

# DIVERSITY, ABUNDANCE, AND PREVALENCE OF INFANT GUT BIFIDOBACTERIA ACROSS DIVERSE POPULATIONS AND FEEDING PRACTICES



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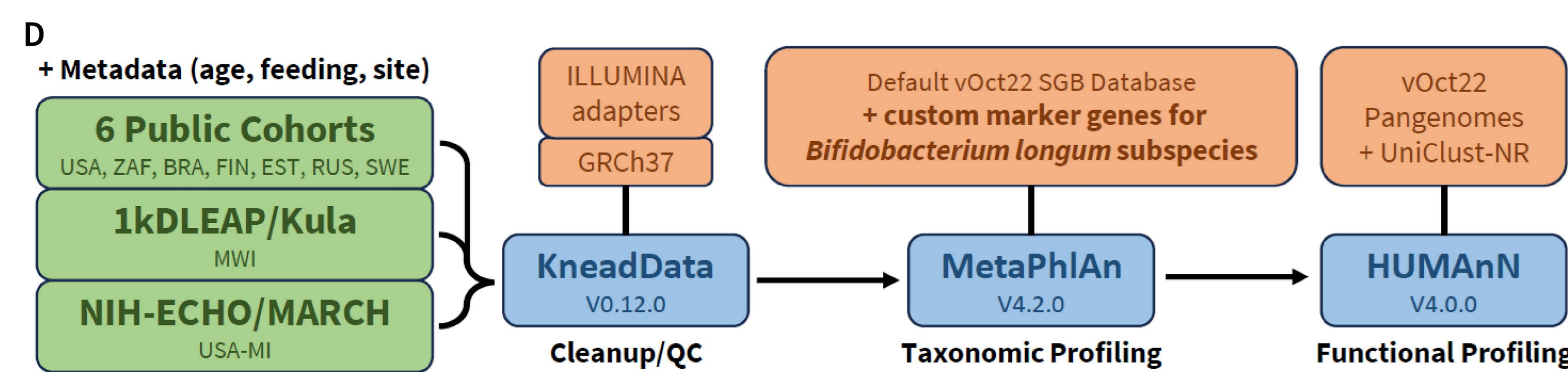
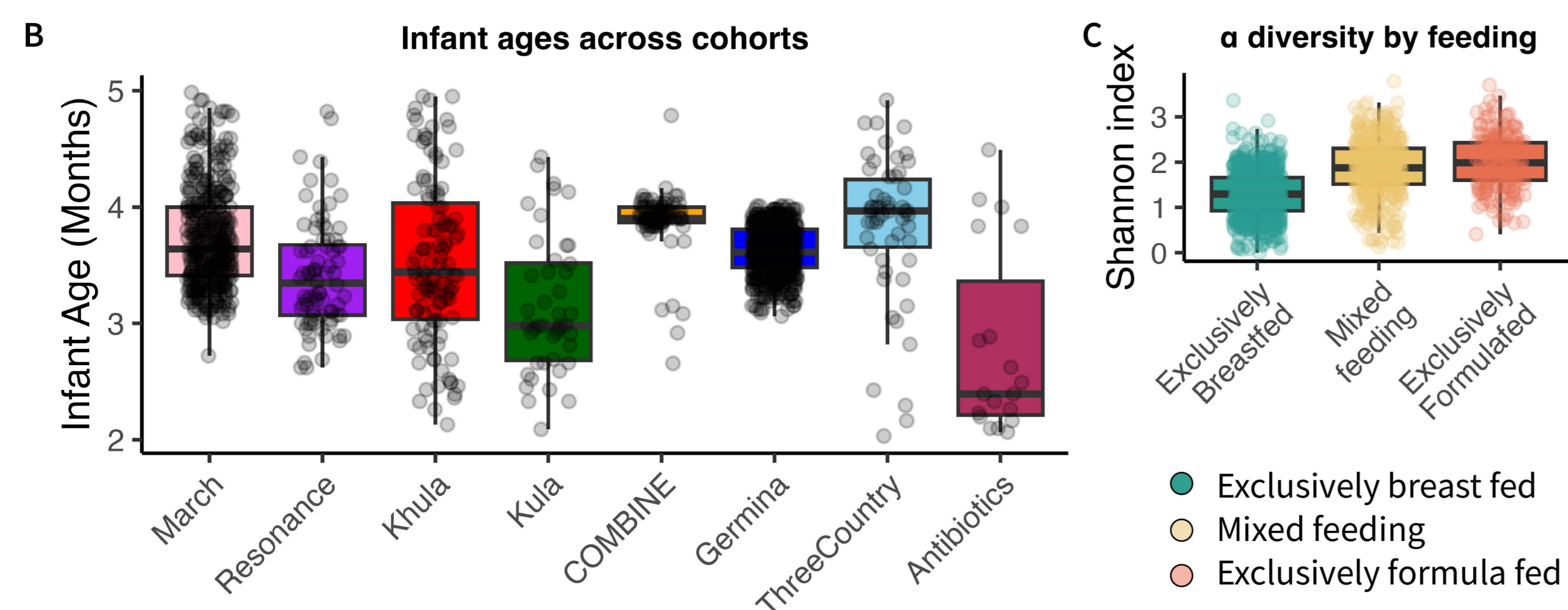
