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.
- 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)	≥ 30 μL	≥40 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 Amplicon 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 PCR Product 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 Nanopore; single band > 5kb for PacBio

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.

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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	
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	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	DV200 ≥ 30%	

* Globin clear applies to human blood only.

2.2 Eukaryotic Total RNA (Long Non-coding RNA) Sequencing

Library Type	Sample Type	Amount	Volume	Concentration	RIN (Agilent 2100)	Purity (NanoDrop™)
Total RNA directional library (rRNA depletion)	Total RNA (animal/ plant/ fungus)	≥ 300 ng	≥ 20 μL	≥ 15ng/μL	≥ 6.5, 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	
Total RNA directional library (Globin removal & rRNA depletion)	Total RNA (human/ mouse blood)	≥ 500 ng	≥ 20 μL	≥ 20 ng/μL	≥5.5, with flat baseline	

* FU: Fluorescent unit

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)	≥2 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	≥10 ng	≥10 μL	-	Fragments between 25-200nt	

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/fungi)	≥ 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 total RNA & 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 total RNA & 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 full-length mRNA 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
Enzymatic Methylation Sequencing	Genomic DNA	≥ 30 ng	≥ 30 μL	≥ 1 ng/μL	0 < OD260/230 < 3; no contamination; Fragments should be above 3000 bp
	cfDNA	≥ 20 ng	≥ 20 μL	≥ 1 ng/μL	Main peak at 170 bp or its integer multiples
Directed DNA Methylation Sequencing (DM-Seq)	Genomic DNA	≥ 20 ng	≥ 20 μL	≥ 1 ng/μL	0 < OD260/230 < 3; no degradation; no contamination
	cfDNA	≥ 20 ng	≥ 20 μL	≥ 1 ng/μL	Main peak at 170 bp or its integer multiples
	FFPE genomic DNA	≥ 20 ng	≥ 20 μL	≥ 1 ng/μL	0 < OD260/230 < 3; Fragments should be above 1000 bp
Reduced Representation Bisulfite Sequencing (RRBS)	Genomic DNA	≥ 1 μg	≥ 20 μL	≥25 ng/μL	0 < OD260/230 < 3; no degradation; no contamination.
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

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	≥ 25 μL
	100 G ≤ X < 375 G	≥ 60 μL
NovaSeq 6000 SP 500 Cycles	X < 30 M reads	≥ 15 μL
	30 M ≤ X < 100 M reads	≥ 25 μL
	100 M ≤ X < 400 M reads	≥ 35 μL
	Lane sequencing	≥ 35 μL/lane (additional 35 μL for one more lane)
NovaSeq X Plus 1.5B 100 Cycles	Flowcell sequencing	≥ 140 μL
DNB T7 PE150 (Uncircularized Library)	X < 50 G	≥ 30 μL
	50 G ≤ X < 200 G	≥ 40 μL
	200 G ≤ X	≥ 50 μL
	Lane sequencing	≥ 50 μL/lane (additional 50 μL for one more lane)
DNB T7 PE100 (DNBelab C4 Single Cell Library)	Lane sequencing	≥ 50 μL/lane (additional 50 μL for one more lane)

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/PE100 (Uncircularized Library)	≥ 2.5 ng/μL, quantified by Qubit® 2.0 (Life Technologies) or ≥ 12 nmol/L quantified by qPCR

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	300-700bp
DNBSEQ-T7 PE150	> 300bp
NovaSeq 100 cycles	< 700bp
NovaSeq 500 cycles	> 370bp

4.4 Important Guidelines & Best Practices

4.4.1 Index Information Guidelines

Accurate Sample-Index Tracking:

- Precisely record the exact index assigned to each sample during library preparation to prevent downstream demultiplexing errors and sample mix-ups.

Recommended Index Strategy:

- Recommended: Use dual-index (8-bp) combinations to ensure faster processing and optimal sequencing turnaround time.
- Not Recommended: Avoid single-index (6-bp or 8-bp) configurations. These have a higher likelihood of index collision, which may delay sequencing scheduling.

Single-Cell Libraries:

- Single-cell libraries frequently exhibit high index duplication rates. We strongly advise distributing index selections across different combinations to prevent index collision within the same batch.

