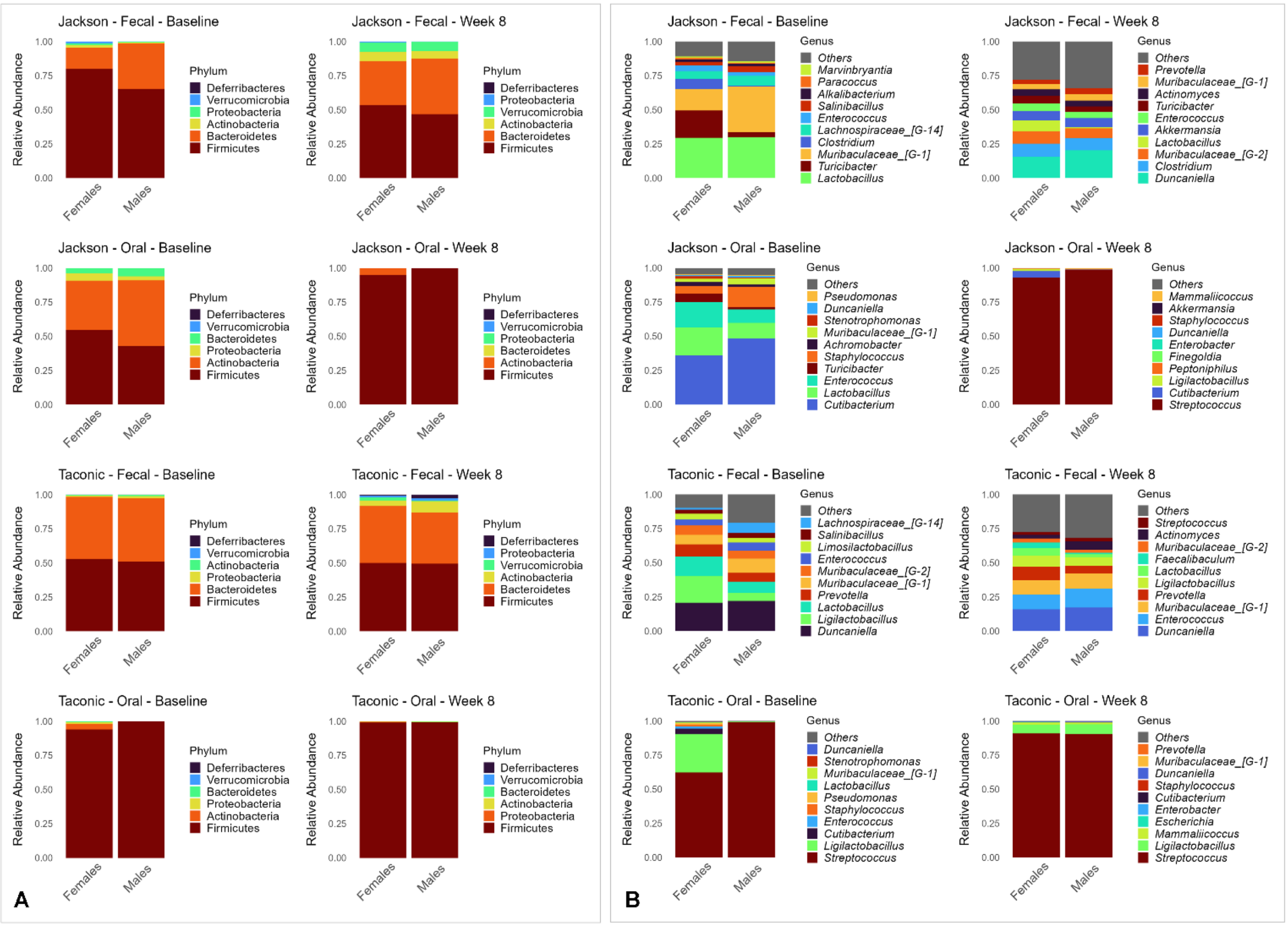
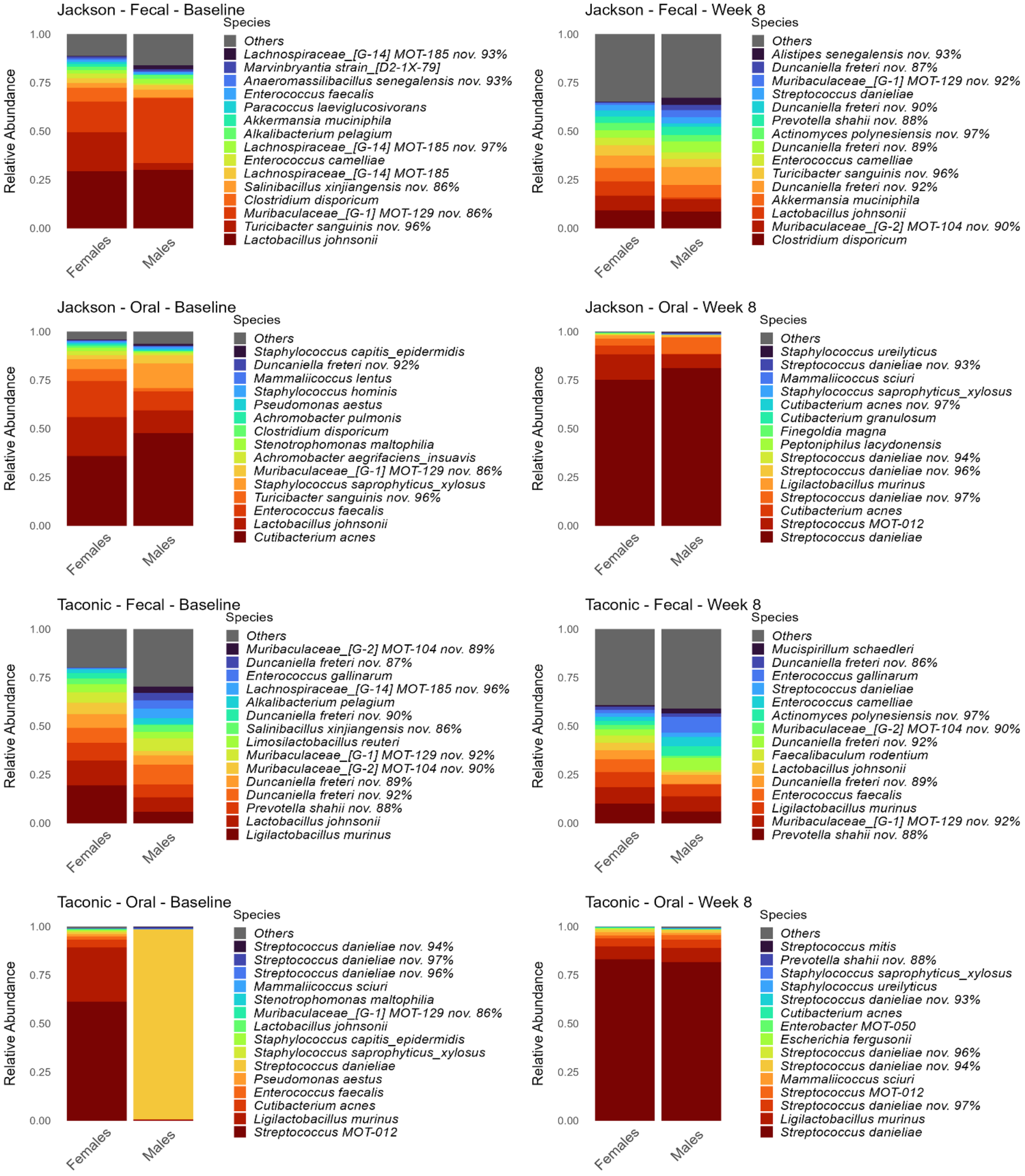
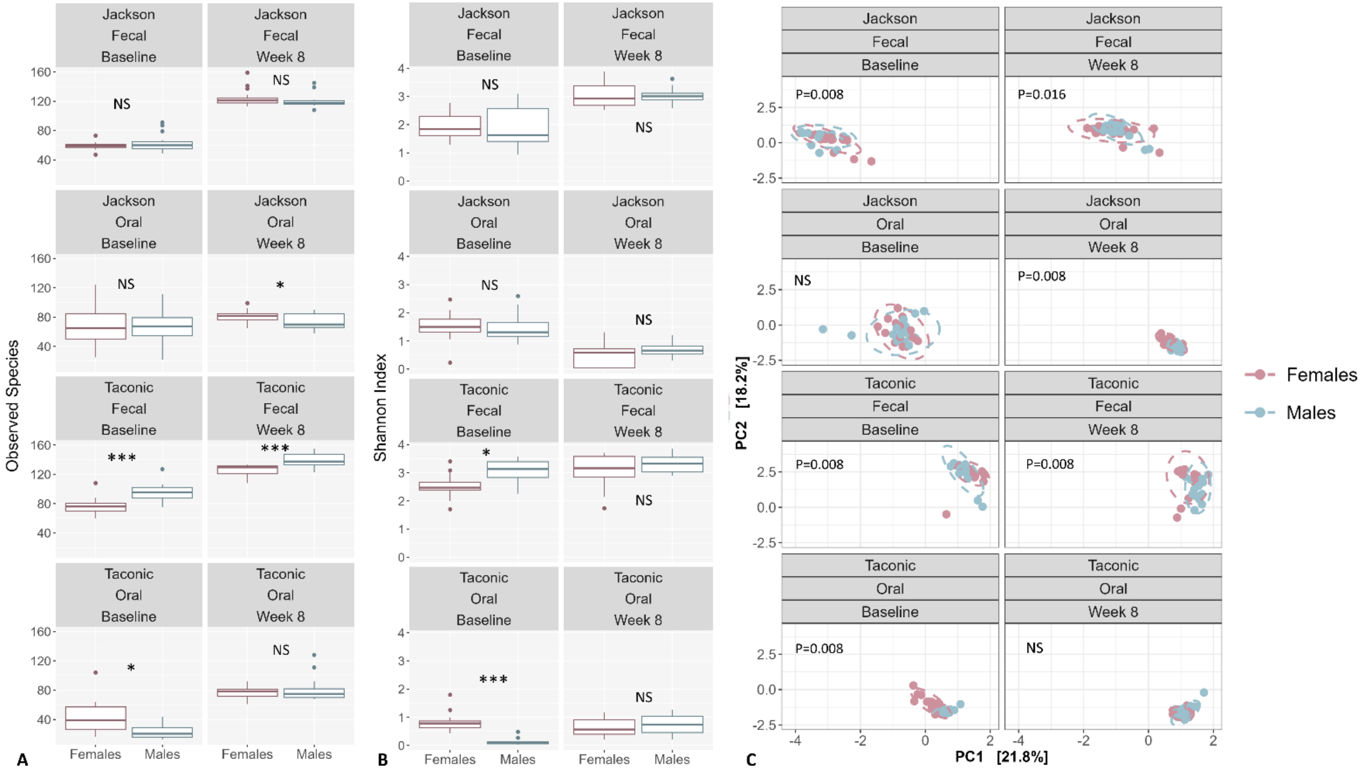


