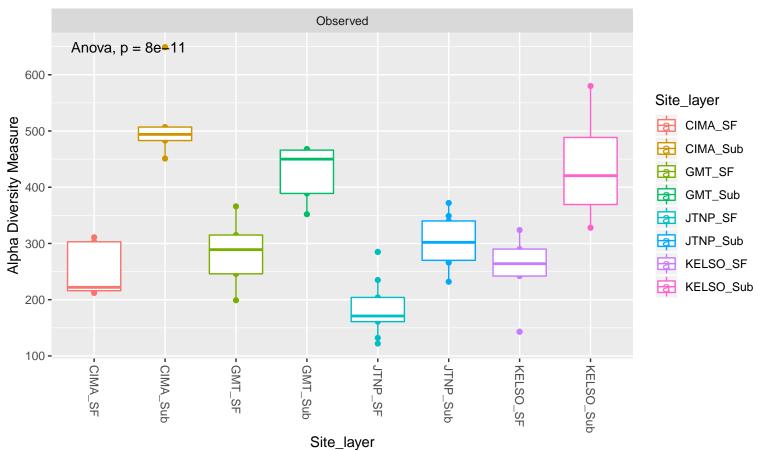
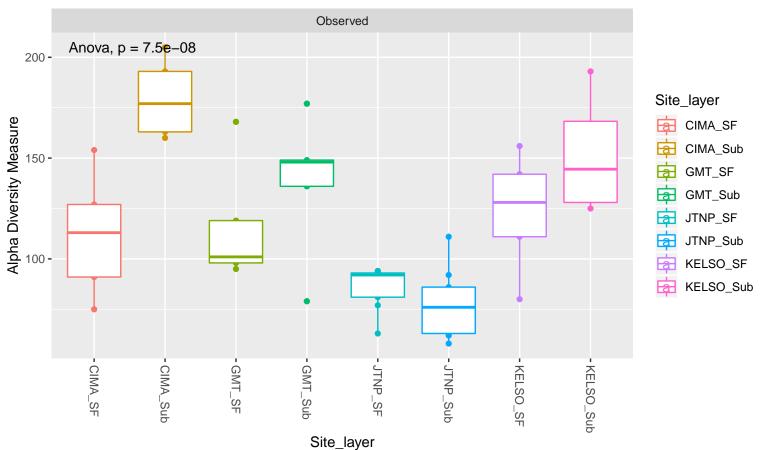
D_1_Proteobacteria



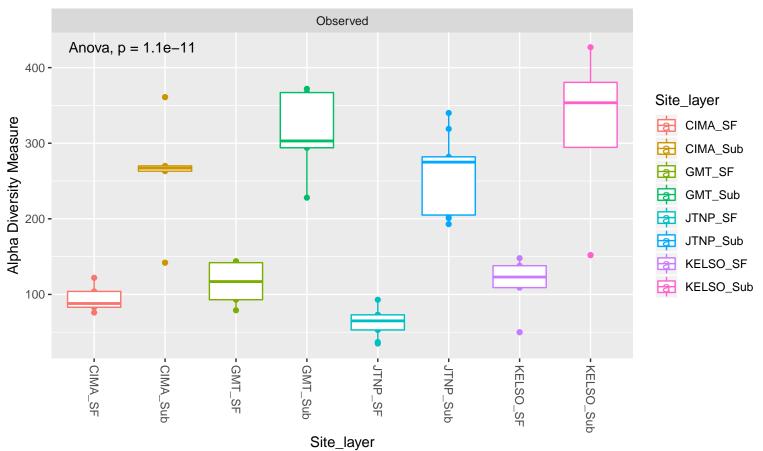
D_1__Firmicutes Observed Anova, p = 0.0001815 -Site_layer Alpha Diversity Measure CIMA_SF CIMA_Sub GMT_SF $\mathsf{GMT}_\mathsf{Sub}$ JTNP_SF JTNP_Sub KELSO_SF KELSO_Sub -KELSO_SF CIMA_SF -GMT_SF KELSO_Sub GMT_Sub JTNP_SF CIMA_Sub JTNP_Sub Site_layer

