

Supplemental Material

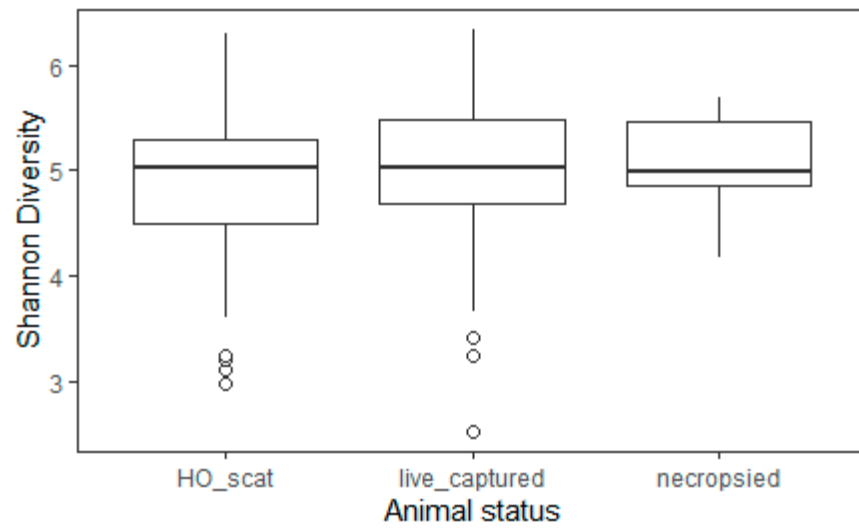


Figure S1. Shannon diversity of seal microbiomes by Animal status at collection (HO_scot: scat collected at haul-out, live_captured: swabs from live captured seals, and necropsied: fecal samples collected upon necropsy. No significant difference in Shannon diversity was found.

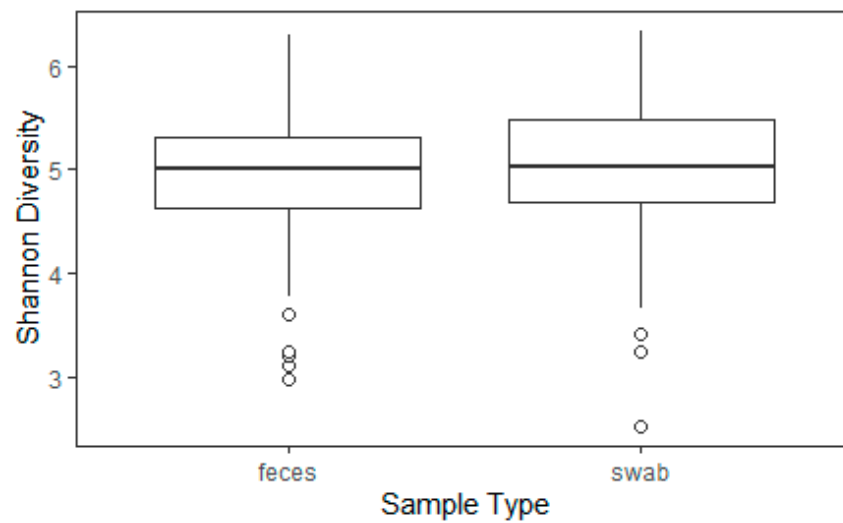


Figure S2. Shannon diversity of seal microbiomes by sample type upon collection, either scat collected or a rectal swab of a live animal in-hand. No significant difference in Shannon diversity was found.

