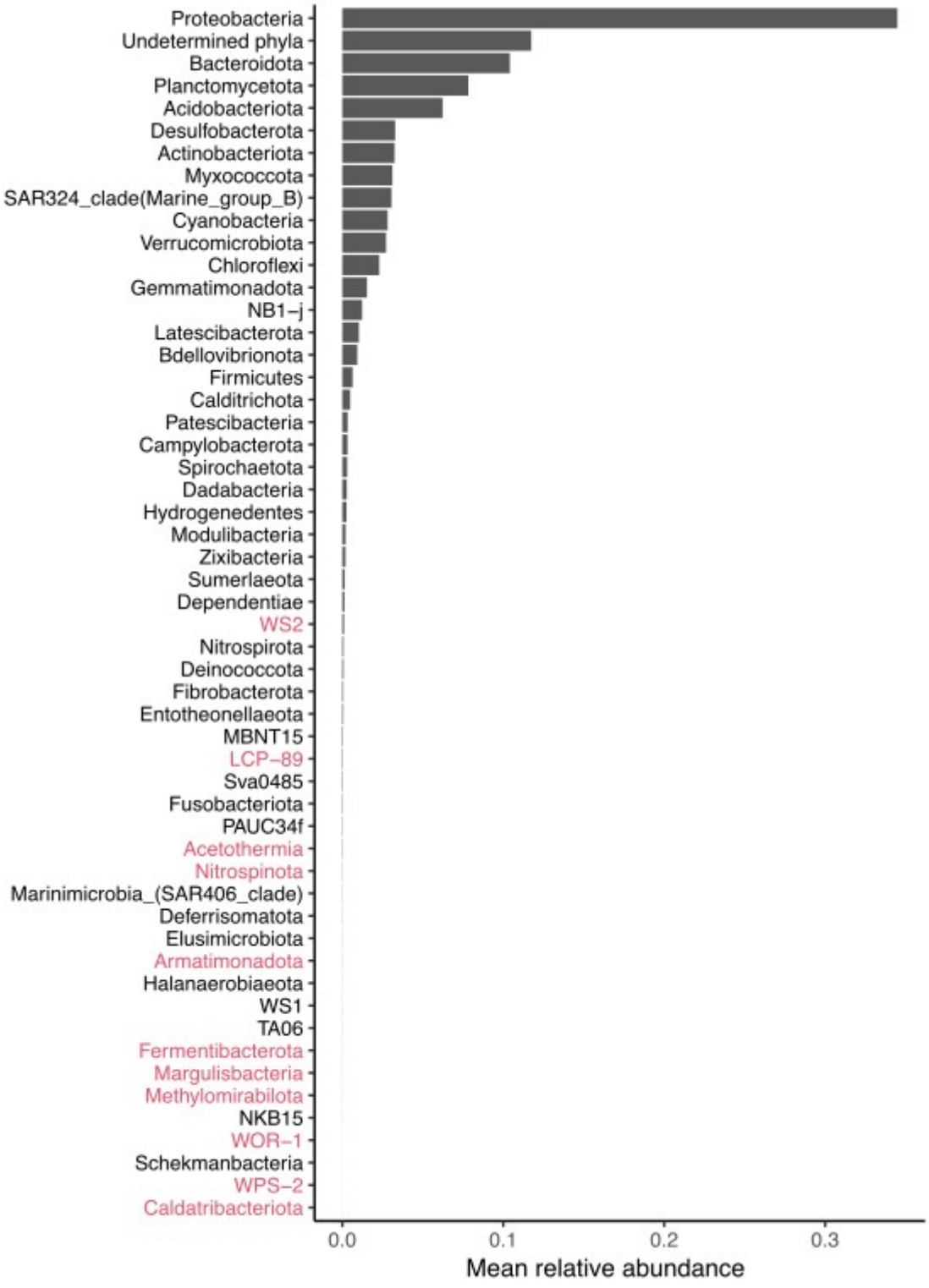

Figure S1. Mean relative abundance of bacterial phyla obtained with LR on Nanopore ; exclusiveLR phyla are in red.

