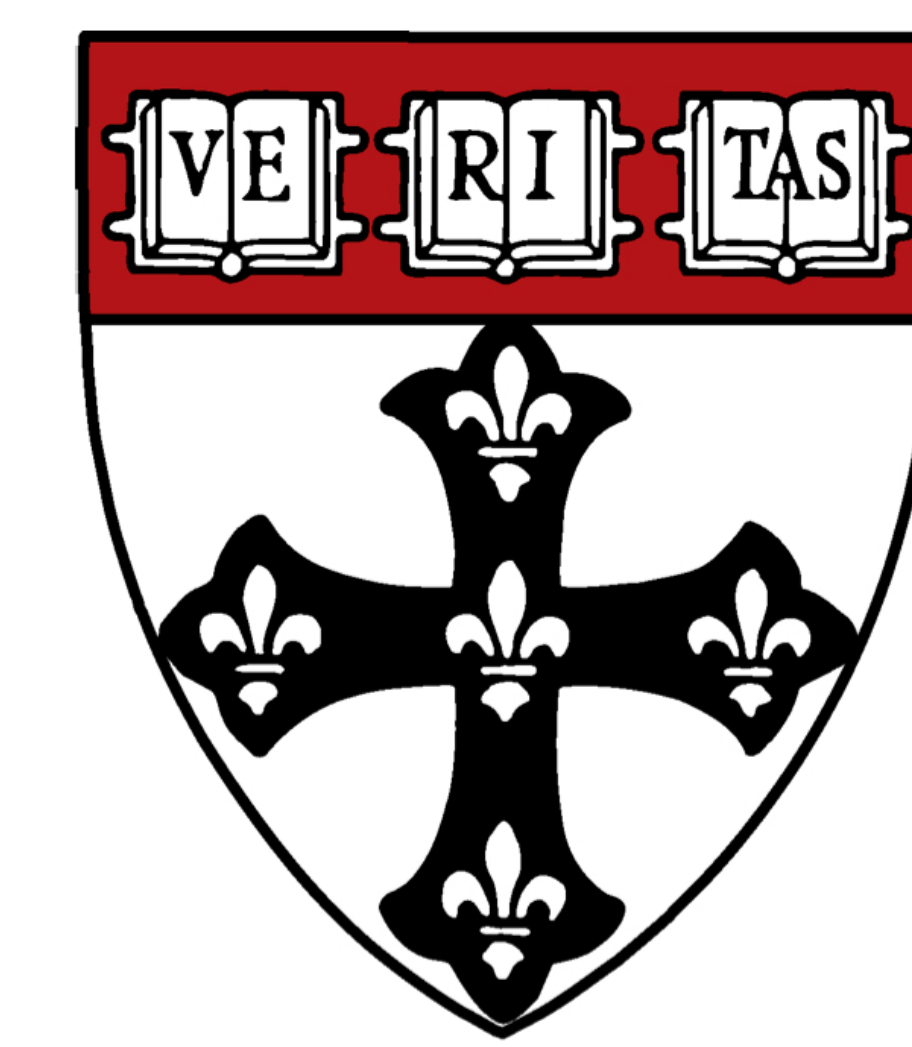




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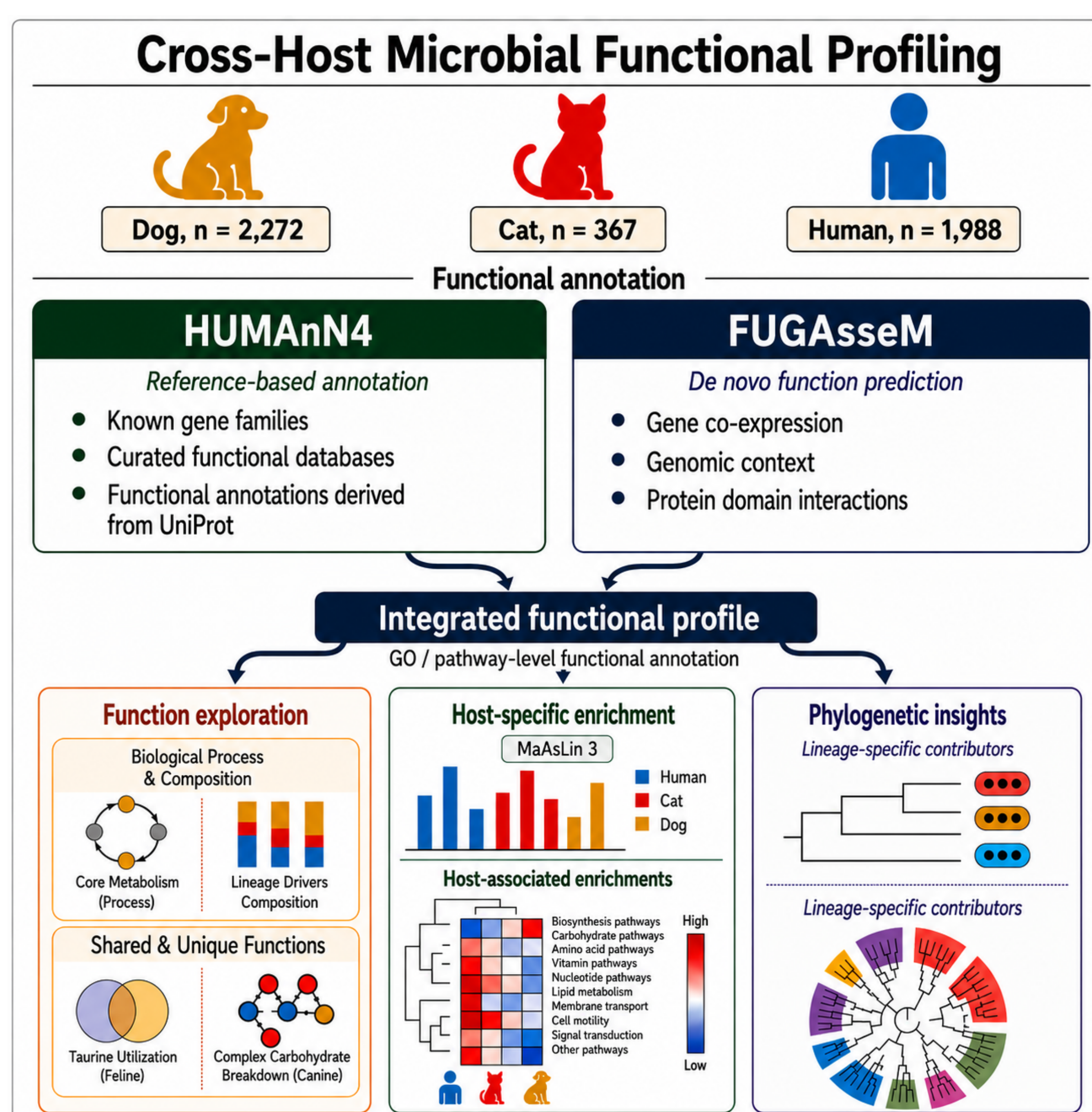
Beyond Taxonomy: Functional Adaptation and Strain Diversity in Human and Companion Animal Gut Microbiomes

