

SUPPLEMENTARY MATERIAL

Microbiome of a reef-building coral displays signs of acclimation to a stressful shallow hydrothermal vent habitat

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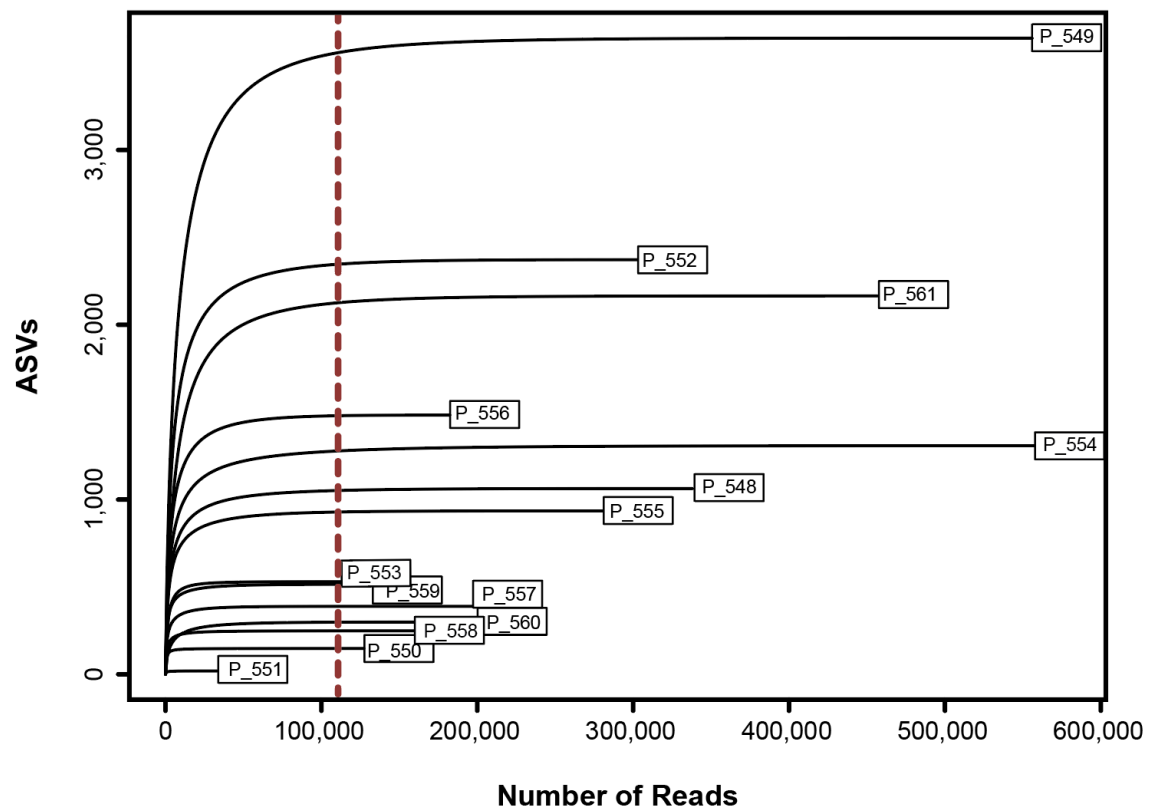
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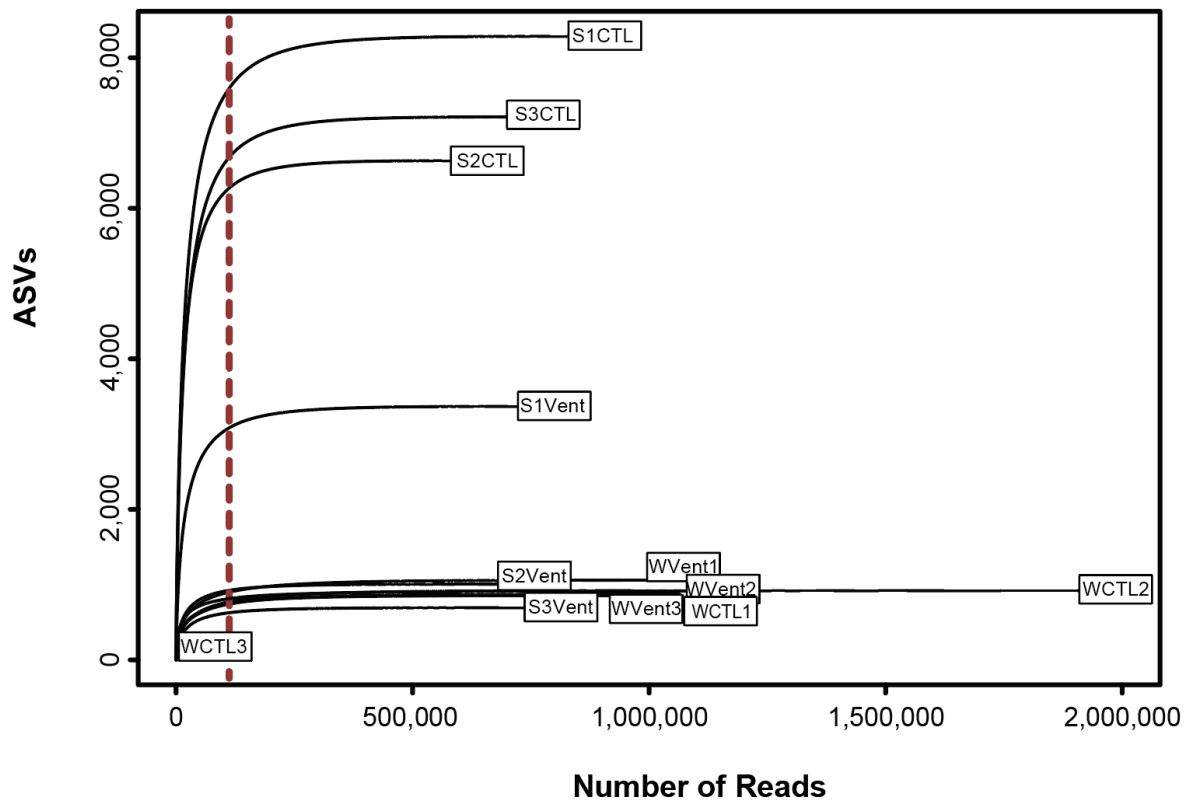
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Supplemental Table 1. Metadata and sequencing information for *Porites panamensis* (n=14), sediment (n=6), water (n=6) and blank (n=2) samples.

