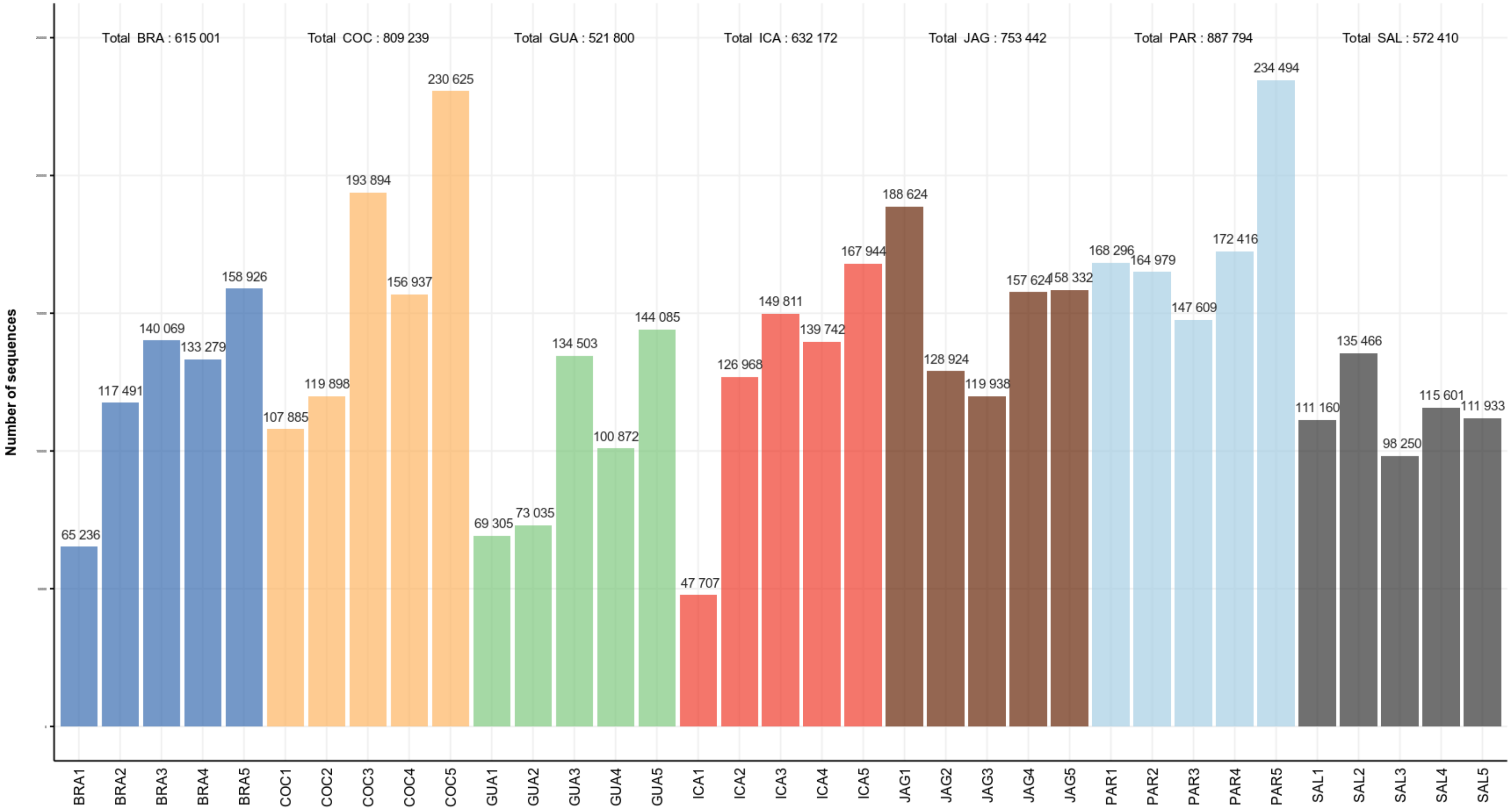
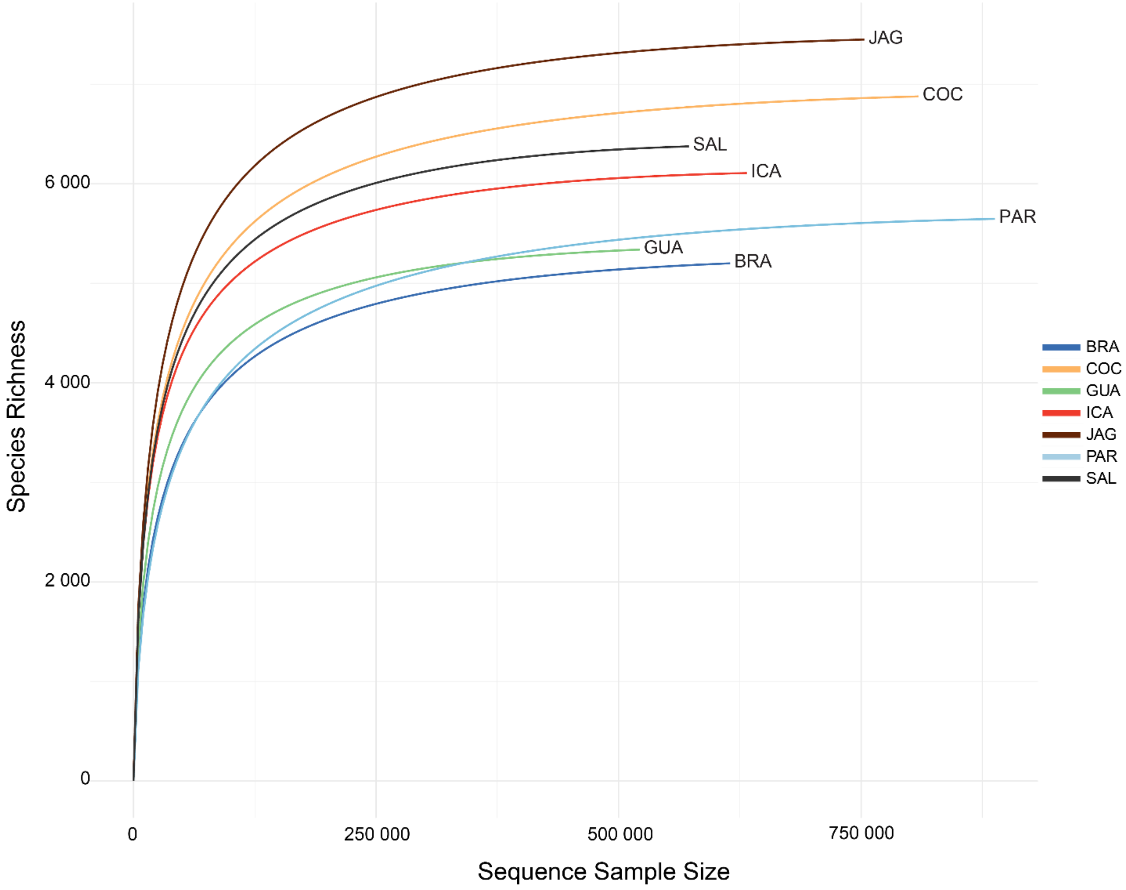
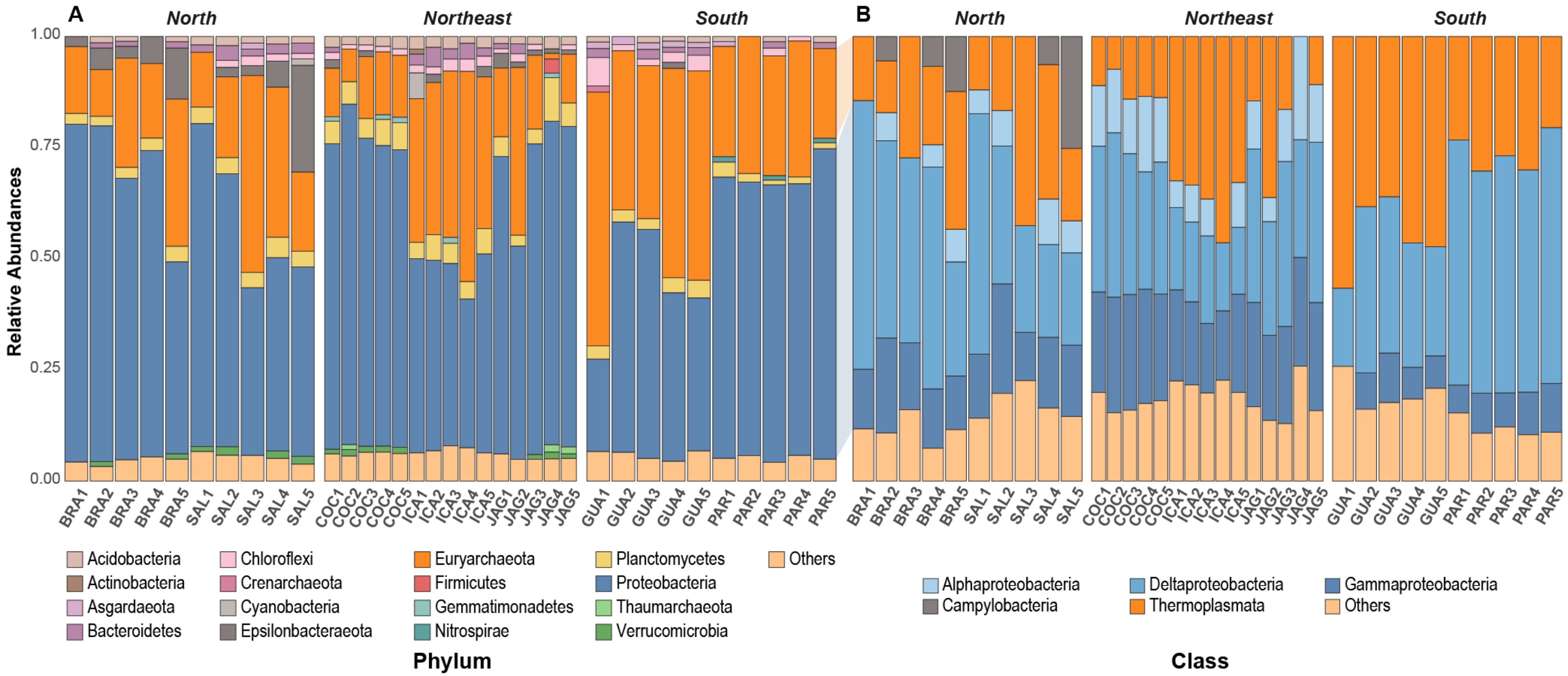
Supplementary information for the manuscript “Brazilian semi-arid mangroves-associated microbiome as pools of richness and complexity in a changing world” by Tavares et al.