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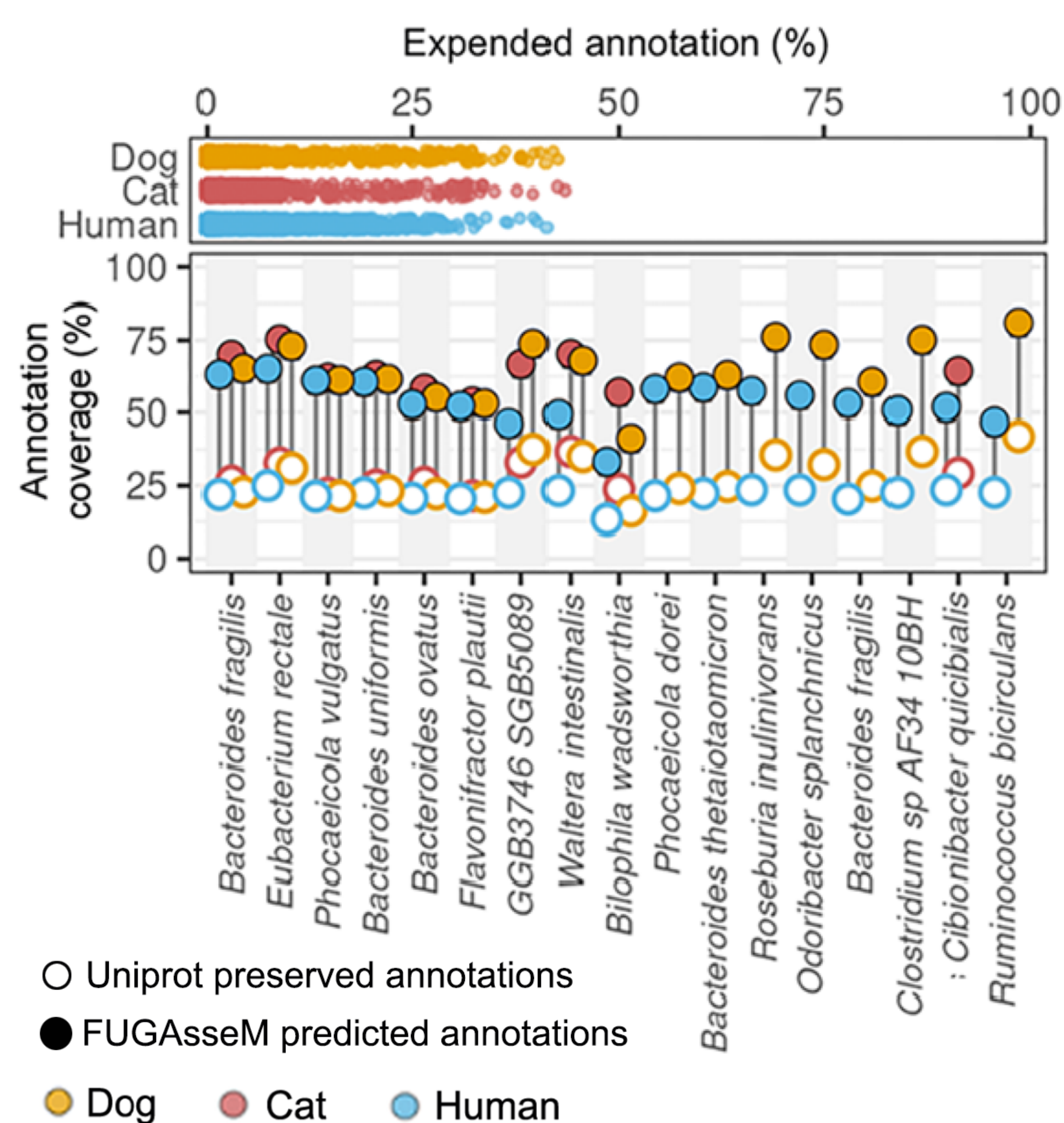


Abstract

The gut microbiome is a functional ecological community in which microbes co-evolve, co-metabolize, and interact with host systems. These dynamic host-microbe interactions shape gut metabolism and physiology, making functional profiling essential for understanding and ultimately harnessing the microbiome to improve host health. Here, we compare human, dog, and cat gut metagenomes to move beyond taxonomy, identify host-specific microbial functions, expand annotation for under-characterized pet-associated microbes, and determine how shared functions may be encoded by distinct host-associated taxa and strains.

