

Table 4: Table 4: Correlation data of OTUs within *Planctomyces* genus across depth

Covariates	Estimate	Std. Error	t-value	Pr(> t)
Otu0125 (Mothur)	-0.0002045	0.0005479	-0.3731784	0.7243139
Otu0144 (Mothur)	-0.0001533	0.0004035	-0.3798581	0.7196506
Otu0401 (Mothur)	-0.0000009	0.0000807	-0.0113619	0.9913741
Otu0592 (Mothur)	-0.0000023	0.0000274	-0.0836392	0.9365887
Asv232 (QIIME2)	-0.0001665	0.0006541	-0.2545201	0.8092302
Asv799 (QIIME2)	-0.0000953	0.0005682	-0.1676505	0.8734282
Asv1021 (QIIME2)	0.0000544	0.0001222	0.4454921	0.6745908
Asv1124 (QIIME2)	-0.0003805	0.0005859	-0.6493922	0.5447317

```

otu_stats <- data.frame()
for (otu in suggestedMOTUs) {
  linear_fit <- workingMTaxa %>% psmelt() %>% filter(OTU ==
    otu) %>% lm(Abundance ~ O2_uM, .) %>% summary()
  otu_stats <- rbind(otu_stats, linear_fit$coefficients["O2_uM",
    ])
}
tmpNames <- paste(suggestedMOTUs, " (Mothur) ")
for (otu in suggestedQOTUs) {
  linear_fit <- workingQTaxa %>% psmelt() %>% filter(OTU ==
    otu) %>% lm(Abundance ~ O2_uM, .) %>% summary()
  otu_stats <- rbind(otu_stats, linear_fit$coefficients["O2_uM",
    ])
}
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 5: Correlation data of OTUs within *Planctomyces* genus across

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Table 5: Table 5: Correlation data of OTUs within *Planctomyces* genus across oxygen concentration

Covariates	Estimate	Std. Error	t-value	Pr(> t)
Otu0125 (Mothur)	-0.0001290	0.0004265	-0.3025609	0.7744070
Otu0144 (Mothur)	-0.0000962	0.0003142	-0.3062077	0.7717866
Otu0401 (Mothur)	-0.0000196	0.0000619	-0.3172313	0.7638869
Otu0592 (Mothur)	-0.0000096	0.0000208	-0.4601604	0.6647195
Asv232 (QIIME2)	-0.0002374	0.0004989	-0.4759372	0.6541875
Asv799 (QIIME2)	-0.0002374	0.0004285	-0.5541303	0.6033590
Asv1021 (QIIME2)	-0.0001100	0.0000831	-1.3250528	0.2424753
Asv1124 (QIIME2)	-0.0000147	0.0004727	-0.0311450	0.9763589