Novogene | Advancing Genomics, Improving Life

NOVOGENE EUROPE SAMPLE REQUIREMENTS

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General submission guidelines

- Nucleic acid samples should be clear, colorless, and free from visible impurities.
- Please submit samples in 1.5-2mL EP tubes with secure caps to avoid leakage during transport.
- For sample extraction services or sample types or library types not listed in this document, please contact us or your local sales representative.
- For human tissue handling, refer to Human Sample Handling Guidelines.
- To ensure smooth processing, we strongly **recommend submitting at least 2× the minimum required amount whenever possible**, to accommodate QC variability and potential repeat testing.

The requirements displayed in this document ensure optimal sequencing quality and turnaround time.

- **Minimum total amount** indicates the minimum acceptable input required for successful library preparation.
- **Minimum volume** is critical to minimize sample loss during quality control procedures.
- **Concentration thresholds** are recommended guidance values and should not be interpreted as absolute cutoffs.

Samples not meeting these guidelines may be placed on hold pending customer confirmation and may proceed under reduced performance expectations. Final outcomes depend on multiple factors beyond our control.

1. GENOME SEQUENCING

Sample buffer and QC recommendations

- Suspend DNA samples in Tris-EDTA (TE) buffer, elution buffer (EB) or Tris-Borate (TB) buffer. For High Molecular Weight (HMW) DNA samples, we recommend EB buffer.
- Use fluorometric quantification (e.g., Qubit), for accuracy. Spectrophotometric methods (e.g., NanoDrop) may overestimate concentration.
- NanoDrop is still useful for assessing purity (OD260/280, OD260/230), but discrepancies may occur during internal QC.

1.1 HUMAN WHOLE GENOME SEQUENCING (WGS)

Service	Sample Type	Minimum amount	Minimum volume	Recommended concentration	Purity
Human WGS	Genomic DNA	≥100 ng	≥20 μL	≥5 ng/μL	OD260/280 = 1.8-2.0. no degradation, no contamination Fragments longer than 1000 bp
	FFPE* DNA	≥300 ng	≥20 μL	≥10 ng/μL	Fragments longer than 1000 bp
	cfDNA/ctDNA*	≥30 ng	-	≥0.5 ng/μL	Fragments of 170 bp or multiples, no genomic DNA contamination
PCR-free human WGS	Genomic DNA	≥1.2 μg	≥20 μL	≥20 ng/μL	OD260/280 = 1.8-2.0. no degradation, no contamination

*FFPE: Formalin-Fixed, Paraffin-Embedded; cell-free DNA, circulating-tumor DNA

1.2 WHOLE EXOME SEQUENCING (WES)

Service	Sample Type	Minimum amount	Minimum volume	Recommended concentration	Purity
Human WES	Genomic DNA	≥300 ng	≥20 μL	≥15 ng/μL	OD260/280 = 1.8-2.0. no degradation, no contamination Fragments longer than 3000 bp
	FFPE* DNA	≥300 ng	≥20 μL	≥15 ng/μL	Fragments longer than 1000 bp
	cfDNA/ctDNA*	≥30 ng	-	≥0.5 ng/μL	Fragments of 170 bp or its multiples, no genomic DNA contamination
Mouse WES	Genomic DNA	≥300 ng	≥15 μL	≥20 ng/μL	OD260/280 = 1.8-2.0. no degradation, no contamination Fragments longer than 3000 bp
	FFPE DNA	≥300 ng	≥20 μL	≥15 ng/μL	Fragments longer than 1000 bp

*FFPE: Formalin-Fixed, Paraffin-Embedded; cell-free DNA, circulating-tumor DNA

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1.3 PLANT & ANIMAL WHOLE GENOME SEQUENCING

