



# Spatiotemporal dynamics of early life microbiome colonization in a canine model

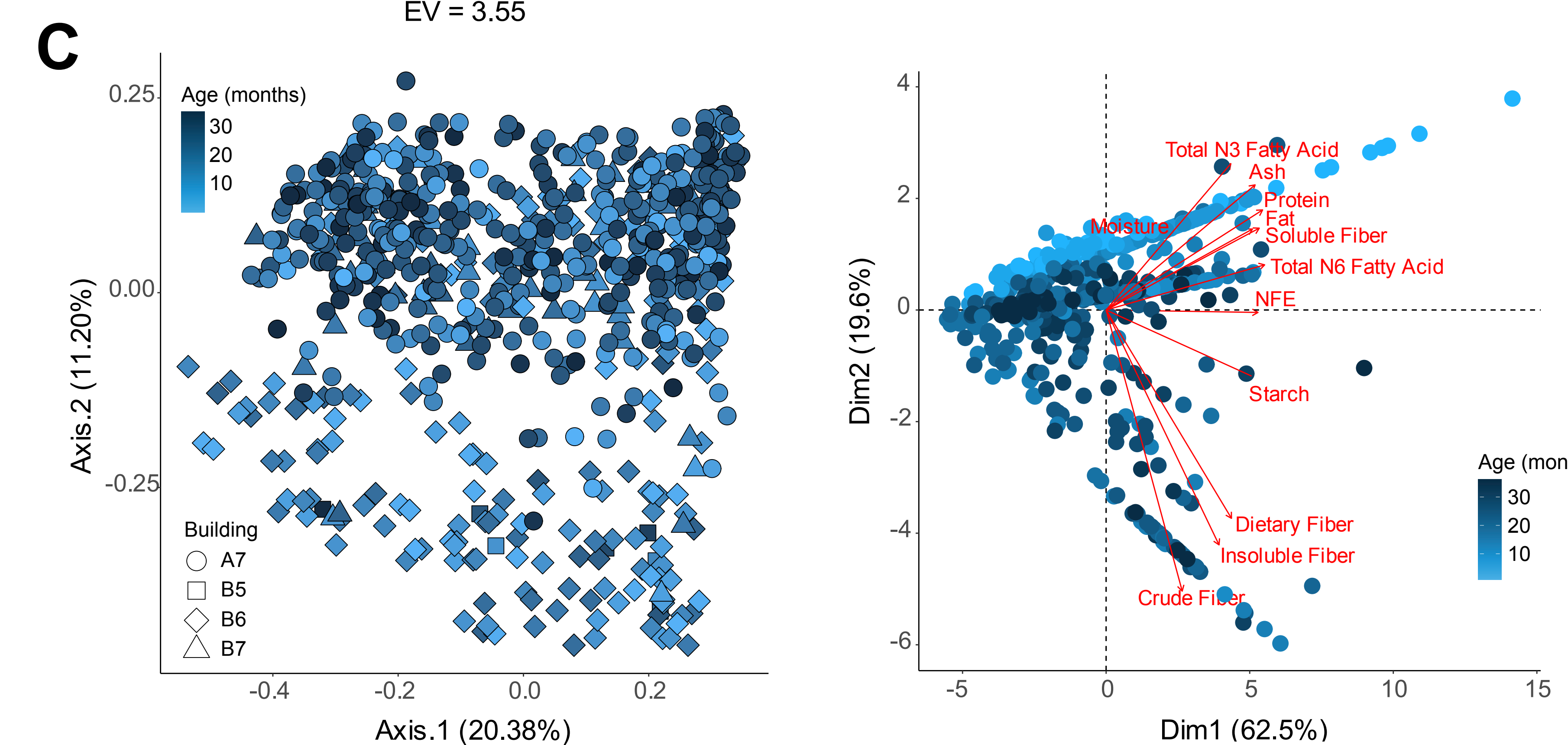
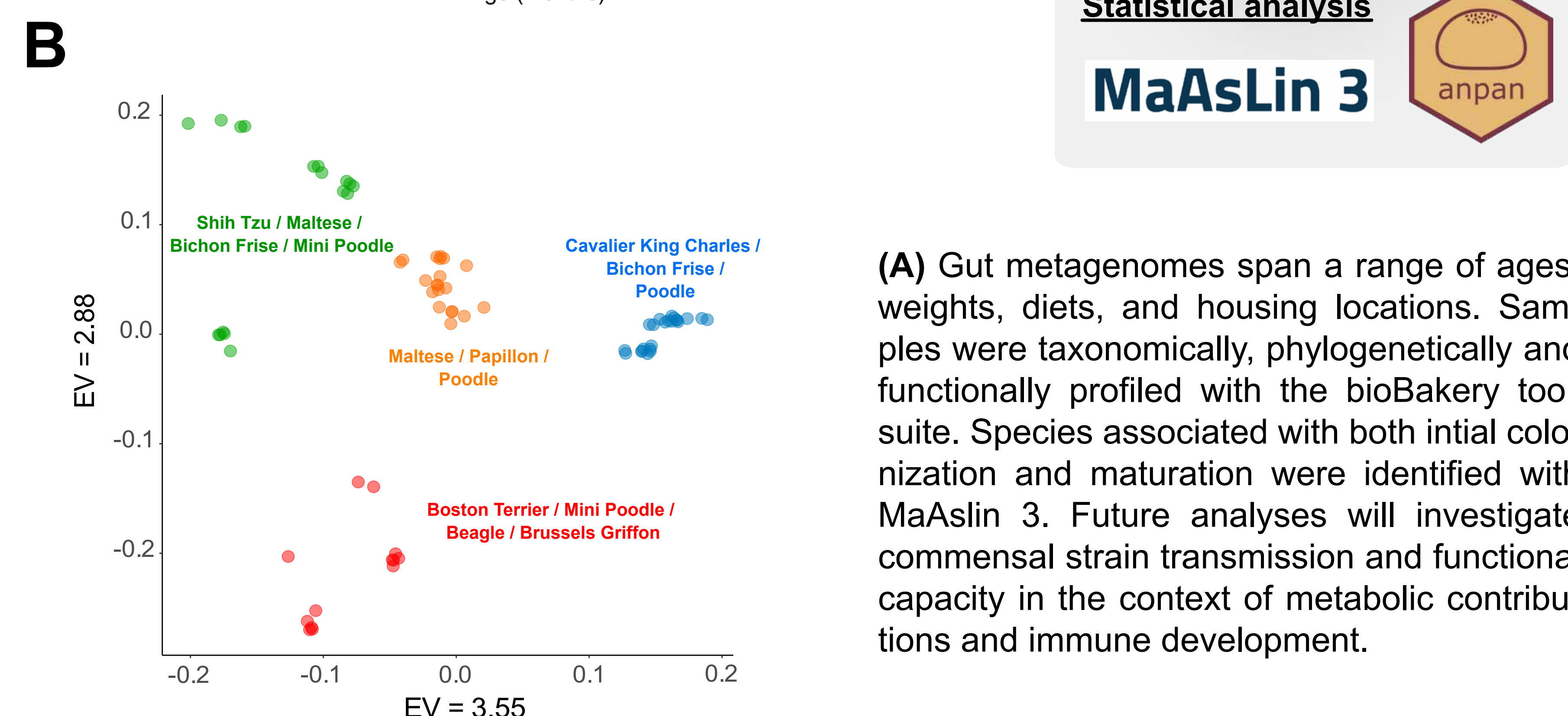
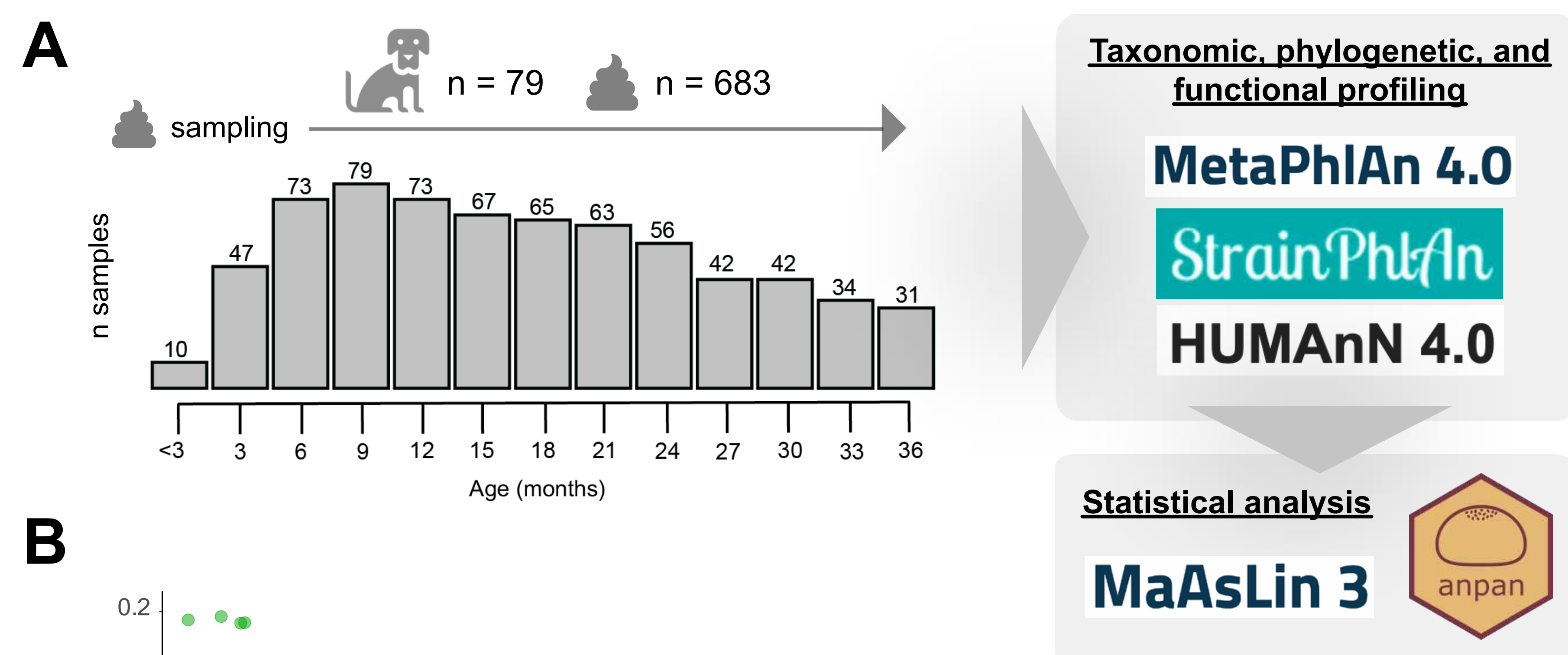
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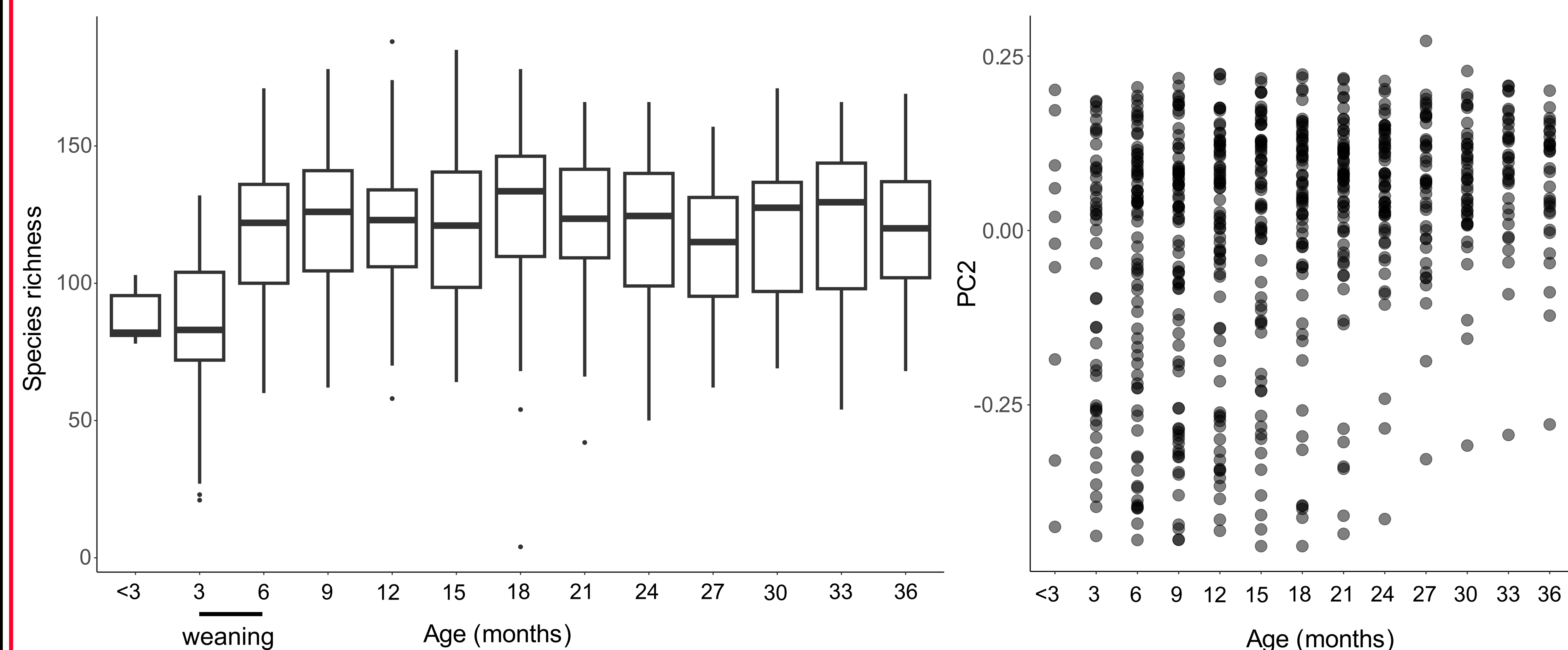
Initial colonization of the mammalian gut microbiome occupies a critical window in early life during which both host immunity and future ecosystem structure are established. These in turn influence disease risk into adulthood including allergies, asthma, and diabetes. Factors such as parental contributions, weaning, diet, environment, and medication play key roles, but many are hard to measure in human infants. We thus employed a precisely tracked canine cohort to understand gut microbiome assembly and stabilization, comprising 683 stool samples from 79 colony dogs sampled approximately every 3 months from 3 months to 3 years of age. Individuals' food intake, housing, breed, medical and medication histories, and lineage records were all recorded. Results showed that, similar to humans, the microbiome became more diverse and adult-like after weaning (3 months in dogs). Certain microbes, like *Megamonas funiformis*, were rare in young dogs but became common in adulthood, while others, like *Blautia hansenii*, were consistently present. Housing, diet, and lineage influenced microbial composition. This cohort offers insights into early gut microbiome development and could help explore disease links and the impact of diet.

