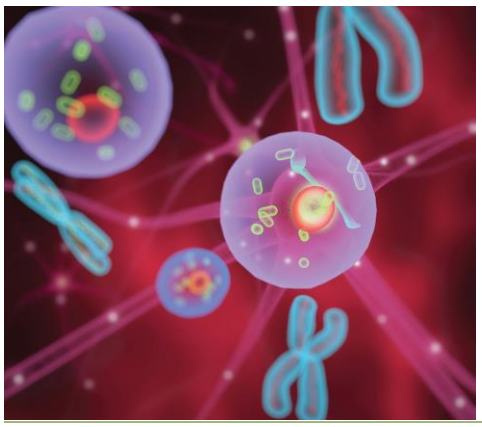
MEDIKONIA
仁 邁 樂 康
Genomic Services & Solutions

Single-cell DNA Sequencing



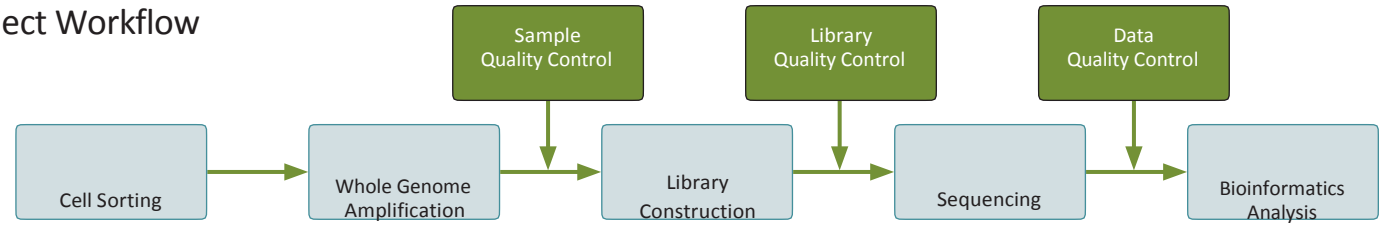
Advances in whole-genome amplification and Medikonia's expertise have made single cell sequencing easily accessible to researchers. Medikonia is one of the few NGS providers with extensive experience in single cell sequencing technology, including single-cell DNA sequencing. We offer the highest quality services in amplification, library construction, sequencing, and bioinformatics analysis to our customers, and our results have been published in leading scientific journals.

With single-cell DNA sequencing, the genomic heterogeneity of cell populations can be explored at the level of the individual cell. Genetic changes, such as point mutations and copy number variation occurring during disease and normal development processes, are profiled using the minute amounts of DNA from single cells. Applications include analysis of genetic heterogeneity within unicellular and multicellular organisms, detection of chromosomal anomalies in germ line cells, preimplantation genomic screening of embryos, and defining the genetic composition of tumors for developing more targeted therapies.

The Advantages

- Leader in single-cell genomics: 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 MALBAC (multiple annealing and looping based amplification cycles) PCR-based method, which provides uniform data while reducing rates of false positives and false negatives.
- Comprehensive processing: Our single-cell sequencing services include amplification, library construction, sequencing, and bioinformatics analysis.

Project Workflow



SEQUENCING STRATEGY

- 350 bp insert DNA library
- HiSeq platform, paired-end 150 bp

DATA QUALITY GUARANTEE

- Q30 ≥ 80%

TURNAROUND TIME

- Amplification: within 10 working days from verification of sample quality
- Library preparation and sequencing: within 22 working days
- Data analysis: 8 working days

SAMPLE REQUIREMENTS

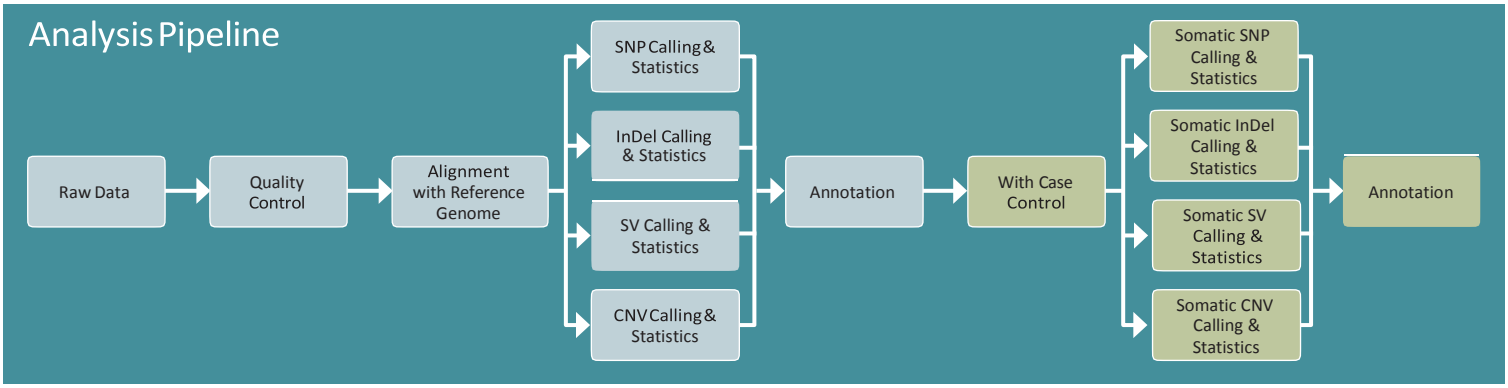
- We accept fresh single cells and laser captured single cells.
- Sorted single cells should be stored in 1X PBS buffer (excluding calcium and magnesium) in a total volume of ≤ 2 **µl**. The stored cells should be freezed in liquid nitrogen and shipped out with dry ice.