Service	Sample Type	Minimum amount	Minimum volume	Recommended concentration	Purity
Plant & Animal WGS	Genomic DNA	≥100 ng	≥20 μL	≥5 ng/μL	OD260/280 = 1.8-2.0. no degradation, no contamination Fragments longer than 1000 bp
PCR-free Plant & Animal WGS (~330 bp insert size)	Genomic DNA	≥1.2 μg	≥20 μL	≥20 ng/μL	OD260/280 = 1.8-2.0. no degradation, no contamination
PCR-free Plant & Animal WGS (custom size, ≤500 bp)	Genomic DNA	≥2 μg	≥20 μL	≥30 ng/μL	

1.4 MICROBIAL WHOLE GENOME SEQUENCING & METAGENOMICS

Service	Sample Type	Minimum amount	Minimum volume	Recommended concentration	Purity
Microbial WGS	Genomic DNA	≥100 ng	≥20 μL	≥5 ng/μL	OD260/280 = 1.8-2.0. no degradation, no contamination Fragments longer than 1000 bp
Shotgun-based metagenomics	Total DNA*	≥100 ng	≥20 μL	≥5 ng/μL	OD260/280 = 1.8-2.0. no degradation, no contamination Fragments longer than 500 bp
PCR-free WGS / PCR-free shotgun-based metagenomics	Genomic DNA / total DNA*	≥1.2 μg	≥20 μL	≥20 ng/μL	OD260/280 = 1.8-2.0. no degradation, no contamination
Amplicon-based metagenomics	Total DNA*	≥200 ng	≥20 μL	≥10 ng/μL	

*Total DNA includes all types of DNA present in a sample, including genomic DNA, mitochondrial DNA and any other extrachromosomal DNA.

1.5 PACBIO SEQUENCING

Service	Sample Type	Minimum amount	Minimum volume	Recommended concentration	Purity
PacBio WGS HiFi library	HMW genomic DNA (Plant & Animal)	≥3 μg	≥50 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
	HMW genomic DNA (Bacteria & Fungus)	≥1.5 μg	≥30 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 Metagenomics HiFi library	HMW genomic DNA (metagenomics)	≥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
PacBio Full -Length 16S/18S/ITS	Isolated DNA	≥150 ng	≥30 μL	≥10 ng/μL	OD260/280 = 1.8-2.0. no degradation, no contamination

*HMW = High Molecular Weight; NC/QC = NanoDrop concentration/Qubit concentration

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1.6 NANOPORE SEQUENCING

Service	Sample Type	Minimum amount	Minimum volume	Recommended concentration	Purity
Nanopore WGS	HMW* genomic DNA (Human)	≥8 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 ⩾20K
Nanopore WGS	HMW genomic DNA (Plant & Animal)	≥8 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 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
Nanopore Metagenomics	HMW genomic DNA (metagenomics)	≥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

*HMW = High Molecular Weight; NC/QC = NanoDrop concentration/Qubit concentration

1.7 PCR PRODUCT SEQUENCING

Service	Sample Type	Minimum amount	Minimum volume	Recommended concentration	Purity
PCR-Free library	PCR product (multiple bands)	≥1.5ug	≥20 μL	≥40 ng/μL	OD260/280 = 1.8-2.0. No/slightly degradation, no/slightly contamination
	PCR product (one single band)	≥200 ng	≥20 μL	≥10 ng/μL	OD260/280 = 1.8-2.0. no degradation, no contamination

2. RNA SEQUENCING

Suspend RNA samples in RNAse-free double-distilled water (ddH_2O). Ethanol is not a recommended solvent as it may interfere with downstream processes.
NanoDrop can be used for purity (OD260/280 and OD260/230) but may **overestimate concentration**.

