Novogene

Microbial Metagenomics Services

In shotgun metagenomic sequencing, genomes from environmental samples are analysed, without the prior isolation and cultivation of individual species. Therefore, it is a powerful technique for studying microbial communities in their natural habitat.

16S/18S/ITS amplicon metagenomic sequencing is frequently used to identify and differentiate microbial species. Short (<500 bp) hypervariable regions of conserved genes are amplified by PCR and analysed using next generation sequencing (NGS) technology.

Applications of our metagenomics services range from identifying a single species in pure culture and characterizing the microbiota of animals or plants, to comparing species diversity and population structure from various environmental sources or geographic regions. Our specialists can advise you on the appropriate analysis for your project.

Why Novogene?

Extensive experience with over 3000 projects

Industry-leading data quality guarantee

In house pipeline to meet different analysis requirement

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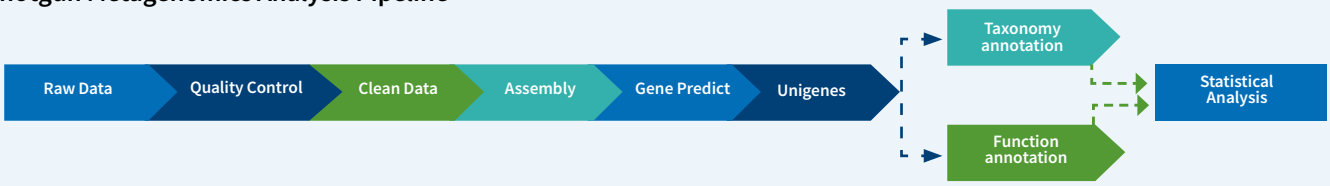
Sample requirements

Service	Sample Type	Amount	Volume	Concentration	Purity
Shotgun metagenomics	Genomic DNA	≥ 200 ng	≥ 20 μL	10 ng/μL	OD260/280: 1.8 –2.0
Amplicon-based metagenomics	Genomic DNA	≥ 200 ng		10 ng/μL	
	PCR product (270-470bp)	≥ 200 ng (pooled samples/library ≥ 1.5μg (one sample/library)		≥ 50 ng/μL	

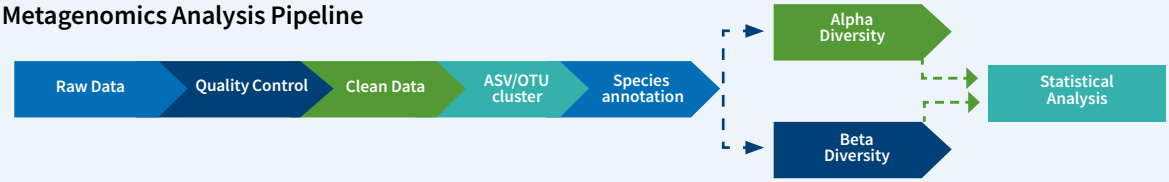
Sequencing parameters

Sample type	Service	Platform	Sequencing strategy	Recommended data volume	Data quality
Genomic DNA	Shotgun metagenomics	Illumina NovaSeq 6000	Pair-end 150	Human Faeces:4-6G Soil samples: 6-8Gb Water samples: 10Gb	Q30 ≥ 85%
	Amplicon-based metagenomics		Pair-end 250	• 30,000 tags • 50,000 tags • 100,000 tags	

Shotgun Metagenomics Analysis Pipeline



Amplicon-based Metagenomics Analysis Pipeline



Publications using Novogene's expertise

Genome Biology, 2020.
Influenza infection elicits an expansion of gut population of endogenous *Bifidobacterium animalis* which protects mice against infection.

Cell Host & Microbe, 2020.
Drosophila Histone Demethylase KDM5 Regulates Social Behavior through Immune Control and Gut Microbiota Maintenance.

Microbiome, 2019.
Mobile antibiotic resistome in wastewater treatment plants revealed by Nanopore metagenomic sequencing.

PNAS, 2019.
Division of labor in honeybee gut microbiota for plant polysaccharide digestion.

Soil Biology and Biochemistry, 2019.
Microbial mechanisms in the reduction of CH4 emission from double rice cropping system amended by biochar: A four-year study.

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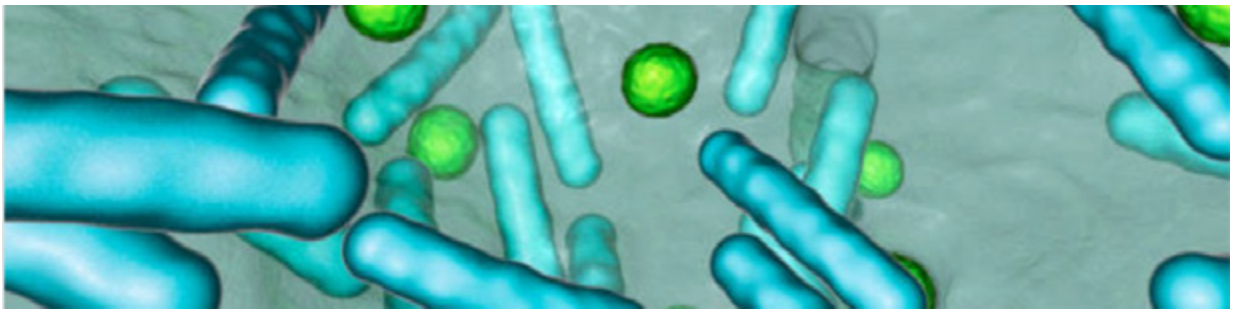
Case study

Influenza infection elicits an expansion of gut population of endogenous Bifidobacterium animalis which protects mice against infection.

