Animal & Plant Whole Genome Sequencing

1.Sample Requirements

Library Type	Sample Type	Amount (Qubit®)	Volume	Concentration	Purity (NanoDrop™/Agarose Gel)
≤ 500 bp Insert DNA Library	Genomic DNA	≥ 200 ng	≥ 20 μL	≥ 10 ng/μL	OD260/280 =1.8~2.0, no degradation, no contamination
	Genomic DNA (PCR-free non- 350 bp)	≥ 5 μg	≥ 20 μL	≥ 30 ng/μL	
	Genomic DNA (PCR-free -350 bp)	≥ 1.2 μg	≥ 20 μL	≥ 20 ng/μL	

2.Sequencing Parameters

Platform	Illumina NovaSeq 6000
Read length	Paired-end 150
Recommended Sequencing Depth	SNP/InDel Detection--over 10× SV/CNV Detection--over 20×
Turnaround time	Guaranteed ≥ 85% bases with Q30 or higher

3. Data Analysis Contents

Standard Analysis
Data quality control: filtering reads containing adapter or with low quality
Alignment with reference genome, statistics of sequencing depth and coverage
Variant (SNP, InDel) calling, annotation and statistics
Advanced Analysis
SV calling, annotation and statistics
CNV calling, annotation and statistics