D_1_Fusobacteria Observed Anova, p = 0.622.0 -Site_layer Alpha Diversity Measure CIMA_SF CIMA_Sub GMT_SF GMT_Sub JTNP_SF JTNP_Sub KELSO_SF KELSO_Sub 0.0 -CIMA_SF -JTNP_SF - KELSO_SF KELSO_Sub CIMA_Sub GMT_SF GMT_Sub JTNP_Sub

D_1__Bacteroidetes



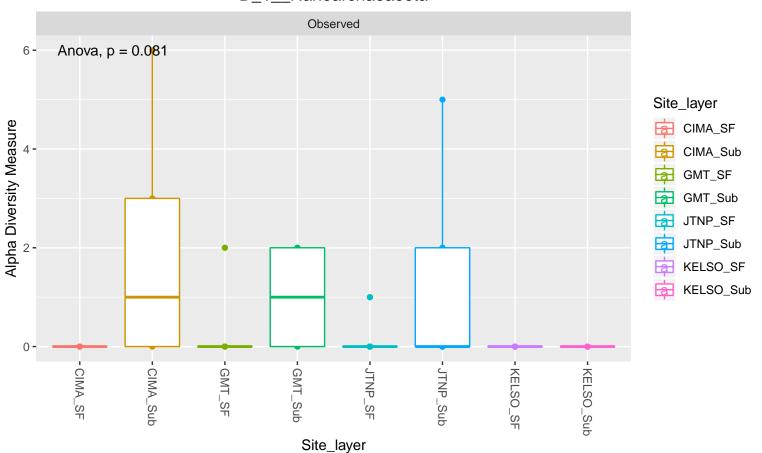
D_1__Actinobacteria



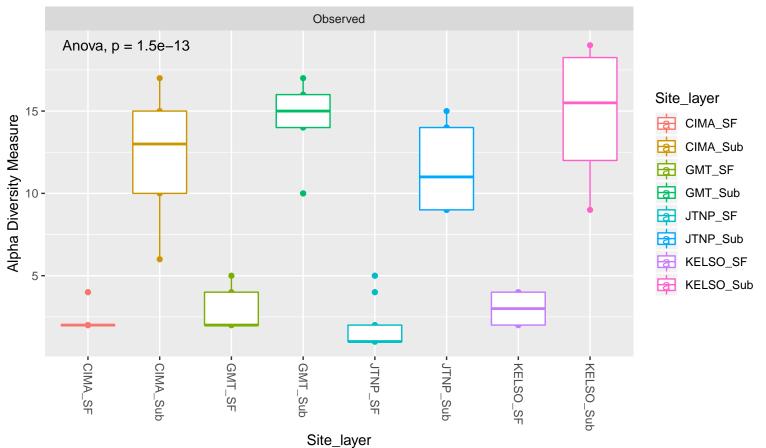
D_1_SAR Observed Anova, p = 0.281.00 -Site_layer Alpha Diversity Measure CIMA_SF CIMA_Sub GMT_SF GMT_Sub JTNP_SF JTNP_Sub KELSO_SF KELSO_Sub 0.00 -- KELSO_Sub - KELSO_SF - CIMA_Sub - GMT_Sub JTNP_Sub JTNP_SF

D_1__Euryarchaeota Observed Anova, p = 0.00146 -Site_layer Alpha Diversity Measure CIMA_SF CIMA_Sub GMT_SF $\mathsf{GMT}_\mathsf{Sub}$ JTNP_SF JTNP_Sub KELSO_SF KELSO_Sub 0 -- GMT_SF -JTNP_SF -KELSO_SF - KELSO_Sub - CIMA_Sub CIMA_SF JTNP_Sub GMT_Sub Site_layer

