Mouse Whole Exome Sequencing

1. Sample Requirements

Sample Type	Amount (Qubit®)	Volume	Concentration	Purity (NanoDrop™)
Genomic DNA	≥ 300 ng	≥ 15 µL	≥ 20 ng/µL	OD260/280=1.8~2.0; no degradation, no contamination
Genomic DNA from FFPE*	≥ 500 ng	-	-	Fragments shouldbe longerthan 1000bp

*FFPE: Formalin-fixed, paraffin-embedded

2. Sequencing Parameters

Platform	Illumina NovaSeq 6000
Read length	Paired-end 150 bp
Recommended sequencing depth	Effective sequencing depth above 50× (6 G)
Data quality	≥ 85% bases with Q30 or higher
**Turnaround time	5~6 weeks from verification of sample quality to data releasing without bioinformatic analysis

**Turnaround time varies depending on the project volume.

3. Data Analysis Contents

Standard analysis
Data quality control
Alignment with reference genome, statistics of sequencing depth and coverage
SNP and InDel calling, annotation and statistics
Somatic SNP/InDel/CNV calling, annotation and statistics (paired tumor samples)