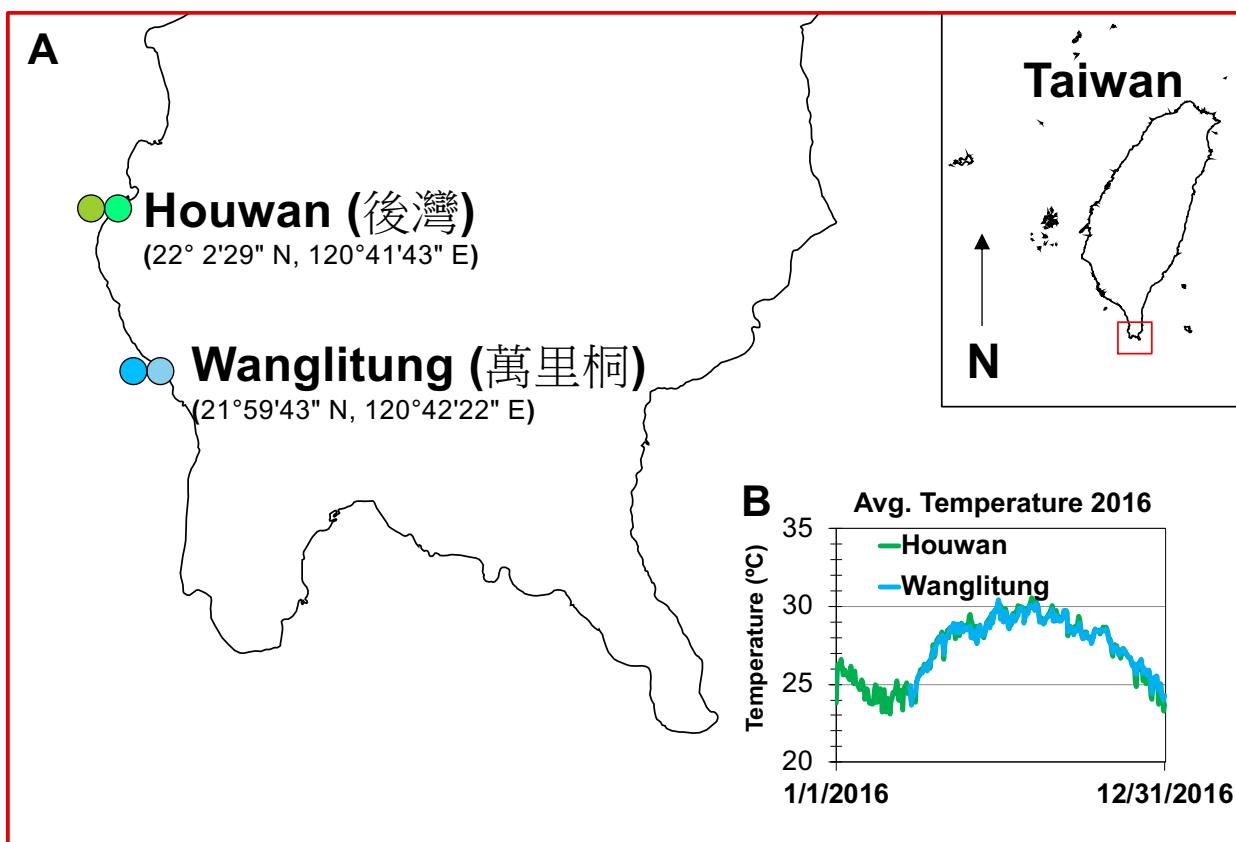


# Coral collection sites in Kenting National Park



Supplementary Fig. 1: Location of coral collection sites in southern Taiwan.

- Map depicting the location of Houwan (後灣 – 22° 2'29" N, 120°41'43" E) and Wanglitung (萬里桐 – 21°59'43" N, 120°42'22" E) reefs. Collection sites were chosen based on the local abundance of *Pocillopora spp.*, and two coral colonies (genotypes) were collected from each site, and will be abbreviated hereafter as HW1, HW2, and WT1, WT2. The colors of the points at each reef represent the colors used to represent each genotype in subsequent plots of gene expression and bacteria community results.
- Time series line plot of average water temperature recorded at Houwan and Wanglitung reefs for the 2016 year that shows no differences in the typical temperatures at each reef site, which ranged from 23 – 30.5°C.

