Supplementary Material: Taxonomic Resolution and Unclassified Fractions — *Culicoides reevesi* Bacteriome

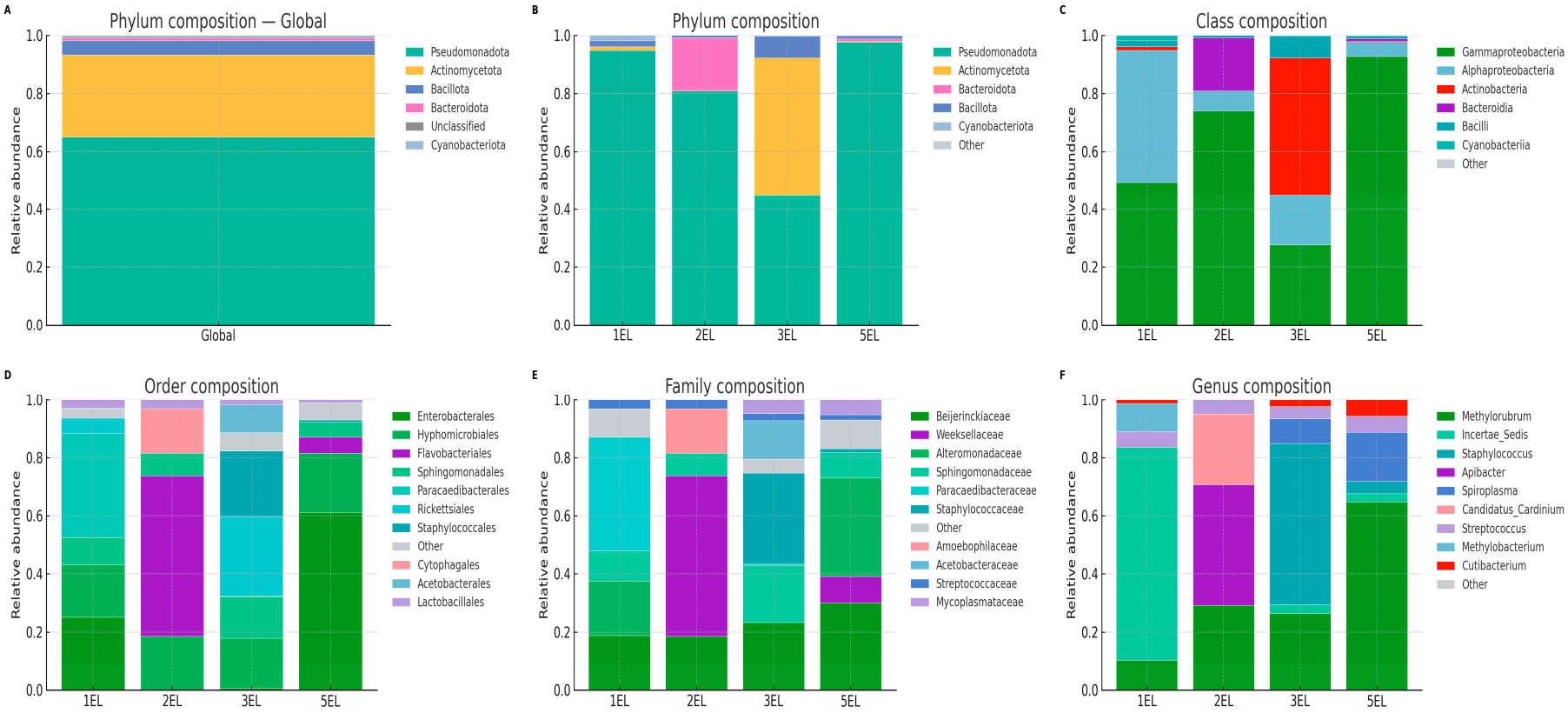


Figure S1. Rank-resolved bacterial composition of *Culicoides reevesi*. (A) Global relative abundance at the Phylum across all pools. (B–F) Pool-specific relative abundances were summarized across Phylum, Class, Order, Family, and Genus (1EL, 2EL, 3EL, 5EL). Stacked bars show relative abundances; low-abundance taxa were grouped as Others. Species-level assignments were not included because the SILVA 138–99 classifier for 515F/806R is validated up to Genus

