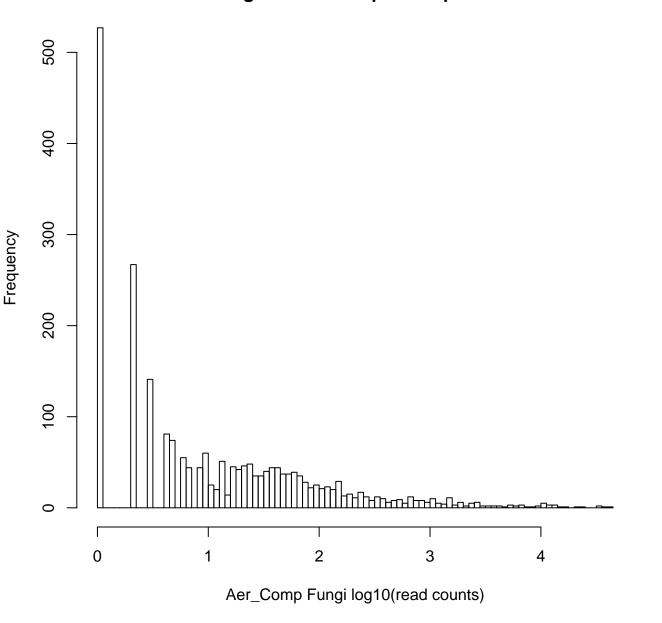
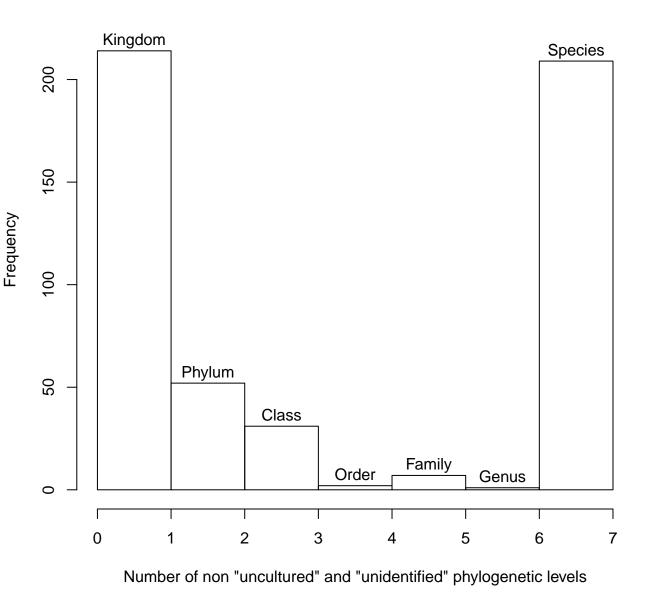
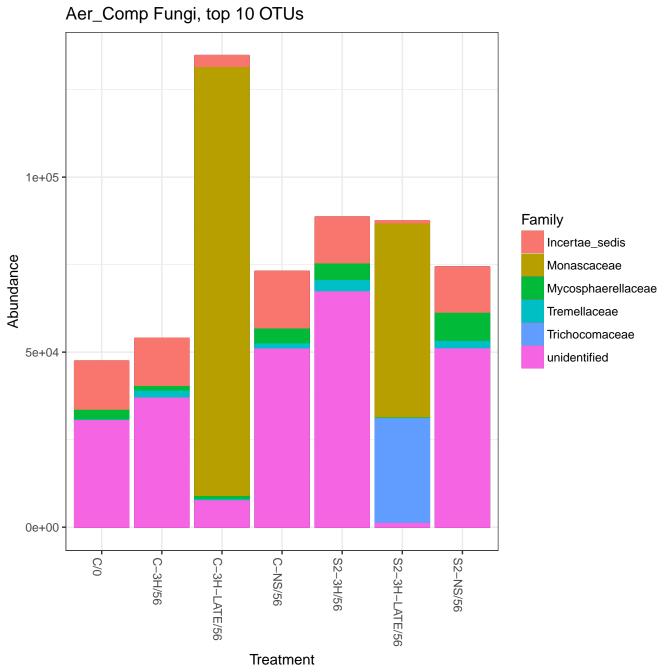
Aer\_Comp Fungi Histogram of reads per sample/OTU

