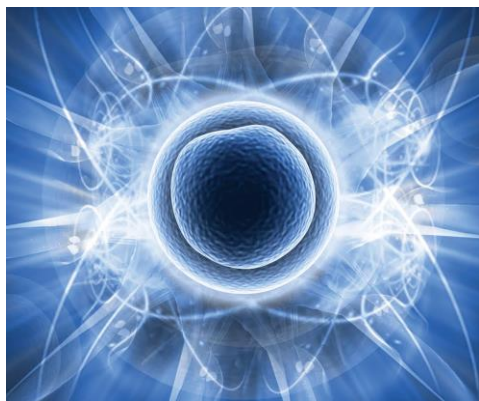




Single-cell RNA Sequencing



Single-cell sequencing is now readily available to researchers through Medikonia's expertise in this field. Medikonia is one of the few NGS providers with extensive experience in single cell sequencing technology, including single-cell RNA-Seq. We offer the highest quality services in amplification, library construction, sequencing, and bioinformatics analysis to our customers, and our results have been published in leading scientific journals.

Single-cell RNA-Seq enables the high-resolution transcriptome profiling of a single cell, and has broad utility for investigating developmental processes and gene regulatory networks, and for revealing heterogeneous gene expression patterns within cell cultures, tissues, and organs. Applications include profiling gene expression changes during stem cell differentiation, organ development, or tumor progression, and characterizing the response of subpopulations of cells to environmental signals and conditions.

Medikonia offers the most advanced techniques for transcriptome analyses for single cells.

The Advantages

- **Leader in single-cell RNA-Seq:** We are one of the few providers of this technology, with the highest ranking in technical capability and experience, and publications in the field.
- **Advanced amplification methods:** We use the SMARTer kit for single cell RNA amplification, which reduces amplification costs, improves amplification rates, and has been utilized in multiple publications. The success rate for amplification from human peripheral blood lymphocytes and mammalian embryonic cells are 100% and >62%, respectively.
- **Comprehensive processing:** Our single-cell RNA sequencing service includes amplification, library construction, sequencing, and extensive bioinformatics analysis.

Project Workflow



SEQUENCING STRATEGY

- 250-300bp insert cDNA library
- HiSeq platform, paired-end 150 bp

DATA QUALITY GUARANTEE

- Q30 ≥ 80%

SAMPLE REQUIREMENTS

- Sorted single cells should be stored in one of the two ways (1) in lysis buffer with RNase inhibitor from SMARTer kit (Clontech) or (2) in 1X PBS buffer (excluding calcium and magnesium) containing RNase inhibitor in a total volume of ≤ 2 µl. The stored cells should be frozen in liquid nitrogen and shipped out with dry ice.

