



Supplement of

Gut microbiomes of the little free-tailed bat (*Mops pumilus*) show high prevalence of potential bacterial pathogens but limited responses to land cover

Julie Teresa Shapiro et al.

Correspondence to: Julie Teresa Shapiro (julie.teresa.shapiro@gmail.com)

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Supplementary Tables

Table S1. Model selection table for ASV richness, model names, model scales, degrees of freedom (df), loglikelihood, Akaike Information Criterion adjusted for small sample size (AICc), delta AICc (Δ AICc), and model weight.

Model	Spatial scale	df	logLik	AICc	Δ AICc	Model weight
Null model	-	2	-868.3	1740.8	-	0.21
Water cover	Landscape	3	-867.3	1741.0	0.14	0.20
Rural cover	Fine	3	-868.0	1742.3	1.44	0.10
Sugarcane cover	Fine	3	-868.2	1742.6	1.83	0.09
Savanna edge density	Landscape	3	-868.2	1742.7	1.87	0.08
Savanna cover	Fine	3	-868.2	1742.7	1.90	0.08
Sugarcane cover	Landscape	3	-868.2	1742.8	1.97	0.08
Rural cover	Landscape	3	-868.3	1742.9	2.05	0.08
Savanna splitting	Landscape	3	-868.3	1742.9	2.12	0.07

Table S2. Model selection table for phylogenetic diversity (Faith's), model names, model scales, degrees of freedom (df), loglikelihood, Akaike Information Criterion adjusted for small sample size (AICc), delta AICc (Δ AICc), and model weight.

Model	Spatial scale	df	logLik	AICc	Δ AICc	Model weight
Water cover	Landscape	4	-242.1	492.6	-	0.16
Sugarcane cover	Fine	4	-242.1	492.7	0.11	0.15
Rural cover	Fine	4	-242.2	492.8	0.22	0.15
Rural cover	Landscape	4	-242.4	493.2	0.62	0.12
Null	-	3	-242.6	493.5	0.89	0.10
Savanna edge density	Landscape	4	-242.6	493.7	1.08	0.09
Savanna cover	Fine	4	-242.7	494.0	1.35	0.08
Sugarcane cover	Landscape	4	-242.8	494.2	1.53	0.08
Savanna splitting	Landscape	4	-243.0	494.5	1.85	0.06

Table S3. Model selection table for *Bartonella* presence, model names, model scales, degrees of freedom (df), loglikelihood, Akaike Information Criterion adjusted for small sample size (AICc), delta AICc (Δ AICc), and model weight.

Model	Spatial scale	df	logLik	AICc	Δ AICc	Model weight
Savanna splitting	Landscape	2	-8.8	22.4	-	0.37
Sugarcane cover	Landscape	2	-9.1	23.0	0.57	0.27
Savanna cover	Fine	2	-9.6	24.1	1.63	0.16
Null	-	1	-11.8	25.8	3.34	0.07
Rural cover	Fine	2	-11.3	27.4	4.94	0.03
Water cover	Landscape	2	-11.3	27.4	4.95	0.03
Sugarcane cover	Fine	2	-11.3	27.4	5.01	0.03
Rural cover	Landscape	2	-11.7	28.2	5.78	0.02
Savanna edge density	Landscape	2	-11.7	28.2	5.81	0.02

Table S4. Model selection table for *Campylobacter* presence, model names, model scales, degrees of freedom (df), loglikelihood, Akaike Information Criterion adjusted for small sample size (AICc), delta AICc (Δ AICc), and model weight.

Model	Spatial scale	df	logLik	AICc	Δ AICc	Model weight
Null	-	1	-7.9	18.1	-	0.22
Rural cover	Landscape	2	-6.9	18.6	0.45	0.18
Savanna splitting	Landscape	2	-6.9	18.7	0.56	0.17
Savanna edge density	Landscape	2	-7.5	19.8	1.65	0.10
Water cover	Landscape	2	-7.6	20.1	2.02	0.08
Rural cover	Fine	2	-7.7	20.3	2.18	0.07
Sugarcane cover	Fine	2	-7.8	20.4	2.27	0.07
Sugarcane cover	Landscape	2	-7.9	20.6	2.53	0.06
Savanna cover	Fine	2	-7.9	20.7	2.54	0.06

Table S5. Model selection table for *Mycoplasma* presence, model names, model scales, degrees of freedom (df), loglikelihood, Akaike Information Criterion adjusted for small sample size (AICc), delta AICc (Δ AICc), and model weight.