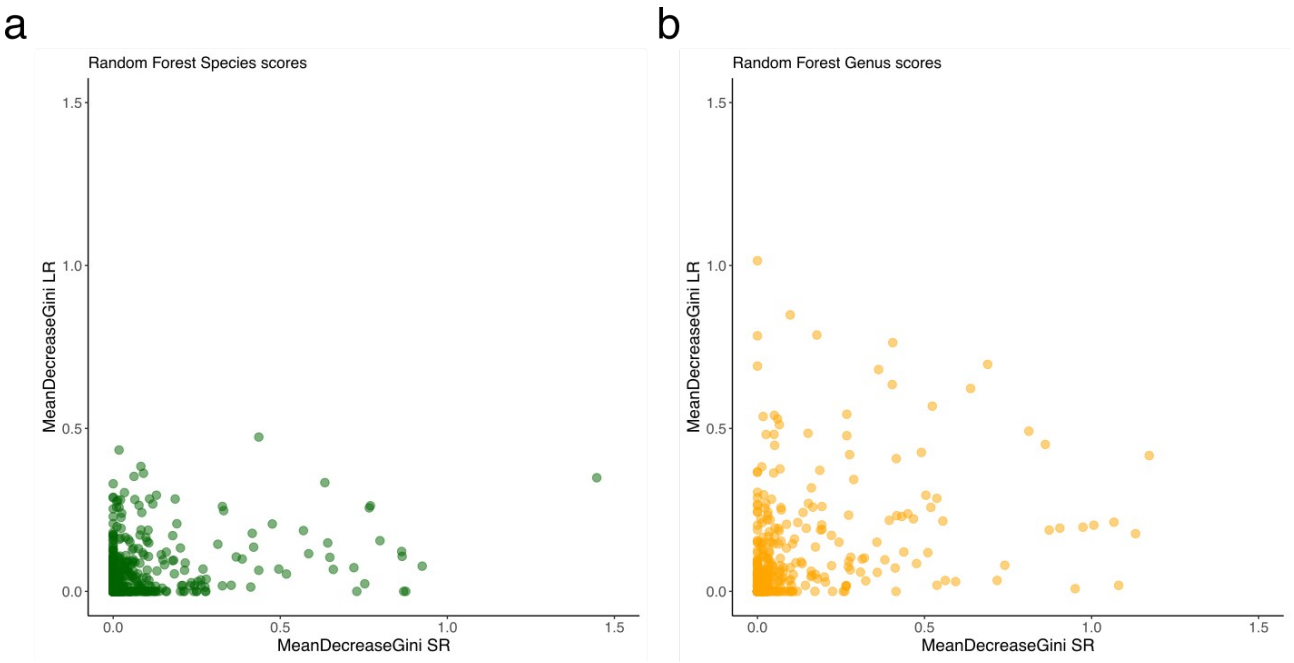

Figure S2. Contribution of Mean Decrease Gini coefficients of common species (**a**) and common genus (**b**) sequenced by short-reads (SR) and long-reads (LR), for [site+(sea-land orientation)] predictors (see details in Table S2). Mean Decrease Gini is a measure of how each variable contributes to 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.

Methods for archaea

SR primers for Illumina (Parada, Needham, and Fuhrman 2016; 515F GTGYCAGCMGCCGCGGTAA and 926R CCGYCAATTYMTTTRAGTTT) did amplified both bacteria and archaea. LR primers used for Nanopore (full-16S for bacteria, ~1.45 kpb; Weisburg et al. 1991; 27F: AGAGTTTGATCMTGGCTCAG ; 1492R: TACGGYTACCTTGTTACGACTT) only amplified bacteria. In Lemoinne et al. 2023, only bacteria were filtered in short-reads for analysis. However, a second LR marker was also chosen for archaea (V1-V6 regions, ~1 kpb; Bahram et al. 2019; SSU1Ar F: TCCGGTTGATCCYGCBRG ; SSU1000Ar R: GGCCATGCAMYWCCTCTC), and presented in this Suppl Mat.

