

Supplementary material

1- Data gathering methodology

1.1 – Sampling effort and OTUs richness data

The quantitative data presented in Figure 1 and table S1 were recovered using the following rules:

- we chose to present one value of sampling effort and richness per species and per study.
- we used only OTUs richness obtained with a 97% similarity cut-off as this is the most frequently used threshold, thus increasing the amount of available data.
- we used the values reported by the original authors when provided in the main text, in tables of in supplementary information. When only rarefaction curves were available, we used a plot digitalization approach (<http://arohatgi.info/WebPlotDigitizer/app/>).
- when no data was directly available we contacted the original authors.
- when available, we used the total number of sequences and OTUs detected for each species analyzed in the original paper.
- when the total numbers were not available, we used the mean richness and sampling effort values estimated across the different location where the species was sampled or across the different replicates analyzed.

1.2 – Estimation of sampling effort - OTUs richness relationship

To estimate the relationship between the sampling effort and the OTUs richness in macro-organisms associated bacterial communities, we used the *mmSAR* package (Guilhaumon *et al.* 2010) to fit species area relationships (SAR). We tested the six following models: power, exponential, monod, logistic, ratio and lomolino. The best model was determined using the Akaike information criteria (AIC).

1.3 – Abundance shifts

The quantitative data presented in Figure 2 and supplementary figures S2-S6 were recovered from the VAMPS database (Huse *et al.* 2014) or from supplementary material of original papers. Figure 2 present data grouped at the genus level. The figures S2-S6 exhibit various level of taxonomic resolution.

1.4 – Spreading distance

The quantitative data presented in Figure 3 were recovered from original papers. When both GTT and SSS were available for one given species we combined them. When a range was presented we used the two extremes values. When no data were available at the species level we use ranges of data collected from various studies on a given group.

