Effects of HIV Viremia on the Gastrointestinal Microbiome of Young Men who have Sex with Men

Supplemental Digital Content

*Sample selection*

Of the 462 participants enrolled in the mSTUDY at the time our study was conducted, we selected a random subsample of 383 based on achieving approximately balanced numbers of HIV+ and HIV- substance users and non-users. The mSTUDY cohort was started to study the effects of non-injection drug use on HIV acquisition and treatment outcomes among Racial/Ethnic minority MSM. As such, substance users are highly represented and we wanted to balance this confounding factor between HIV+ and HIV- groups as well as possible. The total sample size was set in order to achieve 90% power to detect a PERMANOVA effect size of ω2<0.005 at α=0.1, comparing HIV-infected and -uninfected groups (ω2 is a bias-corrected R2 statistic; power analysis was conducted using the R package 'micropower' [1]). Two samples had read counts less than the rarefication depth or did not meet the minimum number of nonzero pairwise read ratios, 10, for inclusion in the size factor calculation and were excluded from alpha diversity, PERMANOVA, ZINB, and LASSO analyses.

*HIV serostatus and RNA quantification.*

HIV negative status was confirmed with the OraQuick Advance® HIV 1/2 (OraSure Technologies, Bethlehem, PA). Among infected participants, plasma HIV RNA was quantified using a standard clinical laboratory assay (Cobas® AmpliPrep/Cobas® TaqMan® HIV-1 Test, Version 2.0, assay range of 20−10,000,000 copies/mL).

*Behavioral and clinical measures*

Demographic data collected included age, Race/Ethnicity, country of origin (United States vs. other countries), employment status, and housing status (homeless or stably housed). Self-reported frequency of methamphetamine, marijuana, and cocaine use in the past six months was measured using the NIDA-modified ASSIST [2]. Due to the relatively low frequency of daily methamphetamine/marijuana use, daily users were combined with weekly users. Cocaine use (including both powder and ‘crack’ cocaine) was overall infrequent, and thus cocaine was treated as a dichotomous variable. Alcohol use in the past six months was measured with the NIAAA recommended alcohol questions [3], assessing frequency and amount of alcohol “bingeing,” consuming six or more drinks on one occasion. Tobacco smoking was measured with the Multicenter AIDS Cohort Study (MACS) questionnaire [4] and sexual behavior, including recency and frequency of receptive anal intercourse, was measured with the American Men’s Internet Survey questionnaire [5]. Obesity was determined by clinician-gathered anthropometrics (height, weight, and waist circumference) and individuals were classified as obese if they had BMI > 30 or waist circumference > 40 inches. Antibiotics used in the past month were also assessed by trained clinical staff. Prior to analysis, we used multiple imputation with the chained equations method [6] to fill in missing covariate data. Amounts of missing data for each covariate are displayed in Table S1.

*Contaminant sequence removal procedure*

Removal of contaminant sequence variants (SVs) was performed by a calculating a ‘contaminant score’ for sequence *i*, set of negative control samples *J*, and read count of sequence *i* in sample *j cij.* Scores range from 0 for sequences that are only observed in “true” samples to 1 for sequences that are only observed in negative controls. Intermediate values are interpreted as an estimate of the likelihood that a given sequence variant was derived from negative controls (i.e. contamination). We used a threshold of *Si*≥ 0.1 to identify and remove contaminant SVs prior to all further analysis.

*Inverse probability of treatment weighting model selection*

Inverse probability of treatment weighting (IPTW) is a balancing procedure used to render the treatment/exposure under study (i.e., HIV viremia group) independent of confounding variables. In essence, weighting by the inverse probability of treatment (or in this case, exposure) transforms the study sample into a “pseudo-population” where exposure status is independent of variables used in the IPTW calculation. It has been shown that if the model used to estimate the weights includes all relevant confounders and is not misspecified, in a weighted population, the effect estimate of exposure on outcome is unbiased [7]. With IPTW, the outcome models are “marginal structural models” instead of conditional on covariates, as in multiple regression. Modeling microbiome data marginally offers several advantages including the ability to control for many confounding factors without inducing overfitting bias [8] or losing efficiency due to overstratification [9].

Mathematically, the IPTW is defined as for exposure levels *x*  1…*n* (*n* = 4 in this study, corresponding to the four HIV viremia categories) and set of confounder variables ***C***. If the treatment probabilities are known (as in, for example, a randomized trial), no estimation is necessary; however, in observational studies the IPTW must be estimated from data. We utilized two methods to estimate the IPTW: a generalized boosted model [10] and multinomial logistic regression. Our covariate set ***C*** included all variables described in the behavioral and clinical covariates section above (see Table 1 and Table S1 for more details).

Prior to fitting the IPTW models, we calculated the standardized mean difference (SMD) in each confounding variable across HIV viremia groups, which measures the severity of imbalance in that variable (higher SMDs indicate greater imbalance; see the R package ‘tableone’ vignette for calculation details: https://cran.r-project.org/web/packages/tableone/tableone.pdf). After fitting each model, we re-calculated the SMD while applying the weights. Table S1 presents SMDs before and after weighting for each variable in the IPTW model plus descriptive statistics of the IPTW themselves. If the IPTW can be flawlessly estimated, all covariates included in the IPTW model will be perfectly balanced across exposure groups in a weighted sample (i.e., SMD = 0). In practice, perfect balance is only achieved in fully nonparametric settings with large amounts of data relative to the number of variables in ***C***, and the SMD measures the severity of the remaining unbalance. We selected the method that produced the lowest average SMD across all confounders, which was the generalized boosted model (Table S1), and used this model to estimate the IPTW.

*Differential abundance testing*

To test for differential abundance of bacterial taxa between HIV viremia groups [HIV-, HIV+ undetectable [HIV RNA < 20 copies/mL (lower limit of detection)], HIV+ suppressed (RNA between 20 and 200 copies/mL), and HIV+ viremic (RNA > 200 copies/mL)], we utilized zero-inflated negative binomial (ZINB) or negative binomial (NB) models with multinomial least absolute shrinkage and selection operator (LASSO) models used as a confirmatory strategy. First, a pre-filtering step excluded genera with less than 100 total reads across all samples or present in less than 10% of samples; after filtering, 78 genera were tested in ZINB and LASSO models. Estimates of relative library sizes (“size factors”) were obtained by calculating geometric means of pairwise read count ratios [11]. ZINB models were normalized by including log size factors as an offset term, and LASSO models utilized a normalized ASV matrix generated by dividing read counts by size factors.

*ZINB model selection and analysis*

Our model selection procedure was as follows: We fit six statistical models to each of 78 bacterial Genus variables. Two were ZINB models, the first including HIV viremia category as a predictor in both the count and zero-inflation components of the model, and the second including HIV only in the count component. We also fit a NB model without a zero-inflation component. Finally, we fit Poisson versions of each of the aforementioned models. All models included HIV viremia group as a categorical predictor and log “size factor” (estimate of relative library size) as an offset term [11]. We selected the optimal model according to minimum AIC, which has been shown to outperform other methods of model selection for microbiome data [12]. ZINB was the selected model for 75/78 taxa (96%) with NB selected to model *Bacteroides, Prevotella,* and *Streptococcus*. Positive counts of these three taxa were observed in nearly all samples (97%, 100%, and 87%, respectively). As has been previously observed [12], the Poisson models were a poor fit for these data, and none were selected as the best model by AIC. Using the optimal statistical model for each taxa, we obtained unadjusted coefficient estimates, standard errors, and *p* values, and corrected all *p* values using FDR. If the first ZINB model was selected (using HIV group in both the count and zero-inflation model components), the coefficients we report are from the count portion of the model. Next, we utilized IPTW to obtain covariate-adjusted estimates. Model-based standard errors are incorrect in inverse probability of treatment-weighted models; therefore, we used the sandwich estimator to obtain robust standard error estimates. Finally, we calculated false coverage rate (FCR)-adjusted 90% confidence intervals [13] for each IPTW-adjusted parameter estimate. FCR adjustment preserves the connection between statistical significance and confidence interval coverage after selection using the FDR method. Adjustment ensures that genera with statistically significant *q* values will have confidence intervals excluding the null value of zero and those that are nonsignificant will include zero.

*LASSO model selection and analysis*

We utilized two multinomial LASSO regression models, one unadjusted and one IPTW-adjusted, as confirmatory methods of feature selection. The models included the same 78 genera from ZINB testing as predictors, and HIV viremia category was the multinomial outcome variable. Prior to fitting the models, each predictor variable (count of bacterial genus) was standardized to have a mean of zero and standard deviation of one. Microbiome data are often on very different scales: Some taxa vary comparatively little across samples, while others may be absent in many samples, but present in huge abundance in others. Standardization was performed so that the scale of each variable did not impact the likelihood of inclusion in the LASSO model.