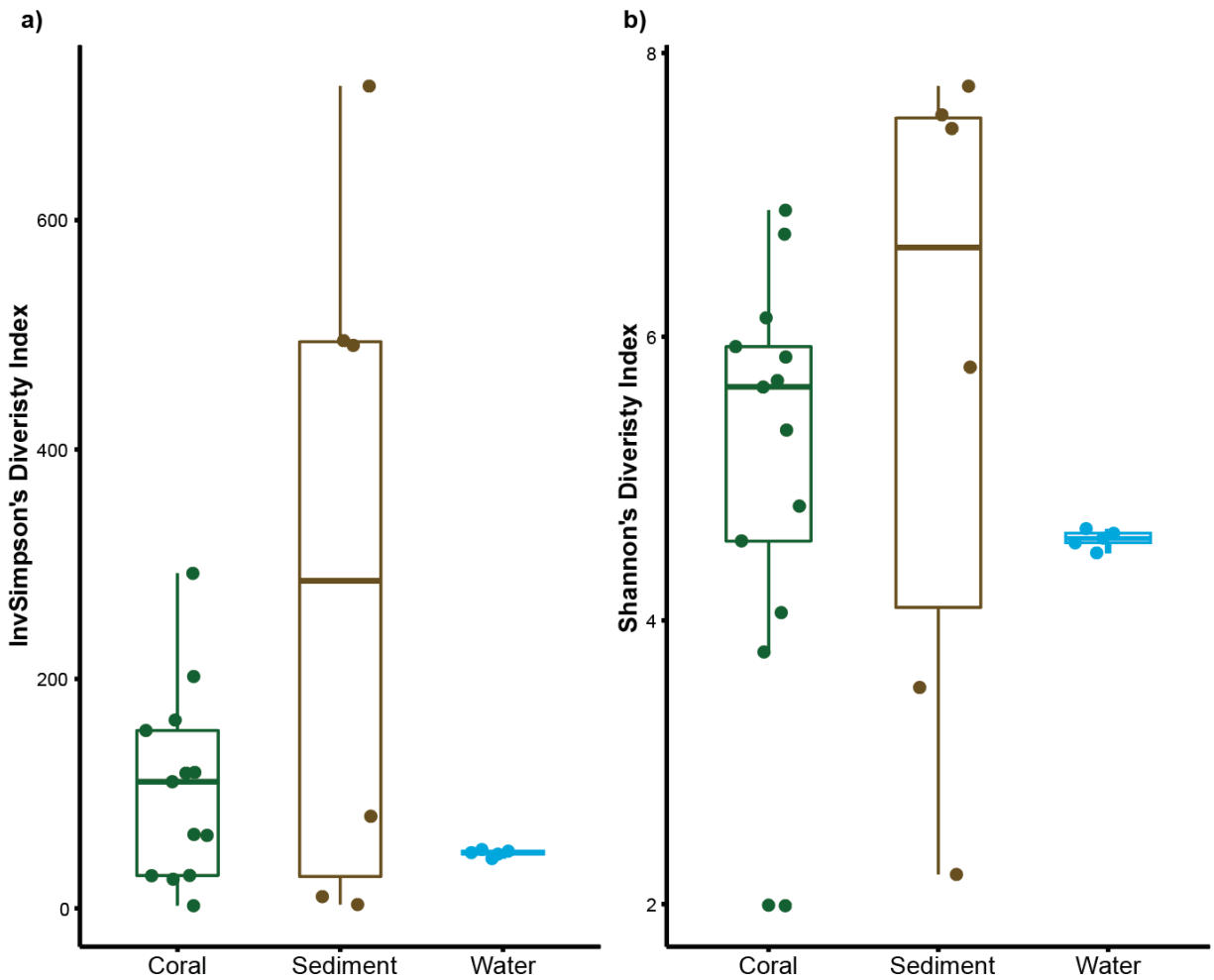
| Sample ID | Type of Sample | Sample Location (on-vent or off-vent) | Sediment Temperature Nearest to Colony (C°) | Transect Distance (meters) | Raw Read Count | Post-QC Bacteria/Archaea Read Count | Rarefied Bacterial/Archaea Read Count | Post-QC <i>Ostreobium</i> Read Count | Rarefied <i>Ostreobium</i> Read Count |
|-----------|----------------------|---------------------------------------|---|----------------------------|----------------|-------------------------------------|---------------------------------------|--------------------------------------|---------------------------------------|
| P 548 | <i>P. panamensis</i> | Off-Vent | 19 | 50.35 | 1,361,791 | 338,088 | 116,035 | 351,094 | 12,445 |
| P 549 | <i>P. panamensis</i> | Off-Vent | 20 | 48.7 | 1,080,968 | 557,155 | 116,035 | 76,640 | 12,445 |
| P 550 | <i>P. panamensis</i> | Off-Vent | 20 | 48.1 | 1,022,894 | 127,246 | 116,035 | 12,445 | 12,445 |
| P 551 | <i>P. panamensis</i> | Off-Vent | 20 | 47.1 | 48,324 | 32,865 | EXCLUDED | 0 | EXCLUDED |
| P 552 | <i>P. panamensis</i> | Off-Vent | 20 | 45 | 628,614 | 302,436 | 116,035 | 15,266 | 12,445 |
| P 553 | <i>P. panamensis</i> | On-Vent | 27 | 31 | 657,048 | 116,035 | 116,035 | 128,462 | 12,445 |
| P 554 | <i>P. panamensis</i> | On-Vent | 27 | 30.3 | 1,233,912 | 581,741 | 116,035 | 133,874 | 12,445 |
| P 555 | <i>P. panamensis</i> | On-Vent | 43 | 16.7 | 558,843 | 280,171 | 116,035 | 27,477 | 12,445 |
| P 556 | <i>P. panamensis</i> | On-Vent | 66 | 13.4 | 325,969 | 182,428 | 116,035 | 52,111 | 12,445 |
| P 557 | <i>P. panamensis</i> | On-Vent | 27 | 30.1 | 852,328 | 196,922 | 116,035 | 194,951 | 12,445 |
| P 558 | <i>P. panamensis</i> | Off-Vent | 25 | 6.8 | 1,035,923 | 162,062 | 116,035 | 19,377 | 12,445 |
| P 559 | <i>P. panamensis</i> | On-Vent | 41 | 5.2 | 579,902 | 135,072 | 116,035 | 60,284 | 12,445 |
| P 560 | <i>P. panamensis</i> | On-Vent | 45 | 14 | 382,097 | 175,654 | 116,035 | 66,298 | 12,445 |
| P 561 | <i>P. panamensis</i> | On-Vent | 30 | 21.5 | 821,537 | 456,609 | 116,035 | 29,480 | 12,445 |
| SCTRL1 | Sediment | Off-Vent | 20 | 6.8 | 994,928 | 826,371 | 116,035 | NA | NA |
| SCTRL2 | Sediment | Off-Vent | 20 | 41 | 675,022 | 582,621 | 116,035 | NA | NA |
| SCTRL3 | Sediment | Off-Vent | 20 | 55 | 822,856 | 706,364 | 116,035 | NA | NA |
| SVENT1 | Sediment | On-Vent | 66 | 13.4 | 941,651 | 721,552 | 116,035 | NA | NA |
| SVENT2 | Sediment | On-Vent | 30 | 21.5 | 791,739 | 681,719 | 116,035 | NA | NA |
| SVENT3 | Sediment | On-Vent | 35 | 31 | 908,095 | 736,671 | 116,035 | NA | NA |
| WCTRL1 | Water | Off-Vent | 20 | 6.8 | 1,060,949 | 932,137 | 116,035 | NA | NA |
| WCTRL2 | Water | Off-Vent | 20 | 41 | 2,156,878 | 1,904,907 | 116,035 | NA | NA |
| WCTRL3 | Water | Off-Vent | 20 | 55 | 116 | 42 | EXCLUDED | NA | NA |
| WVENT1 | Water | On-Vent | 66 | 13.4 | 1,119,412 | 992,704 | 116,035 | NA | NA |
| WVENT2 | Water | On-Vent | 30 | 21.5 | 1,220,951 | 1,064,328 | 116,035 | NA | NA |
| WVENT3 | Water | On-Vent | 35 | 31 | 1,233,856 | 1,067,819 | 116,035 | NA | NA |
| Blank1 | Blank Control | --- | --- | --- | 4,145 | 1,019 | EXCLUDED | NA | NA |
| Blank2 | Blank Control | --- | --- | --- | 6,439 | 5,652 | EXCLUDED | NA | NA |



