



Figure 4: Phylum distribution across samples from QIIME2

3.2 Analysis of abundance information of Planctomyces along with depth and/or oxygen concentration

```
workingMTaxa = subset_taxa(secondMTaxa, Genus == "Planctomyces")
workingQTaxa = subset_taxa(secondQTaxa, Genus == "D_5__Planctomyces")

phylumM <- get_taxa_unique(physeq = secondMTaxa, taxonomic.rank = "Phylum")
phylumQ <- get_taxa_unique(physeq = secondQTaxa, taxonomic.rank = "Phylum")
phylumMQ <- list(phylumM, phylumQ)
phylumMQ <- data.frame(sapply(phylumMQ, "[", seq(max(sapply(phylumMQ,
  length))), stringsAsFactors = FALSE)
phylumMQ[is.na(phylumMQ)] <- " "
colnames(phylumMQ) <- c("Phylums from Mothur", "Phylums from QIIME2")
kable(phylumMQ, caption = "Table 1: Phylums from Mothur vs Phylums from QIIME2")
```