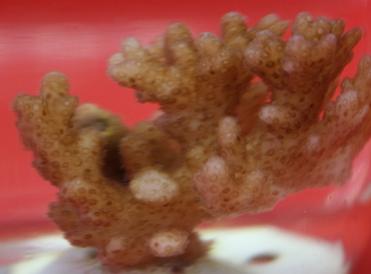
## Control

### Houwan1 (HW1)

*P. damicornis* type 8a  
ORF 23

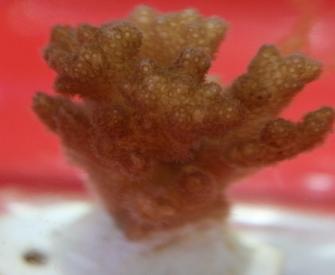


## LPS



### Houwan2 (HW2)

*P. damicornis* type 4a  
ORF09



### Wanglitung1 (WT1)

*P. acuta* type 5  
ORF18

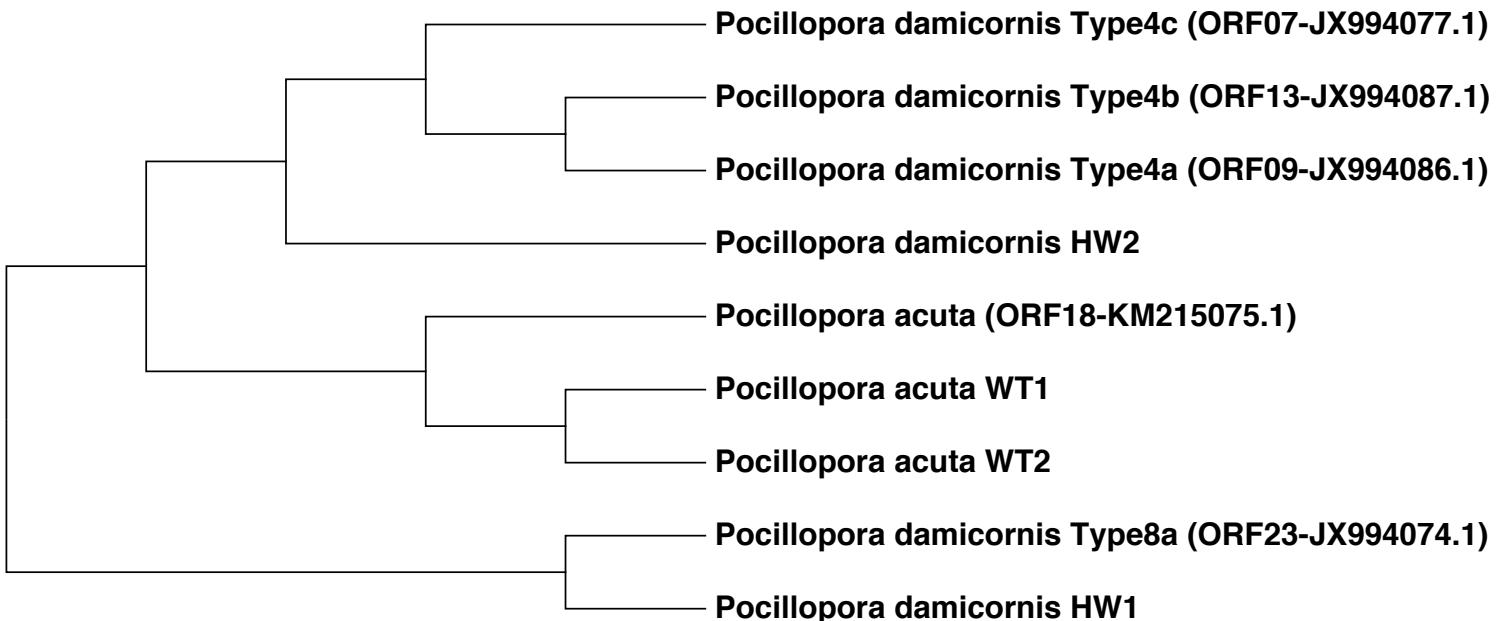


### Wanglitung2 (WT2)

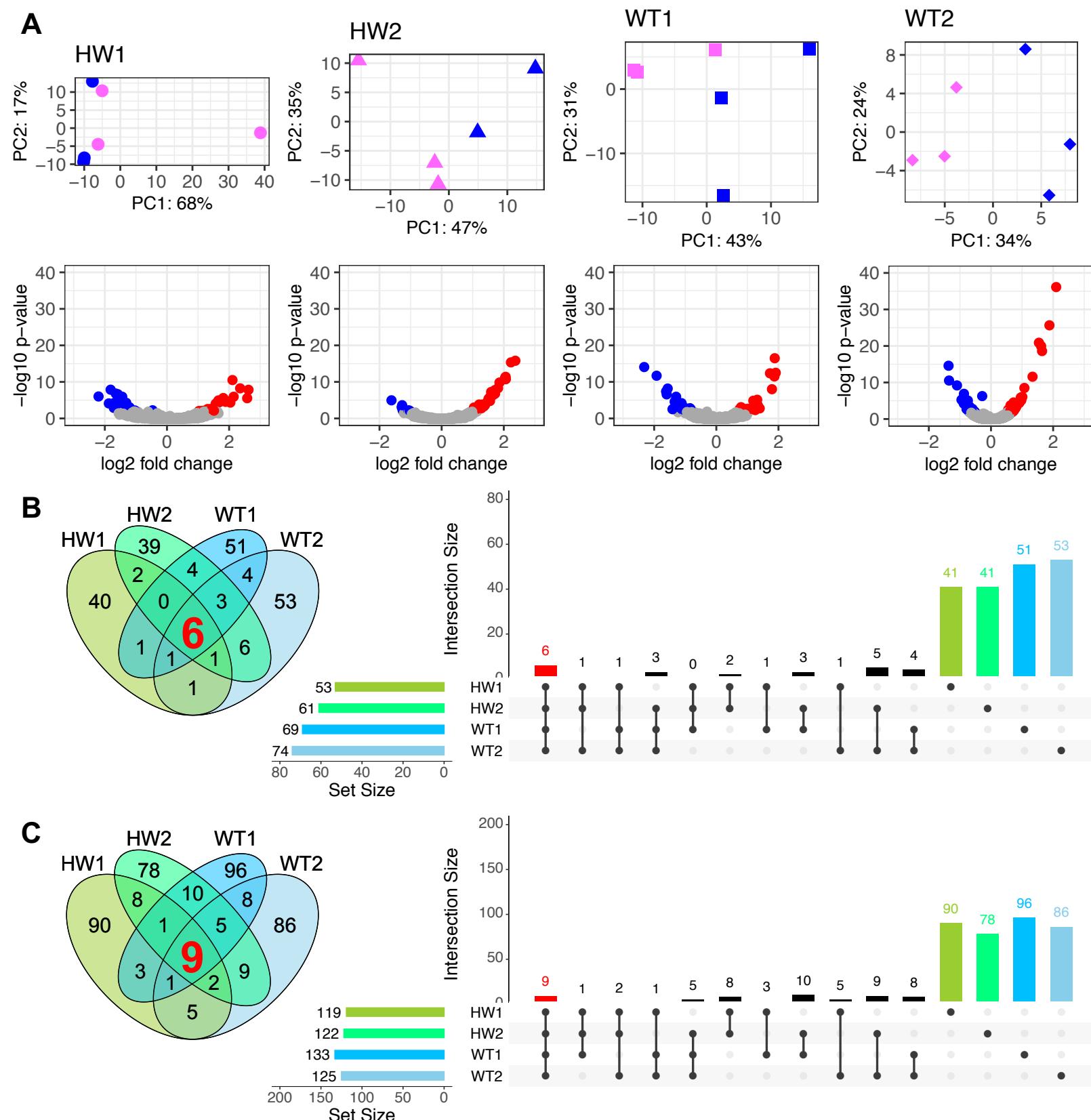
*P. acuta* type 5  
ORF18



Supplementary Fig. 2: Photographs of representative coral fragments in the control treatment and LPS treatment for each coral genotype immediately before sampling. Coral fragments in each treatment ( $n = 3$  per genotype, per treatment, 24 total) appeared completely healthy with extended polyps for the duration of the experiment.

