Supplementary material

Identifying Active Rather Than Total Methanotrophs Inhabiting Surface Soil Is Essential for the Microbial Prospection of Gas Reservoirs

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Table S1. Percentage of MOB in total microorganisms (based on MiSeq sequencing of 16S rRNA genes) in each DNA-SIP fraction of P1 (gas well soil)

Treatment	Fraction	*Methylocystis*	*Methylosarcina*	*Methylocaldum*	*Methylomicrobium*
$^{13}CH_4$	4	**33.76**	2.32	2.20	0.14
	5	**23.39**	7.57	0.89	0.44
	6	**15.57**	4.05	0.26	0.28
	Average	24.24	4.65	1.11	0.28
$^{12}CH_4$	4	1.01	0.04	0.08	0
	5	0.32	0.04	0.04	0
	6	0.04	0.01	0	0
	Average	0.46	0.03	0.04	0
In situ		0.018	0.078	0.006	0.008

Table S2. Percentage of MOB in total microorganisms (based on MiSeq sequencing of 16S rRNA genes) in each DNA-SIP fraction of J3 (dry well soil)

Treatment	Fraction	*Methylocystis*	*Methylosarcina*	*Methylocaldum*	*Methylosinus*
$^{13}CH_4$	4	**13.26**	0	0.04	0.01
	5	**8.71**	0.01	0	0.02
	6	**5.47**	0.01	0	0.01
	Average	9.15	0.01	0.01	0.01
$^{12}CH_4$	4	0.47	0.02	0	0.01
	5	0.11	0.01	0	0
	6	0.28	0.01	0	0
	Average	0.28	0.01	0.01	0.00