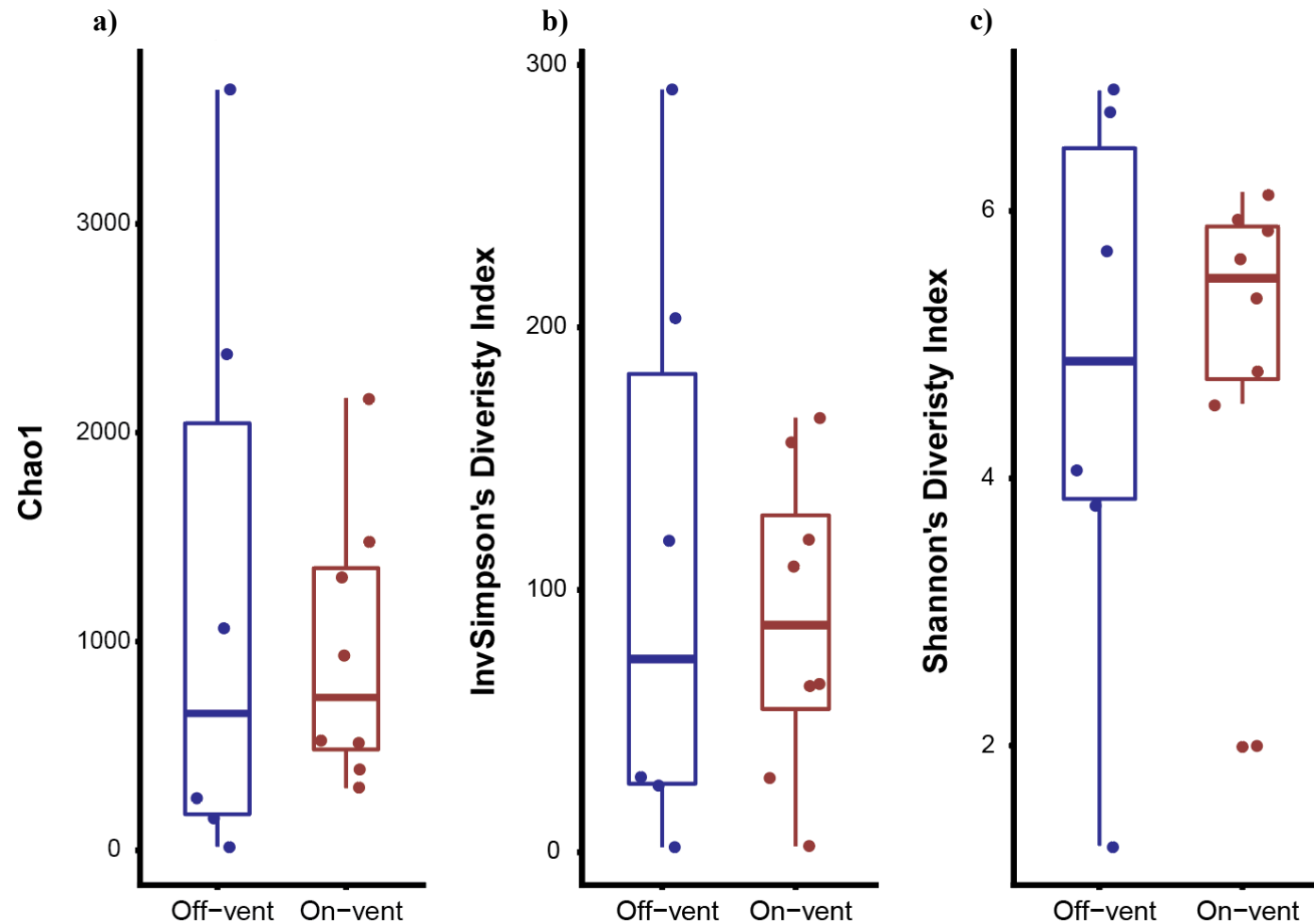
Supplemental Figure 1. Rarefaction curve showing the number of ASVs associated with each *Porites panamensis* sample as read count increases. Black lines are labeled with sample name and end at the maximum number of reads in each sample. The dashed red line indicates the read count chosen for rarefaction (116,035 reads).



