Supplemental information to Salcher et al.:

Table S1: Details of the isolation experiments conducted in Lake Zurich, Switzerland during 2010-2013.

Table S2: Genes involved in methylotrophic pathways present in the genomes of *'Ca.* Methylopumilus planktonicus' MMS-2-53 and *'Ca.* Methylopumilus turicensis' MMS-10A-171.

Figure S1: Relative abundances (in % of DAPI) of microbes affiliated with LD28 (*'Ca.* Methylopumilus planktonicus', upper panel) and PRD01a001B (*'Ca.* Methylopumilus turicensis', lower panel) determined in Lake Zurich, Switzerland, during the investigation period 2008-2011.

Figure S2: Physical (A: water temperature, F: sphaerical irradiance), chemical (B: oxygen content, C: concentration of PO_4-P, D: NO_3-N, E: NH_4-N), and biological (G: concentration of total chlorophyll *a*, H: chlorophyll *a* associated with the cyanobacterium *Planktothrix rubescens*, I: chlorophyll *a* associated with diatoms) parameters determined in Lake Zurich, Switzerland, during the investigation period 2008-2011.

Figure S3: Bootstrapped maximum likelihood tree (GTR-Gamma model) of the 16S rDNA of microbes affiliated with LD28 (*'Ca.* Methylopumilus planktonicus). Sequences in bold represent isolated strains from Lake Zurich (see table S1 for abbreviations). The scale bar at the bottom represents 1 % estimated sequence divergence.

Figure S4: Bootstrapped maximum likelihood tree (GTR-Gamma model) of the 16S rDNA of microbes affiliated with PRD01a001B (*'Ca.* Methylopumilus turicensis). Sequences in bold represent isolated strains from Lake Zurich (see table S1 for abbreviations). The scale bar at the bottom represents 1 % estimated sequence divergence.

Figure S5: Graphic circular map of genome of '*Ca.* Methylopumilus planktonicus' strain MMS-2-53. From outside to the center: Genes on forward strand, genes on reverse strand (both coloured in COG categories), BLASTx comparison to 3 closely related taxa (*'Ca.* Methylopumilus turicensis' strain MMS-10A-171, HTCC2181 of the marine OM43 lineage, and *Methylotenera mobilis* JLW8), GC content, GC skew. COG classification was done with the WebMGA server (Wu et al., 2011) and the genome was displayed with the CGView server (Grant et al. 2008).

Figure S6: Graphic circular map of genome of '*Ca.* Methylopumilus turicensis strain MMS-10A-171. From outside to the center: Genes on forward strand, genes on reverse strand (both coloured in COG categories), BLASTx comparison to 3 closely related taxa ('*Ca.* Methylopumilus planktonicus' MMS-2-53, HTCC2181 of the marine OM43 lineage, and *Methylotenera mobilis* JLW8), GC content, GC skew. COG classification was done with the WebMGA server (Wu et al., 2011) and the genome was displayed with the CGView server (Grant et al. 2008).

Table S1: Details of the isolation experiments conducted in Lake Zurich, Switzerland during 2010-2013.

Date	water temp	med	# wells inoc	# cells /well	# + wells	# pure cult	# Meth	V_{pos}	V_{pure}	V_{Meth}	label	Acc. No.	Meth affil
19/08/2010	19	1	288	1	74	19	-	29.7	6.8	-	MMS-1	-	-
14/10/2010	15.1	1	95	1	10	6	1	11.1	6.5	1.1	MMS-2	LN681407	M. pla.
11/05/2011	16.7	1	95	1.4	-	-	-	-	-	-	MMS-3	-	-
25/05/2011	13.2	1	95	1.4	40	2	1	40.3	1.6	0.8	MMS-4	LN681408	M. pla.
07/06/2011	19.1	1	95	1.4	8	-	-	6.5	-	-	MMS-5	-	-
22/06/2011	19.7	1	95	1.4	11	-	-	9.1	-	-	MMS-6	-	-
06/07/2011	21.5	1	95	1.4	42	-	-	43.0	-	-	MMS-7	-	-
19/07/2011	21.0	1	95	1.4	32	1	-	30.3	0.8	-	MMS-8	-	-
04/08/2011	20.6	2	95	1.4	26	-	-	23.6	-	-	MMS-9	-	-
17/08/2011	21.1	3	95	1.4	39	-	-	38.9	-	-	MMS-10	-	-
24/08/2011	24.7	3	95	1.4	25	-	-	22.5	-	-	MMS-11	-	-
08/09/2011	20.9	3	95	1.4	56	1	1	65.6	0.8	0.8	MMS-12	LN681409	M. pla.
21/09/2011	19.4	3	167	3.2	94	4	4	25.5	0.8	0.8	MMS-13	LN681410-13	M. pla.
05/10/2011	19.4	3	119	2.8	79	7	3	38.8	2.2	0.9	MMS-14	LN681414-16	M. pla.
18/10/2011	15.2	3	119	2.8	88	24	17	47.9	8.0	5.5	MMS-15	LN681417-33	M. pla.
03/11/2011	12.7	3	119	2.8	67	3	2	29.5	0.9	0.6	MMS-16	LN681434-35	M. pla.
16/11/2011	11.3	3	119	2.8	94	18	16	55.6	5.8	5.1	MMS-17	LN681436-51	M. pla.
30/11/2011	9.3	3	119	2.8	21	15	13	6.9	4.8	4.1	MMS-18	LN681452-64	M. pla.
14/12/2011	7.4	3	192	2.8	63	18	18	26.9	5.8	5.8	MMS-19	LN681465-82	M. pla.
10/05/2012	12.1	4	191	2.4	28	25	-	6.7	6.5	-	MMS-20	-	-
25/05/2012	13.5	4	168	2.0	18	17	-	5.7	5.3	-	MMS-21	-	-
01/06/2012	13.5	4	144	2.7	-	-	-	-	-	-	MMS-22	-	-
01/06/2012	13.5	5	144	1.7	-	-	-	-	-	-	MMS-F3	-	-
20/06/2012	17.8	6	24	2.3	10	10	-	23.1	23.1	-	MMS-5H	-	-
20/06/2012	17.8	4	72	2.3	2	2	-	1.2	1.2	-	MMS-3A	-	-
20/06/2012	17.8	4	72	2.3	4	3	-	2.5	1.8	-	MMS-4A	-	-
20/06/2012	17.8	4	72	2.3	1	1	-	0.6	0.6	-	MMS-5A2	-	-
20/06/2012	17.8	5	24	2.3	1	1	-	1.8	1.8	-	MMS-2FG3	-	-
20/06/2012	17.8	5	48	2.3	4	3	-	3.7	2.8	-	MMS-2FG3b	-	-
14/08/2012	23.2	4	96	2	5	5	-	2.7	2.7	-	MMS-7A	-	-
14/08/2012	23.2	4	120	2	14	13	-	6.2	5.7	-	MMS-8A	-	-
14/08/2012	23.2	4	167	1.9	4	3	-	1.3	1.0	-	MMS-9A	-	-
14/08/2012	23.2	4	192	1.8	40	39	12	13.4	13.0	7.4	MMS-10A	LN681522-33	M. tur.
15/08/2012	23.2	4	238	1.8	-	-	-	-	-	-	MMS-11A	-	-
31/08/2012	23.2	4	288	2.4	10	8	3	1.5	1.2	0.43	MMS-12A	LN681483-85	M. pla.
12/11/2012	11.5	7	240	2.3	185	6	-	63.1	1.3	-	MMS-12Awh	-	-
12/11/2012	11.5	7	240	2.3	171	58	1	53.4	12.1	0.2	MMS-14A	LN681486	M. pla.
22/05/2013	13.2	8	120	1.6	20	11	-	11.4	6.0	-	MMS-IA	-	-
22/05/2013	13.2	9	120	1.6	40	22	-	25.3	13.3	-	MMS-IB	-	-
23/05/2013	13.2	9	168	2.0	128	95	2	71.8	44.5	0.6	MMS-IIA	LN681487-88	M. pla.
23/05/2013	13.2	8	168	2.0	92	49	-	39.7	17.2	-	MMS-IIB	-	-
03/06/2013	12.3	10	264	1.7	264	191	-	100	74.4	-	MMS-III	-	-
13/06/2013	15.9	10	288	1.8	74	47	-	17.0	10.2	-	MMS-IV	-	-
15/07/2013	20.1	11	144	1.8	14	6	1	5.8	2.4	0.4	MMS-VA	LN681489	M. pla.
15/07/2013	20.1	12	144	1.8	51	30	19	25.0	13.4	8.1	MMS-VB	LN681490-508	M. pla.
14/08/2013	24.6	12	264	1.7	28	25	13	6.5	5.8	3.0	MMS-VI	LN681509-21	M. pla.
SUM			**6507**		**2077**	**788**	**127**						
MEAN				**2.0**				**24.8**	**8.7**	**2.7**			