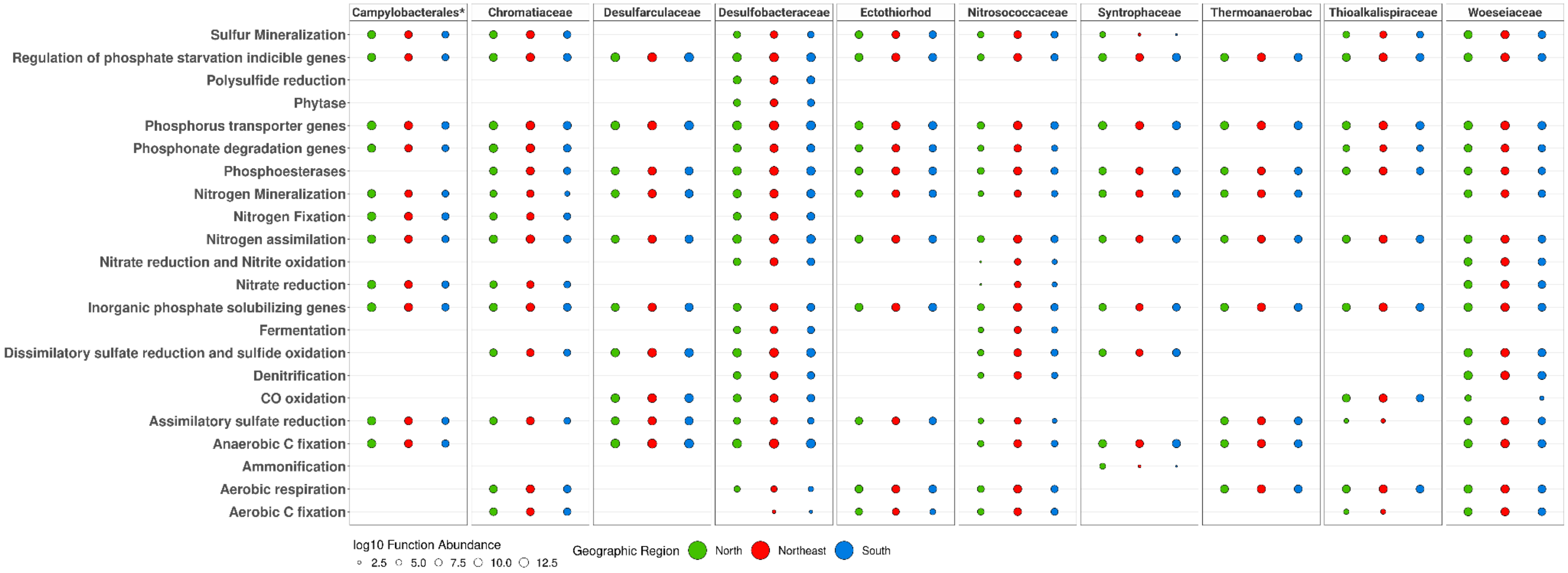
Supplementary Figure 1 - Total number of sequences in each sampling point after quality filtering and removal of chimeric samples, Mitochondria, Chloroplast, Non-assigned and Eukarya reads. The figure displays each of the five sampling points for each mangrove and the total number of sequences per mangrove is shown in the upper zone of the figure. BRA = Bragança (N); SAL = Salinópolis (N); COC = Cocó (NE); JAG = Jaguaribe (NE); ICA = Icapuí (NE); GUA = Guaratuba (S); and PAR = Paranaguá (S).