Model	Spatial scale	df	logLik	AICc	Δ AICc	Model weight
Null	-	1	-6.2	14.6	-	0.25
Savanna splitting	Landscape	2	-5.5	15.8	1.26	0.13
Savanna cover	Fine	2	-5.5	15.9	1.31	0.13
Savanna edge density	Landscape	2	-5.8	16.5	1.95	0.09
Sugarcane cover	Landscape	2	-5.9	16.7	2.09	0.09
Rural cover	Fine	2	-6.0	16.9	2.31	0.08
Sugarcane cover	Fine	2	-6.1	17.0	2.39	0.08
Water cover	Landscape	2	-6.1	17.0	2.40	0.08
Rural cover	Landscape	2	-6.1	17.0	2.43	0.07

Table S6. Model selection table for *Rickettsia* presence, model names, model scales, degrees of freedom (df), loglikelihood, Akaike Information Criterion adjusted for small sample size (AICc), delta AICc (Δ AICc), and model weight.

Model	Spatial scale	df	logLik	AICc	Δ AICc	Model weight
Null	-	1	-11.5	25.3	-	0.20
Savanna cover	Fine	2	-10.4	25.7	0.41	0.16
Savanna splitting	Landscape	2	-10.6	26.1	0.77	0.13
Rural cover	Fine	2	-10.6	26.1	0.77	0.13
Sugarcane cover	Landscape	2	-10.7	26.3	1.00	0.12
Water cover	Landscape	2	-11.0	26.9	1.61	0.09
Savanna edge density	Landscape	2	-11.0	26.9	1.63	0.09
Rural cover	Landscape	2	-11.5	27.9	2.58	0.05
Sugarcane cover	Fine	2	-11.5	27.9	2.58	0.05

Table S7. Model selection table for *Salmonella* presence, model names, model scales, degrees of freedom (df), loglikelihood, Akaike Information Criterion adjusted for small sample size (AICc), delta AICc (Δ AICc), and model weight.

Model	Spatial scale	df	logLik	AICc	Δ AICc	Model weight
Null	-	1	-11.5	25.3	-	0.23
Rural cover	Fine	2	-10.7	26.2	0.91	0.15
Sugarcane cover	Fine	2	-10.8	26.4	1.10	0.13
Savanna splitting	Landscape	2	-11.0	26.8	1.53	0.11
Water cover	Landscape	2	-11.2	27.2	1.90	0.09
Sugarcane cover	Landscape	2	-11.2	27.3	1.95	0.09
Savanna cover	Fine	2	-11.4	27.7	2.43	0.07
Savanna edge density	Landscape	2	-11.5	27.8	2.49	0.07
Rural cover	Landscape	2	-11.5	27.9	2.58	0.06

Table S8. Marginal effects and significance of terms in the forward-selected global distance-based redundancy analysis (db-RDA), including degrees of freedom (df), sum of squares, F statistic, and p value.

Variable	Spatial scale	df	Sum of squares	F	p-value
Rural cover	Fine	1	0.67	1.67	0.001
Sugarcane cover	Landscape	1	0.54	1.35	0.005
Savanna cover	Fine	1	0.69	1.72	0.001
Savanna splitting	Landscape	1	0.51	1.25	0.03
Residuals	-	67	27.0	-	-