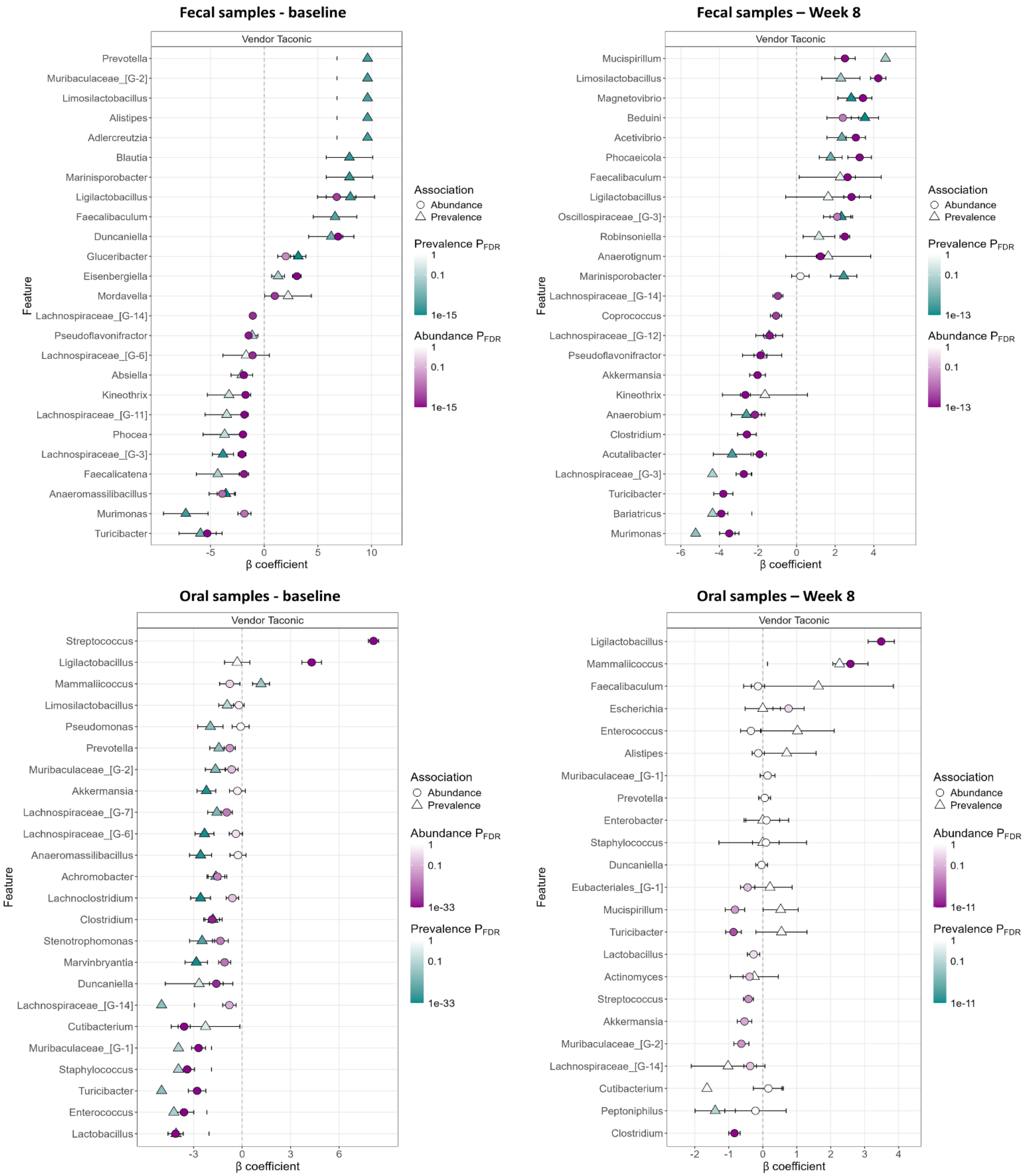
**Supplementary Figure 1. Phylum-level (A) and genus-level (B) taxonomy profiles by sex stratified by vendor, sample type, and 4-NQO treatment (time points).** DNA extracted from oral swab or fecal samples was sequenced for V1-V3 regions of the 16S rRNA gene using paired-end chemistry. Merged, quality-filtered were assigned taxonomies using a BLASTn-based algorithm. Stacked bars represent the average relative abundances of all the identified phyla and top 10 genera across samples. The plots were generated with R.



