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Sample Submission Guideline (Novogene AMEA)

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This sample submission guideline is for customers in the Asia Pacific and Middle East region (AMEA), excluding mainland China. For any questions, please contact your Novogene representative.

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- If you require extraction services that are not covered in this document, or have sample or library types that are not listed, please reach out to marketing_amea@novogeneait.sg or your local sales representative.
- For guidance on how to prepare DNA or RNA samples from various sources, please refer to our Sample Preparation Guide.
- It is recommended to double the sample amount when feasible, in case library re-construction is needed.
- Note that the sample volume for QC (2μL - 5μL) is excluded from the Sample Submission Guidelines.

DISCLAIMER: the requirements displayed in the following pages ensure the delivery of the best possible results and uphold Novogene's quality and performance standards. Samples with suboptimal conditions can be accepted but may not be eligible to meet the delivery standards. Even if all conditions are met, certain sample types or conditions may affect the success rate due to factors beyond our control.

1. Genome Sequencing

- It is recommended to suspend DNA samples in Tris-EDTA (TE) buffer, elution buffer (EB) or Tris-Borate (TB) buffer.
- High Molecular Weight (HMW) DNA samples should be in EB buffer. Please note quantities and conditions are provided as guidelines to optimize sequencing success. However, some sample types may still pose challenges.
- Note: For accurate nucleic acid quantification, we recommend using fluorometric methods (e.g., Qubit), while spectrophotometric methods (e.g., NanoDrop) can be useful for assessing sample purity. Please note that NanoDrop may overestimate nucleic acid concentration, which can result in discrepancies during our sample QC process.

1.1 Human Whole Genome Sequencing (WGS)

Library Type	Sample Type	Amount (Qubit®)	Volume	Concentration	Purity (NanoDrop™/ Agarose Gel)
Human whole genome library	Genomic DNA	≥ 100 ng	≥ 20 μL	≥ 5 ng/μL	OD260/280 = 1.8-2.0; no degradation, no contamination
	FFPE* DNA	≥ 400 ng	≥ 20 μL	≥ 15 ng/μL	Fragments longer than 1,000 bp
Human PCR-free library	Genomic DNA	≥ 1.2 μg	≥ 20 μL	≥ 50 ng/μL	OD260/280 = 1.8-2.0; no degradation, no contamination

* FFPE: Formalin-Fixed, Paraffin-Embedded

1.2 Whole Exome Sequencing (WES)

Library Type	Sample Type	Amount (Qubit®)	Volume	Concentration	Purity (NanoDrop™/ Agarose Gel)
Human WES library	Genomic DNA	≥ 300 ng	≥ 20 μL	≥ 15 ng/μL	OD260/280 = 1.8-2.0; no degradation, no contamination; Main peak is above 3000bp
	FFPE* DNA	≥ 400 ng	≥ 20 μL	≥ 15 ng/μL	Fragments longer than 1000 bp
	cfDNA/ctDNA	≥ 40 ng	≥ 20 μL	≥ 1 ng/μL	Fragments of 170 bp or multiples, no genomic DNA contamination
Mouse WES library	Genomic DNA	≥ 300 ng	≥ 20 μL	≥ 15 ng/μL	OD260/280 = 1.8-2.0; no degradation, no contamination

* FFPE: Formalin-Fixed, Paraffin-Embedded

1.3 Plant & Animal Whole Genome Sequencing

Library Type	Sample Type	Amount (Qubit®)	Volume	Concentration	Purity (NanoDrop™/ Agarose Gel)
Plant & Animal whole genome library	Genomic DNA	≥ 100 ng	≥ 20 μL	≥ 5 ng/μL	OD260/280 = 1.8-2.0; no degradation, no contamination
Plant & Animal PCR-free library	Genomic DNA	≥ 1.2 μg	≥ 20 μL	≥ 50 ng/μL	
GBS (Genotyping by sequencing) library	Genomic DNA	≥ 600 ng	≥ 20 μL	≥ 20 ng/μL	OD260/280 = 1.8-2.0; no degradation, no RNA contamination

