NGS & CTC Services at Prism

Prism Genomic Medicine Inc. is a biotech company located at Texas Medical Center, Houston, we are committed to provide services to facilitate medical research. Because every client's needs are different, we work closely with the researchers to understand the objectives and challenges of each project, we work with our clients to design experiments, then make the rest of process seamless.

Working with our partners, Prism offers wide range of advanced next generation sequencing (NGS) research services as well as our optimized bioinformatics solutions, including whole genome, whole exome, targeted panel sequencing and RNA Seq. We also provide circulating tumor cell (CTC) enumeration and CTC sequencing services.

The Advantage of Prism

- **Advanced technology.** State-of-the-art target enrichment and preparation kits and advanced Illumina sequencing platforms (NovaSeq, HiSeqX Ten, HiSeq4000, NextGen500 and MiSeqDx) to provide the most reliable and high-quality data.
- **Customized Services:** We understand that your project is unique with its own objectives and challenges. Regardless of size or complexity, each project will receive our personalized attention.
- **Fast turnaround times.** Fast and simple workflow, with our advanced sequencing platforms, we can greatly shorten your project cycle.
- **Quality control.** Rigorous quality control in all steps of the preparation and analysis to ensure high quality of final data.
- **Data quality guarantee.** We guarantee our data quality exceeds Illumina's official guarantee
- **Flexibility.** DNA, ctDNA and RNA from plasma, single cell, frozen tissue and FFPE samples are acceptable.
- **Competitive price.** Most cost-effective service for researchers, especially for ultra-deep sequencing coverage needs.
- **Strong NGS analysis.** Our professional bioinformatics team can provide tailored analysis services.
- **Additional bonus.** Free data storage (up to 10 Tb) on Prism computer cluster.

Contact us

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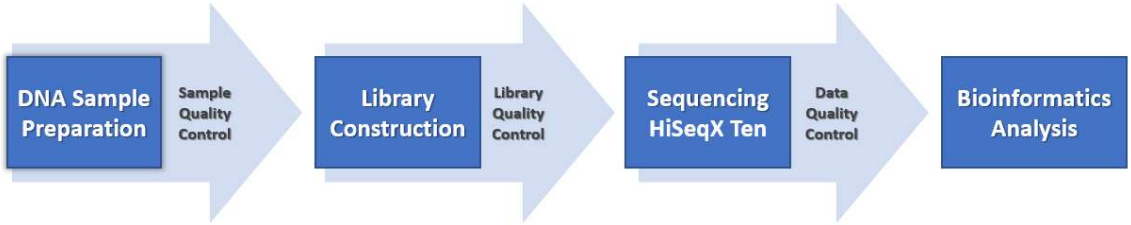
Human Whole Genome Sequencing (WGS)

Human whole genome sequencing enables researchers to catalog the genetic constitution of individuals and capture all the variants present in a single assay. It is applied to the study of cancer and a variety of diseases, as well as human population evolution studies and pharmacogenomics.



Overview of Service:

- State-of-the-art NGS technologies:
  - ✓ 350 bp insert DNA libraries
  - ✓ HiSeq X platform, paired-end 150 bp
- Highest data quality: We guarantee a Q30 score ≥ 80%, exceeding Illumina's official guarantee of ≥75%.
- Bioinformatics analysis:
  - ✓ Data quality control
  - ✓ Alignment with reference genome, statistics of sequencing depth and coverage
  - ✓ SNP/InDel, SV and CNV calling, annotation and statistics
  - ✓ Somatic SNP/InDel, SV and CNV calling, annotation and statistics for tumor-normal paired samples.
- Fast turnaround time:
  - ✓ 20 working days after verification of sample quality (without data analysis)
  - ✓ Additional 8 working days for data analysis

Recommended Sequencing Depth

- For tumor tissues: 50×, adjacent normal tissues and blood 30×
- For rare diseases: 30~50×

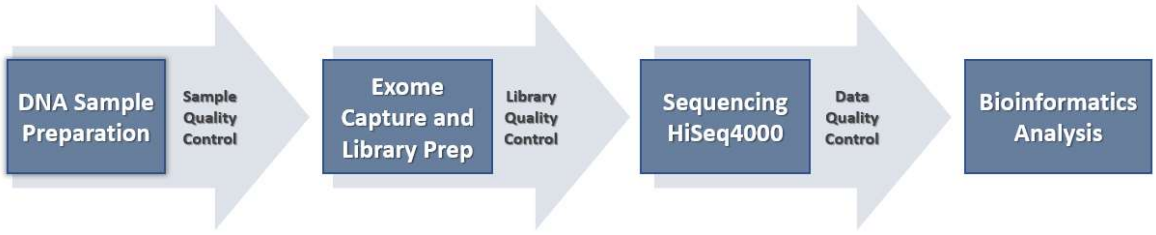
Sample requirements:

Sample Type	Remarks	Amount (μg) measured using Qubit	Volume (ul)	Concentration (ng/ul)	Purity
Genomic DNA	Strongly Recommended	≥1.0 μg	30	≥ 20ng/ul	OD260/280=1.8-2.0 No degradation No RNA contamination
	Required	≥0.5 μg	20		

Price: Depends on the number of samples needing for WGS, the prices start at $1195 per sample for WGS of 30X and 90Gb data.