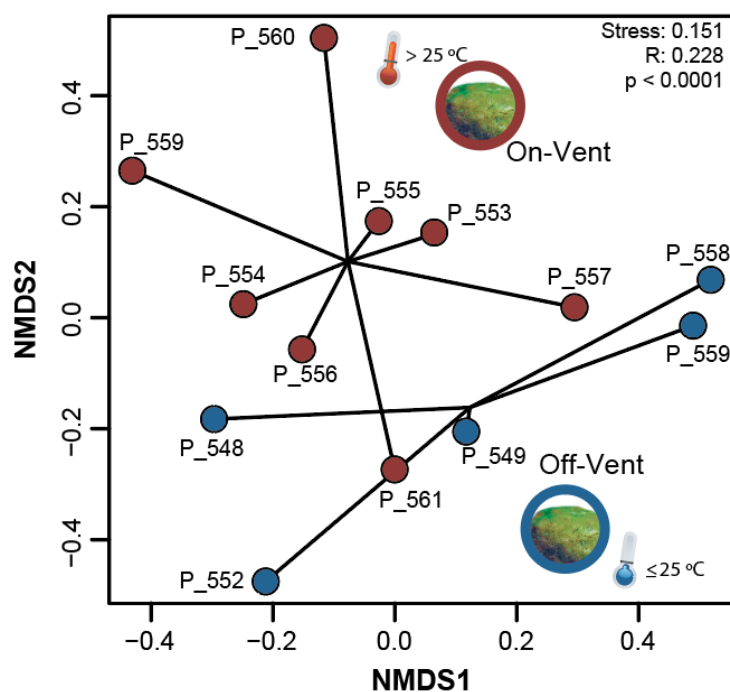
Supplemental Figure 2. Rarefaction curve showing the number of ASVs associated with each abiotic (water or sediment) sample as read count increases. Black lines are labeled with sample name and end at the maximum number of reads in each sample. The dashed red line indicates the read count chosen for rarefaction (116,035 reads).



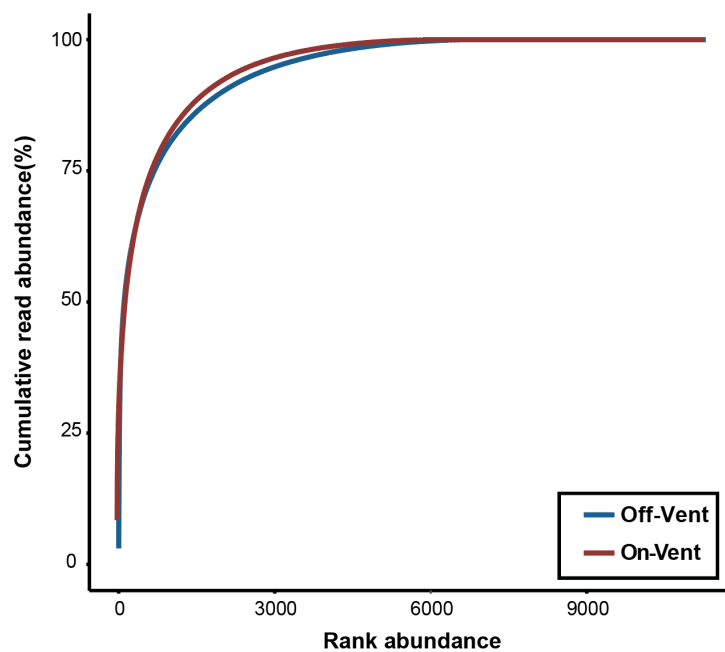
Supplemental Figure 3. Alpha diversity (evenness) for non-rarefied samples of *Porites panamensis*, sediment and water collected from both on- and off-vents. The lower and upper hinges represent the first and third quartiles. The lower and upper whiskers extend to either the largest or smallest value that is no more than 1.5* the interquartile range. The diversity values for each sample are plotted as individual points. a) Inverse Simpson's Diversity Index, and b) Shannon's diversity index.



