```
p3 <- workingQTaxa %>% psmelt() %>% ggplot() + geom_point(aes(x = 02_uM,
            y = Abundance), size = 5, alpha = 0.7) + geom_smooth(method = "lm",
            aes(x = Depth_m, y = Abundance)) + facet_wrap(~OTU, scales = "free_y") +
           labs(title = "Per ASV abundance information")
p4 <- workingQTaxa %>% psmelt() %>% ggplot() + geom_point(aes(x = Sample,
            y = OTU, size = O2_uM, color = OTU)) + scale_size_continuous(range = c(0,
            5)) + theme(axis.text.x = element_text(angle = 45, hjust = 1)) +
            labs(title = "Abundance of ASVs across samples")
figureM <- annotate_figure(ggarrange(p1, p2, ncol = 2, nrow = 1,</pre>
           labels = c("(a)", "(b)")), bottom = text_grob("Mothur", color = "blue",
           face = "bold", size = 12))
figureQ <- annotate_figure(ggarrange(p3, p4, ncol = 2, nrow = 1,
            labels = c("(a)", "(b)")), bottom = text_grob("QIIME2", color = "blue",
           face = "bold", size = 12))
annotate_figure(ggarrange(figureM, figureQ, ncol = 1, nrow = 2,
           labels = c("(a)", "(b)")), bottom = text_grob("Figure 8: Abundance of OTUs/ASVs within *Plants = c("(a)", "(b)")), bottom = text_grob("Figure 8: Abundance of OTUs/ASVs within *Plants = c("(a)", "(b)")), bottom = text_grob("Figure 8: Abundance of OTUs/ASVs within *Plants = c("(a)", "(b)")), bottom = text_grob("Figure 8: Abundance of OTUs/ASVs within *Plants = c("(a)", "(b)")), bottom = text_grob("Figure 8: Abundance of OTUs/ASVs within *Plants = c("(a)", "(b)")), bottom = text_grob("Figure 8: Abundance of OTUs/ASVs within *Plants = c("(a)", "(b)")), bottom = text_grob("Figure 8: Abundance of OTUs/ASVs within *Plants = c("(a)", "(b)")), bottom = text_grob("Figure 8: Abundance of OTUs/ASVs within *Plants = c("(a)", "(a)")), bottom = text_grob("(a)"), bottom = text_grob(
           face = "bold", size = 12))
```