Table S1: Domain based (meta)genome comparison of selected metagenomes of methanotrophs and genomes of selected methanogens*

	Interpro ID	ANME-1-s	ANME-1-m	ANME-2a	ANME-2d-h	ANME-2d-a	AM	A	M-1	M-2	M-3	H-1	H-2	H-3	H-4	S
Dissimilatory sulfate reduction																
Sulphate adenylyltransferase, small subunit	IPR011784	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0
Sulphate adenylyltransferase, large subunit (Sat)	IPR011779	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0
Sulphate adenylyltransferase catalytic domain (Sat)	IPR024951	1	0	0	1	1	0	0	0	0	1	0	0	0	0	1
Sulphate adenylyltransferase (Sat)	IPR002650	0	0	0	1	1	0	0	0	0	1	0	0	0	0	1
Phosphoadenosine phosphosulphate/adenosine 5'-phosphosulphate reductase	IPR004511	0	0	0	1	1	0	0	0	1	1	0	0	0	0	0
Adenosine 5'-phosphosulphate reductase	IPR011798	0	0	0	1	1	0	0	0	1	1	0	0	0	0	0
Phosphoadenosine phosphosulphate reductase	IPR002500	4	1	2	4	3	2	1	2	4	3	2	0	4	3	0
Phosphoadenosine phosphosulphate/adenosine 5'-phosphosulphate reductase	IPR004511	0	0	0	1	1	0	0	0	1	1	0	0	0	0	0
Adenylylsulphate reductase, alpha subunit (Apr)	IPR011803	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Adenylylsulphate reductase, beta subunit (Apr)	IPR011802	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Adenylylsulphate reductase, beta subunit, C-terminal (Apr)	IPR022738	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Sulphite reductase, dissimilatory-type alpha subunit (Dsr)	IPR011806	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Sulphite reductase, dissimilatory-type beta subunit (Dsr)	IPR011808	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Dissimilatory sulphite reductase D	IPR014793	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Sulphur relay, DsrE/F-like protein	IPR003787	4	1	3	8	9	4	2	0	1	0	0	3	3	3	3
Assimilatory sulfate reduction																
SLC26A/SulP transporter	IPR001902	0	1	0	0	0	0	0	0	0	0	0	1	1	0	0
ATP-sulfurylase PUA-like domain	IPR025980	0	0	0	1	1	0	0	0	0	1	0	0	0	0	1
PUA-like domain	IPR015947	30	12	12	14	13	15	11	16	20	13	13	10	13	11	15
Adenosine specific kinase	IPR007153	9	6	0	3	3	0	3	0	0	0	0	3	0	3	3
Adenylyl-sulfate kinase	IPR002891	8	1	0	1	1	0	1	0	0	0	0	0	0	2	2
Sodium/sulphate symporter, conserved site	IPR031312	0	0	1	1	2	0	1	0	0	0	1	0	0	0	0
Sodium/sulphate symporter	IPR001898	11	0	2	2	5	0	0	0	0	0	2	4	0	0	0
Nitrite/sulphite reductase iron-sulphur/sirohaem-binding site	IPR006066	9	3	5	1	8	12	5	11	6	11	5	5	0	8	1
Nitrite/sulphite reductase 4Fe-4S domain	IPR006067	7	1	3	3	4	4	2	4	2	4	2	2	0	4	3
Nitrite/Sulfite reductase ferredoxin-like domain	IPR005117	16	3	7	8	10	9	4	10	4	8	5	4	0	7	9
Thiosulphate sulfurtransferase, conserved site	IPR001307	3	3	0	1	1	0	1	0	0	2	0	1	0	0	0

Table S1 (continued): Domain based (meta)genome comparison of selected metagenomes of methanotrophs and genomes of selected methanogens*