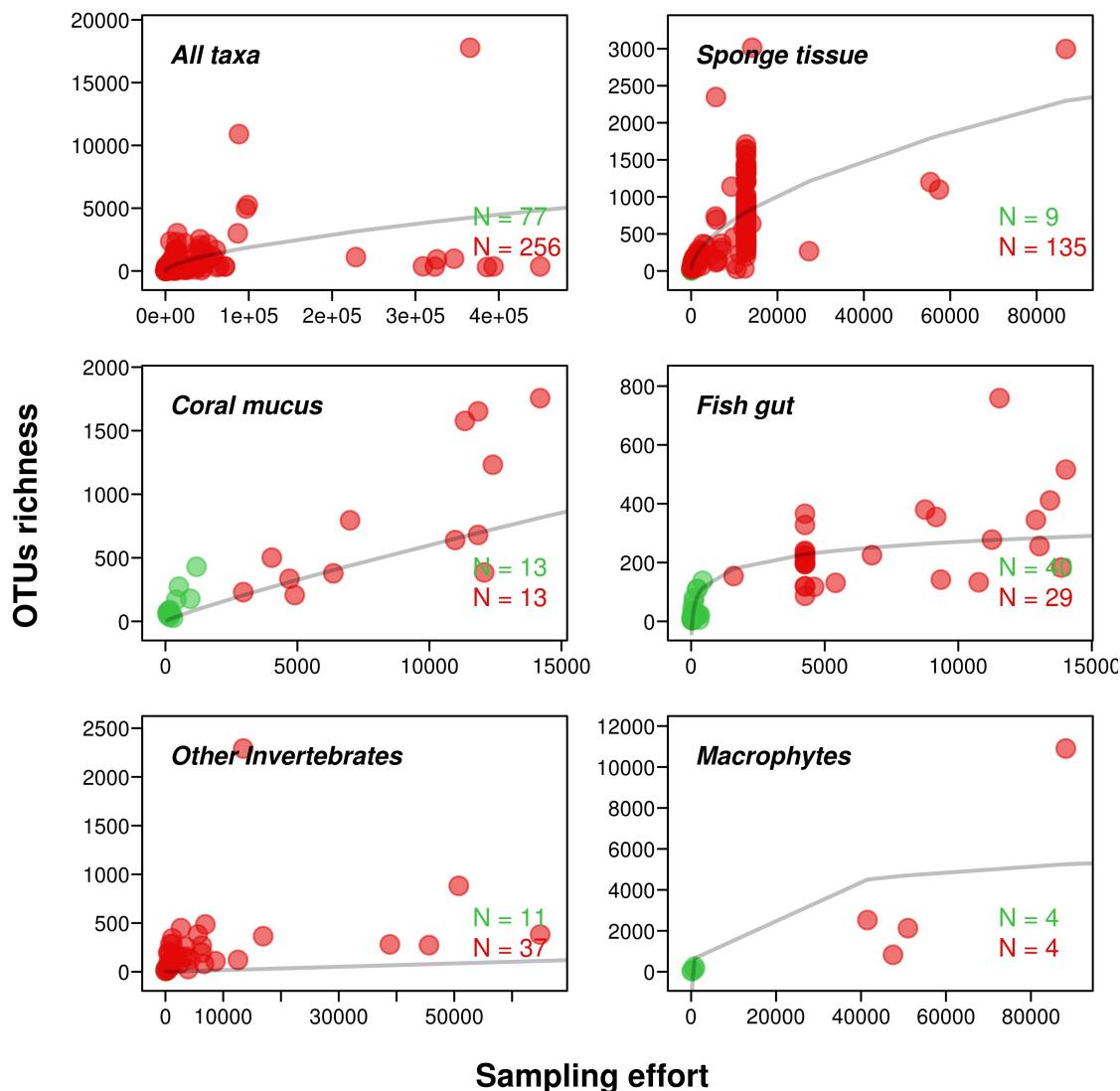
2- Additional results

Table S1 – Results of model comparison.

	All taxa		Sponge tissue		Coral mucus		Fish gut		Other invertebrates		Macrophytes	
	AIC	R2	AIC	R2	AIC	R2	AIC	R2	AIC	R2	AIC	R2
power	4898.35	0.66	2000.36	0.93	452.47	0.83	843.14	0.55	650.82	0.28	191.35	0.29
expo	5161.04	0.26	2296.47	0.48	489.92	0.53	839.26	0.57	648.31	0.31	191.23	0.29
monod	4928.65	0.63	2042.32	0.90	453.49	0.83	837.18	0.58	672.06	-0.06	190.38	0.35
logist	4912.44	0.65	2021.42	0.92	452.07	0.84	839.67	0.58	646.89	0.35	190.62	0.44
ratio	4930.66	0.63	2044.32	0.90	455.04	0.83	839.19	0.58	648.97	0.33	192.38	0.35

Figure S1 – Number of OTUs recorded in bacterial communities associated marine macro-organisms.

Same as figure 1 in the main text but for small sampling effort values. The first figure represents 0.2% of the sampling effort and the second represents 0.05%



