Supplementary Information

Supplementary Methods

Sample sites and benthic cover. Field studies were conducted across four islands in the Southern Line Island archipelago (southern portion) spanning 4°01'S to 11°26'S from October 18 to November 6, 2013. Mean daily PAR at 10m depth on the forereef measured of 312 +/- 214 μmol photons m^{-1} s^{-1} (LI-COR, Inc., www.licor.com) and water temperature ranged from 28.1 +/- 0.5 ^{o}C. The percent cover of benthic corals and algae was estimated in each tent mesocosm using photoquads and the program photogrid as described in Smith et al., (1).

In situ *reef collections.* Collapsible benthic isolation tents (cBITs), referred to in text as benthic chambers, were used to assess effects of specific benthic communities *in situ*. The triangular pyramids, which were developed and built at the Smith and Rohwer laboratories, primarily consist of three transparent polycarbonate side panels joined by flexible polyvinyl chloride strips connected by stainless steel cables (as described in Haas et al., (2)). Benthic chambers were deployed at 10 m on the fore reef habitat on all four southern Line Islands described in this study. All benthic chambers were equipped with autonomous multiprobe (MANTA2 Eureka Water Probes, www.waterprobes.com) that monitored temperature (precision 0.01°C), DO (precision 0.01 mg l-1, accuracy ±1%, automatic temperature and pressure compensated and salinity corrected), pH and conductivity (accuracy ±1%, automatic temperature compensated) at 15 min intervals.

The rate of water exchange in the benthic chambers was calculated using dilution rates of Fluorescein dye. Fluorescein dye was injected into control chambers on Malden, Millennium, and Starbuck and the concentrations measured using a multiprobe sensor with a fluorometer (precision 0.01ppb; Manta2, Eureka Water Probes, TX, USA). Chamber flushing rates, F (liters min^{-1}) were calculated from the dilution rate, D (slope, log10ppb min^{-1} divided by the initial concentration, log10ppb) multiplied by chamber volume (100 liters). Mean flushing rates were 5.04, 5.48, and 2.52 liters min^{-1} for Malden (n=3), Millennium (n=4), and Starbuck (n=5), respectively (Supplementary Figure 1).

Sequence library preparation and bioinformatics. Nucleic acids were extracted from microbial communities collected on Sterivex filters using a modified protocol of the Nucleospin Tissue Kit (Machery-Nagel, Santa Clara, USA) as described previously by Kelly et al., (3). DNA for each sample was normalized to 0.2ng/ul and libraries were built using Nextera XT (Illumina, San Diego, USA). Metagenomic libraries were sequenced on the MiSeq2 using the 600 cycle PE sequencing reagent kit (Illumina, San Diego, USA). The shotgun sequence libraries were post-processed using Prinseq (4) to remove low quality reads (ambiguous bases, low complexity, short read length, replicates). Sequence reads were compared to the SEED database for metabolic and taxonomic assignments using SUPERFOCUS (5), which aligns sequence similarities using RAPSearch2 (6) and performs a 98% clustering of the proteins in the database to reduce computational taxation. Metagenomic reads aligned against the SEED database to get the functional annotation were subsequently extracted to identify the taxa that are encoding the respective protein coding genes from NCBI using Taxonkit (http://bioinf.shenwei.me/taxonkit/). For putative 16S rRNA gene sequences, alignment, classification, sequence distance calculation, OTU clustering, phylogenetic tree construction and calculation of among-sample phylogenetic distances were done using the software package mothur (7) following previously published bioinformatics pipelines (8). Additional phylogenetics were conducted using the SINA multiple

sequence alignment algorithm (9) and the RaxML maximum likelihood phylogeny reconstruction algorithm (10).

Supplementary References

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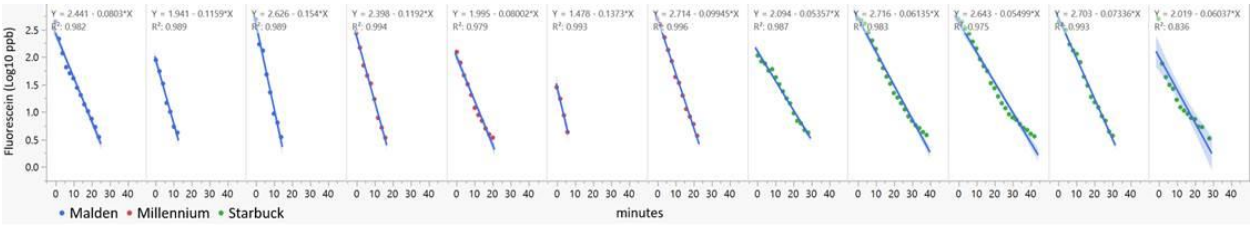

Supplementary Figure 1. Measurement of benthic chamber flushing rates. Estimates of water exchange in the benthic chambers were calculated using Fluorescein dye dilution rates. Dilution of Fluorescein dye was measured in control chambers on Malden, Millennium, and Starbuck using a multiprobe sensor with a fluorometer (Manta2, Eureka Water Probes, TX, USA). Chamber flushing rates, F (liters min^{-1}) were calculated from the dilution rate, D (slope, log10ppb min^{-1} divided by the initial concentration, log10ppb) multiplied by chamber volume (100 liters). Mean flushing rates were 5.04, 5.48, and 2.52 liters min^{-1} for Malden, Millennium, and Starbuck, respectively. Therefore, the turnover rate or *residence time* of seawater within the benthic chambers is estimated to be between 20 and 40 minutes.