Supplementary Figures

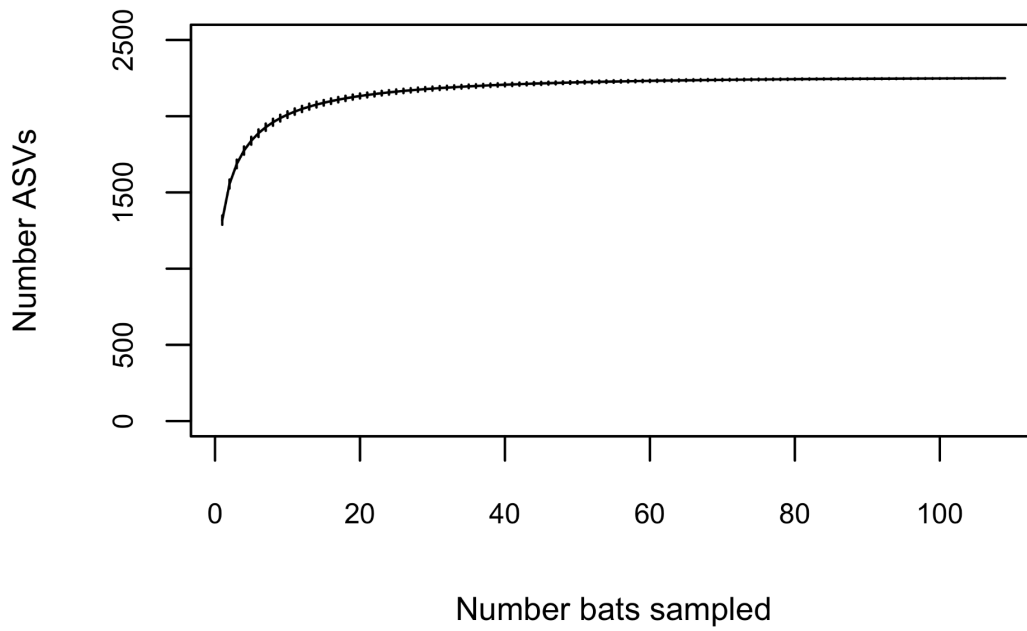


Figure S1. Sample-based rarefaction curve showing the accumulation of ASVs (y axis) as individuals are added (x axis). Vertical lines indicate the 95% confidence interval of the species accumulation curve.