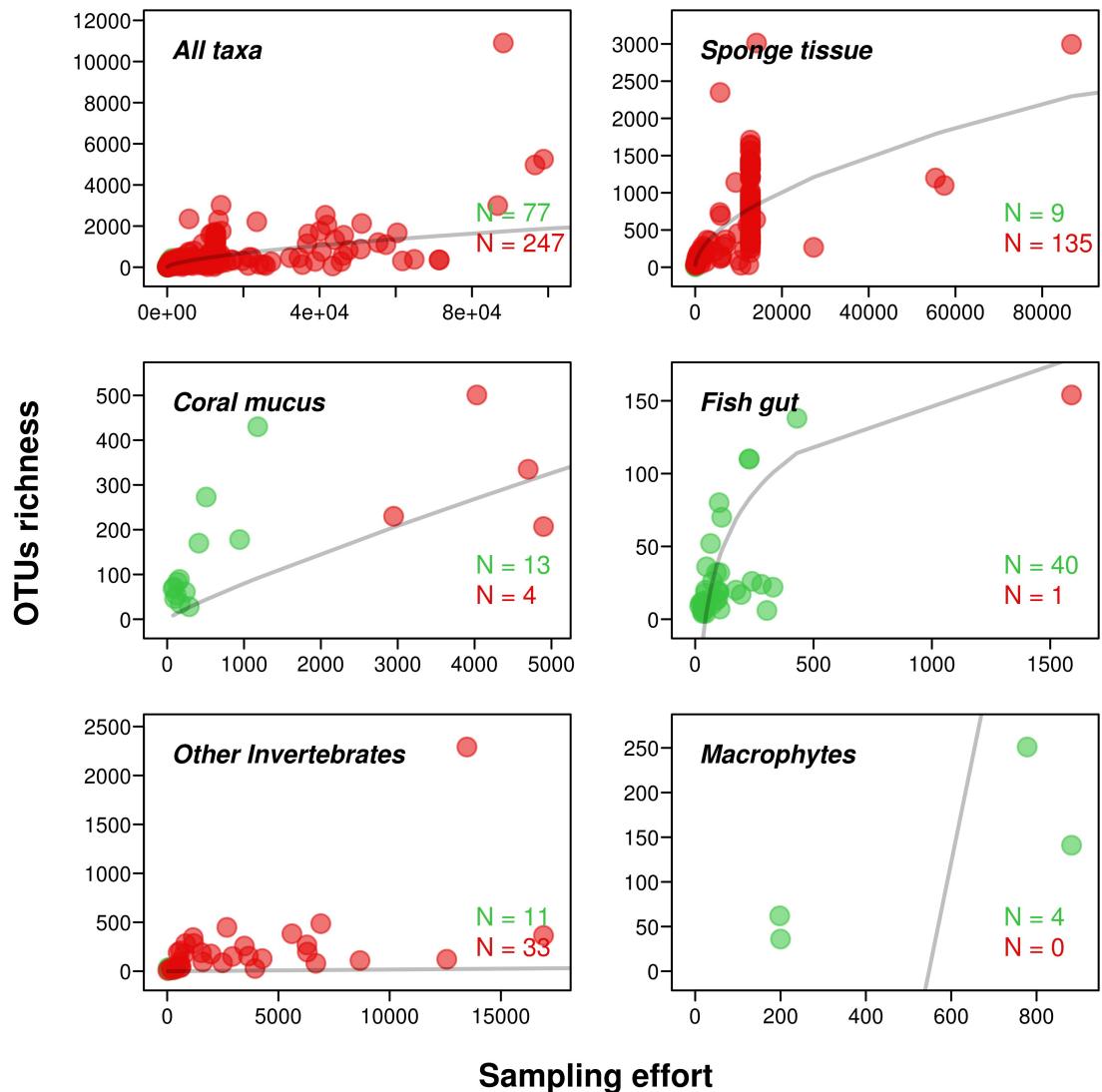