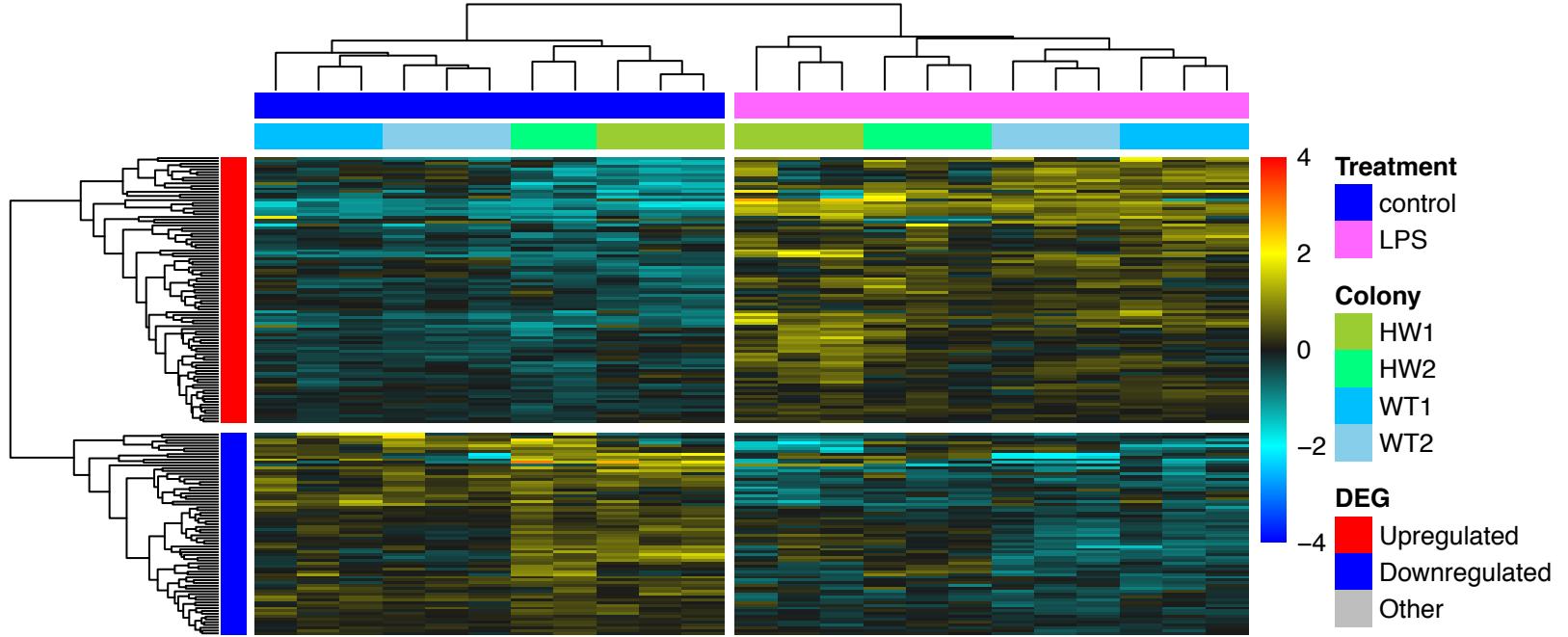


Supplementary Fig. 3: Maximum likelihood phylogenetic tree of *Pocillopora* mtORF sequences shows that the four Taiwan coral genotypes correspond to two different species, *P. damicornis* and *P. acuta*, as well as three different mitochondrial haplotypes. HW1 corresponded to *P. damicornis* type 8a, or ORF23, while HW2 corresponded to *P. damicornis* type 4a or ORF09. WT1 and WT2 shared an identical mtORF haplotype that corresponded to *P. acuta*, type 5 or ORF18. All of the mtORF haplotypes observed in *Pocillopora* colonies collected for this study have been observed in Taiwan previously.