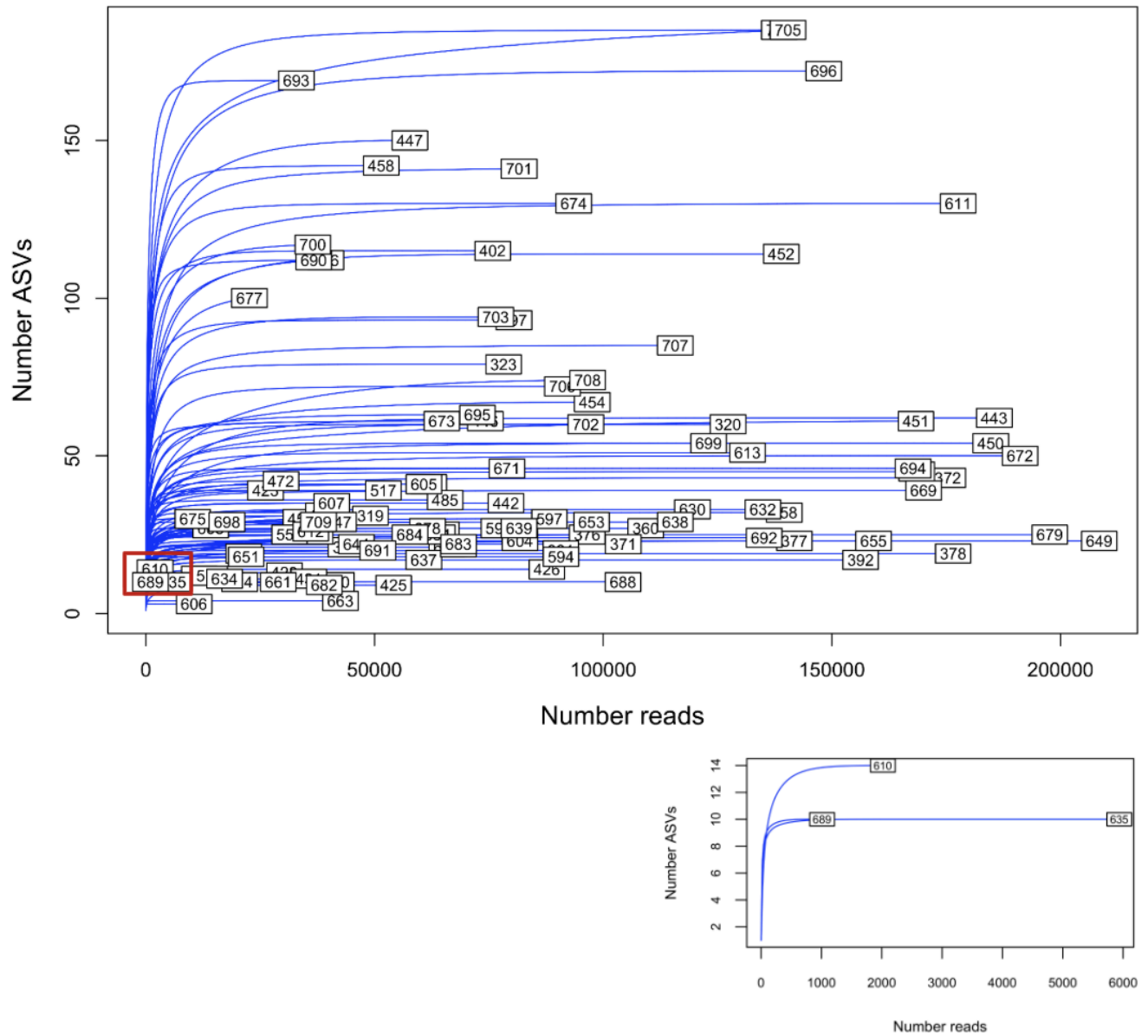


Figure S2. Sample-based rarefaction curve for each individual bat in this study showing the accumulation of ASVs (y axis) as sequencing reads are added (x axis). Vertical lines indicate the 95% confidence interval of the species accumulation curve. The bottom panel shows a zoom for the three samples outlined by the red box in the lower-left corner of the plot.

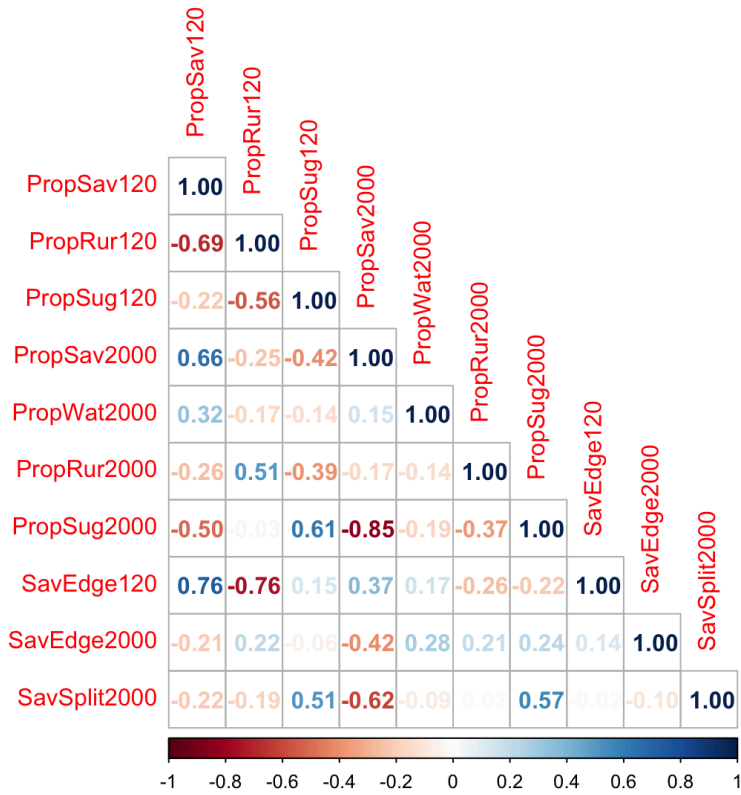


Figure S3. Correlation between land-cover composition and configuration metrics at the fine and landscape scales, indicated by the suffix 120 and 2000, respectively.