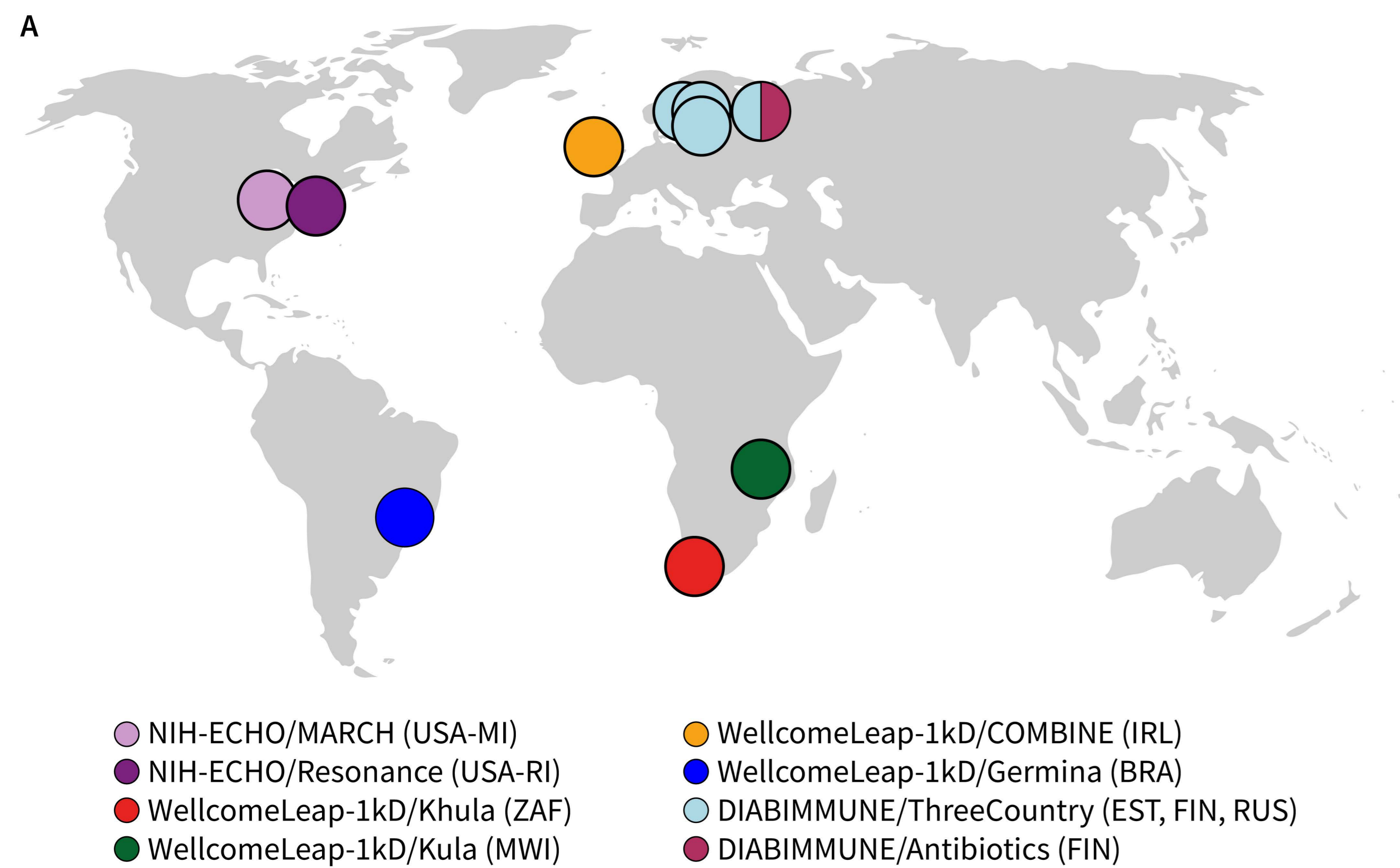
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## GOAL: to perform a global-level survey of *Bifidobacterium* community structure focusing on dominant HMO-utilizing species

