

RNA Sequencing at the Garvan Institute of Medical Research

RNA sequencing generates an overview of a cell's transcriptome that can be used to analyse patterns of gene expression.

The Garvan Institute, through the Sequencing Laboratory in the Kinghorn Centre for Clinical Genomics, offers a full RNA sequencing service including RNA quality control, library preparation with RNA control spike-in, sequencing and data delivery.

Why use RNA Sequencing ?

High sensitivity

RNA sequencing can detect novel transcripts, gene fusions, SNVs and indels with a higher sensitivity than microarrays

Applications across research

Data from RNA sequencing is a powerful tool in cancer that can be used to study alternative splicing, or temporal studies of tumour models

Fully customisable service

Choose from RNA library preparation, sequencing or a full service – from library preparation through to data delivery

Bespoke sequencing

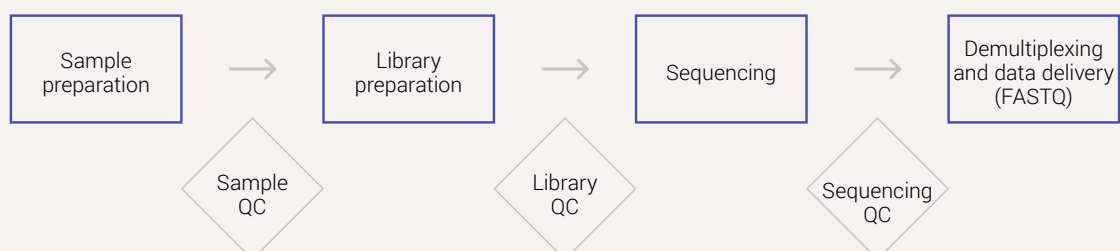
We offer custom RNA sequencing, including single cell sequencing, and can help design a service that fits your research goals

What we offer

The KCCG Sequencing Laboratory offers RNA sequencing on its suite of high throughput Illumina platforms.

- Multiple library preparation options – total RNA, mRNA, total RNA with rRNA depletion, total RNA with globin depletion
- Both high quality RNA and degraded RNA (e.g. from formalin-fixed paraffin embedded tissue) accepted
- Standard turnaround time of 4-6 weeks
- Custom RNA sequencing available, including single cell sequencing
- Access our team of genomic research and bioinformatics experts for advice and support

How it works



Sample specifications

Library Workflow	Type of RNA input	RNA Quantity	RNA Concentration	Species	RNA Quality
Total RNA *	Total RNA	≥1.5 ug	≥100ng/uL	Human, Mouse, Rat	RIN > 6.5
Total RNA	FFPE RNA	≥1.5 ug	≥50ng/uL	Human, Mouse, Rat	DV200 > 50%
mRNA	Total RNA	≥1.5 ug	≥100ng/uL	All except bacterial & viral	RIN > 6.5
mRNA	mRNA**	≥100 ng	≥10ng/uL	All except bacterial & viral	N/A

* Total RNA library preparation includes rRNA depletion

** mRNA enriched through capture of polyA tail, ribosomal RNA depletion or equivalent

Technical specifications

Sequencing platforms	Illumina NovaSeq 6000 Illumina NextSeq 550Dx Illumina HiSeq 2500
Turnaround Time	Standard turn-around time (TAT) of 4-6 weeks from date of acceptance to date of data delivery (dependent on project size)*.
Data format	Raw data delivered as FASTQ
Delivery	Cloud-based data delivery including 90 days of hosting. Hard drive delivery available on request at an additional cost.

* 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 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



Garvan Institute
of Medical Research