVSLVPGNDY
CAE48353_Methylocystis_sp_SC2_pmoB2 : WPQAVARPGESFLNAGEPGPVLIRKSAFVGEV---FAPRSVSLVPGNDY
BAF49661_Methylocaldum_sp_T_025 : WPETVAEPDVAFLNIGIPGPVPIRKASYIGGQ---LVPRSVRLEIGKTY
AAF37894_Methylosinus_trichosporium_OB3b : WPQAVANPKSSFLNAGEPGPVLIRKSAFVGEV---FAPRSVSLVPGNDY
ACE95887_Methylobacter_sp_BB5_1_pmoB2 : WPI SVKPEASFLNISTPGPVLIRTERYLNK---PWNSVALQPPGGDY
ACE95892_Methylomonas_methanica_S1_pmoB2 : WPVSVKPEASFLNISTPGPVLIRTERYLNK---PWNSVALQPPGGDY
CAJ01618_Methylocapsa_acidiphila_B2 : WPVAVAKPEVAFLNVGMPGPVLRREGSFLGGQ---FVPRSTSLLEIGKTY
ABU88156_M_fumariolicum_SolV_pmoB1 : WPHLGFSGIAYINFFEPGPRVLRKETSIVNGO---PVFSMIVKLGDTY
ABU88149_M_fumariolicum_SolV_pmoB2 : WPQETPFGSIFFFNFVPGPQVLRKAIWNEKY---FQFNSVLEKGGVY
ABU88153_M_fumariolicum_SolV_pmoB3 : WPEEIPFTGISFFNFVPGPQVLRKAIWNEKY---FQFNSVLEKGGVY
ABA58954_Nitrosococcus_oceani_ATCC19707 : WPEAVEKPHVSLNAGQPGPVLIRKSAFVGEV---FVPRISGLELGGDY
ABI60299_Nitrosomonas_eutropha_C91 : WPRAAARPDFAFNVGSPSSVYVRLSTKLNH---PWFISGPLELGGDY
ABB74107_Nitrosospira_multiformis_25196 : WPRAVGKPGRAFFNVGSPSPVFRVRLSTKLNH---PTYISGPMELGRDY
AAB86882_Nitrosospira_sp_NpAV_amoB1 : WPRAVGKPGRAFFNVGSPSPVFRVRLSTKLNH---PTYISGPLELGRDY
Methylomirabilis_oxifyfera_Twente_pmoB : WPRAVNTPEISIFLHYSVPGPSMLKKEAWMNGM---PVINATSTQLGGDY
Methylomirabilis_oxifyfera_Ooij_pmoB : WPRAVNTPEISIFLHYSVPGPSMLKKEAWMNGM---PVINATSTQLGGDY

%          %          *          *          120          *          140          *
ABK77030_Cenarchaeum_symbiosum_A : PYEICALALEPGVYHVHTQLNVATVGPGLGPGQTVVVDGE----FILKE
ABY89142_Nitrosopumilus_maritimus_SCM1 : DYQLSAKALEAGVYHVHTQLNVAQVGPGLGPGQTVVVEGE----PIIKP
AAU92183_Methylococcus_capsulatus_Bath : DFRVVLKARRPGDWHVHTMMNVQGGGPIIGPGKWITVEGSMSEFRNPVTT
BAE86886_Methylococcobium_japanense_NI : EFKVLLKARRPGDWHVHTMMNVQGGGPIIGPGKWITITGSMGDFKPNPIT
ACE95889_Methylococcobium_album_BG8_pmb2 : EFKVLLKARRPGDWHVHTMMNVQGGGPIIGPGKWITITGSMGDFKPNPIT
CAE47801_Methylocystis_sp_SC2_pmoB1 : AFSINLRGRRAGRWHVHAQINVEGGGPIIGPGQWIEIKGDMKDFDTPVTL
CAE48353_Methylocystis_sp_SC2_pmoB2 : EYKIVLKARRQGRYHVHVQINVKDGGPIIGPGQWITIKGDMKDFDTPVTL
BAF49661_Methylocaldum_sp_T_025 : DFKVVLKARRPGDWHVHTMMNVQGGGPIIGPGKWITIEGSMSEFKNPVTT
AAF37894_Methylosinus_trichosporium_OB3b : AFSIDLKARRAGRWHVHAQINVEGGGPIIGPGQWIEIKGDMADFKDPVTL
ACE95887_Methylobacter_sp_BB5_1_pmoB2 : -----
ACE95892_Methylomonas_methanica_S1_pmoB2 : DFKVVLKARRLPGRYHIHPFNKLDAGQVMGPGVWLEIGGNPSDFNTTIKT
CAJ01618_Methylocapsa_acidiphila_B2 : EFRVLLKARRQGRWHVHTQLSVDQGGPIIGPGQWIEIKGDMADFKNPVTL
ABU88156_M_fumariolicum_SolV_pmoB1 : DFKVVLKARRPGTWVPGVTMNIKDIGPIVGPPIKVTIDPSSAPFTNTVQT
ABU88149_M_fumariolicum_SolV_pmoB2 : EYKMNQARTPGIWPVGPVMSMEEAGPPIIGPEEFLTIEGSGAGFTNPVKT
ABU88153_M_fumariolicum_SolV_pmoB3 : AYKMNQARNPFIIPMGPMLSMEEAGPPIIGPEEFLTIEGSKGFANPVKT
ABA58954_Nitrosococcus_oceani_ATCC19707 : EFEMTMQGRRPGTWHVHTLLNVQGGGPIIGPGKIITITGDMADFESKITD