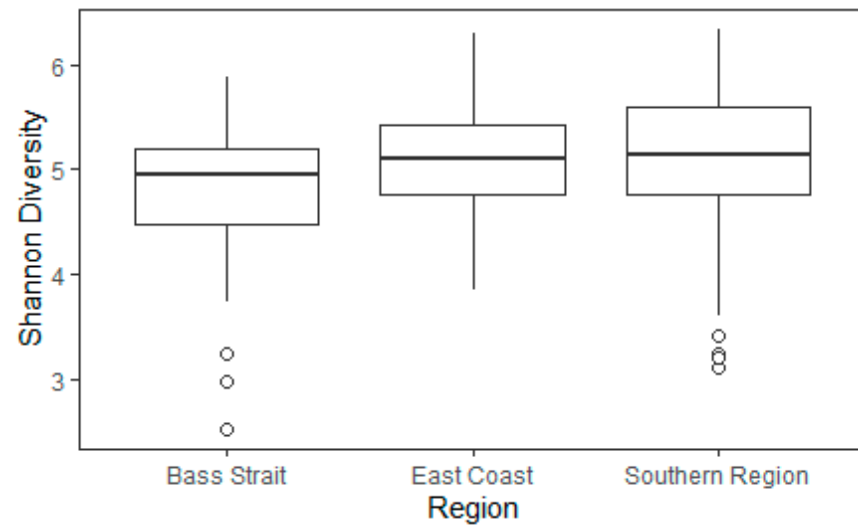


Figure S3. Shannon diversity of seal microbiomes by the region in which they were collected.

