Animal & Plant *De novo* Sequencing

1.Sample Requirements

Library Type	Sample Type	Amount (Qubit®)	Volume	Concentration	Purity (NanoDrop™)
PacBio Library	Genomic DNA	⩾ 10 μg	⩾ 50 μL	⩾ 100 ng/μL	Fragments should be longer than 30 kb; No contamination; Non-viscous; No EDTA contained in DNA elution buffer.

2.Sequencing Parameters

GENOME SURVEY		
Platform	Illumina HiSeq Platform	
Sequencing Libraries	350 bp insert size	
Sequencing Strategy	PE150	
	SIMPLE GENOME *DE NOVO* SEQUENCING	COMPLEX GENOME *DE NOVO* SEQUENCING
Assembly Strategy I	50X PacBio Sequel long read data/Oxford PromethION reads data	
Data Quality Guarantee	Contig N50 ⩾ 1 Mb	Contig N50 ⩾ 300 kb
Assembly Strategy II	High quality de novo assembly (70X PacBio Sequel reads)	
Data Quality Guarantee	Contig N50 ⩾ 2 Mb	Contig N50 ⩾ 500 kb
Assembly Strategy III (Recommended)	Super-scaffold and chromosomal scale de novo assembly integrating PacBio Sequel reads/ Oxford PromethION reads and Hi-C	
Data Quality Guarantee	Contig N50 ⩾ 2 Mb Scaffold N50 ⩾ 4 Mb	Contig N50 ⩾ 500 kb Scaffold N50 ⩾ 1 Mb

3.Data Analysis Contents

Standard Analysis (Assembly)
Data quality control: filtering reads containing adapter or with low quality
Genome assembly with long reads
Quality assessment of genome assembly

Standard Analysis (Annotation)
Repeat Sequence Annotation
Gene Structure Annotation
Gene Function Annotation
Non-coding RNA Annotation

Standard Analysis (Comparative genomic analysis)
Phylogenetic analysis
Gene family analysis
Positive selection analysis
Synteny