ABI60299_Nitrosomonas_eutropha_C91 : AFEVQLRARIPGRHHMHAMLNVDKAGPIAGPGAWMNVGSDWDDFTNPLKL
ABB74107_Nitrosospira_multiformis_25196 : AFEVRLKARIPGRHHMHAMVNIKDGPIAGPAAWNIIGSDWDDFTNPKVL
AAB86882_Nitrosospira_sp_NpAV_amoB1 : AFEVRLKARIPGRHHMHAMVNIKDGPIAGPAAWNIIGSDWDDFTNPKVL
Methylomirabilis_oxifyfera_Twente_pmoB : DYRMINMGRVTGTIVHVPVNIIEGGGPIVGGGFEFVTVGSDWNSFTNNVTT
Methylomirabilis_oxifyfera_Ooij_pmoB : DYRMINMGRVTGTIVHVPVNIIEGGGPIVGGGFEFVTVGSDWNSFTNNVTT

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                                160          *          180          *          200
ABK77030_Cenarchaeum_symbiosum_A : IPYTNIAQSIIGVGYVITFATRPQVI-----
ABY89142_Nitrosopumilus_maritimus_SCM1 : IPYTNIAQSIMIGVGYVITFAT-----
AAU92183_Methylococcus_capsulatus_Bath : LTGQTVLDLENYNEGNTYFWHAFWFAIGVAWIGYWSRRPIFIPRLLMVDAG
BAE86886_Methylomicrobium_japanense_NI : LTGETIDLETYALDGVYGHLLFWYVLGVAMWVYWCRRKPVFIPRRIAVDAG
ACE95889_Methylomicrobium_album_BG8_pmoB2 : -----
CAE47801_Methylocystis_sp_SC2_pmoB1 : LDGSTVDLETYGISRVYAWHLLPWLAVGAAILFWFVRKGI IASYLVRVATG
CAE48353_Methylocystis_sp_SC2_pmoB2 : LEGSTIDLETYGITWTYIYHFFWMAAAAAILYWFMTKGI IIVRYWQVKAG
BAF49661_Methylocaldum_sp_T_025 : LTGQTVLDLETYNEGNTYFWHGASGSAIGMCLGWYWGTVVRRFLPRLPDG
AAF37894_Methylosinus_trichosporium_OB3b : LDGTTVDLETYGDRIYAWHFPWMIAAAAILYWFPKKGI IASYLRISEG
ACE95887_Methylobacter_sp_BB5_1_pmoB2 : -----
ACE95892_Methylomonas_methanica_S1_pmoB2 : INGELIDMESFGFANGVFWHLLF-----
CAJ01618_Methylocapsa_acidiphila_B2 : LNGEVIDLEQYKIGNIYFWHTVWFVAGVAWVYWFRRKRGFVGRYIISVAG
ABU88156_M_fumariolicum_SolV_pmoB1 : LSGQSIINLENYGLSRAMGWSFLWVLLGIGWLLYLLKPTAPRLGLAYLE
ABU88149_M_fumariolicum_SolV_pmoB2 : LLGNTIDLENYEGRMIAWTLTSAIAVWVWVYVWCKPPT-RRGLVAAG
ABU88153_M_fumariolicum_SolV_pmoB3 : LLGNTVDLENYGTARVITWTIFTTLIGVWVWGLYWLAKPPT-RRGLVAAG
ABA58954_Nitrosococcus_oceani_ATCC19707 : LTGNTVNLLETMATGTVIGWHLFWYVLGIAIWWWARRPMFLPRYMRIEAG
ABI60299_Nitrosomonas_eutropha_C91 : LTGETIDSETFNLSNGIFWHLLWMSIGIFWIGIFVARPMFLPRSRVLLAY
ABB74107_Nitrosospira_multiformis_25196 : LTGETIDTETFNFSNGIFWHLLWLSLGIWIGYVVARPMFLPRSRVLLAY
AAB86882_Nitrosospira_sp_NpAV_amoB1 : LTGETIDTETFNFNNGIFWHLLWLGCFWIGYVVARPMFLPRSRVLLAY
Methylomirabilis_oxyfera_Twente_pmoB : IDGTTVNMEVHGQGRIGWLLWTFVGVFWLLWVRRPPT-RRLFQVGVV
Methylomirabilis_oxyfera_Ooij_pmoB : IDGTTVDMVHGQGRIGWLLWTFVGVWLLGWXXRPPT-RRLFQVGVV

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                                *          220          *          240          *
ABK77030_Cenarchaeum_symbiosum_A : -----
ABY89142_Nitrosopumilus_maritimus_SCM1 : -----
AAU92183_Methylococcus_capsulatus_Bath : RAD---ELVSATDRKVMGFLAATILIVVMAMSSANSKYPIITIPLOAGT
BAE86886_Methylomicrobium_japanense_NI : KAD---SLITPTDKKVGMAFAAGTMAIIVAIMGQANEKYPVTTPLQAGL
ACE95889_Methylomicrobium_album_BG8_pmoB2 : -----
CAE47801_Methylocystis_sp_SC2_pmoB1 : KVD---EQVTDDDKRIGAILVALTILATIVGYAVTNSTFPRTIPLQAGL
