P/A *De novo* Genome Assembly

Recommendations on tissue samples

Species	Tissue	Survey	PB	Hi-C
Animal	Visceral tissue	0.5 ~ 1g	≥3.5g	≥2.0g (for each library ≥ 300mg)
	Muscle tissue		≥5.0g	
	Mammalian blood		≥5.0mL	≥2mL/3 libraries
	Poultry/Fish blood		≥0.5mL	
Plant	Fresh Leaf	1 ~ 2g	≥5.0g	≥4.0g (for each library ≥ 1g)
	Petal/Stem	1 ~ 2g	≥10.0g	-
	Root/Seed	1 ~ 2g	≥20.0g	-
Cells	Cultured cell		≥1 x 10^8	≥1 x 10^7

Transcriptome sample for gene prediction	Tissue	NGS-transcriptome	TGS-transcriptome
Common plant	Root/Stem/Petal	450mg	600mg
	Leaf/Seed	300mg	300mg
	Fruit	1.2g	1.2g
Common animal	Heart/Intestine	300mg	300mg
	Viscera/Brain	240mg	240mg
	Muscle	450mg	450mg
	Bones/Hair/Skin	1g	1g
Arthropod	Insect	6	6
	Crustacea	300mg	300mg
Whole blood	blood	1 tube	1 tube

Note: Transcriptome samples used for gene prediction should preferably be mixed samples of multiple tissues to obtain more transcripts.

Nucleotides sample requirements

Species	Concentration and Purity					Integrity
	Qubit Conc.(ng/μl)	Amount(μg)	OD260/280	OD260/230	Nanodrop/Qubit	
PB CCS DNA	≥ 50	10μg/cell/20G	1.7-2.2	1.8-2.5	0.8-2.5	Agarose Gel: No or limited degradation. No or limited contamination.
PB RNA	≥ 120	≥ 0.6	1.7-2.5	0.5-2.5	-	RIN≥8.0 5 ≥ 28S/18S ≥ 1
ONT RNA	≥ 100	≥ 0.6	1.7-2.5	0.5-2.5	-	RIN≥7.5 5 ≥ 28S/18S ≥ 1
Illumina RNA	≥ 20	≥ 0.6	1.7-2.5	0.5-2.5	-	RIN≥6.5 5≥28S/18S≥1

P/A Population Genetics

Recommendations on tissue samples

Species	Tissue	WGS-NGS	WGS-ONT	SLAF
Animal	Visceral tissue	0.5 ~ 1g	≥3.5g	0.5g
	Muscle tissue		≥5.0g	
	Mammalian blood	1.5mL	≥5.0mL	1.5mL
	Poultry/Fish blood		≥0.5mL	
Plant	Fresh Leaf	1 ~ 2g	≥5.0g	0.5 ~1g
	Petal/Stem		≥10.0g	
	Root/Seed		≥20.0g	
Cells	Cultured cell		≥1 x 10^8	

Nucleotides sample requirements

Type	Concentration and Purity					Agarose Gel
	Conc.(ng/μl)	Amount(μg)	OD260/280	OD260/230	Nanodrop/Qubit	
SLAF	≥ 35	≥ 1.6	1.6-2.5	-	-	No or limited degradation. No or limited contamination.
WGS NGS	≥ 1	≥ 0.03	-	-	-	No or limited contamination. No or with degradation (The main band is clear).
WGS ONT	≥ 30	Refer to the table below	1.7-2.2	≥ 1.5	≤ 2	No or limited contamination. No or with degradation (The main band is clear).

Term	Nanopore								
Data Volume (G)	30	60	100	150	200	250	300	350	400
Library Number	1	2	3	4	5	6	7	8	9
Roughly extracted DNA amount (μg)	20	40	60	80	100	120	140	160	180
Purified DNA amount (μg)	10	20	30	40	50	60	70	80	90

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