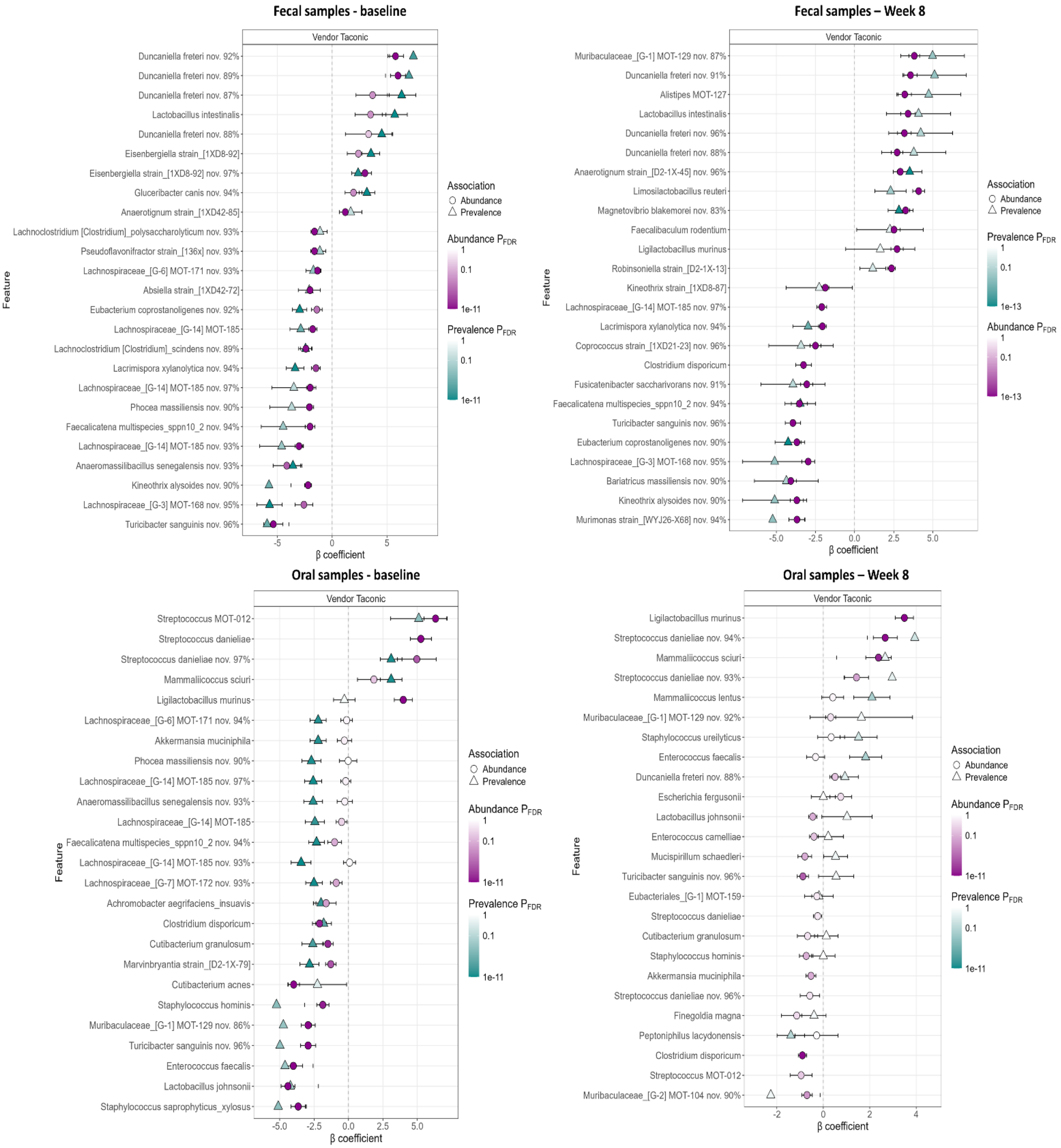
**Supplementary Figure 2. Species-level taxonomy profiles by sex stratified by vendor, sample type, and 4-NQO treatment (time points).** DNA extracted from oral swab or fecal samples was sequenced for V1-V3 regions of the 16S rRNA gene using paired-end chemistry. Merged, quality-filtered were assigned taxonomies using a BLASTn-based algorithm. Stacked bars represent the average relative abundances of top 15 species across samples. The plots were generated with R.