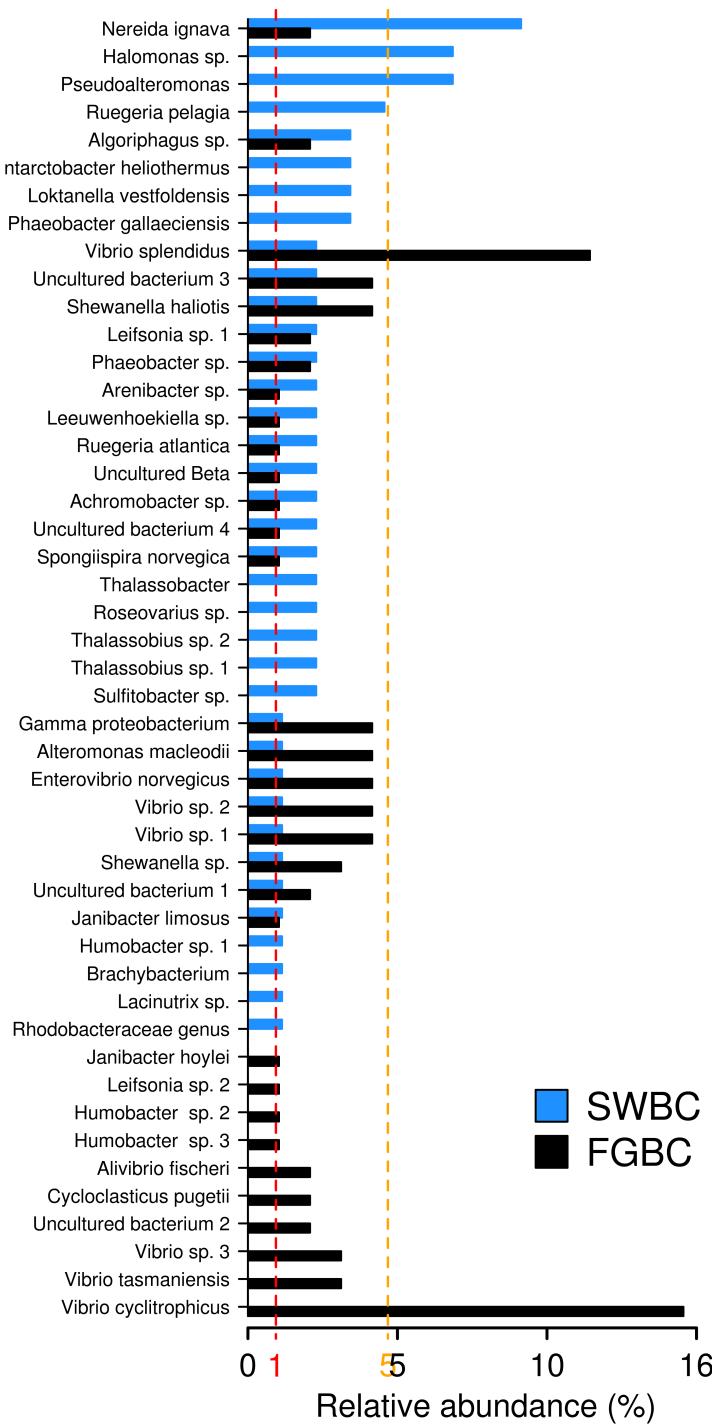