1.4 Microbial Whole Genome Sequencing

Library Type	Sample Type	Amount (Qubit®)	Volume	Concentration	Purity (NanoDrop™/ Agarose Gel)
Bacteria / Fungi whole genome library	Genomic DNA	≥ 100 ng	≥ 20 μL	≥ 5 ng/μL	OD260/280 = 1.8-2.0; no degradation, no contamination
Bacteria / Fungi PCR-free library	Genomic DNA	≥ 1.2 μg	≥ 20 μL	≥ 50 ng/μL	

1.5 Metagenomics

Library Type	Sample Type	Amount (Qubit®)	Volume	Concentration	Purity (NanoDrop™/ Agarose Gel)
Shotgun-based metagenomics library	Total DNA	≥100 ng	≥ 20 μL	≥ 5 ng/μL	OD260/280 = 1.8-2.0; no contamination; Main peak is above 500bp
Shotgun-based metagenomics PCR-free library	Total DNA	≥ 1.2 μg	≥ 20 μL	≥ 50 ng/μL	
Amplicon-based metagenomics	Total DNA	≥ 200 ng	≥ 20 μL	≥ 10 ng/μL	OD260/280 = 1.8-2.0; no degradation, no contamination

1.6 PacBio DNA Sequencing

Library Type	Sample Type	Amount (Qubit®)	Volume	Concentration	Purity
PacBio DNA HiFi library	HMW* Genomic DNA (Human/ Plant/ Animal)	≥3.5 μg (Additional 3 ug per sample per Cell)	≥ 90 μL	≥ 40 ng/μL	OD260/280=1.75~2.0; OD260/230=1.5~2.6; NC/QC**=1.00~2.20; Fragments should be ≥30K
PacBio human low-input DNA HiFi library	HMW* Genomic DNA (Human)	≥ 1.2 μg (Only for 1 time sequencing in 1 Cell)	≥15 μL	≥70 ng/μL	OD260/280=1.75~2.0; OD260/230=1.5~2.6; NC/QC**=0.95~3.00; Fragments should be ≥30K
PacBio DNA HiFi library	HMW* Genomic DNA (Bacteria/ Fungus)	≥ 2 μg	≥ 40 μL	≥ 50 ng/μL	OD260/280=1.75~2.0; OD260/230=1.3~2.6; NC/QC**=1.00~2.20; Fragments should be ≥20K
PacBio DNA HiFi library	HMW* Genomic DNA (Metagenomics)	≥5.5 μg (Additional 5 ug per sample per Cell)	≥ 50 μL	≥ 80 ng/μL	OD260/280=1.75~2.5; OD260/230=1.1~2.6; NC/QC**=1.0~4.0; Fragments should be ≥ 10K
PacBio Full-length 16S library	Genomic DNA	≥ 300 ng	≥30 μL	≥ 10 ng/μL	Clear main band; no degradation; no contamination

* HMW: High Molecular Weight.
** NC/QC: NanoDrop concentration/Qubit concentration

1.7 Nanopore Sequencing

Library Type	Sample Type	Amount (Qubit®)	Volume	Concentration	Purity
Nanopore PromethION DNA library	HMW* Genomic DNA (Human/ Plant/ Animal)	≥ 8.5 μg	≥ 50 μL	≥ 100 ng/μL	OD260/280=1.75~2.0; OD260/230=1.4~2.6; NC/QC**=0.95~3.00 Fragments should be ≥30K
	HMW* Genomic DNA (Bacteria & Fungus)	≥ 3.5 μg	≥ 50 μL	≥ 60 ng/μL	OD260/280=1.7~2.2; OD260/230=1.3~2.6; NC/QC**=0.95~3.00 Fragments should be ≥15K
	HMW* Genomic DNA (Metagenomics)	≥ 5.5 μg	≥ 50 μL	≥ 80 ng/μL	OD260/280=1.7~2.5; OD260/230=1.1~2.6; NC/QC**=0.95~4.00 Fragments should be ≥10K
Nanopore Ultra-long DNA library	uHMW*** Genomic DNA (DNA extracted from Tissue)	≥ 20 μg	≥ 150 μL	≥ 135 ng/μL	OD260/280=1.7-2.0 OD260/230=1.3-2.6 NC/QC**=0.95-3.00 Fragments should be ≥ 100k, no fragments below 30k

	uHMW*** Genomic DNA (DNA extracted from Cell/ Blood)	≥ 30 μg	≥ 600 μL	≥ 50 ng/μL	OD260/280=1.7-2.0 OD260/230=1.3-2.6 NC/QC**=0.95-3.00 Fragments should be ≥ 300k, no fragments below 30k