In-Batch Index Duplication:

- If samples within the same submission batch contain identical index sequences, sequencing turnaround time will be extended to accommodate necessary scheduling adjustments.

Lane Sequencing:

- To maintain optimal base diversity, we strongly recommend pooling at least 5 unique index combinations per lane.

4.4.2 Accurate Library Type Selection

Critical Requirement:

- Accurate identification of the library type is essential. Incorrect library type specification may compromise sequencing strategies, leading to reduced total data yield or uneven lane output.

4.4.3 Non-Compliant / Special Samples

Prior Evaluation:

- If your samples do not fully meet the standard quality or concentration requirements, please consult your assigned Sales Representative or Technical Support Specialist for evaluation prior to submission.

4.4.4 Special Sample Preparation & Storage

Clear Labeling:

- For libraries delivered in non-standard formats (such as lyophilized/freeze-dried powder), please clearly specify the storage state and reconstitution instructions on the Sample Submission Form.

High Viscosity Risk:

- Please ensure samples are thoroughly dissolved and non-viscous. Excessively viscous self-prepared libraries cannot be accurately pipetted, which will prevent successful QC execution.

5. Single Cell Sequencing

Single-cell sequencing enables researchers to investigate cellular heterogeneity by profiling gene expression and other molecular features at single-cell resolution. Unlike conventional bulk sequencing, which measures averaged signals across cell populations, single-cell technologies provide detailed insights into individual cell types, cellular states, and functional diversity.

High-quality sample preparation and proper handling are essential for reliable single-cell sequencing results. Novogene's Single-Cell Sample Submission Guidelines outline sample requirements, preparation, storage, and shipping conditions to help maintain sample integrity. Researchers are encouraged to follow recommended sample preparation protocols and consider pilot studies for rare or challenging sample types.

5.1 Single Cell 3'/5' Gene Expression Sequencing

Library Type	Sample Type	Sample Amount Requirement	Other Requirements	Shipping 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 with ice packs
	Frozen Tissue	Tissue weight ≥ 200 mg (minimum 100mg) Recommend at least two pieces of tissue per sample, in separate 1.5 mL cryovials	Do NOT rinse tissues prior to freezing	Ship with sufficient dry ice
	Fresh Tissue*	Tissue weight ≥ 200 mg (minimum 100mg) Recommend at least two pieces of tissue per sample, in separate 1.5 mL cryovials	Must be processed within 48hrs of harvest	Place in tissue preservation solution, and ship with ice packs.

* Fresh tissue and fresh single-cell suspension samples must be shipped to the Novogene laboratory in the respective region: Singapore samples to the Singapore lab, Japan samples to the Japan lab, and Hong Kong samples to the Hong Kong lab.

5.2 Single Cell Flex v2 (Multiplexing)

Service	Sample Type	Sample Amount Requirement	Other Requirements	Shipping Conditions
Single Cell Flex v2	Fresh*/Frozen Single Cell Suspension	For frozen cell suspension: Single cell number ≥ 2,000,000; Recommend two 1.5 mL cryovials	Cell viability >70% received at lab; Cell diameter: 5-30 μm; Fixation service needed.	Frozen single cell suspension: ship with sufficient dry ice; Fresh single cell suspension: ship with ice packs
	Frozen Tissue	Tissue weight ≥ 200 mg (minimum 100mg) Recommend at least two pieces of tissue per sample, in separate 1.5 mL cryovials	Do NOT rinse tissues prior to freezing	Ship with sufficient dry ice
	Fresh Tissue*	Tissue weight ≥ 200 mg (minimum 100mg) Recommend at least two pieces of tissue per sample, in separate 1.5 mL cryovials	Must be processed within 48hrs of harvest	Place in tissue preservation solution, and ship with ice packs.
	FFPE block (recommended)	1 block, FFPE block must be contained on plastic dehydrating box, otherwise could not be installed on the sectioning device	DV200%≥30%; After embedding store at 4°C, protected from light.	Ship at 4°C (ice pack)

* Fresh tissue and fresh single-cell suspension samples must be shipped to the Novogene laboratory in the respective region: Singapore samples to the Singapore lab, Japan samples to the Japan lab, and Hong Kong samples to the Hong Kong lab.