For each model, the optimal value of the LASSO penalty coefficient *λ* was chosen using 500 repetitions of 10-fold cross-validation (CV). Briefly, for each repetition *i* = 1 to 500, the data were split into 10 randomly selected groups, or folds. Then, for folds *k* = 1 to 10, the *k*th was held out and the other 9 were used to fit the LASSO model. The fitted model was used to predict the holdout data and the mean squared error was recorded. This process was repeated for 100 values of *λ*, ranging from very small (admitting all 78 genera into the model) to comparatively large (allowing no predictors except an intercept term). Results were averaged across the 10 folds, resulting in a CV error curve for repetition *i*. There is significant uncertainty in CV error estimates because of the random selection of folds, so the process was repeated 500 times and the curves were aggregated to obtain the mean CV error for each value of *λ* as well as its standard error. As is standard practice in elastic net regression [14, 15], the optimal value of *λ* was chosen as the minimum value (which is the best fitting model for the data) plus 1 standard error. This choice is recognized as the most parsimonious model that lies within a reasonable degree of uncertainty from the “best” model.

The chosen values of *λ* were then used to fit unweighted and inverse probability of treatment weighted LASSO models, and taxa with nonzero coefficients were recorded as “selected” in the models. Because of the standardization, LASSO effect sizes are not directly comparable with ZINB effect sizes; however, we display in Figure 4 whether each nonzero effect was negative (indicating depletion of that genus) or positive (indicating enrichment).

**Table S1.** Covariates included in the inverse probability of treatment weight models. Standardized mean differences (SMDs) are given before and after weighting. Percent missing is prior to multiple imputation. GBM = generalized boosted model, LRM = logistic regression model, IQR = interquartile range.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Variable | Percent missing | SMD (before) | SMD (GBM) | SMD (LRM) |
| Age | 0 | .405 | .171 | .245 |
| Employment status | 2.9 | .544 | .254 | .336 |
| Race/Ethnicity | 2.1 | .484 | .372 | .364 |
| Country of origin | 0.5 | .118 | .080 | .109 |
| Homelessness | 0.3 | .214 | .176 | .227 |
| Recent RAI | 4.7 | .075 | .070 | .138 |
| Frequency of RAI | 8.9 | .192 | .066 | .133 |
| Methamphetamine use | 0.5 | .539 | .202 | .213 |
| Marijuana use | 0.5 | .296 | .139 | .263 |
| Cocaine use | 0.5 | .159 | .091 | .134 |
| Tobacco smoking | 2.3 | .262 | .150 | .212 |
| Binge drinking | 0.5 | .397 | .145 | .213 |
| Obesity | 0 | .171 | .150 | .051 |
| Antibiotic use | 0 | .209 | .077 | .080 |
| Sample collection type | 0 | .206 | .078 | .162 |
| **Average SMD** |  | **.285** | **.148** | **.192** |
|  |  |  |  |  |
|  | Range | Median | IQR (Q3 – Q1) |  |
| IPTW (GBM) | 0.14 – 3.72 | 0.66 | 0.33 (0.55 – 0.89) |  |
| IPTW (LRM) | 0.14 – 11.74 | 0.71 | 0.49 (0.57 – 1.06) |  |

**Table S2.** Permutational Multivariate ANOVA (PERMANOVA) of HIV category (HIV-, HIV+ undetectable, HIV+ suppressed, HIV+ viremic) on Bray-Curtis, Jaccard, and Jensen-Shannon distance matrices. Unadjusted and covariate adjusted results are shown.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Distance metric | Type | F | R2 | *p* |
| Bray-Curtis | Unadjusted | 1.75 | .014 | .001 |
|  | Adjusted | 1.39 | .011 | .017 |
| Jaccard | Unadjusted | 1.44 | .011 | .005 |
|  | Adjusted | 1.24 | .010 | .030 |
| Jensen-Shannon | Unadjusted | 2.28 | .018 | .001 |
|  | Adjusted | 1.61 | .013 | .019 |

**Table S3.** Comparisons in alpha diversity using inverse probability of treatment weighted quantile regression (median). Values are expected median differences between the group in the ‘Coefficient’ column and the HIV negative reference group.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Statistic | Coefficient | Value | SE | t | *p* | *q* |
| Observeda | Undetectable | 11.00 | 9.43 | 1.16 | 0.245 | 0.374 |
| Observed | Suppressed | 18.00 | 5.93 | 3.03 | 0.003 | 0.022 |
| Observed | Viremic | 15.00 | 11.41 | 1.31 | 0.190 | 0.374 |
| Chao1b | Undetectable | 10.30 | 10.38 | 1.09 | 0.277 | 0.374 |
| Chao1 | Suppressed | 18.80 | 6.44 | 2.92 | 0.004 | 0.022 |
| Chao1 | Viremic | 20.80 | 12.68 | 1.64 | 0.102 | 0.305 |
| Shannonc | Undetectable | 0.016 | 0.099 | 0.16 | 0.873 | 0.873 |
| Shannon | Suppressed | 0.118 | 0.070 | 1.68 | 0.094 | 0.305 |
| Shannon | Viremic | 0.102 | 0.119 | 0.86 | 0.392 | 0.471 |
| Simpsond | Undetectable | -0.005 | 0.008 | -0.60 | 0.552 | 0.602 |
| Simpson | Suppressed | 0.007 | 0.007 | 1.08 | 0.280 | 0.374 |
| Simpson | Viremic | 0.008 | 0.007 | 1.14 | 0.255 | 0.374 |

aKruskal-Wallis test for difference between groups *p* = .025. Kruskal-Wallis tests are not adjusted for confounding.

