Novogene

End-to-end solutions for DNA and RNA sequencing projects from **extraction** to **data analysis**.

Why Novogene?

Highest Quality

Industry-leading Q30 ≥ 85% guarantee

Largest Capacity

280,000 genomes per year

Latest Technology

Illumina, PacBio, Oxford Nanopore and Thermo Fisher systems

Fast Turnaround

Faster than local cores and the vast majority of service providers

Expert Analysis

"Publication-ready" data provided by expert bioinformaticians

For more details on our services and to download product flyers visit: om.novogene.com/flyers

Novogene is a leading provider of genomic services and solutions with cutting edge Next Generation Sequencing (NGS) and bioinformatics expertise. With one of the largest sequencing capacities in the world, we utilise our **deep scientific knowledge, first-class customer service and unsurpassed data quality** to help clients realise their research goals in the rapidly evolving world of genomics. With almost 2,000 employees, multiple locations around the world, 37 NGS related patents and over 790 publications in top tier journals such as Nature and Science, we have rapidly become a world-leader in NGS services.

Genomic Services

Species	Service	Research objective	Platform
Human	WGS/WES/Panel	SNP, SV, InDel and CNV detection	Illumina NovaSeq 6000 PacBio Sequel II/IIe Oxford Nanopore
Animal/Plant/ Microorganism	WGS	SNP, SV, InDel and CNV detection	
Animal/Plant/ Microorganism	*De novo*	Reference genome assembly & annotation	
Microbial community	Amplicon based metagenomics	Species annotation Community diversity investigation	Illumina NovaSeq 6000
Microbial community	Shotgun metagenomics	Metagenome assembly Species annotation Gene prediction & annotation Community diversity investigation	

Applications of Whole Genome Sequencing (WGS) range from disease research to population evolution studies. The protein-coding region of the genome can be analysed in more depth using Whole Exome Sequencing (WES). *De novo* sequencing offers reference genome assembly for rarely studied species. We also identify species within microbial communities with metagenomics.

Clinical & Biopharma Services

Service		Application	Platform
WGS		SNP, SV, InDel and CNV detection	Illumina NovaSeq 6000
PCR-free WGS		SNP, SV, InDel and CNV detection	
WES	Agilent probes	SNP, InDel detection, CNV only for paired samples	
WES	IDT probes	SNP, InDel detection, CNV only for paired samples	
Targeted Panels	NovoFocus CR	Hereditary Cancer Risk	
Targeted Panels	NovoPM2.0	Targeted therapies Immunotherapies (TMB, bTMB, MSI) Hereditary cancer risk genes Efficacy of chemotherapies	
RNA-seq (TruSeq exome)		Expression profiling	

Clinical services offer a range of options for analysis of human samples. Using Illumina NovaSeq 6000 technology, we offer WGS, WES, RNA-seq and target region analysis using our customised panels. Our panels provide enrichment analysis of over 600 cancer-linked genes to aid in the assessment of hereditary risk, diagnosis, and treatment options.

Find out more: om.novogene.com/flyers

Transcriptomic Services

Species	Service	Research objective	Platform
Eukaryotic	mRNA-seq	Transcript characterisation Quantification (gene or transcript level) Target prediction of ncRNA	Illumina NovaSeq 6000
	lncRNA-seq		
	circRNA-seq		
	sRNA-seq		
	Whole transcriptome sequencing (any combination of mRNA, lncRNA, circRNA & sRNA)		
	Full length mRNA-seq	mRNA isoform characterisation	PacBio Sequel II/IIe Oxford Nanopore
Prokaryotic	RNA-seq	Transcript characterisation & quantification	Illumina NovaSeq 6000
Microbial community	Metatranscriptome sequencing	Species annotation & gene quantification	Illumina NovaSeq 6000

RNA services offer whole transcriptome sequencing, as well as specific analysis of individual non-coding RNAs. With long-read PacBio and Nanopore technologies we provide isoform analysis of eukaryotic species. Analysis of prokaryotic species can be done at an individual level, and community level with our metatranscriptomic service.

Epigenetic Services

Service	Research objective	Platform
Whole genome bisulfite sequencing (WGBS)	Methylation characterization & quantification	Illumina NovaSeq 6000
Immunoprecipitated DNA sequencing for ChIP-seq	Characterisation of TF and DBP binding sites	Illumina NovaSeq 6000
Immunoprecipitated RNA sequencing for RIP-seq	Characterisation of RBP binding sites	Illumina NovaSeq 6000

We provide Whole Genome Bisulfite Sequencing (WGBS) for the detection of methylated cytosines on a genome-wide scale with a single nucleotide resolution, offering an insight into the modifying effects of this methylation on gene function and expression. With our ChIP-seq and RIP-seq services, we can analyse protein-DNA interactions (ChIP-seq) and RNA-protein interactions (RIP-seq).