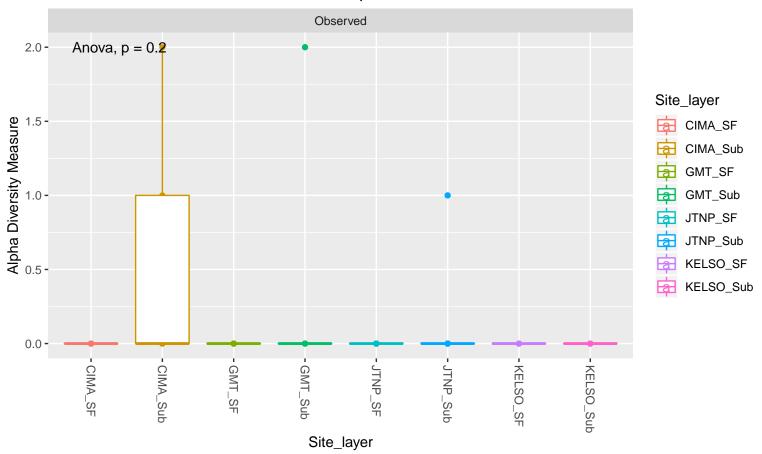
D_1_Nanoarchaeaeota



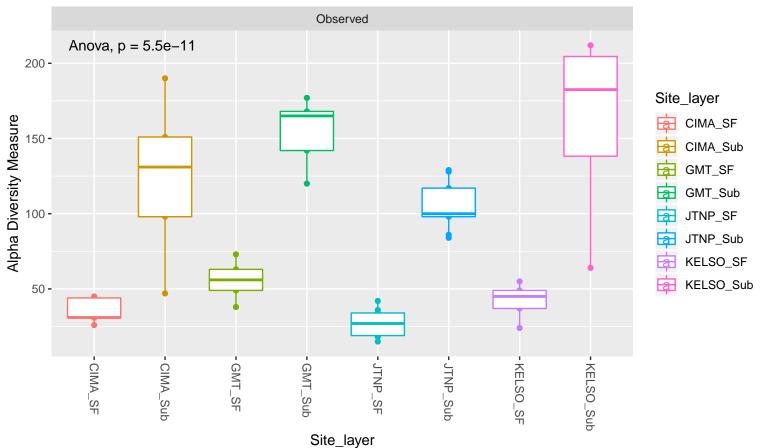
D_1__Thaumarchaeota



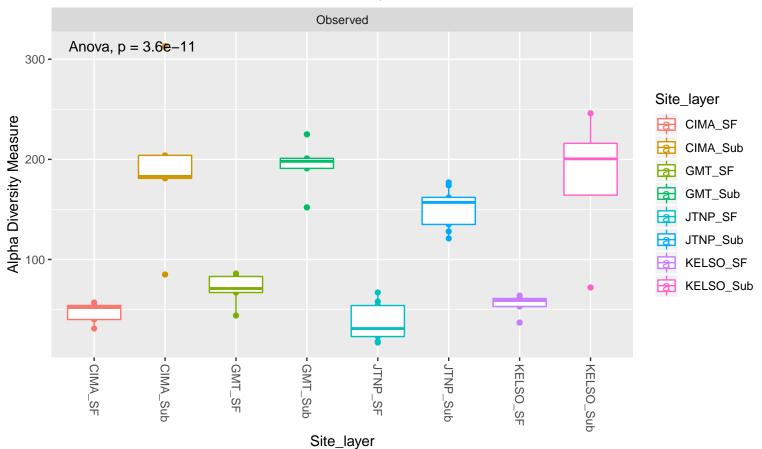
D_1__Omnitrophicaeota



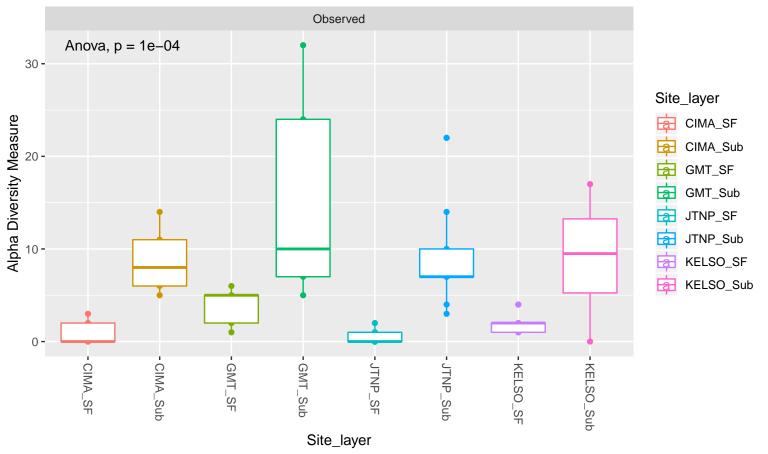
D_1__Acidobacteria



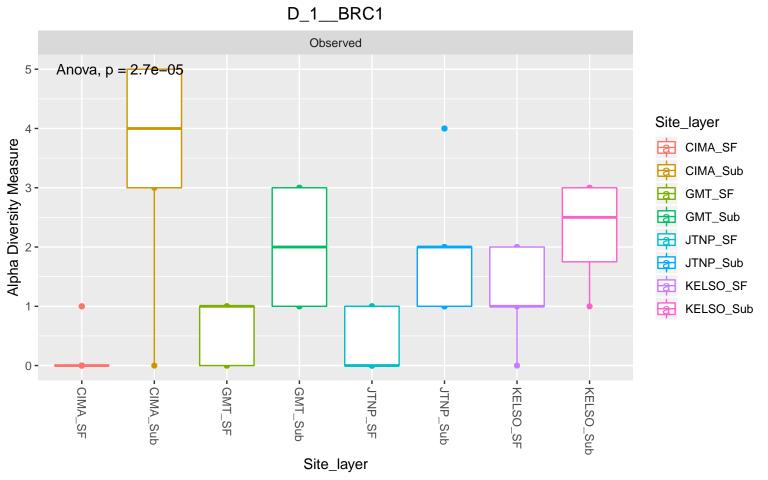
D_1__Planctomycetes