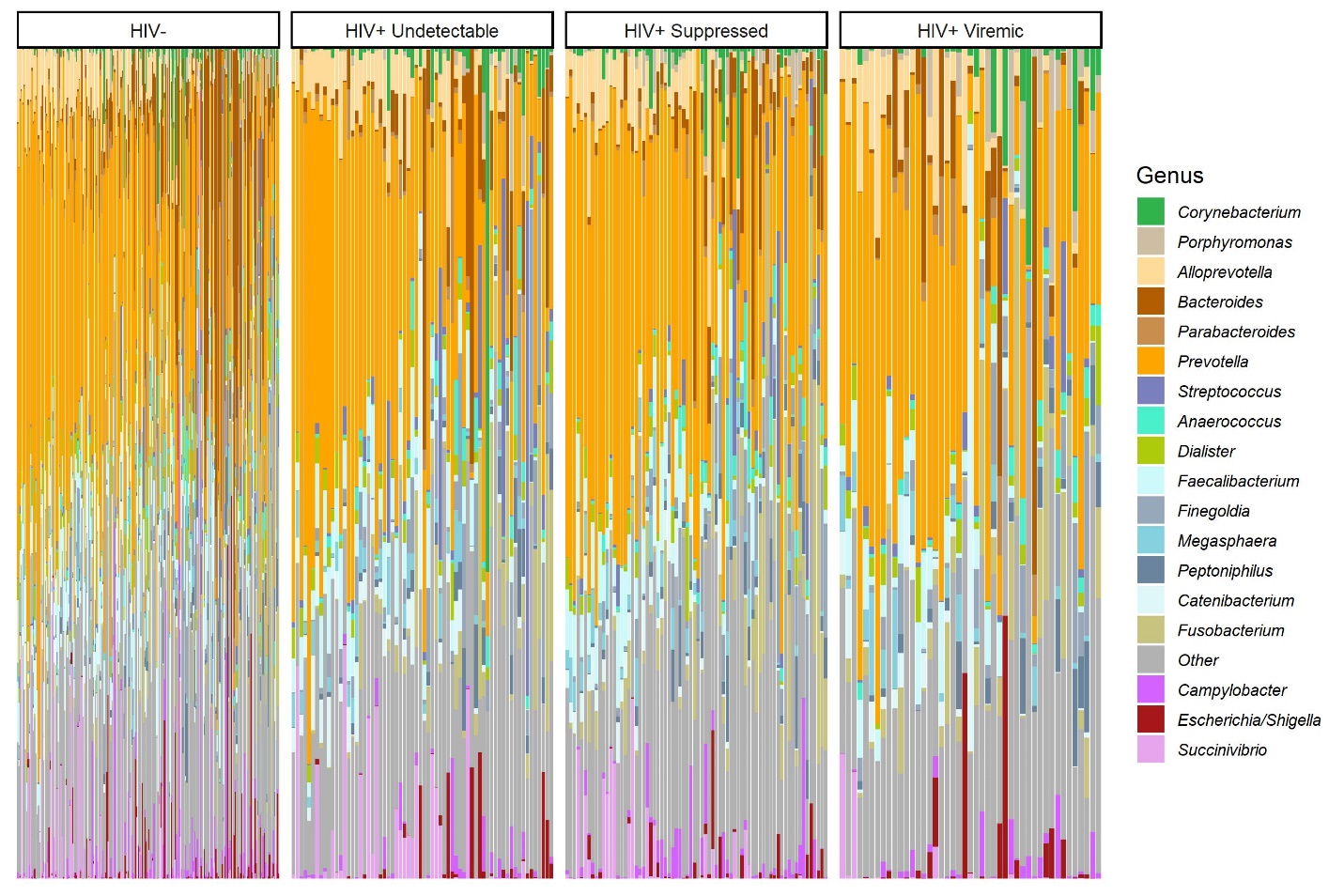
bKruskal-Wallis *p* = .025

cKruskal-Wallis *p* = .332

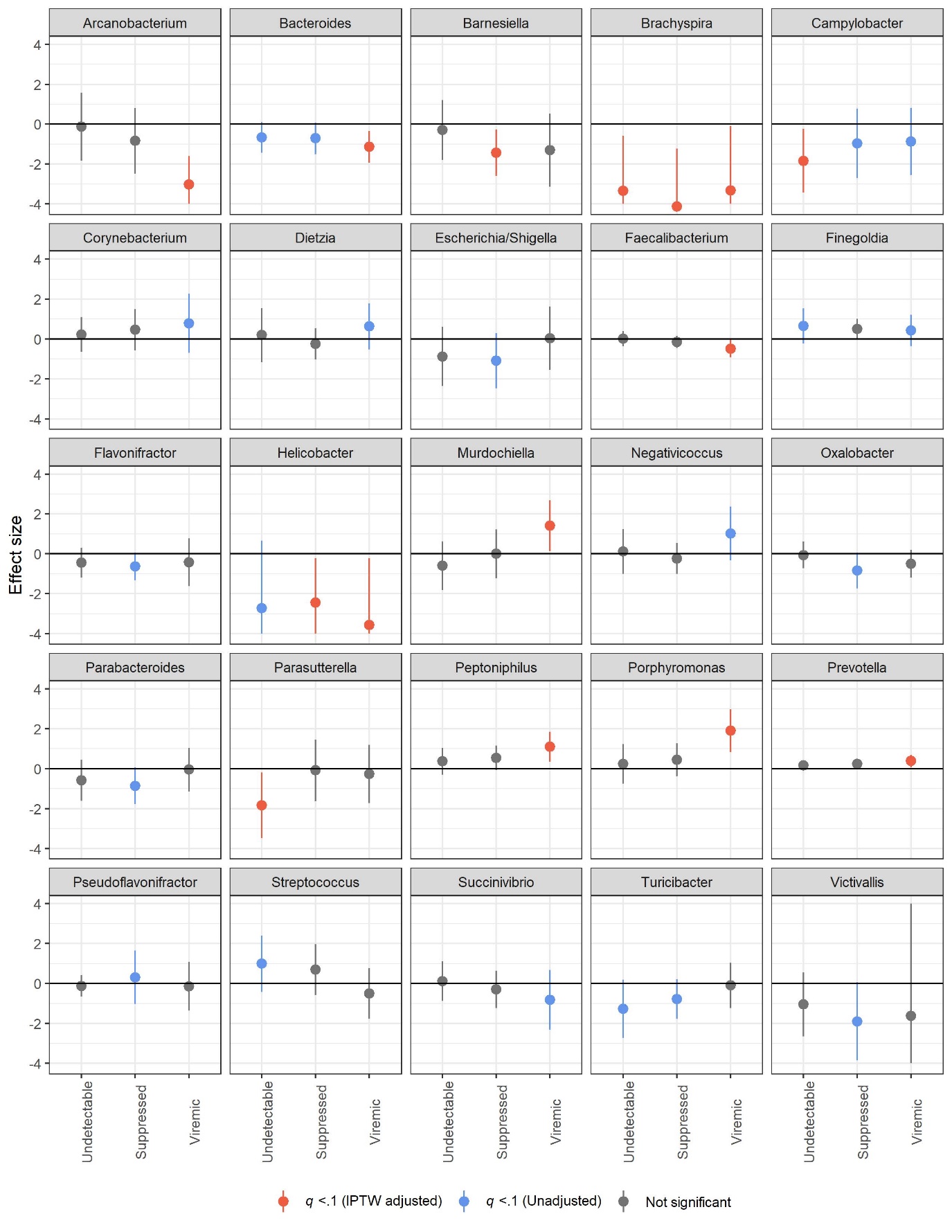
dKruskal-Wallis *p* = .325

**Table S4.** Results of differential abundance tests of bacterial genera between HIV+ undetectable (HIV RNA <20 copies/ml), HIV+ suppressed (HIV RNA >20 and ≤200 copies/ml), HIV+ viremic (HIV RNA >200 copies/ml) participants and HIV- participants. Coefficients are log normalized ratios of bacterial counts comparing each viremia group to the HIV- reference group. N is the total number of samples (of 381 total) with nonzero read counts. Unadjusted and inverse-probability of treatment weighted (IPTW) adjusted results are shown.

