Supplementary materials

Manuscript Title: Antarctic sponges from the Terra Nova Bay (Ross Sea) host a diversified bacterial community

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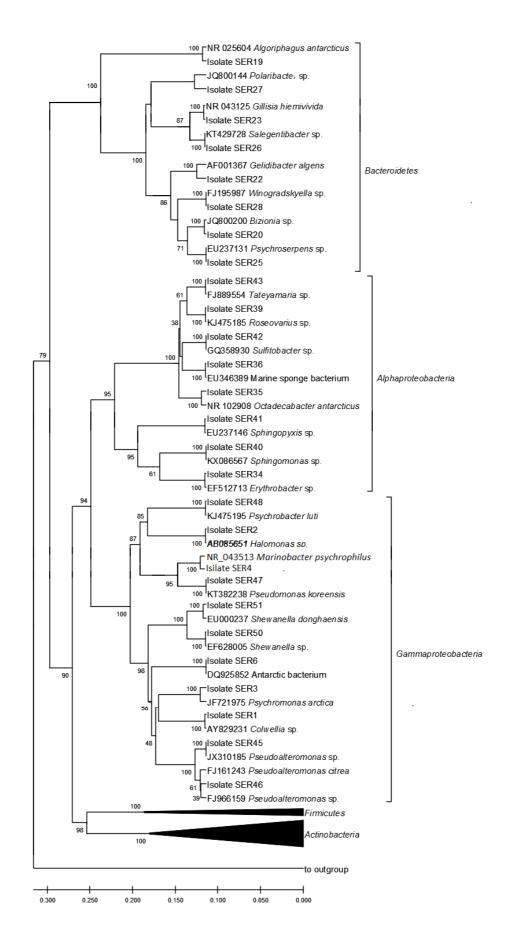
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Supplementary materials

Figure S1. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences of Gram-negative strains (a) and Gram-positive strains (b) isolated from sponge samples.

Figure S2. Non-metric multidimensional scaling analysis (nMDS) computed onBray-Curtis similarity analysis conducted on the bacterial community associated with sponges for sampling site.

Table S1. Ecological indices of Antarctic sponge-associated bacterial communities compared to seawater.



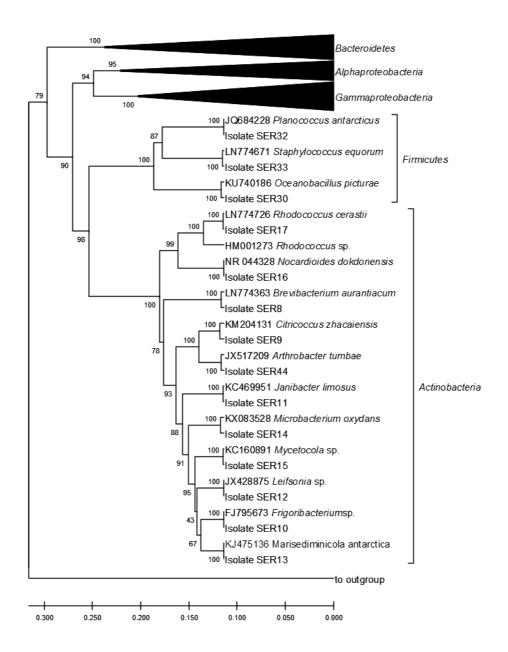


Figure S1. Savoca et al.

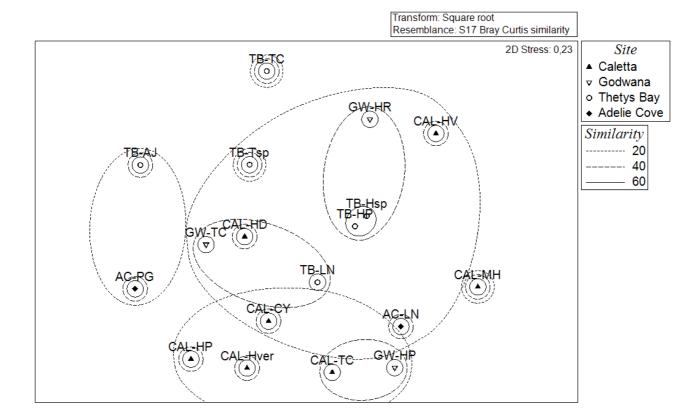


Figure S2. Savoca et al.

Table S1. Ecological indices of Antarctic sponge-associated bacterial communities compared to seawater.

Sample	OTUs			
	Taxa	Chao1	np-Shannon	Simpson
			(H')	(D)
AJ	10.0	12.0	1.9	0.83
LN	6.0	6.0	1.03	0.51
CY	10.0	11.0	2.15	0.88
HP	10.0	10.2	1.78	0.78
PG	12.0	13.5	2.25	0.87
MH	5.0	8.0	0.59	0.27
HD	11.0	14.3	1.12	0.52
HV	6.0	6.5	0.97	0.45
HR	10.0	11.0	2.13	0.86
Hsp	8.0	13.0	0.84	0.39
TC	17.0	16.2	1.80	0.69
TS	7.0	28.0	1.95	0.86
Tsp	13.0	28.0	1.91	0.73
Hver	13.0	15.5	1.74	0.71
Seawater	41.0	54.2	2.14	0.75