



Table S1. Isolates identified among the three studied communities. The identifications were based on 16S rRNA amplification and sequencing.

Microbial communities	Sampled areas	
	Cala do Norte	Barreiro
AMC ^{a1}	<i>Bacillus</i> (<i>B. cereus</i> and <i>B. subtilis</i>) <i>Serratia marcescens</i> <i>Citrobacter freundii</i> <i>Pseudomonas putida</i> <i>Vibrio metschnikovii</i>	<i>Bacillus</i> (<i>B. megaterium</i> , <i>B. cereus</i> , <i>B. subtilis</i> , and <i>B. soli</i>) <i>Vibrio</i> (<i>V. metschnikovii</i> and <i>V. fluvialis</i>) <i>Aeromonas media</i>)
AnMC ^a	<i>Clostridium</i> spp. <i>Clostridium difficile</i> <i>Enterobacteriaceae</i> <i>bacterium</i>	<i>Enterobacteriaceae</i> <i>bacterium</i>
SO ₄ -RMC ^a	<i>Desulfovibrio desulfuricans</i>	<i>Desulfovibrio desulfuricans</i>

^(a) AMC: aerobic microbial community, AnMC: anaerobic microbial community, and SO₄-RMC: sulfate-reducing microbial community.

¹ Part of these data were published in Figueiredo et al. [25].