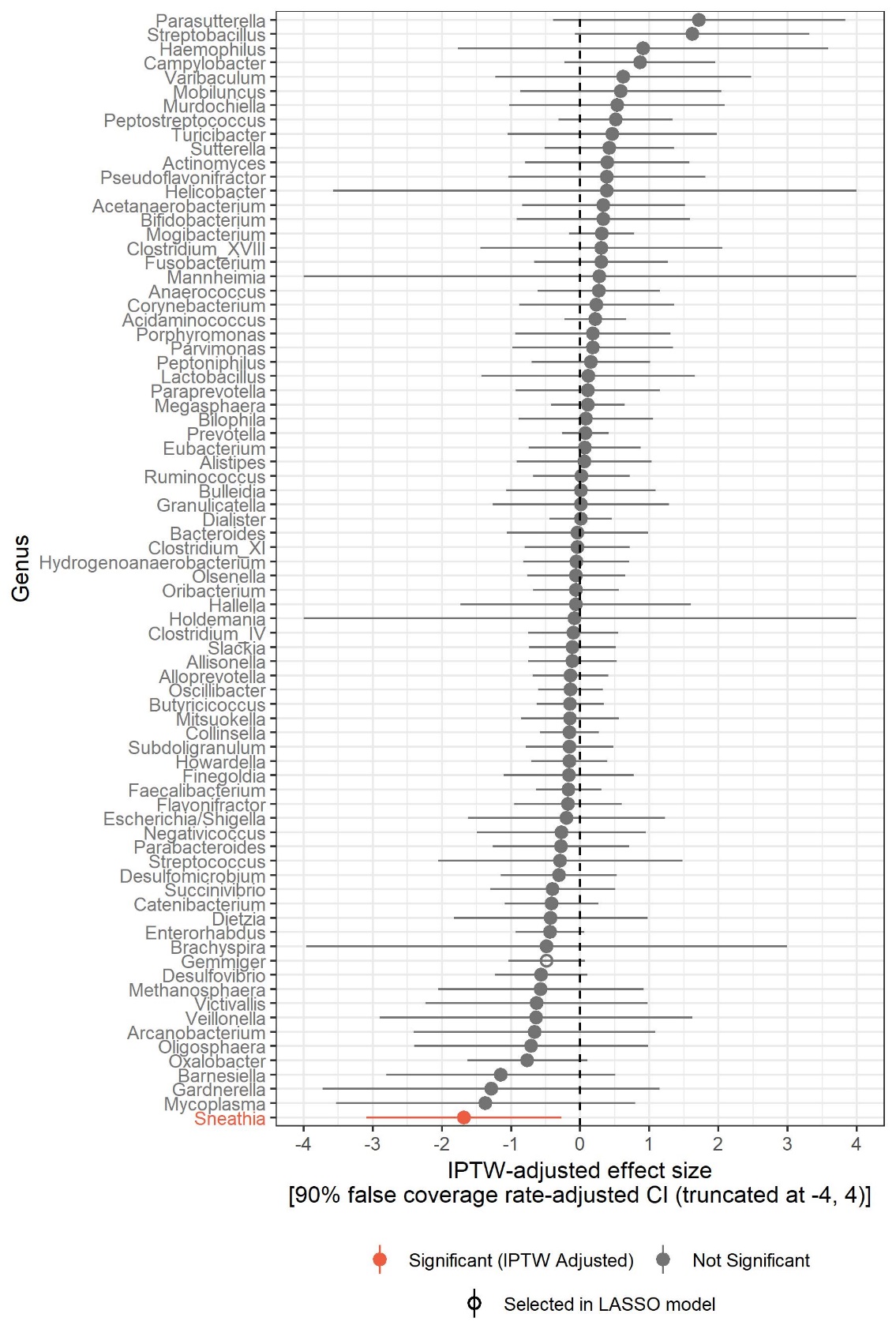
|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Taxonomy | Coefficient | N | Unadjusted | | | | | IPTW-adjusted | | | | |
|  |  |  | Estimate | SE | Z | *p* | *q* | Estimate | SE | Z | *p* | *q* |
| Acetanaerobacterium | Suppressed | 83 | 0.31 | 0.26 | 1.16 | 0.25 | 0.49 | 0.22 | 0.38 | 0.57 | 0.57 | 0.79 |
| Acetanaerobacterium | Undetectable | 83 | -0.13 | 0.31 | -0.41 | 0.68 | 0.86 | -0.17 | 0.24 | -0.70 | 0.48 | 0.74 |
| Acetanaerobacterium | Viremic | 83 | 0.64 | 0.37 | 1.75 | 0.08 | 0.29 | 0.46 | 0.42 | 1.08 | 0.28 | 0.57 |
| Acidaminococcus | Suppressed | 294 | 0.19 | 0.13 | 1.52 | 0.13 | 0.39 | 0.21 | 0.13 | 1.62 | 0.11 | 0.40 |
| Acidaminococcus | Undetectable | 294 | -0.05 | 0.13 | -0.35 | 0.72 | 0.86 | -0.01 | 0.13 | -0.08 | 0.94 | 0.99 |
| Acidaminococcus | Viremic | 294 | -0.08 | 0.16 | -0.53 | 0.60 | 0.78 | 0.15 | 0.22 | 0.67 | 0.50 | 0.74 |
| Actinomyces | Suppressed | 216 | 0.59 | 0.27 | 2.17 | 0.03 | 0.16 | 0.37 | 0.35 | 1.08 | 0.28 | 0.57 |
| Actinomyces | Undetectable | 216 | 0.23 | 0.29 | 0.78 | 0.44 | 0.65 | -0.02 | 0.40 | -0.05 | 0.96 | 0.99 |
| Actinomyces | Viremic | 216 | 0.42 | 0.36 | 1.18 | 0.24 | 0.49 | -0.21 | 0.53 | -0.39 | 0.70 | 0.88 |
| Alistipes | Suppressed | 233 | -0.38 | 0.24 | -1.58 | 0.11 | 0.36 | -0.32 | 0.26 | -1.25 | 0.21 | 0.50 |
| Alistipes | Undetectable | 233 | -0.27 | 0.25 | -1.05 | 0.29 | 0.53 | -0.41 | 0.28 | -1.42 | 0.15 | 0.43 |
| Alistipes | Viremic | 233 | 0.55 | 0.35 | 1.57 | 0.12 | 0.36 | 0.09 | 0.54 | 0.17 | 0.87 | 0.97 |
| Allisonella | Suppressed | 229 | -0.25 | 0.13 | -1.94 | 0.05 | 0.23 | -0.14 | 0.16 | -0.84 | 0.40 | 0.69 |
| Allisonella | Undetectable | 229 | 0.04 | 0.14 | 0.27 | 0.79 | 0.92 | -0.03 | 0.19 | -0.16 | 0.87 | 0.97 |
| Allisonella | Viremic | 229 | 0.02 | 0.16 | 0.10 | 0.92 | 0.97 | 0.10 | 0.22 | 0.45 | 0.65 | 0.86 |
| Alloprevotella | Suppressed | 296 | -0.01 | 0.15 | -0.07 | 0.94 | 0.97 | -0.05 | 0.16 | -0.33 | 0.74 | 0.91 |
| Alloprevotella | Undetectable | 296 | 0.02 | 0.16 | 0.10 | 0.92 | 0.97 | 0.13 | 0.15 | 0.86 | 0.39 | 0.69 |
| Alloprevotella | Viremic | 296 | 0.25 | 0.18 | 1.38 | 0.17 | 0.43 | 0.42 | 0.40 | 1.05 | 0.29 | 0.58 |
| Anaerococcus | Suppressed | 338 | 0.47 | 0.20 | 2.39 | 0.02 | 0.11 | 0.51 | 0.23 | 2.27 | 0.02 | 0.19 |
| Anaerococcus | Undetectable | 338 | 0.32 | 0.21 | 1.52 | 0.13 | 0.39 | 0.24 | 0.27 | 0.90 | 0.37 | 0.67 |
| Anaerococcus | Viremic | 338 | 0.45 | 0.25 | 1.81 | 0.07 | 0.27 | 0.47 | 0.29 | 1.62 | 0.11 | 0.40 |
| Arcanobacterium | Suppressed | 81 | -0.51 | 0.43 | -1.19 | 0.23 | 0.48 | -0.84 | 0.60 | -1.39 | 0.16 | 0.44 |
| Arcanobacterium | Undetectable | 81 | -0.11 | 0.45 | -0.25 | 0.80 | 0.92 | -0.12 | 0.62 | -0.19 | 0.85 | 0.97 |
| Arcanobacterium | Viremic | 81 | -2.61 | 0.62 | -4.22 | 0.00 | 0.00 | -3.03 | 0.52 | -5.77 | 0.00 | 0.00 |
| Bacteroides | Suppressed | 370 | -0.64 | 0.21 | -3.08 | 0.00 | 0.03 | -0.71 | 0.29 | -2.42 | 0.02 | 0.16 |
| Bacteroides | Undetectable | 370 | -0.66 | 0.22 | -3.04 | 0.00 | 0.03 | -0.67 | 0.28 | -2.38 | 0.02 | 0.16 |
| Bacteroides | Viremic | 370 | -0.89 | 0.25 | -3.54 | 0.00 | 0.01 | -1.14 | 0.29 | -3.91 | 0.00 | 0.00 |
| Barnesiella | Suppressed | 62 | -1.76 | 0.46 | -3.85 | 0.00 | 0.00 | -1.43 | 0.43 | -3.36 | 0.00 | 0.03 |
| Barnesiella | Undetectable | 62 | -0.69 | 0.48 | -1.44 | 0.15 | 0.40 | -0.30 | 0.55 | -0.54 | 0.59 | 0.82 |
| Barnesiella | Viremic | 62 | -0.87 | 0.79 | -1.11 | 0.27 | 0.51 | -1.30 | 0.67 | -1.94 | 0.05 | 0.28 |
| Bifidobacterium | Suppressed | 272 | 0.28 | 0.22 | 1.25 | 0.21 | 0.47 | 0.27 | 0.30 | 0.90 | 0.37 | 0.67 |
| Bifidobacterium | Undetectable | 272 | -0.25 | 0.25 | -0.98 | 0.33 | 0.57 | -0.07 | 0.37 | -0.18 | 0.86 | 0.97 |
| Bifidobacterium | Viremic | 272 | 0.35 | 0.28 | 1.28 | 0.20 | 0.46 | 0.54 | 0.38 | 1.44 | 0.15 | 0.43 |
| Bilophila | Suppressed | 228 | 0.04 | 0.21 | 0.21 | 0.83 | 0.92 | 0.26 | 0.29 | 0.91 | 0.36 | 0.67 |
| Bilophila | Undetectable | 228 | 0.22 | 0.22 | 0.99 | 0.32 | 0.57 | 0.18 | 0.27 | 0.69 | 0.49 | 0.74 |
| Bilophila | Viremic | 228 | 0.06 | 0.30 | 0.18 | 0.85 | 0.94 | 0.30 | 0.25 | 1.18 | 0.24 | 0.54 |
| Brachyspira | Suppressed | 40 | -3.47 | 0.78 | -4.43 | 0.00 | 0.00 | -4.13 | 1.06 | -3.88 | 0.00 | 0.00 |
| Brachyspira | Undetectable | 40 | -3.51 | 0.76 | -4.62 | 0.00 | 0.00 | -3.33 | 1.01 | -3.30 | 0.00 | 0.03 |
| Brachyspira | Viremic | 40 | -2.49 | 1.02 | -2.44 | 0.01 | 0.10 | -3.33 | 1.18 | -2.81 | 0.00 | 0.08 |
| Bulleidia | Suppressed | 166 | 0.00 | 0.21 | -0.01 | 0.99 | 0.99 | 0.05 | 0.34 | 0.14 | 0.89 | 0.97 |
| Bulleidia | Undetectable | 166 | 0.04 | 0.21 | 0.18 | 0.86 | 0.94 | 0.02 | 0.24 | 0.09 | 0.93 | 0.99 |
| Bulleidia | Viremic | 166 | 0.05 | 0.23 | 0.21 | 0.83 | 0.92 | 0.08 | 0.35 | 0.23 | 0.82 | 0.96 |
| Butyricicoccus | Suppressed | 338 | -0.14 | 0.11 | -1.22 | 0.22 | 0.48 | -0.20 | 0.13 | -1.52 | 0.13 | 0.43 |
| Butyricicoccus | Undetectable | 338 | -0.14 | 0.11 | -1.22 | 0.22 | 0.48 | -0.05 | 0.14 | -0.37 | 0.71 | 0.89 |
| Butyricicoccus | Viremic | 338 | -0.22 | 0.14 | -1.61 | 0.11 | 0.35 | -0.20 | 0.17 | -1.16 | 0.25 | 0.54 |
| Campylobacter | Suppressed | 294 | -1.11 | 0.28 | -3.98 | 0.00 | 0.00 | -0.97 | 0.64 | -1.52 | 0.13 | 0.43 |
| Campylobacter | Undetectable | 294 | -1.75 | 0.30 | -5.81 | 0.00 | 0.00 | -1.84 | 0.59 | -3.12 | 0.00 | 0.05 |
| Campylobacter | Viremic | 294 | -0.99 | 0.37 | -2.71 | 0.01 | 0.06 | -0.87 | 0.62 | -1.41 | 0.16 | 0.43 |
| Catenibacterium | Suppressed | 292 | -0.19 | 0.17 | -1.11 | 0.27 | 0.51 | -0.27 | 0.18 | -1.51 | 0.13 | 0.43 |
| Catenibacterium | Undetectable | 292 | 0.11 | 0.17 | 0.67 | 0.51 | 0.68 | 0.15 | 0.22 | 0.68 | 0.49 | 0.74 |
| Catenibacterium | Viremic | 292 | 0.36 | 0.20 | 1.84 | 0.07 | 0.26 | 0.46 | 0.64 | 0.72 | 0.47 | 0.73 |
| Clostridium\_IV | Suppressed | 325 | -0.19 | 0.18 | -1.06 | 0.29 | 0.53 | -0.47 | 0.20 | -2.30 | 0.02 | 0.18 |
| Clostridium\_IV | Undetectable | 325 | -0.15 | 0.18 | -0.82 | 0.41 | 0.64 | -0.32 | 0.25 | -1.30 | 0.19 | 0.49 |
| Clostridium\_IV | Viremic | 325 | 0.12 | 0.22 | 0.52 | 0.60 | 0.78 | -0.15 | 0.34 | -0.44 | 0.66 | 0.86 |
| Clostridium\_XI | Suppressed | 211 | -0.41 | 0.24 | -1.73 | 0.08 | 0.29 | -0.39 | 0.22 | -1.73 | 0.08 | 0.34 |
| Clostridium\_XI | Undetectable | 211 | -0.39 | 0.24 | -1.62 | 0.10 | 0.34 | -0.33 | 0.23 | -1.40 | 0.16 | 0.43 |