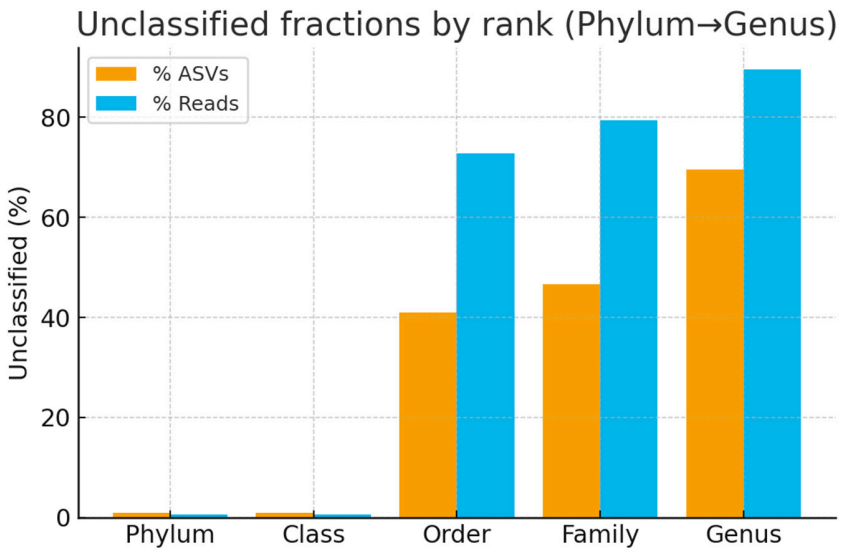


Figure S2. Unclassified fractions by rank (Phylum→Genus). Percentage of *Unclassified* assignments summarized across pools, reported by ASVs (orange) and by reads (blue). Bars show the fraction at each taxonomic rank from Phylum to Genus.

Supplementary Material – Diversity Analysis of the *Culicoides reevesi* bacteriome

