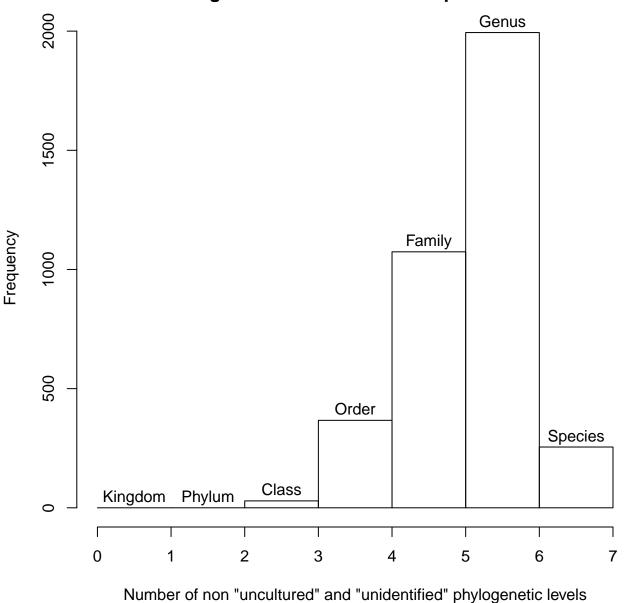
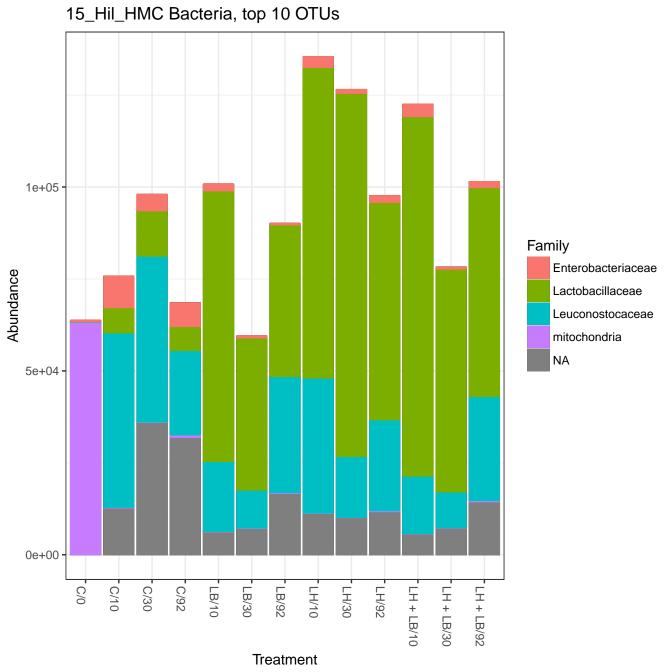
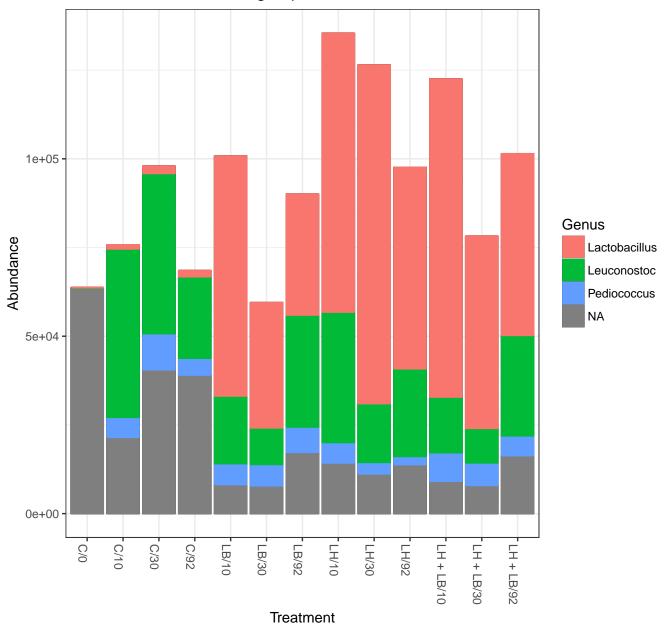


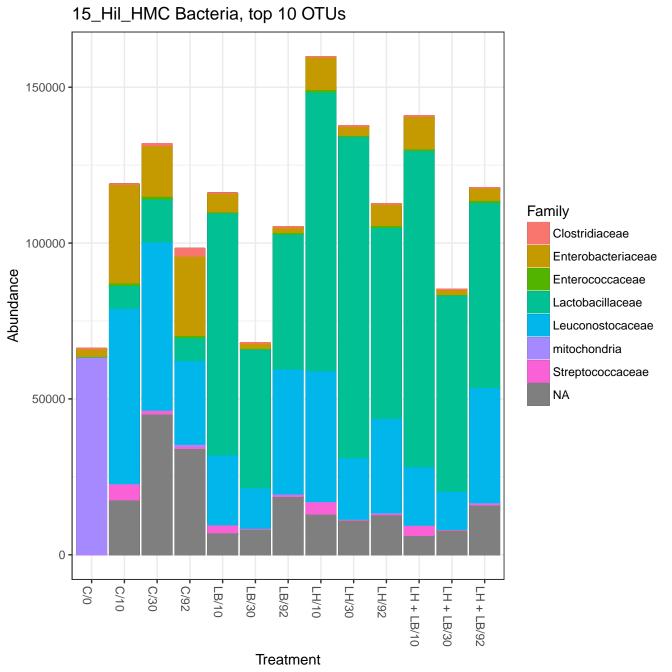
## 15\_Hil\_HMC Bacteria Histogram of INFERRED most specific rank