For library of archeal LR, PCRs were performed in 3 small-volume replicates of 12,5 µl each, containing 6,25µl of LongAmp Taq 2x Master Mix (NEB), 4,25µl of milliQ water, 1 µl of DNA (~10ng.μl^{-1}), 0,25 µl of forward primer, 0,25 µl of reverse primer (10nM each). The following PCR parameters are for archaea primers. PCR cycles consisted of initial denaturing for 3 min at 95°C, followed by 32 cycles composed of denaturation for 30 s at 95°C, hybridization for 30 s at 55°C, and elongation for 45 s at 65 °C and final elongation for 10 min at 65°C. All first PCR products were verified by agarose gel electrophoresis, re-amplified if negative until they were positive, and positive triplicates were pooled into one before the indexation PCR. Concentrations were measured by the Qubit fluorometer (dsDNA BR kit) and brought back to a concentration of 1ng/µl. Indexation PCR was realized according to the Nanopore « PCR barcoding (96) amplicons (SQK-LSK109) » protocol. Indexed amplicons were pooled into one tube per primer/marker and purified with magnetic beads (Nucleomag Macherey Nagel, 1:0.8 ratio). Indexed and purified products were verified on agarose gel electrophoresis.

Sequencing and processing of archaeal LR was done following the same protocol as for bacterial full-16S described in the manuscript, except for filtering size of raw reads (900 and 1.1kbp for 16S V1-V6). The circular diagram showing archaean OTUs the most contributing to PCA structure in each sample was obtained with the ord_plot_iris function from microViz R package (Barnett 2023).
#######

Results for archaea

With 16SV4-V5 degenerated primers on a single flow-cell, SR read coverage for archaea (mean 193 reads/sample, min 29 - max 620) was much lower than those of LR for archaea, with archaeal specific primers and a dedicated flow-cell (mean 4817 reads/sample, min 2384 - max 6701). Therefore SR archaean taxa are just mentioned here, but not interpreted. LR detected 171 archaean OTUs in 11 phyla, almost all belonging to core communities in samples (Table S1).
########

Figure S3 (next page). (**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.