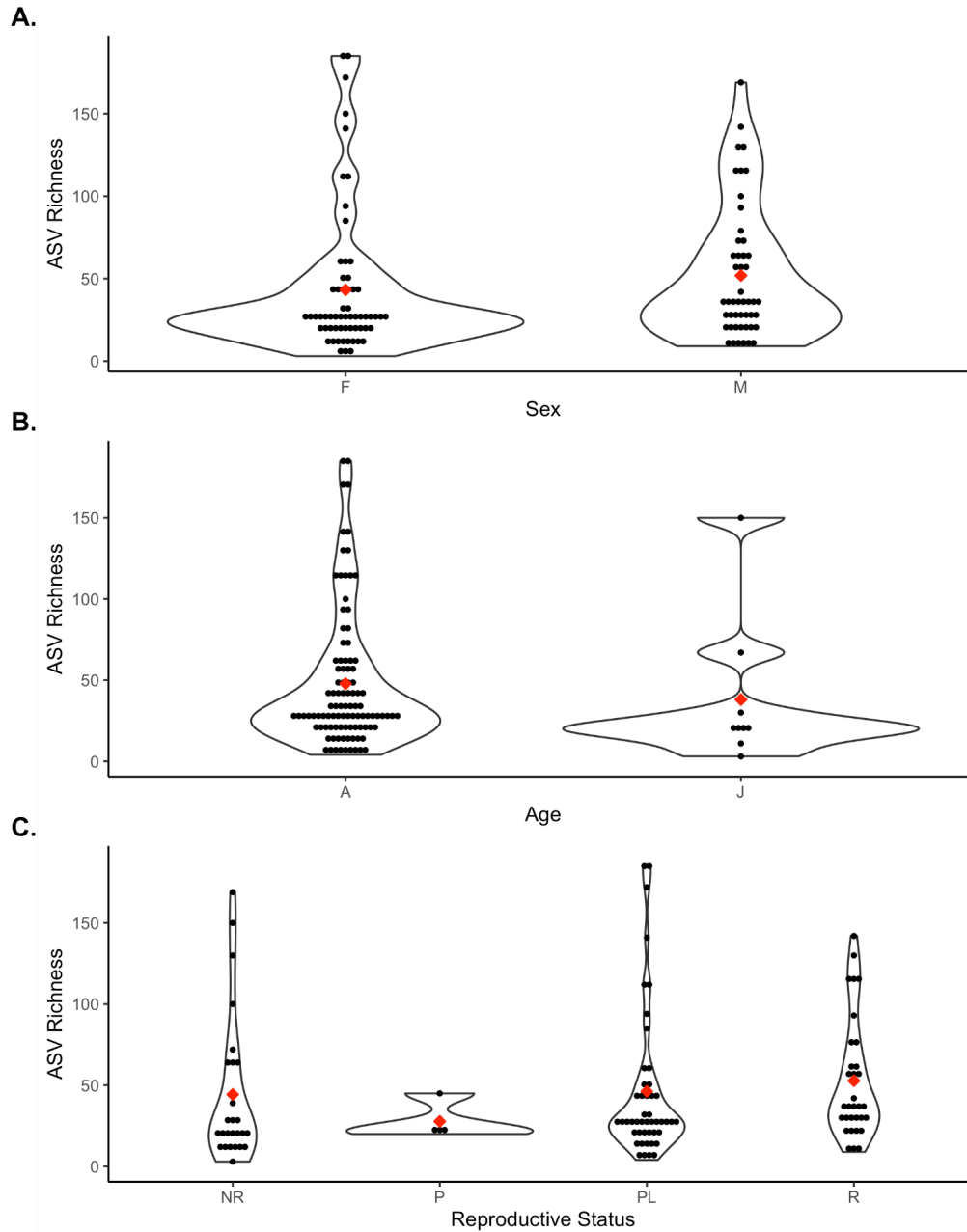


Figure S4. Violin plots of bacterial ASV richness by: A. Sex (F = Female, M = Male), B. Age (A = Adult, J = Juvenile), C. Reproductive status (NR = Non-reproductive male and female, P = Pregnant, PL = Post-lactating, R = Reproductive male). Each dot represents an individual bat, the red diamonds indicate the mean bacterial species richness for each group.