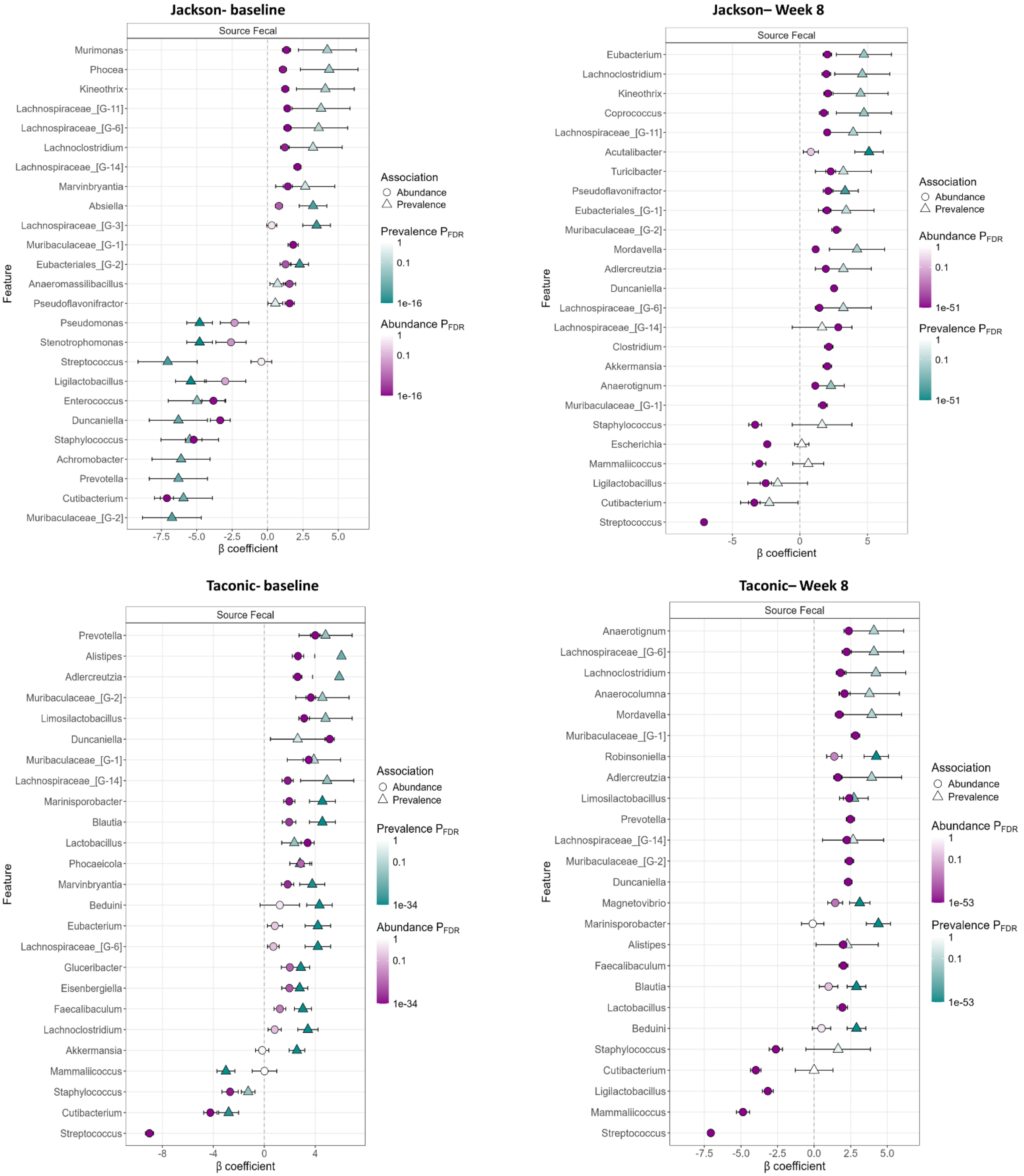
**Supplementary Figure 3. Species richness, alpha and beta-diversity by sex stratified by vendor, sample type, and 4-NQO treatment (time points).** Rarified taxonomic profiles were used to calculate observed species (A) and Shannon's alpha diversity index (B). Statistical significance was assessed with t-test or Mann-Whitney test as appropriate. * Adjusted p-value ≤ 0.05; *** Adjusted p-value ≤ 0.001; NS, not significant. Principle Component Analysis (C) was performed using Aitchison distances calculated from centered log-ratio (CLR) transformed taxonomic profiles. Statistical significance was sought using PERMANOVA; NS, not significant. The plots were generated with R.



**Supplementary Figure 4. Differentially abundant/prevalent genera by vendor (Taconic vs. Jackson) stratified by sample type and 4NQO treatment (time point).** Centered log ratio (CLR) transformed data were analyzed with Multivariate Association with Linear Models (MaAsLin3 package in R) to identify differentially abundant genera (FDR ≤ 0.1).