2.1 EUKARYOTIC MESSENGER RNA SEQUENCING

Service	Sample Type	Minimum amount	Minimum volume	Recommended concentration	RIN	Purity
Eukaryotic mRNA (polyA enrichment)	Total RNA (animal)	≥100 ng	≥10 μL	≥10 ng/μL	≥4.0, with flat baseline	OD260/280≥2.0. OD260/230≥2.0. no degradation, no contamination
	Total RNA (plant, fungus)	≥100 ng	≥10 μL	≥10 ng/μL	≥4.0, with flat baseline	
	Total RNA (blood)	≥400 ng	≥20 μL	≥20 ng/μL	≥5.0, with flat baseline	
	Double stranded cDNA	≥100 ng	≥10 μL	≥10 ng/μL	Fragments between 400 bp-5000 bp, main peak at ~2000 bp	
Strand-specific Eukaryotic mRNA (polyA enrichment)	Total RNA (animal)	≥200 ng	≥10 μL	≥20 ng/μL	≥5.0, with flat baseline	
	Total RNA (plant, fungus)	≥200 ng	≥10 μL	≥20 ng/μL	≥5.0, with flat baseline	
	Total RNA (blood)	≥400 ng	≥20 μL	≥20 ng/μL	≥5.0, with flat baseline	

2.2 TRANSCRIPTOME SEQUENCING

Service	Sample Type	Minimum amount	Minimum volume	Recommended concentration	RIN	Purity
Eukaryotic strand-specific lncRNA (rRNA depletion)	Total RNA (animal)	≥300 ng	≥10 μL	≥20 ng/μL	≥5.5, with flat baseline	OD260/280≥2.0. OD260/230≥2.0. no degradation, no contamination
	Total RNA (plant, fungus)	≥300 ng	≥10 μL	≥20 ng/μL	≥5.5, with flat baseline	
	Total RNA (blood)	≥500 ng	≥10 μL	≥20 ng/μL	≥5.5, with flat baseline	
	Exosome RNA (human, mouse, rat)	≥5 ng	≥12 μL	-	Fragments between 25-200nt, FU*>10, with flat baseline	
	Exosome RNA (animal or plant)	≥20 ng	≥12 μL	-	Fragments between 25-200nt, FU*>10, with flat baseline	
	FFPE** RNA	≥400ng	≥10 μL	≥20 ng/μL	≥6.5, with flat baseline	
Prokaryotic strand-specific RNA (rRNA depletion)	Total RNA	≥300 ng	≥10 μL	≥20 ng/μL	≥6.0, with flat baseline	
Metatranscriptome (Double rRNA depletion)	Total RNA	≥300 ng	≥20 μL	≥15 ng/μL	≥5.8, with flat baseline	

*FU = Fluorescent unit
**FFPE: Formalin-Fixed, Paraffin-Embedded. RIN ≥6.5 is listed for internal QC flagging only; samples below this may still be acceptable.

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2.3 EUKARYOTIC SMALL RNA SEQUENCING

Service	Sample Type	Minimum amount	Minimum volume	Recommended concentration	RIN	Purity
Eukaryotic sRNA (18-40 bp insert)	Total RNA (animal)	≥1 μg	≥20 μL	≥50 ng/μL	≥7.5, with flat baseline	OD260/280≥2.0. OD260/230≥2.0. no degradation, no contamination
	Total RNA (plant, fungus)	≥1 μg	≥20 μL	≥50 ng/μL	≥7.0, with flat baseline	
	Exosome RNA (human, mouse, rat)	≥10 ng	≥10 μL	-	Fragments between 25-40nt, FU*>10, with flat baseline	
	Exosome RNA (animal or plant)	≥25 ng	≥10 μL	-	Fragments between 25-40nt, FU*>10, with flat baseline	

*FU = Fluorescent unit

2.4 EUKARYOTIC CIRCULAR RNA SEQUENCING

Service	Sample Type	Minimum amount	Minimum volume	Recommended concentration	RIN	Purity
Eukaryotic circRNA (rRNA and linear RNA depletion)	Total RNA (animal)	≥1 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, fungus)	≥1 μg	≥20 μL	≥50 ng/μL	≥6.5, with flat baseline	