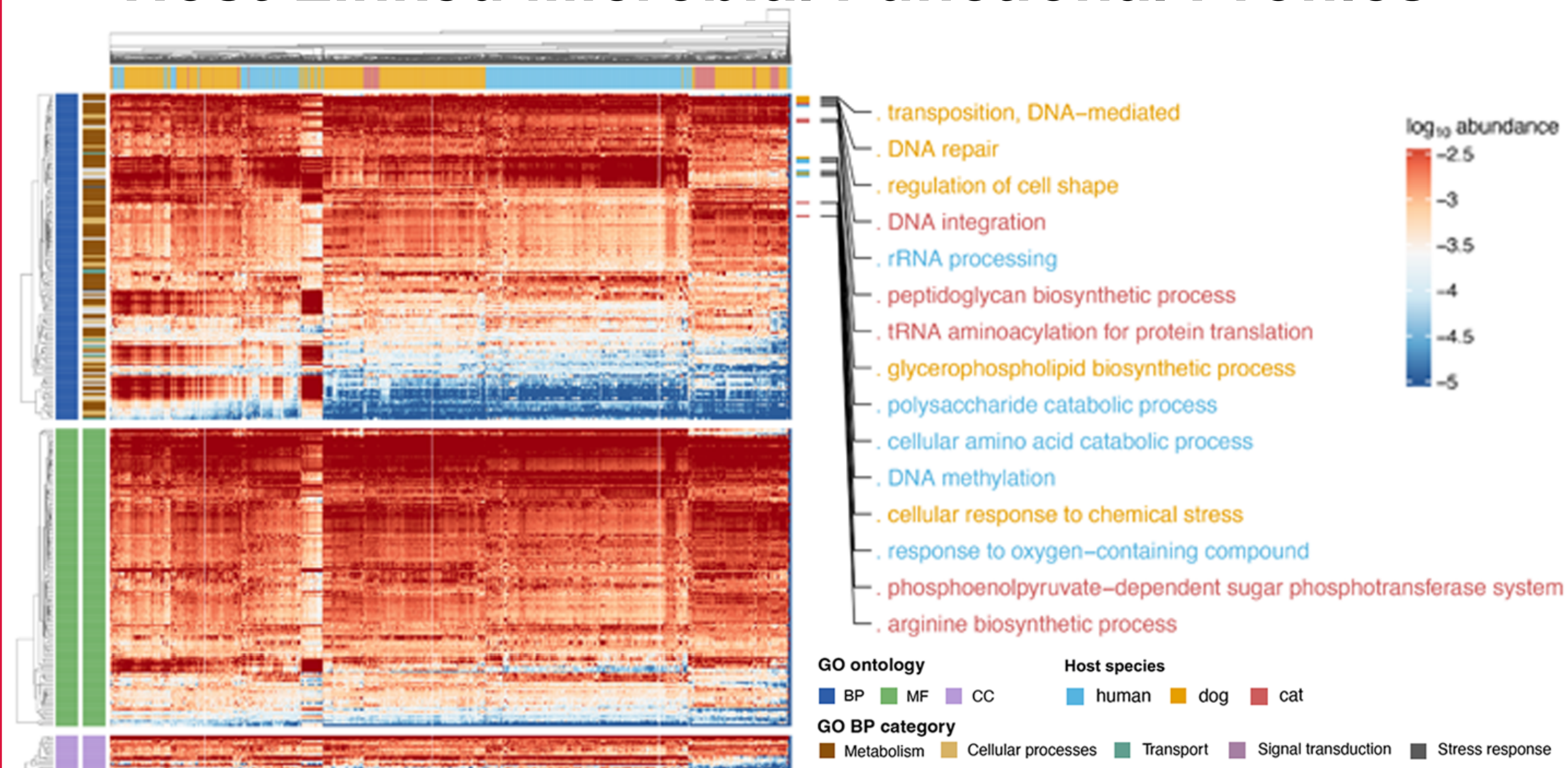


Annotation Gains Across Hosts



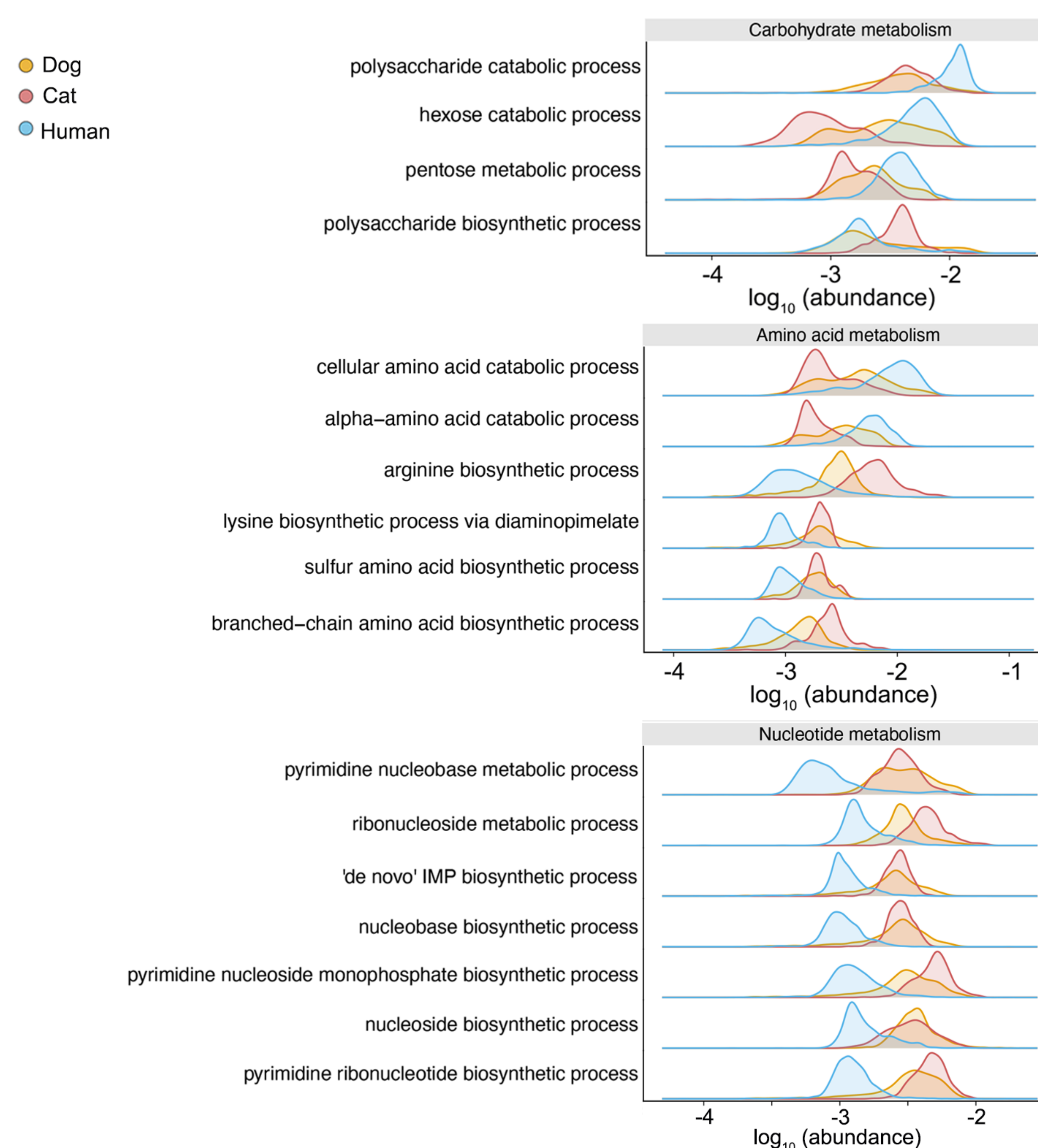
Integrated functional profiling substantially expands functional gene annotations across hosts. This improves both cross-host comparisons in shared taxa and the annotation of companion animal-associated microbes where reference gaps are lacking.