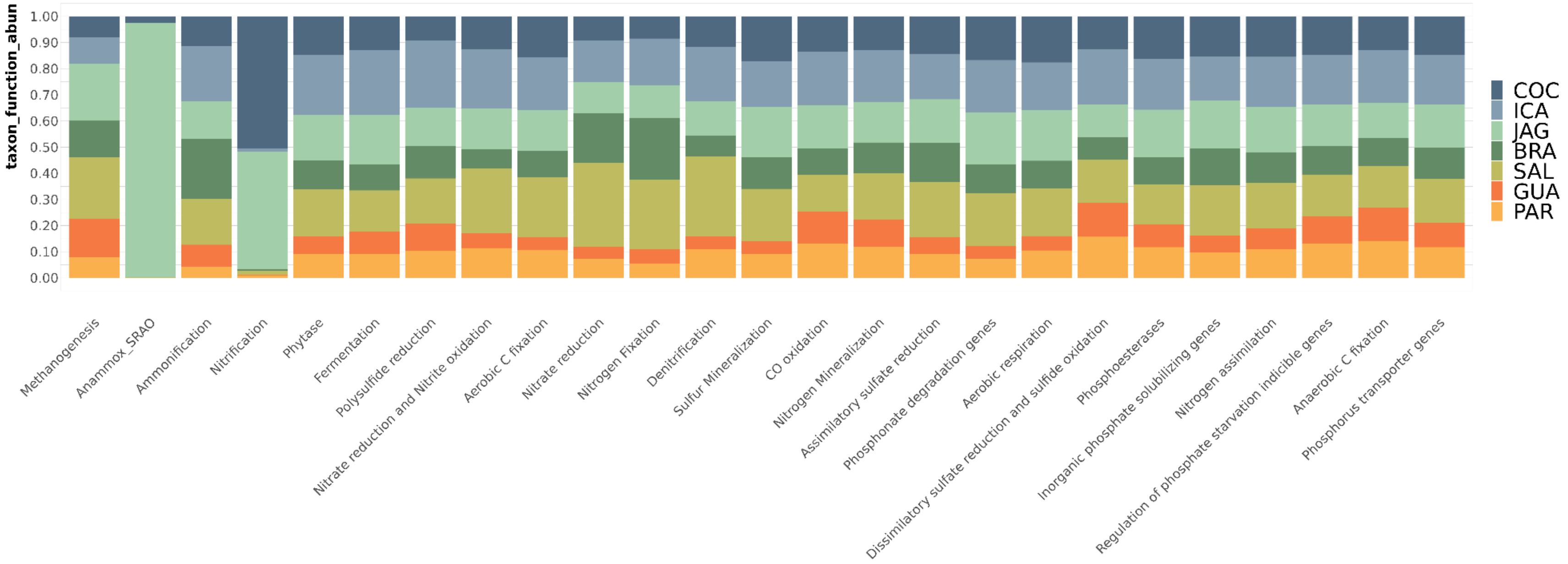
Supplementary Figure 2 – Rarefaction curves generated from the species richness for the seven studied mangroves. The X-axis presents the number of sequences in each mangrove, while the Y-axis shows the number of species (BRA = Bragança (N); SAL = Salinópolis (N); COC = Cocó (NE); JAG = Jaguaribe (NE); ICA = Icapuí (NE); GUA = Guaratuba (S); and PAR = Paranaguá (S).