The early-life gut microbiome is shaped by environmental exposures during infancy, with human milk oligosaccharides (HMOs) selectively enriching HMO-utilizing taxa such as *Bifidobacterium* spp.

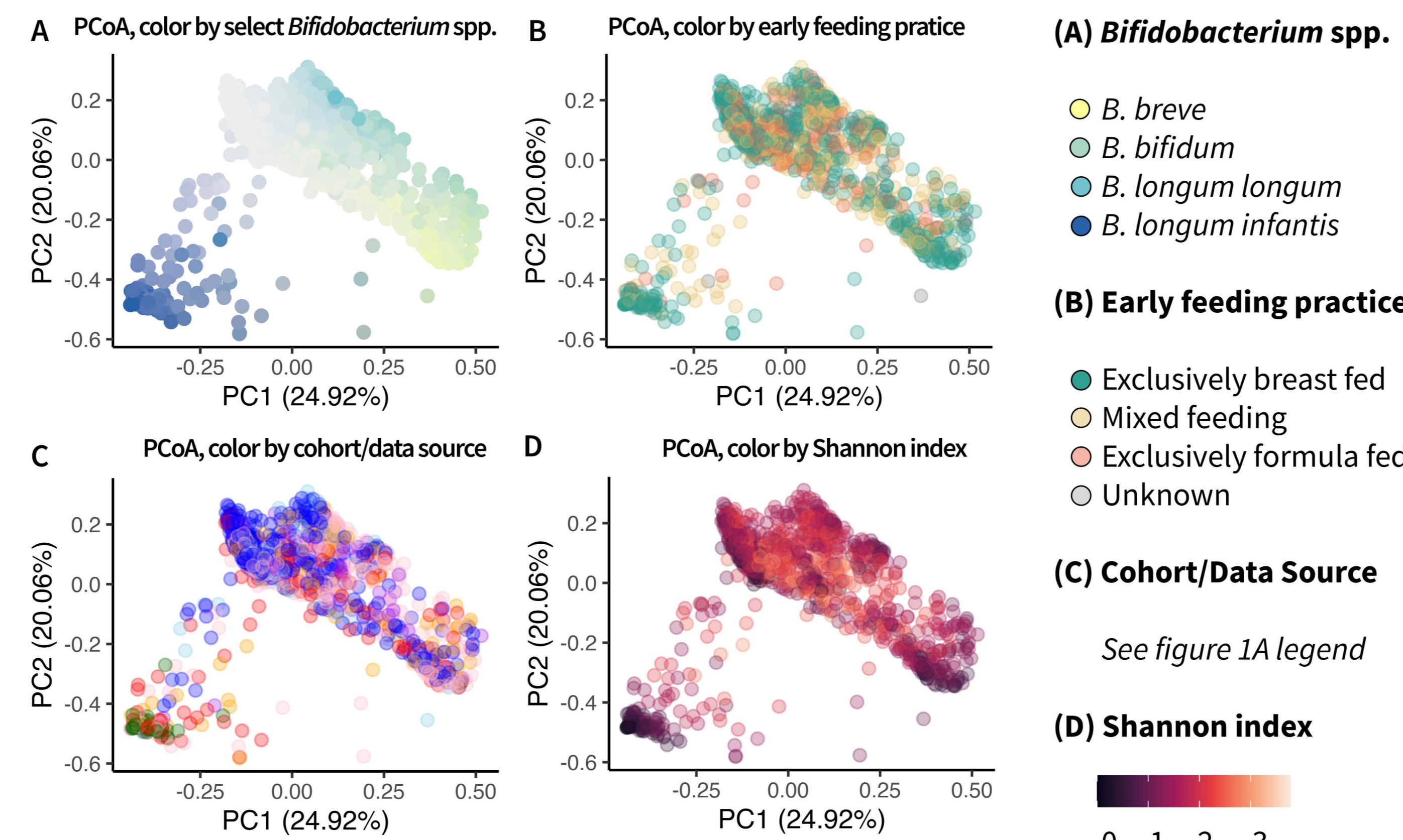
Here, we use subspecies-level metagenomic profiling across >1,500 infants from diverse global cohorts to investigate patterns of coexistence and exclusion among dominant HMO-utilizing Bifidobacteria.