| Clostridium\_XI | Viremic | 211 | -0.22 | 0.30 | -0.72 | 0.47 | 0.67 | 0.06 | 0.41 | 0.14 | 0.89 | 0.97 |
| Clostridium\_XVIII | Suppressed | 111 | -0.22 | 0.32 | -0.67 | 0.50 | 0.68 | -0.69 | 0.58 | -1.20 | 0.23 | 0.53 |
| Clostridium\_XVIII | Undetectable | 111 | -0.84 | 0.37 | -2.25 | 0.02 | 0.14 | -1.03 | 0.51 | -2.03 | 0.04 | 0.24 |
| Clostridium\_XVIII | Viremic | 111 | 0.76 | 0.83 | 0.93 | 0.35 | 0.59 | 0.61 | 0.97 | 0.63 | 0.53 | 0.76 |
| Collinsella | Suppressed | 335 | 0.07 | 0.10 | 0.63 | 0.53 | 0.71 | 0.09 | 0.11 | 0.80 | 0.42 | 0.70 |
| Collinsella | Undetectable | 335 | 0.18 | 0.11 | 1.66 | 0.10 | 0.32 | 0.24 | 0.13 | 1.82 | 0.07 | 0.31 |
| Collinsella | Viremic | 335 | 0.05 | 0.13 | 0.36 | 0.72 | 0.86 | 0.16 | 0.23 | 0.68 | 0.50 | 0.74 |
| Corynebacterium | Suppressed | 289 | 0.36 | 0.27 | 1.36 | 0.17 | 0.43 | 0.46 | 0.38 | 1.22 | 0.22 | 0.52 |
| Corynebacterium | Undetectable | 289 | 0.21 | 0.28 | 0.76 | 0.45 | 0.65 | 0.23 | 0.32 | 0.72 | 0.47 | 0.73 |
| Corynebacterium | Viremic | 289 | 1.23 | 0.32 | 3.80 | 0.00 | 0.00 | 0.78 | 0.54 | 1.43 | 0.15 | 0.43 |
| Desulfomicrobium | Suppressed | 82 | -0.03 | 0.22 | -0.15 | 0.88 | 0.95 | -0.06 | 0.31 | -0.19 | 0.85 | 0.97 |
| Desulfomicrobium | Undetectable | 82 | 0.16 | 0.22 | 0.74 | 0.46 | 0.66 | 0.26 | 0.20 | 1.30 | 0.19 | 0.49 |
| Desulfomicrobium | Viremic | 82 | 0.44 | 0.34 | 1.31 | 0.19 | 0.45 | 0.05 | 0.33 | 0.15 | 0.88 | 0.97 |
| Desulfovibrio | Suppressed | 232 | -0.22 | 0.16 | -1.35 | 0.18 | 0.43 | -0.30 | 0.18 | -1.69 | 0.09 | 0.37 |
| Desulfovibrio | Undetectable | 232 | 0.16 | 0.17 | 0.97 | 0.33 | 0.57 | 0.26 | 0.24 | 1.10 | 0.27 | 0.57 |
| Desulfovibrio | Viremic | 232 | -0.02 | 0.20 | -0.12 | 0.91 | 0.97 | -0.11 | 0.22 | -0.48 | 0.63 | 0.84 |
| Dialister | Suppressed | 347 | 0.00 | 0.14 | 0.02 | 0.98 | 0.99 | 0.01 | 0.15 | 0.03 | 0.97 | 1.00 |
| Dialister | Undetectable | 347 | 0.01 | 0.14 | 0.06 | 0.95 | 0.98 | 0.00 | 0.12 | -0.03 | 0.98 | 1.00 |
| Dialister | Viremic | 347 | 0.23 | 0.17 | 1.37 | 0.17 | 0.43 | 0.33 | 0.17 | 1.88 | 0.06 | 0.29 |
| Dietzia | Suppressed | 182 | -0.08 | 0.23 | -0.35 | 0.73 | 0.86 | -0.25 | 0.29 | -0.86 | 0.39 | 0.69 |
| Dietzia | Undetectable | 182 | -0.15 | 0.26 | -0.57 | 0.57 | 0.75 | 0.20 | 0.50 | 0.41 | 0.68 | 0.88 |
| Dietzia | Viremic | 182 | 0.94 | 0.30 | 3.10 | 0.00 | 0.03 | 0.63 | 0.42 | 1.50 | 0.13 | 0.43 |
| Enterorhabdus | Suppressed | 105 | -0.09 | 0.16 | -0.57 | 0.57 | 0.75 | -0.23 | 0.16 | -1.44 | 0.15 | 0.43 |
| Enterorhabdus | Undetectable | 105 | 0.21 | 0.14 | 1.45 | 0.15 | 0.39 | 0.20 | 0.18 | 1.16 | 0.25 | 0.54 |
| Enterorhabdus | Viremic | 105 | 0.24 | 0.22 | 1.09 | 0.27 | 0.52 | 0.29 | 0.22 | 1.32 | 0.19 | 0.48 |
| Escherichia/Shigella | Suppressed | 236 | -0.89 | 0.36 | -2.47 | 0.01 | 0.10 | -1.09 | 0.51 | -2.14 | 0.03 | 0.21 |
| Escherichia/Shigella | Undetectable | 236 | -0.49 | 0.38 | -1.30 | 0.19 | 0.45 | -0.87 | 0.55 | -1.59 | 0.11 | 0.41 |
| Escherichia/Shigella | Viremic | 236 | 0.38 | 0.44 | 0.86 | 0.39 | 0.61 | 0.04 | 0.58 | 0.07 | 0.95 | 0.99 |
| Eubacterium | Suppressed | 148 | -0.35 | 0.24 | -1.48 | 0.14 | 0.39 | -0.33 | 0.26 | -1.24 | 0.22 | 0.50 |
| Eubacterium | Undetectable | 148 | -0.24 | 0.31 | -0.77 | 0.44 | 0.65 | -0.40 | 0.29 | -1.40 | 0.16 | 0.43 |
| Eubacterium | Viremic | 148 | 0.50 | 0.28 | 1.80 | 0.07 | 0.28 | 0.41 | 0.50 | 0.82 | 0.41 | 0.70 |
| Faecalibacterium | Suppressed | 365 | -0.08 | 0.11 | -0.70 | 0.48 | 0.68 | -0.15 | 0.11 | -1.42 | 0.15 | 0.43 |
| Faecalibacterium | Undetectable | 365 | -0.04 | 0.11 | -0.37 | 0.71 | 0.86 | 0.01 | 0.14 | 0.10 | 0.92 | 0.99 |
| Faecalibacterium | Viremic | 365 | -0.28 | 0.13 | -2.12 | 0.03 | 0.17 | -0.48 | 0.16 | -3.03 | 0.00 | 0.05 |
| Finegoldia | Suppressed | 363 | 0.46 | 0.20 | 2.30 | 0.02 | 0.13 | 0.50 | 0.19 | 2.64 | 0.01 | 0.11 |
| Finegoldia | Undetectable | 363 | 0.69 | 0.21 | 3.30 | 0.00 | 0.02 | 0.66 | 0.32 | 2.05 | 0.04 | 0.24 |
| Finegoldia | Viremic | 363 | 0.67 | 0.24 | 2.75 | 0.01 | 0.05 | 0.43 | 0.29 | 1.48 | 0.14 | 0.43 |
| Flavonifractor | Suppressed | 171 | -0.65 | 0.21 | -3.06 | 0.00 | 0.03 | -0.63 | 0.26 | -2.45 | 0.01 | 0.16 |
| Flavonifractor | Undetectable | 171 | -0.46 | 0.21 | -2.16 | 0.03 | 0.16 | -0.45 | 0.28 | -1.62 | 0.10 | 0.40 |
| Flavonifractor | Viremic | 171 | -0.52 | 0.28 | -1.84 | 0.07 | 0.26 | -0.42 | 0.44 | -0.96 | 0.34 | 0.65 |
| Fusobacterium | Suppressed | 308 | 0.37 | 0.25 | 1.50 | 0.13 | 0.39 | 0.28 | 0.30 | 0.91 | 0.36 | 0.67 |
| Fusobacterium | Undetectable | 308 | 0.24 | 0.26 | 0.91 | 0.36 | 0.59 | -0.04 | 0.33 | -0.13 | 0.90 | 0.97 |
| Fusobacterium | Viremic | 308 | 0.40 | 0.30 | 1.33 | 0.18 | 0.44 | 0.29 | 0.40 | 0.72 | 0.47 | 0.73 |
| Gardnerella | Suppressed | 55 | -0.33 | 0.61 | -0.54 | 0.59 | 0.78 | -0.34 | 0.50 | -0.68 | 0.49 | 0.74 |
| Gardnerella | Undetectable | 55 | 1.34 | 0.57 | 2.36 | 0.02 | 0.12 | 0.91 | 0.89 | 1.03 | 0.30 | 0.59 |
| Gardnerella | Viremic | 55 | 0.78 | 0.63 | 1.23 | 0.22 | 0.48 | 0.67 | 0.53 | 1.27 | 0.20 | 0.50 |
| Gemmiger | Suppressed | 325 | -0.01 | 0.13 | -0.06 | 0.95 | 0.98 | -0.12 | 0.13 | -0.93 | 0.35 | 0.67 |
| Gemmiger | Undetectable | 325 | 0.26 | 0.13 | 2.01 | 0.04 | 0.21 | 0.37 | 0.17 | 2.14 | 0.03 | 0.21 |
| Gemmiger | Viremic | 325 | -0.24 | 0.15 | -1.54 | 0.12 | 0.38 | -0.42 | 0.21 | -1.98 | 0.05 | 0.26 |
| Granulicatella | Suppressed | 183 | 0.25 | 0.29 | 0.86 | 0.39 | 0.61 | 0.21 | 0.42 | 0.50 | 0.62 | 0.83 |
| Granulicatella | Undetectable | 183 | 0.36 | 0.31 | 1.15 | 0.25 | 0.50 | 0.19 | 0.52 | 0.36 | 0.72 | 0.90 |
| Granulicatella | Viremic | 183 | 0.29 | 0.32 | 0.91 | 0.36 | 0.59 | -0.11 | 0.49 | -0.23 | 0.82 | 0.96 |
| Haemophilus | Suppressed | 187 | 0.86 | 0.40 | 2.16 | 0.03 | 0.16 | 1.28 | 0.69 | 1.87 | 0.06 | 0.29 |
| Haemophilus | Undetectable | 187 | 0.17 | 0.42 | 0.42 | 0.68 | 0.86 | 0.49 | 0.80 | 0.61 | 0.54 | 0.77 |
| Haemophilus | Viremic | 187 | -1.15 | 0.47 | -2.45 | 0.01 | 0.10 | -0.97 | 0.55 | -1.78 | 0.08 | 0.32 |
| Hallella | Suppressed | 63 | -0.08 | 0.37 | -0.23 | 0.82 | 0.92 | -0.20 | 0.38 | -0.51 | 0.61 | 0.82 |
| Hallella | Undetectable | 63 | 0.13 | 0.55 | 0.23 | 0.81 | 0.92 | -0.14 | 0.55 | -0.26 | 0.79 | 0.95 |
| Hallella | Viremic | 63 | -0.43 | 0.42 | -1.04 | 0.30 | 0.54 | -0.07 | 0.43 | -0.16 | 0.87 | 0.97 |
| Helicobacter | Suppressed | 41 | -2.31 | 0.82 | -2.83 | 0.00 | 0.04 | -2.45 | 0.82 | -2.98 | 0.00 | 0.05 |
| Helicobacter | Undetectable | 41 | -3.14 | 0.87 | -3.60 | 0.00 | 0.01 | -2.71 | 1.24 | -2.19 | 0.03 | 0.21 |