Abbreviations: water temp, water temperature, med, medium; # wells inoc, number of wells inoculated; # cells/well, number of cells inoculated per well; # + wells, number of wells with cells growing; # pure cult, number of pure cultures; # Meth, number of cultures affiliated with *Methylophilaceae*; V_{pos}, total viability; V_{pure}, viability of pure cultures; V_{meth}, viability of isolates affiliated with *Methylophilaceae*; label, labeling scheme for pure cultures; Acc No, accession numbers; Meth affil, affiliation of isolated *Methylophilaceae*, M. pla., *'Candidatus* Methylopumilus planktonicus' (LD28); M. tur., *'Candidatus* Methylopumilus turicensis' (PRD01a001B).

Media:

1: filtered and autoclaved lake water (LW) + minimal carbon medium (MC)#1
2: LW + MC#1 + Vitamins (V)
3: LW + MC#1 + V + amino acids (AA)
4: LW + 10x MC#2 + V + AA
5: artificial lake water (ALW) + TES + 10x MC#2 + medium 4 (1:1)
6: ALW + 10x MC#2
7: LW + 10x MC#2 + MC#3 + V + AA
8: LW + MC#2 + MC#3 + inorganic basal medium (IBM) + stock4 + V + 10xAA
9: LW + pyruvate (50 µM) + urea (0.5 µM) + MC#4 + V + 10xAA
10: LW+ V + 10xAA
11: LW + MC#2 + pyruvate (50 µM) + urea (0.5 µM) + V + 10xAA
12: LW + pyruvate (50 µM) + urea (0.5 µM) + V + 10xAA

Minimal carbon medium (MC)#1: 1 µM NH_4Cl, 0.1 µM K_2HPO_4, 11.1 µM D-glucose, 13.3 µM D-ribose, 22.7 µM pyruvate, 21.7 µM glycerol, 9 µM N-acetylglucosamine, 0.1 µM glutamate, 0.1 µM glutamine, 0.05 µM arginine, 0.1 µM methionine, 0.1 µM glycine

MC#2: 1 µM NH_4Cl, 0.1 µM K_2HPO_4, 55.5 µM D-glucose, 66.6 µM D-ribose, 217.2 µM formate, 217.2 µM ethanol, 84.7 µM succinate, 131.5 µM glycolate, 108.6 µM glycerol, 45.2 µM N-acetylglucosamine

MC#3: 62.1 µM putrescine, 39.3 µM spermidine, 66.6 µM D-xylose, 66.6 µM arabinose

MC#4: 30 µM NH_4Cl, 50 µM oxaloacetate, 50 µM taurine, 1 µM betaine, 40 µM $CaCl_2$

Amino acid solution (AA): 0.5 µM isoleucine, leucine, lysine, methionine, alanine, phenylalanine, threonine, tryptophane, valine, arginine, histidine, asparagine, aspartate, cysteine, proline, serine, tyrosine, 2 µM glutamine, glutamate, glycine

Vitamine solution (V): 0.593 µM thiamine, 0.08 µM niacin, 0.000074 µM cobalamine, 0.005 µM para-amino benzoic acid, 0.074 µM pyridoxine, 0.081 µM pantothenic acid, 0.004 µM biotin, 0.004 µM folic acid, 0.555 µM myo-inositol