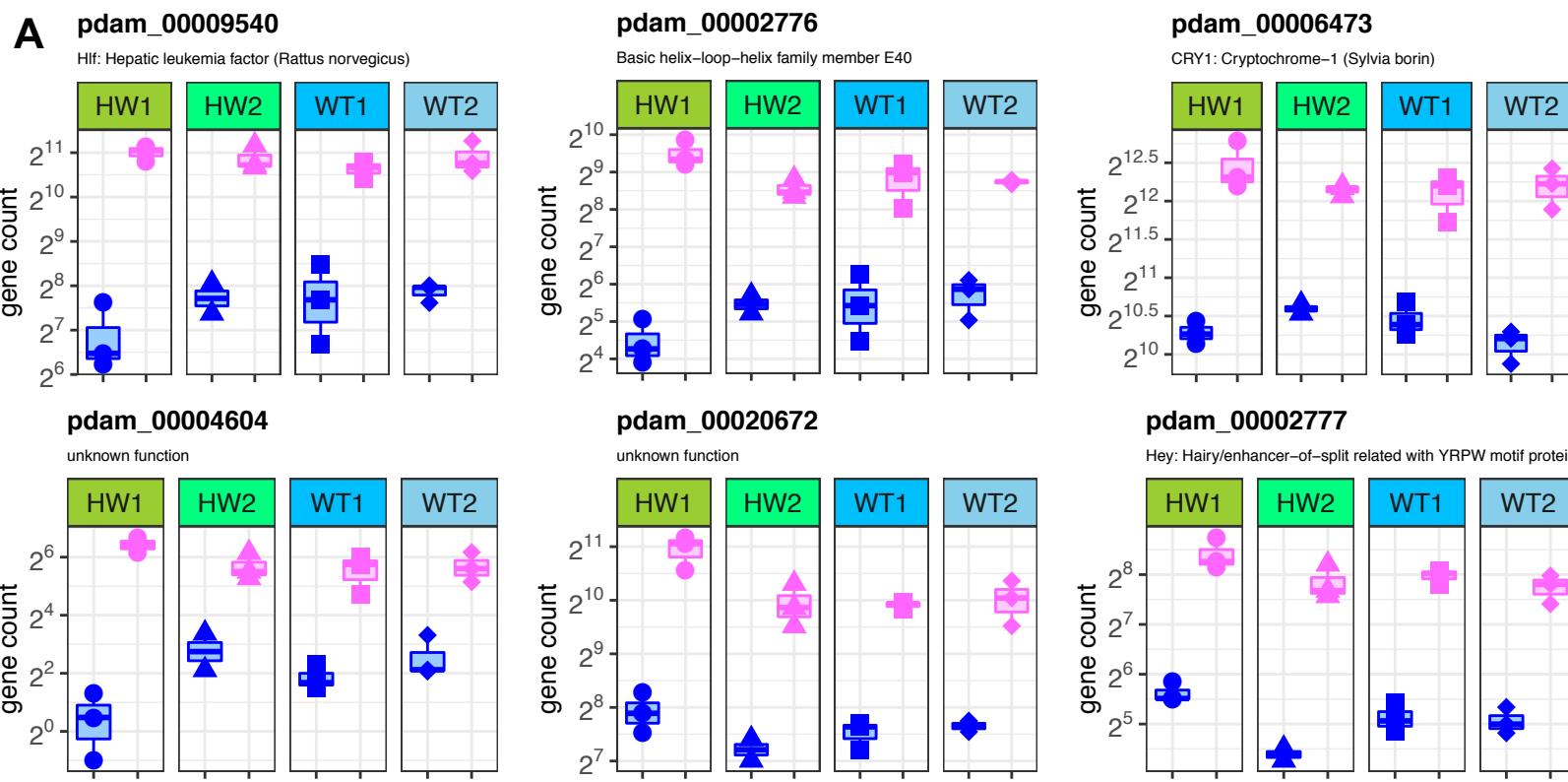


Supplementary Fig. 4: Genotype-specific DESeq2 model differential expression results and UpSetR analysis reveal genotype-specific responses to LPS by identifying unique and shared DEGs among *Pocillopora* coral genotypes.

- For each coral genotype (Houwan1, Houwan2, Wanglitung1 and Wanglitung2), a PCA plot and volcano plot depict the key differential gene expression results and show that control treatment and LPS treatment samples cluster separately along PC1 within each genotype.
- Venn and UpSetR diagrams of set sizes for genotype-specific DEG lists that are unique to and shared among different *Pocillopora* coral genotypes at the  $p<0.01$  significance threshold.
- Venn and UpSetR diagrams of set sizes for genotype-specific DEG lists that are unique to and shared among different *Pocillopora* coral genotypes at the  $p<0.05$  significance threshold.