CAE48353_Methylocystis_sp_SC2_pmoB2 : KGR---ELIQDEKRIGAVTLAAVLLAVLVFYASANREFPRTPLMQAGL
BAF49661_Methylocaldum_sp_T_025 : RSGSCERADFGVTKKVMGFAAATILIVIFAMSSANSKYPIITIPLOAGT
AAF37894_Methylosinus_trichosporium_OB3b : KDE---EQIGDDDRRVGAIVLAVTILATIIGYAVTNSTFPRTIPLQAGL
ACE95887_Methylobacter_sp_BB5_1_pmoB2 : -----
ACE95892_Methylomonas_methanica_S1_pmoB2 : -----
CAJ01618_Methylocapsa_acidiphila_B2 : KGG---ELITPLERQIGAGALAAATLLVVIISYALTASEFPRTIPLQAGN
ABU88156_M_fumariolicum_SolV_pmoB1 : KED---ELVTKQDQKFGFLFLAIVIVLVFGGAFITSKQFPPIVPLQKTF
ABU88149_M_fumariolicum_SolV_pmoB2 : RKE---DLFSPMDRQVCFLLFTIGTIVLVAAMITKAQYPIITIPLOQETK
ABU88153_M_fumariolicum_SolV_pmoB3 : RKE---ELFNPDLRQVCFLLFTVGTIVIVAAAALITKAQYPIITIPLOQETK
ABA58954_Nitrosococcus_oceani_ATCC19707 : EAN---DLVTAQDKKLTIGVLVGVLLIILFGFKSAEDKFPVTTIPLQAGL
ABI60299_Nitrosomonas_eutropha_C91 : GDD---LLLDPMDDKKTIVWVLAALLTALIVWGGYRYTETKHPYTVPIQAGE
ABB74107_Nitrosospira_multiformis_25196 : GDE---LLLDPMDDKVAWVLLITFGIVWGGYRYTETKHPYTVPIQAGE
AAB86882_Nitrosospira_sp_NpAV_amoB1 : GDD---LLLDPMDDKVAWVLLIATFGIVWGGYRYTETKHPYTVPIQAGE
Methylomirabilis_oxyfera_Twente_pmoB : PEE---ELVSPGDRTLGLVLMIAATVLIIVAIYVVTNGAYPIITIPLOQTR
Methylomirabilis_oxyfera_Ooij_pmoB : PEE---ELVSSGDRTLGLVLMIAATVLIIVAIYVVTNGAYPIITIPLOQTR

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                                260          *          280          *          300
ABK77030_Cenarchaeum_symbiosum_A : -----
ABY89142_Nitrosopumilus_maritimus_SCM1 : -----
AAU92183_Methylococcus_capsulatus_Bath : MRGMKPLELPAP-----TVSVKVEDATYRVVPGRAMRMKLTITNHGNSPI
BAE86886_Methylomicrobium_japanense_NI : MRGIKSLELPQP-----TVSVKVVDSYRVVPGRAMQMTLEITNNGDSAV
ACE95889_Methylomicrobium_album_BG8_pmoB2 : -----
CAE47801_Methylocystis_sp_SC2_pmoB1 : QKPLTPLVTDGTAGVGKERVTSSELNGGVYKVPGRELTINVKVTNSTSEPL
CAE48353_Methylocystis_sp_SC2_pmoB2 : LTGISPIDEPR-----STVAVQFKGGSYTVVPGRELRI RAKVTNNGKEPI
BAF49661_Methylocaldum_sp_T_025 : LRGIQPIIEPK-----ATVAVKVNDASRVVPGRAMRMKLTITNNGDKPV
AAF37894_Methylosinus_trichosporium_OB3b : QKPLTPIIEBGTAGVGHVVTAEELKGGVYKVPGRELTIQVKVTNKTDDEPL
ACE95887_Methylobacter_sp_BB5_1_pmoB2 : -----
ACE95892_Methylomonas_methanica_S1_pmoB2 : -----
CAJ01618_Methylocapsa_acidiphila_B2 : IRAIDALNIPE-----SPIKVEYLRGTYKVPGRELVATYKITNTGKPEV
ABU88156_M_fumariolicum_SolV_pmoB1 : VRINPLPKEST-----FVEAKVSKATYVYVQQRSLDFDLITVTKGNEKV
ABU88149_M_fumariolicum_SolV_pmoB2 : YIIKPLPPEPA-----LIQAEVTDATYDVPGRITLSFHLQVKNIGDKPV
ABU88153_M_fumariolicum_SolV_pmoB3 : YIIKPLPPEPT-----LIQAEVTDATYDVPGRITLSFHLQVKNIGDKPV
ABA58954_Nitrosococcus_oceani_ATCC19707 : LGTIDSLPVDYN-----SMVSNVVKANYRVVPGRTISMTVEITNHTDQVI
ABI60299_Nitrosomonas_eutropha_C91 : SKVAPLVPAPN-----PVAIKITDANYDVPGRALRVSMVETNNGDTPV
ABB74107_Nitrosospira_multiformis_25196 : SKVEPLPVKPN-----PIAIKVTHANYDVPGRALRVSMVETNNGDTPV
AAB86882_Nitrosospira_sp_NpAV_amoB1 : SKVQPMVPKPN-----PIAIKVTHANYDVPGRALRVSMVETNNGDTPV