* HMW: High Molecular Weight
** NC/QC: NanoDrop concentration/Qubit concentration
***uHMW: Ultra-High Molecular Weight

1.8 PCR Product Sequencing

Library Type	Sample Type	Amount (Qubit®)	Volume	Concentration	Purity (NanoDrop™/ Agarose Gel)
PCR-free library	PCR product	≥ 1.5 μg	≥ 20 μL	≥ 60 ng/μL	OD260/280 = 1.8-2.0; no degradation, no contamination
Library with PCR	PCR product	≥ 200 ng	≥ 20 μL	≥ 10 ng/μL	
PacBio/ Nanopore amplicon library	PCR product	≥ 2 μg	≥ 20 μL	≥ 50 ng/μL	OD260/280=1.75~2.0; OD260/230=1.4~2.6; NC/QC**=0.95~3.00 Single band >1kb

For all Genome Sequencing products,

- It is recommended to double the sample amount when feasible, in case library re-construction is needed.
- Note that the sample volume for QC (2μL - 5μL) is excluded from the Sample Submission Guidelines.

2. RNA Sequencing

It is recommended to suspend RNA samples in RNase-free double-distilled water (ddH2O). Ethanol is not a recommended solvent as it may interfere with downstream processes. Please note quantities and conditions are provided as guidelines to optimize sequencing success. However, some sample types may still pose challenges.

Note: For accurate nucleic acid quantification, we recommend using fluorometric methods (e.g., Qubit), while spectrophotometric methods (e.g., NanoDrop) can be useful for assessing sample purity. Please note that NanoDrop may overestimate nucleic acid concentration, which can result in discrepancies during our sample QC process. For RNA integrity, RIN values (or equivalent metrics) are acceptable.

2.1 Transcriptome Sequencing

Library Type	Sample Type	Amount	Volume	Concentration	RIN (Agilent 2100)	Purity (NanoDrop™)
Eukaryotic mRNA library (polyA enrichment)	Total RNA (animal/ plant/ fungus)	≥ 200 ng	≥ 20 μL	≥ 10 ng/μL	≥ 4.0, with flat baseline	OD260/280 ≥ 2.0; OD260/230 ≥ 2.0; no degradation, no contamination
	Total RNA (blood)	≥ 400 ng	≥ 20 μL	≥ 20 ng/μL	≥ 5.0, with flat baseline	
	Double stranded cDNA	≥ 100 ng	≥ 20 μL	≥ 5 ng/μL	Fragments between 400 bp-5000 bp, main peak at ~2000 bp	
Eukaryotic mRNA library (Globin removal & polyA enrichment)	Total RNA (human blood)	≥ 400 ng	≥ 20 μL	≥ 20 ng/μL	≥5.0, with flat baseline	
Eukaryotic strand-specific mRNA library (polyA enrichment)	Total RNA (animal/ plant/ fungus)	≥ 400 ng	≥ 20 μL	≥ 20 ng/μL	≥5.0, with flat baseline	
Eukaryotic strand-specific mRNA library (Globin removal & polyA enrichment)	Total RNA (human blood)*	≥ 400 ng	≥ 20μL	≥ 20 ng/μL	≥5.0, with flat baseline	
Prokaryotic strand-specific RNA library (rRNA depletion)	Total RNA	≥ 400 ng	≥ 20 μL	≥ 20 ng/μL	≥6.0, with flat baseline	
Dual RNA library (double rRNA depletion)	Total RNA	≥ 400 ng	≥20 μL	≥ 20 ng/μL	≥6.5, with flat baseline	

Metatranscriptome library (double rRNA depletion)	Total RNA	≥ 400 ng	≥ 20 μL	≥ 20 ng/μL	≥5.8, with flat baseline	
FFPE RNA library (TruSeq RNA Exome Panel)	FFPE total RNA	≥ 200 ng	≥ 10 μL	≥ 10 ng/μL	DV200 ≥ 30%	
FFPE RNA library (rRNA depletion and strand-specific library)	FFPE total RNA	≥ 400 ng	≥ 20μL	≥ 20 ng/μL	≥6.5, with flat baseline	Has main bands of 18S and 28S; no genomic contamination

* Globin clear applies to human blood only.