	Interpro ID	ANME-1-s	ANME-1-m	ANME-2a	ANME-2d-h	ANME-2d-a	AM	A	M-1	M-2	M-3	H-1	H-2	H-3	H-4	S
Heme-copper oxidase subunit II																
Multicopper oxidase, type 1	IPR001117	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0
Multicopper oxidase, type 2	IPR011706	0	0	0	2	3	0	0	0	0	0	0	0	0	0	0
Multicopper oxidase, type 3	IPR011707	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0
Multicopper oxidase, copper-binding site	IPR002355	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0
Multicopper oxidases, conserved site	IPR033138	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
Copper centre Cu(A), identified in cytochrome c oxidase and nitrous oxide reductase	IPR001505	0	0	0	2	2	0	0	0	0	0	0	0	0	0	2
EfeO-type cupredoxin-like domain, iron uptake system	IPR028096	0	0	0	6	7	5	0	0	0	1	0	0	0	2	1
Multi-domain cupredoxins, periplasmic domain of cytochrome c oxidase subunit II	IPR008972	2	2	6	43	45	18	0	2	6	8	0	2	2	6	4
Nitrate reduction																
Flavoprotein pyridine nucleotide cytochrome reductase	IPR001709	0	0	0	10	0	0	0	0	4	0	0	0	0	0	0
Rieske iron-sulphur protein, C-terminal	IPR005805	0	0	0	6	6	3	0	0	0	0	0	0	0	0	0
Rieske [2Fe-2S] iron-sulphur domain	IPR017941	3	0	0	13	6	6	0	3	12	0	0	3	0	0	0
Cytochrome c nitrite reductase, small subunit (NrfH)	IPR017571	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0
NapC/NirT cytochrome c, N-terminal	IPR005126	0	1	0	3	3	0	0	0	0	0	0	0	0	0	0
Cytochrome c552 (NrfA)	IPR003321	0	0	0	3	3	0	0	1	1	0	0	0	0	0	0
Cytochrome cd1-nitrite reductase-like, haem d1 domain	IPR011048	2	1	0	2	0	2	0	1	0	0	0	0	1	0	0
DMSO/Nitrate reductase chaperone, NarJ	IPR020945	6	3	0	9	9	0	0	0	0	0	0	0	0	0	6
NarG-like domain	IPR023234	6	0	2	5	7	3	2	2	3	2	0	0	0	0	12
Periplasmic nitrate reductase NapB subunit, heme binding domain	IPR027406	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0
Respiratory nitrate reductase beta, C-terminal	IPR029263	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
Nitrate reductase chaperone, NarJ	IPR003765	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Nitrate reductase, gamma subunit	IPR003816	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Nitrate reductase, alpha subunit	IPR006468	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Nitrate reductase, beta subunit	IPR006547	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
DMSO/Nitrate reductase chaperone	IPR020945	6	3	0	9	9	0	0	0	0	0	0	0	0	0	6
Nitrite reductase [NAD(P)H] small subunit, NirD	IPR012748	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CbbQ/NirQ/NorQ, C-terminal	IPR013615	2	2	0	0	0	0	0	0	1	1	0	0	0	0	0
Cytochrome c-552/DMSO reductase-like, haem-binding domain	IPR019020	0	0	0	4	6	0	0	0	0	0	0	0	0	0	0
Copper centre Cu(A), has been identified in cytochrome c oxidase and nitrous oxide reductase	IPR001505	0	0	0	2	2	0	0	0	0	0	0	0	0	0	2
Cytochrome c-552/4, tetra-heme cytochrome	IPR023155	11	2	17	22	20	2	0	6	3	16	0	0	0	0	3
Heme b synthase (heme D1)	IPR030896	0	0	1	1	1		0	1	1	1	0	0	0	0	0
Siroheme synthase, central domain (for nitrite reductase)	IPR028281	0	0	1	0	1	0	0	0	1	0	0	0	0	1	0
Sirohaem synthase, N-terminal (for nitrite reductase)	IPR006367	9	0	2	2	2	2	2	3	2	2	2	2	2	2	2
12,18-didecarboxysiroheme deacetylase	IPR030894	1	0	1	1	1	1	0	0	1	1	0	0	0	0	0

Table S1 (continued): Domain based (meta)genome comparison of selected metagenomes of methanotrophs and genomes of selected methanogens*

	Interpro ID	ANME-1-s	ANME-1-m	ANME-2a	ANME-2d-h	ANME-2d-a	AM	A	M-1	M-2	M-3	H-1	H-2	H-3	H-4	S
NADH:cytochrome b5 reductase (CBR)	IPR001834	0	0	4	12	0	4	0	4	4	4	0	0	0	0	0
Cytochrome b5-like heme/steroid binding domain	IPR001199	3	0	0	6	0	3	0	3	3	3	0	0	0	0	0
Cytochrome b/b6, C-terminal	IPR005798	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0
Cytochrome b/b6-like domain	IPR027387	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0
Cytochrome b/b6, N-terminal	IPR005797	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0

* Domain abundance in every (meta)genome is indicated by numbers which are darkened according to abundance. S-AOM performing ANME include ANME-1-s [1], ANME-1-m [2], and ANME-2a [3]. N-AOM performing ANME include ANME-2d-h [4] and ANME-2d-a [5]. The acetoclastic (A) and methylotrophic (M) methanogens include *Methanosarcina acetivorans* C2A (AM), *Methanosaeta concilii* GP6 (A), *Methanococcoides burtonii* DSM6242 (M-1), *Methanolobus tindarius* DSM2278 (M-2), and *Methanohalophilus mahii* DSM5219 (M-3). Hydrogenotrophic methanogens (H) include *Methanospirillum hungatei* JF-1 (H-1), *Methanobacterium formicicum* DSM3637 (H-2), *Methanococcus maripaludis* C5 (H-3), and *Methanoregula formicica* SMSP (H-4). The sulfate-reducing archaeon (S) is *Archaeoglobus fulgidus* DSM 4304.