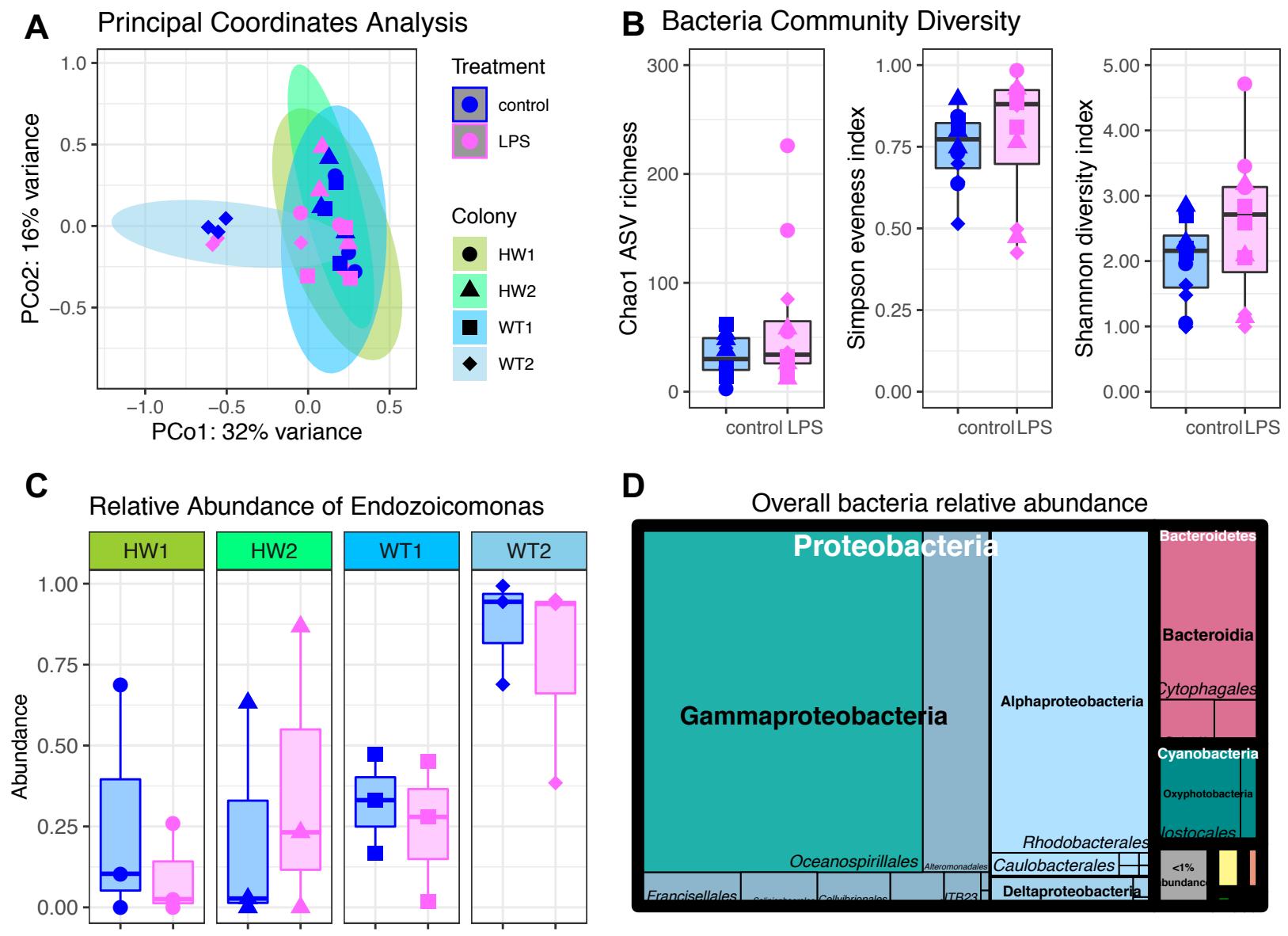


Supplementary Fig. 5: Heatmap of all DEGs ( $p_{adj} < 0.01$ ) between the control and LPS treatment samples. The heatmap depicts the regularized logarithm (rlog) transformed expression values for each DEG, with color scaled from red for overexpression to blue for underexpression relative to the mean expression level for each DEG. A hierarchical clustering tree for all coral samples is depicted on the upper x-axis, with colors denoting the sample treatment as blue for the control treatment and pink for the LPS treatment, and also the sample parent colony with green shades for the Houwan colonies and blue shades for the Wanglitung colonies. A hierarchical clustering tree for the individual DEGs is depicted on the y-axis, showing gene clustering based on expression patterns with colors denoting whether each DEG was upregulated or downregulated.