2.2 Eukaryotic Long Non-coding RNA Sequencing

Library Type	Sample Type	Amount	Volume	Concentration	RIN (Agilent 2100)	Purity (NanoDrop™)
Directional RNA library (rRNA depletion)	Total RNA (animal/ plant/ fungus)	≥ 300 ng	≥ 20 μL	≥ 15ng/μL	≥ 5.5, with flat baseline	OD260/280 ≥ 2.0; OD260/230 ≥ 2.0; no degradation, no genomic contamination
	Exosome RNA	⩾ 10 ng	⩾10 μL	-	Fragments between 80-200nt, no peaks> 2000nt, FU*>10, with flat baseline	
Directional RNA library (Globin removal & rRNA depletion)	Total RNA (human/ mouse blood)**	≥ 500 ng	≥ 20μL	≥ 20 ng/μL	≥5.5, with flat baseline	

* FU: Fluorescent unit
** Ribo-Zero Globin applies to human/mouse blood.

2.3 Eukaryotic Small RNA Sequencing

Library Type	Sample Type	Amount	Volume	Concentration	RIN (Agilent 2100)	Purity (NanoDrop™)
Eukaryotic small RNA library (18-40 bp insert)	Total RNA (animal/ plant/ fungus)	≥1.5 μg	≥20 μL	≥50 ng/μL	≥6.5, with flat baseline	OD260/280 ≥ 2.0; OD260/230 ≥ 2.0; no degradation, no contamination
	Exosome Total RNA	≥20 ng	≥20 μL	-	Fragments between 25-200nt, FU*>10, with flat baseline	

* FU: Fluorescent unit

2.4 Eukaryotic Circular RNA Sequencing

Library Type	Sample Type	Amount	Volume	Concentration	RIN (Agilent 2100)	Purity (NanoDrop™)
Eukaryotic circRNA directional library (rRNA and linear RNA depletion)	Total RNA (animal)	≥ 2 μg	≥ 20 μL	≥ 50 ng/μL	≥ 7.0, with flat baseline	OD260/280 ≥ 2.0; OD260/230 ≥ 2.0; no degradation, no contamination
	Total RNA (plant)	≥ 2 μg	≥ 20 μL	≥ 50 ng/μL	≥ 6.5, with flat baseline	

2.5 Eukaryotic Whole Transcriptome Sequencing

Library Type	Sample Type	Amount	Volume	Concentration	RIN (Agilent 2100)	Purity (NanoDrop™)
Eukaryotic lncRNA & small RNA library	Total RNA	≥ 2.5 μg	≥ 30 μL	≥ 50 ng/μL	≥ 7.5, with flat baseline	OD260/280 ≥ 2.0; OD260/230 ≥ 2.0; no degradation, no genomic contamination
Eukaryotic lncRNA & small RNA & circRNA library	Total RNA	≥ 4 μg	≥ 50 μL	≥ 50 ng/μL		

2.6 Long Read Transcriptome Sequencing

Library Type	Sample Type	Amount	Volume	Concentration	RIN (Agilent 2100)	Purity (NanoDrop™)
PacBio Kinnex full-length RNA library	Total RNA	≥ 1.2 ug	≥ 30 μL	≥ 40 ng/μL	≥ 6.5 with flat baseline	OD260/280=1.8-2.2; OD260/230=1.3-2.5; NC/QC* ≤ 2

* NC/QC: NanoDrop concentration/Qubit concentration

For all RNA Sequencing products,

- It is recommended to double the sample amount when feasible, in case library re-construction is needed.
- Note that the sample volume for QC (2μL - 5μL) is excluded from the Sample Submission Guidelines.

