

### 3.3 Estimate richness (number of OTUs/ASVs) for *Planctomyces*

```
suggestedMOTUs <- colnames(otu_table(workingMTaxa))
suggestedQOTUs <- rownames(otu_table(workingQTaxa))
suggestedMQOTUs <- list(suggestedMOTUs, suggestedQOTUs)
suggestedMQOTUs <- data.frame(sapply(suggestedMQOTUs, "[", seq(max(sapply(suggestedMQOTUs,
  length))))))
colnames(suggestedMQOTUs) <- c("OTUs from Mothur", "ASVs from QIIME2")
kable(suggestedMQOTUs, caption = "Table 3: OTUs from Mothur vs ASVs from QIIME2")
```

Table 3: Table 3: OTUs from Mothur vs ASVs from QIIME2

OTUs from Mothur	ASVs from QIIME2
Otu0125	Asv232
Otu0144	Asv799
Otu0401	Asv1021
Otu0592	Asv1124

Table 3 shows that in our analysis we observe only 4 OTUs/ASVs within the *Planctomyces* genus.

### 3.4 Interpretation of abundance information of OTUs/ASVs of *Planctomyces* along with depth and/or oxygen concentration

```
otu_stats <- data.frame()
for (otu in suggestedMOTUs) {
  linear_fit <- workingMTaxa %>% psmelt() %>% filter(OTU ==
    otu) %>% lm(Abundance ~ Depth_m, .) %>% summary()
  otu_stats <- rbind(otu_stats, linear_fit$coefficients["Depth_m",
    ])
}
tmpNames <- paste(suggestedMOTUs, " (Mothur) ")
for (otu in suggestedQOTUs) {
  linear_fit <- workingQTaxa %>% psmelt() %>% filter(OTU ==
    otu) %>% lm(Abundance ~ Depth_m, .) %>% summary()
  otu_stats <- rbind(otu_stats, linear_fit$coefficients["Depth_m",
    ])
}
tmpNames <- c(tmpNames, paste(suggestedQOTUs, " (QIIME2) "))
otu_stats <- cbind(tmpNames, otu_stats)
colnames(otu_stats) <- c("Covariates", "Estimate", "Std. Error",
  "t-value", "Pr(>|t|)")
kable(otu_stats, caption = "Table 4: Correlation data of OTUs within *Planctomyces* genus across")
```