Supplemental Figure 4. Alpha diversity for non-rarefied samples of *Porites panamensis* from off- (blue) and on-vent (red) sites. The lower and upper hinges represent the first and third quartiles. The lower and upper whiskers extend to either the largest or smallest value that is no more than 1.5* the interquartile range. The diversity values for each sample are plotted as individual points. a) Chao1, b) Inverse Simpson's Diversity Index, and c) Shannon's diversity index.



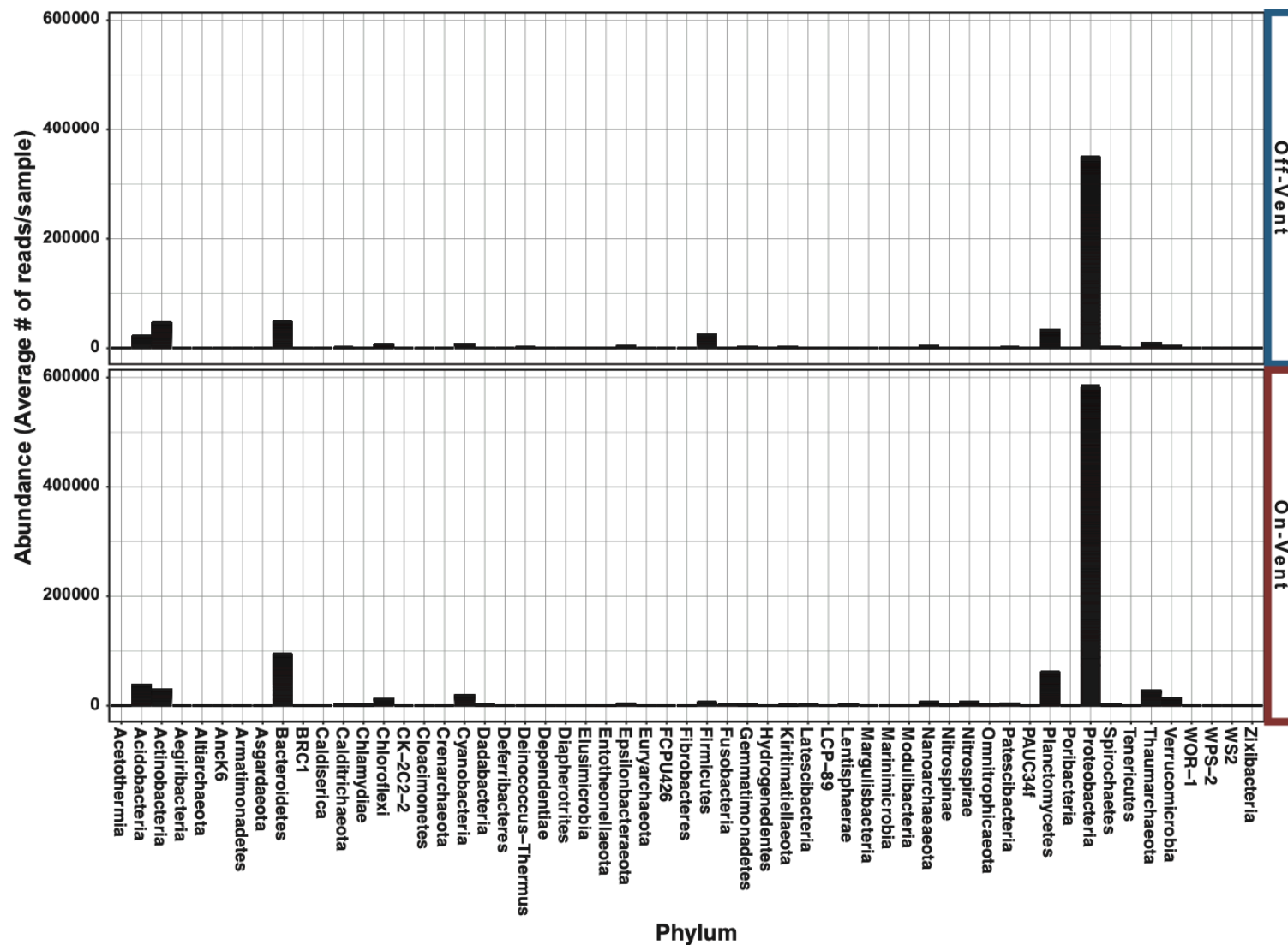
Supplemental Figure 5. NMDS plot of microbial community beta diversity (Bray-Curtis) for off- (blue) and on-vent (red) samples of *Porites panamensis* samples for including all ASVs and all samples. Black lines connect samples of the same group to the centroid for that group.



