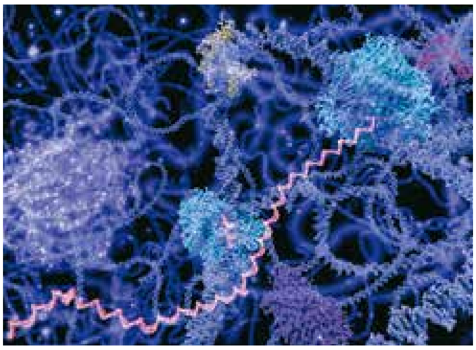
LncRNA-Seq



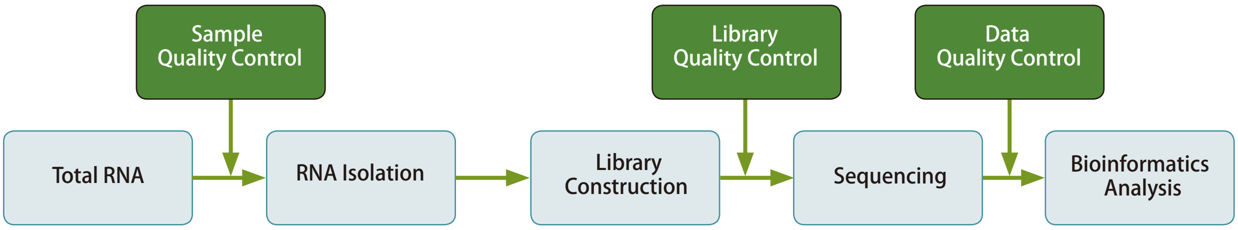
Long non-coding RNAs (LncRNAs) are transcribed RNAs longer than 200 nt that do not encode for proteins. LncRNAs are involved in a wide range of important cellular processes such as X-chromosome inactivation, imprinting, maintenance of pluripotency, lineage commitment and apoptosis. LncRNAs are also known to be involved with human diseases such as cancer, cardiovascular disease and neurological disorders, and are of significant interest to researchers.

Novogene bioinformatics team provides comprehensive analysis for both lncRNAs and mRNAs, enabling access to lncRNA and mRNA information in a single sequencing run. Applications include comparison of lncRNA and mRNA expressions in different stages of development and in different tissues, as well as unveiling key functions of mRNAs and lncRNAs.

The Novogene Advantage

- Extensive experience with thousands of samples successfully sequenced.
- Unsurpassed data quality with a guaranteed Q30 score ⩾ 80% that exceeds Illumina s official guarantee.
- Comprehensive analysis using widely accepted mainstream software and mature in-house pipeline.

Project Workflow



Sample Quality Control

Library Quality Control

Data Quality Control

Total RNA → RNA Isolation → Library Construction → Sequencing → Bioinformatics Analysis

SEQUENCING STRATEGY

- 250~300 bp insert strand-specific cDNA library
- Illumina platform, paired-end 150 bp.

DATA QUALITY GUARANTEE

- Our data quality guarantee, as measured by the percentage of bases with a sequencing quality score above Q30 (PE150, ⩾ 80%), exceeds Illumina's official guarantee (PE150, ⩾ 75%).

TURNAROUND TIME

- Within 15 working days from verification of sample quality (without data analysis)
- The data analysis turnaround is project-dependent.

RECOMMENDED SEQUENCING DEPTH

- Minimum: 10G per sample
  Recommended: 15G per sample

SAMPLE REQUIREMENTS

- Total RNA amount: ⩾ 2 μg; RNA concentration: ⩾ 50 ng / μl
- RIN value ⩾ 6.3 for plants and fungi
  RIN value ⩾ 6.8 for animals
- Purity: OD260/280 ⩾ 2.0
  OD260/230 ⩾ 2.0, without degradation or contamination
- FFPE sample: > 10 scrolls or slides.
  Samples should be tested and pre-qualified by gel electrophoresis.

NOVOGENE (UK) COMPANY LTD.
25 Cambridge Science Park
Milton Road
Cambridge, CB4 0FW
United Kingdom

Tel: +44(0)1223 628750
Eml: **europe@novogene.com**
Web: **www.novogene.com**
China · China Hong Kong · Singapore · UK · USA

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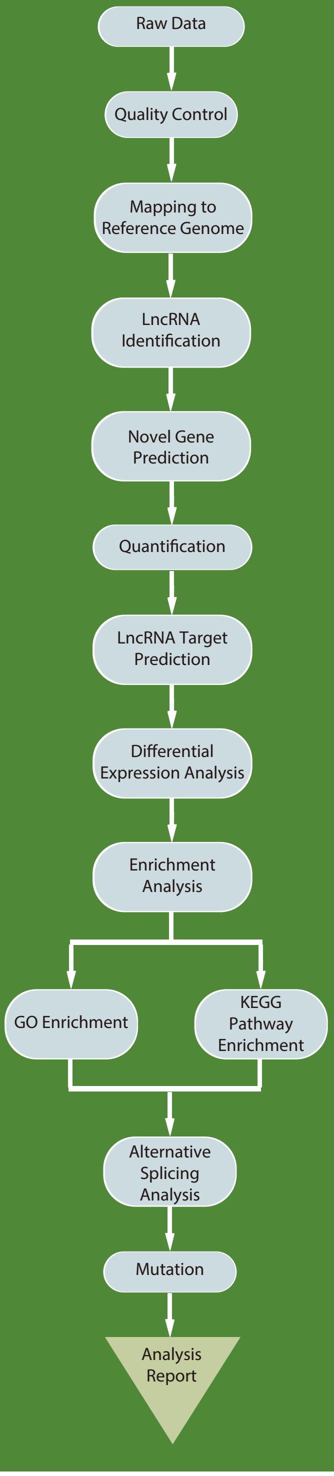
Analysis Pipeline