Methylomirabilis_oxyfera_Twente_pmoB : MDTPELKPTTEFTPYSHATVKARPVTAVYTVVPGRLGMVIEVTNGSNRPQ
Methylomirabilis_oxyfera_Ooij_pmoB : MDTPELKATTEFTPYAHATVKARPVTAVYTVVPGRLGMVIEVTNGSNRPQ

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*           320           *           340           *
ABK77030_Cenarchaeum_symbiosum_A : -----
ABY89142_Nitrosopumilus_maritimus_SCM1 : -----
AAU92183_Methylococcus_capsulatus_Bath : RLGEFYTASVRFLLSDVYKDTTGYPEDLLAEDGLSVSDNSPLAPGETRTV
BAE86886_Methylococcobium_japanense_NI : RLAEFNTASVRFLLDADVYEDDTNYPDDLLAEEGLSVSDNSPLAPGETRTV
ACE95887_Methylococcobium_album_BG8_pmB2 : -----
CAE47801_Methylocystis_sp_SC2_pmoB1 : RLGEYTAAGLRFLNPDVFTTKPDFDYLLADRGLS-TDPTPIAPGETKEI
CAE48353_Methylocystis_sp_SC2_pmoB2 : RLGEFTSAGLRFLNPDVFTTRPDPDYLLADRGLSVSDPNPIAPGETRDL
BAF49661_Methylocaldum_sp_T_025 : RLGEFYTASVRFLLDADVYKDTTGYPEDLLADDGLSEVSDNSPIQGETRTV
AAF37894_Methylosinus_trichosporium_OB3b : KLGEYTAAGLRFLNPDVFTTKPEFPDYLLADRGLS-TDPTPLAPGETKTI
ACE95887_Methylobacter_sp_BB5_1_pmoB2 : -----
ACE95892_Methylomonas_methanica_S1_pmoB2 : -----
CAJ01618_Methylocapsa_acidiphila_B2 : RVGEFATATLRFLLNPDVYTKVDYPEYILAERGLSLSDNAP IAPGETKEL
ABU88156_M_fumariolicum_SolV_pmoB1 : YLRRFQTANVAFLNPAAPDNQWPADSPVNGGELQITPNEPILPGETKQL
ABU88149_M_fumariolicum_SolV_pmoB2 : VLKEFLTANVRFLLNPDVPGNTWNNENNPEVNGGPMRVTPEP INPGETKTL
ABU88153_M_fumariolicum_SolV_pmoB3 : VLKEFLTANVRFLLNPDIPGNTWNPSPFPEVNGGPMKVSPEP INPGETKTI
ABA58954_Nitrosococcus_oceani_ATCC19707 : SIGEFNTGGIRFMNANVRVDETDYPELLAPEGLEVSQDD-IAPGETVVV
ABI60299_Nitrosomonas_eutropha_C91 : TFGFETTAGIRFVNSTGRKYLDQYPRLELVAVGLNFDDGAIQGETKQL
ABB74107_Nitrosospira_multiformis_25196 : RIGFETTAVGRFINKVGLKHLDRGYPKELVATGLSFDNETPIQGETREV
AAB86882_Nitrosospira_sp_NpAV_amoB1 : RIGFETTAVGRFINKVGLKHLDRNYPKELVATGLSFDNDAP IQGETREV
Methylomirabilis_oxifera_Twente_pmoB : QLGGFTTANLQFRDPALFPDSR-----LKKIKVEPAGPIPPGQVTVM
Methylomirabilis_oxifera_Ooij_pmoB : QLGGFTTANLQFRDPALFPDSR-----LKKIKVEPAGPIAPGQVTVL

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360           *           380           *           400
ABK77030_Cenarchaeum_symbiosum_A : -----
ABY89142_Nitrosopumilus_maritimus_SCM1 : -----
AAU92183_Methylococcus_capsulatus_Bath : DVTASDAAEVYRLSDI IYDPDSRFAGLLFFFDATGNRQVVQIDAPLIPS
BAE86886_Methylococcobium_japanense_NI : DVTASDAAEVYRLADLIYDPDSRFAGLLFFIDEDGNRQMTMVDAPLIPT
ACE95889_Methylococcobium_album_BG8_pmB2 : -----
CAE47801_Methylocystis_sp_SC2_pmoB1 : AVKQDARWDIERLSLAYDSDS QIGGLMFFSPTGRRFAAIEGGPVIPK
CAE48353_Methylocystis_sp_SC2_pmoB2 : EVIVQDARFDIERLSLAYDSDS QFGGLLFFS PSEGERQRAEIEGGPVIPK
BAF49661_Methylocaldum_sp_T_025 : EVTASDAAEVYRLSDI IYDPDSRFAGLLFFFDQGGQRIYVQIDAPLIPS
AAF37894_Methylosinus_trichosporium_OB3b : EVKQDARWDIERLSLAYDSDS QIGGLMFFS PSEGERQRAEIEGGPVIPK
ACE95887_Methylobacter_sp_BB5_1_pmoB2 : -----
ACE95892_Methylomonas_methanica_S1_pmoB2 : -----