D_1__Patescibacteria

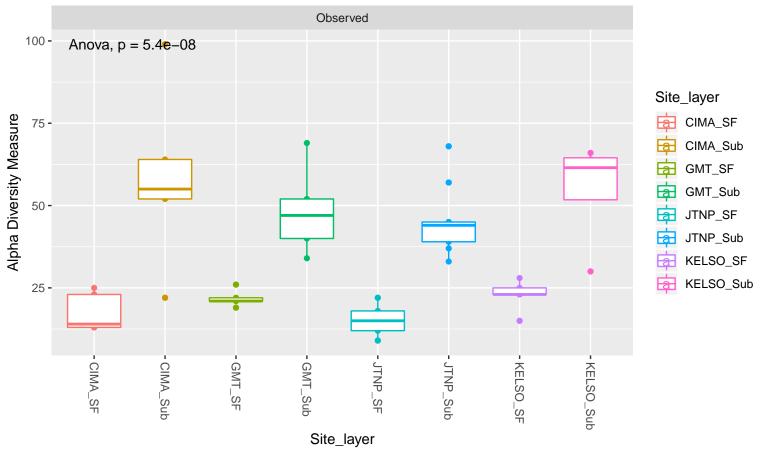


D_1__Dependentiae Observed Anova, p = 0.00423 -Site_layer Alpha Diversity Measure CIMA_SF CIMA_Sub GMT_SF $\mathsf{GMT}_\mathsf{Sub}$ JTNP_SF JTNP_Sub KELSO_SF KELSO_Sub 0 -CIMA_Sub -GMT_SF -JTNP_SF -KELSO_SF - KELSO_Sub -CIMA_SF JTNP_Sub GMT_Sub