Human Whole Exome Sequencing (WES)

Exome sequencing provides a cost-effective alternative to whole genome sequencing as it targets only the protein coding region of the human genome responsible for a majority of known disease related variants. Whether you are conducting studies in rare Mendelian disorders, complex disease, cancer research, or human population studies, Prism's comprehensive human whole exome sequencing service provides a high-quality, affordable and convenient solution.



Overview of Service:

- State-of-the-art exome capture and sequencing:
  - ✓ Agilent SureSelect Human All Exome V6 (58 M) is used.
  - ✓ Accurate variant calling with longer read length up to 150 bp.
  - ✓ Sequencing using HiSeq4000 platform, 150 PE
  - ✓ Unsurpassed data quality: Guarantee a Q30 score ≥80%
- Bioinformatics analysis:
  - ✓ Data quality control
  - ✓ Alignment with reference genome, statistics of sequencing depth and coverage;
  - ✓ SNP/InDel, SV and CNV calling, annotation and statistics
  - ✓ Somatic SNP/InDel, SV and CNV calling, annotation and statistics (only apply for tumor normal paired samples
- Fast turnaround time: Within 25 working days after verification of sample quality, additional 5 working days for data analysis

Recommended Sequencing Depth:

- For Mendelian disorder/rare disease: effective sequencing depth above 50× (6Gb)
- For tumor sample: effective sequencing depth above 100× (12Gb)

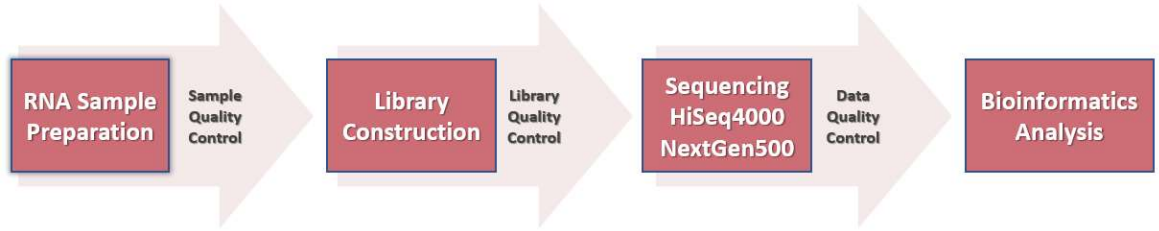
Sample requirements:

Sample Type	Remarks	Amount (μg) measured using Qubit	Volume (ul)	Concentration (ng/ul)	Purity
Genomic DNA	Strongly Recommended	≥1.2 μg	30	≥ 20ng/ul	OD260/280=1.8-2.0 No degradation No RNA contamination
	Required	≥0.6 μg	20		
FFPE slides	> 10 scrolls or slides or total RNA ≥1.5 μg				DV200 ≥ 25

Prices: Depending on sequencing depth and the number of samples to be sequenced, the price is estimated to be $549 per sample.

RNA-Sequencing

RNA-Seq provides a precise and complete snapshot of the transcriptome and enables the identification of novel transcripts, alternative splicing and gene fusion events. RNA-Seq also provides an alternative and affordable approach for gene expression quantification and differential gene expression analysis among groups of samples.



Overview of Service:

Sequencing Strategy:

- ✓ Library preparation using total RNA from frozen tissues and FFPRE tissues.
- ✓ Sequencing 150 x2 PE or 75x2 PE using HiSeq4000 or NextGene500 platform.

Bioinformatic analysis:

- Gene expression analysis (≥ 20 million reads recommended)
  - ✓ Mapping, alignment, and expression level reports
  - ✓ Comparison of expression levels between samples or sample groups
  - ✓ Go enrichment analysis and KEGG pathway analysis
- Transcriptomic data analysis (≥ 40 million reads recommended)
  - ✓ Mapping, alignment and expression level reports
  - ✓ Protein-protein interaction analysis
  - ✓ Functional annotation of transcription factors
  - ✓ Alternative splicing analysis
  - ✓ Fusion gene analysis
  - ✓ SNP/InDel analysis

Turnaround time: 20-30 days

Sample requirements:

Sample Type	Remarks	Amount (μg) measured using Qubit	Volume (ul)	Concentration (ng/ul)	Purity
Total RNA	Strongly Recommended	≥1.0 μg	30	≥ 20ng/ul	OD260/280=1.8-2.0 RIN ≥ 6.8 No DNA contamination
	Required	≥0.5 μg	20		
FFPE slides	> 10 scrolls or slides or total RNA ≥1.5 μg				DV200 ≥ 25

Prices: Depends on the data size needed for your research, our competitive price is estimated to be $330 per sample.

Single Cell DNA Sequencing

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.