CAJ01618_Methylocapsa_acidiphila_B2 : TVKQDARWDTERLADLAYDVSS FAGLMFFFTPSGARYEVETGGPVIPK
ABU88156_M_fumariolicum_SolV_pmoB1 : HIKAQGAWEVERLSTIYKESRRFGLLIPFGDTAGNRNIIAIDQFVVP
ABU88149_M_fumariolicum_SolV_pmoB2 : EVMSQSAEWEENQRLT-MYHETNRFGLLFFFTDTSGTQVFAIADQI VIP
ABU88153_M_fumariolicum_SolV_pmoB3 : EVMSQSAEWEENQRLT-MYNETNRFGLLFFFTDPSGTQVFAIADQI VIP
ABA58954_Nitrosococcus_oceani_ATCC19707 : DISATDAAEVYQRMADVIYDPDSRFAGLIFVDPVEGNEIPIPIGGPLVPT
ABI60299_Nitrosomonas_eutropha_C91 : RMEAKDALWEIQRLMALLGDPESRFGGLLMSWDSSEGRHINSIAGPVIPV
ABB74107_Nitrosospira_multiformis_25196 : KMEAKDALWEVQRLMALLGDPESRFGGLLMTWSDGDRNINSIAGAVIPV
AAB86882_Nitrosospira_sp_NpAV_amoB1 : KMVAKDALWEVQRLMALLGDPESRFGGLLMTWSDGDRNINSIAGAVIPV
Methylomirabilis_oxifera_Twente_pmoB : SIDATDAAEVYQRLAELIYDSRSRYGGLLEFFFDADKNRQIIVEVGGP-VIP
Methylomirabilis_oxifera_Ooij_pmoB : SVDATDAAEVYQRLAELIYDSRSRYGGLLEFFFDADKNRQIIVEVGGP-VIP

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## C

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*           20           *           40           *
ABK77035_Cenarchaeum_symbiosum_A : -MLMAQMPALIPKEVEIQRLKKIWMIMIAMGSAASVEVDNFVDSGLHQT
ABY89141_Nitrosopumilus_maritimus_SCM1 : MITMAQMPALIPKEVEIQRLKKIWLIVIAMGSTAASVEVDNFVDSGLHQT
AAU92181_Methylococcus_capsulatus_Bath : WMNPLYTEIVLEIVTASILWGYLWKT-RDR--NLAALTPREELRRNFT-H
BAE86884_Methylococcobium_japanense_NI : WMNPLYTEIVLEIVTASILWGYLWKS-RDR--KVMSTPREELRRHLLT-H
CAE47799_Methylocystis_sp_SC_pmoC1 : WMSILWTEIPLLEISGIGLAGFLWKT-RTR--DFSTLTAREEMRRLVV-E
CAE48351_Methylocystis_sp_SC2_pmoC2 : WMNLMWTELEPVEVAFVFCGIGGYLWKT-RDR--NIDAVAPREEMRRLIT-L
BAF49659_Methylocaldum_sp_T_025_pmoC : WMNPLYTEIVLEVVTSILWGYLWKT-RDR--NMAALAPREELRRNMT-H
AAF37893_Methylosinus_trichosporium_OB3b : WLSILWTEIPLLEVSGLALAGLWKT-RDR--NVDVAPREELRRHV-L
CAJ01616_Methylocapsa_acidiphila_pmoC : WMTILYIEEPTLEIAFLGLIGYLWKT-RPN--DLDTVAPREELRRIFY-L
ABU88150_M_fumariolicum_SolV_pmoC1 : WMSILYTELILEPTTLIALCSWLWVT-RDR--AMENLAPAEELRRYWN-L
ABU88151_M_fumariolicum_SolV_pmoC2 : WMNLLALELALAEALSFIACVTLWLVVT-RDR--NLENI SPVEELRRYWN-L
ABU88154_M_fumariolicum_SolV_pmoC3 : WMNLFWGITIMNVIWGLTWGWIWVYRDR--HLEQLNPGEEELKRWYSNW
ABA58956_Nitrosococcus_oceani_ATCC_19707 : WMNLLYIELVVEALATAALVSYLIKT-RDR--NMEAMTPREELRRYCT-L
ABI60301_Nitrosomonas_eutropha_C91 : WMGLWRVHMAIMPLFALVTVGWIWKT-RDTEEQLNNDPKLEIKRYFY-Y
ABB74105_Nitrosospira_multiformis_25196 : WMGLWRVHMIVMPLFALITWGIWKT-RDTEQQLDNLDPKLEVCRYFY-W
AAC69319_Nitrosospira_sp_NpAV_amoC1 : WMGLWRVHMIVMPLFALVTVGWIWKT-RDT--NLDNLDPKLEIKRYFY-W
Methylomirabilis_oxifera_Twente_pmoC2 : WMNMLIGELIEGAVLTFALGYIWKTRDR--NLDKIPPEELRRFWG-L
Methylomirabilis_oxifera_Twente_pmoC1 : WMNMLIGELIEGAVLTFALGYIWKTRDR--NLDKIPPEELRRFWG-L
Methylomirabilis_oxifera_Ooij_pmoC1 : WMNMLIGELIEGAVLVFTLGYIWKTRDR--NLDRI TPPEELRRFWG-L
Methylomirabilis_oxifera_Ooij_pmoC2 : WMNMLIGELIEGAVLVFTLGYIWKTRDR--NLDRI TPPEELRRFWG-L