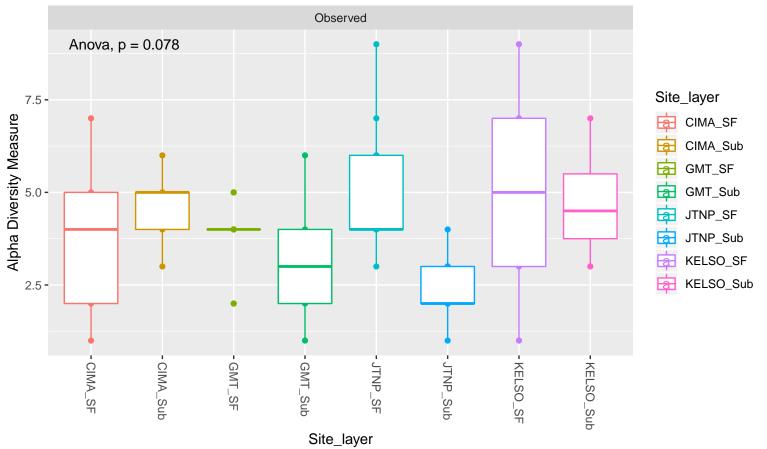


D_1__Elusimicrobia Observed 10.0 -Anova, p = 0.0011Site_layer 7.5 -Alpha Diversity Measure CIMA_SF CIMA_Sub GMT_SF $\mathsf{GMT}_\mathsf{Sub}$ 5.0 -JTNP_SF JTNP_Sub KELSO_SF 2.5 -KELSO_Sub 0.0 -- CIMA_Sub - GMT_Sub - KELSO_SF -CIMA_SF - JTNP_Sub - KELSO_Sub JTNP_SF Site_layer

