Supplementary Methods

Calculation of regression slopes

When calculating the clearance slope, we did not include the final data point for participants that achieve eradication. The resulting regression slope would be biased (too shallow) if the eradication time was included using the corresponding threshold value. Alternatively, assigning the qPCR measurement at the final observation time to zero introduces two problems: 1) on the log-scale, a zero count corresponds to negative infinity and 2) the true zero may occur before or after the final observation time resulting in an unpredictable bias (either too shallow or steep) for the subject-specific regressions. We also did not estimate slope lines as trends for participants that experienced eradication in 1 or 2 days because there was not enough information to establish a trend under these conditions.

Assumptions for bacterial group clearance rate comparison

For this analysis, we used clearance rates instead of half-lives to meet the normality assumptions of the regression. To compare rate differences between each bacterial group, we repeated this regression using each bacterial group as the reference group.

Predictors of BV-associated bacteria re-emergence.

To find determinants of bacterial re-emergence after suppression we looked at several potential predictors including baseline bacterial levels, time until bacterial suppression, estimated clearance rates, and presence of *L. crisptus* or *L. jensenii*. Presence of *Lactobacillus* spp. was defined as any positive swab throughout the 28-day observation

period. Using a generalized logistic regression controlling for within subject correlation, we estimated odds ratio for each of these predictors (Table A1).

Predictors of Lactobacillus spp. emergence.

To find determinants of *L. crispatus* and *L. jensenii* emergence (Supplementary Figure 3) we looked at several potential predictors including mean clearance rate, mean clearance time, baseline *L. iners* concentration, mean BV-associated bacteria concentration, and total BV-associated bacteria present at baseline. Using the Kolmogorov-Smirnov two-sample test, we compared episodes with emergent Lactobacillus spp. to episodes without across these predictors (Figure A1).

Supplementary Results

Sensitivity analysis of repeat enrollments

To test the effect of repeated enrollments on our results, all of the results presented in the results section were recreated with exclusion of the 4 repeat enrollments. There were some slight differences in this analysis but most of the results were robust. Initial values were slightly lower in repeat enrollments (Figure A2). The results from the regression of clearance time on initial values were only slightly different. With all 15 episodes, we found that a one log increase in initial value results in a 0.50 days (95% CI: 0.19, 0.81) increase in clearance time; without repeat enrollments, the estimate is 0.66 days (95% CI: 0.27, 1.05). We found the ICC estimates to remain relatively stable (changes under 0.02 for both estimates): therefore, in both analyses, variability in clearance rates occurs more due to treatment session than individual species. The correlation of initial values and

clearance rates (discussed in the supplementary data) across all bacteria did not change. The comparison of estimated clearance rates (Figure 3B) was relatively robust, though there was minor change in statistical significance likely attributable to smaller sample size (Figure A3). For estimated half-lives, an aggregate re-analysis was not conducted as the repeat enrollments are delineated in Figure 4 in the manuscript for comparison. There were no noticeable changes in the *Lactobacillus* spp. and corresponding summed composition analysis.