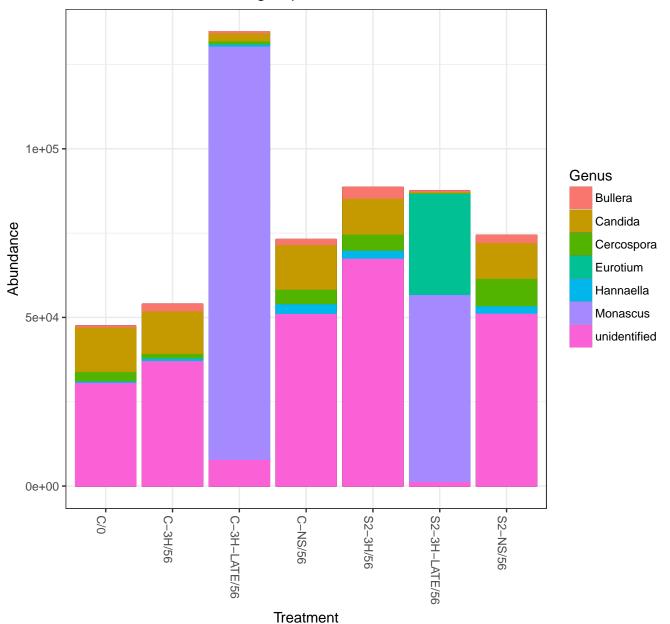


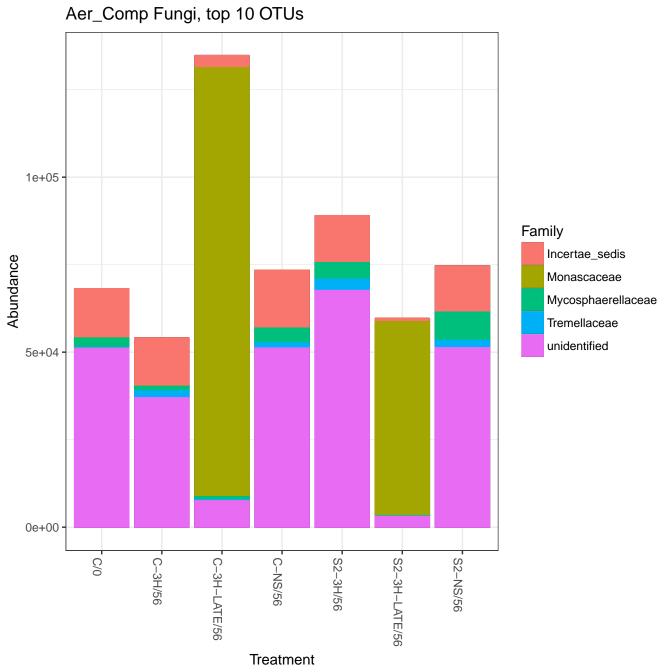
## Aer\_Comp Fungi Histogram of INFERRED most specific rank