## Diverse infant cohorts enable global-scale profiling of HMO-utilizing *Bifidobacterium* spp.



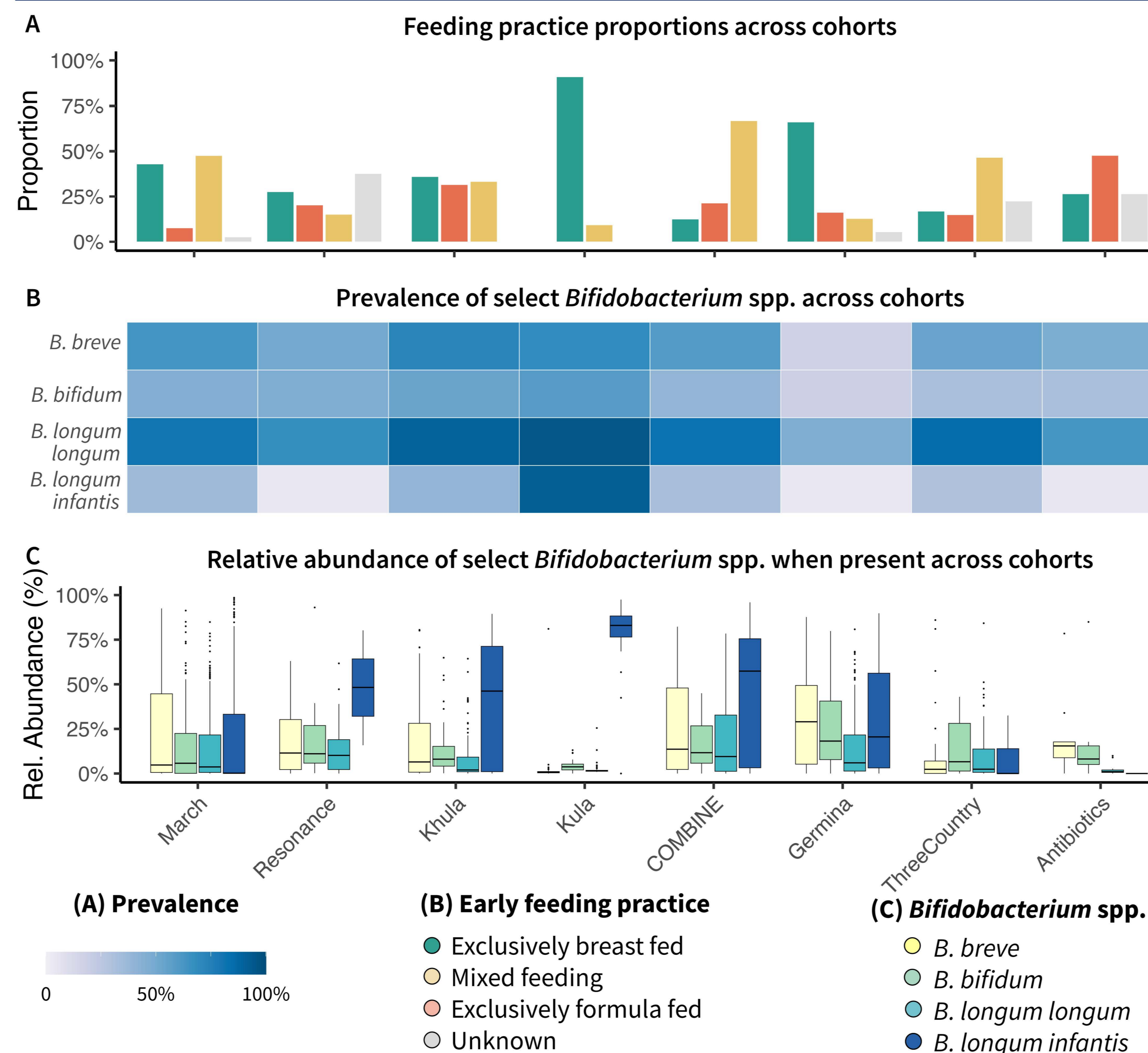
**Figure 1. Cohort and methodology description for the global survey into *Bifidobacterium* ecology.** (A) Approximate geographical sources of cohort data. (B) Infant age (in months) at biospecimen collection. Each participant contributed a single sample. (C) Alpha diversity measured as Shannon Index for every gut microbial community, stratified by infant feeding practice. (D) Data pooling and metagenomic profiling pipeline. Data from 8 cohorts underwent taxonomic and functional profiling with the BioBakery 4 suite.