## Longitudinal sampling from a canine model and study methodology



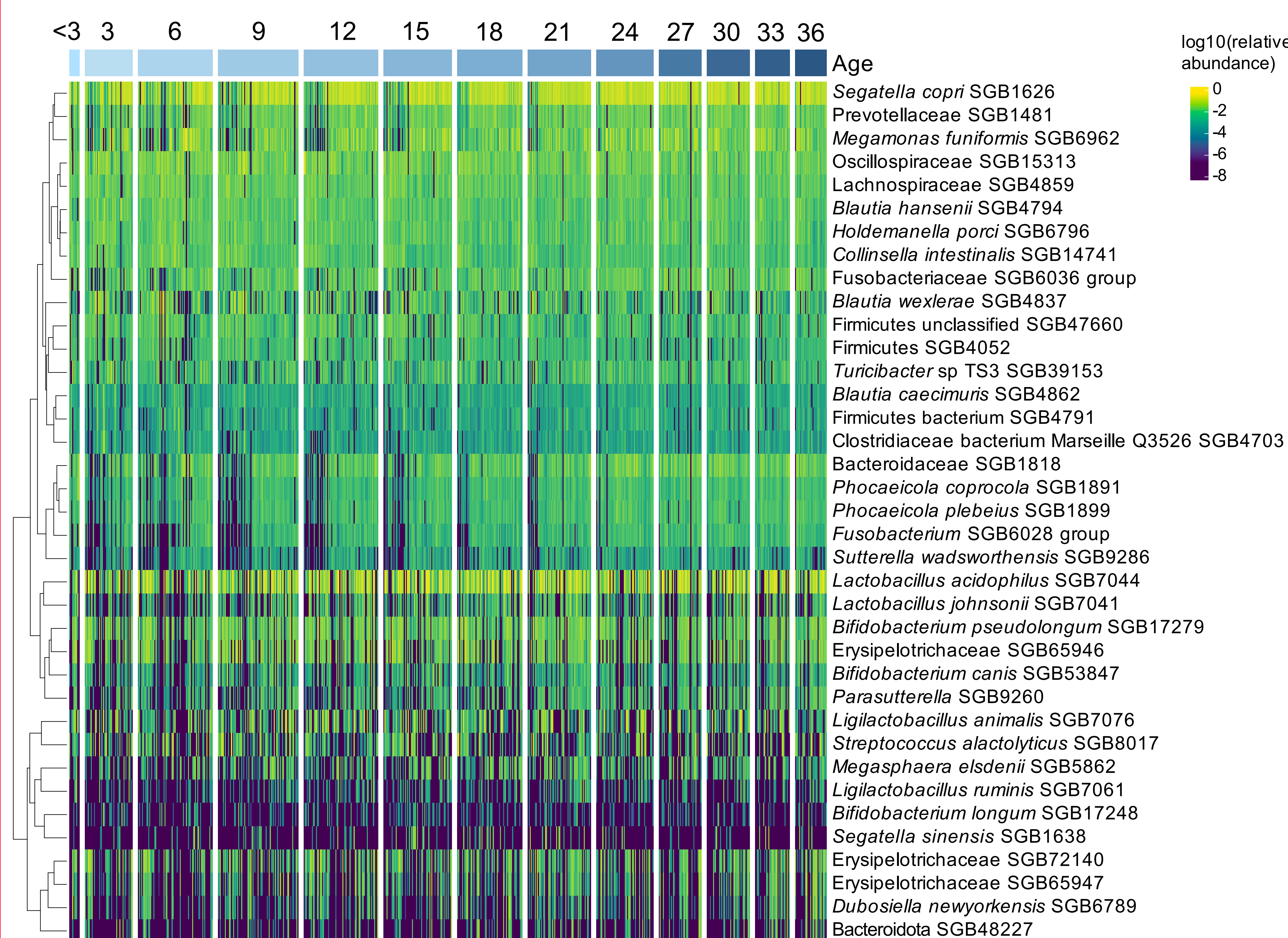
**(B)** Dogs spanned a mix of small breeds and were grouped into four main “breed categories” based on SNP genotyping data. At the time of sampling, animals spanned a **(C)** range of housing communities (different rooms and pens) and **(D)** consumed diverse diets (profiles displayed are for a subset of animals).

