



Figure 3: A) Non-metric multidimensional scaling of microbial community samples using Unifrac distances derived from 16S amplicon data. A dashed ellipse denotes the 3 coral stress treatments while a solid ellipse denotes the coral Control treatment. **B)** Two-way heatmap of the most abundant bacterial families in each treatment. Abundant families were defined as: relative abundance $\geq .005$ in samples ≥ 3 or a relative abundance $\geq .1$ in samples ≥ 1 . Each cell represents the z-scored mean relative abundance of a given family in a treatment. Cells are colored according to z-score, with warmer colors indicating enrichment and cooler colors indicating depletion. Clustering was performed using Euclidian distances. **C)** Visualization of the 31 OTUs determined to be significantly differentially abundant (DA) in at least one of the three stress treatments compared to Control samples by DESeq2. Dotplot of the log2 fold-change values for the 31 significantly DA OTUs in the three coral stress treatments. Each dot represents a given OTU in a given treatment. Dot height on the y-axis and color correspond to log2 fold-change values. Error bars depict the standard error of each log2 fold-change value calculated by DESeq2. Dot size corresponds to mean raw abundance. Each OTU is labeled according to its class, family, and Genus_OTUNumber on the x-axis. Asterisks denote a significantly DA ASV in a treatment.