3. Epigenetics Sequencing

- It is recommended to suspend DNA samples in Tris-EDTA (TE) buffer, elution buffer (EB) or Tris-Borate (TB) buffer, and RNA samples in RNase-free double-distilled water (ddH2O).
- RIP-seq input controls should be rRNA-depleted prior to sample shipment.

3.1 Epigenetics Sequencing

Service	Sample Type	Amount (Qubit®)	Volume	Concentration	Purity or fragment size (NanoDrop™/Agarose Gel)
Whole Genome Bisulfite Sequencing (WGBS)	Genomic DNA	≥ 200 ng	≥ 20 μL	≥ 5 ng/μL	0 < OD260/230 < 3; no degradation; no contamination
Reduced Representation Bisulfite Sequencing (RRBS)	Genomic DNA	≥ 1 μg	≥ 20 μL	≥25 ng/μL	0 < OD260/230 < 3; no degradation; no contamination.
Enzymatic Methylation Sequencing	Genomic DNA	≥ 30 ng	≥ 30 μL	≥ 1 ng/μL	0 < OD260/230 < 3; no contamination; Fragments should be above 3000bp
Enzymatic Methylation Sequencing	cfDNA	≥ 20 ng	≥ 20 μL	≥ 1 ng/μL	Main peak at 170 bp or its integer multiples
ChIP-seq	Enriched DNA	≥ 20 ng	≥ 20 μL	≥ 1 ng/μL	Main peak within 100 bp-500 bp
RIP-seq	Enriched RNA (after rRNA depletion)	≥ 30 ng	≥ 30 μL	≥ 1 ng/μL	Main peak ≥ 80
Me-RIP	Total RNA	≥ 30 μg	≥ 600 μL	≥ 50 ng/μL	RIN ≥ 5 with flat baseline; no degradation; no contamination.
Me-RIP low-input library	Total RNA (Human/Mouse)	≥ 2 μg	≥ 40 μL	≥ 50 ng/μL	RIN ≥ 5 with flat baseline; no degradation; no contamination.
Ribo-seq	RPF (Ribosome-Protected Fragment)	≥ 600 ng	≥ 6 μL	≥ 100 ng/uL	No observable color

4. Premade Library Sequencing

Premade libraries should be colourless. Sub-libraries must be pooled together prior to library shipment. Please note quantities and conditions are provided as guidelines to optimize sequencing success. However, some sample types may still pose challenges.

4.1 Library Volume

Sequencing platform & sequencing strategy	Sequencing data amount	Volume requirements
NovaSeq X Plus 10B PE150	Lane sequencing	≥70 μL (additional 70 μL for one more lane)
NovaSeq X Plus 25B PE150	Lane sequencing	≥ 130 μL/lane (additional 130 μL for one more lane)
NovaSeq X Plus PE150	X < 30 G	≥ 15 μL
	30 G ≤ X < 100 G	≥ 30 μL
	100 G ≤ X < 375 G	≥ 70 μL
NovaSeq 6000 SP 500 Cycle/ SE50	X < 30 M reads	≥ 15 μL
	30 M ≤ X < 100 M reads	≥ 25 μL
	100 M ≤ X < 400 M reads	≥ 50 μL
	Lane sequencing	≥ 70 μL/lane (additional 70 μL for one more lane)
NovaSeq6000 SP PE50/ SE50	Flowcell sequencing	≥ 140 μL/flowcell
DNB T7 PE150 (Illumina Linear Library)	X < 50 G reads	≥ 40 μL
	50 G ≤ X < 200 G reads	≥ 60 μL
	200 G ≤ X	≥ 80 μL
	Lane sequencing	≥ 80 μL/lane (additional 80 μL for one more lane)
DNB T7 PE100	Please check with our representatives	

4.2 Library Concentration

Sequencing platform & sequencing strategy	Library concentration
NovaSeq Platforms	≥ 2 ng/μL, quantified by Qubit® 2.0 (Life Technologies) or ≥ 2 nmol/L quantified by qPCR
DNB T7 PE150 (Illumina Linear Library)	≥ 2.5 ng/μL, quantified by Qubit® 2.0 (Life Technologies) or ≥ 12.6 nmol/L quantified by qPCR
DNB T7 PE100	Please check with our representatives

4.3 Library Size

- Library size includes: insert + adapters (120 bp) ± 50 bp (Does not apply to small RNA library)
- Libraries should have a single main peak, no multiple peaks, no adapter contamination, and no primer dimers.