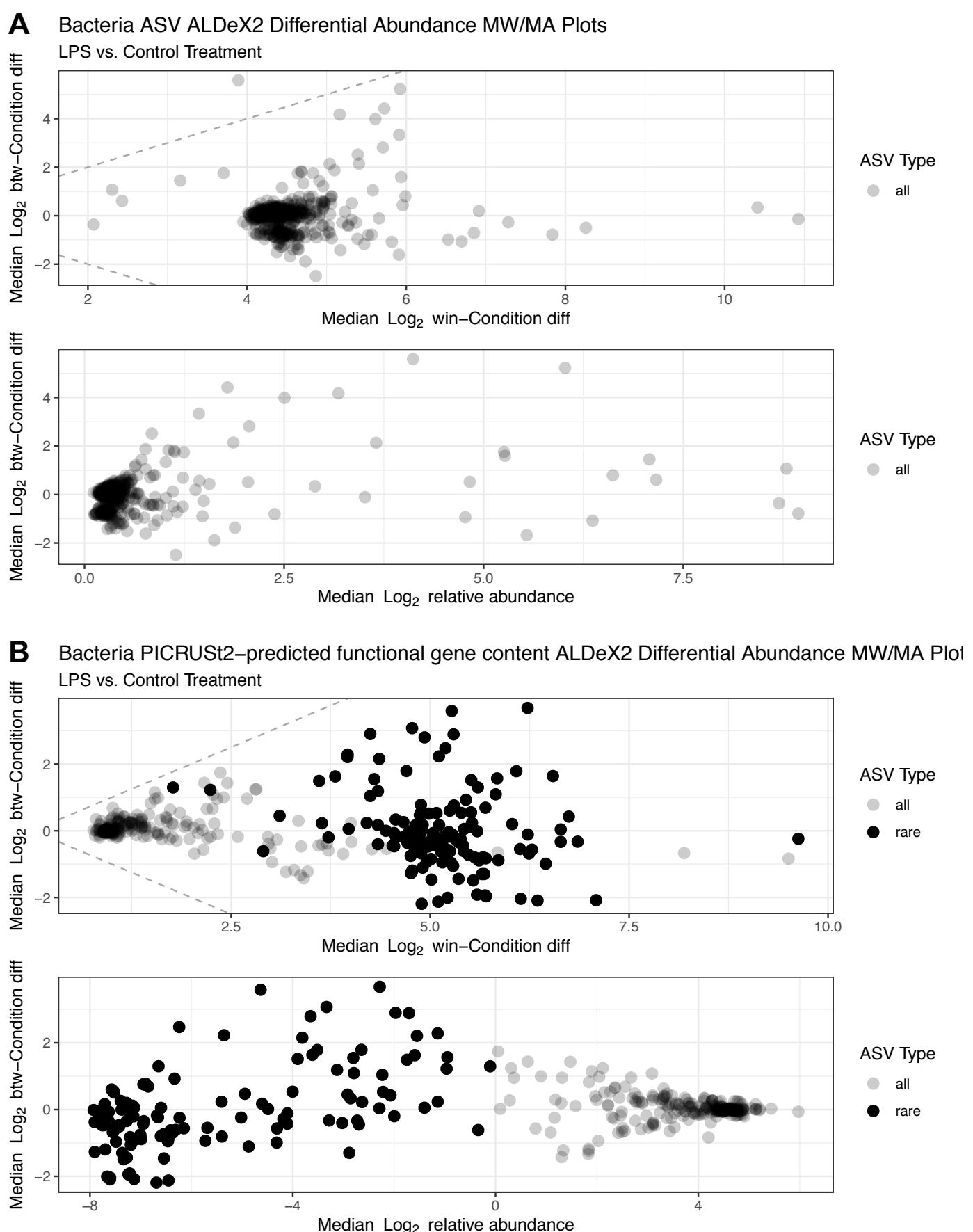
Supplementary Fig. 6: Boxplots of consensus upregulated DEGs among *Pocillopora* coral genotypes.

A. Gene counts boxplots for the six consensus upregulated DEGs, faceted according to *Pocillopora* coral genotype to demonstrate upregulation to LPS treatment in each genotype in the experiment.