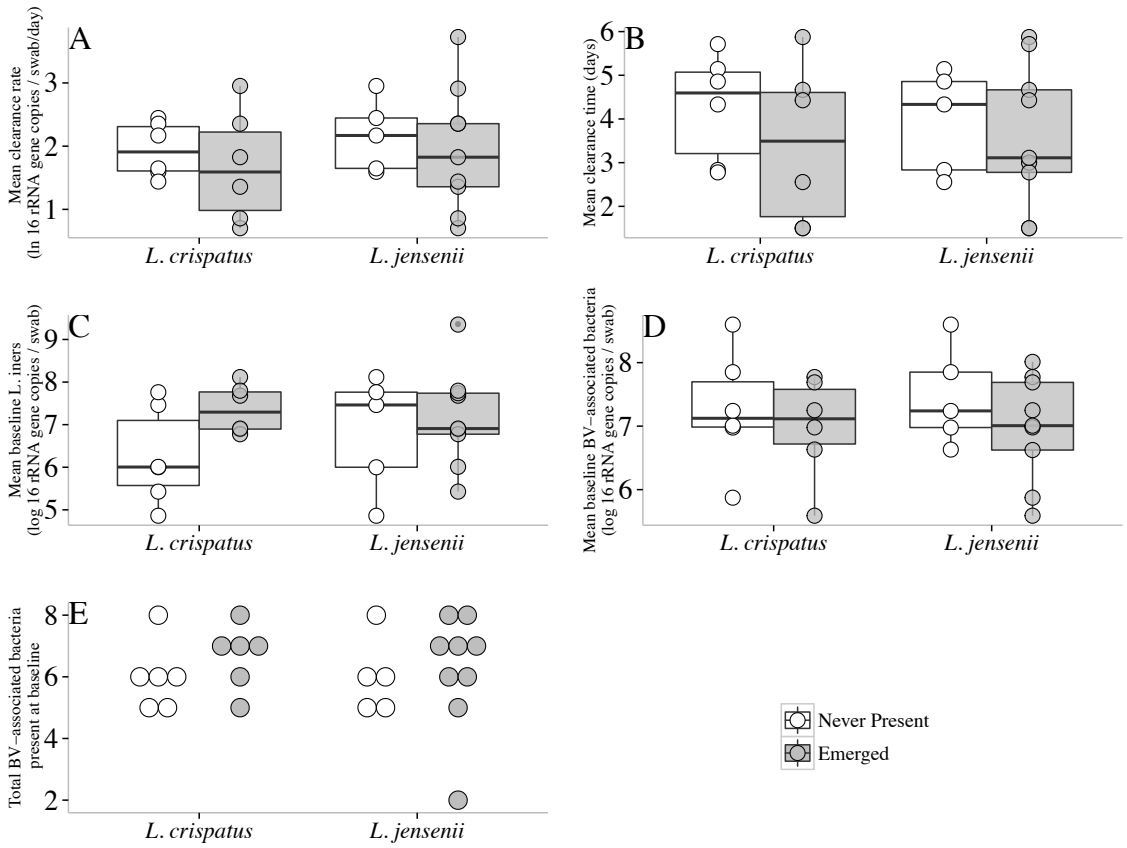

Fig. A1: Emergence of *Lactobacillus* spp. was not associated with factors we analyzed. Comparison of episodes where *Lactobacillus* spp. emerged (gray: 6 episodes for *L. crispatus* and 8 episodes for *L. jensenii*) to episodes with no positive swabs (white: 6 episodes for *L. crispatus* and 5 episodes for *L. jensenii*) across A) mean episode clearance rates, B) mean episode clearance time, C) baseline *L. iners* concentration, D) mean baseline BV-associated bacteria concentration, and E) total BV-associated bacteria present at baseline. Boxes represent the interquartile range (IQR) of the data, the whiskers extend to cover all data within 1.5IQR of the first or third quartile, and circles represent raw data. No distributions were statistically significantly different by group (comparing emergent to never present within *Lactobacillus* spp.) at the 0.1 level using the Kolmogorov-Smirnov two-sample test.

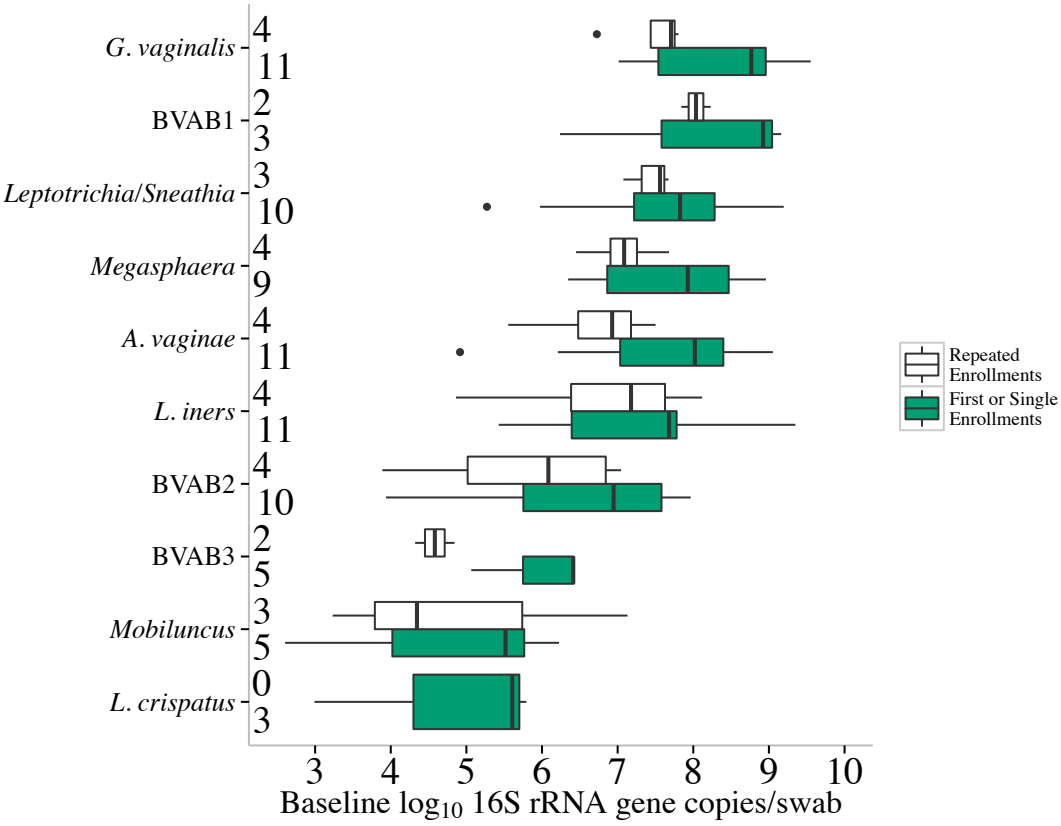

Figure A2: Pre-treatment ranges for bacterial concentration during bacterial vaginosis comparing repeated enrollments with first or single enrollments.