## β-diversity landscape reflects community dominance by distinct *Bifidobacterium* spp.



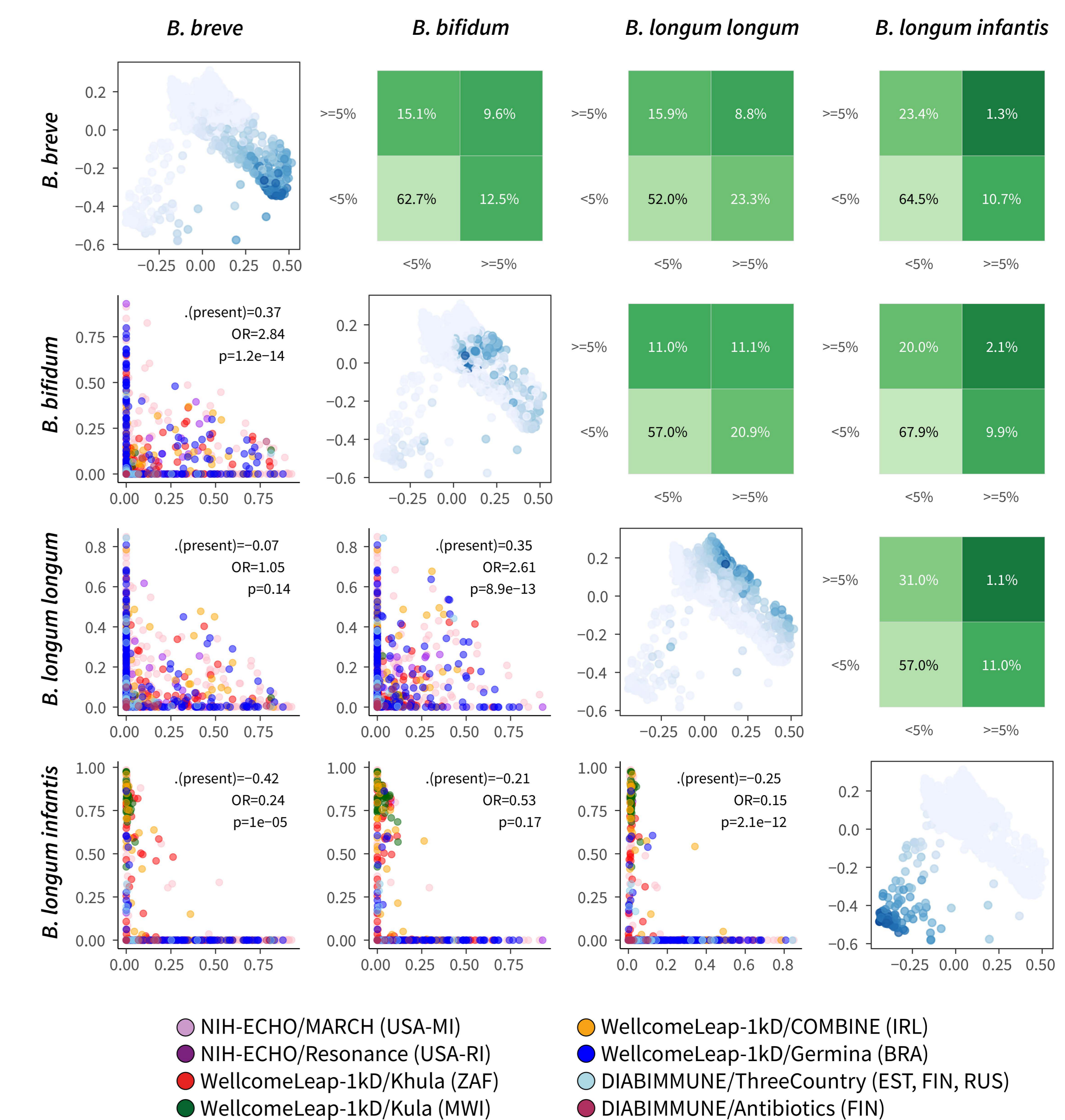
**Figure 2. Subspecies-level profiling of *Bifidobacterium* spp. enables emergence of unique ecological patterns.** β-diversity ordination by nonmetric multidimensional scalins (nMDS) of Bray-Curtis distances between the 1,500 profiled metagenomes, colored by (A) Select *Bifidobacterium* spp; (B) Data source/cohort; (C) Feeding practice (3-category: Exclusive Breast fed, Mixed, and Exclusive Formulafed); (D) Shannon Index

## *Bifidobacterium longum* subsp. *infantis* follows unique compositional patterns across cohorts



**Figure 3. Abundance patterns for select *Bifidobacterium* spp. across cohorts.** (A) Feeding practice proportion across cohorts. (B) Prevalence of select *Bifidobacterium* spp. across cohorts. (C) Average relative abundance of select *Bifidobacterium* spp. across cohorts. (A), (B), and (C) share the same x-axis.

## Communities dominated by *BL. infantis* are “exclusive clubs” depleted of other Bifidobacteria



**Figure 4. Subspecies-level data support competitive relationships among key *Bifidobacterium* spp. in the infant gut.** (Main Diagonal) PCoA plots colored by relative abundance of each species. (Lower Triangle) intra-sample abundance; and (Upper Triangle) co-occurrence matrix for each pair of *Bifidobacterium* spp. A cutoff of 5% was applied to define “occurrence” of a certain species in a gut microbial community.

## Next steps

Future work will focus on experimentally characterizing candidate competitive mechanisms underlying these exclusionary community structures, including bacteriocin-associated systems and other strategies that may selectively suppress competing HMO-utilizing taxa.

Complementary co-culture experiments may help explain how certain bifidobacteria resist exclusion or re-establish within *B. longum infantis*-dominated communities.

Across all studied populations, we observed conserved patterns of ecological partitioning among HMO-utilizing bifidobacteria, particularly reflected in the contrasting and rarely co-dominant distributions of *B. longum infantis*, *B. longum longum* and *B. breve*; *B. infantis*-dominated communities consistently depleted of other HMO-utilizing bifidobacteria, including more broadly co-occurring taxa such as *B. bifidum*.