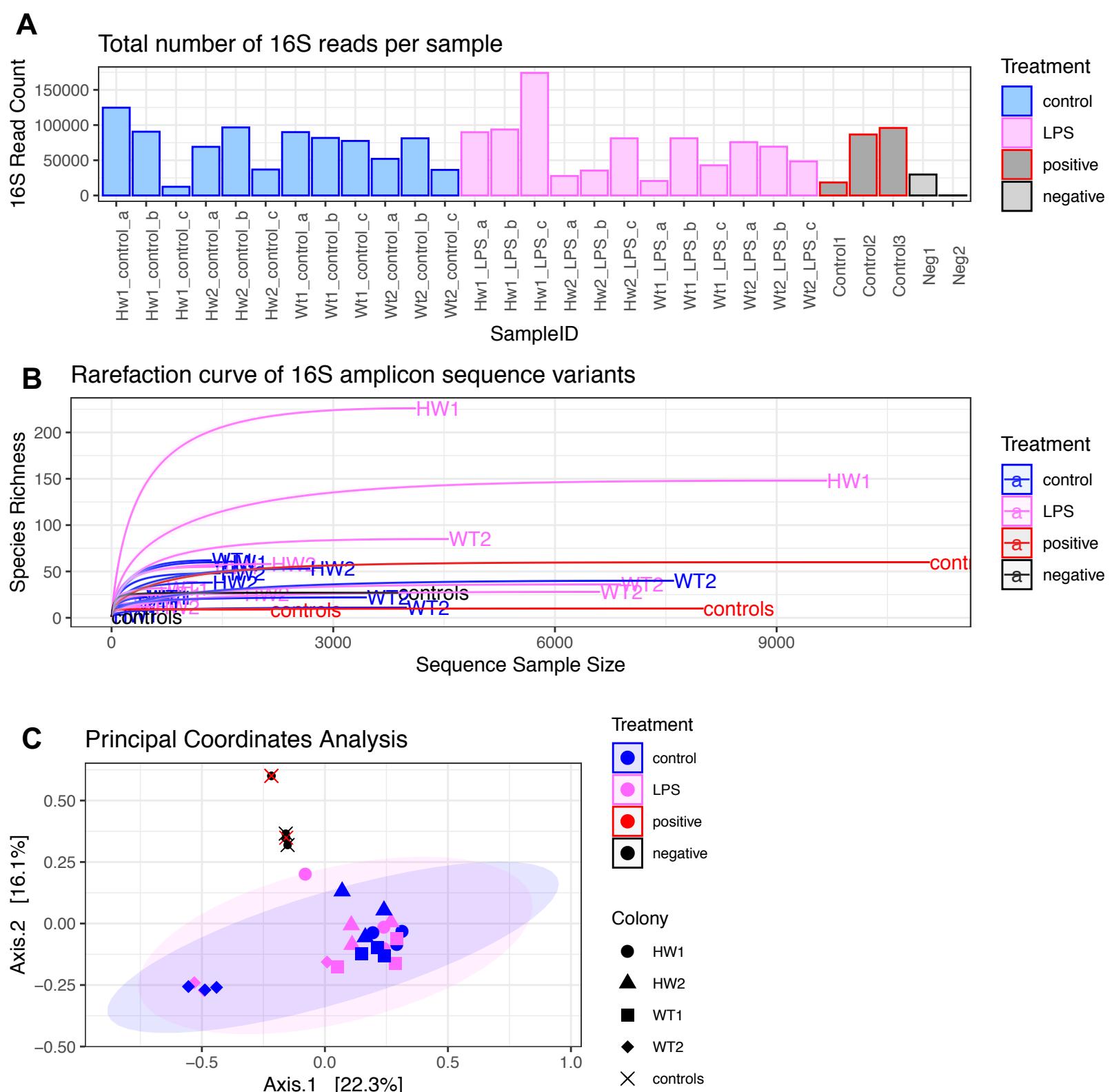
Supplementary Fig. 7: Coral bacteria community composition and diversity results that genotypic differences have a stronger effect on the bacteria community.

- Principal coordinates analysis (PCoA) plot of coral bacteria community Bray-Curtis distances demonstrates that LPS treatment does not have an effect on coral bacteria community composition. Point shape represents the sample colony (genotype), and color represents the treatment, with blue for the control treatment and pink for the LPS treatment. Colored ellipses represent normal confidence ellipses.
- Boxplots of the Chao1 richness estimator, Simpson evenness and Shannon diversity indices demonstrate that LPS treatment does not significantly alter coral bacteria community alpha diversity metrics.
- Boxplot of the relative abundance of *Endozoicomonas* bacteria across all *Pocillopora* genotypes, indicating that the differences in the relative abundance contribute to genotypic variation.
- Treemap of overall bacteria relative abundance across all samples in the experiment, showing the dominant bacteria phyla (white text labels), classes (black text labels), and orders (italicized text labels) as hierarchical nested areas. The dominant bacteria phyla are Proteobacteria, Bacteroidetes, and Cyanobacteria, the dominant bacteria classes (black labels) are Gammaproteobacteria, Alphaproteobacteria, Bacteroidia, and Oxyphotobacteria, and the most dominant bacteria order was Oceanospirillales, which was mostly comprised of bacteria belonging to the genus *Endozoicomonas*.



Supplementary Fig. 8: Bacteria 16S ASV and PICRUSt2-predicted functional gene content ALDeX2 results.

- Bacteria ASV ALDeX2 Bland-Atlmann (MA) and effect (MW) plots, demonstrating no differentially abundant ASVs between treatments.
- Bacteria PICRUSt2-predicted functional gene content ALDeX2 MA and MW plots.



Supplementary Fig. 9: Bacteria 16S sequencing read depth and taxonomic assignment results.

- Barplot of total read count for each sample after removal of mitochondria and chloroplast sequences.
- Alpha-diversity sequence rarefaction curves.
- Bacteria community PCoA with included sequencing controls.