Distributions of pre-treatment $\log_{10}$16S rRNA gene copies/swab for each measured bacteria ordered by increasing mean. Boxes represent the interquartile range (IQR) of the data, the whiskers extend to cover all data within 1.5 IQR of the first or third quartile, and solid dots represent outliers. Sample sizes at baseline are given for each species (out of 11 single/first episodes and 4 repeated episodes). *L. jensenii* was removed due to small sample size (a single episode with baseline $\log_{10}$16S rRNA gene copies/swab count of 6.40).

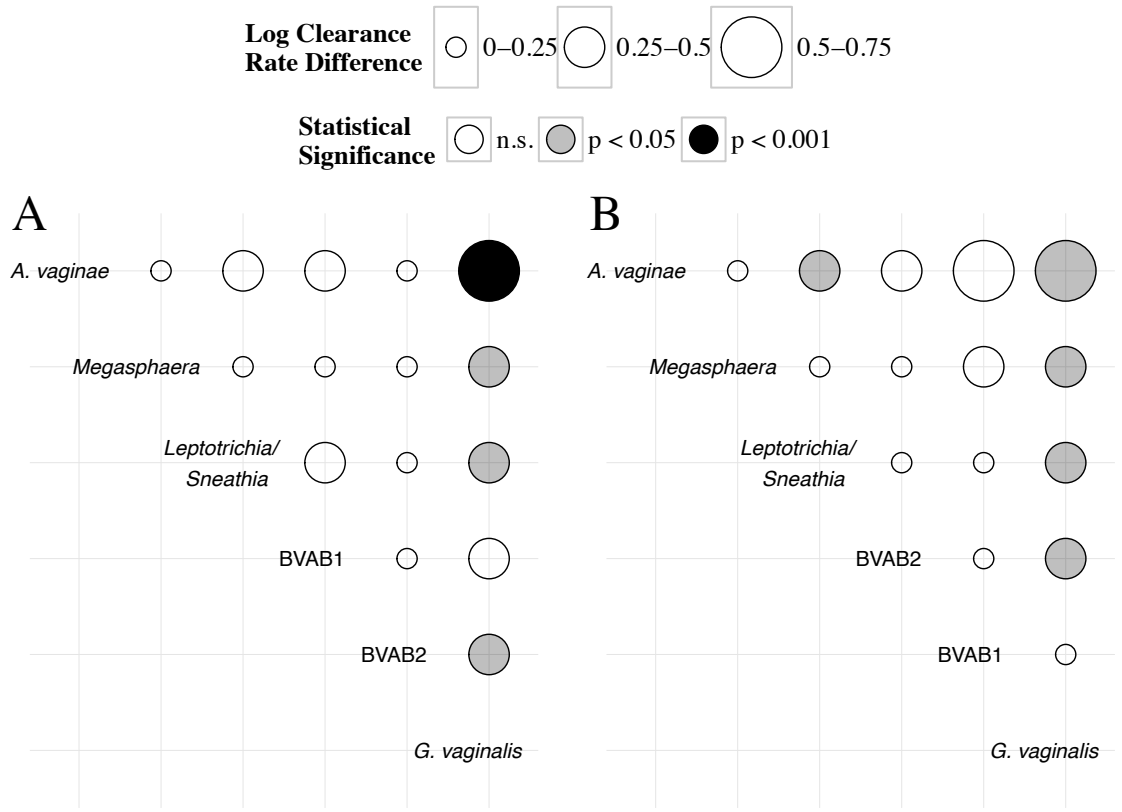

Figure A3: Bacterial clearance rate comparison for A) all episodes (same as Figure 3B) and B) excluding repeated enrollments. Each bubble represents the mean differences in clearance rates ($\log_{10}$ 16S rRNA gene copies/swab/day) between the bacterial group listed to the left and the bacterial group listed below. Rate differences and p-values were estimated using a linear mixed model.

Table A1: Logistic regression models for re-emergence

Predictor[a]	Odds Ratio[b] (95% CI)	Interpretation
Baseline count	1.22 (0.85, 1.79)	Per $\log_{10}$ increase in baseline $\log_{10}$ count
Treatment days until suppression	1.12 (0.84, 1.52)	For each one day increase in treatment time until suppression
Clearance rate	1.68 (0.87, 3.63)	Per 0.5 $\log_{10}$ increase in clearance rate
L. crispatus presence[c]	0.46 (0.12, 1.64)	Compared to no detection of *L. crispatus*
L. jensenii presence[c]	0.83 (0.17, 3.87)	Compared to no detection of *L. jensenii*
Presence[c] of either *L. crispatus* or *L. jensenii*	0.40 (0.08, 1.79)	Compared to no detection of either *Lactobacillus* spp.

[a]Each model fit separately

[b]Times increase in odds of re-emergence

[c]Positive swab anytime during observation period (through day 28)