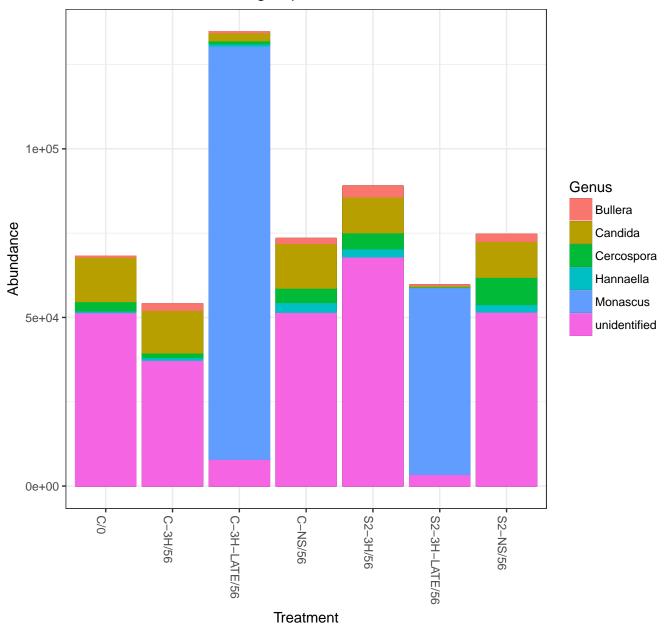


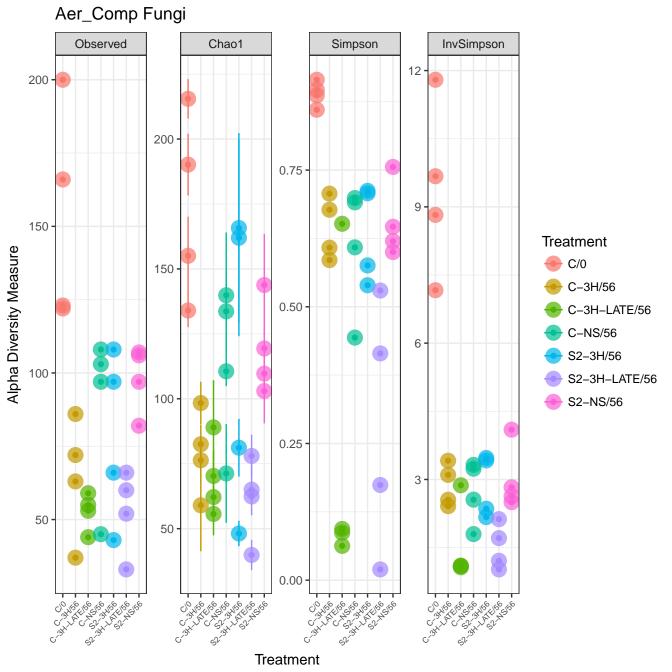
Aer\_Comp Fungi, OTUs with at least 1/100 of max reads/sample/OTU in at least one treatment group

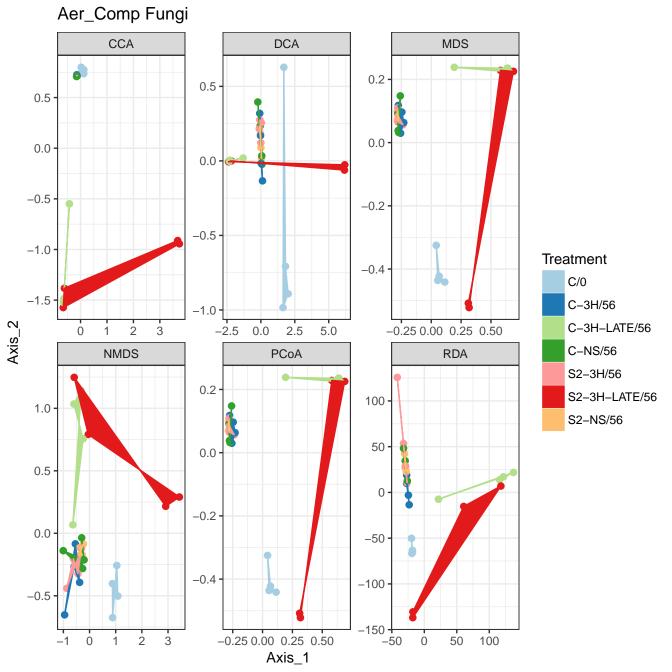


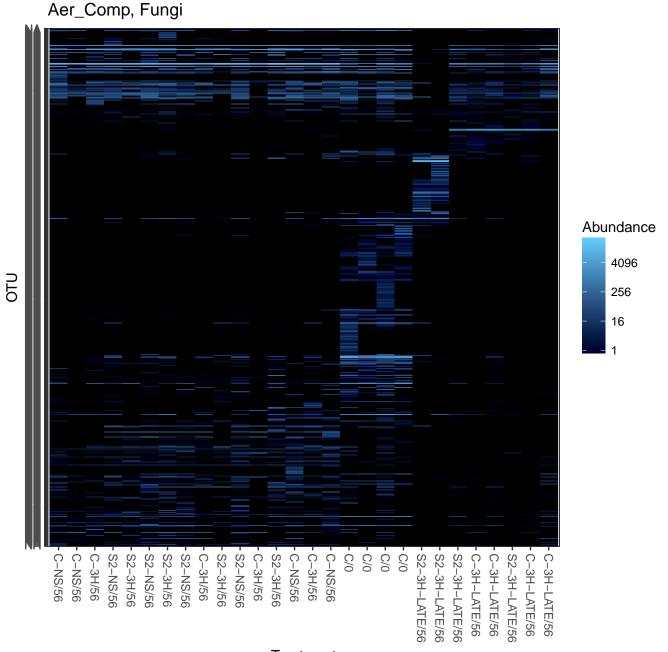


Aer\_Comp Fungi, OTUs with at least 1/100 of max reads/sample/OTU in at least one treatment group









Treatment

Aer\_Comp Fungi: Differential abundance ratio, C/0 vs. S2-3H-LATE/56 @ 0.05 8 4 log2FoldChange Phylum Ascomycota Basidiomycota unidentified Dothideomycetes Eurotiomycetes Class