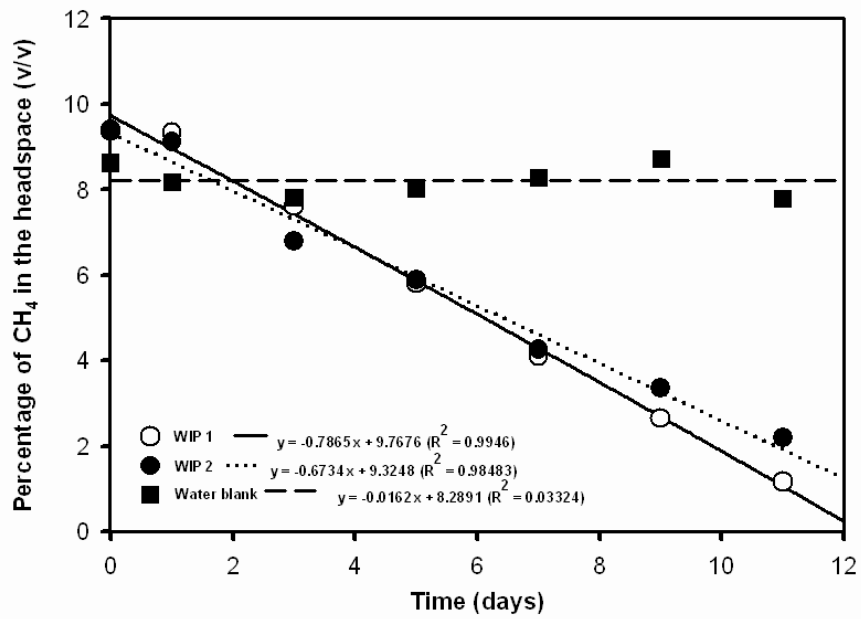


1 **Supplementary Figure 1** Representative methane oxidation time courses of replicate samples
2 from Pond B sampled in August, 2011, along with one control blank, with the results of linear
3 regressions.
4



5
6
7

1 **Supplementary Figure 2** (next page) Results of *pmoA*-microarray analysis of three samples
2 from oilsands tailings ponds A and B. Genes were amplified using primers 189f/661r (first 3
3 rows) or 189f/682r (next 3 rows). The colour gradient represents % of the maximum signal as
4 achieved by hybridising a pure target against the probe. For details of the probes see Stralis-
5 Pavese *et al.* (2011). The probe names listed as the column headers are described in detail in
6 Supplementary Table 5.

1 **Supplementary Table 1:** Chemical analysis of water from the surface 1-m depth of Ponds A and B
 2 based on measurements made on two dates (Pond A: July 22, 2010 and July 7, 2011; Pond B July
 3 22, 2010 and June 9, 2011). Data are means and standard errors of duplicates, or are based on a
 4 single sample where SE is not reported. Data were obtained using standard methods (Syncrude,
 5 1995).
 6

	Pond A		Pond B	
	Mean	SE	Mean	SE
pH (units)	8.0	0.0050	7.8	0.13
Conductivity ($\mu\text{S cm}^{-1}$)	3610	20.0	3120	80.2
Temperature ($^{\circ}\text{C}$)	20.0		21.9	1.10
Dissolved solids (%)	0.24	0.018	0.19	0.0033
Total solids content (%)	0.27		0.23	
Alkalinity (mg L^{-1})	1010	338	840	311
Chemical O_2 demand (mg L^{-1})	240		230	
Dissolved O_2 at 30-cm depth (mg L^{-1})	0.27		0.030	
O_2 penetration depth (cm) ($\leq 0.01 \text{ mg L}^{-1}$)	150		60	
Redox potential (mV)	54		148	
Sulphides (mg L^{-1})	0.012	0.012	0.090	0.020
Dissolved organic Carbon (mg C L^{-1})	40	1.0	46	2.0
o-Phosphate (mg P L^{-1})	0.015	0.0070	0.015	0.0045
Ammonia (mg N L^{-1})	7.8	2.0	17	6.9
Nitrate + Nitrite (mg N L^{-1})	0.015	0.0050	0.011	0.0010
Total Nitrogen (mg N L^{-1})	9.9	0.1	18	8.3
Total major ions (mg L^{-1}) ^a	2770	12.4	2290	27.2

7
 8 ^a Includes Na^+ , K^+ , Mg^{2+} , Ca^{2+} , F^- , Cl^- , Br^- , SO_4^{2-} , CO_3^{2-} , HCO_3^-
 9

10 Syncrude Canada Ltd. (1995). Syncrude analytical methods manual. 4th ed. Syncrude Canada
 11 Ltd., Edmonton, AB.
 12
 13
 14
 15

1 **Supplementary Table 2A-D** The top 25 OTUs of each sample site based on % of total reads in
 2 16S rRNA gene pyrotag sequencing analysis. OTUs were clustered based on 97% identity using
 3 QIIME. Where multiple samples were obtained from a site the averages equally represent each
 4 sample. The table is divided into 4 parts based on the sample sites: Table 2A represents the
 5 natural bitumen samples (n=2), Table 2B is Pond B (n=7); Table 2C is Pond A (n=7); and Table 2D
 6 is other tailings ponds (n=6)

7
 8
 9 **Supplementary Table 2A** Natural bitumen samples from Saline Creek (2 samples, Sept, 2009)
 10

Rank	% Reads	Phylum	Class	Order	Family	Genus
1	4.88	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Methylococcales</i>	<i>Crenotrichaceae</i>	<i>Crenothrix</i>
2	2.21	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Chromatiales</i>	<i>Ectothiorhodospiraceae</i>	
3	2.00	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Methylococcales</i>	<i>Crenotrichaceae</i>	<i>Crenothrix</i>
4	1.84	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Rhodocyclales</i>		
5	1.81	<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidimicrobiales</i>		
6	1.74	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Methylococcales</i>	<i>Methylococcaceae</i>	
7	1.69	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>			
8	1.50	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Chromatiales</i>		
9	1.29	<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Acidimicrobiales</i>	EB1017	
10	0.96	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Methylococcales</i>	<i>Methylococcaceae</i>	
11	0.95	<i>Chloroflexi</i>	SOGA31			
12	0.94	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Methylococcales</i>	<i>Crenotrichaceae</i>	<i>Crenothrix</i>
13	0.92	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodospirillales</i>	<i>Rhodospirillaceae</i>	
14	0.80	<i>Chloroflexi</i>	SOGA31			
15	0.67	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>		
16	0.56	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>		<i>Methylbium</i>
17	0.54	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Oxalobacteraceae</i>	
18	0.53	<i>Bacteroidetes</i>	<i>Sphingobacteria</i>	<i>Sphingobacteriales</i>	<i>Flexibacteraceae</i>	<i>Cytophaga</i>
19	0.51	<i>Bacteroidetes</i>	<i>Sphingobacteria</i>	<i>Sphingobacteriales</i>	<i>Flexibacteraceae</i>	<i>Cytophaga</i>
20	0.50	<i>Chloroflexi</i>	<i>Anaerolineae</i>	envOPS12		
21	0.47	<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomycetales</i>	<i>Microbacteriaceae</i>	
22	0.47	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Methylococcales</i>	<i>Crenotrichaceae</i>	<i>Crenothrix</i>
23	0.46	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Bradyrhizobiaceae</i>	<i>Bradyrhizobium</i>
24	0.46	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>		
25	0.46	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Rhodocyclales</i>	<i>Rhodocyclaceae</i>	<i>Methyloversatilis</i>