Table S2: Gene structure of the gene containing the Fae domain found in the metagenomes of ANME-1 [1, 2]*

Meyerdierks et al.,2010		
Gene position	**Interpro identifier**	
1996565-1995378	IPR013785	Aldolase-type TIM barrel
	IPR011060	Ribulose-phosphate binding barrel
	IPR014826	Formaldehyde-activating enzyme
	IPR001754	Orotidine 5'-phosphate decarboxylase domain
	IPR014826	Formaldehyde-activating enzyme
	IPR020568	Ribosomal protein S5 domain 2-type fold
	IPR014826	Formaldehyde-activating enzyme
Stokke et al.,2012		
Gene position	**Interpro identifier**	
18911-1996565	IPR013785	Aldolase-type TIM barrel
	IPR011060	Ribulose-phosphate binding barrel
	IPR014826	Formaldehyde-activating enzyme
	IPR001754	Orotidine 5'-phosphate decarboxylase domain
	IPR014826	Formaldehyde-activating enzyme
	IPR020568	Ribosomal protein S5 domain 2-type fold
	IPR014826	Formaldehyde-activating enzyme

*The position of the genes corresponds to the position on the contig where the specific domains were found.

Table S3: Gene structure of the iron hydrogenase gene found in the metagenomes of ANME-1 (gene 1) and the surrounding genes (gene 2 and gene 3)*

Meyerdierks et al., 2010	**Gene position**	**Interpro identifier**	
Gene 1	925906-927615	IPR003149	Iron hydrogenase, small subunit
		IPR019574	NADH:ubiquinone oxidoreductase, subunit G, iron-sulphur binding
		IPR009016	Iron hydrogenase
		IPR013352	Iron hydrogenase, subset
		IPR001041	2Fe-2S ferredoxin-type iron-sulfur binding domain
		IPR017896	4Fe-4S ferredoxin-type, iron-sulphur binding domain
		IPR000283	NADH:ubiquinone oxidoreductase, 75kDa subunit, conserved site
		IPR003149	Iron hydrogenase, small subunit
		IPR004108	Iron hydrogenase, large subunit, C-terminal
		IPR019574	NADH:ubiquinone oxidoreductase, subunit G, iron-sulphur binding
Gene 2	927628-928404	IPR011538	NADH-ubiquinone oxidoreductase 51 kDa subunit, FMN-binding domain
		IPR019554	Soluble ligand binding domain
		IPR019575	NADH-ubiquinone oxidoreductase 51 kDa subunit, iron-sulphur binding domain
		IPR001949	NADH:ubiquinone oxidoreductase, 51kDa subunit, conserved site
		IPR019575	NADH-ubiquinone oxidoreductase 51 kDa subunit, iron-sulphur binding domain
Gene 3	928501-928854	IPR011538	NADH-ubiquinone oxidoreductase 51 kDa subunit, FMN-binding domain
		IPR002023	NADH-quinone oxidoreductase subunit E-like
		IPR012336	Thioredoxin-like fold

* The position of the genes corresponds to the position on the contig where the specific domains were found.

Table S3 (continued): Gene structure of the iron hydrogenase gene found in the metagenomes of ANME-1 (gene 1) and the surrounding genes (gene 2 and gene 3)*

Stokke et al., 2012	**Gene position**	**Interpro identifier**	
Gene 1	927615-925906	IPR003149	Iron hydrogenase small subunit
		IPR019574	NADH:ubiquinone oxidoreductase, subunit G, iron-sulphur binding
		IPR009016	Iron hydrogenase
		IPR013352	Iron hydrogenase, subset
		IPR001041	2Fe-2S ferredoxin-type iron-sulfur binding domain
		IPR017896	4Fe-4S ferredoxin-type, iron-sulphur binding domain
		IPR017900	4Fe-4S ferredoxin, iron-sulphur binding, conserved site
		IPR012675	Beta-grasp domain
		IPR000283	NADH:ubiquinone oxidoreductase, 75kDa subunit, conserved site
		IPR003149	Iron hydrogenase, small subunit
		IPR004108	Iron hydrogenase, large subunit, C-terminal
Gene 2	928404-927628	IPR011538	NADH-ubiquinone oxidoreductase 51 kDa subunit, FMN-binding domain
		IPR019554	Soluble ligand binding domain
		IPR019575	NADH-ubiquinone oxidoreductase 51 kDa subunit, iron-sulphur binding domain
		IPR001949	NADH:ubiquinone oxidoreductase, 51kDa subunit, conserved site
Gene 3	928854-928501	IPR011538	NADH-ubiquinone oxidoreductase 51 kDa subunit, FMN-binding domain
		IPR002023	NADH-quinone oxidoreductase subunit E-like
		IPR002023	NADH-quinone oxidoreductase subunit E-like
		IPR012336	Thioredoxin-like fold

*The position of the genes corresponds to the position on the contig where the specific domains were found.

References

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