Figure S2-S6 – Abundance distribution of OTUs within macro-organisms associated bacterial community and the surrounding seawater bacterial communities.

The following plots were constructed in the same way as the figure 2 in the main text. However, the retrieved data have a coarser level of resolution which varies depending on the study. Only the taxa with total abundance > 0.5% are represented.

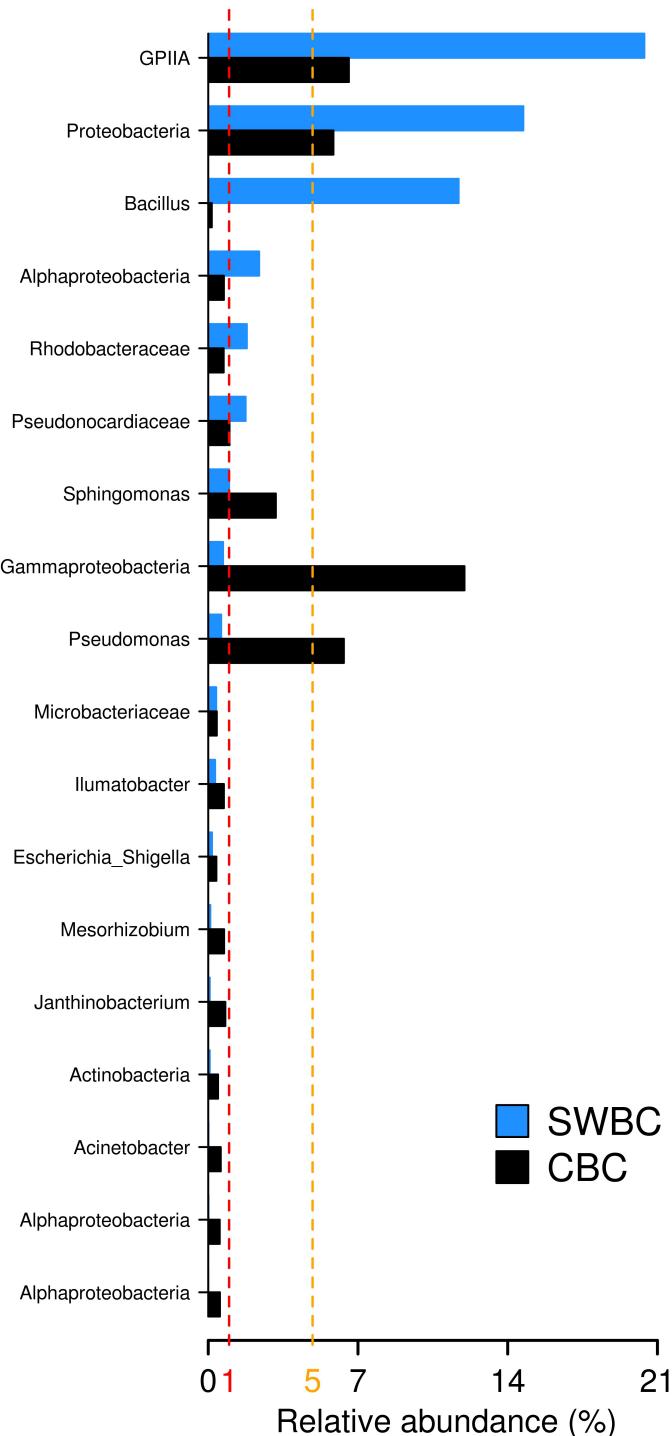
Data from Balcazar *et al.* 2010

Hippocampus guttulatus

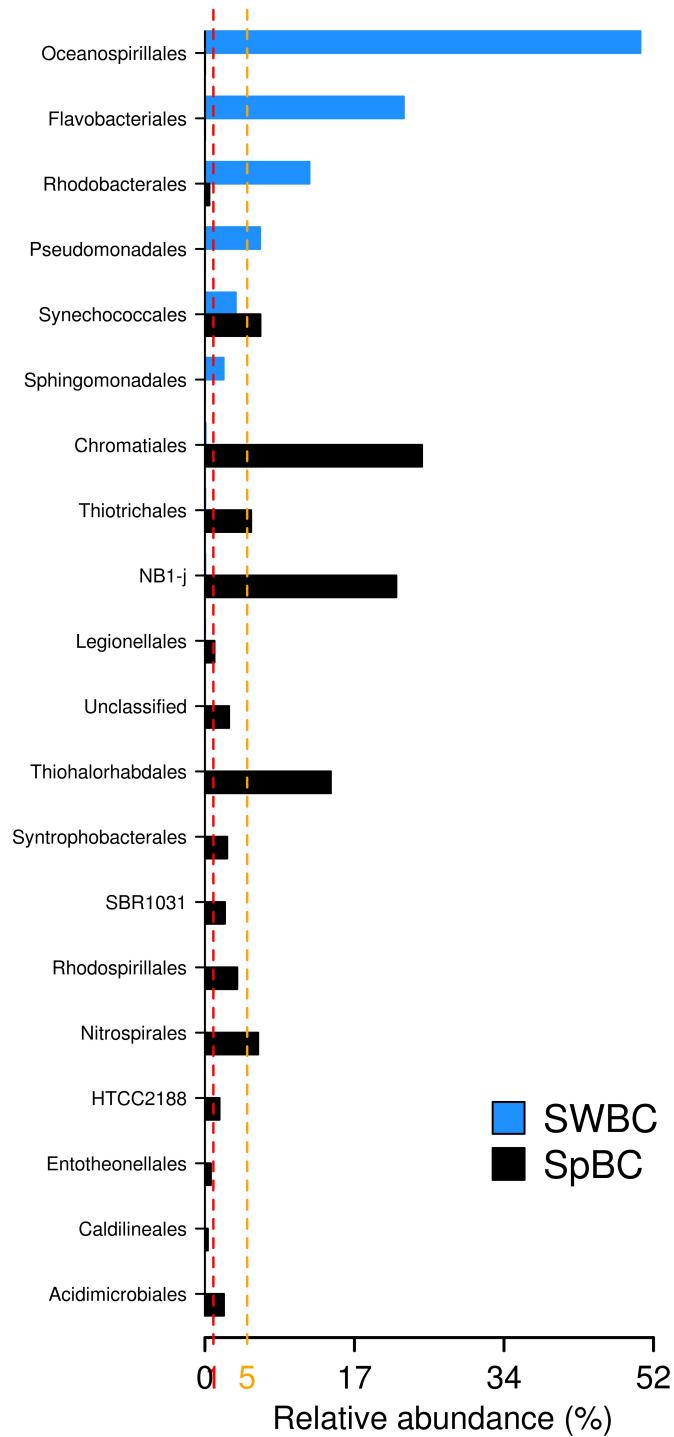


Data from Carlos *et al.* 2013

Madracis decactis, Mussismilia hispida, Palythoa caribaeorum, and Tubastraea coccinea