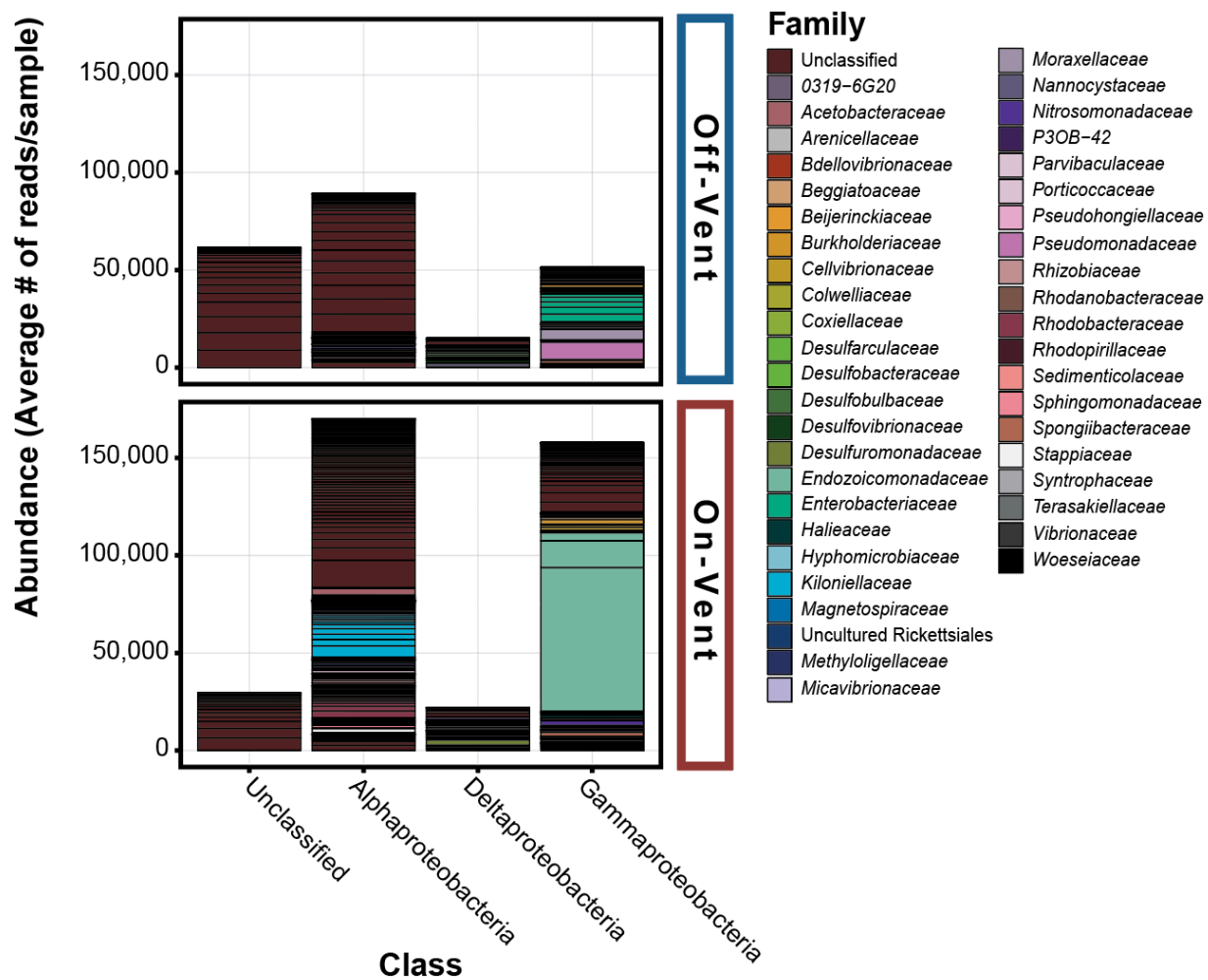
Supplemental Figure 6. Rank abundance curve showing the rank abundance of individual ASVs and the cumulative read abundance for off- (blue) and on-vent (red) *P. panamensis* samples.

Supplemental Table 2. Comparison (% relative abundance) between the 355-high abundance ASVs and all ASVs for the most abundant microbial phyla across all *Porites panamensis* samples and the most abundant microbial families in both on-vent and off-vent *P. panamensis* samples.