Host-Linked Microbial Functional Profiles



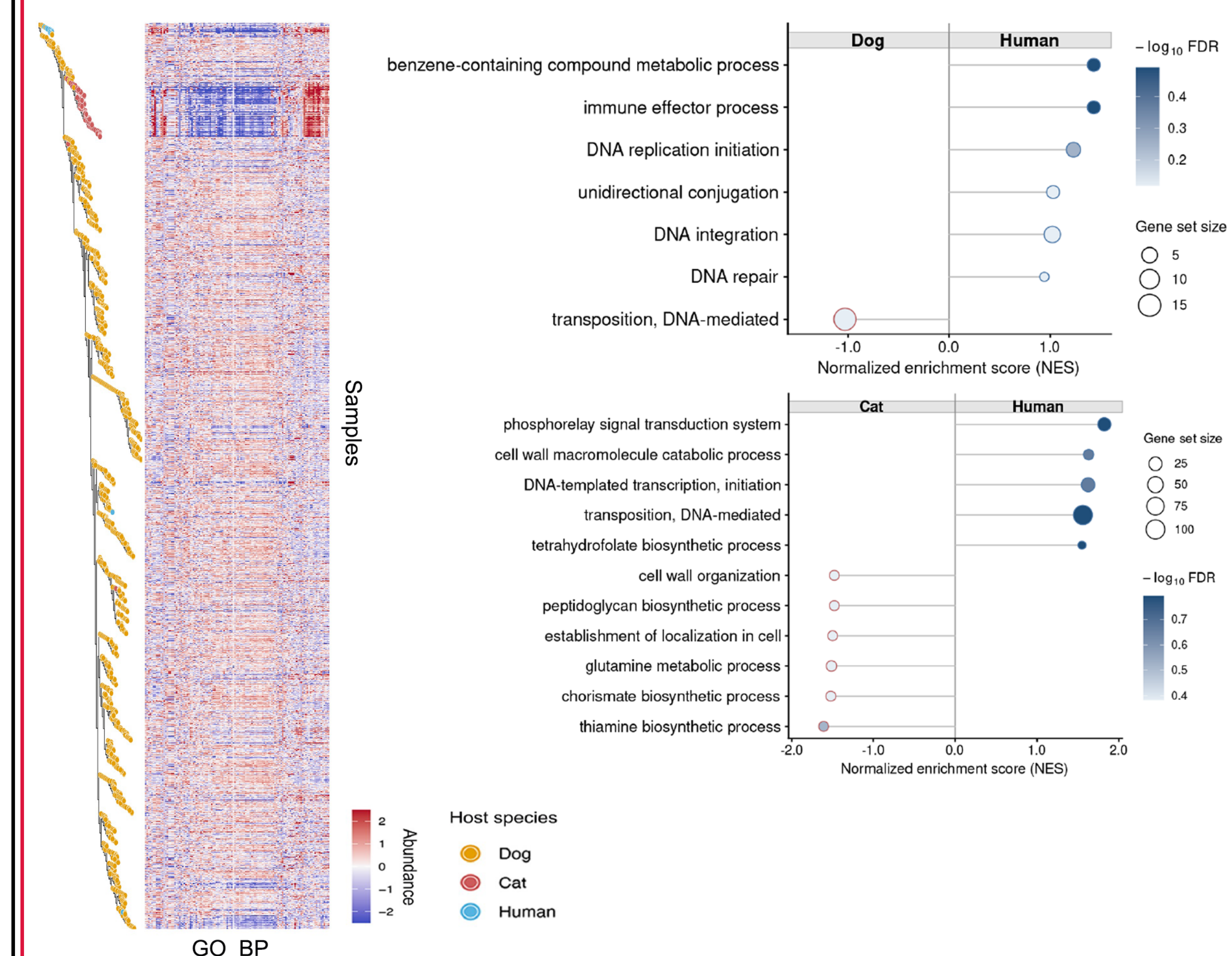
Microbial functional profiles show structured variation across host-associated species, revealing both broadly conserved biological processes and host-linked differences in metabolism, stress response, genome maintenance, and cell-surface functions.

Host-linked Differences in Microbial Metabolism



Differences in the abundance of biological process functional genes suggest host-associated metabolic patterns. Microbial functions show distinct patterns across the hosts based on carbohydrate catabolism, amino acid catabolism and biosynthesis, membrane lipid remodeling, and nucleotide biosynthesis. Overall, these shifts suggests distinct nutrient-processing and cellular biosynthesis programs across dog, cat, and human gut environments

Host-Driven Functional Specialization at the Strain Level



Host-associated *R. gnavus* strains carry distinct functional programs. Functional variation follows strain lineage, with cat- and human-associated clades showing distinct GO biological process profiles. Enrichment analysis links these differences to genome mobility, DNA maintenance, cell-wall remodeling, signaling, and biosynthetic metabolism, supporting host-associated functional specialization at the strain level.

Take-home message

Gut microbiomes differ not only in species composition, but also in functional potential across hosts. By integrating reference-based and predicted functional annotations, we improve detection of microbial functions in human, dog, and cat gut metagenomes, especially among under-characterized pet-associated microbes. Cross-host comparisons reveal distinct metabolic strategies, with human-associated microbiomes enriched in carbohydrate and amino acid catabolism, while dog and cat microbiomes show stronger biosynthetic potential. At the strain level, host-associated *R. gnavus* lineages carry distinct biological process profiles, indicating that host adaptation operates from broad community metabolism down to strain-specific functional specialization.

Acknowledgments

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