## Concordant with human infants, the canine gut microbiome converges post-weaning



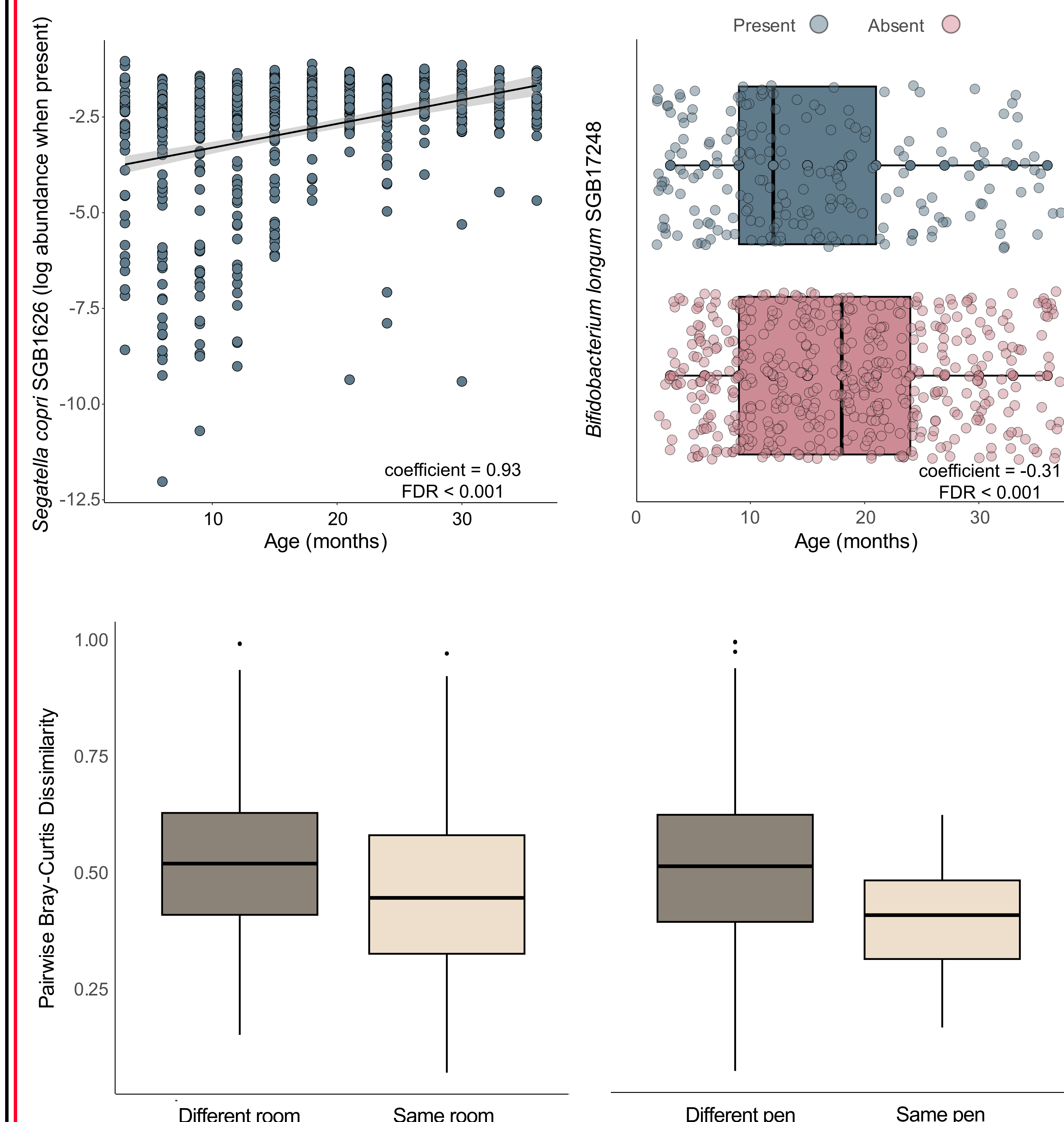
With the shift from milk to solid food, the canine gut microbial communities became more diverse and stabilized. This trend has been observed in the developing gut of human infants and in other mammals such as mice. **LEFT:** Strain richness for samples increased with age. Microbial communities become more similar in the number of different microbes as the animals mature (consume more diverse diets and with increasing exposure to other dogs). **RIGHT:** Interindividual variation with respect to age (second principal component [explained variance = 11.06%]).

## Age-specific gut microbial profiles



Taxonomic profiles are more similar between animals of the same age. Certain species (e.g., *Megamonas funiformis*, *Phocaeicola plebeius*, and *Sutterella wadsworthensis*) were present in very few young samples, but became more prevalent and abundant as the animals matured. Other species (e.g., *Lactobacillus acidophilus*, *Segatella sinensis*, and an unknown species of Bacteroidota) were variably present regardless of life stage.

## Community assemblage is shaped by life stage and cohousing



**TOP LEFT:** *Segatella copri*, a common and diverse gut commensal, became more abundant with age. **TOP RIGHT:** *Bifidobacterium longum*, which is known to colonize the gut of human infants and for its utilization of human milk oligosaccharides, was significantly observed in younger dogs compared to adults. **BOTTOM:** The gut microbiome of animals housed in the same room or pen tend to have more similar gut microbiomes than those housed separately (pairwise Bray-Curtis distances between animals with samples collected on the same day).

## Next steps

- Understand how microbiome stabilization corresponds to immune development in dogs and how this compares to humans and other mammals.
- Determine how the early life gut microbiome in dogs predicts the onset and severity of diseases known to be linked to the gut microbiome such as dermatitis.
- Understand functional changes through canine development as related to immunity and metabolic requirements.
- Evaluate commensal transmission through strain tracking.

## Acknowledgments

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