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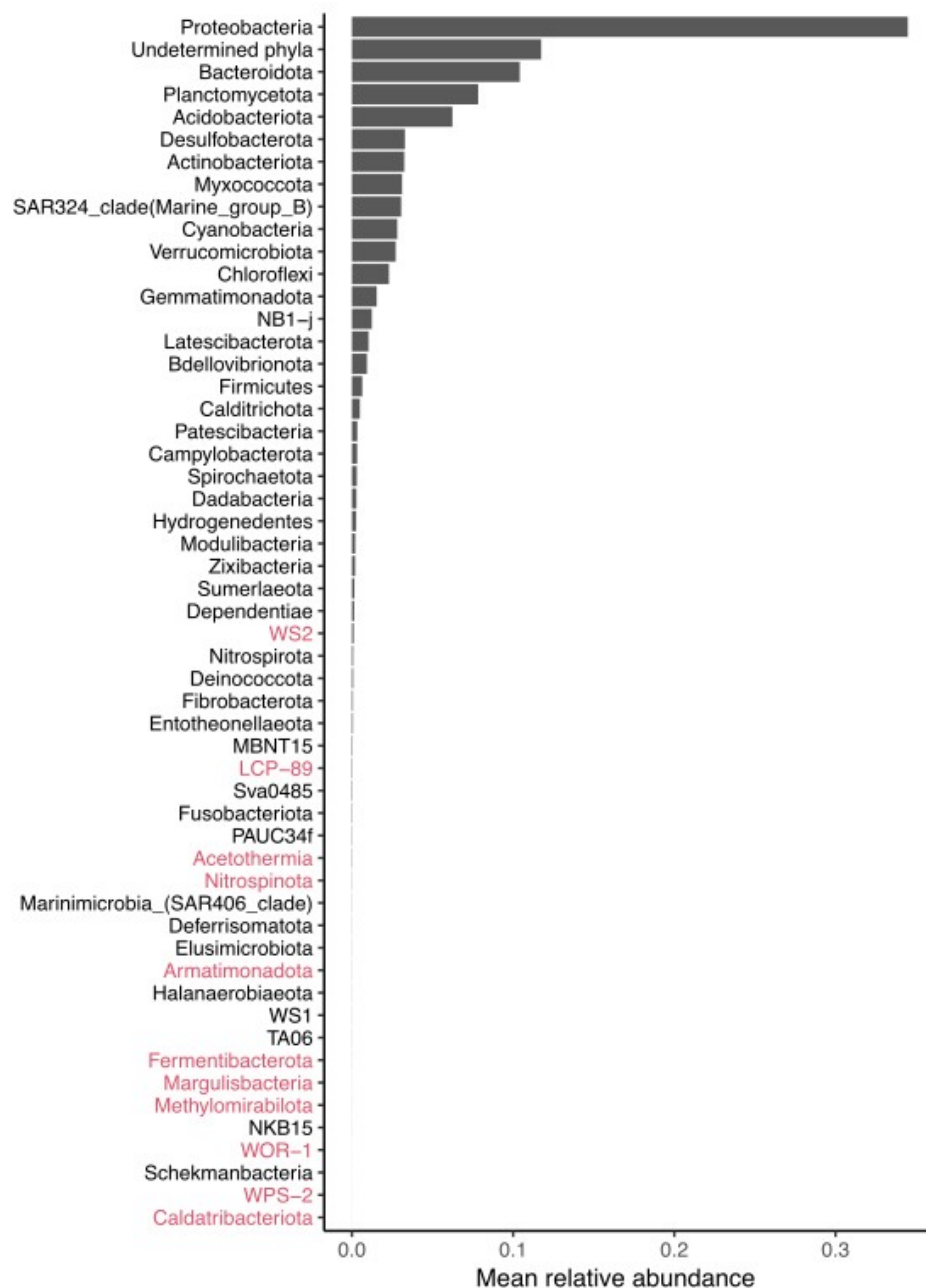
Figure S2. (**a-b**) Archaean taxa (genus level) contributing to structuring the communities in samples sequenced by Nanopore (rarefied at 5500 reads per sample, 97% OTUs with a minimum coverage of 50 reads) : (**a**) PCA on relative abundances, (**b**) iris plot of the relative abundances for taxa the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

Figure S3. Mean relative abundance of Nanopore phyla ; exclusive Nanopore phyla are in red.