Sequencing platform & sequencing strategy	Library size
NovaSeq PE150	> 300bp
DNBSEQ-T7 PE150	> 300bp
NovaSeq 6000 SE50/PE50	< 700bp
NovaSeq 500 cycles	> 370bp

5. Single Cell Sequencing

- Novogene's AMEA labs, dedicated to supporting basic research, operate at a BSL-1 safety level. For toxic animal or plant samples, or tissues from organisms classified above BSL-1, please contact Novogene representatives in advance to confirm safety acceptance.
- The quality of tissue or nucleic acid extraction is influenced by various factors, including species, tissue type, collection method, preservation conditions, extraction protocol, operator proficiency, laboratory equipment, and environment.
- To ensure high-quality cell/nuclei, please refer to the sample preparation protocols and run the pilot study for the rare sample type if necessary.

5.1 Single Cell 3'/5' Gene Expression Sequencing

Library Type	Sample Type	Sample Amount Requirement	Other Requirements	Shipment conditions
Single Cell 3' / 5' Gene Expression Sequencing	Fresh/Frozen Single Cell Suspension	Single cell number ⩾ 1,000,000; Recommend two 1.5 mL cryovials	Cell viability >70% received at lab Cell diameter: 5-30 μm	Frozen single cell suspension: ship with sufficient dry ice; Fresh single cell suspension: ship on wet ice
	Frozen Tissue	Tissue weight ≥ 50 mg Recommend at least two pieces of tissue per sample, in separate 1.5 mL cryovials	Do NOT rinse tissues prior to freezing	Shipment with sufficient dry ice
	Fresh Tissue*	Tissue weight ≥ 50 mg Recommend at least two pieces of tissue per sample, in separate 1.5 mL cryovials	Must be processed within 48hrs of harvest	Fresh tissue ship on wet ice
	Fresh Single Nuclei Suspension**	Single cell number ⩾ 1,000,000	Cell viability <10% Nuclei diameter: 5-30 μm	Onsite service

* Fresh tissue/fresh single cell suspension: For Singapore samples sent to Singapore Novogene lab. For Japan samples, please consult with technical specialist.

** Fresh Single nuclei suspension: On-site service only, as single nuclei cannot be frozen or shipped by ice.

5.2 Single Cell Immune Profiling (VDJ)

Library Type	Sample Type	Sample Amount Requirement	Other Requirements
Single Cell TCR/BCR library	Fresh Single Nuclei Suspension*	Single Cell Number ⩾ 1,000,000	Cell viability <10% Nuclei diameter: 5-30 μm
	Frozen Single Cell Suspension	Single cell number ⩾ 1,000,000; Recommend two 1.5 mL cryovials	Cell viability >85% before freezing Cell viability >70% received at lab Cell diameter: 5-30 μm

* Fresh Single Nuclei Suspension: For onsite service in Singapore Only

5.3 Single Cell ATAC Sequencing

Library Type	Sample Type	Sample Amount Requirement	Other Requirements
Single Cell ATAC library	Frozen Tissue	Tissue weight ≥ 50 mg Recommend at least two pieces of tissue per sample, in separate 1.5 mL cryovials	Do NOT rinse tissues prior to freezing

5.4 Single Cell Long Read Sequencing

Library Type	Sample Type	Sample Amount Requirement	Other Requirements
Nanopore cDNA Library	Single Cell Suspension*	Single Cell Number ⩾ 1,000,000	Viability ⩾ 80%, Diameter: 5-40 μm
	cDNA	≥ 50 ng	Peak Size: 1-1.8 kb Concentration > 2 ng/ul No more than 2 months storage under -20℃/-80℃

* Single Cell Suspension: For onsite service in Singapore only.