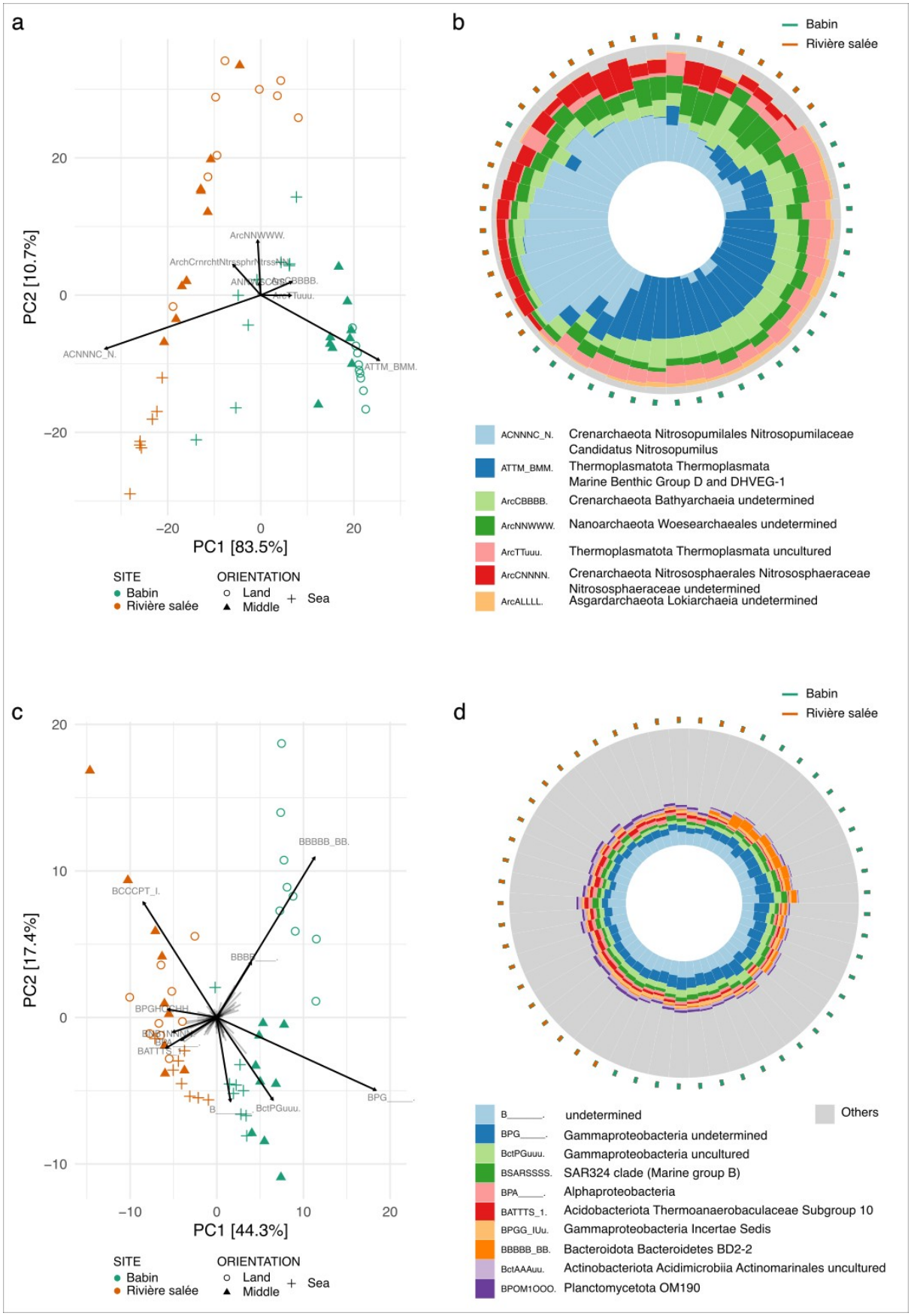
a
b
c
d
PC2 [10.7%]
PC1 [83.5%]
ArcNNWWW.
ACNNNC_N.
ATTM_BMM.
SITE
Babin
Rivière salée
ORIENTATION
Land
Middle
Sea
Babin
Rivière salée
ACNNNC_N. Crenarchaeota Nitrosopumilales Nitrosopumilaceae Candidatus Nitrosopumilus
ATTM_BMM. Thermoplasmatota Thermoplasmata Marine Benthic Group D and DHVEG-1
ArcCBBBB. Crenarchaeota Bathyarchaeia undetermined
ArcNNWWW. Nanoarchaeota Woesearchaeales undetermined
ArcTTuuu. Thermoplasmatota Thermoplasmata uncultured
ArcCNNNN. Crenarchaeota Nitrososphaerales Nitrososphaeraceae Nitrososphaeraceae undetermined
ArcALLLL. Asgardarchaeota Lokiarchaeia undetermined
PC2 [17.4%]
PC1 [44.3%]
BBBBB_BB.
BCCCPT_I.
BPG_____.
BctPGuuu.
SITE
Babin
Rivière salée
ORIENTATION
Land
Middle
Sea
Babin
Rivière salée
Others
B_____. undetermined
BPG_____. Gammaproteobacteria undetermined
BctPGuuu. Gammaproteobacteria uncultured
BSARSSSS. SAR324 clade (Marine group B)
BPA_____. Alphaproteobacteria
BATTTS_1. Acidobacteriota Thermoanaerobaculaceae Subgroup 10
BPGG_IUu. Gammaproteobacteria Incertae Sedis
BBBBB_BB. Bacteroidota Bacteroidetes BD2-2
BctAAAuu. Actinobacteriota Acidimicrobiia Actinomarinales uncultured
BPOM1OOO. Planctomycetota OM190

Figure S3.

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 SR were mentioned but the read coverage by sample was much lower than those for archaeal LR.

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
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.