| Helicobacter | Viremic | 41 | -3.18 | 1.07 | -2.98 | 0.00 | 0.03 | -3.56 | 1.23 | -2.90 | 0.00 | 0.06 |
| Holdemania | Suppressed | 96 | -0.04 | 0.31 | -0.13 | 0.90 | 0.97 | -0.52 | 0.62 | -0.84 | 0.40 | 0.69 |
| Holdemania | Undetectable | 96 | -0.23 | 0.30 | -0.76 | 0.45 | 0.65 | -0.55 | 0.48 | -1.16 | 0.25 | 0.54 |
| Holdemania | Viremic | 96 | 0.37 | 0.36 | 1.02 | 0.31 | 0.55 | -0.51 | 0.70 | -0.72 | 0.47 | 0.73 |
| Howardella | Suppressed | 225 | -0.11 | 0.13 | -0.80 | 0.42 | 0.65 | -0.17 | 0.15 | -1.13 | 0.26 | 0.56 |
| Howardella | Undetectable | 225 | 0.03 | 0.13 | 0.21 | 0.84 | 0.92 | -0.02 | 0.20 | -0.09 | 0.93 | 0.99 |
| Howardella | Viremic | 225 | -0.23 | 0.16 | -1.45 | 0.15 | 0.39 | -0.33 | 0.18 | -1.87 | 0.06 | 0.29 |
| Hydrogenoanaerobacterium | Suppressed | 122 | 0.34 | 0.23 | 1.48 | 0.14 | 0.39 | 0.22 | 0.24 | 0.93 | 0.35 | 0.67 |
| Hydrogenoanaerobacterium | Undetectable | 122 | 0.18 | 0.24 | 0.74 | 0.46 | 0.66 | 0.26 | 0.23 | 1.13 | 0.26 | 0.56 |
| Hydrogenoanaerobacterium | Viremic | 122 | 0.01 | 0.29 | 0.03 | 0.98 | 0.99 | -0.23 | 0.23 | -0.99 | 0.32 | 0.62 |
| Lactobacillus | Suppressed | 97 | -0.46 | 0.42 | -1.11 | 0.27 | 0.51 | -0.55 | 0.42 | -1.29 | 0.20 | 0.49 |
| Lactobacillus | Undetectable | 97 | -0.74 | 0.44 | -1.67 | 0.10 | 0.32 | -0.72 | 0.51 | -1.42 | 0.16 | 0.43 |
| Lactobacillus | Viremic | 97 | 0.28 | 0.42 | 0.66 | 0.51 | 0.68 | 0.39 | 0.46 | 0.84 | 0.40 | 0.69 |
| Mannheimia | Suppressed | 43 | 1.28 | 0.88 | 1.46 | 0.14 | 0.39 | 1.51 | 1.13 | 1.33 | 0.18 | 0.48 |
| Mannheimia | Undetectable | 43 | 1.90 | 0.80 | 2.37 | 0.02 | 0.11 | 12.45 | 18.82 | 0.66 | 0.51 | 0.75 |
| Mannheimia | Viremic | 43 | 1.49 | 1.17 | 1.27 | 0.20 | 0.46 | 1.95 | 1.08 | 1.81 | 0.07 | 0.31 |
| Megasphaera | Suppressed | 271 | 0.08 | 0.18 | 0.42 | 0.67 | 0.85 | 0.18 | 0.17 | 1.10 | 0.27 | 0.57 |
| Megasphaera | Undetectable | 271 | 0.04 | 0.19 | 0.22 | 0.83 | 0.92 | 0.06 | 0.16 | 0.38 | 0.70 | 0.89 |
| Megasphaera | Viremic | 271 | 0.23 | 0.23 | 0.97 | 0.33 | 0.57 | 0.46 | 0.22 | 2.14 | 0.03 | 0.21 |
| Methanosphaera | Suppressed | 65 | -0.69 | 0.35 | -1.95 | 0.05 | 0.23 | -0.88 | 0.45 | -1.96 | 0.05 | 0.26 |
| Methanosphaera | Undetectable | 65 | -0.10 | 0.39 | -0.25 | 0.81 | 0.92 | -0.32 | 0.54 | -0.59 | 0.56 | 0.78 |
| Methanosphaera | Viremic | 65 | -0.20 | 0.58 | -0.35 | 0.73 | 0.86 | -0.86 | 0.79 | -1.10 | 0.27 | 0.57 |
| Mitsuokella | Suppressed | 236 | -0.16 | 0.17 | -0.93 | 0.35 | 0.59 | -0.16 | 0.21 | -0.78 | 0.44 | 0.72 |
| Mitsuokella | Undetectable | 236 | 0.05 | 0.17 | 0.27 | 0.78 | 0.92 | -0.01 | 0.20 | -0.07 | 0.94 | 0.99 |
| Mitsuokella | Viremic | 236 | -0.29 | 0.21 | -1.36 | 0.17 | 0.43 | -0.14 | 0.23 | -0.62 | 0.53 | 0.76 |
| Mobiluncus | Suppressed | 144 | 0.44 | 0.25 | 1.78 | 0.07 | 0.28 | 0.38 | 0.43 | 0.89 | 0.37 | 0.67 |
| Mobiluncus | Undetectable | 144 | -0.37 | 0.27 | -1.37 | 0.17 | 0.43 | -0.21 | 0.39 | -0.52 | 0.60 | 0.82 |
| Mobiluncus | Viremic | 144 | 0.14 | 0.39 | 0.37 | 0.71 | 0.86 | -0.10 | 0.40 | -0.26 | 0.80 | 0.95 |
| Mogibacterium | Suppressed | 278 | 0.10 | 0.12 | 0.81 | 0.42 | 0.64 | 0.21 | 0.14 | 1.46 | 0.14 | 0.43 |
| Mogibacterium | Undetectable | 278 | -0.10 | 0.13 | -0.77 | 0.44 | 0.65 | -0.10 | 0.15 | -0.66 | 0.51 | 0.75 |
| Mogibacterium | Viremic | 278 | 0.30 | 0.15 | 1.98 | 0.05 | 0.23 | 0.50 | 0.25 | 2.04 | 0.04 | 0.24 |
| Murdochiella | Suppressed | 141 | -0.41 | 0.34 | -1.21 | 0.23 | 0.48 | 0.00 | 0.45 | 0.00 | 1.00 | 1.00 |
| Murdochiella | Undetectable | 141 | -0.82 | 0.43 | -1.93 | 0.05 | 0.23 | -0.59 | 0.45 | -1.32 | 0.19 | 0.48 |
| Murdochiella | Viremic | 141 | 1.54 | 0.49 | 3.12 | 0.00 | 0.03 | 1.40 | 0.47 | 3.00 | 0.00 | 0.05 |
| Mycoplasma | Suppressed | 60 | -0.74 | 0.65 | -1.14 | 0.26 | 0.50 | -1.02 | 1.71 | -0.60 | 0.55 | 0.78 |
| Mycoplasma | Undetectable | 60 | 0.25 | 0.71 | 0.36 | 0.72 | 0.86 | 0.02 | 1.07 | 0.02 | 0.99 | 1.00 |
| Mycoplasma | Viremic | 60 | -0.34 | 0.67 | -0.51 | 0.61 | 0.79 | -1.06 | 1.06 | -1.00 | 0.32 | 0.62 |
| Negativicoccus | Suppressed | 84 | -0.22 | 0.33 | -0.67 | 0.51 | 0.68 | -0.23 | 0.29 | -0.81 | 0.42 | 0.70 |
| Negativicoccus | Undetectable | 84 | 0.32 | 0.36 | 0.88 | 0.38 | 0.60 | 0.12 | 0.41 | 0.30 | 0.76 | 0.92 |
| Negativicoccus | Viremic | 84 | 1.28 | 0.33 | 3.89 | 0.00 | 0.00 | 1.02 | 0.49 | 2.07 | 0.04 | 0.24 |
| Oligosphaera | Suppressed | 74 | 0.14 | 0.35 | 0.41 | 0.68 | 0.86 | -0.06 | 0.59 | -0.10 | 0.92 | 0.99 |
| Oligosphaera | Undetectable | 74 | 0.52 | 0.35 | 1.49 | 0.14 | 0.39 | 0.59 | 0.32 | 1.83 | 0.07 | 0.31 |
| Oligosphaera | Viremic | 74 | -0.37 | 0.41 | -0.91 | 0.37 | 0.59 | -0.67 | 0.35 | -1.92 | 0.05 | 0.28 |
| Olsenella | Suppressed | 182 | -0.01 | 0.15 | -0.09 | 0.93 | 0.97 | 0.00 | 0.22 | -0.01 | 0.99 | 1.00 |
| Olsenella | Undetectable | 182 | 0.15 | 0.17 | 0.92 | 0.36 | 0.59 | 0.06 | 0.17 | 0.33 | 0.74 | 0.91 |
| Olsenella | Viremic | 182 | 0.33 | 0.19 | 1.77 | 0.08 | 0.28 | 0.19 | 0.26 | 0.74 | 0.46 | 0.73 |
| Oribacterium | Suppressed | 141 | -0.14 | 0.19 | -0.72 | 0.47 | 0.67 | -0.11 | 0.25 | -0.43 | 0.66 | 0.86 |
| Oribacterium | Undetectable | 141 | 0.10 | 0.21 | 0.46 | 0.65 | 0.83 | -0.04 | 0.20 | -0.18 | 0.85 | 0.97 |
| Oribacterium | Viremic | 141 | -0.26 | 0.22 | -1.21 | 0.23 | 0.48 | -0.37 | 0.25 | -1.49 | 0.14 | 0.43 |
| Oscillibacter | Suppressed | 325 | -0.08 | 0.11 | -0.68 | 0.50 | 0.68 | -0.12 | 0.13 | -0.90 | 0.37 | 0.67 |
| Oscillibacter | Undetectable | 325 | 0.15 | 0.12 | 1.27 | 0.20 | 0.46 | 0.02 | 0.13 | 0.17 | 0.86 | 0.97 |
| Oscillibacter | Viremic | 325 | -0.08 | 0.14 | -0.61 | 0.54 | 0.72 | -0.21 | 0.17 | -1.25 | 0.21 | 0.50 |
| Oxalobacter | Suppressed | 64 | -0.66 | 0.25 | -2.70 | 0.01 | 0.06 | -0.83 | 0.33 | -2.51 | 0.01 | 0.14 |
| Oxalobacter | Undetectable | 64 | -0.05 | 0.23 | -0.23 | 0.82 | 0.92 | -0.06 | 0.24 | -0.25 | 0.80 | 0.95 |
| Oxalobacter | Viremic | 64 | -0.36 | 0.31 | -1.16 | 0.25 | 0.49 | -0.50 | 0.25 | -1.96 | 0.05 | 0.26 |
| Parabacteroides | Suppressed | 272 | -0.79 | 0.24 | -3.25 | 0.00 | 0.02 | -0.85 | 0.34 | -2.54 | 0.01 | 0.14 |
| Parabacteroides | Undetectable | 272 | -0.47 | 0.25 | -1.91 | 0.06 | 0.23 | -0.58 | 0.38 | -1.53 | 0.13 | 0.43 |
| Parabacteroides | Viremic | 272 | 0.15 | 0.35 | 0.43 | 0.67 | 0.85 | -0.05 | 0.40 | -0.11 | 0.91 | 0.98 |
| Paraprevotella | Suppressed | 213 | 0.08 | 0.21 | 0.40 | 0.69 | 0.86 | 0.09 | 0.32 | 0.28 | 0.78 | 0.93 |
