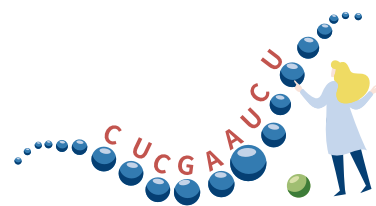




Eukaryotic mRNA Sequencing

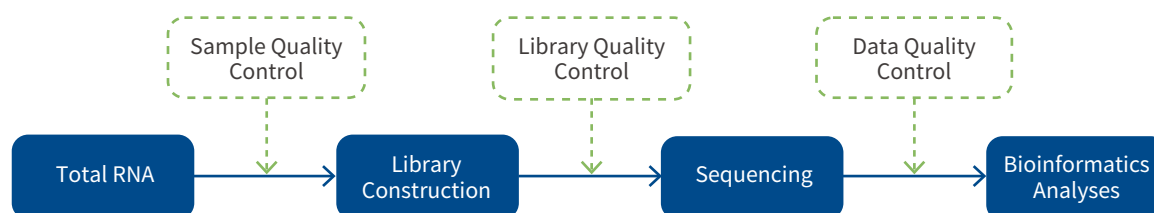


The use of next-generation sequencing (NGS) technology for mRNA-Seq allows researchers to analyze the continuous change of the cellular transcriptome. At Novogene, we use the state-of-the-art Illumina platform for all mRNA-Seq projects. We offer advanced, affordable, and comprehensive solutions for research relating to gene profiling and functions, structural analyses, and more. Our highly experienced bioinformaticians use widely accepted mainstream software and a mature in-house pipeline. Our standard or customized data analysis packages come with publication-ready results to meet virtually any project request.

Novogene Advantages

- More than 200,000 samples successfully sequenced at an industry-leading turnaround time
- Extraordinary NGS intelligent delivery system applied to provide more efficient and reliable services
- Exceptional data quality guarantee (Q30 $\geq$ 80%, exceeding Illumina's benchmarks)
- Free in-house bioinformatics software to visualize data flexibly

Project Workflow



Service Highlights



Sequencing Strategy

NovaSeq 6000 platform, paired-end 150 bp, 250-300 bp insert cDNA library, 6 Gb raw data/sample (recommended)



Sample Requirement

Total RNA as low as 400ng; for a low-input library, please contact us for details



Turnaround Time

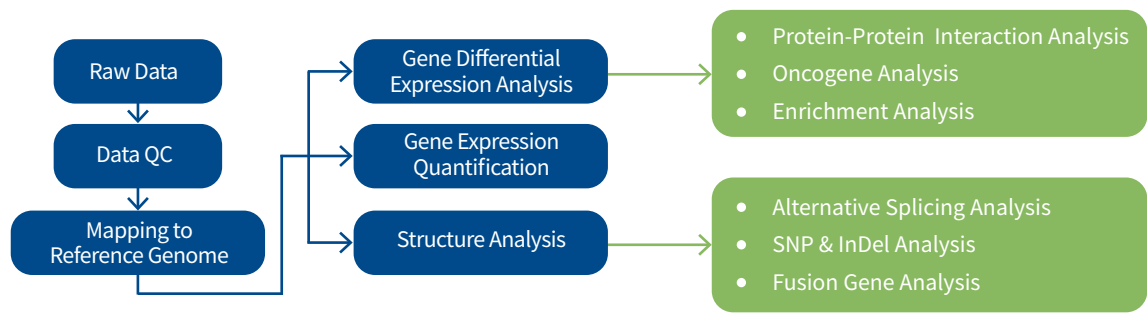
As fast as 14 business days after sample quality verification



Bioinformatics Analysis

Disease-oriented analysis content (fusion gene, oncogene analysis and more) specially catered for human and mouse mRNA sequencing projects

Bioinformatics Analysis Pipeline



Standard analysis process for species of human and mouse.
Customized analysis is also available. Please contact us for details.

Novogene Powered Literature

Drosophila histone demethylase KDM5 regulates social behavior through immune control and gut microbiota maintenance

Background: Increasing evidence suggests that gut microbiota can affect the symptoms of intellectual disability (ID) and autism spectrum disorder (ASD) diseases. Host genes influence the composition of gut microbiota, but the molecular mechanisms that regulate host-commensal microbiota homeostasis remain mostly unknown.

Results

$kdm5^{K6801/10424}$ flies showed a decrease on KDM5 protein and mRNA expression (Figure 1) in intestinal tissue. Which it was also associated with an increase in histone H3 lysine 4 trimethylation (H3K4me3).
The gut microbiota of $kdm5^{K6801/10424}$ flies had a lower number of observed species compared to the wild type (Figures 2A and 2B). The gut microbiota of $kdm5^{K6801/10424}$ flies showed increased levels of Proteobacteria and decreased levels of Firmicutes (Figure 2C).

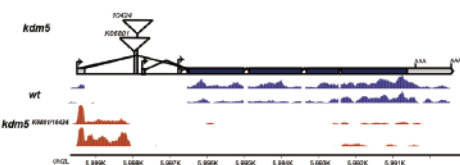


Figure 1. Transcription levels of *kdm5* in intestine tissues from wild type (wt) and $kdm5^{K6801/10424}$ flies using RNA-seq analysis.

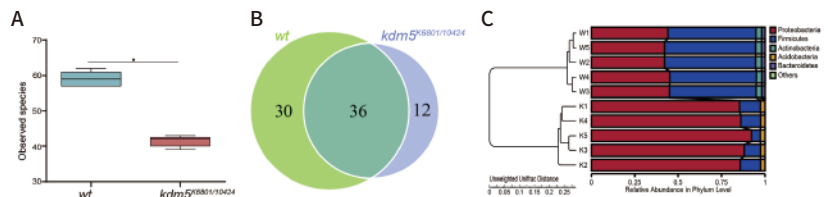


Figure 2 (A). Observed bacterial species' richness in gut samples from wt and $kdm5^{K6801/10424}$ flies. (B). Overlap of observed bacterial operational taxonomic units (OTUs) in gut samples from wt and $kdm5^{K6801/10424}$ flies. (C). Hierarchical clustering of wt and $kdm5^{K6801/10424}$ flies

Conclusion: This study used a genetic approach to dissect the role of KDM5 in the gut-microbiome-brain axis. It suggests that modifying the gut microbiome may provide therapeutic benefits for ID and ASD patients.

Reference: Chen Kun, Luan XT, Liu QS, *et al.* Drosophila histone demethylase KDM5 regulates social behavior through immune control and gut microbiota maintenance [J]. *Cell Host & Microbe*, 2019, 25 (4): 537–552

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