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                                # # # *
ABK77035_Cenarchaeum_symbiosum_A : SIRDSAFTPAHWWLYSHFVALPLGWGSVAIYDR-----
ABY89141_Nitrosopumilus_maritimus_SCM1 : SIRDSAFTPAHWWLYSHFVALPLGWGSAAIYDR-----
AAU92181_Methylococcus_capsulatus_Bath : LVWLVAWAWAIYWGASYFTEQDGTWHQTVIRDTDFTPSHIIEFYLSYPIY
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CAE47799_Methylocystis_sp_SC_pmoC1 : VQWLVVYAAAIYWGASFFTEQDGTWHMTVIRDTDFTPSHIIEFYMSYPIY
CAE48351_Methylocystis_sp_SC2_pmoC2 : IGWLAVYAFSVYWGASYFTEQDGTWHQTVIRDTDFTPSHIIEFYLSYPIY
BAF49659_Methylocaldum_sp_T_025_pmoC : LIWLFAYAWAIYWGASYFTEQDGTWHQTVIRDTDFTPSHIIEFYLSYPIY
AAF37893_Methylosinus_trichosporium_OB3b : VEWLVVYAVAIYWGASFFTEQDGTWHMTVIRDTDFTPSHIIEFYMSYPIY
CAJ01616_Methylocapsa_acidiphila_pmoC : FNWIFVYGVAIYWGASYFTEQDGTWHQTVIRDTDFTPSHIIEFYMSYPIY
ABU88150_M_fumariolicum_SolV_pmoC1 : GLYLVVYTTLLYWGASYFTEQDGTWHQTVIRDTDFTPSHIIEFYQSYPIY
ABU88151_M_fumariolicum_SolV_pmoC2 : GLFIVVYTVGLYWGASYFTEQDGTWHQTVIRDTDFTPSHIIEFYQSYPIY
ABU88154_M_fumariolicum_SolV_pmoC3 : LITLGVYAWCLVW-AVFFVEQDGVWHSSMIRDETEPTPSHIFNFYLSWPIF
ABA58956_Nitrosococcus_oceani_ATCC_19707 : YMWVVYGVGLFWGASFFTEQDGAWHQTVVIRDTDFTPSHIIEFYMSYPIY
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ABB74105_Nitrosospora_multiformis_25196 : MMWLVYIFGVYWGGSFFTEQDASWHQVIIRDTSFTPSHVYVYFSGFPMY
AAC69319_Nitrosospora_sp_NpAV_amoC1 : MMWLVYIFGVYWGGSFFTEQDASWHQVIIRDTSFTPSHVYVYFSGFPMY
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Methylomirabilis_oxifera_Twente_pmoC1 : GQWIATPAWAVYWGASFFTEQDGTWHQTVIRDTDFTPSHIIEFYLSYPIY
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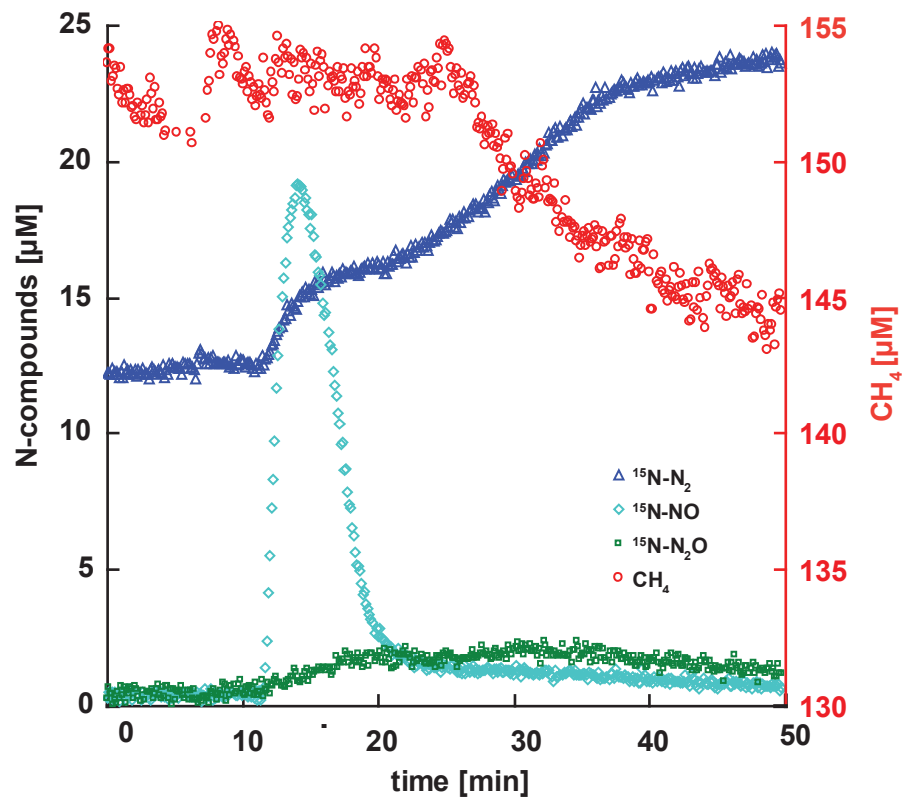
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AAU92181_Methylococcus_capsulatus_Bath : IITGFAAFIYAKTRLPFFAKGISLP---YLVLVVGGPFMILPNVGLNEWGH
BAE86884_Methylococcobium_japanense_NI : IITGGASFLYAKTRLPYQOGLS---LQYLVVVVGGPFMILPNVGLNEWGH
CAE47799_Methylocystis_sp_SC_pmoC1 : SVIAGVGFYAKTRLPYFAKGS-YS---VAYLIVAIQPFMILPNVGLNEWGH
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BAF49659_Methylocaldum_sp_T_025_pmoC : IITGGGAFLYAHTRLPYFQTTTKGLSLAYLILWTGPFMILPNVGLNEWGH
AAF37893_Methylosinus_trichosporium_OB3b : SIMAVGAFFYAKTRIPYFAHG-FS---LAFILVAIQPFMILPNVGLNEWGH
CAJ01616_Methylocapsa_acidiphila_pmoC : IITGGVGFYARTRLPTFGSKGS---VAYLIVVGGPFMILPNVGLNEWGH
ABU88150_M_fumariolicum_SolV_pmoC1 : IVAGVGSVMYAMTRLPQYAKAFSVP---YAVLVGSPMLIFPNVGLNEFQH
ABU88151_M_fumariolicum_SolV_pmoC2 : IILGVGSFMYAITRLPMFARFSIP---YAVLVGSPMLIFPNVGLNEFQH
ABU88154_M_fumariolicum_SolV_pmoC3 : INFVAGLMLTRTRLPVGMKWLPL---LVMEVAVMIFMILPILIGNEWGH
ABA58956_Nitrosococcus_oceani_ATCC_19707 : VMVGLGSFTYAKTRIPYFAKGSVP---YLMVLVGGPFMILPNVGLNEWGH
ABI60301_Nitrosomonas_eutropha_C91 : IIVGVATYLYAMTRLPYFHRGISFP---LVMAIAGPLMILPNVGLNEWGH
ABB74105_Nitrosospora_multiformis_25196 : IIVGSIASLYAMTRLPYSRGTSFP---LVMAIAGPLMILPNVGLNEWGH
