

FIG. S1 Rarefaction curve showing the relationship between the number of observed species and the sampling effort. The x-axis represents the sample size and the y-axis represents the number of species which is represented by the number OTUs observed. As the sample size increases, the curve grows rapidly and approaches a plateau, indicating that the observed species diversity has saturated. The plateau phase was reached at <10,000 reads for most samples.

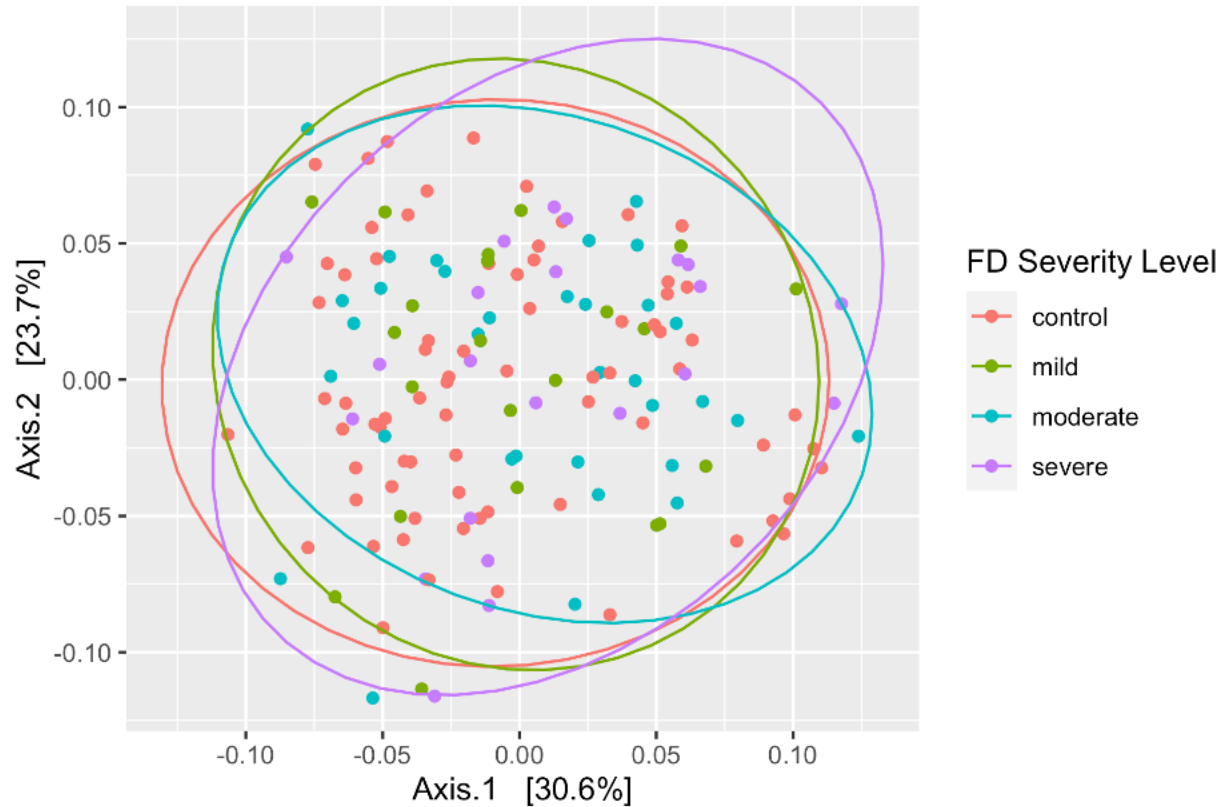


FIG. S2 No apparent microbial composition differences in mice with varying levels of FD, as indicated by the Weighted UniFrac beta diversity PCoA plot. The beta diversity PCoA plot shows no clear clustering distinction between healthy control mice (red), mice with mild FD (green), mice with moderate FD (blue), and mice with severe FD (purple). However, PERMANOVA statistical analysis indicated a significant difference between all groups ($p=0.001$). Control $n=74$, Mild $n=22$, Moderate $n=33$, Severe $n=22$.