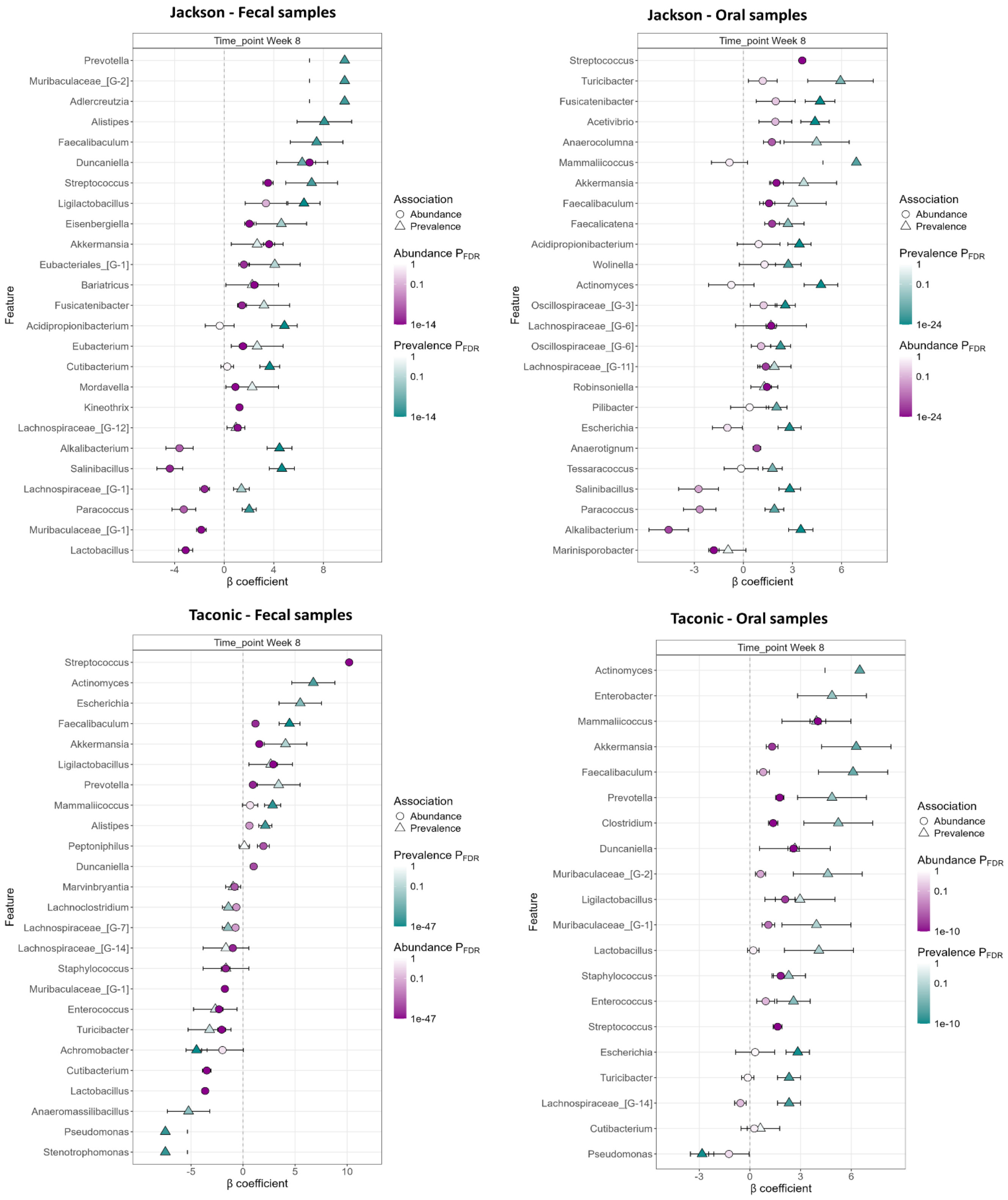


**Supplementary Figure 5. Differentially abundant/prevalent species by vendor (Taconic vs. Jackson) stratified by sample type and 4NQO treatment (time point).** Centered log ratio (CLR) transformed data were analyzed with Multivariate Association with Linear Models (MaAsLin3 package in R) to identify differentially abundant species (FDR ≤ 0.1).