2.5 EUKARYOTIC WHOLE TRANSCRIPTOME SEQUENCING

Service	Sample Type	Minimum amount	Minimum volume	Recommended concentration	RIN	Purity
Eukaryotic lncRNA & sRNA	Total RNA	≥1.5 μg	≥30 μL	≥50 ng/μL	≥7.5, with flat baseline (animal) ≥7.0, with flat baseline (plant, fungus)	OD260/280≥2.0. OD260/230≥2.0. no degradation, no contamination
Eukaryotic lncRNA & sRNA & circRNA	Total RNA	≥2.5 μg	≥50 μL	≥50 ng/μL		

2.6 LONG READ TRANSCRIPTOME SEQUENCING

Service	Sample Type	Minimum amount	Minimum volume	Recommended concentration	RIN	Purity
PacBio Full-length Transcriptome Sequencing (polyA enrichment)	Total RNA	≥600 ng	≥15 μL	≥40 ng/μL	≥6.5 with flat baseline	OD260/280=1.8-2.2. OD260/230=1.3-2.5. NC/QC*≤2
Nanopore RNA (polyA enrichment)	Total RNA	≥100 ng	≥10 μL	≥10 ng/μL		

*NC/QC = NanoDrop concentration/Qubit concentration

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2.7 SINGLE CELL TRANSCRIPTOMICS

Service	Assay	Sample Type	Recommended amount	Other details
snRNA-seq	3' GEX	Fresh Frozen tissues/organoids	> 50 mg	• Shipped in cryovials with dry ice.
scRNA-seq	3' GEX 5' GEX + VDJ* (*Mouse and human only*)	Cryopreserved cell suspensions	2-3 M cells Cell viability > 70%	• Samples should be cryopreserved with freezing media. • Shipped in cryovials with dry ice.
		Fresh tissues/organoids	> 50 mg	• Novogene will ship tissue storage solution. • Tissues must be placed in tissue storage solution immediately after retrieval and arrive in the lab within 48 hours. • Shipped with ice packs.
		Whole blood/Bone marrow (Mouse, Human, Rat)	2-4 mL	• Collected in EDTA vacutainer tubes. • Shipped with ice packs.

2.8 SPATIAL TRANSCRIPTOMICS

Service	Species Type	Sample Type	Minimum amount	RNA QC	Other Details
Spatial Transcriptomics (10X Genomics Visium HD, Probe-based)	Human Mouse	FFPE block	1 FFPE block Block thickness > 1mm	DV200 ≥ 30%	**For optimal capture area usage:** Multiple tissue pieces can be embedded into FFPE or OCT blocks 2 FFPE tissue sections can be placed on 1 glass slide, without overlap
		FFPE tissue sections	2-4 tissue sections on glass slides and RNA scrolls (Thickness > 50 μm)		
		Fresh (frozen) tisssues (Embedded in OCT blocks)	1 OCT block Block thickness > 1mm	RIN ≥ 4	

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3. EPIGENETICS SEQUENCING

Sample buffer and QC recommendations

- Suspend DNA samples in elution buffer (EB) or Tris-Borate (TB) buffer.
- For DNA methylation projects, **EDTA-containing buffers are not recommended**. Please submit DNA in nuclease-free water, as EDTA can chelate divalent cations and negatively affect enzyme activity in enzyme-based sequencing workflows.
- Use fluorometric quantification (e.g., Qubit), for accuracy. Spectrophotometric methods (e.g., NanoDrop) may overestimate concentration.
- NanoDrop is still useful for assessing purity (OD260/280, OD260/230), but discrepancies may occur during internal QC.

