Phylums from Mothur	Phylums from QIIME2

Table 1: Table 1: Phylums from Mothur vs Phylums from QIIME2

Phylums from Mothur	Phylums from QIIME2
Proteobacteria	D_1__Proteobacteria
Bacteroidetes	D_1__Bacteroidetes
Thaumarchaeota	D_1__Planctomycetes
Actinobacteria	D_1__Thaumarchaeota
Marinimicrobia_(SAR406_clade)	D_1__Actinobacteria
Planctomycetes	D_1__Deferribacteres
Gemmatimonadetes	D_1__Verrucomicrobia
Verrucomicrobia	D_1__Firmicutes
Nitrospinae	D_1__Lentisphaerae
SBR1093	D_1__Cyanobacteria
TM6_(Dependentiae)	
Chloroflexi	
Cyanobacteria	
Euryarchaeota	
PAUC34f	
Woesearchaeota_(DHVEG-6)	
Gracilibacteria	
Parcubacteria	

Based on Fig. 3, the phylum Proteobacteria was found to be the most abundant from depth of 10m to 200m compared to the other phyla. The abundance of phylum Thaumarchaeota was found to be decreasing from 100m to 200m. The abundance of the other phyla Actinobacteria, Bacteroidetes, Chloroflexi, Cyanobacteria, Euryarchaeota, Gemmatimonadetes, Gracilibacteria, Marinimicrobia_(SAR406_clade), Nitrospinae, Parcubacteria, PAUC34f, Planctomycetes, Proteobacteria, SBR1093, Thaumarchaeota, TM6_(Dependentiae), Verrucomicrobia, and Woesearchaeota_(DHVEG-6) were observed as depth-independent. In the QIIME2 data, there were much less phyla presented (10 types of phyla) in comparison with the Mothur data (18 types of phyla), see Table 1. The abundance of Bacteriodetes seemed to be decreasing from depth 10m to 200m. The abundance of Thaumarcheota was found to be decreasing from depth of 100m to 165m. There was no significant relationship found between the abundance of Proteobacteria and Planctomycetes in regards to depth. Overall, it was observed that the distribution of phyla was changing with depth in the Mothur and QIIME2 data.

```
subMTaxa <- subset_taxa(secondMTaxa, Phylum == "Planctomycetes")
colourCount <- length(unique(tax_table(subMTaxa)[, "Genus"]))
myColors <- colorRampPalette(brewer.pal(8, "Accent"))(colourCount)
myColors[5] <- colorPlanctomycetes
p1 <- plot_bar(subMTaxa, fill = "Genus") + geom_bar(aes(color = Genus,
    fill = Genus), stat = "identity", position = "stack") + scale_fill_manual(values = myColors
    scale_colour_manual(values = myColors)
```