11
 12

1
2**Supplementary Table 2B** Tailings pond B (7 samples, 2010-2011)

Rank	% Reads	Phylum	Class	Order	Family	Genus
1	18.15	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	
2	16.37	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Rhodocyclales</i>	<i>Rhodocyclaceae</i>	
3	5.39	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	
4	3.52	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Alcaligenaceae</i>	
5	3.45	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonadales</i>	<i>Erythrobacteraceae</i>	<i>Erythromicrobium</i>
6	2.56	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Chromatiales</i>	<i>Chromatiaceae</i>	<i>Thiocapsa</i>
7	2.16	<i>Bacteroidetes</i>	<i>Flavobacteria</i>	<i>Flavobacteriales</i>	<i>Flavobacteriaceae</i>	<i>Flavobacterium</i>
8	1.56	<i>Bacteroidetes</i>	<i>Flavobacteria</i>	<i>Flavobacteriales</i>	<i>Flavobacteriaceae</i>	<i>Flavobacterium</i>
9	1.38	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodospirillales</i>	<i>Rhodospirillaceae</i>	
10	1.18	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	
11	1.02	<i>Tenericutes</i>	<i>Erysipelotrichi</i>	<i>Erysipelotrichales</i>	<i>Erysipelotrichaceae</i>	PSB-M-3
12	0.87	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Desulfuromonadales</i>	<i>Geobacteraceae</i>	<i>Geobacter</i>
13	0.84	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Rhodoferax</i>
14	0.82	<i>Firmicutes</i>	<i>Clostridia</i>	<i>Clostridiales</i>	FamilyXI. <i>Incertae Sedis</i>	
15	0.80	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodobacterales</i>	<i>Rhodobacteraceae</i>	<i>Rhodobacter</i>
16	0.74	<i>Acidobacteria</i>	<i>Chloracidobacteria</i>			
17	0.73	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Hydrogenophaga</i>
18	0.72	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Xanthobacteraceae</i>	<i>Xanthobacter</i>
19	0.68	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Acidovorax</i>
20	0.67	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pseudomonadales</i>	<i>Moraxellaceae</i>	<i>Acinetobacter</i>
21	0.60	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Xanthomonadales</i>	<i>Xanthomonadaceae</i>	<i>Ancylobacter</i>
22	0.56	<i>Bacteroidetes</i>	<i>Flavobacteria</i>	<i>Flavobacteriales</i>	<i>Flavobacteriaceae</i>	
23	0.52	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Rhodoferax</i>
24	0.52	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	
25	0.48	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	

3
4

1
2**Supplementary Table 2C** Tailings pond A (7 samples, 2010-2011)

Rank	% Reads	Phylum	Class	Order	Family	Genus
1	21.87	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	
2	3.56	<i>Acidobacteria</i>	<i>Chloracidobacteria</i>			
3	3.16	<i>Euryarchaeota</i>	<i>Methanomicrobia</i>	<i>Methanosarcinales</i>	<i>Methanosaetaceae</i>	<i>Methanosaeta</i>
4	2.53	<i>Bacteroidetes</i>	<i>Flavobacteria</i>	<i>Flavobacteriales</i>	<i>Flavobacteriaceae</i>	
5	2.24	<i>Bacteroidetes</i>	<i>Flavobacteria</i>	<i>Flavobacteriales</i>	<i>Flavobacteriaceae</i>	<i>Flavobacterium</i>
6	2.07	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodospirillales</i>	<i>Rhodospirillaceae</i>	
7	1.97	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	
8	1.85	<i>Euryarchaeota</i>	<i>Methanomicrobia</i>	<i>Methanosarcinales</i>	<i>Methanosaetaceae</i>	<i>Methanosaeta</i>
9	1.80	<i>Euryarchaeota</i>	<i>Methanomicrobia</i>	<i>Methanomicrobiales</i>		<i>Candidatus Methanoregula</i>
10	1.55	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Alcaligenaceae</i>	
11	1.49	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Methylococcales</i>	<i>Methylococcaceae</i>	<i>Methylocaldum</i>
12	1.40	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Hydrogenophaga</i>
13	1.24	<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomycetales</i>		
14	1.18	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Rhodocyclales</i>	<i>Rhodocyclaceae</i>	
15	1.13	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Burkholderiaceae</i>	
16	0.94	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Rhodocyclales</i>	<i>Rhodocyclaceae</i>	<i>Methyloversatilis</i>
17	0.84	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Methylophilales</i>	<i>Methylophilaceae</i>	
18	0.84	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Limnohabitans</i>
19	0.83	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Burkholderiaceae</i>	<i>Limnobacter</i>
20	0.73	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhizobiales</i>	<i>Xanthobacteraceae</i>	<i>Xanthobacter</i>
21	0.71	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Rhodoferax</i>
22	0.69	<i>Bacteroidetes</i>	<i>Flavobacteria</i>	<i>Flavobacteriales</i>	<i>Flavobacteriaceae</i>	<i>Flavobacterium</i>
23	0.65	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Pseudomonadales</i>	<i>Pseudomonadaceae</i>	<i>Pseudomonas</i>
24	0.54	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonadales</i>	<i>Sphingomonadaceae</i>	
25	0.52	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonadales</i>	<i>Erythrobacteraceae</i>	<i>Erythromicrobium</i>

3
4
5
6

1
2**Supplementary Table 2D** Various tailings ponds (6 samples from 2 ponds, Sept, 2009)