Zhang et al., 2020. Genome Biology. DOI: 10.1186/s13059-020-02007-1.



This study used Novogene's shotgun and amplicon-based metagenomics services to identify Bifidobacterium animalis as the primary species in the gut microbiome of mice that provides protection against influenza infection.

Results

16S rRNA amplicon sequencing was used to analyse the diversity of mouse gut microbiome in mice that died from infection (GX.DG), mice that survived (GX.SG), mice that were inoculated with an attenuated virus as a negative control (NC) and mice inoculated with PBS saline (PBS).

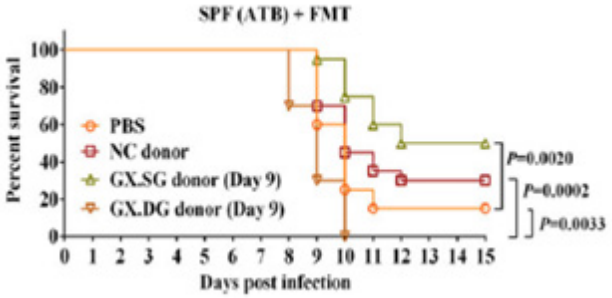


Figure 1
Venn diagram showing the overlap of (a) m6A peaks and (b) m6A modified genes in newborn, suckling, and adult samples.

Faecal microbiome transplants (FMT) from the 4 above categories were carried out on germ free mice, resulting in the highest survival rate among those inoculated with the gut microbiota of GX.SG mice (fig. 1), suggesting a beneficial change in gut microbiota of mice that survived influenza infection.

Taxanomic analysis revealed *B. animalis* and *B. pseudolongum* as the species with increased abundance in GX.SG mice when compared with all other cohorts, with individual inoculation of *B. animalis* showing the largest effect on survival rate in germ free mice.

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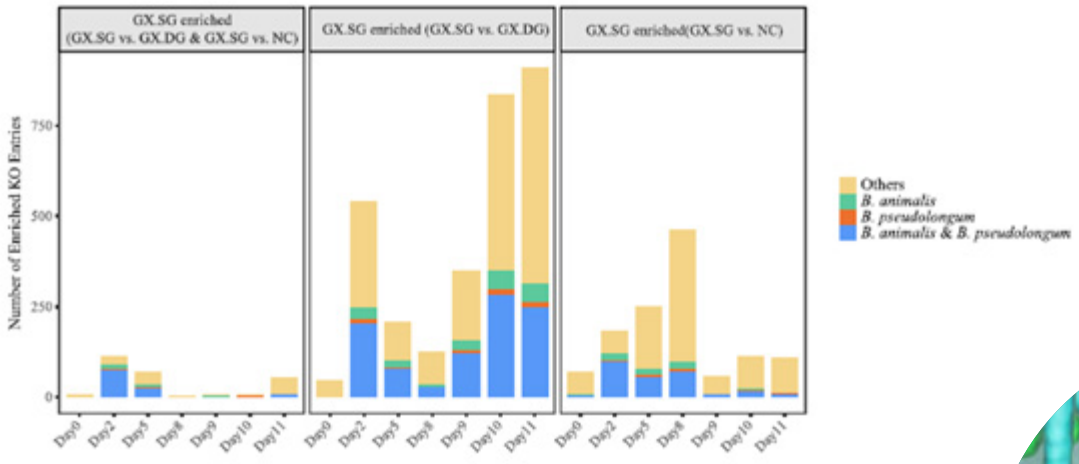
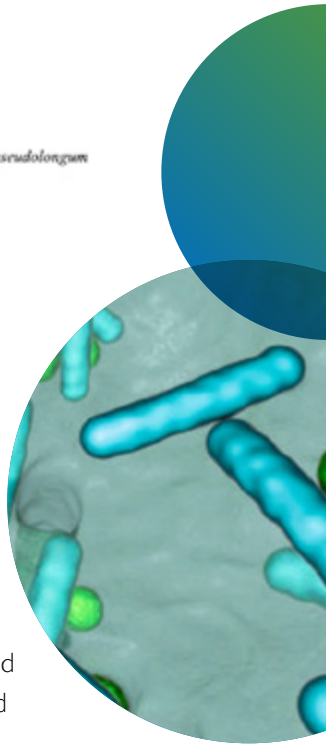


Figure 2
KO enrichment of GX.SG mice microbiome up to 11 days post-infection.



A functional metagenome analysis was then carried out and KEGG ontology (KO) gene enrichment was found in GX.SG samples (fig. 2) in pathways involved in carbohydrate and lipid synthesis, energy metabolism and amino acid metabolism. Of these, *B. animalis* was enriched specifically in valine, isoleucine, lysine and enzyme CoA biosynthesis.

Mice inoculated with *B. animalis* only also showed increased cytokine levels in the earlier stages of infection, a trend similar to that found when mice were orally administered valine. These findings suggested that *B. animalis* elicits its protective effects against influenza infection by modification of the immune response with valine.

Conclusions

This study provides an example of the ability of the gut microbiome to protect the host against an extraintestinal infection. It establishes *B. animalis* as the primary species that exerts this protective effect in mice against influenza infection. It also establishes the potential of gut microbiota as biomarkers for the prediction of the severity of influenza infection in patients, which may lead to the development of precision medicine on a case by case basis in the future.

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