Artificial lake water (ALW, Zotina et al. 2003): 2 mM $NaHCO_3$, 30 µM KNO_3, 200 µM $MgSO_4$, 40 µM $CaCl_2$, 160 µM $CaSO_4$, 30 µM NH_4Cl, 0.322 µM K_2HPO_4

TES (trace element solution): 12 µM $FeCl_3$, 16 µM H_3BO_3, 1 µM $MnCl_2$, 0.1 µM $ZnSO_4$, 0.04 µM $CuSO_4$, 0.04 µM $CoCl_2$, 0.03 µM $NaMoO_4$, 0.4 µM $NiCl_2$,

Inorganic basal medium (IBM, Hahn et al. 2003): 304 µM $MgSO_4$, 182 µM $Ca(NO_3)_2$, 190 µM $NaHCO_3$, 20 µM KCl, 16 µM K_2HP_4, 17 µM Na_2EDTA-Fe, 0.1 ml TES

References:

Hahn M, Lünsdorf H, Wu Q, Schauer M, Höfle M, Boenigk J *et al* (2003). Isolation of novel ultramicrobacteria classified as *Actinobacteria* from five freshwater habitats in Europe and Asia. *Appl Environ Microbiol* **69:** 1442-1451.

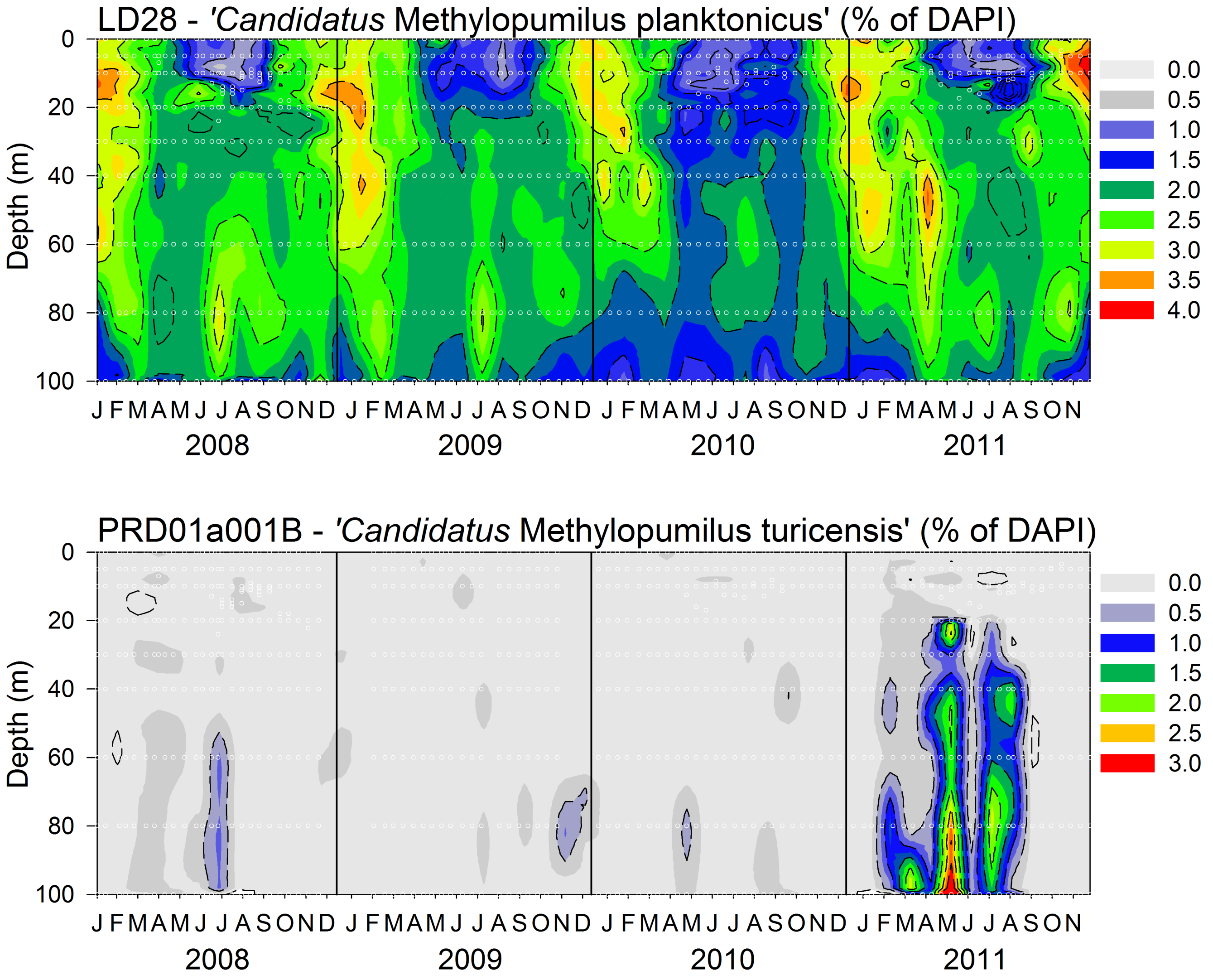
Zotina T, Köster O, Jüttner F (2003). Photoheterotrophy and light-dependent uptake of organic and organic nitrogenous compounds by *Planktothrix rubescens* under low irradiance. *Freshwater Biol* **48:** 1859-1872.

Table S2: Genes involved in methylotrophic pathways present in the genomes of *'Ca.* Methylopumilus planktonicus' MMS-2-53 (Acc. No. LN827929) and *'Ca.* Methylopumilus turicensis' MMS-10A-171 (Acc. No LN794158).

