LC Sciences

Human Whole Exome Sequencing

The human exome contains about 180,000 exons. These constitute about 1% of the human genome or about 30 megabases. The goal of this approach is to identify the functional variation that is responsible for both mendelian and common diseases without the high costs associated with whole-genome sequencing while maintaining high coverage in sequence depth. Thus, whole exome sequencing (WES) is a less expensive but still effective alternative to whole genome sequencing (WGS).

Applications

Cancer research

Human population studies

Genetic disease screening

Discovery of biomarkers and therapeutic targets

Our Features & Advantages

Quality Services

We have both Twist and Agilent exome probes available, and we have an official collaboration with agilent that can provide excellent service.

Extensive Experience

We have reliable sample processing capabilities and have successfully extracted tens of thousands of samples of all types, including blood, tissue, FFPE, swabs, etc.

Specialist Team

We have experienced experts to assist you with experimental design and data interpretation.

Reliable & Fast Turnaround Time

A dedicated project manager will be provided and the results will be given to you within 15 business days after sample quality verification.

Project Workflow

Sequencing Strategy: illumina Novaseq platform, PE150 bp, 20 Gb raw data/sample

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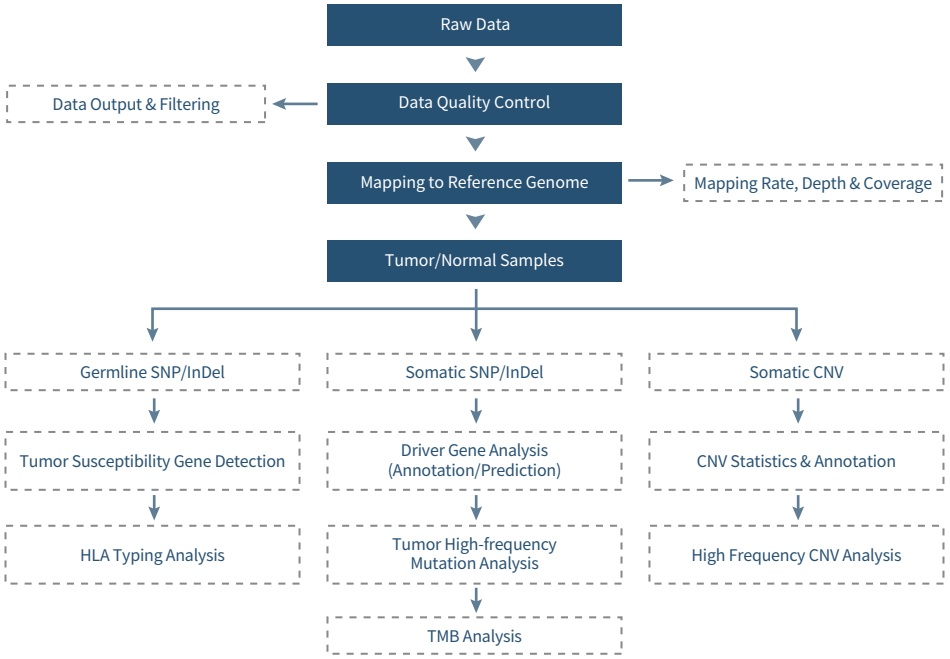
Bioinformatics Analysis Pipeline



Sample Requirements

Library Preparation	Sample Type	Amount	RIN	Purity
Exonme captured cDNA library	Genomic DNA	⩾1 μg	⩾20 ng/μl	260/280=1.8~2.0

Recent Publications

Journal	IF	Title	Year
Nature Communications	16.6	Lipid droplet-associated lncRNA LIPTER preserves cardiac lipid metabolism	2023
Nature Communications	16.6	Injectable, Self-Contained, Subaqueously Cross-Linking Laminous Adhesives for Biophysical-Chemical Modulation of Osteochondral Microenvironment	2023
Clinical Cancer Researchr	11.5	Design of fast-onset antidepressant by dissociating SERT from nNOS in the DRN	2022

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