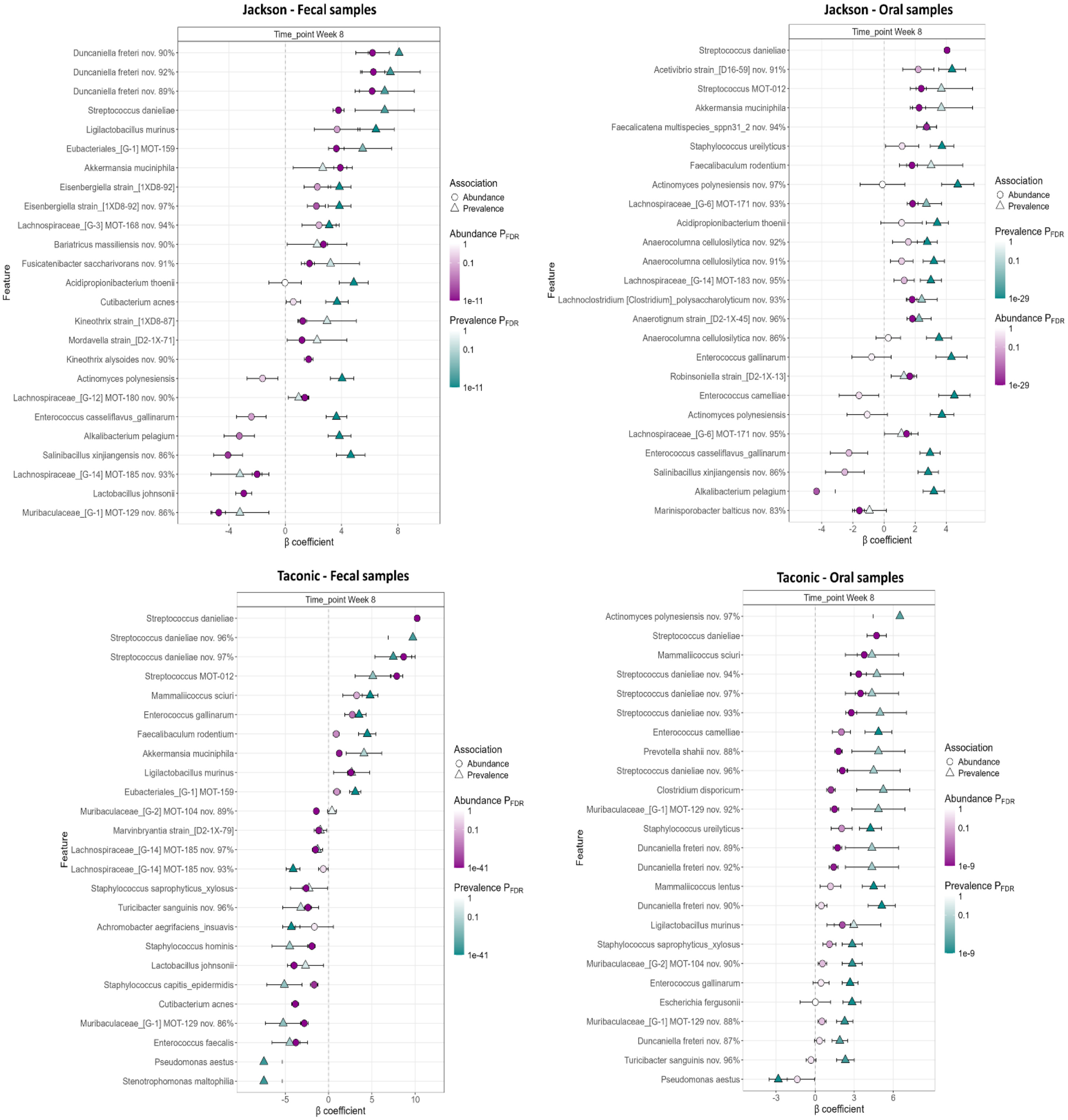


**Supplementary Figure 6. Differentially abundant/prevalent genera by sample type (Fecal vs. Oral) stratified by vendor and 4NQO treatment (time point).** Centered log ratio (CLR) transformed data were analyzed with Multivariate Association with Linear Models (MaAsLin3 package in R) to identify differentially abundant genera (FDR ≤ 0.1).

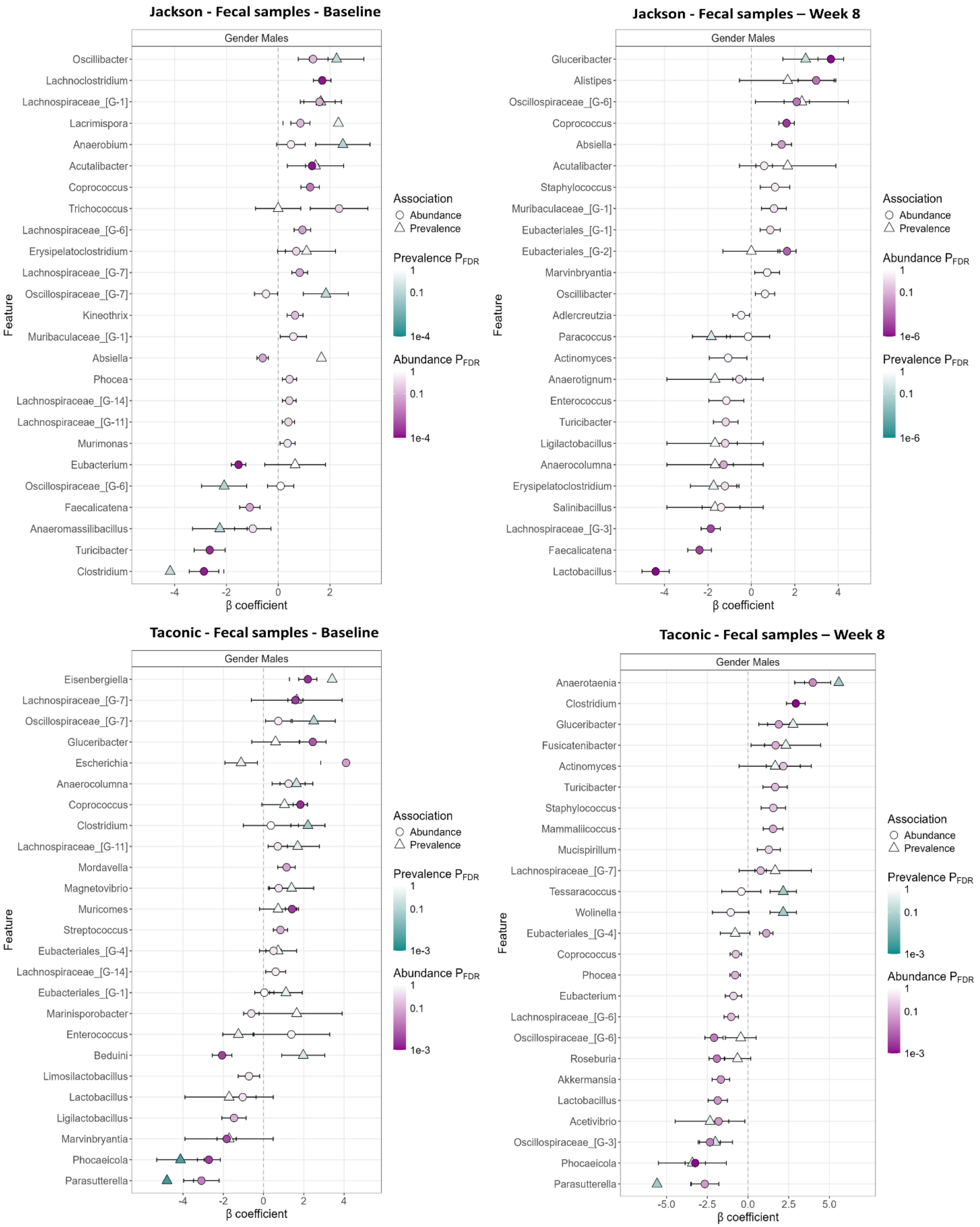
**Supplementary Figure 7. Differentially abundant/prevalent species by sample type (Fecal vs. Oral) stratified by vendor and 4NQO treatment (time point).** Centered log ratio (CLR) transformed data were analyzed with Multivariate Association with Linear Models (MaAsLin3 package in R) to identify differentially abundant species (FDR ≤ 0.1).



