```
figureM <- annotate_figure(ggarrange(p1, ncol = 1, nrow = 1,
    widths = 0.7, heights = 0.2), bottom = text_grob("Mothur",
    color = "blue", face = "bold", size = 12))

subQTaxa = subset_taxa(secondQTaxa, Phylum == "D_1__Planctomycetes")
colourCount <- length(unique(tax_table(subMTaxa)[, "Genus"]))
myColors <- colorRampPalette(brewer.pal(8, "Accent"))(colourCount)
myColors[4] <- colorPlanctomycetes
p2 <- plot_bar(subQTaxa, fill = "Genus") + geom_bar(aes(color = Genus,
    fill = Genus), stat = "identity", position = "stack") + scale_fill_manual(values = myColors
    scale_colour_manual(values = myColors)
figureQ <- annotate_figure(ggarrange(p2, ncol = 1, nrow = 1,
    widths = 0.7, heights = 0.2), bottom = text_grob("QIIME2",
    color = "blue", face = "bold", size = 12))
annotate_figure(ggarrange(figureM, figureQ, ncol = 1, nrow = 2),
    bottom = text_grob("Figure 5: Genus distribution of Planctomycetes across samples",
        face = "bold", size = 12))
```