Figure 3: Phylum distribution across samples from Mothur

```
colourCount <- length(unique(tax_table(secondQTaxa)[, "Phylum"]))
myColors <- colorRampPalette(brewer.pal(8, "Accent"))(colourCount)
myColors[7] <- colorPlanctomycetes

p2 <- plot_bar(secondQTaxa, fill = "Phylum") + geom_bar(aes(color = Phylum,
    fill = Phylum), stat = "identity", position = "stack") +
    scale_fill_manual(values = myColors) + scale_colour_manual(values = myColors)
annotate_figure(ggarrange(p2, ncol = 1, nrow = 1), bottom = text_grob("Figure 4: Phylum distri
    face = "bold", size = 12))
```