

```
figureQ <- ggarrange(p1, p2, p3, p4, ncol = 2, nrow = 2, labels = c("(a)",
  "(b)", "(c)", "(d)"))
annotate_figure(figureQ, bottom = text_grob("Figure 2: QIIME2",
  face = "bold", size = 12))
```

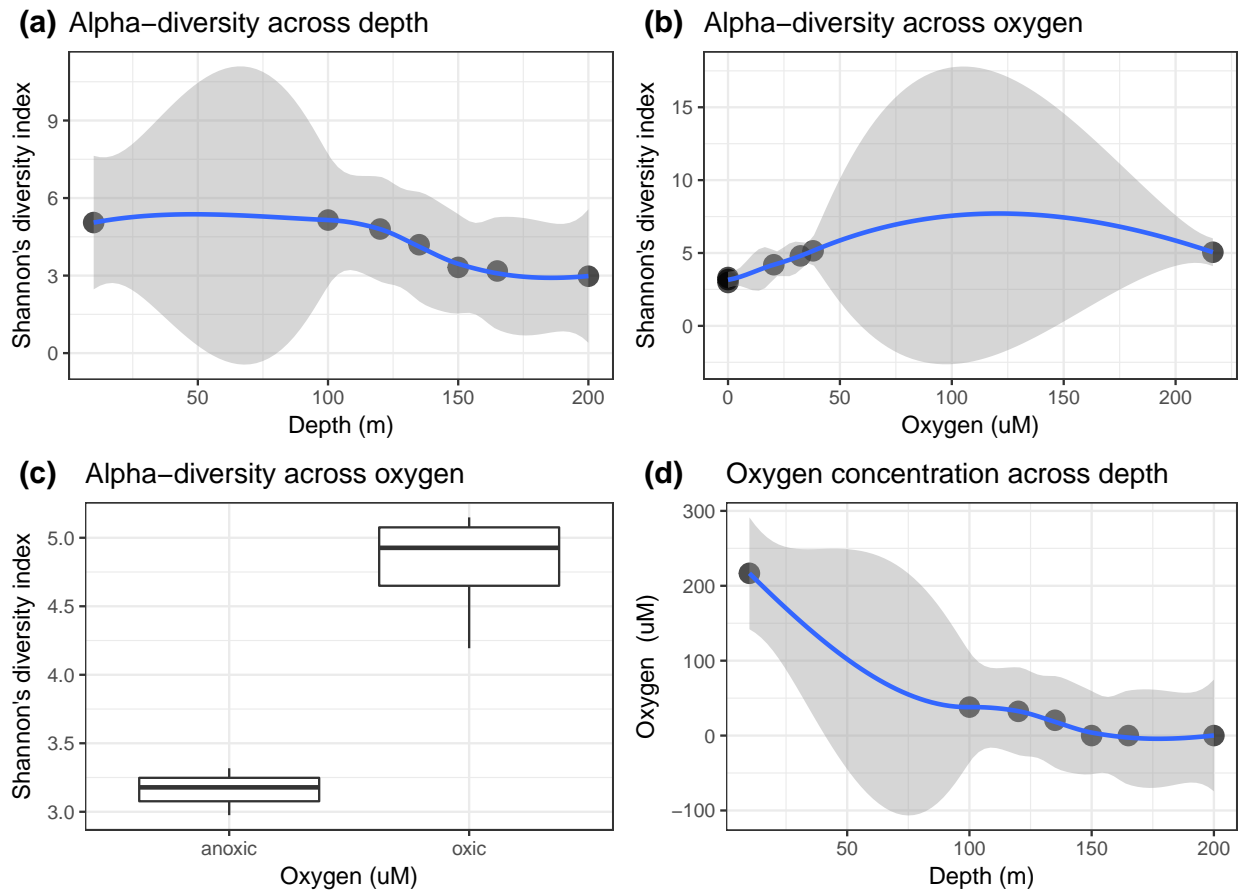


Figure 2: QIIME2

```
colorPlanctomycetes <- "black"

colourCount <- length(unique(tax_table(secondMTaxa[, "Phylum"])))
myColors <- colorRampPalette(brewer.pal(8, "Accent"))(colourCount)
myColors[12] <- colorPlanctomycetes
p1 <- plot_bar(secondMTaxa, 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(p1, ncol = 1, nrow = 1), bottom = text_grob("Figure 3: Phylum distrib",
  face = "bold", size = 12))
```