Pathway	Gene	Protein/function	*'Ca.* M. planktonicus' MMS-2-53	*'Ca.* M. turicensis' MMS-10A-171
Methanol oxidation	*xoxF*	Homologue of MDH large subunit	BN1208_1208	BN1209_1575
	xoxJ	unknown	BN1208_1207	BN1209_1574
	xoxG	cytochrome c, electron acceptor from MDH	BN1208_1206	BN1209_1572, BN1209_1573
	mxaR	unknown	BN1208_0638	BN1209_0567
	mxaS	unknown	BN1208_0637	BN1209_0566
	mxaA	Ca2+ insertion into MDH	BN1208_0636	BN1209_0565
	mxaC	Ca2+ insertion into MDH	BN1208_0635	BN1209_0564
	mxaK	Ca2+ insertion into MDH	BN1208_0634	BN1209_0563
	mxaL	Ca2+ insertion into MDH	BN1208_0633	BN1209_0562
	mxaD	unknown	BN1208_0373	BN1209_0453
	pqqB	PQQ biosynthesis	BN1208_0720	BN1209_0756
	pqqC	PQQ biosynthesis	BN1208_0721	BN1209_0757
	pqqD	PQQ biosynthesis	BN1208_0722	BN1209_0758
	pqqE	PQQ biosynthesis	BN1208_0723	BN1209_0759
	pqqF	PQQ biosynthesis	BN1208_1061	BN1209_1323
	pqqG	PQQ biosynthesis	BN1208_1060	BN1209_1322
H_4F-linked formaldehyde oxidation	*folD*	Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) / Methylenetetrahydrofolate cyclohydrolase (EC 3.5.4.9)	BN1208_0070	BN1209_0056
	fhs	Formate-tetrahydrofolate ligase	BN1208_0733	-
	metF	5,10-methylenetetrahydrofolate reductase	BN1208_0111	BN1209_0102, BN1209_0103
	ygfZ	glycine cleavage T protein (aminomethyl transferase)	BN1208_0632	BN1209_0560
H_4MPT-linked formaldehyde oxidation	*fhcA*	formyltransferase/hydrolase complex subunit A	-	BN1209_0742
	fhcD	formyltransferase/hydrolase complex subunit D	-	BN1209_0741
	fhcC	formyltransferase/hydrolase complex subunit C	-	BN1209_0740
	mptG	beta-ribofuranosylamino-benzene 5-phosphate synthase	-	BN1209_0744
	mtdB	methylene H_4MPT dehydrogenase	-	BN1209_0745
	orfY	unknown	-	BN1209_0746
	mch	methenyl H_4MPT cyclohydrolase	-	BN1209_0747
	orf5	biosynthesis of H_4MPT	-	BN1209_0748
	orf7	unknown	-	BN1209_0749
	fae	formaldehyde activating enzyme	-	BN1209_1682
	orf17	unknown	-	BN1209_0773
	orf1	unknown	-	BN1209_0774
	orf9	biosynthesis of H_4MPT	-	BN1209_0775
	pabB	para-aminobenzoate synthase component I	-	BN1209_0776, BN1209_1662
	orf21	biosynthesis of H_4MPT	-	BN1209_0777
	pcbD	unknown	-	BN1209_0778
	orf22	biosynthesis of H_4MPT	-	BN1209_0842
	orf19	biosynthesis of H_4MPT	-	BN1209_0841
	orf20	biosynthesis of H_4MPT	-	BN1209_0840
	afp	dihydromethanopterin reductase	-	BN1209_0839

Pathway	Gene	Protein/function	‘*Ca.* M. planktonicus’ MMS-2-53	‘*Ca.* M. turicensis’ MMS-10A-171
Formate oxidation	*fdhA*	formate dehydrogenase alpha subunit	BN1208_1192	BN1209_0677
	fdhB	formate dehydrogenase beta subunit	BN1208_1193	BN1209_0676, BN1209_1191
	fdhC	formate dehydrogenase gamma subunit	BN1208_1194	BN1209_0675
	fdhD	formate dehydrogenase accessory protein	BN1208_1191	BN1209_0678
	fdhE	formate dehydrogenase delta subunit	BN1208_1190	BN1209_0679
Ribulose monophosphate (RuMP) cycle for formaldehyde assimilation/oxidation	*hps*	3-hexulose-6-phosphate synthase	BN1208_0845	BN1209_0202, BN1209_0771
	hpi	6-phospho-3-hexuloisomerase	BN1208_0844	BN1209_0772
	tal	transaldolase	BN1208_0846, BN1208_0901	BN1209_0770
	pgi	glucose 6-phosphate isomerase	BN1208_0816	BN1209_0914
	zwf	glucose 6-phosphate dehydrogenase	BN1208_0649	BN1209_0580
	pgl	6-phosphogluconolactonase	BN1208_0650	BN1209_0581
	gndA	6-phosphogluconolactonase	BN1208_0651	BN1209_0582
	gndB	6-phosphogluconate dehydrogenase (NADP)	-	BN1209_0428
	edd	6-phosphogluconate dehydratase	BN1208_1051	BN1209_1306
	eda	2-dehydro-3-deoxy-phosphogluconate aldolase	BN1208_1050	BN1209_1305
	tkt	transketolase	BN1208_1157	BN1209_1513
	rpe	ribulose-phosphate 3-epimerase	BN1208_1297	BN1209_1663
	ppi	ribose-5-phosphate isomerase	BN1208_0100, BN1208_0677	BN1209_0087, BN1209_0663

Figure S1: Relative abundances (in % of DAPI) of microbes affiliated with LD28 ('*Cand.* Methylopumilus planktonicus', upper panel) and PRD01a001B (*'Cand*. Methylopumilus turicensis', lower panel) determined in Lake Zurich, Switzerland, during the investigation period 2008-2011.



LD28 - *'Candidatus* Methylopumilus planktonicus' (% of DAPI)

PRD01a001B - *'Candidatus* Methylopumilus turicensis' (% of DAPI)

Figure S2: Physical, chemical, and biological parameters determined in Lake Zurich, Switzerland, during the investigation period 2008-2011.