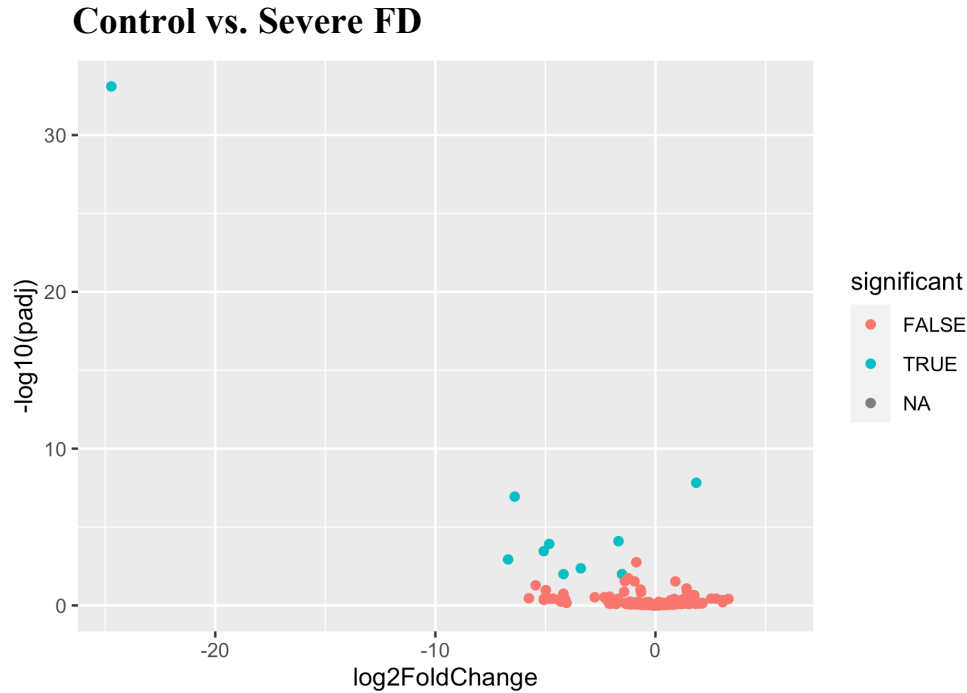


FIG. S3 Volcano plot of DESeq2 analysis shows differential abundance between healthy control mice and mice with severe FD. The x-axis represents log2 fold change and the y-axis represents negative log10 adjusted p-value. Significantly differentially abundant taxa (adjusted $p < 0.05$ and \log_2 fold change > 1.5) are shown in blue, while red points indicate taxa not significantly differentially abundant in severe FD mice compared to controls. Control $n=74$, Severe $n=22$.

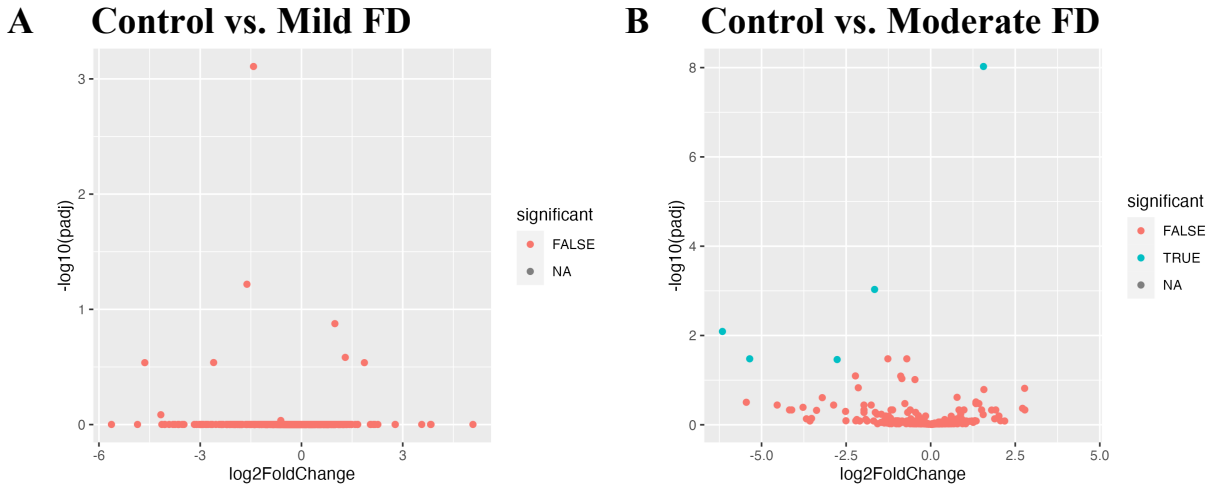


FIG. S4 Volcano plot of DESeq2 analysis shows differential abundance in moderate FD mice compared to healthy controls, but no difference between the control and mild FD mice. (A) The differential abundance analysis between the control and mild FD mice shows no difference in the abundance of shared taxa. The x-axis represents log₂ fold change and the y-axis represents negative log₁₀ adjusted p-value. Red points indicate taxa that are not significantly differentially abundant taxa in the mild FD group. Significantly differentially abundant taxa were set to have an adjusted $p < 0.05$ and log₂ fold change > 1.5 . Control $n=74$, Mild $n=22$. (B) The differential abundance analysis between the control and moderate FD mice shows 5 differentially abundant taxa in the moderate FD group. The x-axis represents log₂ fold change and the y-axis represents negative log₁₀ adjusted p-value. Significantly differentially abundant taxa (adjusted $p < 0.05$ and log₂ fold change > 1.5) are shown in blue, while red points indicate taxa not significantly differentially abundant in moderate FD mice compared to controls. Control $n=74$, Moderate $n=33$.