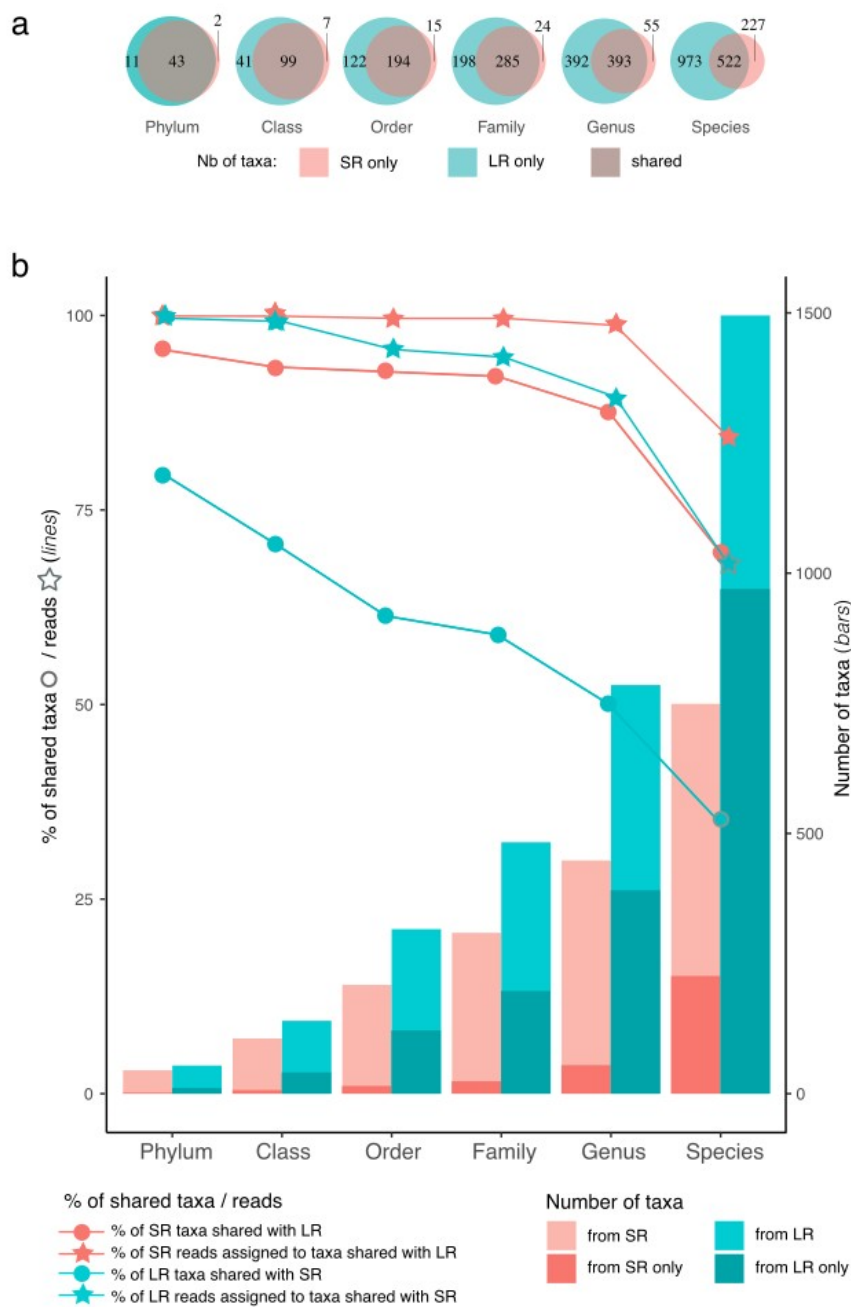
Figure S4. (**a**) Venn diagrams showing the proportions of bacterial taxa shared and unshared between both primer pairs, at each phylogenetic rank (numbers in the discs refer to the numbers of taxa of the portion of the disc it is written on) ; (**b**) On left axis, proportion of bacterial taxa shared between both primer pairs (lines with dots) and proportion of reads assigned to taxa shared between both primer pairs (lines with stars), number of shared and unshared taxa (bars, right axis), at each phylogenetic rank ; more details in Table 1.