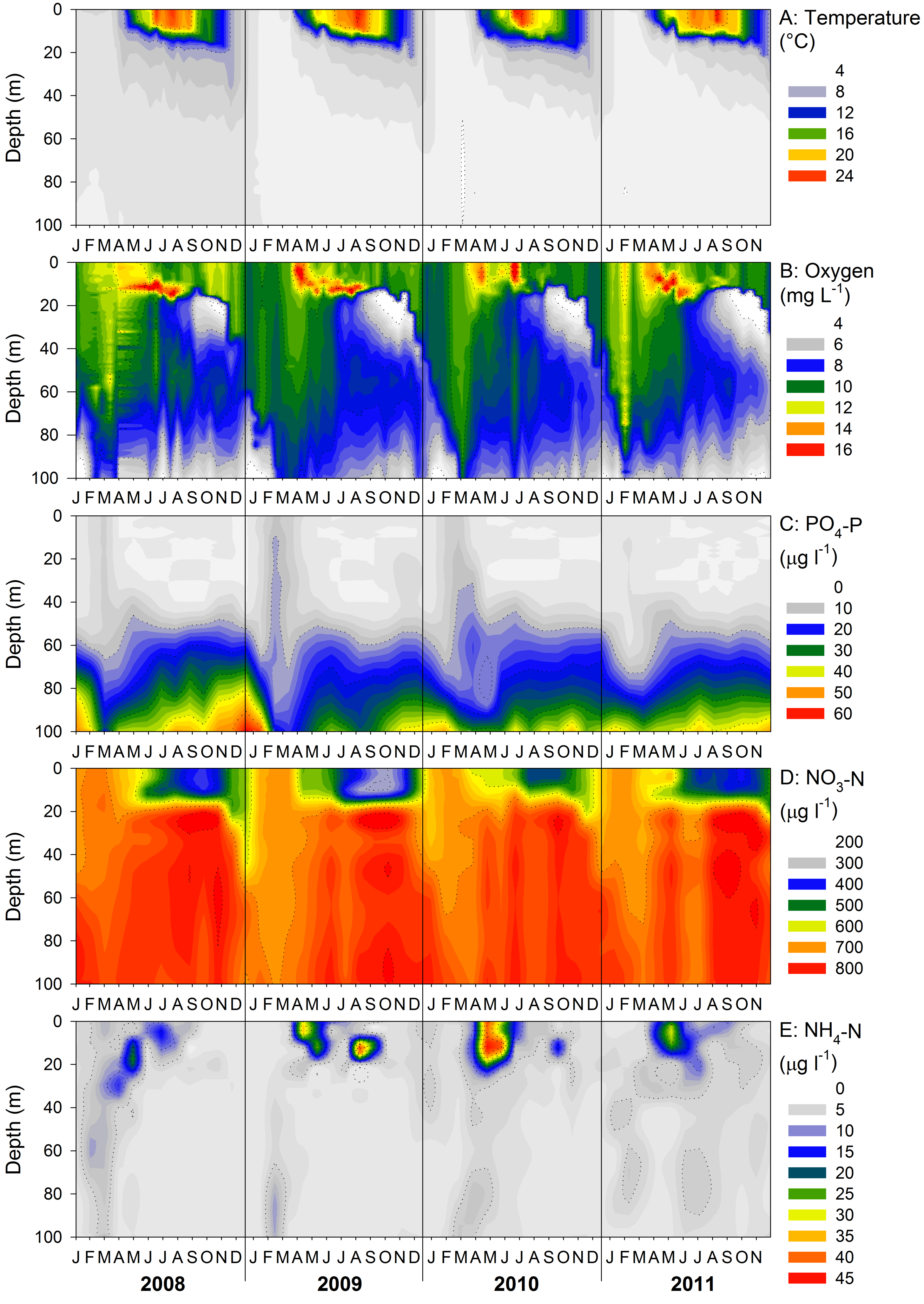


Figure S2 continued

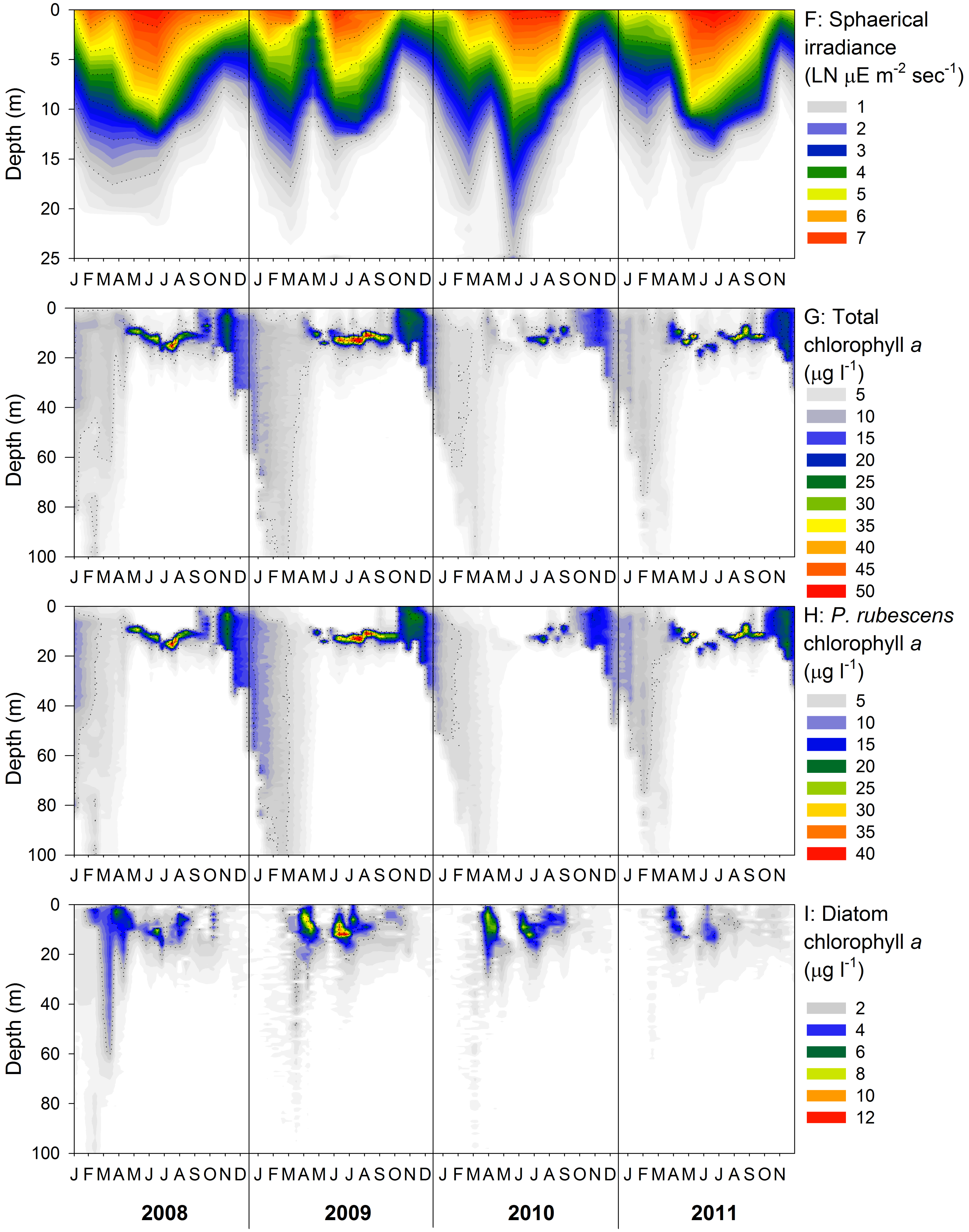
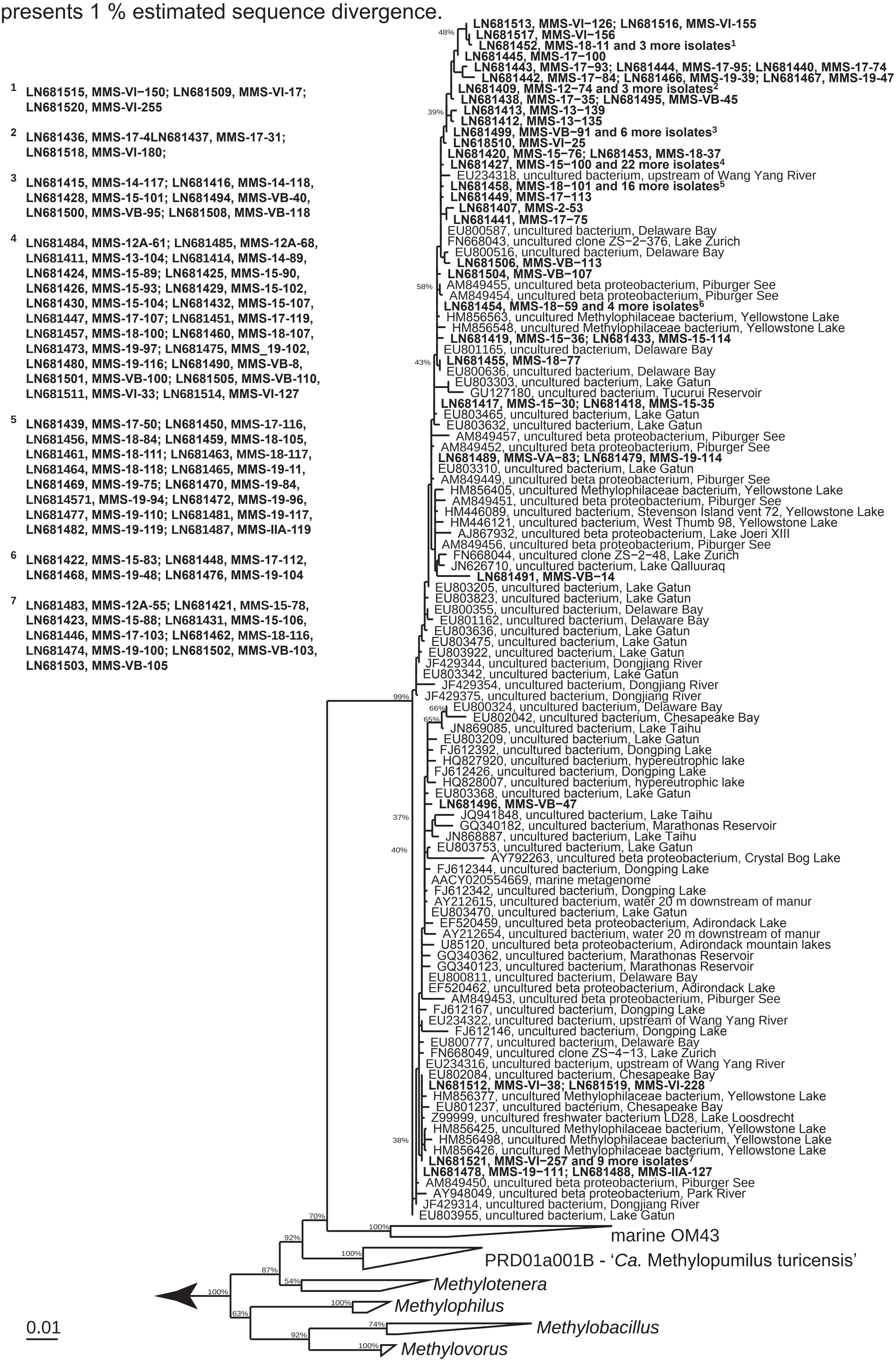


Figure S3: Bootstrapped maximum likelihood tree (GTR-Gamma model) of the 16S rDNA of microbes affiliated with LD28 (‘*Ca.* Methylopumilus planktonicus). Sequences in bold represent isolated strains from Lake Zurich (see table S1 for abbreviations). The scale bar at the bottom represents 1 % estimated sequence divergence.