Rank	% Reads	Phylum	Class	Order	Family	Genus
1	11.89	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Rhodocyclales</i>	<i>Rhodocyclaceae</i>	<i>Thauera</i>
2	10.48	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Rhodocyclales</i>	<i>Rhodocyclaceae</i>	
3	7.96	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Chromatiales</i>	<i>Chromatiaceae</i>	<i>Thiocapsa</i>
4	3.79	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Desulfuromonadales</i>	<i>Geobacteraceae</i>	<i>Geobacter</i>
5	3.32	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	
6	2.39	<i>Actinobacteria</i>	<i>Actinobacteria</i>	<i>Actinomycetales</i>	ACK-M1	
7	2.01	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	<i>Limnohabitans</i>
8	1.69	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Rhodocyclales</i>	<i>Rhodocyclaceae</i>	<i>Thauera</i>
9	1.55	<i>Bacteroidetes</i>	<i>Flavobacteria</i>	<i>Flavobacteriales</i>	<i>Flavobacteriaceae</i>	<i>Flavobacterium</i>
10	0.98	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Sphingomonadales</i>	<i>Sphingomonadaceae</i>	
11	1.01	<i>Bacteroidetes</i>	<i>Flavobacteria</i>			
12	0.92	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Rhodocyclales</i>	<i>Rhodocyclaceae</i>	
13	0.85	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Alcaligenaceae</i>	
14	0.84	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Burkholderiaceae</i>	<i>Polynucleobacter</i>
15	0.83	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Desulfobacterales</i>	<i>Desulfobulbaceae</i>	<i>Desulfocapsa</i>
16	0.82	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Rhodocyclales</i>	<i>Rhodocyclaceae</i>	<i>Thauera</i>
17	0.7	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Desulfovibrionales</i>	<i>Desulfomicrobiaceae</i>	<i>Desulfomicrobium</i>
18	0.58	<i>Spirochaetes</i>	<i>Spirochaetes</i>	<i>Sphaerochaetales</i>	<i>Sphaerochaetaceae</i>	<i>Sphaerochaeta</i>
19	0.57	<i>Bacteroidetes</i>	<i>Bacteroidia</i>	<i>Bacteroidales</i>		
20	0.55	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>	<i>Comamonadaceae</i>	
21	0.57	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Rhodocyclales</i>	<i>Rhodocyclaceae</i>	<i>Thauera</i>
22	0.55	<i>Proteobacteria</i>	<i>Gammaproteobacteria</i>	<i>Aeromonadales</i>	<i>Aeromonadaceae</i>	<i>Aeromonas</i>
23	0.54	<i>Proteobacteria</i>	<i>Betaproteobacteria</i>	<i>Burkholderiales</i>		<i>Aquabacterium</i>
24	0.53	<i>Proteobacteria</i>	<i>Alphaproteobacteria</i>	<i>Rhodobacterales</i>	<i>Rhodobacteraceae</i>	
25	0.53	<i>Proteobacteria</i>	<i>Deltaproteobacteria</i>	<i>Desulfobacterales</i>	<i>Desulfobulbaceae</i>	<i>Desulfocapsa</i>

3
4

1 **Supplementary Table 3** Summary of the genera of methanotrophs (and the *Methylophilaceae*
2 family of methylotrophs) detected in the heavy fractions of 5 separate SIP incubations using the
3 surface waters of Ponds A and B. Two SIP experiments that were heavily grazed based on large
4 proportions of amoebae detected in the heavy fraction are not included.
5

	Mean	SE
<i>Methylocaldum</i>	17.4	1.93
<i>Methylomonas</i>	42.5	4.22
<i>Methylomicrobium</i>	2.37	0.625
<i>Methylobacter</i>	6.10	2.23
<i>Crenothrix/Methylosoma</i>	0.184	0.0178
<i>Methylophilaceae</i>	7.80	0.974

6
7

1 **Supplementary Table 4** 16S rRNA genes, and genes encoding key nitrogen metabolism and
2 methylotrophy functions detected in the ¹³CH₄-labeled SIP metagenome, and their top BLAST hits
3 (to a cultured organism) against the non-redundant database. The minimum aligned length was
4 200 nucleotides (for 16S rRNA) or 50 amino acids (for all protein-encoding genes).
5

Contig	Gene	BLAST top hit	Identity %	E-value	Length
16S rRNA genes					
ckmer87_3163	16S rRNA	<i>Methylocaldum tepidum</i> strain LK6	94	0.0	389
ckmer83_2241	16S rRNA	<i>Methylotenera mobilis</i> JLW8	96	0.0	728
ckmer87_1975	16S rRNA	<i>Methylomicrobium kenyense</i>	94	0.0	486
ckmer87_1181	16S rRNA	<i>Methylosarcina lacus</i> strain LW14	98	0.0	388
kmer83_2127001	16S rRNA	<i>Methylococcus mobilis</i>	99	0.0	341
ckmer79_3890	16S rRNA	<i>Methylovorus</i> sp. MP688	96	0.0	568
kmer79_2448064	16S rRNA	<i>Methylomonas</i> sp. LW16	97	0.0	386
Kmer63_4200339	16S rRNA	<i>Aquimonas voraii</i> strain GPTSA	96	4e-177	255
Kmer59_4688829	16S rRNA	<i>Porphyrobacter</i> sp. BZ35	100	e-135	247
kmer63_4172340	16S rRNA	<i>Methylomicrobium buryaticum</i> strain 7G	98	e-123	238
ckmer87_4706	16S rRNA	<i>Methylomonas fodinarum</i> strain JB13	89	9e-88	244
kmer87_1766037	16S rRNA	<i>Methylobacter</i> sp. LW12	98	e-108	214
kmer87_1822475	16S rRNA	<i>Methylomonas methanica</i>	99	0.0	541
ckmer87_2696	16S rRNA	<i>Pseudomonas putida</i> GB-1	90	e-165	342
ckmer79_1140	16S rRNA	<i>Pseudomonas argentinensis</i> strain PA01	92	0.0	786
Methylotrophy genes					
ckmer79_1733	<i>pmoA</i>	<i>Methylocaldum</i> sp. T-025	87	e-134	274
ckmer87_3841	<i>pmoA</i>	<i>Methylomicrobium album</i> BG8	97	e-143	250
ckmer63_2136	<i>pmoA</i>	<i>Methylomonas methanica</i> MC09	98	3e-45	89
kmer83_2092985	<i>pmoA</i>	<i>Methylosoma</i> sp. TFB	87	2e-50	86
kmer63_4256224	<i>pmoA</i>	<i>Methylomonas</i> sp. LW13	86	2e-067	144
kmer59_4724056	<i>pmoA</i>	<i>Methylomonas</i> sp. M5	96	1e-053	104
kmer59_4742331	<i>pmoA</i>	<i>Methylomonas methanica</i>	100	4e-62	113
kmer67_3724384	<i>pmoA</i>	<i>Methylocaldum</i> sp. T-025	91	1e-30	68
kmer59_4677095	<i>pmoA</i>	<i>Methylomonas methanica</i>	98	6e-42	77
ckmer79_1733	<i>pmoB</i>	<i>Methylocaldum</i> sp. T-025	87	e-134	247
ckmer87_3841	<i>pmoB</i>	<i>Methylomicrobium album</i> BG8	97	e-143	250
ckmer87_4803	<i>pmoB</i>	<i>Methylococcus capsulatus</i> str. Bath	86	2e-037	90
kmer83_2122116	<i>pmoB</i>	<i>Methylococcus capsulatus</i> str. Bath	84	1e-37	90
kmer87_1785776	<i>pmoB</i>	<i>Methylocaldum</i> sp. T-025	73	1e-32	94
kmer87_1785788	<i>pmoB</i>	<i>Methylocaldum</i> sp. T-025	72	9e-32	94
kmer87_1781460	<i>pmoB</i>	<i>Methylococcus capsulatus</i> str. Bath	72	1e-34	91
kmer87_1781266	<i>pmoB</i>	<i>Methylococcus capsulatus</i> str. Bath	71	4e-34	91
kmer83_2107215	<i>pmoB</i>	<i>Methylococcus capsulatus</i> str. Bath	68	1e-30	96
kmer59_4653614	<i>pmoB</i>	<i>Methylococcus capsulatus</i> str. Bath	88	4e-28	69
ckmer87_2237	<i>pmoB</i>	<i>Methylomicrobium alcaliphilum</i>	88	1e-26	68
ckmer75_2666	<i>pmoB</i>	<i>Methylomonas</i> sp. LW13	96	2e-56	107
ckmer87_1889	<i>pmoC</i>	<i>Methylococcus capsulatus</i> str. Bath	86	2e-95	160
ckmer83_77	<i>pmoC</i>	<i>Methylomicrobium album</i> BG8	97	1e-157	225
ckmer67_4696	<i>pmoC</i>	<i>Methylococcus capsulatus</i>	84	1e-56	96
ckmer87_3382	<i>pmoC</i>	<i>Methylococcus capsulatus</i>	89	2e-48	97
kmer67_3793325	<i>pmoC</i>	<i>Methylococcus capsulatus</i>	70	3e-24	81
kmer87_1772609	<i>pmoC</i>	<i>Methylomicrobium alcaliphilum</i>	98	8e-25	53
ckmer79_1733	<i>pmoC</i>	<i>Methylocaldum</i> sp. T-025	87	e-134	247
ckmer67_808	<i>pmoC</i>	<i>Methylococcus capsulatus</i> str. Bath	67	4e-13	52
ckmer872165	<i>glyA</i>	<i>Methylomicrobium alcaliphilum</i>	87	0.0	416
ckmer833613	<i>sga</i>	<i>Methylomicrobium alcaliphilum</i>	79	0.0	387
ckmer872620	<i>sga</i>	<i>Methylococcus capsulatus</i>	81	2e-111	187
ckmer87_199	<i>hpr</i>	<i>Methylomicrobium alcaliphilum</i>	75	0.0	323
kmer59_4774671	<i>hpr</i>	<i>Methylomicrobium alcaliphilum</i>	71	3e-91	191
ckmer87_1730	<i>mxal</i>	<i>Methylococcus capsulatus</i>	57	1e-75	240
ckmer87_1730	<i>mxac</i>	<i>Methylococcus capsulatus</i>	58	1e-079	275
ckmer87_1730	<i>mxar</i>	<i>Methylococcus capsulatus</i>	56	e-107	336
ckmer87_1730	<i>mxaj</i>	<i>Methylococcus capsulatus</i>	79	2e-059	137
ckmer87_1730	<i>mxaj</i>	<i>Methylobacter tundripaludum</i>	55	1e-82	257
ckmer87_1730	<i>mxaf</i>	<i>Methylococcus capsulatus</i>	87	0.0	573
ckmer87_781	<i>mxae</i>	<i>Methylobacillus flagellatus</i>	84	0.0	625
ckmer79_3087	<i>mxaf</i>	<i>Methylococcus capsulatus</i>	82	0.0	599
ckmer79_3087	<i>mxaj</i>	<i>Methylococcus capsulatus</i>	60	2e-084	247
ckmer87_384	<i>mxaj</i>	<i>Methylococcus capsulatus</i>	50	5e-075	261