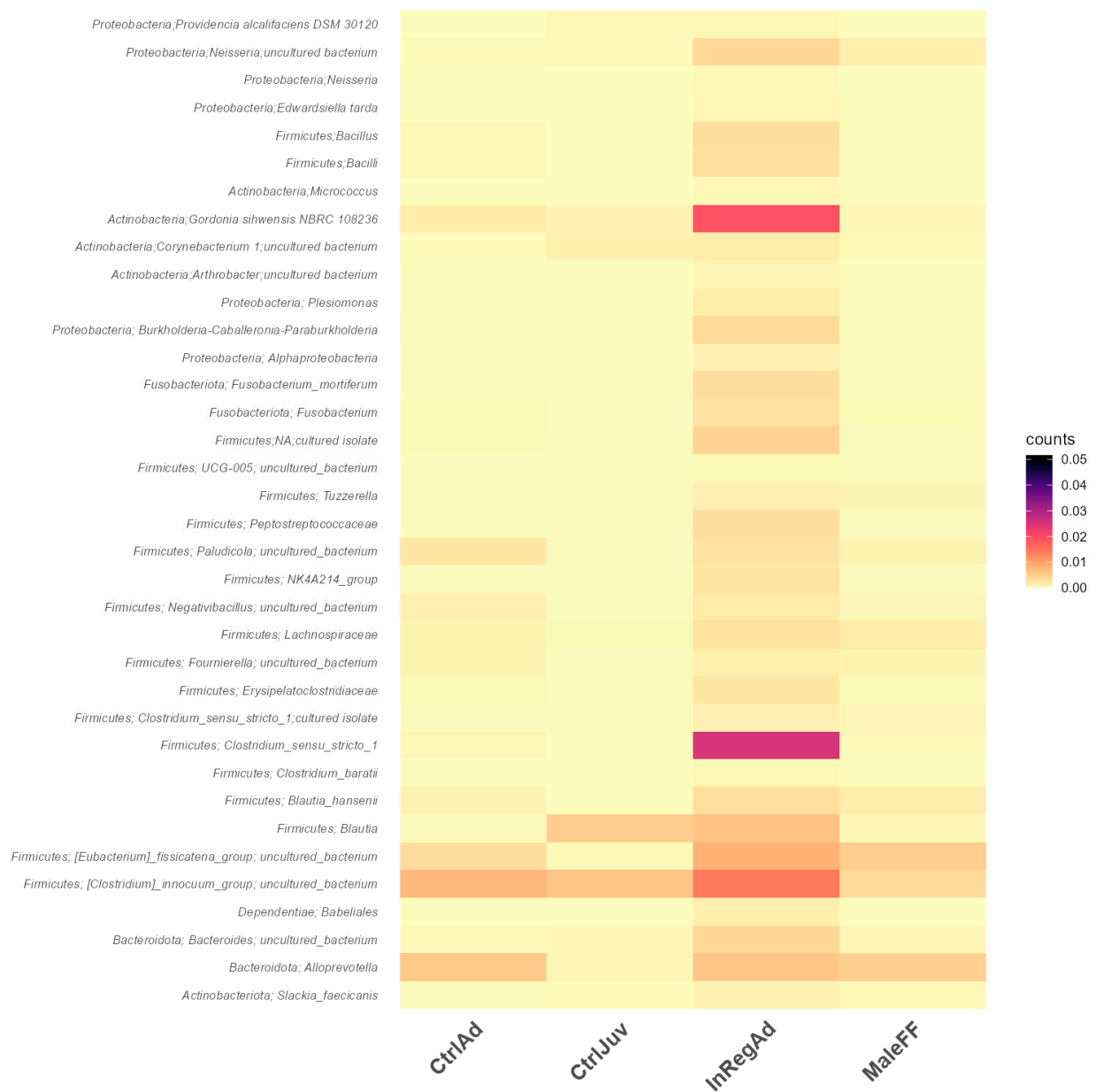


Figure S4. Heatmap of 72 ASVs aggregated at the taxon level (39 taxa) found in significantly higher abundance in the adults sampled in the region around farms (InRegAd) than any of the other three groups of seals tested: Males at the farms (MaleFF), control adults (CtrlAd) or control juveniles (CtrlJuv). These ASVs were found differentially abundant through ANCOM analysis of ASVs in all seals sampled when assessing variability between groups and accounting for the co-variability of regionality and using a W-statistic threshold of 0.7.

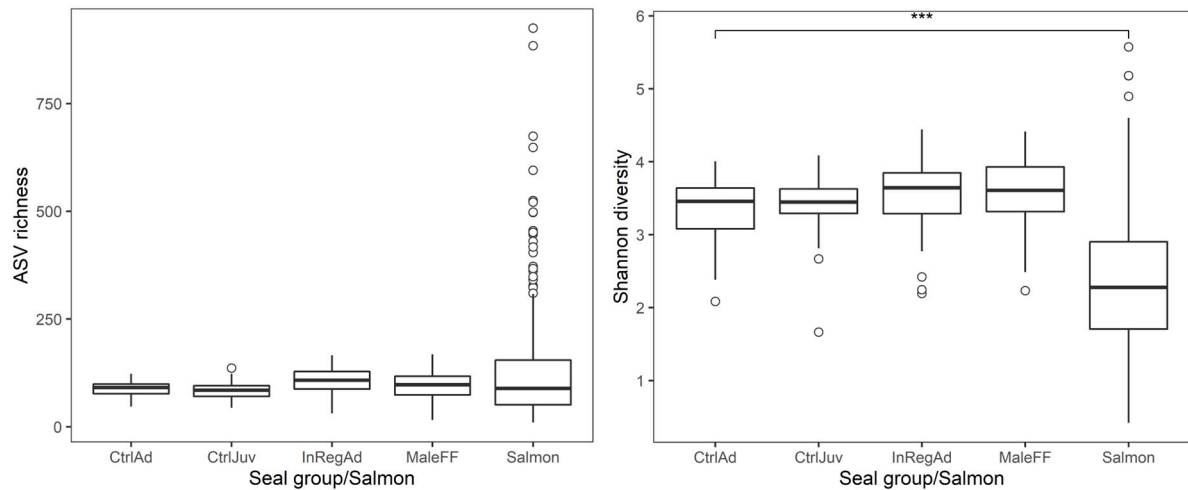


Figure S5. Richness (left panel) and Shannon diversity (right panel) differences between seal groups and salmon gut microbiomes.