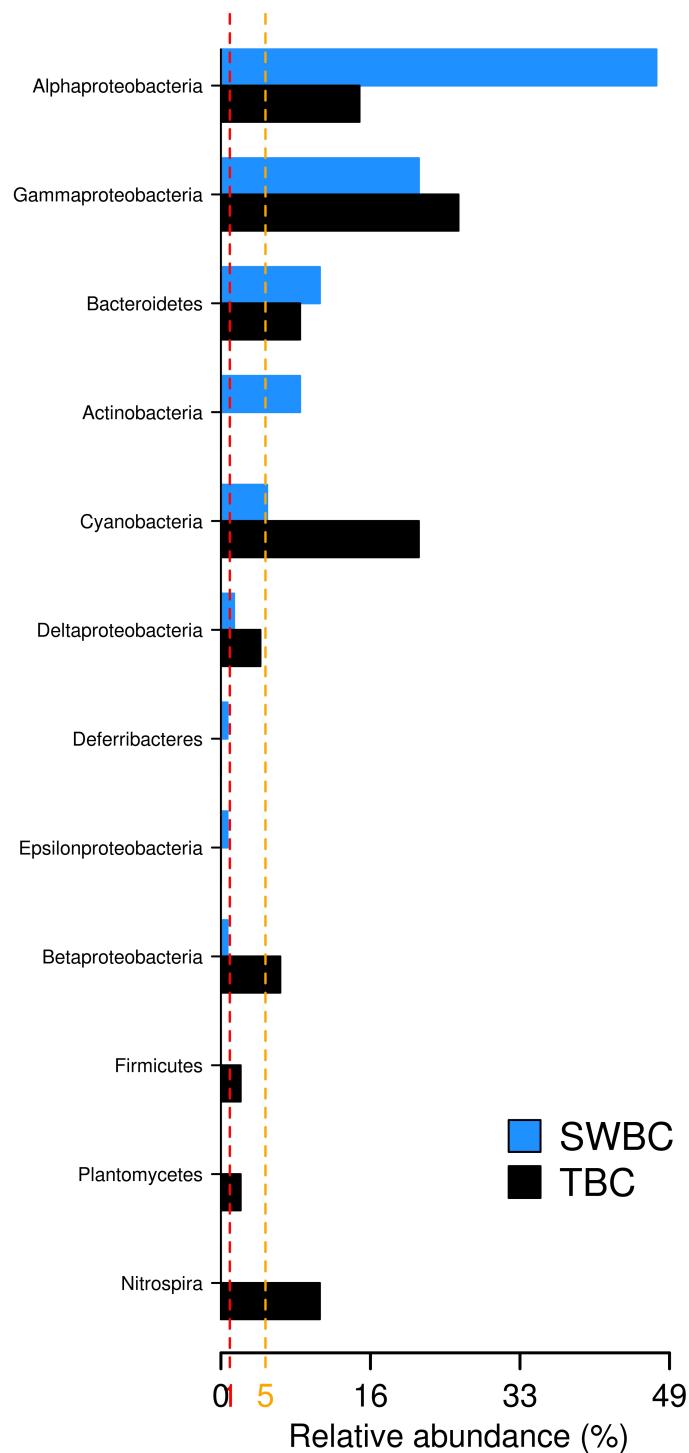


Data from de Voogd *et al.* 2015
Styliissa massa and *Xestospongia testudinaria*

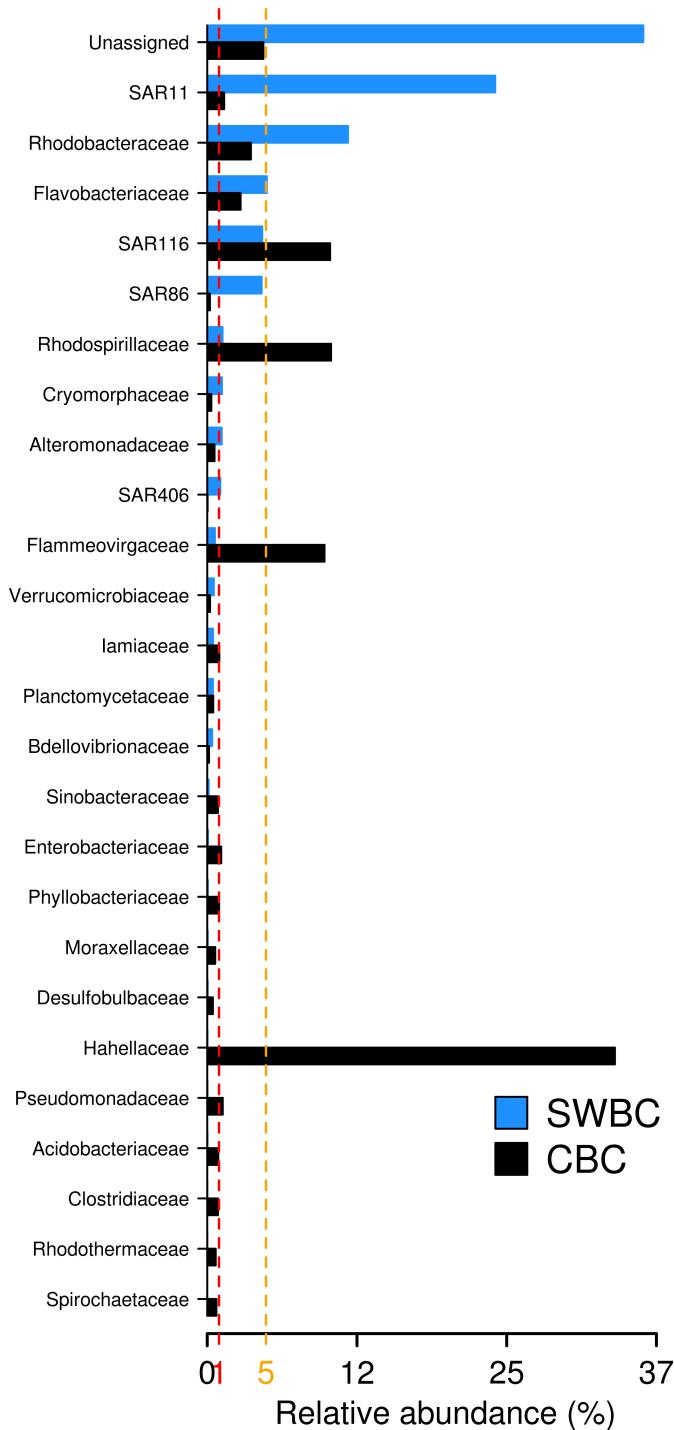


Data from Erwin *et al.* 2011

Didemnum sp.

