Table S1. Summary of sequencing output, DADA2 processing, and final dataset characteristics used for downstream analyses.

Analysis Step	Parameter	Value
Sequencing input	Samples included in downstream analyses	29
	Read pairs entering DADA2, total	2,708,855
	Read pairs per sample, median (range)	89,763 (50,695-172,346)
DADA2 processing	Quality-filtered reads	2,579,792 (95.2%)
	Denoised reads	2,409,864 (89.0%)
	Merged reads	2,115,509 (78.1%)
	Non-chimeric reads	1,776,928 (65.6%)
Feature table	ASVs generated by DADA2	30,646
Final dataset used for downstream analyses	ASVs retained after taxonomic filtering	4,433
	Reads retained in the final feature table	1,299,088
	Rarefaction depth	10,000 reads/sample
	Samples retained after rarefaction	29/29 (100%)