Raw Data

Quality Control

Mapping to Reference Genome

LncRNA Identification

Novel Gene Prediction

Quantification

LncRNA Target Prediction

Differential Expression Analysis

Enrichment Analysis

GO Enrichment

KEGG Pathway Enrichment

Alternative Splicing Analysis

Mutation

Analysis Report

Novogene Data

REPRESENTATIVE DATA QUALITY RESULTS OF lnc RNA SEQUENCING (PE 150) FROM NOVOGENE:

Sample Name	# of Raw Reads	# of Clean Reads	Clean Bases	Error Rate (%)	Q20 (%)	Q30 (%)	GC Content (%)
Sample1	118726766	117424068	17.61G	0.01	97.70	94.09	52.33
Sample2	133948474	132481702	19.87G	0.01	97.85	94.40	50.66
Sample3	144285430	142696176	21.4G	0.01	97.84	94.42	52.15
Sample4	133066914	132086794	19.81G	0.01	98.27	95.50	49.99
Sample5	133570278	131801718	19.77G	0.01	98.28	95.49	53.05
Sample6	111400698	107732776	16.16G	0.01	97.82	94.31	51.56

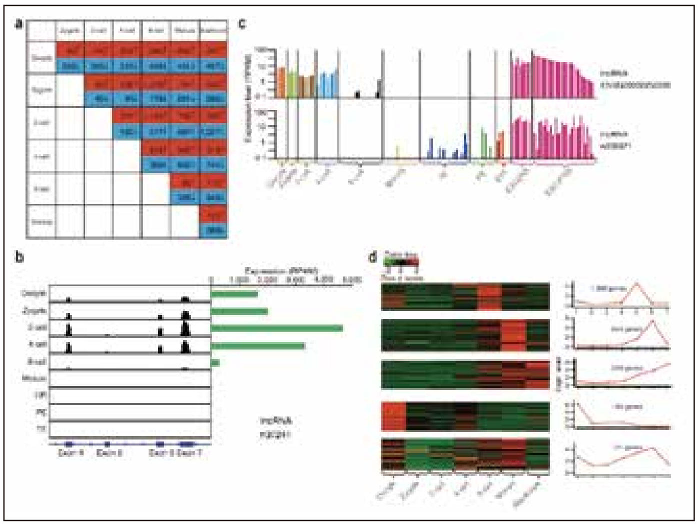
Project Example

The following study utilized Novogene's expertise.

Single-cell RNA-Seq profiling of human preimplantation embryos and embryonic stem cells .

Nature Structural & Molecular Biology 20, 1131 – 1139 (2013)

Measuring gene expression in individual cells is crucial for understanding the gene regulatory network controlling human embryonic development. Here we apply single-cell RNA sequencing analysis to 124 individual cells from human preimplantation embryos and human embryonic stem cells (hESCs) at different passages. The number of maternally expressed genes detected in our data set is 22,687, including 8,701 long noncoding RNAs (lncRNAs), which represents a significant increase from 9,735 maternal genes detected previously by cDNA microarray. We discovered 2,733 novel lncRNAs, many of which are expressed in specific developmental stages. To address the long-standing question whether gene expression signatures of human epiblast (EPI) and in vitro hESCs are the same, we found that EPI cells and primary hESC outgrowth have dramatically different transcriptomes, with 1,498 genes showing differential expression between them. This work provides a comprehensive framework of the transcriptome landscapes of human early embryos and hESCs.



Expression patterns of known long noncoding RNA (lncRNA) genes during human preimplantation development and derivation of hESCs.

Year	Journal	Article
2016	Scientific Reports	Analyses of Long Non-Coding RNA and mRNA profiling using RNA sequencing during the pre-implantation phases in pig endometrium
2016	Scientific Reports	Transcriptome Analysis Reveals Distinct Gene Expression Profiles in Eosinophilic and Noneosinophilic Chronic Rhinosinusitis with Nasal Polyps
2016	BMC Genomics	Genome-Wide Analysis of Long Non-Coding RNAs at Early Stage of Skin Pigmentation in Goats (Capra hircus)
2016	Biology of Reproduction	Systematic Identification of Long Non-coding RNAs in Immature and Mature Porcine Testes
2013	Nature Structural & Molecular Biology	Single-cell RNA-Seq Profiling of Human Preimplantation Embryos and Embryonic Stem Cells