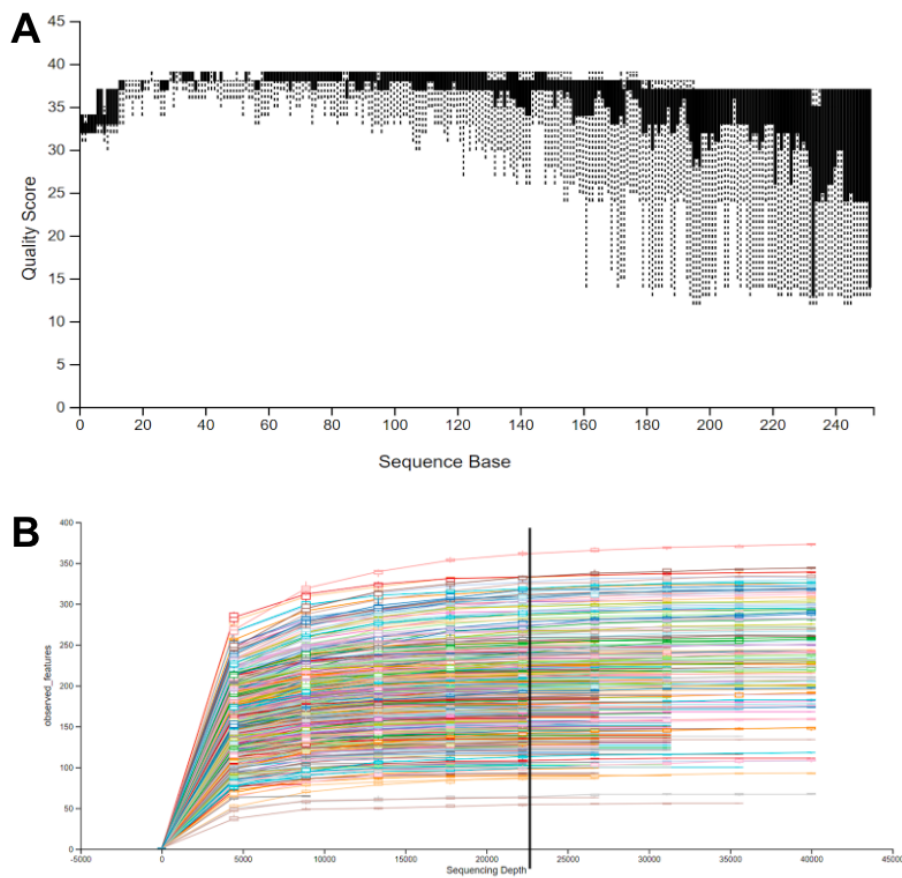# SUPPLEMENTAL MATERIAL

FIG. S1 Data processing in QIIME2. (A) Sequence quality plot. Sequences were truncated at 248bp for downstream analyses. **(B)** Alpha-rarefaction curve. Sequencing depth of 22700 was chosen. Both figures were produced in QIIME2 view.
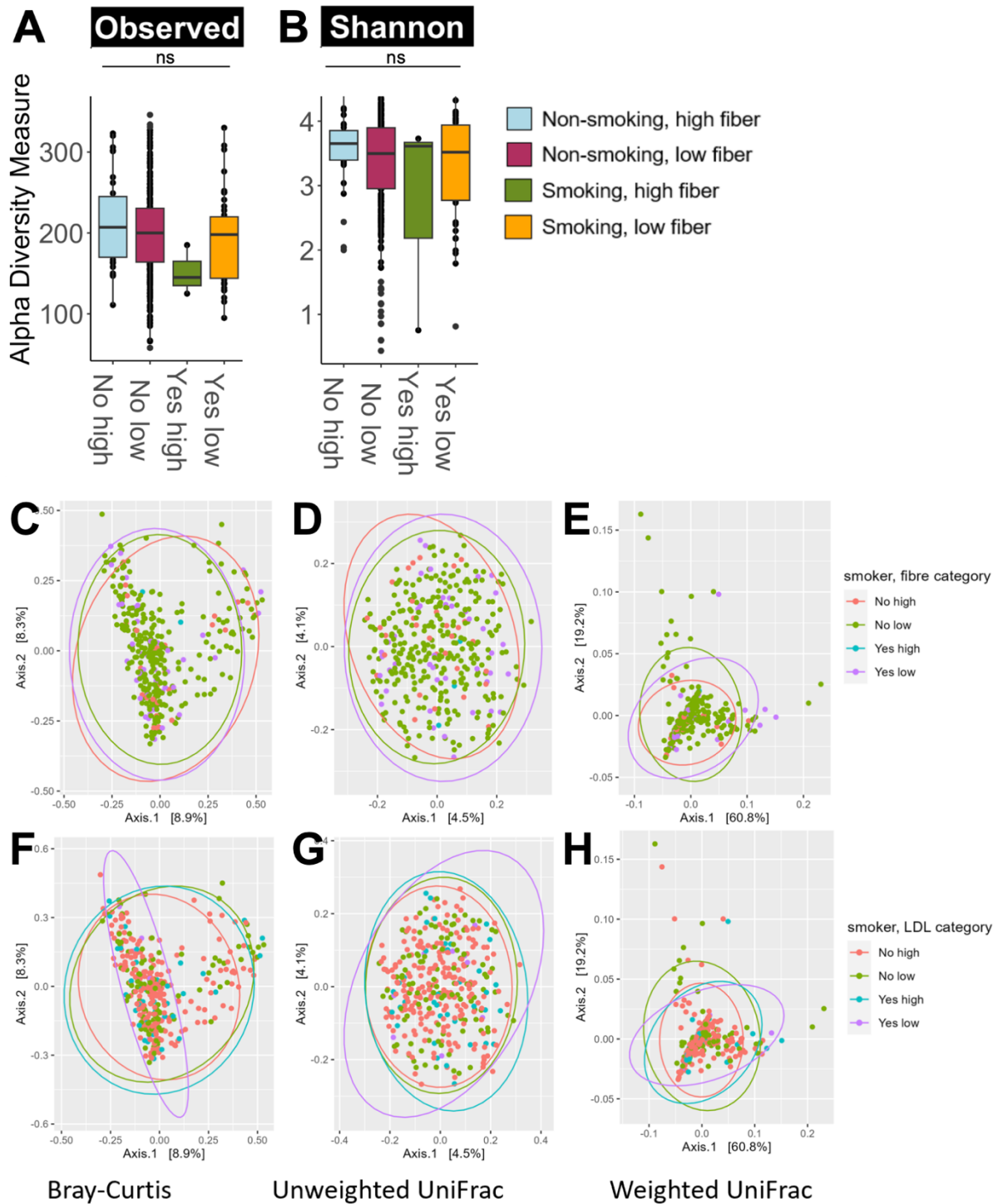
FIG. S2 No significant effect on population diversity metrics observed between different smoking and fiber, LDL populations. Alpha diversity measured using **(A)** Observed Features and **(B)** Shannon's Diversity Metric shows no significant difference (ns) of fiber consumption between four population categories, assessed using One-Way ANOVA with minimum $p<0.05$ cutoff. Beta diversity assessed for fiber and LDL level respectively using **(C,F)** Bray-Curtis, **(E,G)** Unweighted UniFrac, and **(E,H)** Weighted UniFrac shows no significant difference between four population categories. Beta diversity significance assessed using PERMANOVA with minimum $p<0.05$ cutoff.
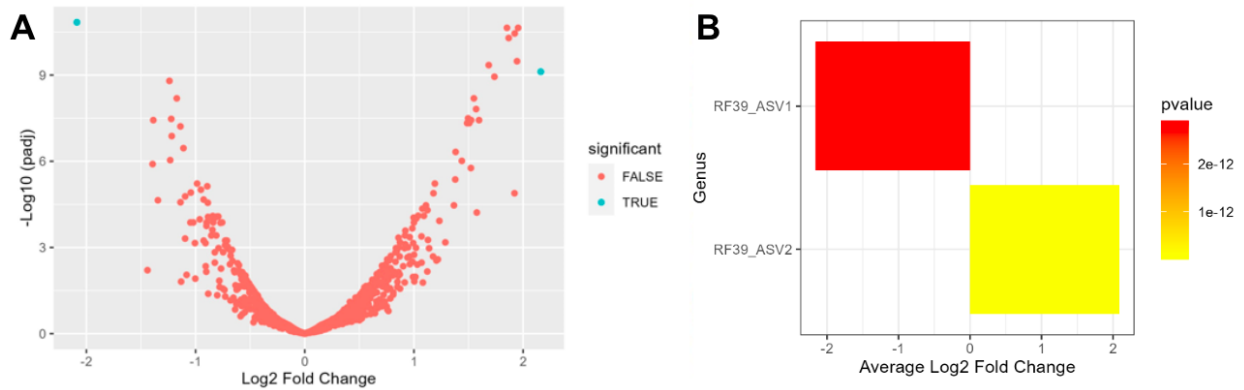
FIG. S3 Non-smokers with high LDL experience less LDL-associated up and down regulation of gut bacteria relative to non-smokers with low LDL. (A) Comparing differential abundances of bacterial ASVs. Volcano plot blue dots: |Log2 Fold Change|> 2 of non-smokers with high LDL vs. low LDL, p adj < 0.01. **(B)** Taxa bar plot. Differential expression of 2 significant ASVs within the same genus and corresponding Log2 fold changes in non-smokers with high LDL vs. low LDL. p adj < 0.01 and |Log2 Fold Change| > 2.