| Paraprevotella | Undetectable | 213 | -0.01 | 0.21 | -0.03 | 0.98 | 0.99 | 0.01 | 0.28 | 0.04 | 0.96 | 0.99 |
| Paraprevotella | Viremic | 213 | 0.38 | 0.28 | 1.35 | 0.18 | 0.43 | 0.12 | 0.31 | 0.40 | 0.69 | 0.88 |
| Parasutterella | Suppressed | 87 | 0.04 | 0.46 | 0.08 | 0.94 | 0.97 | -0.08 | 0.57 | -0.14 | 0.89 | 0.97 |
| Parasutterella | Undetectable | 87 | -1.38 | 0.53 | -2.60 | 0.01 | 0.07 | -1.84 | 0.60 | -3.05 | 0.00 | 0.05 |
| Parasutterella | Viremic | 87 | -0.61 | 0.64 | -0.96 | 0.34 | 0.58 | -0.26 | 0.54 | -0.49 | 0.63 | 0.84 |
| Parvimonas | Suppressed | 199 | 0.37 | 0.28 | 1.36 | 0.17 | 0.43 | 0.26 | 0.30 | 0.87 | 0.39 | 0.69 |
| Parvimonas | Undetectable | 199 | 0.30 | 0.29 | 1.03 | 0.30 | 0.54 | 0.12 | 0.42 | 0.29 | 0.77 | 0.93 |
| Parvimonas | Viremic | 199 | 0.25 | 0.33 | 0.77 | 0.44 | 0.65 | 0.43 | 0.54 | 0.80 | 0.42 | 0.70 |
| Peptoniphilus | Suppressed | 348 | 0.47 | 0.20 | 2.31 | 0.02 | 0.13 | 0.54 | 0.23 | 2.35 | 0.02 | 0.16 |
| Peptoniphilus | Undetectable | 348 | 0.33 | 0.21 | 1.57 | 0.12 | 0.37 | 0.37 | 0.25 | 1.50 | 0.13 | 0.43 |
| Peptoniphilus | Viremic | 348 | 0.95 | 0.25 | 3.83 | 0.00 | 0.00 | 1.09 | 0.27 | 3.99 | 0.00 | 0.00 |
| Peptostreptococcus | Suppressed | 253 | 0.50 | 0.24 | 2.11 | 0.04 | 0.17 | 0.41 | 0.25 | 1.63 | 0.10 | 0.40 |
| Peptostreptococcus | Undetectable | 253 | -0.05 | 0.25 | -0.21 | 0.83 | 0.92 | -0.09 | 0.26 | -0.35 | 0.72 | 0.90 |
| Peptostreptococcus | Viremic | 253 | 0.31 | 0.28 | 1.12 | 0.26 | 0.51 | 0.42 | 0.36 | 1.17 | 0.24 | 0.54 |
| Porphyromonas | Suppressed | 234 | 0.28 | 0.30 | 0.94 | 0.35 | 0.59 | 0.44 | 0.30 | 1.45 | 0.15 | 0.43 |
| Porphyromonas | Undetectable | 234 | 0.03 | 0.32 | 0.08 | 0.93 | 0.97 | 0.25 | 0.36 | 0.68 | 0.50 | 0.74 |
| Porphyromonas | Viremic | 234 | 1.63 | 0.36 | 4.57 | 0.00 | 0.00 | 1.91 | 0.39 | 4.89 | 0.00 | 0.00 |
| Prevotella | Suppressed | 381 | 0.23 | 0.10 | 2.20 | 0.03 | 0.16 | 0.23 | 0.09 | 2.61 | 0.01 | 0.12 |
| Prevotella | Undetectable | 381 | 0.16 | 0.11 | 1.47 | 0.14 | 0.39 | 0.16 | 0.10 | 1.57 | 0.12 | 0.43 |
| Prevotella | Viremic | 381 | 0.22 | 0.13 | 1.74 | 0.08 | 0.29 | 0.38 | 0.11 | 3.39 | 0.00 | 0.03 |
| Pseudoflavonifractor | Suppressed | 72 | 0.71 | 0.23 | 3.05 | 0.00 | 0.03 | 0.31 | 0.49 | 0.63 | 0.53 | 0.76 |
| Pseudoflavonifractor | Undetectable | 72 | 0.01 | 0.27 | 0.03 | 0.98 | 0.99 | -0.12 | 0.20 | -0.62 | 0.53 | 0.76 |
| Pseudoflavonifractor | Viremic | 72 | 0.32 | 0.36 | 0.89 | 0.37 | 0.59 | -0.14 | 0.45 | -0.30 | 0.76 | 0.92 |
| Ruminococcus | Suppressed | 287 | 0.13 | 0.18 | 0.77 | 0.44 | 0.65 | -0.05 | 0.22 | -0.22 | 0.83 | 0.96 |
| Ruminococcus | Undetectable | 287 | -0.05 | 0.19 | -0.25 | 0.80 | 0.92 | -0.01 | 0.19 | -0.04 | 0.96 | 0.99 |
| Ruminococcus | Viremic | 287 | -0.27 | 0.23 | -1.20 | 0.23 | 0.48 | -0.34 | 0.26 | -1.27 | 0.20 | 0.50 |
| Slackia | Suppressed | 141 | -0.05 | 0.14 | -0.36 | 0.72 | 0.86 | -0.11 | 0.15 | -0.73 | 0.46 | 0.73 |
| Slackia | Undetectable | 141 | 0.11 | 0.15 | 0.78 | 0.44 | 0.65 | 0.00 | 0.20 | 0.00 | 1.00 | 1.00 |
| Slackia | Viremic | 141 | 0.19 | 0.19 | 0.96 | 0.34 | 0.58 | 0.31 | 0.29 | 1.07 | 0.29 | 0.57 |
| Sneathia | Suppressed | 52 | -0.61 | 0.60 | -1.01 | 0.31 | 0.55 | -0.90 | 0.51 | -1.78 | 0.07 | 0.32 |
| Sneathia | Undetectable | 52 | 0.73 | 0.67 | 1.08 | 0.28 | 0.52 | 0.78 | 0.51 | 1.51 | 0.13 | 0.43 |
| Sneathia | Viremic | 52 | 0.10 | 0.67 | 0.16 | 0.88 | 0.95 | 0.01 | 0.66 | 0.02 | 0.98 | 1.00 |
| Streptobacillus | Suppressed | 72 | 0.97 | 0.50 | 1.95 | 0.05 | 0.23 | 1.20 | 0.49 | 2.43 | 0.02 | 0.16 |
| Streptobacillus | Undetectable | 72 | -0.49 | 0.53 | -0.92 | 0.36 | 0.59 | -0.31 | 0.58 | -0.53 | 0.60 | 0.82 |
| Streptobacillus | Viremic | 72 | 0.95 | 0.56 | 1.69 | 0.09 | 0.32 | 0.95 | 0.43 | 2.20 | 0.03 | 0.21 |
| Streptococcus | Suppressed | 331 | 0.58 | 0.27 | 2.13 | 0.03 | 0.17 | 0.70 | 0.47 | 1.51 | 0.13 | 0.43 |
| Streptococcus | Undetectable | 331 | 1.21 | 0.28 | 4.26 | 0.00 | 0.00 | 0.99 | 0.52 | 1.91 | 0.06 | 0.28 |
| Streptococcus | Viremic | 331 | 0.22 | 0.33 | 0.68 | 0.50 | 0.68 | -0.50 | 0.47 | -1.06 | 0.29 | 0.58 |
| Subdoligranulum | Suppressed | 212 | -0.21 | 0.18 | -1.19 | 0.23 | 0.48 | -0.50 | 0.23 | -2.16 | 0.03 | 0.21 |
| Subdoligranulum | Undetectable | 212 | -0.38 | 0.17 | -2.21 | 0.03 | 0.15 | -0.34 | 0.24 | -1.41 | 0.16 | 0.43 |
| Subdoligranulum | Viremic | 212 | -0.43 | 0.22 | -1.92 | 0.05 | 0.23 | -0.72 | 0.32 | -2.23 | 0.03 | 0.20 |
| Succinivibrio | Suppressed | 156 | -0.27 | 0.40 | -0.67 | 0.50 | 0.68 | -0.29 | 0.35 | -0.85 | 0.39 | 0.69 |
| Succinivibrio | Undetectable | 156 | 0.13 | 0.40 | 0.33 | 0.74 | 0.87 | 0.13 | 0.36 | 0.34 | 0.73 | 0.90 |
| Succinivibrio | Viremic | 156 | -1.25 | 0.48 | -2.62 | 0.01 | 0.07 | -0.82 | 0.55 | -1.49 | 0.14 | 0.43 |
| Sutterella | Suppressed | 217 | -0.02 | 0.21 | -0.08 | 0.94 | 0.97 | -0.15 | 0.32 | -0.45 | 0.65 | 0.86 |
| Sutterella | Undetectable | 217 | -0.42 | 0.22 | -1.91 | 0.06 | 0.23 | -0.56 | 0.24 | -2.37 | 0.02 | 0.16 |
| Sutterella | Viremic | 217 | -0.02 | 0.29 | -0.08 | 0.94 | 0.97 | 0.33 | 0.45 | 0.72 | 0.47 | 0.73 |
| Turicibacter | Suppressed | 91 | -0.88 | 0.32 | -2.72 | 0.01 | 0.06 | -0.78 | 0.36 | -2.16 | 0.03 | 0.21 |
| Turicibacter | Undetectable | 91 | -1.12 | 0.35 | -3.19 | 0.00 | 0.02 | -1.27 | 0.54 | -2.37 | 0.02 | 0.16 |
| Turicibacter | Viremic | 91 | 0.14 | 0.41 | 0.33 | 0.74 | 0.87 | -0.09 | 0.41 | -0.22 | 0.83 | 0.96 |
| Varibaculum | Suppressed | 133 | 0.40 | 0.32 | 1.26 | 0.21 | 0.47 | 0.24 | 0.46 | 0.52 | 0.61 | 0.82 |
| Varibaculum | Undetectable | 133 | -0.50 | 0.36 | -1.39 | 0.16 | 0.43 | -0.39 | 0.53 | -0.73 | 0.47 | 0.73 |
| Varibaculum | Viremic | 133 | -0.15 | 0.42 | -0.35 | 0.73 | 0.86 | 0.21 | 0.50 | 0.41 | 0.68 | 0.88 |
| Veillonella | Suppressed | 91 | -0.54 | 0.45 | -1.20 | 0.23 | 0.48 | -0.74 | 0.60 | -1.25 | 0.21 | 0.50 |
| Veillonella | Undetectable | 91 | -0.05 | 0.54 | -0.09 | 0.93 | 0.97 | -0.14 | 0.72 | -0.20 | 0.84 | 0.97 |
| Veillonella | Viremic | 91 | 0.89 | 0.59 | 1.51 | 0.13 | 0.39 | 1.09 | 1.01 | 1.07 | 0.28 | 0.57 |
| Victivallis | Suppressed | 45 | -1.37 | 0.45 | -3.03 | 0.00 | 0.03 | -1.90 | 0.72 | -2.64 | 0.01 | 0.11 |
| Victivallis | Undetectable | 45 | -0.76 | 0.43 | -1.78 | 0.07 | 0.28 | -1.04 | 0.59 | -1.76 | 0.08 | 0.33 |
| Victivallis | Viremic | 45 | -0.64 | 0.59 | -1.08 | 0.28 | 0.52 | -1.62 | 2.18 | -0.74 | 0.46 | 0.73 |