ckmer87_384	<i>mxoE</i>	<i>Methylobacter tundripaludum</i>	93	0.0	455
ckmer87_478	<i>mxoA</i>	<i>Methylobacter sp.</i>	30	1e-28	286
ckmer87_1247	<i>mxoD</i>	<i>Methylococcus capsulatus</i>	61	8e-051	159
ckmer87_781	<i>xoxF</i>	<i>Methylobacillus flagellatus</i>	84	0.0	625
ckmer79_3087	<i>xoxF</i>	<i>Methylococcus capsulatus</i>	82	0.0	599
ckmer7930871	<i>xoxF</i>	<i>Methylococcus capsulatus</i>	82	0.0	619
ckmer877811	<i>xoxF</i>	<i>Methylovorus glucosetrophus</i>	86	0.0	625
ckmer872165	<i>mtaA</i>	<i>Methylomonas methanica</i>	86	0.0	325
ckmer793685	<i>mtaA</i>	<i>Methylococcus capsulatus</i>	65	5e-095	286
ckmer633897	<i>mtaA</i>	<i>Methylomonas methanica</i>	94	2e-048	101
kmer594735825	<i>mtaA</i>	<i>Methylobacter tundripaludum</i>	92	4e-28	66
ckmer833088	<i>mtaA</i>	<i>Methylomonas methanica</i>	86	0.0	325
ckmer871371	<i>mtaB</i>	<i>Methylococcus capsulatus</i>	80	3e-170	300
ckmer83569	<i>mtaB</i>	<i>Methylomicrobium alcaliphilum</i>	86	0.0	301
ckmer87_108	<i>mhc</i>	<i>Methylobacillus flagellatus</i>	87	e-144	325
ckmer87_2998	<i>hps</i>	<i>Methylomonas sp. 16a</i>	100	2e-148	214
ckmer87_189	<i>hps</i>	<i>Methylomicrobium album BG8</i>	95	5e-120	190
Nitrogen metabolism genes					
kmer59_4774971	<i>haoA</i>	<i>Methylomonas sp. 16A</i>	96	0.0	328
ckmer83_3946	<i>haoA</i>	<i>Methylomonas sp. 16A</i>	99	e-105	182
ckmer83_1928	<i>haoA</i>	<i>Methylomonas sp. 16A</i>	92	e-156	300
kmer59_4729129	<i>haoA</i>	<i>Methylomonas sp. 16A</i>	84	0.0	105
ckmer87_48	<i>norB</i>	<i>Methylobacter mobilis JLW8</i>	78	e-151	323
ckmer83_2227	<i>norB</i>	<i>Methylobacter mobilis JLW8</i>	72	0.0	233
ckmer87_148	<i>norB</i>	<i>Methylomicrobium album BG8</i>	90	0.0	345

- 1
- 2 *hao* hydroxylamine oxidoreductase
- 3 *nor* nitric oxide reductase
- 4 *pmo* particulate methane monooxygenase
- 5 *glyA* serine hydroxymethyltransferase
- 6 *sgaA* serine-glyoxylate aminotransferase
- 7 *hpr* hydroxypyruvate reductase
- 8 *mxo*, *xox* methanol dehydrogenase
- 9 *mtaA* bifunctional methylene-H4MPT/ methylene-H4F dehydrogenase
- 10 *mtaB* methylene-H4MPT dehydrogenase
- 11 *mch* methenyl-H4MPT cyclohydrolase
- 12 *hps* hexulose phosphate synthase
- 13

1 Supplementary Table 5: Probes used in the *pmoA*-microarray (listed in the the columns of
 2 Supplementary Figure 2), with intended specificities.