Premade Libraries

We offer sequencing-only services for the following libraries:

- Illumina compatible libraries
- PacBio compatible libraries

For full details and sample requirements please visit our website or contact us to discuss your needs.

Publication-Ready Results

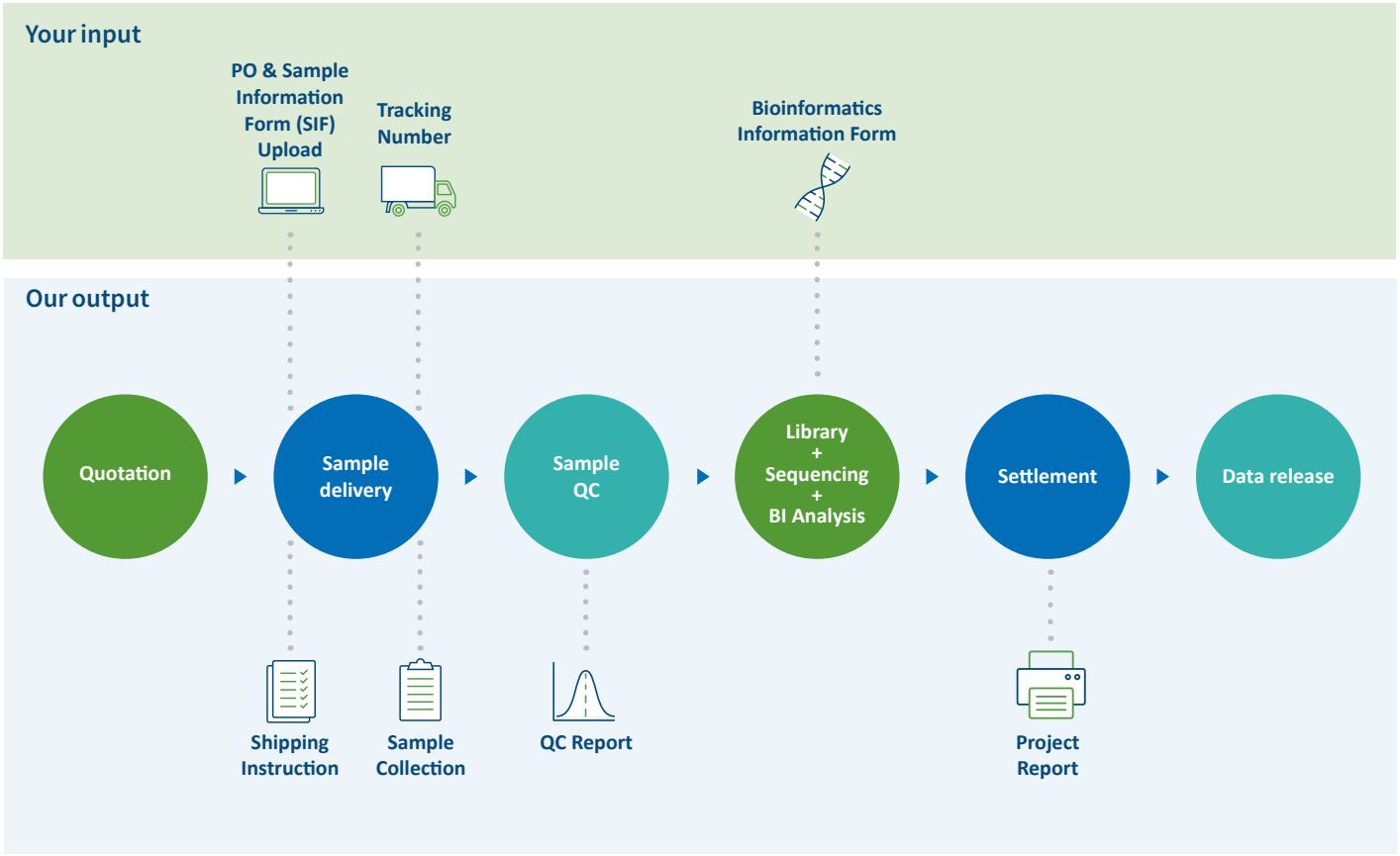
Generating useful information from your sequencing project can be difficult. Our accomplished bioinformaticians can analyse your data and help you generate publication-ready results.

- Automated systems for standard analysis
- Expert bioinformatics support for custom analysis
- Full-service solutions available

Our Platforms

illumina® PACBIO® Oxford NANOPORE Technologies

Our Workflow



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Contact Details

Our Sequencing Centre

Our Sequencing Centre on the Cambridge Science Park offers our customers an unrivalled sequencing service with a quick turn-around, exceptional data quality and expert PhD level advice and support throughout your project.

Our Locations

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For more details on our services and to download product flyers visit:
om.novogene.com/flyers

Novogene

Leading Genomic Services and Solutions