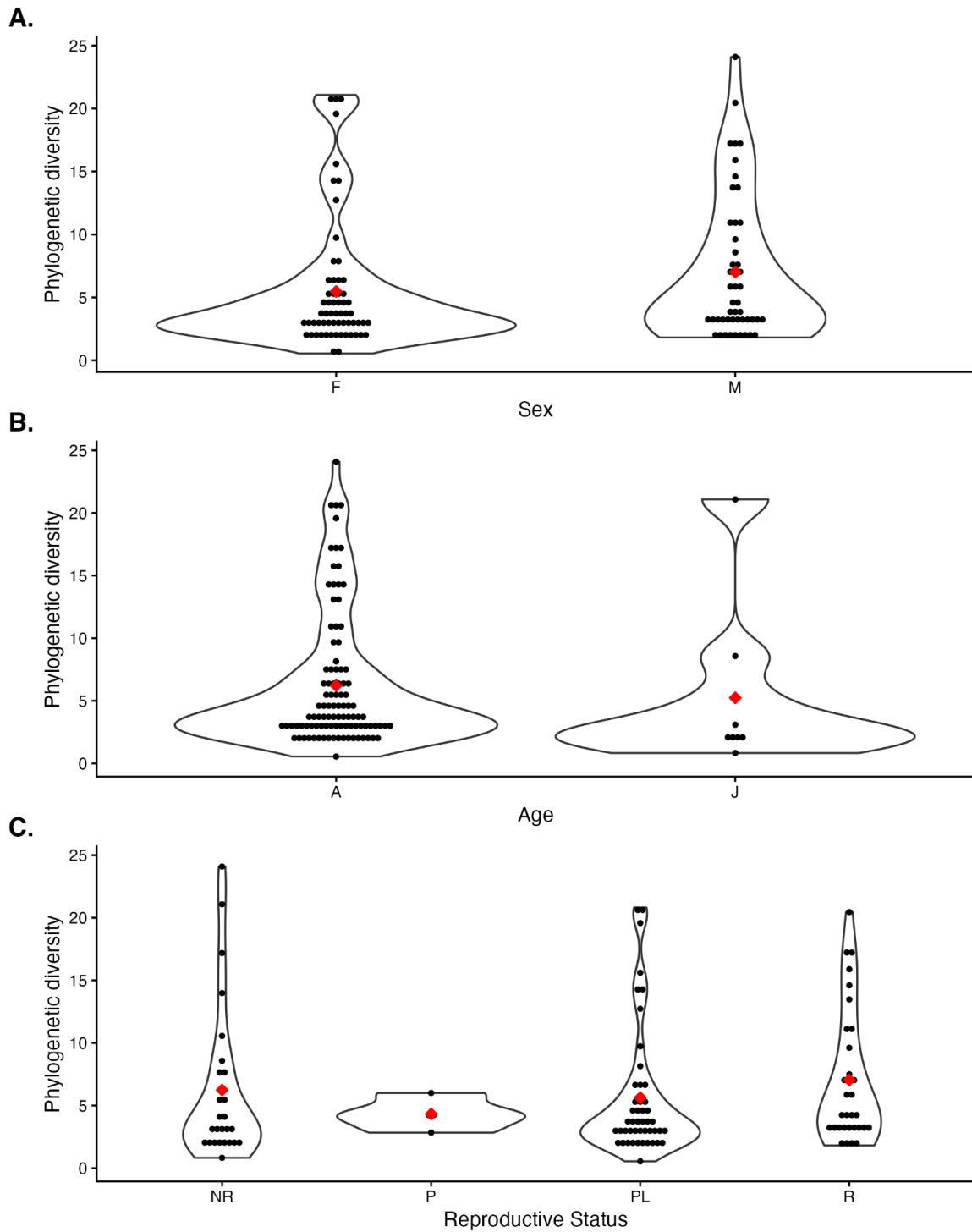


Figure S5. Violin plots of bacterial phylogenetic diversity by: A. Sex (F = Female, M = Male), B. Age (A = Adult, J = Juvenile), C. Reproductive status (NR = Non-reproductive male and female, P = Pregnant, PL = Post-lactating, R = Reproductive male). Each dot represents an individual bat, the red diamonds indicate the mean bacterial phylogenetic diversity (Faith's D) for each group.

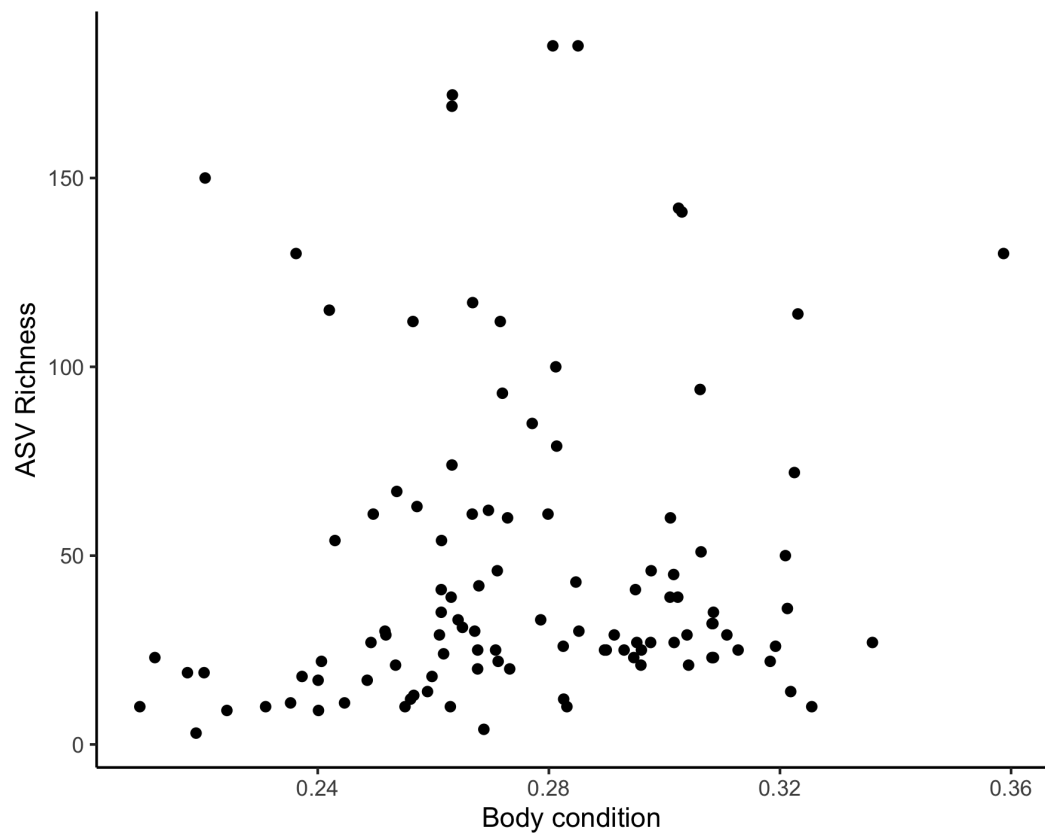


Figure S6. Correlation between bat body condition and ASV richness.

