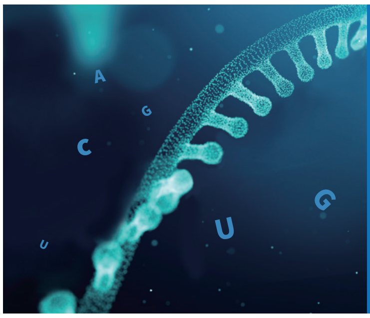
Novogene

Eukaryotic mRNA Sequencing



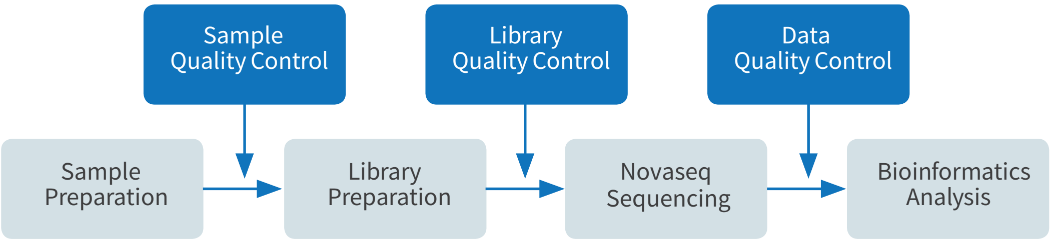
mRNA-Seq uses next-generation sequencing (NGS) to reveal the presence and quantity of messenger RNA in a biological sample at a given moment, analyzing the continuously changing cellular transcriptome. Novogene' s mRNA-Seq, based on state-of-the-art Illumina NovaSeq platforms with paired-end 150 bp sequencing strategy, offers complete solutions for gene expression quantification and differential gene expression analysis among groups of samples, as well as for identification of novel transcripts, alternative splicing, and gene fusion events, etc. Our experienced bioinformaticians work closely with customers to provide standard and customized data analysis and publication ready results for species with and without a reference genome.

Extensive experience with
over 30,000 samples

Data quality exceeds
Illumina's official guarantee

In house pipeline to meet
different analysis requirement

Project workflow



Sequencing parameter

Platform	Illumina NovaSeq 6000	
Read length	Pair-end 150	
Recommended Sequencing Depth	Recommended: 15G for animals and plants 3G for fungi	Minimum: 6G for animals and plants 2G for fungi
Data quality	Guaranteed Q30 ⩾ 80%, exceeding Illumina's official benchmark of ⩾ 75%	
Turnaround time	Express service: 15 working days from sample delivery to data delivery (<24 samples)	

Samples requirement

Library Type	Sample Type	Amount Required	Volume	Concentration	RNA Integrity Number (Agilent 2100)	Purity (NanoDrop$^{\text{TM}}$)
Eukaryotic RNA-Seq (cDNA library)	Total RNA	⩾ 0.4 µg	⩾ 20 µL	⩾ 20 ng/µL	⩾ 6.8 (Animal), smooth base line ⩾ 6.3 (Plant and Fungus), smooth base line	OD260/280 ⩾ 2.0, OD260/230 ⩾ 2.0, No degradation, No contamination

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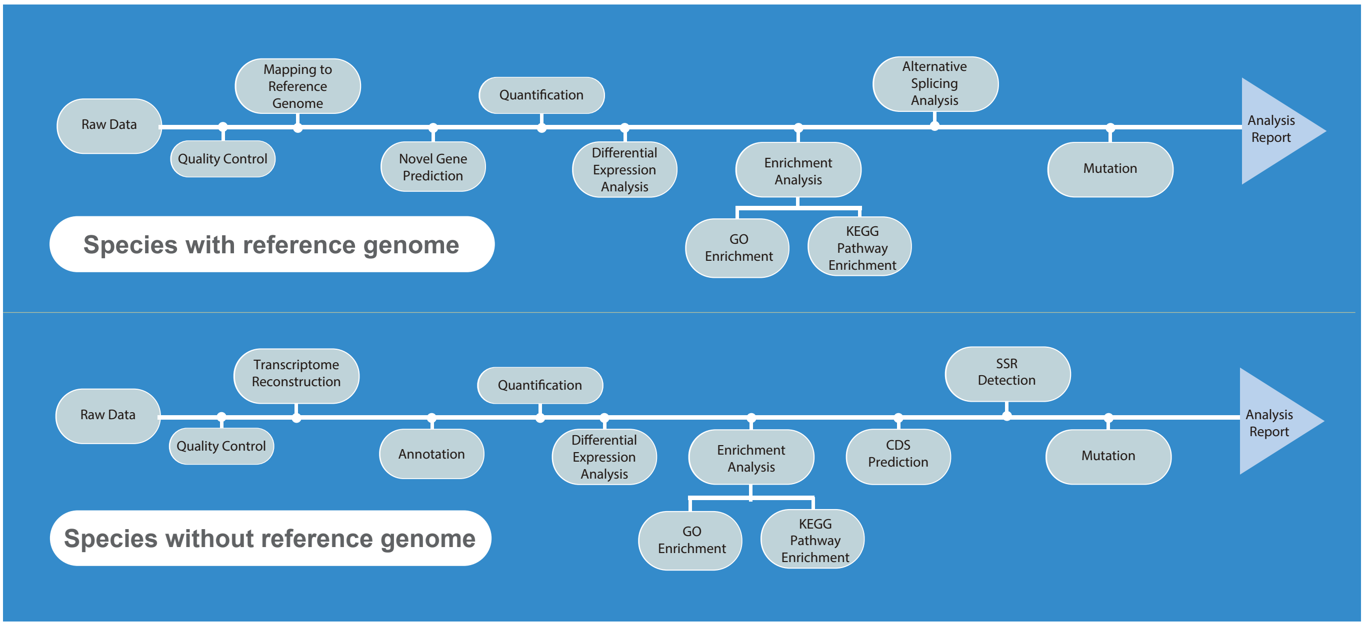
Analysis Pipeline