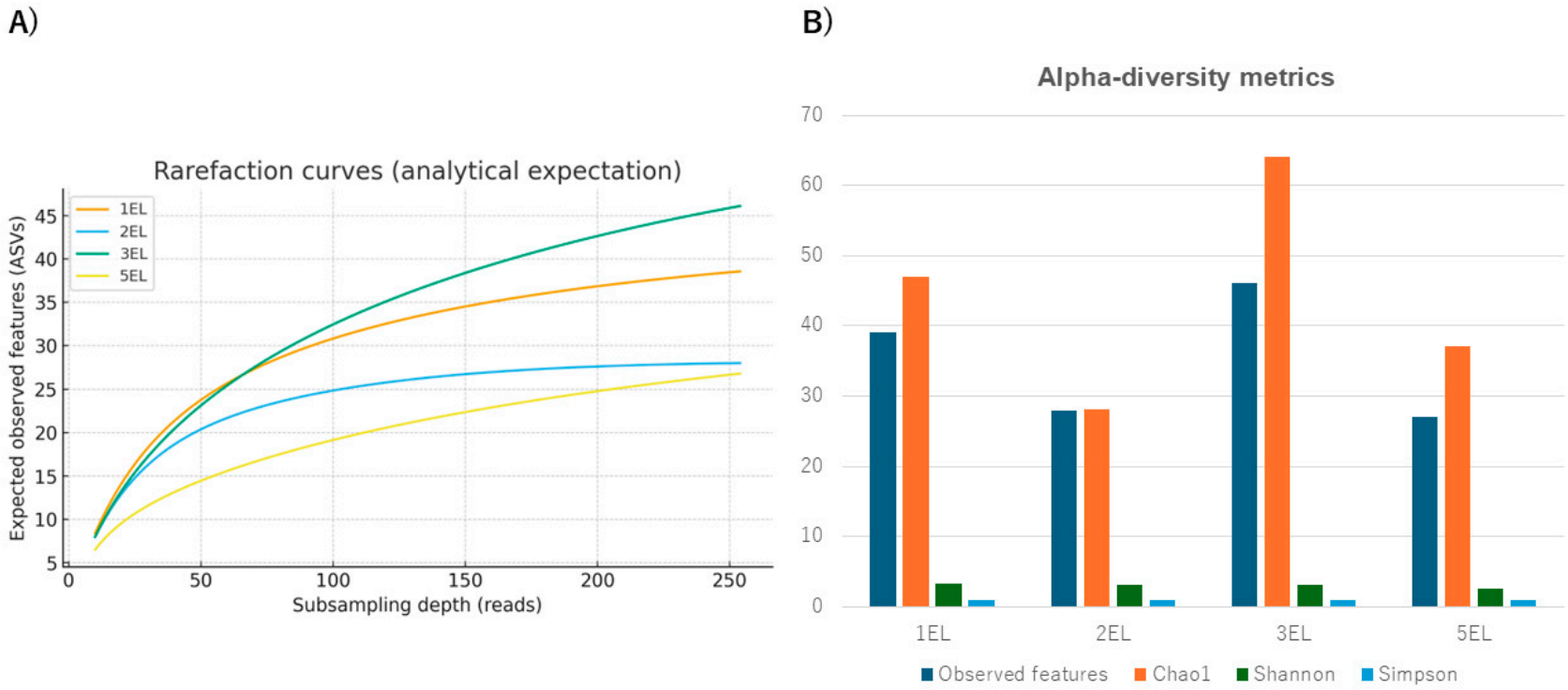


Figure S3. Rarefaction and alpha diversity. Rarefaction curves of expected Observed ASVs up to a subsampling depth of 254 reads. (B) Alpha-diversity at depth 254 (Observed, Chao1, Shannon, Simpson [1–D]) for pools 1EL, 2EL, 3EL, and 5EL. Values were calculated from the rarefied feature table (depth = 254).

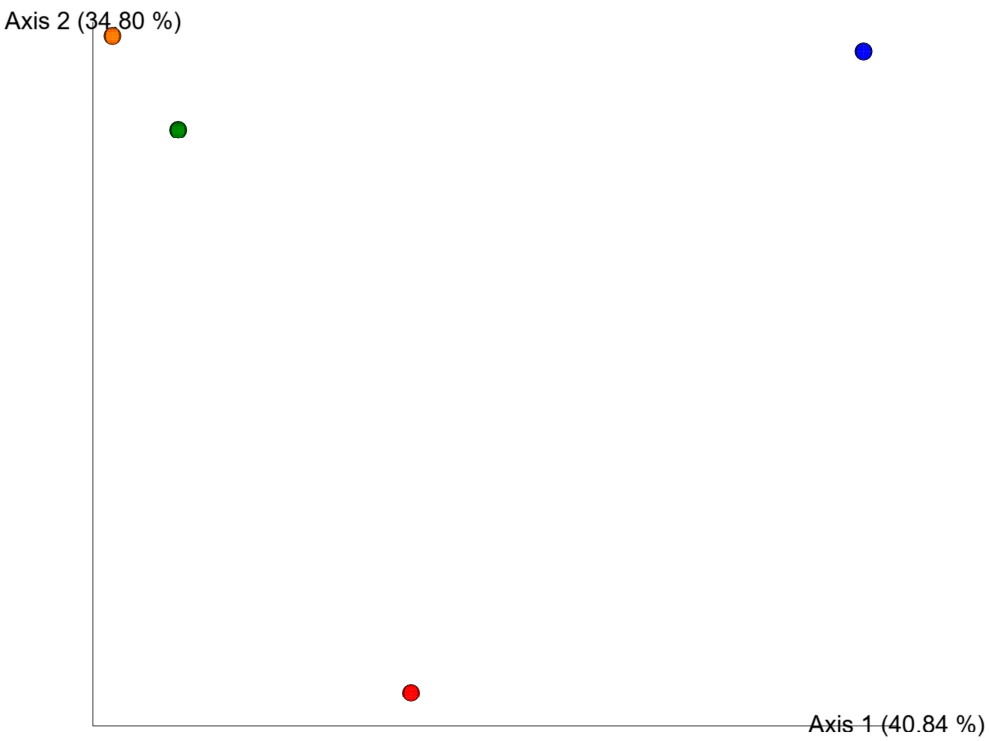


Figure S4. Principal coordinates analysis (PCoA) based on Bray–Curtis dissimilarity. Axis labels indicate the proportion of variance explained.