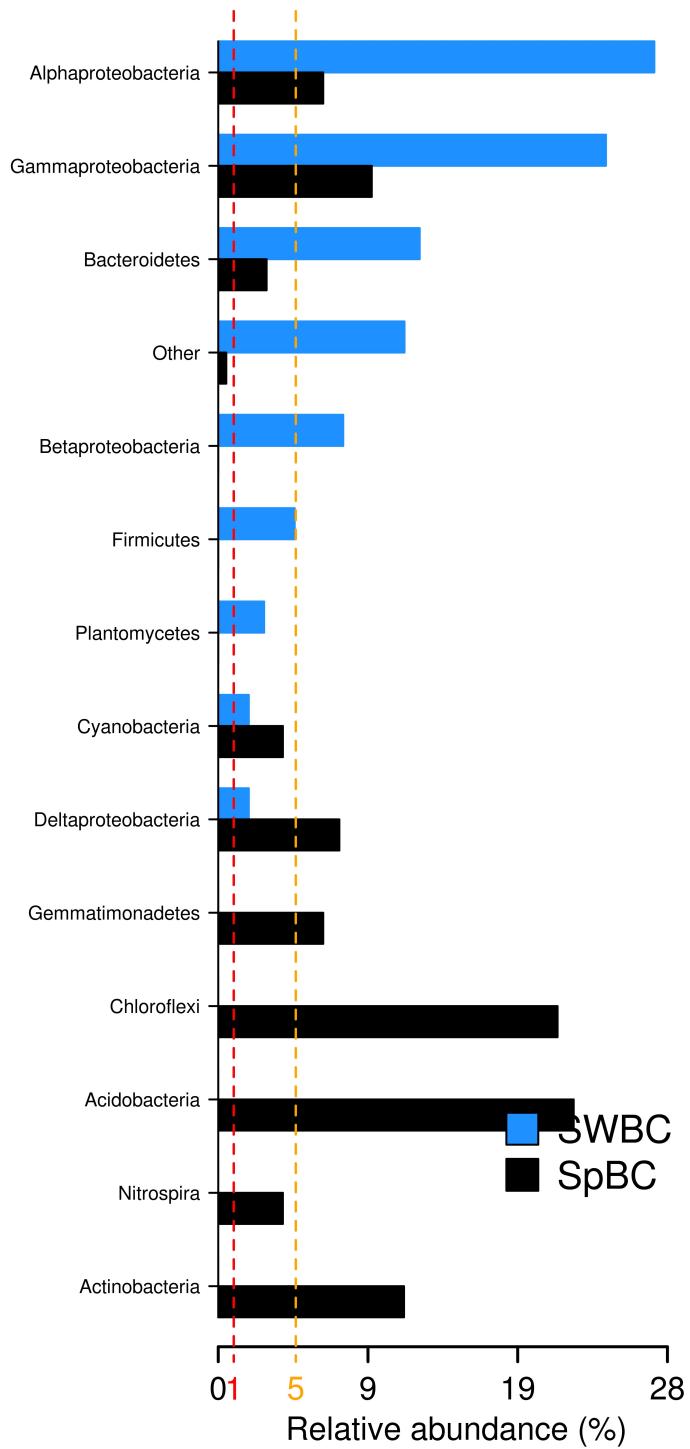


Data from Sunagawa *et al.* 2010 (VAMPS project: ICM_CCB_Bv6)
Montastraea spp., Diploria strigosa, Porites astreoides, Acropora spp. Gorgonia ventalina



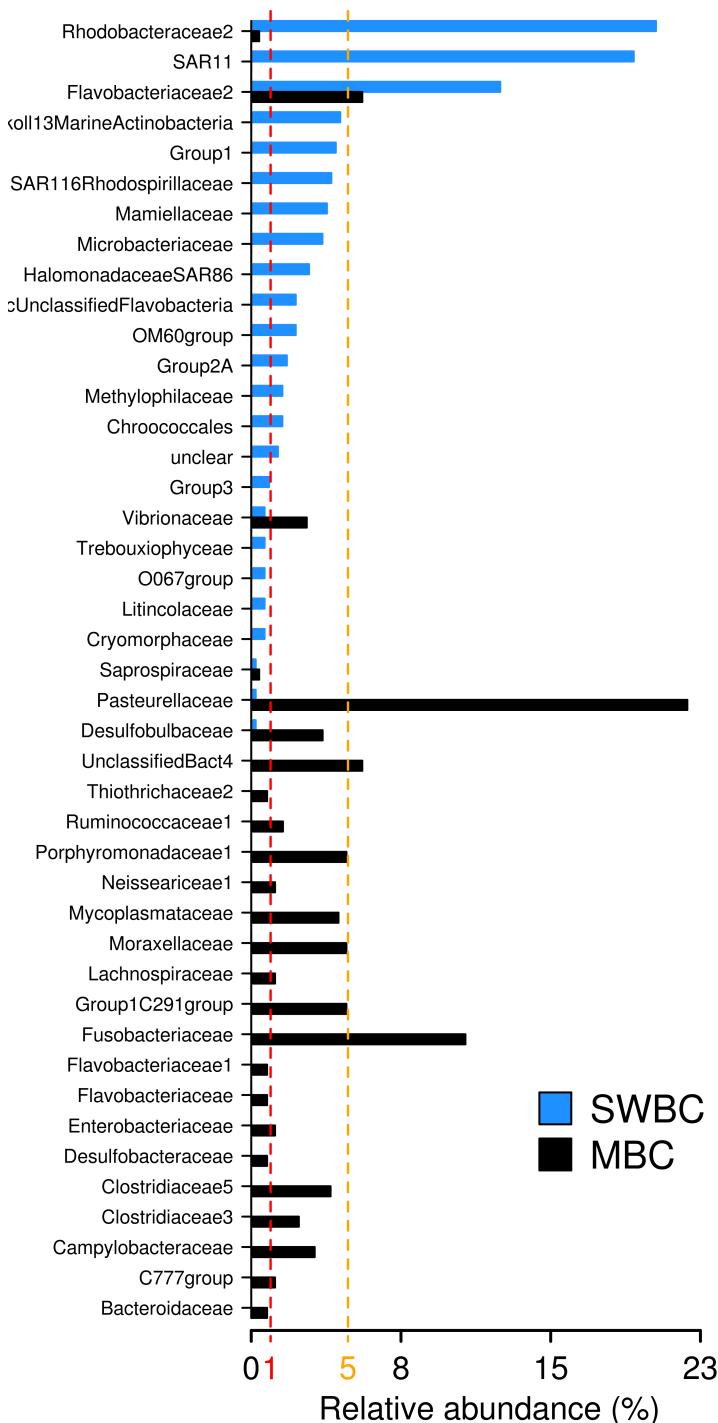
Data from Hentschel *et al.* 2006

Several species



Data from Bik *et al.* 2016

Several mammals



3- References used in tables

3.1 – References used in Table S1

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