5.3 Single Cell Immune Profiling (VDJ)

Library Type	Sample Type	Sample Amount Requirement	Other Requirements	Shipping Conditions
Single Cell TCR/BCR library	Fresh*/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	Frozen single cell suspension: ship with sufficient dry ice; Fresh single cell suspension: ship with ice packs
	Fresh tissue*	Tissue weight ≥ 200 mg (minimum 100mg) Recommend at least two pieces of tissue per sample, in separate 1.5 mL cryovials	Must be processed within 48hrs of harvest	Place in tissue preservation solution, and ship with ice packs.

* Fresh tissue and fresh single-cell suspension samples must be shipped to the Novogene laboratory in the respective region: Singapore samples to the Singapore lab, Japan samples to the Japan lab, and Hong Kong samples to the Hong Kong lab.

5.4 Single Cell ATAC Sequencing

Library Type	Sample Type	Sample Amount Requirement	Other Requirements	Shipping Conditions
Single Cell ATAC library	Frozen Tissue	Tissue weight ≥ 200 mg (minimum 100mg) Recommend at least two pieces of tissue per sample, in separate 1.5 mL cryovials	Do NOT rinse tissues prior to freezing	Ship with sufficient dry ice

5.5 Single Cell Long Read Sequencing

Library Type	Sample Type	Sample Amount Requirement	Other Requirements	Shipping Conditions
Nanopore cDNA Library	Fresh*/Frozen Single Cell Suspension*	Single Cell Number ≥ 1,000,000	Viability ≥ 80%, Diameter: 5-40 μm	Frozen single cell suspension: ship with sufficient dry ice; Fresh single cell suspension: ship with ice packs
	Fresh tissue*	Tissue weight ≥ 200 mg (minimum 100mg) Recommend at least two pieces of tissue per sample, in separate 1.5 mL cryovials	Must be processed within 48hrs of harvest	Place in tissue preservation solution, and ship with ice packs.
	cDNA	≥ 50 ng	Peak Size: 1-1.8 kb; Conc. > 2 ng/ul; No more than 2 months storage under -20℃/-80℃	Ship with dry ice

* Fresh tissue and fresh single-cell suspension samples must be shipped to the Novogene laboratory in the respective region: Singapore samples to the Singapore lab, and Hong Kong samples to the Hong Kong lab.

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 HD Spatial Transcriptome

Service	Sample Type	Sample Amount Requirements	Preservation	Sample QC	Shipping Conditions
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 (ice pack)
	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 < 4 weeks	DV200% ≥30%	4°C (ice pack)

* From FFPE section to library prep, try to keep the interval within 14 days as much as possible.

6.2 Stereo-seq Spatial Transcriptome

Service	Sample Type	Sample Amount Requirements	Preservation	Sample QC	Shipping Conditions
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)
	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 section into a new 50 ml centrifuge tube for library prep	Dry and sealed, storage time at -20°C < 4 weeks	DV200% ≥30%	Dry ice

6.3 10x Atera Spatial Transcriptome

Service	Sample Type	Sample Amount Requirements	Preservation	Sample QC	Shipping Conditions
10x Atera 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. Recommended to be stored <1 year	DV200% ≥30%	4-8°C (ice pack)
	FFPE slide	4 FFPE glass slides (1 for H&E staining, 1 for actual run, 2 as backups), tissue thickness is 5 μm. Must use the recommended slide type.	Dry and sealed, protected from light. After slicing, storage time at room temperature < 4 weeks	DV200% ≥30%	4-8°C (ice pack)
	FFPE section	5-10 FFPE (5μm thickness) scrolls in 1.5mL tube for sample QC; ≥4 FFPE (5μm thickness) tissue sections, place each FFPE section into a new 50 ml centrifuge tube for Atera run	Store at -80°C less than 4 weeks	DV200% ≥30%	Ship with dry ice

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, Cell/Tissue Lysates, etc. *Please contact us for more information				

8. Mass Spectrometry

For the sample guidelines of Untargeted Metabolomics and Quantitative Proteomics, please refer to the link below for details:

https://oss-website-sgp-ec.novogene.com/wp-content/uploads/2026/09/Novogene-AMEA-Sample-Submission-Guideline_Metabolomics-and-Proteomics-2026-09-V1_updated.pdf

https://amea.novogene.com/
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