



# Whole Genome Sequencing

## at the Garvan Institute of Medical Research

Whole genome sequencing (WGS) generates a comprehensive overview of an organism's genomic makeup, including both coding and non-coding regions.

The Garvan Institute, through the Sequencing Laboratory in the Kinghorn Centre for Clinical Genomics, offers NATA (ISO15189) accredited WGS on its Illumina platforms. Our team have extensive experience in genomic research and can help create a bespoke service that fits your project goals.

### Why use whole genome sequencing?

#### Uniform coverage of the genome

WGS provides consistent, genome-wide coverage including protein-coding genes, non-coding RNAs, mitochondria and regulatory regions, regardless of annotation

#### Detect structural variations

WGS makes it possible to call copy number variations and structural variations (including translocations and inversions), as well as SNVs and indels

#### Applications across genomic research

WGS is a powerful tool for the diagnosis of inherited conditions, biomarker discovery, characterisation of cancer drivers, and much more

#### Flexible data analysis

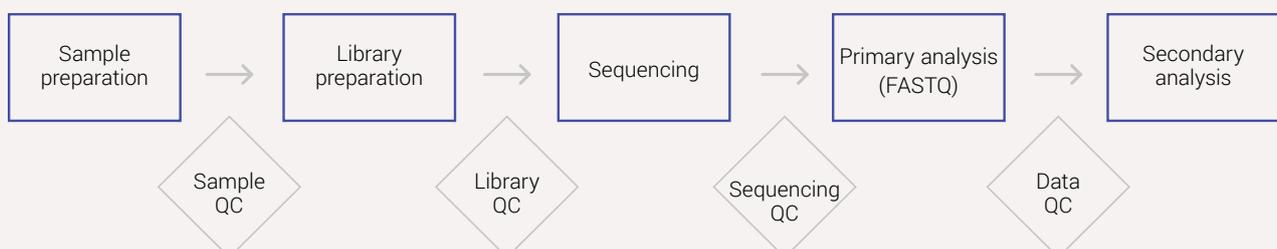
Data generated from WGS can be reanalysed and reinterpreted at any time, such as when new functional elements are identified, or to answer new research questions that arise

### What we offer

The KCCG Sequencing Laboratory is highly experienced in WGS, with over 20,000 whole genomes sequenced to date. We offer:

- Clinical grade end-to-end service, from library preparation through to data analysis
- Fast turnaround time with WGS data available within 6 weeks
- $\geq 75\%$  of bases above Q30 guaranteed
- Automated liquid handling and library preparations, with streamlined workflow for maximum efficiency
- Access to our team of genomic research and bioinformatics experts for advice and support

### How it works



## Technical specifications

<b>Sample</b>	100µL of gDNA with a concentration between 12-100ng/ul and A260:A280 of >1.8
<b>Sample type</b>	Genomic DNA from blood, fresh frozen tissue, saliva, cell lines or single cells
<b>Sequencing platforms</b>	Illumina HiSeq X Illumina HiSeq 2500 Illumina NovaSeq 6000
<b>Turn-around Time</b>	Standard turn-around time (TAT) of 4-6 weeks from date of acceptance to date of data delivery (dependent on project size)*.
<b>Data specifications</b>	>100GB, ≥75% bases above Q30, 2x150bp paired end reads
<b>Data format</b>	Raw data (FASTQ) delivered for all samples. Alignments (Bam) and variants (VCF) available as secondary analysis through our bioinformatics service
<b>Bioinformatics Services</b>	Clinically accredited pipeline using industry best practices (GATK) and reference genome hs37d5 (1000 Genome Project GRCh37 plus decoy) ClinSV pipeline for structural variant detection
<b>Delivery</b>	Cloud-based data delivery including 90 days of hosting. Hard drive delivery available on request at an additional cost.
<b>Coverage</b>	~30x for most human samples Coverage for non-human samples depends on genome size and project aims. Some projects may require deep sequencing. Our team can help to decide what coverage is required. We calculate coverage per Illumina specifications, read more at <a href="https://www.illumina.com/content/dam/illumina-marketing/documents/products/technotes/hiseq-x-30x-coverage-technical-note-770-2014-042.pdf">https://www.illumina.com/content/dam/illumina-marketing/documents/products/technotes/hiseq-x-30x-coverage-technical-note-770-2014-042.pdf</a>

\* Please contact the laboratory for any TAT concerns or specific requirements

## Location

KCCG Sequencing Laboratory is part of the Garvan Institute of Medical Research in Darlinghurst, NSW, Australia.

We receive samples from all over the world – visit [garvan.org.au/sequencing](https://garvan.org.au/sequencing) for international sample requirements, or contact our team to discuss further.

## Contact

To find out more or discuss your specific project needs, contact the KCCG Sequencing Laboratory team at [kccgseq@garvan.org.au](mailto:kccgseq@garvan.org.au)



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