

Novogene is a world-leader in Next Generation Sequencing and Bioinformatics. From our state-of-the-art facility in Cambridge UK, our leading-edge platforms, well-developed bioinformatics pipeline, extensive NGS experience, and highly skilled and supportive team help life science research and development organisations advance human health, agriculture and environmental protection.



We provide a complete end-to-end solution for DNA and RNA sequencing projects from extraction to data analysis.

Publication-ready analysis



Personalised service

- ▶ **Library construction:**
Send us your DNA or RNA samples. Choose the library type required. We will make your library ready for sequencing.
- ▶ **Pre-made libraries:**
We accept pre-made libraries.
- ▶ **Nucleic acid extraction:**
Simply send us your samples and we will do the rest.
- ▶ **Bioinformatics support:**
If you already have your data and need support for Bioinformatic analysis, we have various pipelines to meet different research objectives.

Your guide to sample requirements...

DNA SAMPLE REQUIREMENTS

SERVICE TYPE	SPECIES	SAMPLE TYPE	AMOUNT (QUBIT®)	VOLUME	CONCENTRATION	PURITY (NANODROPTM/AGAROSE GEL)
Whole genome sequencing	Human, Animal, Plant & Microbe	Genomic DNA	≥ 0.2 µg	≥ 20 µL	≥ 10 ng/µL	OD260/280 = 1.8-2.0, no degradation, no contamination
	Human, Animal & Plant	Genomic DNA (PCR-free low input)	≥ 1.5 µg	≥ 20 µL	≥ 20 ng/µL	
	Microbe				≥ 50 ng/µL	
	Human	FFPE* DNA	≥ 0.8 µg	-	-	Fragments should be longer than 1500 bp
Whole exome sequencing	Human & Mouse	Genomic DNA	≥ 0.4 µg	≥ 20 µL	≥ 20 ng/µL	OD260/280 = 1.8 – 2.0, no degradation, no contamination
		FFPE**	≥ 0.8µg	-	-	Fragments should be longer than 1000 bp
	Human	cfDNA/ctDNA	≥ 50 ng	-	-	Fragments should be in multiples of 170bp, no genomic contamination
Shotgun metagenomics		Genomic DNA	≥ 200 ng	≥ 20 µL	≥ 10 ng/µL	
Amplicon based metagenomics	Microbe	Genomic DNA	≥ 200 ng	≥ 20 µL	≥ 20 ng/µL	OD260/280 = 1.8 – 2.0, no degradation, no contamination
		PCR product	≥ 1.5 µg	≥ 20 µL	≥ 50 ng/µL	
De novo sequencing (Illumina)	Microbe	Genomic DNA	≥ 1 µg	≥ 20 µL	≥ 20 ng/µL	
De novo sequencing (PacBio)	Animal, Plant & Microbe	Genomic DNA (*HMW)	≥ 10 µg	≥ 50 µL	≥ 100 ng/µL	Fragments should be longer than 40K bp; no contamination; non-viscous; no EDTA contained in DNA elution buffer OD260/280=1.8-2.0; OD260/230=2.0-2.2; no degradation, no contamination
De novo sequencing (Nanopore)	Animal & Plant	Genomic DNA (*HMW)	≥ 10 µg	≥ 50 µL	≥ 100 ng/µL	OD260/280=1.8-2.0; OD260/230=2.0-2.2; no degradation or RNA contamination mainbands should be longer than 40K

RNA SAMPLE REQUIREMENTS

SERVICE TYPE	SAMPLE TYPE	AMOUNT	VOLUME	CONCENTRATION	RNA INTEGRITY NUMBER (AGILENT 2100)	PURITY (NANODROPTM)
Eukaryotic RNA-Seq	Total RNA (Animal)				≥ 6.8, with flat base line	
	Total RNA (Plant and Fungus)	≥ 0.4 µg	≥ 20 µL	≥ 20 ng/µL	≥ 6.3, with flat base line	
	Total RNA (Blood)	≥ 0.8 µg	≥ 20 µL	≥ 20 ng/µL	≥ 6.8, with flat base line	
	Amplified cDNA (double-stranded) or total RNA (single cell)	≥ 100ng	≥ 20 µL	≥ 10 ng/µL	Fragments distributing between 400 bp~5000 bp, with the main peak at ~2000bp	
Eukaryotic RNA-Seq (strand specific library)	Total RNA (Animal)				≥ 6.8, with flat base line	
	Total RNA (Plant and Fungus)	≥ 0.8 µg	≥ 20 µL	≥ 20 ng/µL	≥ 6.3, with flat base line	
Eukaryotic small RNA sequencing	Total RNA (Animal)	≥ 2 µg	≥ 20 µL	≥ 50 ng/µL	≥ 7.5, with smooth base line	OD260/280 ≥ 2.0; OD260/230 ≥ 2.0, no degradation, no contamination
	Total RNA (Plant and Fungus)				≥ 7, with smooth base line	
	Exosome RNA	≥ 20 ng	≥ 10 µL	-	Fragments distributing between 25-200 nt (by high sensitive Agilent 2100 Bioanalyzer), FU> 10, with no peak > 2000nt	
Eukaryotic lncRNA sequencing	Total RNA (Animal)				≥ 6.5, flat base line	
	Total RNA (Plant and Fungus)	≥ 2 µg	≥ 20 µL	≥ 50 ng/µL	≥ 6, flat base line	
	Exosome RNA	≥ 20 ng	≥ 10 µL	-	Fragments distributing between 25-200 nt (by high sensitive Agilent 2100 Bioanalyzer), FU> 10, with no peak > 2000nt	
Eukaryotic circRNA sequencing	Total RNA (Animal)	≥ 5 µg	≥ 20 µL	≥ 50 ng/µL	≥ 7, flat base line	
	Total RNA (Plant and Fungus)				≥ 6.5, flat base line	
Prokaryotic RNA-seq	Total RNA	≥ 3 µg	≥ 20 µL	≥ 50 ng/µL	≥ 6.0, with flat base line	
Meta-transcriptomics	Total RNA	≥ 2.5 µg	≥ 20 µL	≥ 50 ng/µL	≥ 6.5, with flat base line	

Sample delivery address:

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