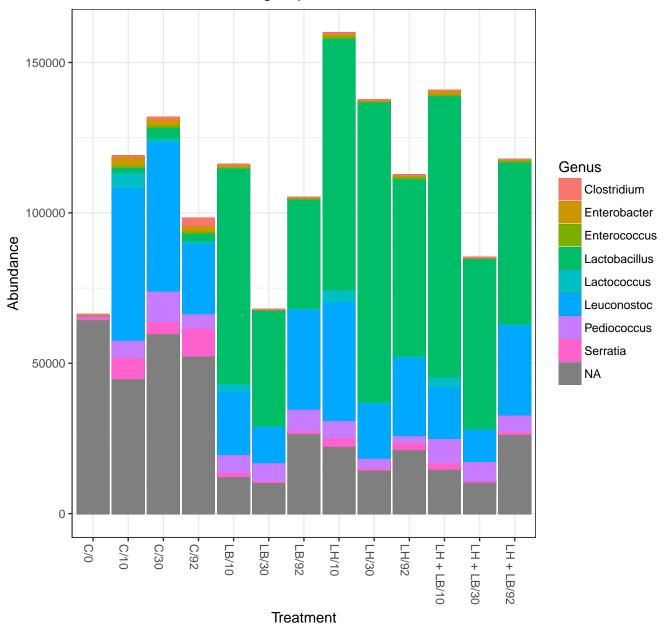


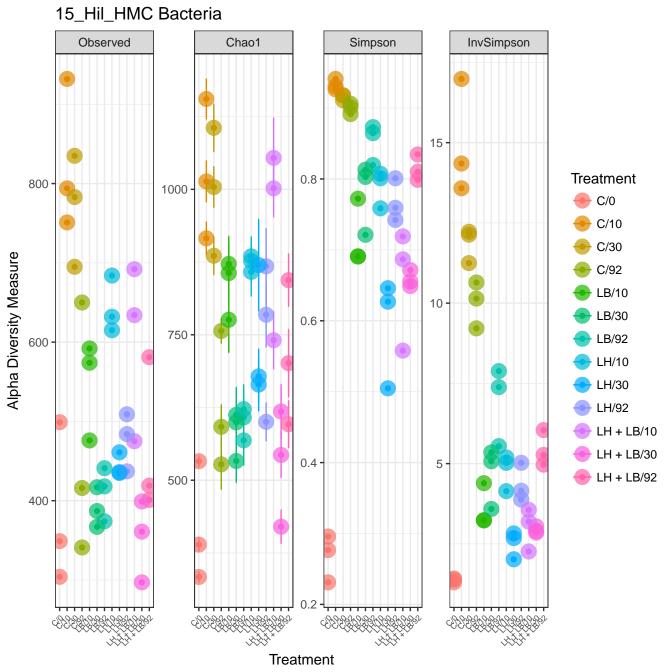
15\_Hil\_HMC Bacteria, OTUs with at least 1/100 of max reads/sample/OTU in at least one treatment group



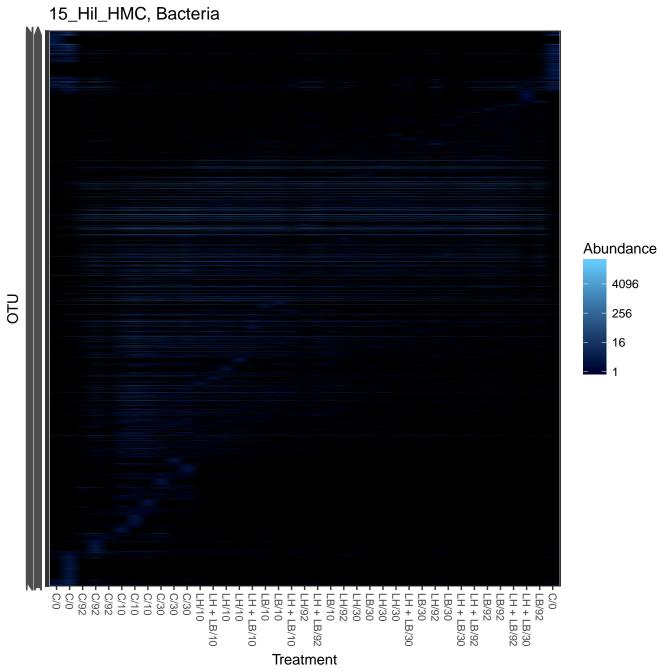


15\_Hil\_HMC Bacteria, OTUs with at least 1/100 of max reads/sample/OTU in at least one treatment group





15\_Hil\_HMC Bacteria CCA DCA MDS 2 0.4 -0.8 1 0.2 0.4 Treatment 0.0 C/0 0 0.0 -C/10 C/30 -0.2 **-**-0.4C/92 -1 LB/10 Axis\_2 3 LB/30 2 4 3 -0.50 -0.25 0.00 i Ö 2 4 0.25 1 LB/92 NMDS PCoA **RDA** LH/10 1.0 LH/30 0.4 -LH/92 0 LH + LB/10 0.5 0.2 LH + LB/30 LH + LB/92 -100 0.0 0.0 -0.2 **-**-200 **-**-0.5-2 -0.50 -0.25 0.00 0.25 -4 -50 0 50 100 Axis\_1



15\_Hil\_HMC Bacteria: Differential abundance ratio, C/0 vs. LH/30 @ 0.05 10 5 log2FoldChange Phylum Proteobacteria 0 -**Bacteroidetes** Firmicutes -5 -10 Bacilli Alphaproteobacteria Betaproteobacteria Gammaproteobacteria [Saprospirae] Class