

Table S4. Alpha and beta diversity by collection method using different minimum read thresholds and normalization methods

Sequence Read Threshold	Normalization Method	Shannon	Inverse Simpson	Observed Richness	Pielou's Evenness	Bray Curtis (R²)	WUF (R²)	UUF (R²)
100 reads	Rarefaction	.49	.72	.04	.17	.01 (.04)	.59 (.03)	.01 (.04)
	Relative Abundance	.24	.93	.006	.013	.007 (.04)	.40 (.03)	.002 (.07)
	DESeq2	.24	.93	.006	.013	.01 (.04)	.55 (.03)	.003 (.07)
*300 reads	Rarefaction	.19	.49	.01	.094	.01 (.05)	.10 (.06)	.003 (.09)
	*Relative Abundance	.11	.79	.002	.011	.005 (.06)	.31 (.04)	.01 (.07)
	DESeq2	.11	.79	.002	.011	.02 (.06)	.25 (.05)	.001 (.11)
700 reads	Rarefaction	.07	.46	.01	.12	.002 (.07)	.07 (.07)	.001 (.14)
	Relative Abundance	.10	.64	.005	.032	.006 (.07)	.24 (.06)	.003 (.13)
	DESeq2	.10	.64	.005	.032	.008 (.07)	.16 (.06)	.001 (.14)

1000 reads	Rarefaction	.02	.57	.004	.13	.008 (.08)	.19 (.08)	.001 (.17)
	Relative Abundance	.04	.65	.004	.055	.008 (.09)	.13 (.08)	.002 (.15)
	DESeq2	.04	.65	.004	.055	.016 (.08)	.06 (.09)	.001 (.16)
2000 reads	Rarefaction	.08	.94	.016	.11	.04 (.10)	.10 (.11)	.003 (.19)
	Relative Abundance	.11	.94	.016	.11	.03 (.10)	.06 (.12)	.003 (.16)
	DESeq2	.11	.94	.016	.11	.07 (.10)	.15 (.11)	.003 (.17)

P values for Wilcoxon signed-rank test and for PERMANOVA are reported to demonstrate statistical significance of alpha and beta diversity measures between urine collected by cystocentesis versus midstream voiding. R^2 values are listed in parentheses for beta diversity measures. *P* values < .05 are in bold. Each analysis is designated by a number of reads, which represents the minimum sequence read threshold that samples must possess to be included in that analysis. The number is followed by rarefaction, relative abundance, or DESeq2 to indicate which normalization method was used. The primary analysis is designated by an asterisk (*). WUF = Weighted UniFrac; UUF = Unweighted UniFrac.