[1] **LN681515, MMS-VI−150; LN681509, MMS-VI-17; LN681520, MMS-VI-255**

[2] **LN681436, MMS-17-4LN681437, MMS-17-31; LN681518, MMS-VI-180;**

[3] **LN681415, MMS-14-117; LN681416, MMS-14-118, LN681428, MMS-15-101; LN681494, MMS-VB-40, LN681500, MMS-VB-95; LN681508, MMS-VB-118**

[4] **LN681484, MMS-12A-61; LN681485, MMS-12A-68, LN681411, MMS-13-104; LN681414, MMS-14-89, LN681424, MMS-15-89; LN681425, MMS-15-90, LN681426, MMS-15-93; LN681429, MMS-15-102, LN681430, MMS-15-104; LN681432, MMS-15-107, LN681447, MMS-17-107; LN681451, MMS-17-119, LN681457, MMS-18-100; LN681460, MMS-18-107, LN681473, MMS-19-97; LN681475, MMS_19-102, LN681480, MMS-19-116; LN681490, MMS-VB-8, LN681501, MMS-VB-100; LN681505, MMS-VB-110, LN681511, MMS-VI-33; LN681514, MMS-VI-127**

[5] **LN681439, MMS-17-50; LN681450, MMS-17-116, LN681456, MMS-18-84; LN681459, MMS-18-105, LN681461, MMS-18-111; LN681463, MMS-18-117, LN681464, MMS-18-118; LN681465, MMS-19-11, LN681469, MMS-19-75; LN681470, MMS-19-84, LN6814571, MMS-19-94; LN681472, MMS-19-96, LN681477, MMS-19-110; LN681481, MMS-19-117, LN681482, MMS-19-119; LN681487, MMS-IIA-119**

[6] **LN681422, MMS-15-83; LN681448, MMS-17-112, LN681468, MMS-19-48; LN681476, MMS-19-104**

[7] **LN681483, MMS-12A-55; LN681421, MMS-15-78, LN681423, MMS-15-88; LN681431, MMS-15-106, LN681446, MMS-17-103; LN681462, MMS-18-116, LN681474, MMS-19-100; LN681502, MMS-VB-103, LN681503, MMS-VB-105**

Figure S4: Bootstrapped maximum likelihood tree (GTR-Gamma model) of the 16S rDNA of microbes affiliated with PRD01a001B (*'Ca.* Methylopumilus turicensis). Sequences in bold represent isolated strains from Lake Zurich (see table S1 for abbreviations). The scale bar at the bottom represents 1 % estimated sequence divergence.

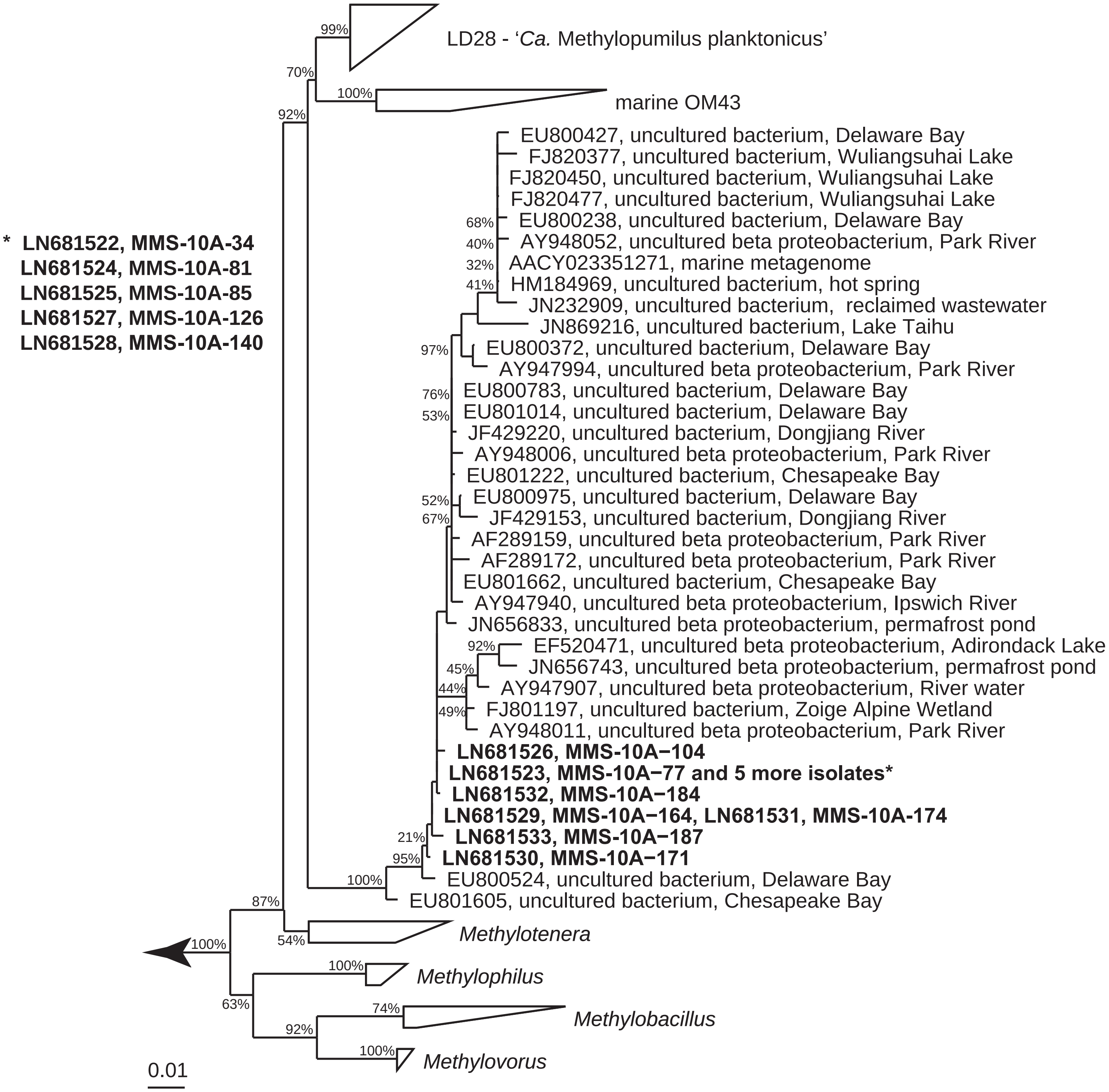
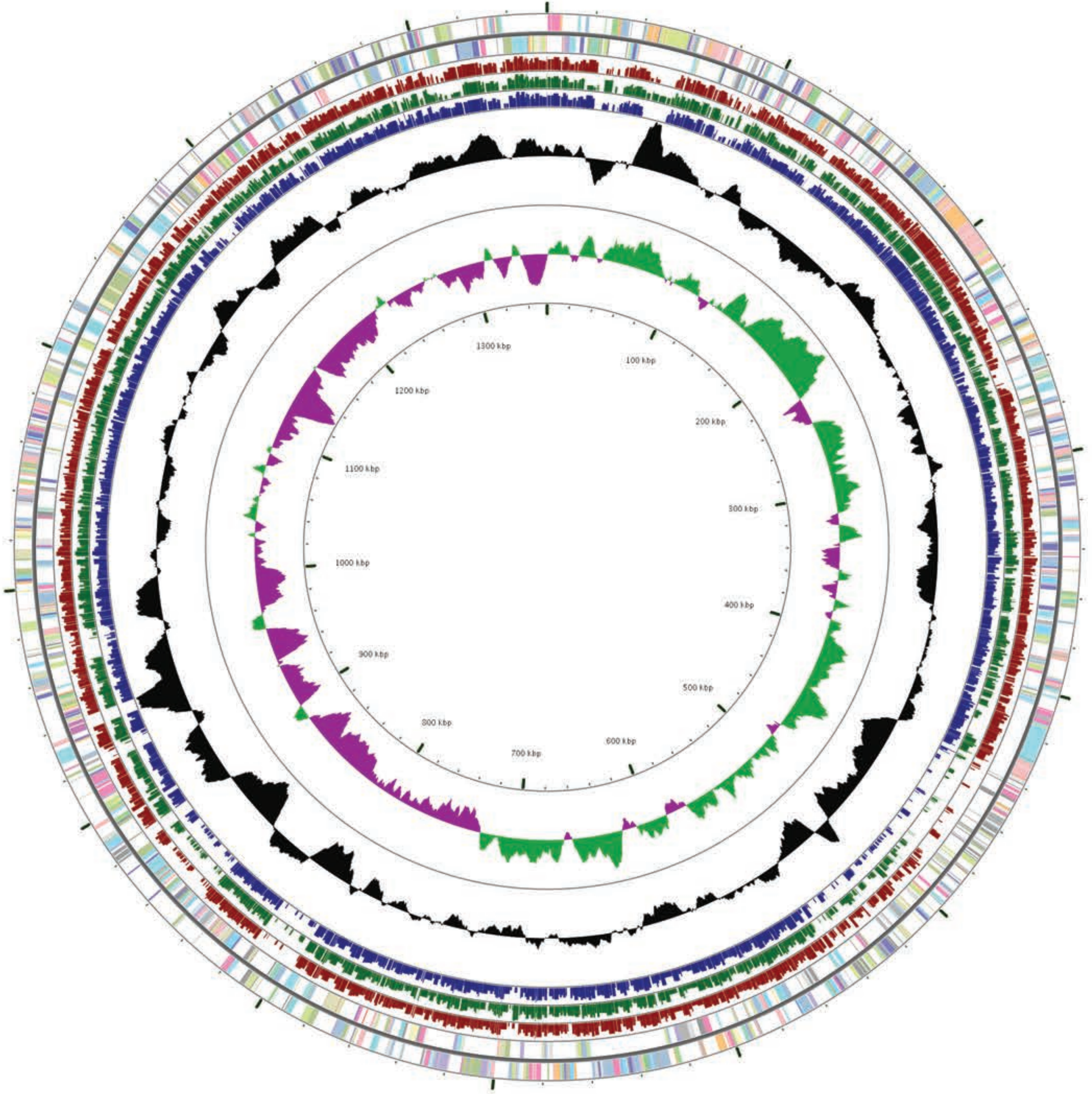