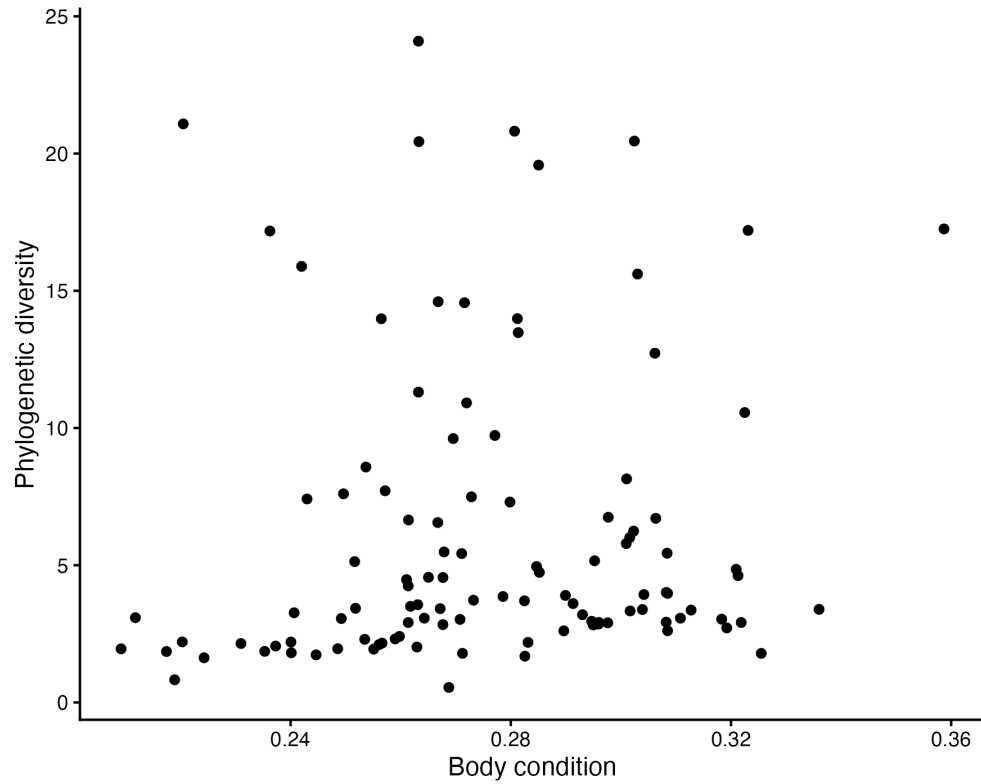


Figure S7. Correlation between bat body condition and phylogenetic diversity (Faith's D).

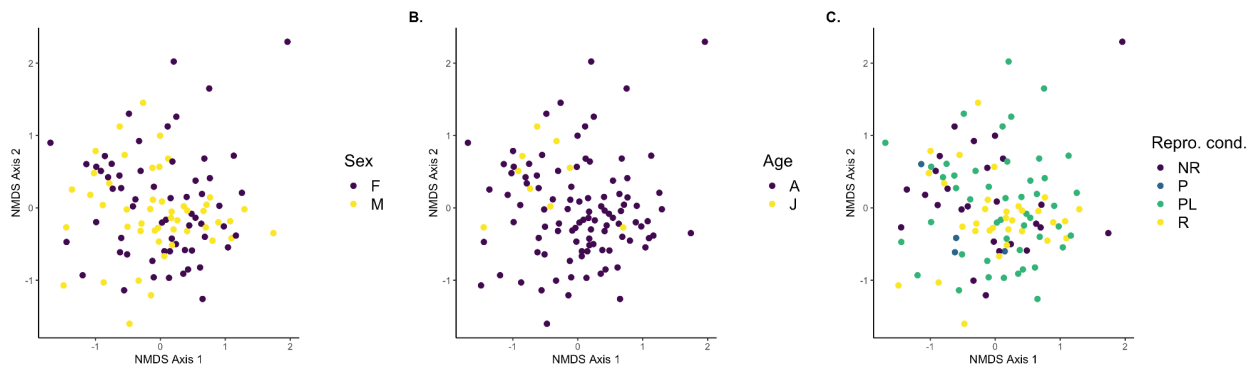


Figure S8. Non-metric multidimensional scaling (NMDS) plots showing variation in bacterial communities between bats based on A. sex, B. age, C. reproductive condition (non-reproductive, pregnant, post-lactating, reproductive male). Each point represents an individual bat and each color represents the characteristics. Values are based on Jaccard's distance.