AAC69319_Nitrosospora_sp_NpAV_amoC1 : IIVGVASLYAMTRLPYARGTSFP---LVMAIAGPLMILPNVGLNEWGH
Methylomirabilis_oxifera_Twente_pmoC2 : IIGISAYMWARTRLPLFSKAHSIP---FMLTVGGPAMIFVNVALNEWGH
Methylomirabilis_oxifera_Twente_pmoC1 : IIGISAYMWARTRLPLFSKAHSIP---FMLTVGGPAMIFVNVALNEWGH
Methylomirabilis_oxifera_Ooij_pmoC1 : IIGINAYMWARTRLPLFSKXXXXP---FMLTVGGPAMIFVNVALNEWGH
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ABY89141_Nitrosopumilus_maritimus_SCM1 : -FWFVEEIFAVPNHWMFNMGVVAFMGALAYVVRVYARLIELGAEPTGEN
AAU92181_Methylococcus_capsulatus_Bath : TFWFMEELFVAPLHYGFVIFGWLALA-VMGTLTQTFYFAQGGGLQSLCE
BAE86884_Methylococcobium_japanense_NI : TFWFMEELFVAPLHYGFVFFGWSALG-VLGVNIEBGLSKLLKDLA--
CAE47799_Methylocystis_sp_SC_pmoC1 : TFWFMEELFVAPLHWGFVFFRWMLG-VFGVVLQLLINIQRLIKGEGVAL
CAE48351_Methylocystis_sp_SC2_pmoC2 : TFWFMEELFTAPLHWGFVFFGWFALA-VFGVARQVLDLDRVIELSKYEKDA
BAF49659_Methylocaldum_sp_T_025_pmoC : TFWFMEELFVAPLHYGFVIFGWLALA-IMGVLLQIFASVSN-LMGKEICE
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CAJ01616_Methylocapsa_acidiphila_pmoC : TFWFMEELFVAPLHWMFVFFGWFMLS-VFGVSLQLLGRIKELCTGVEDVV
ABU88150_M_fumariolicum_SolV_pmoC1 : TFWFMEELFVAPLHWGFVFMFGWALA-ILGTVLQICPRILELIKQVYVYK
ABU88151_M_fumariolicum_SolV_pmoC2 : TFWFMEELFVAPLHWGFVAFGWFALA-IMGVWLQACPRVYELIKQVYVYK
ABU88154_M_fumariolicum_SolV_pmoC3 : SAWILEEWFAPLHWTVPFPAWAAVW-PLNGFDMFPRIAAVLKATYFGE
ABA58956_Nitrosococcus_oceani_ATCC_19707 : TFWFMEELFVAPLHWGFVFFAWFILA-VFGVFLQVQPRMKELIGRELQOS
ABI60301_Nitrosomonas_eutropha_C91 : TFWFMEELFVAPLHWGFVVLGWAGLF-QGGVAAQIITRYSNLTDVWVWNGQ
ABB74105_Nitrosospora_multiformis_25196 : AFWFMEELFVAPLHWGFVILGWSGLF-AGGIAAQIITRYSNLTDVWVWNGQ
AAC69319_Nitrosospora_sp_NpAV_amoC1 : TFWFMEELFVAPLHWGFVILGWSGLF-AGGIAAQIITRYSNLTDVWVWNGQ
Methylomirabilis_oxifera_Twente_pmoC2 : TFWFMEELFVAPLHWGFVTLGWCLFG-VYGVAAACMPRIFELIRITSGGK
Methylomirabilis_oxifera_Twente_pmoC1 : TFWFMEELFVAPLHWGFVTLGWCLFG-VYGVAAACMPRIFELIRITSGGK
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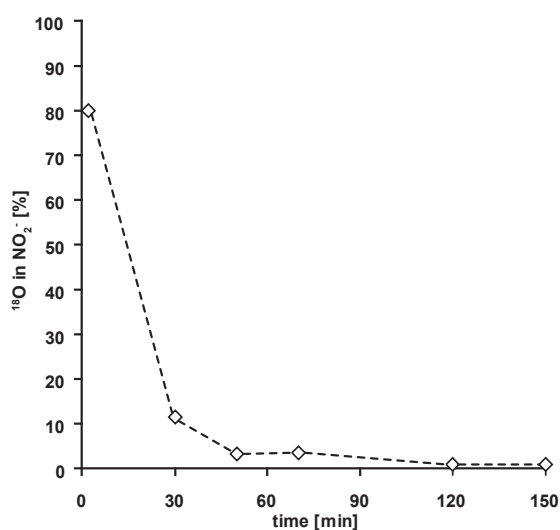
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**Supplementary Figure 4** | Alignments of representatives of partial (a) PmoA and AmoA, (b) PmoB and AmoB and (c) PmoC and AmoC sequences, including those from *M. oxyfera* enrichment cultures “Twente” and “Ooij”. Highly conserved positions in both PmoA and AmoA, as identified in ref. 45, are highlighted in yellow, with those positions that differ in *M. oxyfera* shown in red. Positions found to be conserved in the PmoA of all methane oxidisers and different in AmoA of ammonia oxidisers are highlighted in dark green, while those conserved in AmoA of all proteobacterial ammonia oxidisers and differing in PmoA are identified in dark blue. Also positions identified in ref. 44 as zinc ligands (#), mononuclear copper ligands (+) and dinuclear copper ligands (%) in *M. capsulatus* (Bath) pMMO are marked.