6. Spatial Transcriptome Sequencing

- Spatial omics allows researchers to map gene expression within the spatial architecture of tissues, preserving the context of cellular organization. Unlike conventional RNA sequencing that aggregates data from bulk tissue samples, spatial transcriptomics retains the spatial distribution of gene expression, enabling a detailed exploration of cellular interactions and tissue heterogeneity.
- This technology reveals critical insights into the spatial arrangement and functional states of cells within their native microenvironments, which is essential for understanding developmental biology, pathology, and therapeutic responses. Novogene's spatial omics services provide comprehensive solutions, from spatial gene expression profiling to advanced data analysis, empowering researchers to decode the spatial complexity of tissues with precision.

6.1 10x Visium V2 (CytAssist) Spatial Transcriptome / 10x Visium HD Spatial Transcriptome

Service	Sample Type	Sample Amount Requirement	Preservation	Sample QC	Shipping
10x Visium V2/ 10x Visium HD Spatial Transcriptome	FFPE block (recommended)	1 block, FFPE block must be contained on plastic dehydrating box, otherwise could not be installed on the sectioning device	After embedding store at 4°C, protected from light	DV200% ⩾30%	4°C or Room Temperature
	FFPE slide	5-10 FFPE (10μm thickness) scrolls in tube for sample QC; 2-4 FFPE (5μm thickness) tissue sections on glass slides for library prep*	Dry and sealed, storage time at 4°C < 14 days	DV200% ⩾30%	4°C or Room Temperature
	Fresh Frozen (OCT embedded block)	Tissue thickness > 1mm, area < 6.5×6.5mm	Store at -80°C in a refrigerator	RIN⩾4	Dry ice

* From FFPE section to library prep, try to keep the interval within 14 days as much as possible.
* FFPE blocks should be no older than 3 years.

6.2 Stereo-seq Spatial Transcriptome

Service	Sample Type	Sample Amount Requirement	Preservation	Sample QC	Shipping
Stereo-seq Spatial Transcriptome	FFPE block* (recommended)	1 block, FFPE block must be contained on plastic dehydrating box, otherwise could not be installed on the sectioning device	After embedding store at 4°C, protected from light	DV200% ⩾30%	4-8°C (ice pack) or Room Temperature
	FFPE section	10-15 FFPE (5μm thickness) scrolls in 1.5mL tube for sample QC; 4-6 FFPE (5μm thickness) tissue sections, place each FFPE sections into a new 50 ml centrifuge tubes for library prep	Dry and sealed, storage time at 4°C < 14 days	DV200% ⩾30%	4-8°C (ice pack) or Room Temperature
	Fresh frozen (OCT embedded block)	For samples with a thickness greater than 1mm, the area should be less than 0.9cm × 0.9cm	Store at -80°C in a refrigerator	RIN⩾4	Dry ice

*FFPE blocks should be no older than 3 years.

6.3 10x Xenium Spatial Transcriptome

Service	Sample Type	Sample Amount Requirement	Preservation	Sample QC	Shipping
10x Xenium Spatial Transcriptome	FFPE block	Tissue thickness greater than 1 mm, area less than 10.5 mm × 22.5 mm.	storage time at 4°C within 1 year	RIN⩾4 DV200%⩾30%	4-8°C (ice pack) or Room Temperature

7. Olink Proteomics

- The Olink Explore HT and Olink Reveal are multiplex, high-throughput biomarker analysis platform based on Proximity Extension Assay (PEA) technology. PEA technology combines an antibody-based immunoassay with the powerful properties of next generation sequencing (NGS). This provides a scalable multiplex protein biomarker platform with exceptional specificity and sensitivity while using minimal sample volumes.
- Olink enables proteomic profiling, biomarker discovery, and mechanism insight across diverse areas of clinical research.

7.1 Olink Proteomics

Service	Sample Type	Sample Amount Requirement	Preservation	Sample QC	Shipping
Olink Proteomics	Serum/Plasma	50 μL or more in 1.5μL clear tubes	Store sample at -80°C immediately after extraction. Hemolysis may affect analysis results.	It is recommended to perform a visual inspection of the hemolysis level before sample submission. For more details, please consult our specialist.	Please include sufficient dry ice and send by frozen delivery, to avoid sample thawing during shipping
	Other sample matrices: CSF, lysates, etc. *Please contact us for more information				

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