Order	Name	Intended specificity	Sequence 5' → 3'	L	GC%	T _m
1	MbA557	<i>Methylobacter</i>	CAATGGCATGATGTTCACTCTGGCT	25	48.0	61.5
2	MbA486	<i>Methylobacter</i>	AGCATGACATTGACAGCGGTTGTT	24	45.8	61.6
3	Mb460	<i>Methylobacter</i>	GACAGTTACAGCGTAATCGGTGG	24	54.2	60.9
4	Mb_LW12-211	<i>Methylobacter</i>	CGTCTTTGGGTTACTGTTGTGCC	23	52.2	60.0
5	Mb_SL#3-300	<i>Methylobacter</i>	GGCGCTGTTGTTTGTGTATTGGGT	24	50.0	62.2
6	Mb_SL299	soda lake <i>Methylobacter</i> isolates and clones	GGGGTGCAACTCTGTGTATCTTAGG	25	52.0	60.5
7	Mb_SL#1-418	soda lake <i>Methylobacter</i> isolates and clones	GCGATCGTATTAGACGTTATCCTGATG	27	44.4	58.6
8	MmbB284	<i>Mmb. Buryatense</i> - same region as <i>Jpn284</i> , but 3 MM vs. that one <i>Methylobacter</i> and Japanese strain related	ATCGCATCGCTTGGGGTGCAA	21	57.1	62.5
9	Jpn284	clone Jpn 07061	ACCGTATCGCATGGGGTG	18	61.1	58.0
10	BB51-302	<i>Methylobacter</i>	CGGTTGTTTGTGTCTTAGGTCTG	23	47.8	57.2
11	Mb267	<i>Methylobacter</i>	GCATGCTTGTGGTTCCGTTAC	21	52.4	58.1
12	Mb292	<i>Methylobacter</i>	CCGTTACCGTCTGCCTTTCCG	20	60.0	59.1
13	Mb282	<i>Methylobacter</i>	TTACCGTCTGCCTTTCCGGC	19	57.9	58.6
14	Mb_URC278	<i>Methylobacter</i>	GTTCCGTTACAGACTGCCTTTCCGG	24	54.2	61.3
15	511-436	<i>Methylobacter</i>	GTTTTGATGCTGTCTGGCAG	20	50.0	55.5
16	511-436L	<i>Methylobacter</i> 511 group	GUUUUGAUGCUGUCUGGCAGCA	22	50.0	60.0
17	LP10-424	<i>Methylobacter</i> LP 10 group	GTACTTGATTGTATCTTGATGCTGTGAC	28	39.3	55.7
18	LF1a-456	<i>Methylobacter</i> LF 1a group	CATGGTATTGACTGCTGTTATCGGTG	26	46.2	57.7
19	Mb_C11-403	<i>Methylobacter</i>	CAAACCTTCATGCCTGGTGCTATCGT	25	48.0	61.4
20	Mb380	<i>M. bacter</i> broad group A universal?	CAGTAAATTTCTGCTTCCCTTCAAATCT	28	35.7	55.8
21	Mb271	<i>Methylobacter</i>	TTGTGGTGGCGTTACCGT	18	55.6	58.0
22	S14m2-270	Marine type Ia cluster, S14m#2	CTTATGGTACCGTTACAGATTGCCTTA	27	40.7	56.4
23	S14m2-406	Marine type Ia cluster, S14m#2	TTAATTCCTGGTGCAATTGCACTTGAC	27	40.7	58.3
24	PS80-291	clone PS-80	ACCAATAGGCGCAACACTTAGT	22	45.5	58.3
25	MS1-440	Marine type Ia cluster, Marine sediment #1	TGATGTTGTCTGGTAGCTTCACATTAAC	28	39.3	57.1
26	Mm_pel467	<i>Methylomicrobium pelagicum</i>	ACTGCGGTAATCGATGGTTTGGC	23	52.2	61.6
27	Kuro18-205	Marine type Ia cluster, Kuro18	AGACGTTTGTGGGTGACAGTTGC	23	52.2	60.0
28	DS1-401	Deep sea cluster #1	GCGCGGTAGTTTGTGTTATGGCT	23	52.2	61.7
29	Mm531	<i>Methylomonas</i>	CTCCATTGCACGTGCCTGTAGA	22	54.5	60.7
30	Mm_M430	<i>Methylomonas</i>	TGGACGTGATTTTGTGTTGGGCAA	25	44.0	61.6
31	Mm_RS311	<i>Mm. methanica</i> , RS clade(10-286)	CTGTTGTTGCTCTGATGCTGGG	22	54.5	58.6
32	Mm_ES294	<i>Methylomonas</i>	CCAATCGGTGCAACAATTTCTGTAGT	26	42.3	59.8
33	Mm_ES543	<i>Methylomonas</i>	GTGCCAGTTGAGTATAACGGCATGA	25	48.0	60.9
34	Mm_ES546	<i>Methylomonas</i>	CCAGTTGAGTATAACGGCATGATGAT	26	42.3	58.7
35	Mm_MV421	<i>Methylomonas</i>	CTATCGTGCTGGATAACAATCCTGATGT	27	44.4	60.0
36	Mm451	<i>Methylomonas</i>	CTGATGTTGGGTAACAGCATGACT	24	45.8	58.8
37	Mm275	<i>Methylomonas</i>	GTGGTGGAGATACCGTTTGCC	21	57.1	59.2