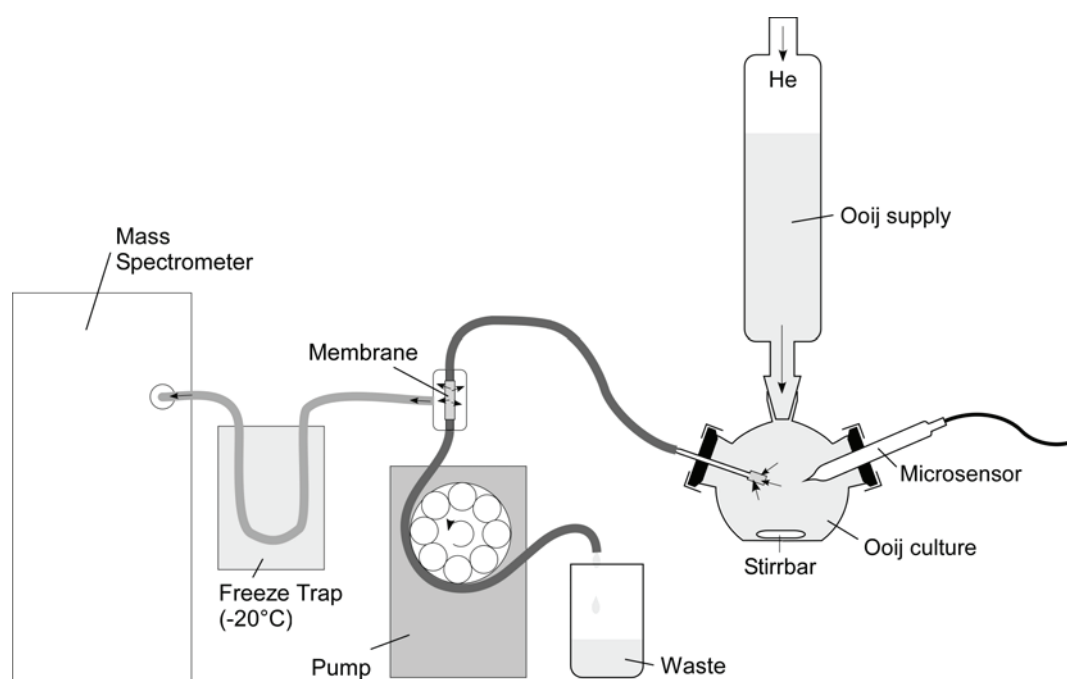




**Supplementary Figure 5** | Production of <sup>15</sup>N-labelled dinitrogen gas and consumption of methane after addition (t = 11 min) of <sup>15</sup>N-labelled nitric oxide (<sup>15</sup>NO). Like nitrite, nitric oxide apparently sustains methane oxidation. Experimental conditions are the same as for Figure 3. Red circles: CH<sub>4</sub>; turquoise diamonds: <sup>15</sup>NO; blue triangles: <sup>15,15</sup>N<sub>2</sub> and <sup>14,15</sup>N<sub>2</sub>; green squares: <sup>15,15</sup>N<sub>2</sub>O and <sup>14,15</sup>N<sub>2</sub>O.



**Supplementary Figure 6** | Oxygen-exchange between <sup>18</sup>O-nitrite and (unlabelled) water mediated by *M. oxyfera* enrichment culture “Ooij”. <sup>18</sup>O-labelled NO<sub>2</sub><sup>-</sup> was prepared according to ref. 50, and the labelling percentage was measured by GC-MS as described in the method section after conversion to N<sub>2</sub>O (ref. 51). Control incubations of <sup>18</sup>O-NO<sub>2</sub><sup>-</sup> in identical medium without biomass showed no measurable O-exchange over a period of 4 h.



**Supplementary Figure 7** | Schematic setup for the measurement of nitrogenous intermediates by microsensors and membrane-inlet mass spectrometry (see Figure 3 and Supplementary Figure 5).