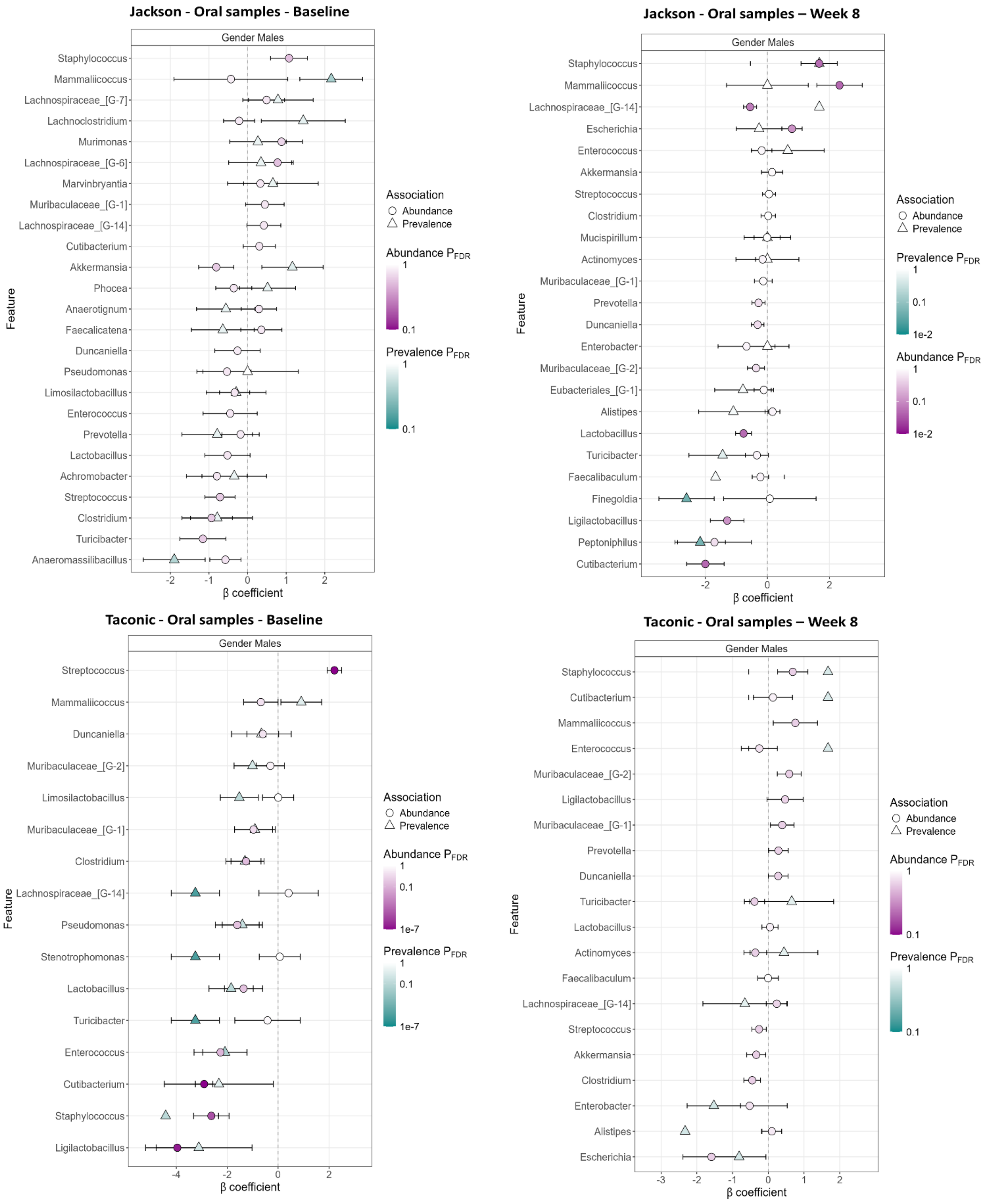
**Supplementary Figure 8. Differentially abundant/prevalent genera by 4NQO treatment (Baseline vs. Week 8) stratified by vendor and sample type.** Centered log ratio (CLR) transformed data were analyzed with Multivariate Association with Linear Models (MaAsLin3 package in R) to identify differentially abundant genera (FDR ≤ 0.1).



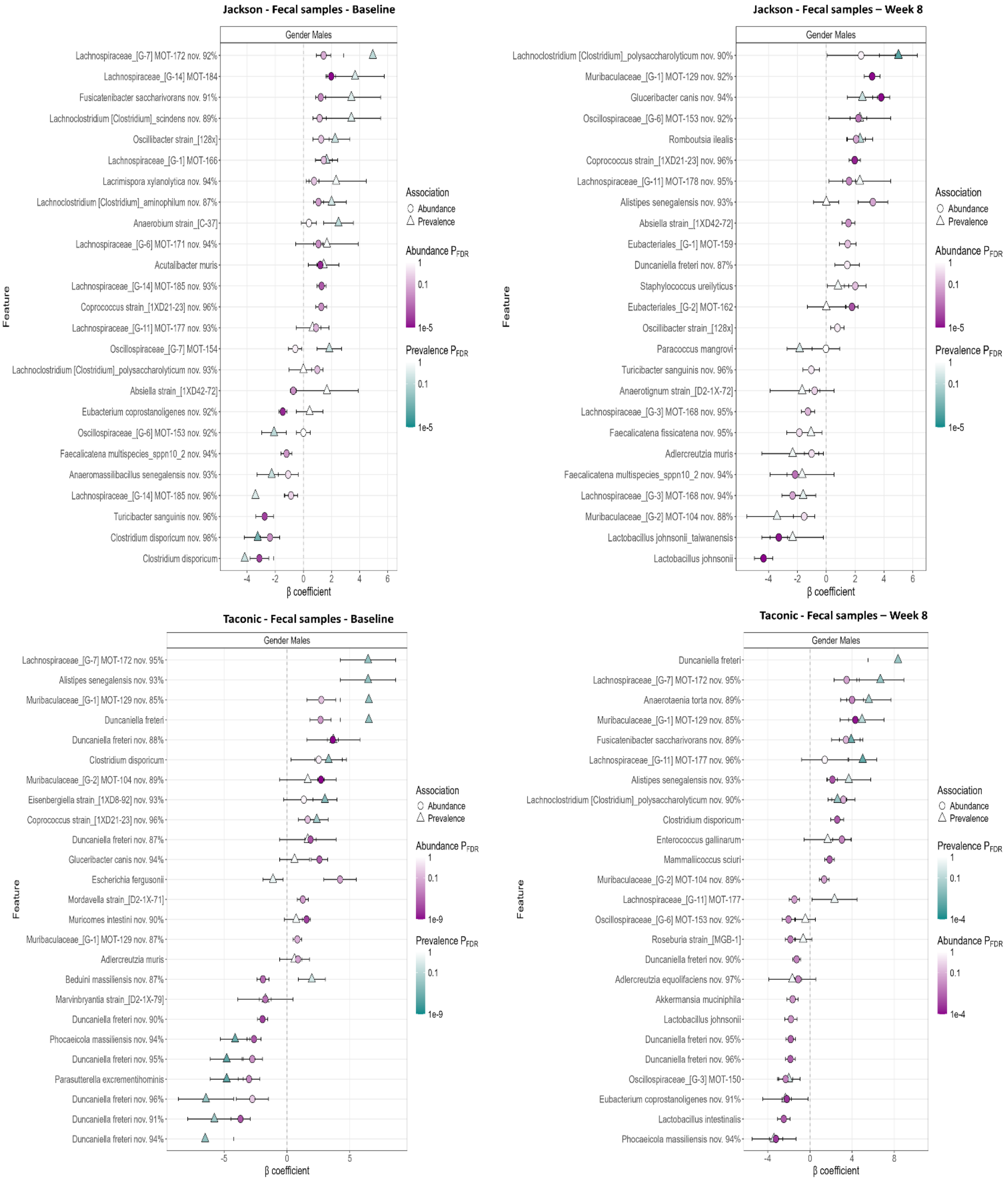
**Supplementary Figure 9. Differentially abundant/prevalent species by 4NQO treatment (Baseline vs. Week 8) stratified by vendor and sample type.** Centered log ratio (CLR) transformed data were analyzed with Multivariate Association with Linear Models (MaAsLin3 package in R) to identify differentially abundant species (FDR ≤ 0.1).