38	Alp7-441	<i>Alpine soil Methylomonas, Alp#7 (10-282)</i>	GATGTTAGGTAACAGCATGACACTGAC	27	44.4	57.4
39	peat_1_3-287	<i>Methylomonas</i> -related peat clones	AACTGCCTTTAGGCGCTACC	20	55.0	58.6
40	Est514	<i>Methylochromium</i> -related clones	AATTGGCCTATGGTTGCGCC	20	55.0	59.9
41	Mmb259	<i>Methylochromium album</i> + Landfill <i>M. microbia</i>	CTGTTCAAGCAGTTGTGTGGTATCG	25	48.0	59.8
42	Mmb303	<i>Methylochromium album</i>	CAATGCTGGCTGTTCTGGGC	20	60.0	60.3
43	Mmb304	<i>Methylochromium album</i> + Landfill <i>M. microbia</i> and related	ATGCTGGCTGTTCTGGGCTTG	21	57.1	60.6
44	LW14-639	<i>Methylochromium LW14</i> group	AAAAGGUACUUGGAGAACCUUCGGU	25	44.0	60.0
45	Mmb_RS2-443	<i>Methylochromium, Mmb_RS2</i>	TGCTGGGCAACAGCATGCAGT	21	57.1	62.8
46	Mmb562	<i>Mmb. album</i> and <i>Methylosarcina</i>	ATGGTAATGACCCCTGGCTGACTTG	24	50.0	60.6
47	Mm229	<i>Deep-branching M. monas</i> (?) group (<i>WHmb3</i> related group)	CCAATCGTTGGAATCACTTTCCAGC	26	50	60.2
48	MsQ290	<i>M. sarcina quisquiliarum</i> related	TGCCATTCGGCGCTGTAATTTAGTA	26	46.2	60.8
49	MsQ295	<i>M. sarcina quisquiliarum</i>	CGGCGCGGTTCTTTCTGTACTG	22	59.1	60.6
50	LP20-644	<i>Methylochromium</i> -related clones	GTACACTGCGTACTTTGCGTAA	22	45.5	56.0
51	LP20-607	<i>LP20</i> group (Type Ia, deep branching- <i>Mmb</i> ?)	ACTGGTATGCCTGAATACATCCGTA	25	44	57.4
52	Ia193	Type Ia (<i>M. bacter-M. monas-M. microbium</i>)	GACTGGAAAGATAGACGTCTATGGG	25	48.0	57.8
53	Ia575	Type Ia (<i>M. bacter-M. monas-M. microbium-M. sarcina</i>)	TGGCTGACTTGCAAGGTTACCAC	23	52.2	61.3
54	Bsed516	<i>Marine sediment #2, Bsed</i>	AACTGGCCAATGGTTGCTCCA	21	52.4	59.9
55	SW11-375	<i>Marine sediment #2, SW#1</i>	TGCTGGCGCTATGGGTTGG	19	63.2	60.9
56	SW11-377	<i>Marine sediment #2, SW#1</i>	TGGCGCTATGGGTTGGGTT	20	60	62.1
57	Nc_oce426	<i>Nitrosococcus oceani</i>	CTTGGATGCCATGCTTGCGA	20	55.0	59.8
58	DS2-287	<i>Deep sea #2, subgroup (N. coccus and Deep sea Type Ia 10-298)</i>	GAATCCCATTTGGCGGACTTTGTG	25	52	61.0
59	AIMS1-442	<i>Deep sea #2, AIMS#1</i>	TTGTTGACAGGTAGCTATTTGGCAAC	26	42.3	57.7
60	DS2-220	<i>Deep sea #2, subgroup</i>	ACGGTGACTCCGATTGTGTGTAT	23	47.8	58.2
61	DS2-626	<i>Deep sea #2, subgroup</i>	ATTGCTGGTCTGCATCAGCCTG	22	54.5	60.2
62	USCG-225	Upland soil cluster Gamma	CTGACGCCGATCATGTGCAT	20	55.0	59.1
63	USCG-225b	Upland soil cluster Gamma	CTGACGCCGATCATGTGCATCA	22	54.5	61.2
64	JR2-409	JR cluster #2 (California upland grassland soil)	TTATTTCCCGCGCTATCATGATCG	24	50.0	60.5
65	JR2-468	JR cluster #2 (California upland grassland soil)	ACAGCCATAATTGGACCATTCTTCTG	26	42.3	59.2
66	JR3-505	JR cluster #3 (California upland grassland soil)	TGTATCTACCAATTGGCCTCATCTG	26	46.2	60.1
67	JR3-593	JR cluster #3 (California upland grassland soil)	CTATCAGTATGTGCGGACAGGC	22	54.5	58.6
68	501-375	<i>Methylococcus</i> - related marine and freshwater sediment clones	CTTCCCGGTGAACCTTCGTGTTCC	23	56.5	61.3
69	501-286	<i>Methylococcus</i> - related marine and freshwater sediment clones	GTCAGCCGTGGGGCGCCA	18	77.8	66.7
70	USCG-305	Upland soil cluster #3	CACGGTCTGCGTTCTGGC	18	66.7	59.5
71	Mc396	<i>Methylococcus</i>	CCCTGCCTCGCTGGTGCC	18	77.8	64.4
72	MclT272	<i>Methylocaldum tepidum</i>	GGCTTGGGAGCGGTTCCG	18	72.2	61.9
73	MclG281	<i>Methylocaldum gracile</i>	AAAGTTCCGCAACCCCTGGG	20	60.0	61.5
74	MclS402	<i>Methylocaldum szegediense</i>	GCGCTGTTGGTTCCGGGT	18	66.7	61.8

75	MclS394	<i>Methylocaldum</i> <i>szegeiensense</i> and related	TTCCCGGCGCTGTTGGTTCC	20	65	63.3
76	MclS400	<i>Methylocaldum</i> <i>szegeiensense</i> and related	CGGCGCTGTTGGTTCCGGGT	20	70	65.7
77	MclE302	<i>Methylocaldum</i> E10	CGCAACCATGGCCGTTCTG	19	63.2	60.3
78	Mcl404	<i>Mcl.tepidum</i> - <i>Mcl. Gracile</i> - <i>Mcl.Szeg</i> and related	TTTTGGTTCCGGGTGCGATTT	21	47.6	58.0
79	Mcl408	<i>Methylocaldum</i> fw-1 group: <i>M.coccus</i> - <i>M.caldum</i> related marine and freshwater sediment clones	GGTTCGGGTGCGATTTTG	19	57.9	57.8
80	fw1-286	fw-1 group: <i>M.coccus</i> - <i>M.caldum</i> related marine and freshwater sediment clones	ATCGTCAACCGTGGGGCG	18	66.7	61.1
81	fw1-639	fw-1 group: <i>M.coccus</i> - <i>M.caldum</i> related marine and freshwater sediment clones	GAAGGGCACGCTGCGTACG	19	68.4	62.0
82	fw1-641	fw-1 group: <i>M.coccus</i> - <i>M.caldum</i> related marine and freshwater sediment clones	AGGGCACGCTGCGTACGTT	19	63.2	63.3
83	JHTY1-267	<i>JH-TY#1</i>	TTGGTTGTGGGAAAACCTCCGT	22	45.5	57.4
84	JRC4-432	Japanese rice cluster #4	GACGTTGTCCTGGCTCTGAG	20	60.0	58.3
85	OSC220	Finnish organic soil clones and related	TCACCGTCGTACCTATCGTACTGG	24	54.2	60.8
86	OSC300	Finnish organic soil clones and related	GGCGCCACCGTATGTGTA CTG	21	61.9	61.4
87	JRC3-535	Japanese Rice Cluster #3	CGTTCACGTTCCGGTTGAG	20	60.0	59.3
88	LK580	fw-1 group + Lake Konstanz sediment cluster	CCGACATCATTGGCTACA ACTATGT	25	44.0	58.7
89	RSM1-419	<i>RSM#1</i>	CCATTCTGCTCGACGTGGTTCT	22	54.5	59.4
90	JHTY2-562	<i>JH-TY#2</i>	ATGCTGTTGTGCGATCGCCGACTTGC	25	56.0	63.6
91	JHTY2-578	<i>JH-TY#2</i>	CCGACTTGCAAGGCTACA ACTATGTC	26	50.0	59.5
92	JRC2-447	Japanese Rice Cluster #2	CTGAGCACCAGCTACCTGTTCA	22	54.5	60.2
93	LW21-374	LW21 group	CTACTTCCCGATCACCATGTGCT	23	52.2	60.2
94	LW21-391	LW21 group	TGTGCTTCCCTCGCAGATC	20	60.0	60.5
95	M90-574	<i>M.coccus</i> - <i>M.caldum</i> related marine and freshwater sediment clones	ATCGCCGACCTGCTGGGTTA	20	60.0	62.2
96	M90-253	<i>M.coccus</i> - <i>M.caldum</i> related marine and freshwater sediment clones	GCTGCTGTACAGGCGTTCCTG	21	61.9	61.7
97	Mth413	<i>Methylothermus</i>	CACATGGCGATCTTTTTAGACGTTG	25	44.0	58.3
98	Mha-500	<i>Methylohalobius</i> - <i>M.thermus</i> and related ?	TGATGTACCCGGGCAACTGGC	21	61.9	62.3
99	DS3-446	Deep sea cluster #3	AGCTGTCTGGCAGTTTCCTGTTCA	24	50.0	62.5
100	PmoC640	<i>PmoC</i>	AAGGGAACGCTTCGTACGTTTGG	23	52.2	59.8
101	PmoC308	<i>PmoC</i>	CCTGTGTGCTGGCGATTCTGCT	22	62.3	59.1
102	lb453	Type I b (<i>M.thermus</i> - <i>M.coccus</i> - <i>M.caldum</i> and related)	GGCAGCTACCTGTTCACCGC	20	65.0	61.7
103	lb559	Type I b (<i>M.thermus</i> - <i>M.coccus</i> - <i>M.caldum</i> and related)	GGCATGCTGATGTCGATTGCCG	22	59.1	62.5
104	McyB304	<i>M.cystis B</i> (<i>parvus/echinoides</i> /strain M)	CGTTTTCGCGGCTCTGGGC	19	68.4	62.7
105	Mcy255	<i>M.cystis B</i> (<i>parvus/echinoides</i> /strain M)	GGCGTCGCAGGCTTTCTGG	19	68.4	62.3
106	Mcy459	<i>Methylocystis</i>	GTGATCACGGCGATTGTTGGTTC	23	52.2	60.2
107	Mcy264	<i>Methylocystis</i>	CAGGCGTTCTGGTGGGTGAA	20	60.0	61.0
108	Mcy270	<i>Methylocystis</i>	TTCTGGTGGGTGAACTCCGTCT	23	52.2	61.8
109	Mcy413	<i>Methylocystis</i>	TTCCGGCGATCTGGCTTGACG	21	61.9	63.2
110	Mcy522	<i>Methylocystis</i> A + peat	GGCGATTGCGGCGTTCCA	18	66.7	62.3