Service	Sample Type	Minimum amount	Minimum volume	Recommended concentration	Purity or fragment size
Whole Genome Bisulfite Sequencing (WGBS)	Genomic DNA	≥100 ng	≥20 μL	≥5 ng/μL	0 < OD260/230 < 3; no degradation, no contamination
Reduced Representation Bisulfite Sequencing (RRBS)	Genomic DNA	≥800 ng	≥20 μL	≥24 ng/μL	0 < OD260/230 < 3; no degradation, no contamination
Enzymatic Methylation Sequencing	Genomic/FFPE* DNA	≥100 ng	≥20 μL	≥5 ng/μL	0 < OD260/230 < 3; Fragments above 5000 bp, main peak above 13 kb
	cfDNA/ctDNA*	≥20 ng	-	≥3 ng/μL	Fragments of 170 bp or multiples, no genomic DNA contamination
DM-seq (TAPS+ or 5-base)	Genomic/FFPE* DNA	≥35 ng	≥15 μL	≥2 ng/μL	0 < OD260/230 < 3; no degradation, no contamination
	cfDNA/ctDNA*	≥20 ng	-	≥0.5 ng/μL	Fragments of 170 bp or multiples, no genomic DNA contamination
ChIP-seq	Enriched DNA	≥20 ng	≥12 μL	-	Main peak within 100 bp and 500 bp
Enriched RNA Sequencing (e.g. RIP-seq)	Enriched RNA (rRNA-depleted)	≥20 ng	≥10 μL	≥2 ng/μL	Fragments longer than 80 nt
	Total RNA	≥50 ng	≥20 μL	≥2.5 ng/μL	Fragments longer than 80 nt

*FFPE: Formalin-Fixed, Paraffin-Embedded; cell-free DNA, circulating-tumor DNA

4. OLINK PROTEOMICS

Service	Species Type	Sample Type*	Sample Minimum Volume	Other details
Olink® HT Explore or Olink® Reveal	Human	Plasma or serum	≥50 μL	• Frozen transport and storage (-80° C) • Hemolysis will affect the results

*Other sample types (e.g. cell culture supernatant, urine, CSF, saliva, tissue lysate, bone marrow, etc.) may be accepted if pre-treated according to Olink's protocol. Please contact us before preparing these samples.

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5. 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 library types may still pose challenges.

5.1 LIBRARY VOLUME

Sequencing platform & sequencing strategy	Sequencing data amount	Minimum volume requirement
NovaSeq X Plus PE150	<30 Gb	≥15 μL
	30 Gb ≤ X < 100 Gb	≥30 μL
	100 Gb ≤ X < 375 Gb	≥70 μL
	375 Gb ≤ X < 1 Tb	≥130 μL
	Lane sequencing on 10B	≥70 μL (additional 70 μL for one more lane)
	Lane sequencing on 25B	≥130 μL (additional 130 μL for one more lane)
NovaSeq series SE50/PE50/PE250	<20 M reads	≥15 μL
	20 M reads ≤ X < 50 M reads	≥25 μL
	50 M reads ≤ X ≤ 150 M reads	≥50 μL
	Lane sequencing	≥70 μL (additional 70 μL for one more lane)
AVITI24 SE50/PE50/PE75	per flow cell sequencing (2 lanes)	≥140 μL
AVITI24 PE150	per flow cell sequencing (2 lanes)	≥70 μL
AVITI24 PE300	per flow cell sequencing (1 lane)	≥70 μL

Illumina Only: For flow cell sequencing projects where custom sequencing primers (R1, R2, index) are needed, please send them with 100 μM concentration and 50 μL volume.

5.2 LIBRARY CONCENTRATION

- ≥ 2 ng/μL, quantified by Qubit® 2.0 (Life Technologies)
  ≥2 nM, quantified by qPCR

5.3 LIBRARY SIZE

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

Sequencing platform	Sequencing strategy	Library size
NovaSeq series / AVITI24	SE50/PE50 & PE75 (AVITI24 only)	<700 bp
NovaSeq X Plus / AVITI24	PE150	300 bp ~ 600 bp
NovaSeq 6000	PE250	>370 bp
AVITI24	PE300	>450 bp

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