



**Fig. S4 Relative abundances (in cumulative percentage) of the most abundant bacterial classes in seawater.** Bacterial community compositions were shown for each sample ( $n=3$  per treatment) after 0, 4, 8 and 11 weeks of incubation in the benthic mesocosms under different conditions (see ‘Materials and Methods’ section; a, ambient; +, elevated). Analysis is based on bacterial 16S rDNA (V1-V2) amplicon sequences (Illumina MiSeq). Low abundant classes ( $\leq 1\%$ ) were summarized as “other”.