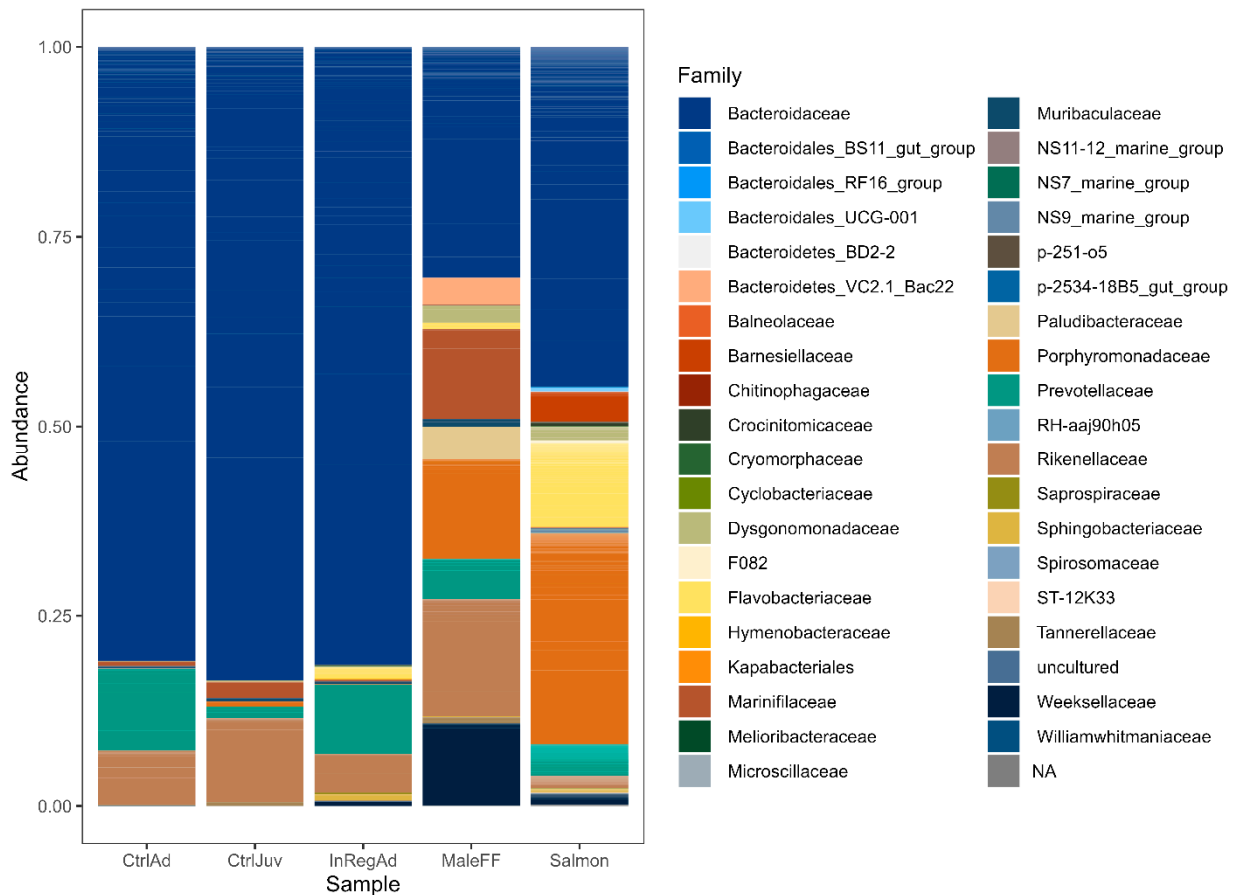


Figure S6. The relative abundance of families in the phylum *Bacteroidota* found in all seal groups samples and representative salmon microbiomes; males at fish farms (MaleFF), adults/scats sampled in the region directly around salmon (InRegAd), juveniles sampled outside of the regions around farms (CtrlJuv), adults/scats sampled outside the regions around farms (CtrlAd), and farmed salmon (Salmon).