RECOMMENDED SEQUENCING DEPTH

- For normal sample: effective sequencing depth of 30×
- For tumor sample: effective sequencing depth of 50×

REPRESENTATIVE DATA QUALITY RESULTS OF SINGLE CELL DNA SEQUENCING FROM MEDIKONIA

Sample Name	Raw Reads	Raw Data (%)	Effective (%)	Error (%)	Q20 (%)	Q30 (%)	GC (%)
G6_10	119752154	34.59	99.80	0.03	95.64	89.85	44.74
G6_11	114546150	33.26	99.80	0.04	94.00	87.43	44.87
G6_12	116002747	33.57	99.80	0.04	95.29	89.95	44.91
G5_9	127417212	37.23	99.70	0.03	96.42	91.15	44.99



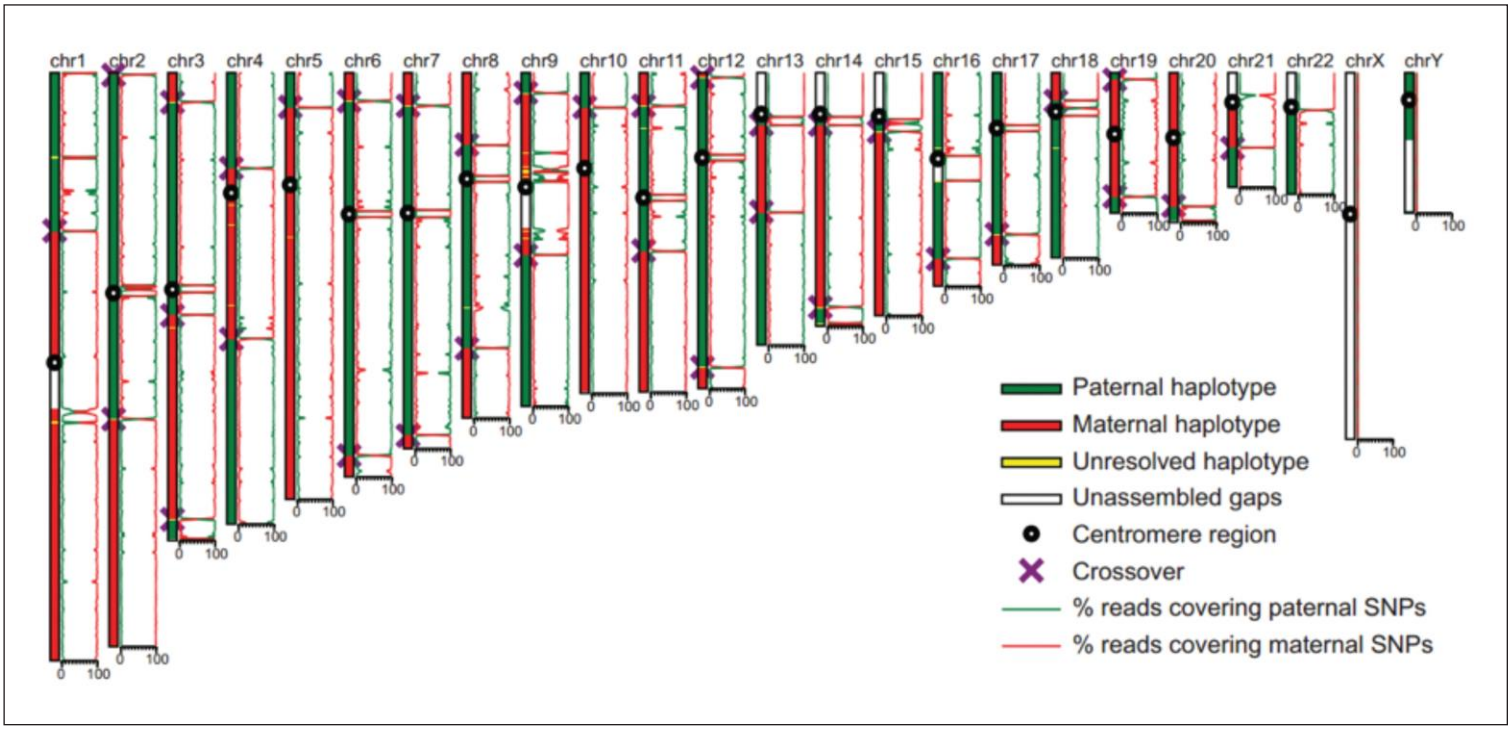
Project Example

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

Probing meiotic recombination and aneuploidy of single sperm cells by whole-genome sequencing.

Science, 338:1627-1630 (2012).

In this study, Medikonia's single-cell DNA sequencing technology was used to analyze the genomes of individual human sperm following amplification by MALBAC. The results revealed variation in the distribution of recombination events along the genome and provided new insights into meiotic mechanisms



Identifiying crossover positions in individual sperm cells