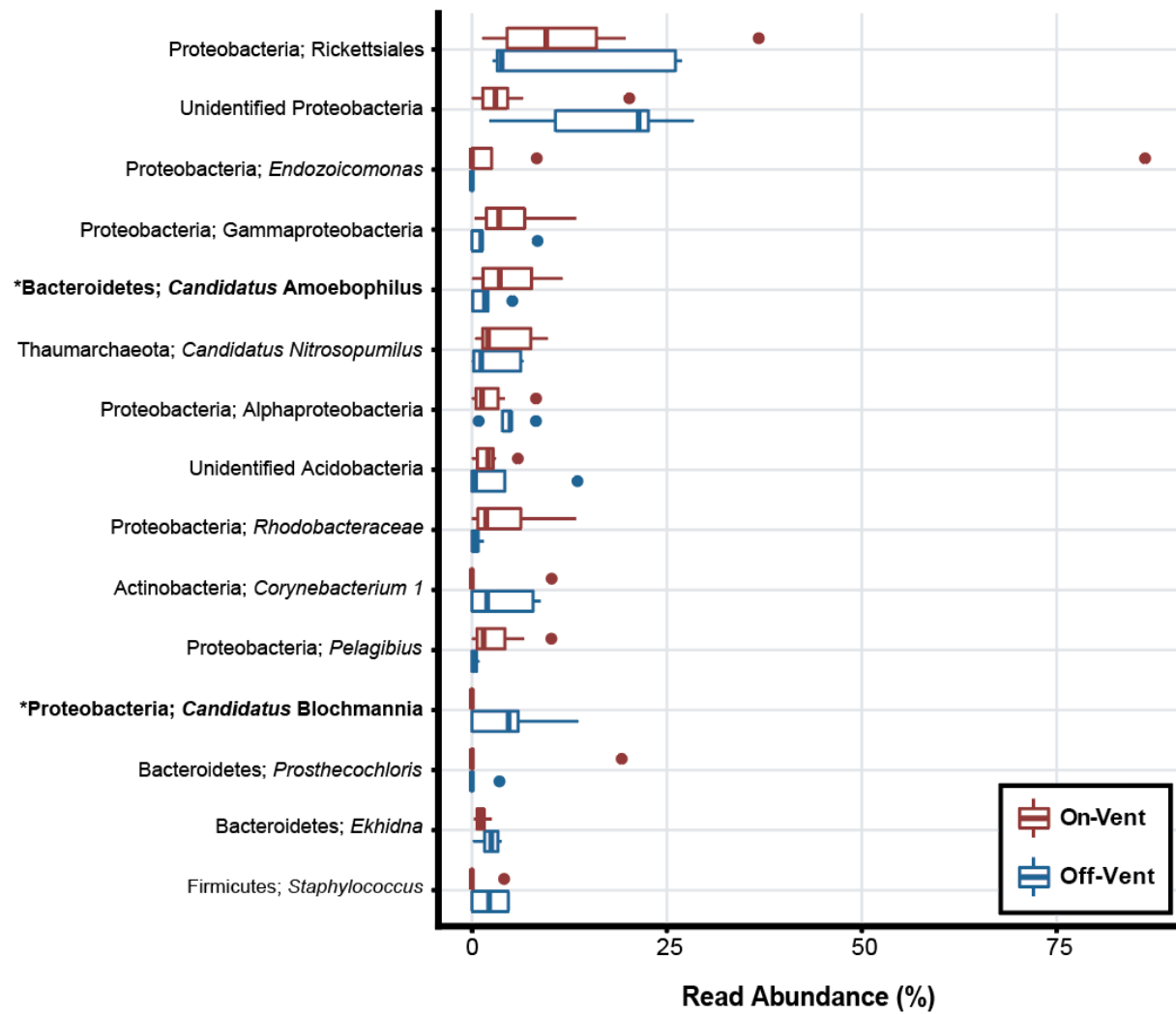
| Sample Group | Most Abundant Phyla (% Relative Abundance) | | Most Abundant Families On-Vent (% Relative Abundance) | | | Most Abundant Families Off-Vent (% Relative Abundance) | |
|-------------------|--|---------------|---|-----------------------|------------------------|--|---------------------------|
| | Proteobacteria | Bacteroidetes | <i>Endozoicomonadaceae</i> | <i>Kiloniellaceae</i> | <i>Amoebophilaceae</i> | <i>Enterobacteriaceae</i> | <i>Corynebacteriaceae</i> |
| On-Vent HA ASVs | 69.6% | 11.5% | 11.9% | 6.2% | 4.9% | 0.3% | 2.4% |
| On-Vent All ASVs | 63% | 10.2% | 14.1% | 6.2% | 4.4% | 0.2% | 1.5% |
| Off-Vent HA ASVs | 69.8% | 8.3% | 0% | 2.1% | 2.0% | 5% | 4.2% |
| Off-Vent All ASVs | 60.1% | 8.4% | 0.1% | 2.7% | 2.4% | 4.6% | 5.6% |



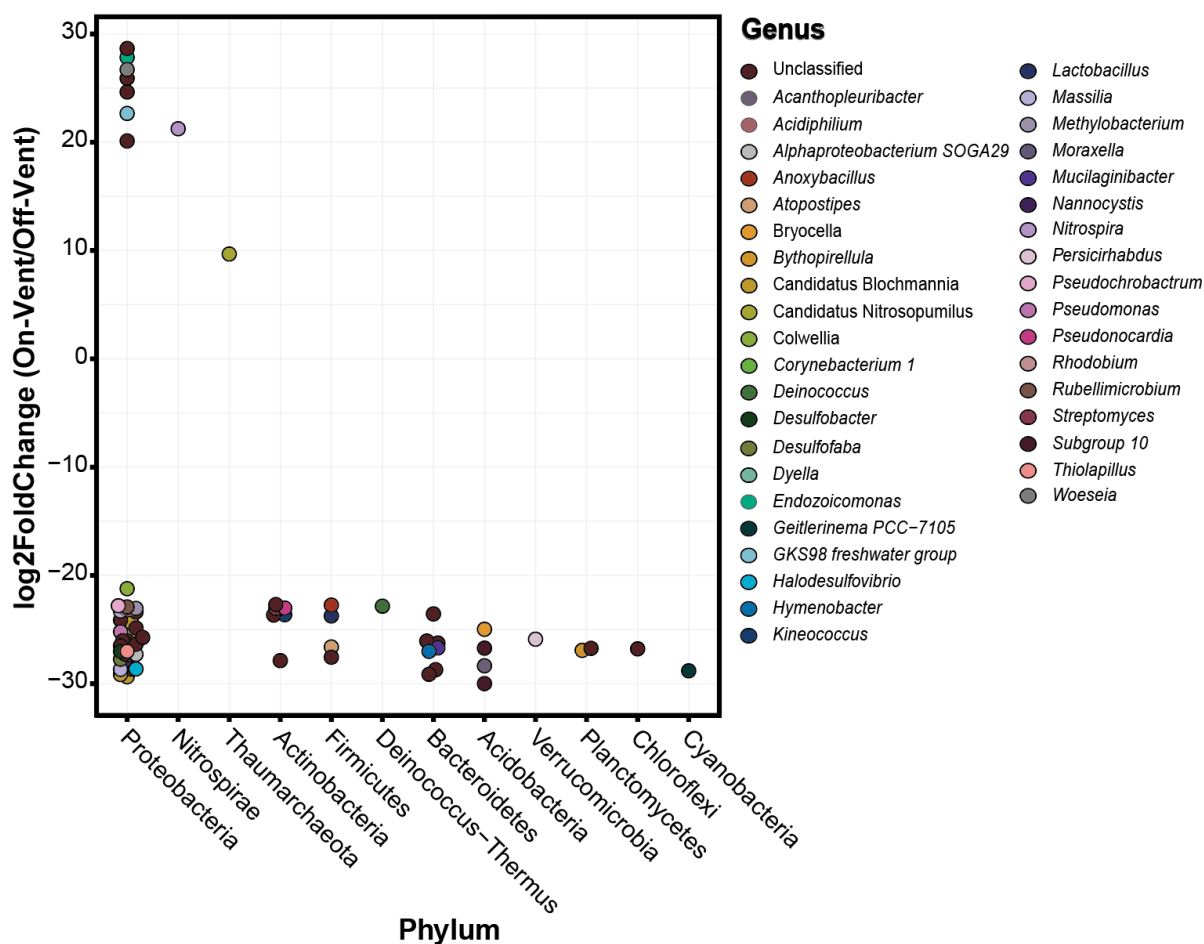
Supplemental Figure 7. Relative abundance plots of all ASVs for off- (top) and on-vent (bottom) *Porites panamensis* samples. ASVs are clustered by phylum designation. Compare phylum-level abundance patterns to those displayed in Figure 4 for high abundance ASVs only.