Fig. S5: Graphic circular genome map of *'Ca.* Methylopumilus planktonicus' strain MMS-2-53.
From outside to the center: Genes on forward strand, genes on reverse strand (both coloured in COG categories), BLASTx comparison to 3 closely related taxa (*'Ca*. Methylopumilus turicensis' MMS-10A-171, HTCC2181 of the marine OM43 lineage, and *Methylotenera mobilis* JLW8), GC content, GC skew.
COG classification was done with the WebMGA server (Wu et al., 2011) and the genome was displayed with the CGView server (Grant et al. 2008).

References:
Wu S, Zhu Z, Fu L, Niu B, Li W (2011). WebMGA: a customizable web server for fast metagenomic sequence analysis. BMC Genomics 12: 444.
Grant JR, Stothard P (2008) The CGView Server: a comparative genomics tool for circular genomes. Nucleic Acids Res 36:W181-W184.



COG categories:

- ■ A
- ■ B
- ■ J
- ■ K
- ■ L
- ■ D
- ■ O
- ■ M
- ■ N
- ■ P
- ■ T
- ■ U
- ■ V
- ■ W
- ■ Y
- ■ Z
- ■ C
- ■ G
- ■ E
- ■ F
- ■ H
- ■ I
- ■ Q
- ■ R
- ■ S
- ■ unknown COG
- ■ tRNA
- ■ rRNA
- ■ BLAST results *'Ca.* M. tur.' MMS-10A-171
- ■ BLAST results marine HTCC2181 (OM43)
- ■ BLAST results *Methylotenera mobilis* JLW8
- ■ GC content
- ■ GC skew +
- ■ GC skew -

Fig. S6: Graphic circular genome map of *'Ca.* Methylopumilus turicensis' strain MMS-10A-171**.**
From outside to the center: Genes on forward strand, genes on reverse strand (both coloured in COG categories), BLASTx comparison to 3 closely related taxa (*'Ca*. Methylopumilus planktonicus' MMS-2-53, *Methylotenera mobilis* JLW8, and *Methylobacillus flagellatus* KT), GC content, GC skew. COG classification was done with the WebMGA server (Wu et al., 2011) and the genome was displayed with the CGView server (Grant et al. 2008).

References:

Wu S, Zhu Z, Fu L, Niu B, Li W (2011). WebMGA: a customizable web server for fast metagenomic sequence analysis. BMC Genomics 12: 444.

Grant JR, Stothard P (2008) The CGView Server: a comparative genomics tool for circular genomes. Nucleic Acids Res 36:W181-W184.