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
			Illumina			
OTU499	Dadabacteria	Dadabacteriia	Dadabacteriales	—	—	2,26
OTU295	Planctomycetota	Planctomycetes	Pirellulales	Pirellulaceae		0,81
OTU293					*Blastopirellula*	0,99
OTU277					*Pirellula*	0,44
OTU209	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales inc. sed.	*Bauldia*	0,40
OTU161		Gammaproteobacteria	Ectothiorhodospirales	Ectothiorhodospiraceae	*Thiogranum*	0,53
OTU134			HOC36	HOC36	*HOC36*	1,13
OTU111			Pseudomonadales	Nitrincolaceae	*Marinobacterium*	1,10
OTU92			Thiomicrospirales	Thiomicrospiraceae	*endosymbionts*	2,48
OTU107			Pseudomonadales	Pseudohongiellaceae	*Pseudohongiella*	0,50
OTU118				Halieaceae	*Parahaliea*	0,37
OTU111				Nitrincolaceae	*Marinobacterium*	1,10
OTU139			Gammaproteobacteria inc. sd.	Unknown_Family	*uncultured*	0,39
OTU190			uncultured	uncultured	*uncultured*	0,48
OTU503	Cyanobacteria	Cyanobacteriia	Phormidesmiales	Nodosilineaceae	*MBIC10086*	0,60
OTU52	Verrucomicrobiota	Kiritimatiellae	Kiritimatiellales	Kiritimatiellaceae	*R76-B128*	0,32
OTU528	Chloroflexi	Dehalococcoidia	FS117-23B-02	FS117-23B-02	*FS117-23B-02*	0,60
OTU637	Bacteroidota	Bacteroidia	Flavobacteriales	Flavobacteriaceae	*Hoppeia*	1,19

OTU	Phylum	Class	Order	Family	Genus	MDG
OTU643					*Actibacter*	0,36
OTU703			Bacteroidales	SB-5	*SB-5*	0,53
OTU709				Prolixibacteraceae	*Draconibacterium*	0,55
Nanopore						
OTU_b563	Dadabacteria	Dadabacteriia	Dadabacteriales	__	__	0,81
OTU_b120	Planctomycetota	Planctomycetes	Pirellulales	Pirellulaceae	__	0,73
OTU_b118					*Blastopirellula*	0,39
OTU_b84					*Pir4_lineage*	0,81
OTU_b221	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales inc. sed.	*Bauldia*	0,75
OTU_b1395			Defluviicoccales	Defluviicoccaceae	*Defluviicoccus*	1,14
OTU_b18		Gammaproteobacteria	__	__	__	0,94
OTU_b420			Ectothiorhodospirales	Ectothiorhodospiraceae	*uncultured*	0,42
OTU_b157				Thioalkalispiraceae	*Thiohalophilus*	0,86
OTU_b98			HOC36	HOC36	*HOC36*	0,65
OTU_b454			Pseudomonadales	Nitrincolaceae	*Marinobacterium*	0,85
OTU_b1960				Alcanivoracaceae	*Ketobacter*	0,81
OTU_b355			Thiomicrospirales	Thiomicrospiraceae	*endosymbionts*	0,51
OTU_b1138			Chromatiales	Sedimenticolaceae	*Sedimenticola*	0,85
OTU_b365			pItb-vmat-80	pItb-vmat-80	*pItb-vmat-80*	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	*Mycobacterium*	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.