MetaGene™ Mouse
Translational mouse microbiome profiling

Features of MetaGene Mouse

- Strain-level taxonomy profiles
- Functional pathway characterization
- Alpha/beta diversity metrics
- Optimized fecal pellet extraction
- Standardized library preparation
- Metagenomic sequencing starting at 2 million reads
- Project consultation
- Dedicated study coordinator
- Quality-controlled data

Mouse microbiome research has provided valuable insights into human diseases, including cancer, diabetes and obesity.

However, taxonomic and functional characterization of mouse microbial communities is limited by incomplete microbial reference databases and a lack of bioinformatics tools geared toward mouse-associated bacteria.
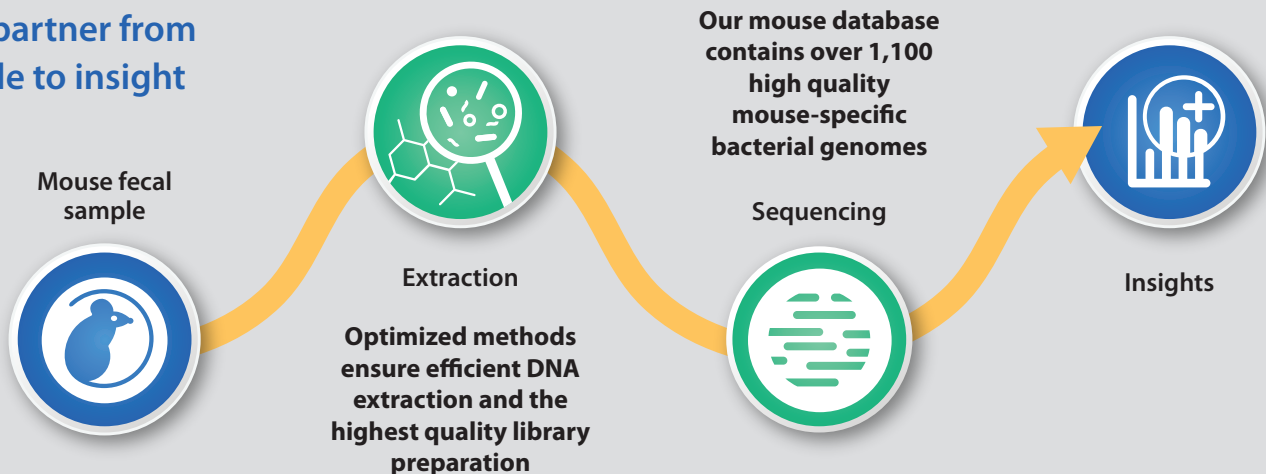
Diversigen's team of scientists developed MetaGene™ Mouse, a comprehensive service that overcomes translational mouse model research gaps by combining optimized pre-analytical steps, including DNA extraction and sequencing, with tailored analytics based on our curated database to provide strain-level resolution and functional characterization.

MetaGene Mouse
generates more taxanomic and functional data than traditional 16S methods

	MetaGene Mouse	Other mouse microbiome platforms
Genus-level resolution	✓	✓
Species-level resolution	✓	✗
Strain-level resolution	✓	✗
Direct functional characterization	✓	✗
Curated mouse database	✓	✗

Your partner from sample to insight

Mouse fecal sample

Extraction

Optimized methods ensure efficient DNA extraction and the highest quality library preparation

Our mouse database contains over 1,100 high quality mouse-specific bacterial genomes

Sequencing

Insights

## Improve your interpretation of the mouse microbiome:

- Species and strain identification
- Functional characterization for biomarker discovery
- Significantly improved mapping rates to find key interactions and pathways

Looking for more analytics?

Ask us about CorePlus™ analysis for data-driven insights with innovative custom bioinformatics

Dedicated metagenomics service for mouse and humanized mouse models

- Identify strains and biomarkers with improved specificity and sensitivity

- Capture functional pathways and interactions within the mouse microbiome

- Annotate data with over 1,100 high quality mouse-specific bacterial genomes, whole genome assemblies and metagenome-assembled genomes
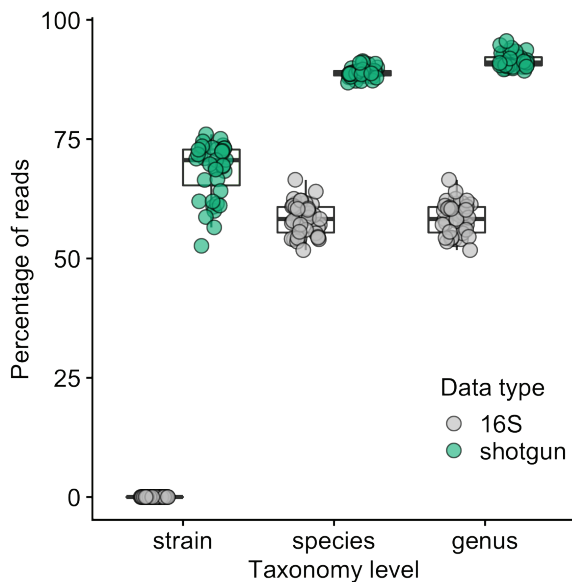
MetaGene Mouse results in higher resolution taxonomic profiling in comparison to amplicon 16S methods.
16S V4 sequencing data (grey) and corresponding shotgun data (green) for each sample[1] was annotated with Dada2 and MetaGene Mouse, respectively. The percentage of reads annotated at each level of taxonomy from strain to genus is shown.
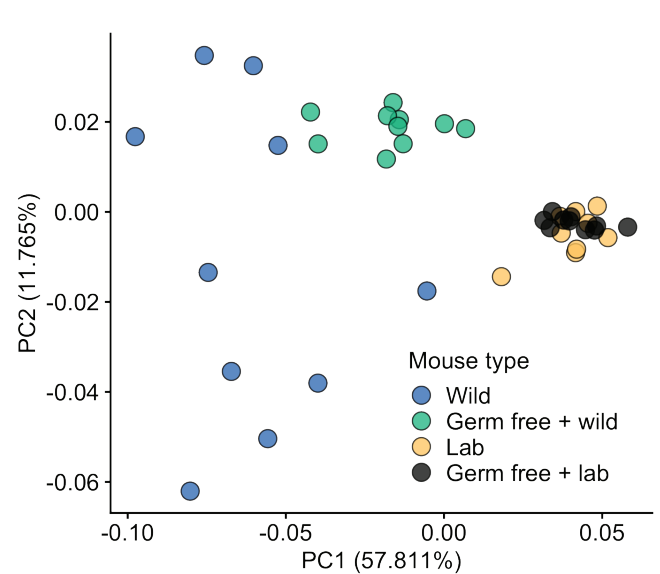
Functional profiles correlate with biological differences in mice.
Mouse shotgun sequencing samples were annotated with the MetaGene Mouse pipeline and KEGG functional profiles were used to plot a principal coordinate analysis (PCoA) of Bray Curtis distances. This dataset[1] consists of fecal microbiome samples from wild mice (Wild), laboratory raised mice (Lab) and germ free mice colonized with the microbiome of wild or lab mice (Germ free + wild/lab).

Our accessible team of scientists is ready to help at every step of your project. Interested in maximizing the value of your mouse microbiome projects?

Contact us at **info@diversigen.com** or **www.diversigen.com**

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