Comprehensive View of Eukaryotic mRNA Sequencing

Eukaryotic mRNA Sequencing Introduction

Novogene offers competitive sequencing services for eukaryotic mRNA transcripts of species either with or without reference genomes. In addition to providing alternative and affordable approaches to gene expression profiling among sample groups, eukaryotic mRNA sequencing, short as mRNA-seq, also enables the identification of novel transcripts, the detection of alternative splicing, gene fusion events, and provides customized data analysis and publication-ready results to meet bioinformatic requests.

The Novogene Advantages

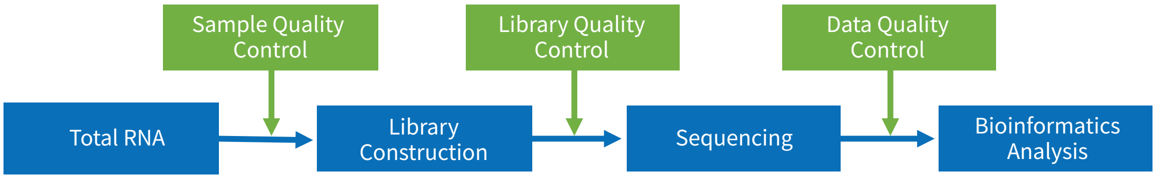
Extensive experience with 200, 000+ samples sequenced

Data

Industry leading data quality exceeding Illumina benchmarks

Free in-house software to visualize data flexibly per project needs

Project Workflow



Sample Quality Control

Library Quality Control

Data Quality Control

Total RNA → Library Construction → Sequencing → Bioinformatics Analysis

Sequencing Specifications

Sequencing Strategy

PE150 on Illumina platform, 250-300bp insert cDNA library

Sequencing Depth

⩾6 G raw data/sample

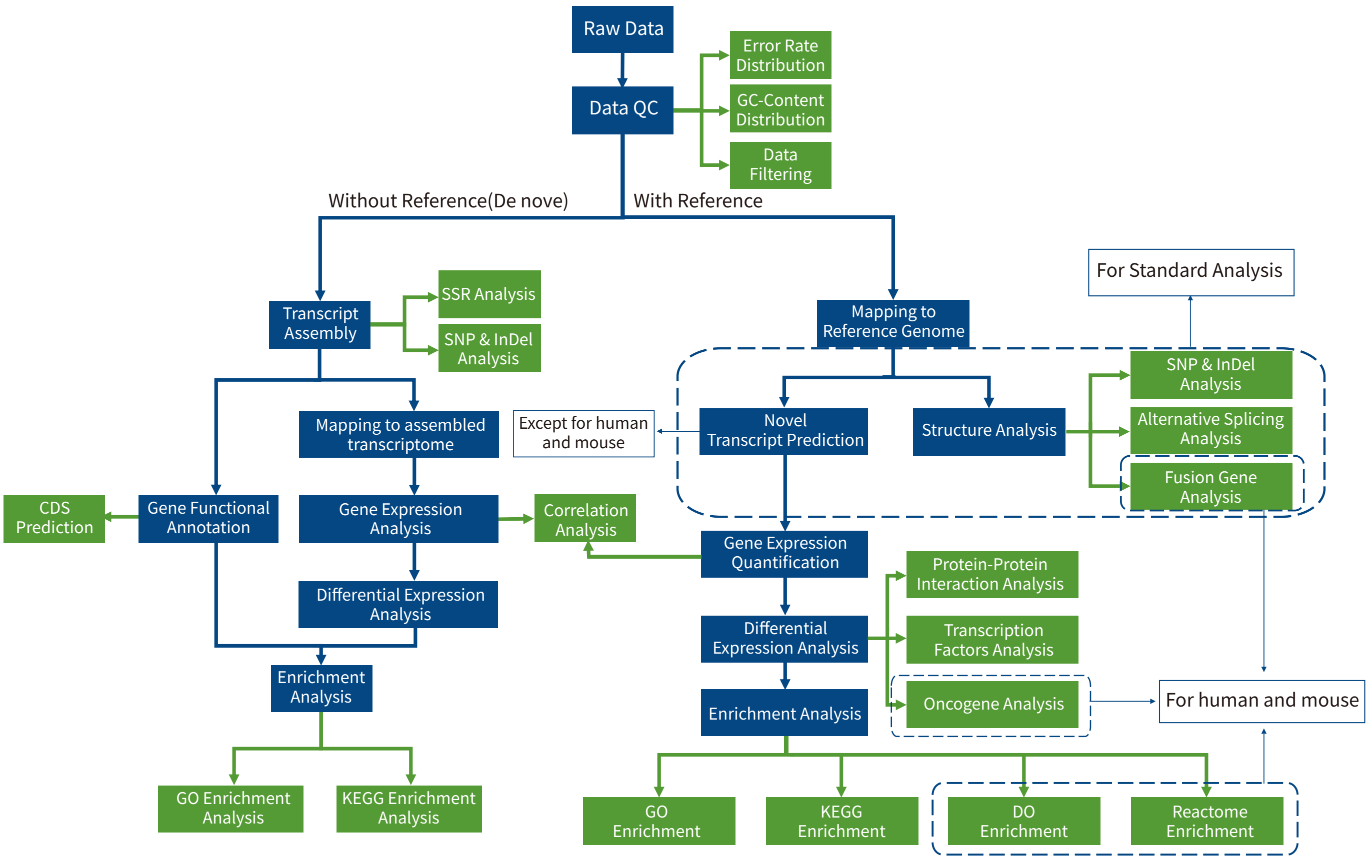
Data Quality Guarantee

Q30⩾80%, exceeding Illumina's official guarantee of ⩾75%

Turnaround Time

Quickest turnaround for your project

Analysis Pipeline



Novogene Powered Literature

Targeting Epigenetic Crosstalk as a Therapeutic Strategy for EZH2-Aberrant Solid Tumors

Background

Mutations or aberrant upregulation of EZH2 occur frequently in human cancers. This paper profiles global posttranslational histone modification changes in cancer cell lines with various sensitivities to EZH2 inhibitor.

Results

RNA-seq, H3K27ac *ChIP-seq*, and proteomics analysis helps to examine the cellular pathways affected by EPZ-6438 and to further demonstrate the linkage between H3K27ac modification and pathway activations (Figure 1).

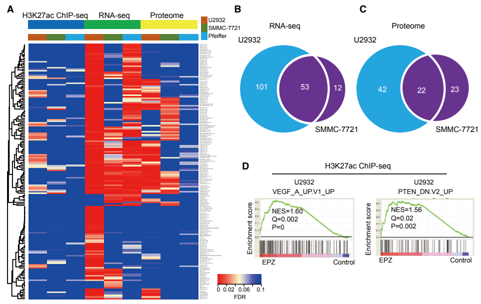


Figure 1. Feedback H3K27 acetylation change drives oncogenic transcriptional reprogramming.

Conclusion

Epigenetic crosstalk targeting together with MLL1-based stratification and inhibiting feedback MAPK activation expand EZH2 inhibitors'therapeutic utility and efficacy in patient-derived solid tumor models.

Reference: Huang X, Yan J, Zhang M *et al.* Targeting Epigenetic Crosstalk as a Therapeutic Strategy for EZH2-Aberrant Solid Tumors[J]. *Cell*, 2018, 175: 186–199.

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