Species with reference genome

Raw Data
Quality Control
Mapping to Reference Genome
Novel Gene Prediction
Quantification
Differential Expression Analysis
Enrichment Analysis
GO Enrichment
KEGG Pathway Enrichment
Alternative Splicing Analysis
Mutation
Analysis Report

Species without reference genome

Raw Data
Quality Control
Transcriptome Reconstruction
Annotation
Quantification
Differential Expression Analysis
Enrichment Analysis
GO Enrichment
KEGG Pathway Enrichment
CDS Prediction
SSR Detection
Mutation
Analysis Report

Project experience

Background

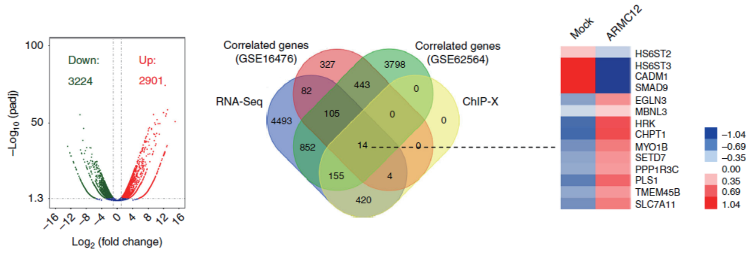
Neuroblastoma (NB), one of the most common malignant solid tumors in pediatric population that arises from neural crest-derived cells, constitutes 15% of cancer related mortality in childhood. Poor clinical outcome in patients suffering from high risk NB. The mechanisms essential for the aggressiveness and progression of NB still warrant further investigation.

Sample and sequencing strategy

Tumor cells with/ without MYCN amplification
Library preparation: RNA-seq library
2 Sequencing: Illumina platform

Conclusion

ARMC12 plays a crucial role in tumor progression and could be a potential therapeutic approach for NB. Mechanistically, ARMC12 physically interacts with retinoblastoma binding protein 4 (RBBP4) to facilitate the formation and activity of polycomb repressive complex 2, resulting in transcriptional repression of tumor suppressive genes



Ectopic expression of ARMC12 represses the expression of PRC2 downstream tumor suppressive genes in NB cells.

Publications using Novogene's expertise

Year	Journal	Article
2019	Applied and Environmental Microbiology	l-Rhamnose metabolism in clostridium beijerinckii strain DSM 6423
2018	Scientific Reports	Csde1 binds transcripts involved in protein homeostasis and controls their expression in an erythroid cell line
2018	Int J Mol Sci	Overexpression of the Rybp Gene inhibits differentiation of bovine myoblasts into myotubes
2018	Lung Cancer	Identification of MET exon14 skipping by targeted DNA- and RNA-based next-generation sequencing in pulmonary sarcomatoid carcinomas
2018	Nature communication	Armadillo repeat containing 12 promotes neuroblastoma progression through interaction with retinoblastoma binding protein 4
2017	PeerJ	Integration of lncRNA-miRNA-mRNA reveals novel insights into oviposition regulation in honey bees
2017	Mol Ecol	Insights into deep-sea adaptations and host-symbiont interactions: A comparative transcriptome study on Bathymodiolus mussels and their coastal relatives