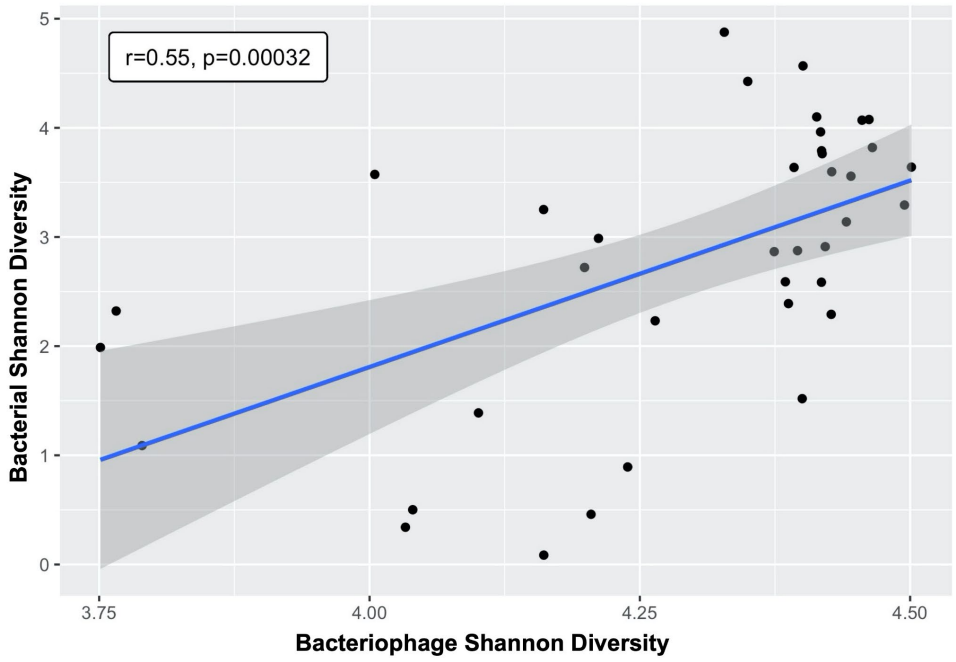
Supplement to:

Transkingdom Analysis of the Female Reproductive Tract Reveals Bacteriophages Form Communities

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Supplementary Figure S1: Transkingdom Correlation between Bacterial and Bacteriophage Diversity in the FRT. Scatter plot showing the correlation with 95% confidence interval (dark grey) of the regression line (blue) between the sample bacterial and bacteriophage Shannon diversity.

Supplementary Table S1: Comparison of Community Group (CG) and Community State Types (CST)

	CG 1	CG 2	CG 3	CG 4	CG 5
Total N	15	54	64	30	75
CST III	8	54	13	1	7
CST IV-A	0	0	0	1	27
CST IV-B	5	0	51	28	36
CST IV-C	2	0	0	0	5
Average Similarity Score	0.0882	0.9180	0.5218	0.3174	0.1330

Average VALENCIA similarity score (not including CG2): 0.2966

Supplementary Table S2A: Statistical values for Figure 5A taxa

	***p*-val (BV)**	**FDR adj. *p*-val (BV)**
Lactobacillus	0.000112	0.000475
Lactobacillus iners	0.000281	0.000955
Gardnerella	0.005973	0.014506
Prevotella	7.70E-05	0.000439
Megasphaera	4.10E-05	0.000439
Atopobium vaginae	0.012197	0.025918
Sneathia	7.30E-05	0.000439
Dialister	0.000362	0.001024

Supplementary Table S2B: Statistical values for Figure 5D taxa

	***p*-val (BV)**	**FDR adj. *p*-val (BV)**
unassigned_*Spounavirinae*	0.001167	0.019058
Bacillus_virus_Camphawk	0.001137	0.019058
unclassified_P22likevirus	0.002274	0.028879
Escherichia_virus_FV3	0.001896	0.027874
Bacillus_virus_Pony	0.000364	0.014546
Yersinia_virus_R1RT	0.000164	0.014546
Synechococcus_phage_S_RIM8	0.00106	0.019058
unclassified_E125virus	0.000535	0.015739
Mycobacterium_virus_Send513	0.001025	0.019058
Cronobacter_virus_GAP31	0.000216	0.014546