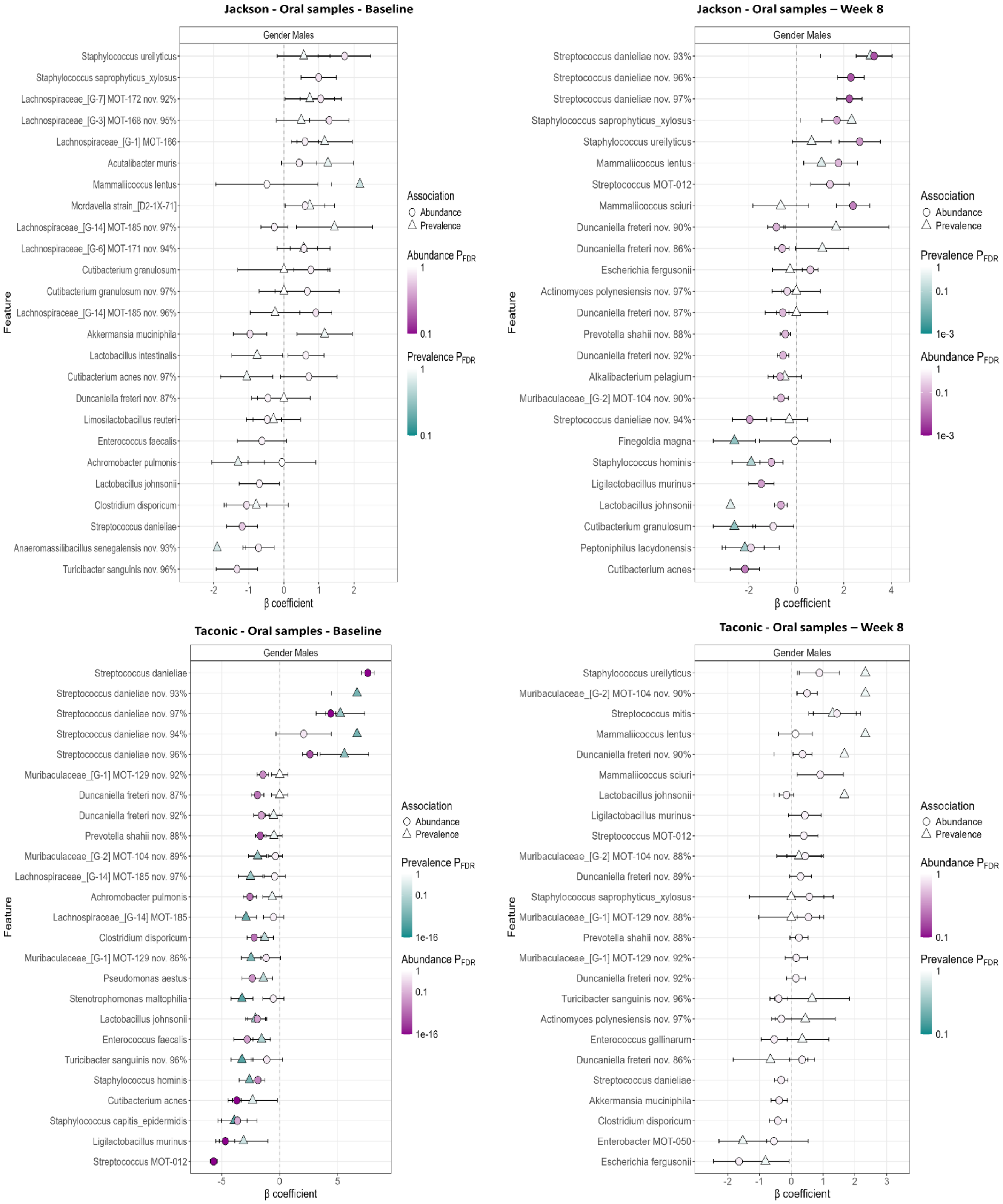
**Supplementary Figure 10. Differentially abundant/prevalent genera by sex (Males vs. Females) stratified by vendor and 4NQO treatment (time point) –Fecal samples.** Centered log ratio (CLR) transformed data were analyzed with Multivariate Association with Linear Models (MaAsLin3 package in R) to identify differentially abundant genera (FDR ≤ 0.1).



**Supplementary Figure 11. Differentially abundant/prevalent genera by sex (Males vs. Females) stratified by vendor and 4NQO treatment (time point) –Oral samples.** Centered log ratio (CLR) transformed data were analyzed with Multivariate Association with Linear Models (MaAsLin3 package in R) to identify differentially abundant genera (FDR ≤ 0.1).



**Supplementary Figure 12. Differentially abundant/prevalent species by sex (Males vs. Females) stratified by vendor and 4NQO treatment (time point) –Fecal samples.** Centered log ratio (CLR) transformed data were analyzed with Multivariate Association with Linear Models (MaAsLin3 package in R) to identify differentially abundant species (FDR ≤ 0.1).


Jackson - Oral samples - Baseline

Jackson - Oral samples – Week 8

Taconic - Oral samples - Baseline

Taconic - Oral samples – Week 8

**Supplementary Figure 13. Differentially abundant/prevalent species by sex (Males vs. Females) stratified by vendor and 4NQO treatment (time point) –Oral samples.** Centered log ratio (CLR) transformed data were analyzed with Multivariate Association with Linear Models (MaAsLin3 package in R) to identify differentially abundant species (FDR ≤ 0.1).