TURNAROUND TIME

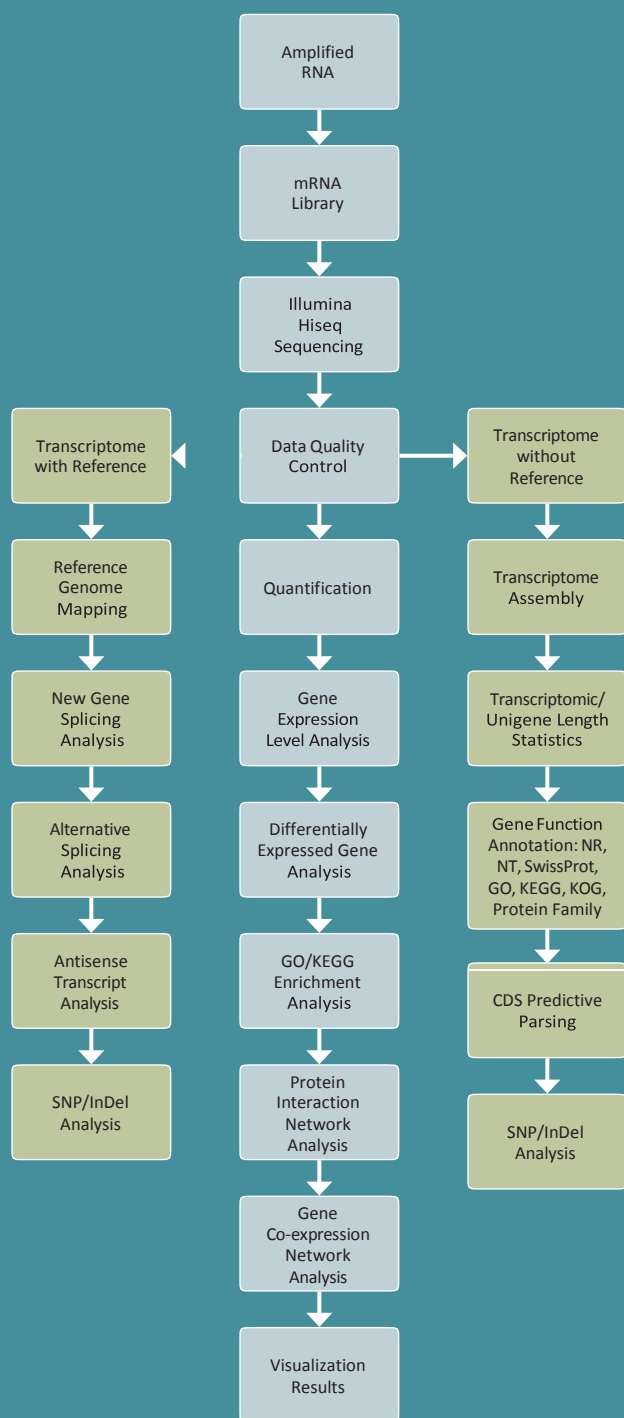
- Amplification: 7 working days from verification of sample quality
- Library preparation and sequencing: within 15 working days
- The turnaround for data analysis is project dependent

Medikonia Data

REPRESENTATIVE DATA QUALITY RESULTS OF SINGLE CELL RNA SEQUENCING FROM MEDIKONIA

Sample	Raw Reads	Clean Reads	Clean Bases	Error (%)	Q20 (%)	Q30 (%)	GC (%)
Sample 1_1	20594409	20132577	2.52G	0.03	96.16	92.32	43.60
Sample 1_2	20594409	20132577	2.52G	0.04	93.57	88.31	43.56
Sample 2_1	22213754	21739346	2.72G	0.03	96.22	92.38	43.69
Sample 2_2	22213754	21739346	2.72G	0.04	93.90	88.87	43.65

Analysis Pipeline



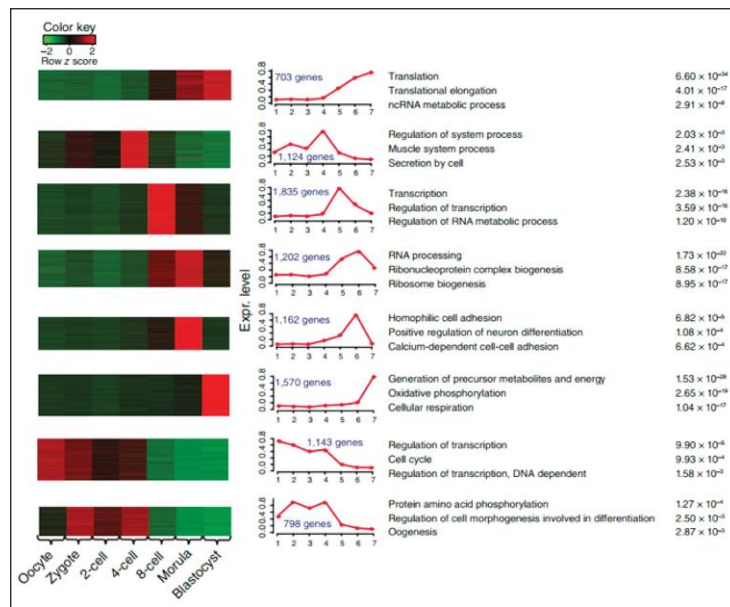
Project Example

The following study utilized Medikonia's expertise in single-cell RNA-Seq.

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

Nature Structural & Molecular Biology, 20:1131-1139 (2013).

In this study, the transcription profiles of human embryonic stem cells and cells from human preimplantation embryos were examined at different developmental stages. Results demonstrated markedly different expression patterns between cell groups, and revealed over 2,000 novel long noncoding RNAs.



Expression patterns during human preimplantation development and derivation of human embryonic stem cells (hESCs)