D_1__Armatimonadetes

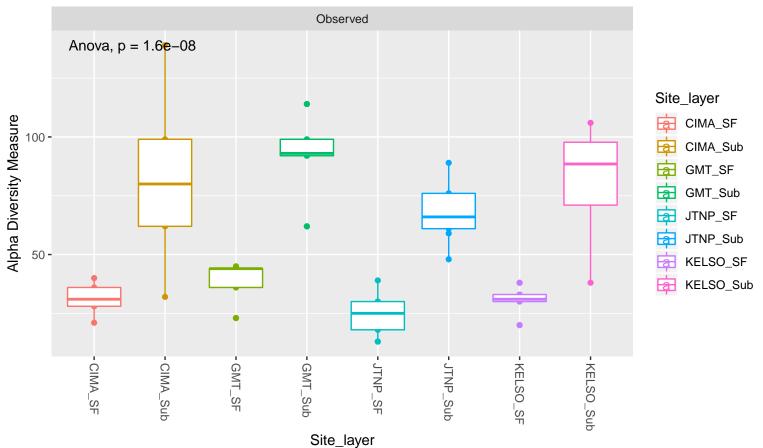


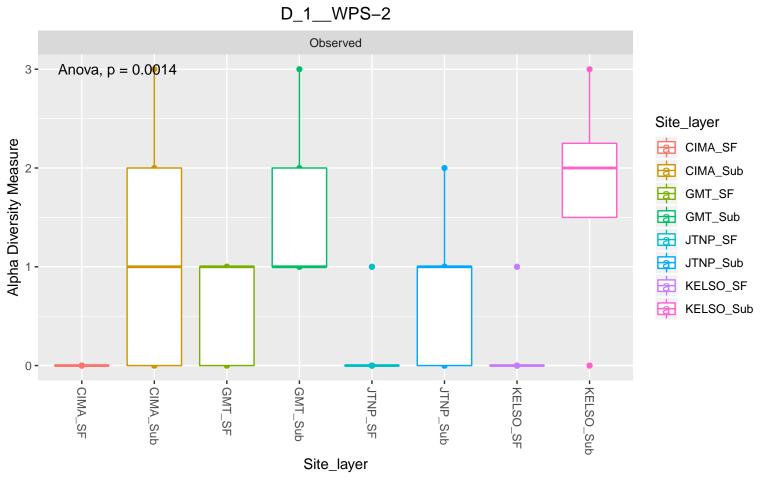
D_1__Deinococcus-Thermus



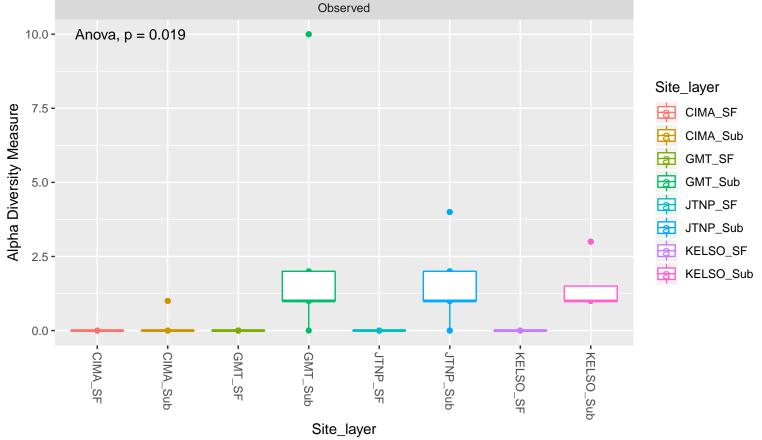
D_1__Chloroflexi Observed Anova, p = 2.3e-10300 -Site_layer Alpha Diversity Measure CIMA_SF CIMA_Sub GMT_SF 200 - $\mathsf{GMT}_\mathsf{Sub}$ JTNP_SF JTNP_Sub KELSO_SF 100 -KELSO_Sub - CIMA_Sub GMT_Sub KELSO_SF KELSO_Sub CIMA_SF JTNP_SF JTNP_Sub