clones						
111	Mcy233	<i>Methylocystis</i>	ATTCTCGGCGTGACCTTCTGC	21	57.1	60.9
112	McyM309	<i>M.cystis</i> strain M and related	GGTTCTGGGCTGATGATCGG	21	61.9	61.0
113	Peat264	peat clones	GGCGTTTTTCTGGGTCAACTTCC	23	52.2	60.3
114	MsS314	<i>Methylosinus sporium</i>	GGTTCTGGGTCTGCTCATCGG	21	61.9	60.8
115	MsS475	<i>Methylosinus sporium</i>	TGGTCGGCGCCCTGGGCT	18	77.8	68.3
116	Msi263	<i>Methylosinus sporium</i> + 1 <i>Msi.trichosporium</i> subcluster	GGCGTTCCTGTGGGAGAACTTC	22	59.1	61.2
117	Msi423	<i>Methylosinus</i>	CTGTGGCTGGACATCATCCTGC	22	59.1	61.4
118	MsT214	<i>Methylosinus trichosporium</i> OB3b and rel.	TGGCCGACCGTGGTTCCG	18	72.2	63.5
119	Msi520	<i>Methylosinus trichosporium</i>	GCGATCGCGGCTCTGCA	17	70.6	61.6
120	Msi269	<i>Methylosinus trichosporium</i>	TCTTCTGGGAGAACTTCAAGCTGC	24	50.0	60.6
121	Msi294	<i>Methylosinus</i>	GTTCGGCGCGACCTTCGC	18	72.2	62.5
122	ARC2-518	Deep branching type II clade ARC2 - <i>Methylosinus</i> <i>trichosporium</i> 15-084 group?	GGCCGGCGATTGGTCAGTATCA	22	59.1	61.7
123	Msi232	<i>M.sinus</i> + most <i>M.cystis</i> - considered as additional type II probe	ATCCTGGGCGTGACCTTCGC	20	65.0	63.3
124	II509	Type II	CGAACAACTGGCCGGCGAT	19	63.2	61.7
125	II630	Type II	CATGGTCGAGCGCGGCAC	18	72.2	62.4
126	Alp8-468	Type II novel <i>pmoA</i> , Alpine cluster Alp#8	CGCGCTCCTTGGCTCGTTGG	20	70.0	64.0
127	xb6-539	Novel <i>pmoA</i> copy of type II and related environmental clones	AGGCCGCCGAGGTCGAC	17	76.5	63.0
128	LP21-190	Novel <i>pmoA</i> copy of type II and related environmental clones	ATCGACTTCAAGGATCGCCG	20	55.0	58.2
129	LP21-260	Novel <i>pmoA</i> copy of type II and related environmental clones	CGCAGTCCTTCTTCTGGACG	20	60.0	58.6
130	NMcy1-247	Novel <i>pmoA</i> copy of <i>M.cystis</i> #1 (?)	TCGACATCGTGCTGATGATCTCGG	24	54.2	62.1
131	NMsi1-469	Novel <i>pmoA</i> copy of <i>M.sinus</i>	GCGCTGGTCGGCTCCATGG	19	73.7	64.3
132	NMcy2-262	Novel <i>pmoA</i> copy of <i>M.cystis</i> #2 (?)	CAGTCCTTCTTCTGGCAGAAGTTCC	25	52.0	60.9
133	LP21-436	<i>Mcy</i> + <i>Msi</i> novel <i>pmoA</i> #1 groups	GTGCTGATGATGTCGGGCAGCTGGC	25	64.0	66.1
134	NMsiT-271	Novel <i>pmoA</i> copy of <i>M.sinus trichosporium</i> (?)	AGCGCTTCCGTCTGCCGAT	19	63.2	62.9
135	LP21-232	Novel <i>pmoA</i> copy of type II and related environmental clones	ATCGTCGCCATGTGCTTCGC	20	60.0	61.9
136	RA14-299	RA14 related clones	GCGCGACGTTCTTTGTGTC	20	60.0	59.5
137	RA14-594	RA14 related clones	CCACAACGTTCTGACCTCGA	20	55.0	57.9
138	RA14-591	RA14 related clones	GGCTTCCACAACGTTCTGACCT	22	54.5	60.9
139	Wsh1-566	Watershed + flodded upland cluster 1	GCTCATGAGCTTGGCCGACATC	22	59.1	61.8
140	Wsh2-491	Watershed + flodded upland cluster 2	TCATTTGGCCAACCTCTCTCATTCC	25	48.0	60.9
141	Wsh2-450	Watershed + flodded upland cluster 2	CAAGAGCTGGATCATCACGATG	22	50.0	56.8
142	B2rel251	<i>Methylocapsa</i> -related clones	CCGCCGCGGCCAGTATTA	19	68.4	63.4
143	B2-400	<i>Methylocapsa</i>	ACCTCTTTGGTCCCGGCTGC	20	65.0	63.4
144	B2-261	<i>Methylocapsa</i>	TCAGGCCTATTTCTGGGAAAGCT	23	47.8	58.3
145	B2all343	<i>Methylocapsa</i> and related clones	AACCGCTACACCAATTTCTGGGG	23	52.2	61.2
146	B2all341	<i>Methylocapsa</i> and related	TCAACCGCTACACCAATTTCTGGG	24	50.0	61.1