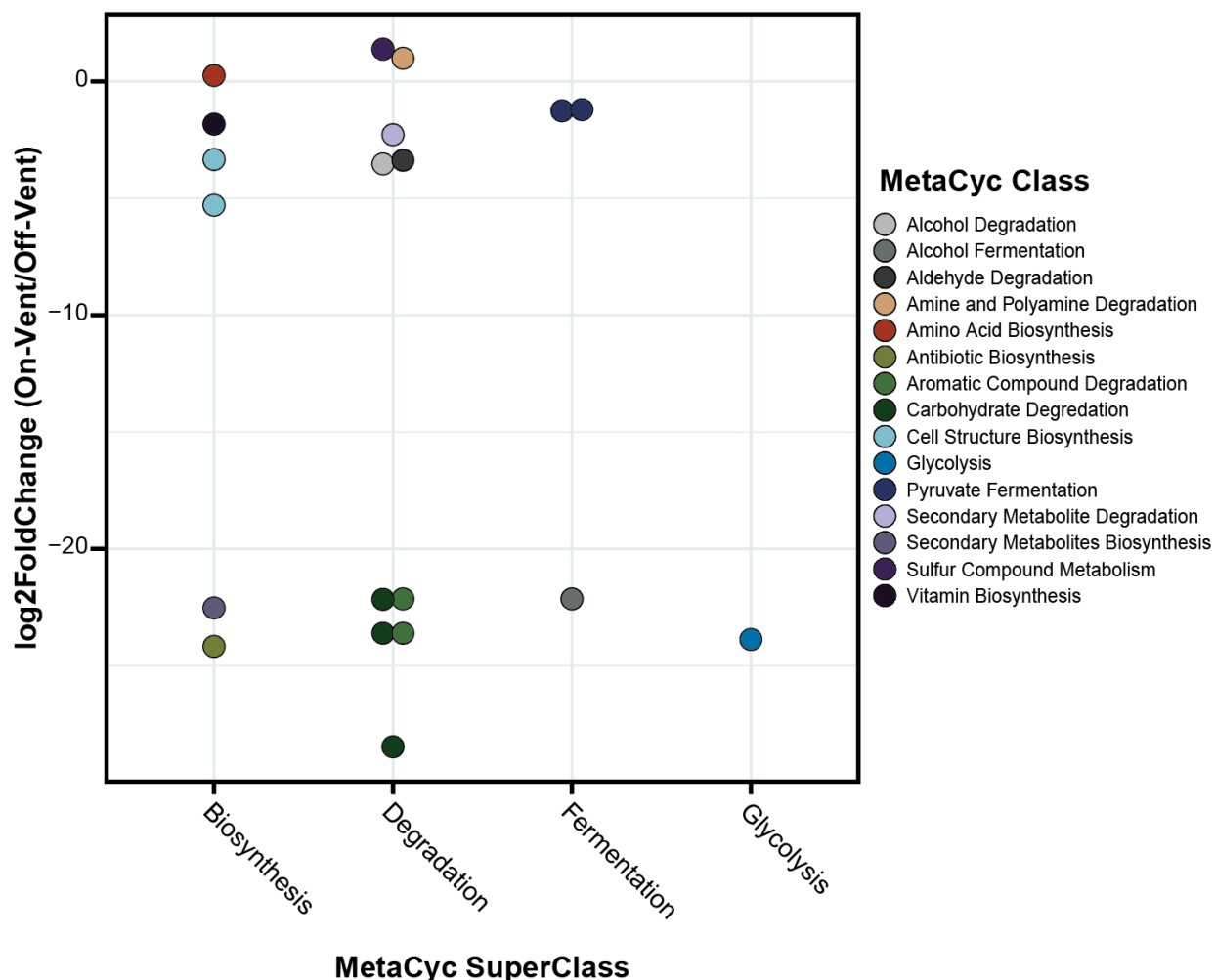
Supplemental Figure 8. Relative abundance plots of high abundance ASVs (>500 reads) in the phylum Proteobacteria for off- (top) and on-vent (bottom) *Porites panamensis* samples. Black lines separate ASVs. ASVs are clustered by Class designation and colored by Family.



Supplemental Figure 9. Relative abundance (in descending order) box plots for the 15 most abundant high abundance ASVs (>500 reads) in on- (blue) and off-vent (red) *Porites panamensis* samples. Asterisks denote ASVs that were differentially abundant between off- and on-vent colonies.



Supplemental Figure 10. Differentially abundant high abundance ASVs (>500 reads) between off- and on-vent samples of *P. panamensis*. Log2Fold change is shown as increases or decreases in on-vent microbiomes. Individual ASVs are plotted according to phylum and colored by genus.



Supplemental Figure 11. Differentially abundant biological pathways between site types. Dots represent individual pathways and are grouped by MetaCyc Superclass and colored by MetaCyc Class (as identified by the MetaCyc Database).