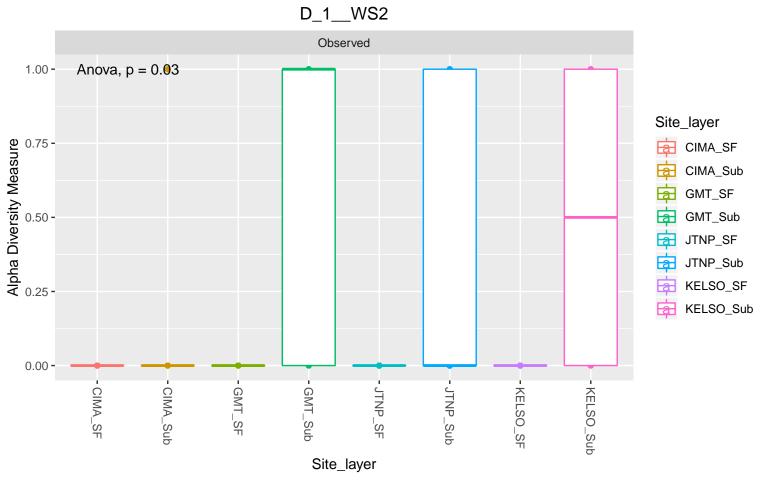
D_1__Gemmatimonadetes



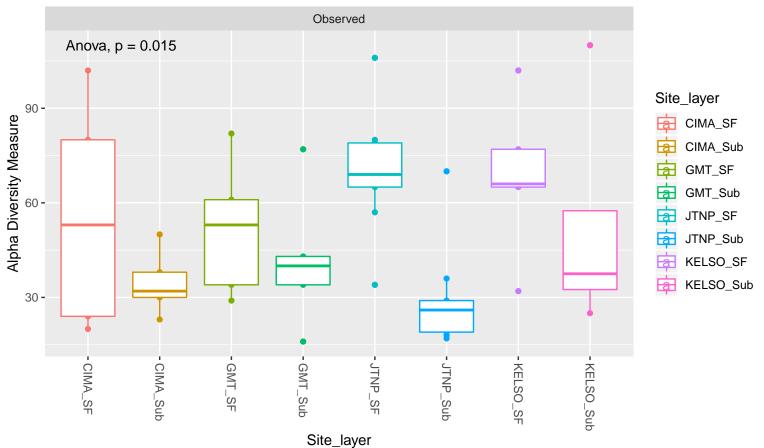


D_1__Entotheonellaeota Observed

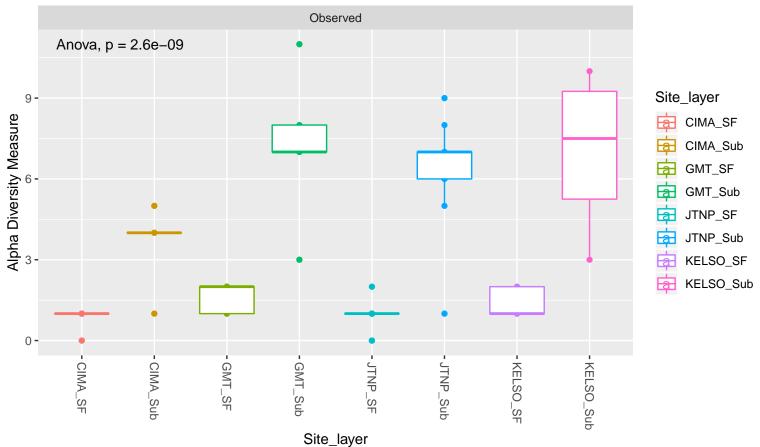


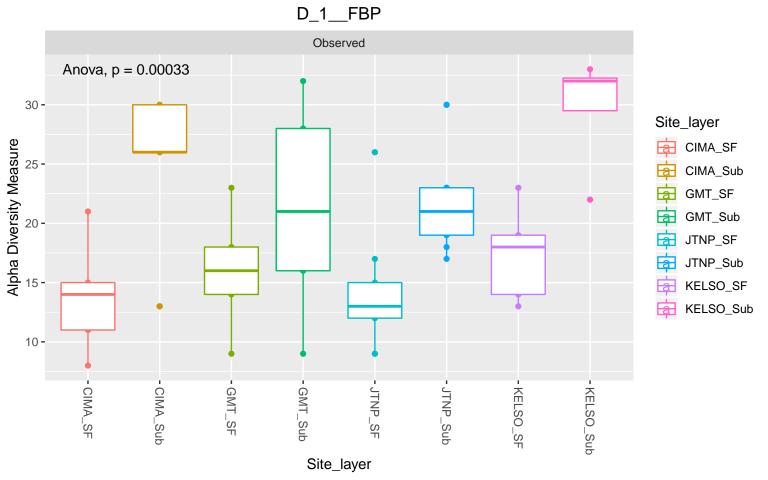


D_1__Cyanobacteria

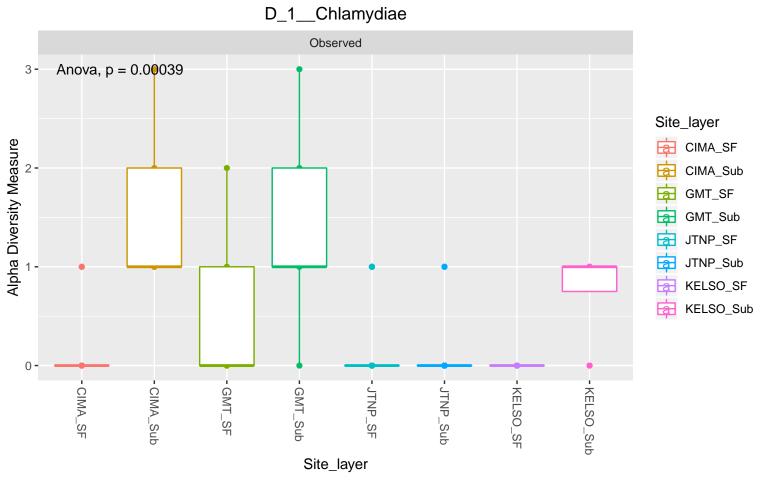


D_1_Nitrospirae





D_1_Fibrobacteres Observed Anova, p = 0.0463 -Site_layer Alpha Diversity Measure CIMA_SF CIMA_Sub GMT_SF $\mathsf{GMT}_\mathsf{Sub}$ JTNP_SF JTNP_Sub KELSO_SF KELSO_Sub 0 -- CIMA_SF CIMA_Sub - GMT_SF -JTNP_SF -KELSO_SF - KELSO_Sub JTNP_Sub GMT_Sub Site_layer



D_1__Rokubacteria Observed 2.0 -Anova, p = 0.3Site_layer Alpha Diversity Measure CIMA_SF CIMA_Sub GMT_SF GMT_Sub JTNP_SF JTNP_Sub KELSO_SF KELSO_Sub 0.0 -CIMA_SF -JTNP_SF - KELSO_SF KELSO_Sub CIMA_Sub GMT_SF GMT_Sub JTNP_Sub

D_1__Verrucomicrobia