clones						
147	pmoAMO3-400	clone pmoA-MO3	ACCCAGATGATCCCGTCGGC	20	65.0	62.6
148	pmoAMO3-486	MO3 group	ggGATGGGGCCTTCTCATGTACC	23	60.9	61.5
149	pmoAMO3-511	MO3 group	AGCAACTGGCAGGTCTCTCG	19	63.2	60.2
150	Ver330	<i>Verrucomicrobia</i> , all pmoA1+pmoA2	TGGTCAGTGGATGAATAGGTATTGGA	26	42.3	57.3
151	Ver307	<i>Verrucomicrobia</i> , all pmoA2	TTCAGCTGTGCCGGATTGTTTT	22	45.5	57.9
152	Ver285	<i>Verrucomicrobia</i> , <i>Ma.fum</i> pmoA2+ <i>Ma.kam.</i> pmoA2	TAAAGCGCCTATAGGAGCAACCT	23	47.8	58.0
153	Ma_F1-355	<i>Ma.fum.</i> pmoA1	AACTTCTGGGGTTGGGGCACTT	22	54.5	61.5
154	Ma_F1-594	<i>Ma.fum.</i> pmoA1	TGAATACATCCGGACTTCTACCCC	24	50.0	57.9
155	Ma_I1-312	<i>Ma.inf.</i> pmoA1	AACCGTTGGGCTTTTCTTTGGC	22	50.0	59.1
156	Ma_I1-401	<i>Ma.inf.</i> pmoA1	AAACATTAATCCCCAGGCTGTCTGT	25	44.0	58.9
157	Ma_F3-638	<i>Ma.fum.</i> pmoA3	AAAGTGGGACTCTTCGGACCTT	22	50.0	58.1
158	Ma_F3-542	<i>Ma.fum.</i> pmoA3	AACCCTTAGAAGCCTTAGGCCA	22	50.0	58.1
159	ESR-579	ESR (Eastern Snake River) cluster	GACCTGATCGGATTCGAGAACATC	24	50.0	58.5
160	M84P22-514	environmental clones of uncertain identity	AACTGGGCCTGGCTGGG	17	70.6	61.0
161	TUSC409	Tropical Upland Soil Cluster #2	CGATCCCGGGCGCGATTC	18	72.2	61.8
162	TUSC502	Tropical Upland Soil Cluster #2	TCTTCTACTTCGGCAACTGGC	21	52.4	58.3
163	mtrof173	Universal	GGbGACTGGGACTTCTGG	18	66.7	57.4
164	mtrof362-l	Methanotrophs	TGGGGCTGGACCTACTTCC	19	63.2	59.5
165	mtrof661	Methanotrophs	GGTAARGACGTTGCKCCGG	19	63.2	60.4
166	mtrof662-l	Methanotrophs	GGTAAGGACGTTGCGCCGG	19	68.4	61.9
167	mtrof656	Methanotrophs	ACCTTCGGTAAGGACGT	17	52.9	53.2
168	NmNc533	<i>Nitrosomonas-Nitrosococcus</i>	CAACCCATTTGCCAATCGTTGTAG	24	45.8	58.6
169	Nsm_eut381	<i>Nitrosomonas eutropha</i>	CCACTCAATTTTGTAAACCCAGGTAT	26	42.3	59.0
170	PS5-226	<i>Nitrosococcus</i> related clones	ACCCCGATTGTTGGGATGATGTA	23	47.8	59.9
171	PI6-306	<i>Nitrosomonas-Nitrosococcus</i> related clones	GGCACTCTGTATCGTATGCCTGTTAG	26	50.0	60.5
172	NsNv207	<i>Nitrosospira-Nitrosovibrio</i>	TCAATGGTGGCCGGTGG	17	64.7	58.5
173	NsNv363	<i>Nitrosospira-Nitrosovibrio</i>	TACTGGTGGTCGCACTACCC	20	60.0	59.6
174	SV308	Svalbard clade	TGAGCATCTCTGGGCTTGTCGT	22	54.5	60.7
175	SVrel583	Svalbard clade and related	TACATGGGATTCACATTTGTGAGGAC	26	42.3	57.0
176	Nit_rel471	AOB related clones/probably methanotrophs	CGTTCGCGATGATGTTTGGTCC	22	54.5	60.1
177	Sed585	Ssed#1	GGGCATTTCGCGATGATGTTTTATCCGA	27	48.1	61.2
178	Sed422	Ssed#1 and related	TGATCCTAGACTGCACCCTGTTG	23	52.2	58.5
179	Nit_rel223	AOB related clones/probably methanotrophs	GTCACACCGATCGTAGAGGT	20	55.0	56.9
180	Nit_rel417	Arctic soil related #1, subgroup	CGCGTTGATCTTTGATTGCACCCTGTT	27	48.1	61.8
181	Nit_rel419	Arctic soil related #1, subgroup	CGTTGATCCTTGATTGCACCCTGTT	25	48.0	59.8
182	Nit_rel526	JRC#1+CCd#1 groups	GCCATCAACCATTGGTTGCGGA	22	54.5	60.8
183	Nit_rel652	Arctic soil MOB	CGTACATTCGGTGGTCCACTG	22	54.5	57.9
184	ARC529	AOB related clones/probably methanotrophs	TAAGCAGCCGATGGTCGTGGAT	22	54.5	62.2
185	Nit_rel470	AOB related	CGATATTCGGGGTATGGGCG	20	60.0	58.4

		clones/probably methanotrophs AOB related				
186	Nit_rel351	clones/probably methanotrophs	GTTTGCCTGGTACTGGTGGG	20	60.0	59.2
187	gp17-438	<i>environmental clones of uncertain identity - gp17</i> AOB related	ACTCTTATTGACCAGGAATTGGACCTTG	28	42.9	58.5
188	Nit_rel304	clones/probably methanotrophs - <i>Crenothrix</i> and related	CGCTCTGCATTCTGGCGCT	19	63.2	61.8
189	NLw303	environmental clones of uncertain identity - NL wetland	AACGATCACTATTCTGGCTCTTGCCTTT	28	42.9	60.1
190	M84P105- 451	environmental clones of uncertain identity	AACAGCCTGACTGTCCACCAG	20	55.0	58.1
191	WC306_54- 385	environmental clones of uncertain identity	AACGAAGTACTGCCGGCAAC	20	55.0	59.2
192	WC306-54- 516	environmental clones of uncertain identity	AACTGGCCGATTTTTGGCATGTT	23	43.5	58.4
193	gp23-454	environmental clones of uncertain identity	AACGCGCTGCTCACTGCG	18	66.7	62.3
194	MR1-348	environmental clones of uncertain identity	AATCTTCGGTTGGCACGGCT	20	55.0	61.1
195	gp619	environmental clones of uncertain identity	CGGAATATCTGCGCATCATCGAGC	24	54.2	61.5
196	gp391	environmental clones of uncertain identity	ATCTGGCCGGCGACCATG	18	66.7	61.1
197	gp2-581	environmental clones of uncertain identity	ACATGATCGGCTACGTGTATCCG	23	52.2	60.0
198	RA21-466	clone RA21 - environmental clone of uncertain identity	CGGCGTTCTTGGCGGCAT	18	66.7	62.4