Supplementary Figure 3 – Comparison of taxonomic distributions of Bacteria and Archaea at the phylum (A) and class (B) level in *Rhizophora mangle* root-associated soil. Stacked bar plot of the relative abundance above 0.01 for each sampling point (summed from three replicates each). Phyla and classes with relative abundance < 0.01 are displayed as “Others”.



Supplementary Figure 4 – Main microbial contributors to KEGG Orthologs associated with Carbon, Nitrogen, Sulphur, and Phosphorus cycles based on PICRUSt2 analysis generated by using the 16S rDNA data on *Rhizophora mangle* root-associated soil microbiomes. In the figure, "Ectothiorhod" refers to Ectothiorhodospiraceae, "Thermoanaerobac" refers to Thermoanaerobaculaceae, and "Campylobacterales*" refers to Campylobacterales Incertae Sedis.



Supplementary Figure 5 – PICRUSt2 analysis of predicted KEGG Orthologs associated with Carbon, Nitrogen, Sulphur, and Phosphorus cycles generated by using the 16S rDNA data on mangrove-associated microbiomes.

Supplementary Table 1 – Counts of raw sequencing reads during quality processing and total number of filtered reads (nonchim). Five sampling points for each mangrove were sampled, with triplicates subsamples for each, totaling 105 samples (five samples with three subsamples per mangrove). Input represents the total resulting number of raw sequences; filtered represents the total number of samples after quality filtering; and nonchim represent the total number of non-chimeric samples.

Supplemented as Excel file.

Supplementary Table 2 – General characterization of the datasets and alpha diversity. No. seqs = number of sequences; No. sing = number of singletons; Good's = Goods coverage; S obs = observed richness.

Mangroves	**No. seqs**	**No. sing**	**Good's**	**Inverse Simpson**	**Shannon**	**S obs**	**Chao1**
Bragança (N)	615 001	243	99.96	28.83	5.74	5 200	5274.82
Salinópolis (N)	572 410	174	99.97	75.43	6.64	6 375	6405.78
Cocó (NE)	809 239	209	99.97	140.44	6.95	6 877	6928.75
Jaguaribe (NE)	753 442	195	99.97	76.67	6.85	7 448	7490.79
Icapuí (NE)	632 172	138	99.98	233.64	6.94	6 107	6129.56
Guaratuba (S)	521 800	202	99.96	86.56	6.22	5 338	5391.99
Paranaguá (S)	887 794	198	99.98	14.10	5.31	5 647	5693.44

Supplementary Table 3 – List of the 33 significant indicator genera ($P < 0.05$) for *Rhizophora mangle* root-associated soil microbiomes and their respective values for North, Northeast, and South regions. The values were obtained by using the function *multipatt* from *indicspecies* package in R.

Indicator genus	**stat**	***P*-value**	**Indicator value**
North			
Sulfurovum	0.921	0.036	0.8482
Blastocatella	0.914	0.025	0.8361
Thiofractor	0.88	0.009	0.7745
Truepera	0.868	0.009	0.7536
Algiphilus	0.864	0.036	0.7459
Thiovulum	0.825	0.02	0.6804
Thermotomaculum	0.774	0.037	0.5988
Altererythrobacter	0.727	0.009	0.528
*Verrucomicrobia 01 **	0.696	0.04	0.4848
Northeast			
Pontibacillus	1	0.022	1
Halomonas	1	0.022	1
Magnetovibrio	1	0.022	1
Roseimarinus	1	0.022	1
Modicisalibacter	0.99	0.022	0.9801
Candidatus_Babela	0.979	0.022	0.9575
Fulvivirga	0.971	0.022	0.9437
Bradymonas	0.966	0.022	0.9335
Halobacillus	0.944	0.022	0.8912
Tepidibacter	0.936	0.022	0.8767
X3PJM14	0.923	0.022	0.8518
Tistlia	0.918	0.022	0.8433
Halovulum	0.912	0.022	0.8317
Hypnocyclicus	0.91	0.022	0.8286
Reinekea	0.904	0.022	0.8174
Salinirepens	0.901	0.022	0.8114

Bythopirellula	0.883	0.022	0.779
OM60.NOR5. clade	0.881	0.022	0.7753
Orenia	0.856	0.022	0.7333
Aquimixticola	0.849	0.033	0.7214
Pelagibius	0.848	0.022	0.7191
Vulgatibacter	0.8	0.022	0.6397
South			
Planktotalea	0.825	0.036	0.68
SEEP.SRB1	0.67	0.045	0.4482