We offer the highest quality single cell sequencing services including DNA amplification, library construction, sequencing and bioinformatics analysis using our unique technologies. We use a method has high fidelity amplification, thus, avoid artifact caused by cytosine deamination (mostly C - > T). It reduces error rate to ~ 200 false SNVs per single cell from > 20,000 false SNVs per single cell from most commonly used kit, and enables the discovery of accurate somatic single nucleotide variations (SNVs) in single cells.

Sequencing Strategy

- DNA amplification using a method allows yielding ~3ug DNA from a single cell for sequencing.
- 350 bp insert DNA library
- HiSeq platform, paired-end 150 bp

Data Quality Guarantee: Q30 ≥ 80%

Sample Requirements

- We accept fresh single cells and laser captured single cells from FFPE slides.
- Single CTC cell may be dissected using NanoVelcro-LCM technology.
- Sorted single cells should be stored in 1 x PBS buffer in a total volume of ≤ 2 μL.

Turnaround Time

- Amplification: within 12 working days from verification of sample quality
- Library preparation and sequencing: within 26 working days
- Data analysis: 8 working days

Recommended Sequencing Depth

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

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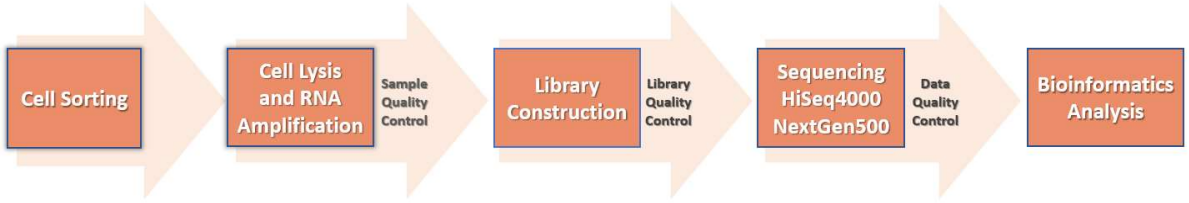
Single Cell RNA Sequencing

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. We offer the highest quality of single-cell RNA-Seq service includes amplification, library construction, sequencing, and bioinformatics analysis.



Sequencing Strategy

- SMARTer kit for single cell RNA amplification.
- 250-300 bp insert cDNA library
- Sequencing using HiSeq4000 or NextGene500 platform.

Data Quality Guarantee: Q30 ≥ 80%

Sample Requirements

- We accept fresh single cells and laser captured single cells from FFPE slides.
- Circulating tumor cells (CTC) may be purified using our Thermoresponsive CTC purification system and used for RNAseq.
- 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 cell should be frozen in liquid nitrogen and shipped out with dry ice.

Turnaround Time: 25 working days

Recommended Sequencing Depth

- ≥ 20 million reads for gene expression studies
- ≥ 40 million reads for transcriptome studies

Metagenomic Sequencing

Metagenomic sequencing is used to analyze the genomes of various species found in environmental samples. This powerful technique is used to study microbial communities in their natural habit. At Prism, we can provide the service you need to identify the species, genes and pathways represented in your samples. Our service is provided using the Illumina HiSeq platform with an assembly-first strategy and our bioinformatics analyses provide gene predictions, function annotations and taxonomic annotations. At Prism, we can guarantee high quality service, fast turnaround times at a low cost.

Sequencing Strategy

- 300 bp insert DNA library
- Illumina platforms, paired-end 150 bp

Data Quality Guarantee

- Q30 score ≥ 80%, exceeding Illumina's official guarantee of ≥75%

Sample Requirements

Sample Type	Remarks	Amount (μg) measured using Qubit	Volume (μl)	Concentration (ng/ul)	Purity
Genomic DNA	Strongly Recommended	≥1.6 μg	≥20 μL	≥ 50 ng/ul	OD260/280=1.8-2.0 No degradation No RNA contamination
	Required	≥0.8 μg			

Turnaround Time: 22 working days starting after we receive the library preparation confirmation from client, additional working days for data analysis

Prism Genomic Medicine

NanoVelcro Circulating Tumor Cells Assays

CTC technology provides an alternative to biopsies for areas with low tissue resources, and advanced studies using the isolated CTCs. Working with our partners, we provide circulating tumor cell (CTC) enumeration and CTC sequencing services.

- 1st-platform: NanoVelcro Chip, composed of a silicon nanowire substrate and an overlaid microfluidic chaotic mixer, allows capture CTCs for CTC enumeration and for CTC biomarker immunostaining.
- 2nd-platform: NanoVelcro-LCM technology can be used to enrich/identify/isolate CTCs with single-cell precision.
- 3rd-platform: Thermoresponsive CTC Purification System: By grafting thermoresponsive polymer brushes onto nanosubstrates, CTCs can be captured and released of CTCs at 37 and 4°C, respectively. The temperature-dependent conformational changes of polymer brushes can effectively alter the accessibility of the capture agent on nanosubstrates, allowing for rapid CTC purification with desired viability and molecular integrity.
- Purified CTCs can be subjected to a variety of molecular analyses, including mutational analysis by RT-PCR and Sanger sequencing, as well as NGS at both whole exome and whole genome levels.