**Figure S1.** Rectal microbial composition of study participants, N = 383. Columns represent the relative composition of each subject’s microbiome at the genus level. Within HIV viremia groups, subjects are ordered by the first principal coordinate of a Bray-Curtis pairwise distance matrix. Genera representing less than 1% of the composition on average across samples were combined into “Other.”



**Figure S2.** Zero-inflated negative binomial effect sizes comparing HIV-infected undetectable (RNA <20 copies/mL), suppressed (RNA ≥20-200 copies/mL), and viremic (RNA > 200 copies/mL) to HIV-uninfected participants. All taxa with at least one significant difference between groups are shown. Inverse probability of treatment-weighted effect sizes and 90% false coverage rate-adjusted confidence intervals (truncated at -4, 4) are plotted, with statistical significance (*q* < 0.1) indicated in color. Effect sizes are log ratios of normalized genera counts.



**Figure S3.** Forest plot of results of zero-inflated negative binomial models comparing genus-level bacterial counts between HIV+ suppressed (RNA ≥20-200 copies/mL) and HIV+ undetectable (RNA < 20 copies/mL, lower limit of detection) participants. Inverse probability of treatment-weighted effect sizes and 90% false coverage rate-adjusted confidence intervals (truncated at -4, 4) are plotted, with statistical significance (*q* < 0.1) indicated in color. Effect sizes are log ratios of normalized genera counts.

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