



**Figure S1.** Contribution of Mean Decrease Gini coefficient (MDG) of common genus **(a)** and common families **(b)** sequenced by Illumina and Nanopore, for [site+(sea-land orientation)] predictors (see details in Table S2). Mean Decrease Gini is a measure of how each variable contributes to the homogeneity of the nodes and leaves in the resulting random forest (see Methods for details) ; the higher the value of MDG score, the higher the importance of the variable in the model.

**Figure S2** (next page). **(a-b)** Archaeal taxa (genus level) contributing to structuring the communities in samples sequenced by Nanopore (rarefied at 5500 reads per sample, 97% OTUs with a minimum coverage of 50 reads) : **(a)** PCA on relative abundances, **(b)** iris plot of the relative abundances for taxa the most contributing to the PCA in (a). **(c-d)** same for bacterial taxa (genus level), sequenced by Nanopore.



Kingdom	sequencer (primers)	Taxa / reads	Phylum	Class	Order	Family	Genus	Species
Archaea	Illumina (515F + 926R)	detected (% assigned)	6 (83.3%)	7 (85.7%)	10 (90.0%)	14 (85.7%)	15 (86.7%)	31 (71.0%)
	Nanopore (SSU1Ar F + SSU1000Ar)	detected (% assigned)	11 (90.9%)	23 (78.3%)	34 (79.4%)	50 (80.0%)	83 (80.7%)	171 (67.8%)
	shared		6	7	10	13	14	24
	% of shared taxa for Illumina		100%	100%	100%	92.9%	93.3%	77.4%
	% of shared taxa for Nanopore		54.6%	30.4%	29.4%	26.0%	16.9%	14.0%

**Table S1.** Archaea detected by Illumina were mentioned but the read coverage by sample was much lower than those for Nanopore Archaea.

OTU#	Phylum	Class	Order	Family	Genus	MDG
<b>Illumina</b>						
OTU499	Dadabacteria	Dadabacteriia	Dadabacteriales	—	—	2,26
OTU295	Planctomycetota	Planctomycetes	Pirellulales	Pirellulaceae	—	0,81
OTU293					<i>Blastopirellula</i>	0,99
OTU277					<i>Pirellula</i>	0,44
OTU209	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales inc. sed.	<i>Bauldia</i>	0,40
OTU161		Gammaproteobacteria	Ectothiorhodospirales	Ectothiorhodospiraceae	<i>Thiogranum</i>	0,53
OTU134			HOC36	HOC36	<i>HOC36</i>	1,13
OTU111			Pseudomonadales	Nitrincolaceae	<i>Marinobacterium</i>	1,10
OTU92			Thiomicrospirales	Thiomicrospiraceae	<i>endosymbionts</i>	2,48
OTU107			Pseudomonadales	Pseudohongiellaceae	<i>Pseudohongiella</i>	0,50
OTU118				Haliaceae	<i>Parahalia</i>	0,37
OTU111				Nitrincolaceae	<i>Marinobacterium</i>	1,10
OTU139			Gammaproteobacteria inc. sd.	Unknown_Family	<i>uncultured</i>	0,39
OTU190			uncultured	uncultured	<i>uncultured</i>	0,48
OTU503	Cyanobacteria	Cyanobacteriia	Phormidesmiales	Nodosilineaceae	<i>MBIC10086</i>	0,60
OTU52	Verrucomicrobiota	Kiritimatiellae	Kiritimatiellales	Kiritimatiellaceae	<i>R76-B128</i>	0,32
OTU528	Chloroflexi	Dehalococcoidia	FS117-23B-02	FS117-23B-02	<i>FS117-23B-02</i>	0,60
OTU637	Bacteroidota	Bacteroidia	Flavobacteriales	Flavobacteriaceae	<i>Hoppeia</i>	1,19
OTU643					<i>Actibacter</i>	0,36
OTU703			Bacteroidales	SB-5	<i>SB-5</i>	0,53
OTU709				Prolixibacteraceae	<i>Draconibacterium</i>	0,55
<b>Nanopore</b>						
OTU_b563	Dadabacteria	Dadabacteriia	Dadabacteriales	—	—	0,81
OTU_b120	Planctomycetota	Planctomycetes	Pirellulales	Pirellulaceae	—	0,73
OTU_b118					<i>Blastopirellula</i>	0,39
OTU_b84					<i>Pir4_lineage</i>	0,81
OTU_b221	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales inc. sed.	<i>Bauldia</i>	0,75
OTU_b1395			Defluviicoccales	Defluviicoccaceae	<i>Defluviicoccus</i>	1,14
OTU_b18		Gammaproteobacteria	—	—	—	0,94
OTU_b420			Ectothiorhodospirales	Ectothiorhodospiraceae	<i>uncultured</i>	0,42
OTU_b157				Thioalkalispiraceae	<i>Thiohalophilus</i>	0,86
OTU_b98			HOC36	HOC36	<i>HOC36</i>	0,65
OTU_b454			Pseudomonadales	Nitrincolaceae	<i>Marinobacterium</i>	0,85
OTU_b1960				Alcanivoracaceae	<i>Ketobacter</i>	0,81
OTU_b355			Thiomicrospirales	Thiomicrospiraceae	<i>endosymbionts</i>	0,51
OTU_b1138			Chromatiales	Sedimenticolaceae	<i>Sedimenticola</i>	0,85
OTU_b365			pItb-vmat-80	pItb-vmat-80	<i>pItb-vmat-80</i>	1,47
OTU_b202	NB1-j	—	—	—	—	0,77
OTU_b502	Acidobacteriota	Vicinamibacteria	Subgroup_9	—	—	0,77
OTU_b115		Subgroup_22	—	—	—	0,48
OTU_b744	Actinobacteriota	Actinobacteria	Corynebacteriales	Mycobacteriaceae	<i>Mycobacterium</i>	0,48
OTU_b862		Thermoleophilia	Solirubrobacterales	67-14	—	0,94

**Table S2.** Bacterial genus contributing the most importantly to the site effect, after a random forest analysis on Illumina and Nanopore datasets. In green : OTUs common to both datasets. MDG : mean decrease in Gini coefficient, a measure of how each variable contributes to the homogeneity of the nodes and leaves in the resulting random forest ; the higher the value of MDG score, the higher the importance of the variable in the model.