

University of Auckland Genomics Facility

Sequencing Platforms

We offer access to a range of Illumina sequencing platforms (MiSeq, NextSeq), as well as access, via our network, to HiSeq, X10 and PacBio.

A full ABI Sanger sequencing and genotyping service is also available

Libraries

We can prepare all standard library types, including:

- DNA libraries, both low and standard input
- Small RNA Libraries
- Amplicon Indexing/Metagenomic Libraries
- Nextera/Low Input Nextera Libraries
- Bisulfite Libraries
- Targeted Resequencing
- Illumina VeriSeq Embryonic Preimplantation Genetic Screening
- Small Genome Resequencing
- Single Cell RNAseq (late 2017)
- mRNA Sequencing – including molecular indexing

Affymetrix Genotyping and Gene Expression Arrays

All array types can be processed.

Genomic DNA Extraction, QC and submission for X10 or PacBio

We can assist researchers in the production of high-molecular weight DNA required for long reads and other whole genome sequencing applications. We can provide QC of DNA, complete the sample submission process and arrange shipping/customs clearance.

Bioinformatics services

Our bioinformatics team is available to discuss scientific collaborations on a case-by-case basis.

In addition, we can provide the following bioinformatics service and support:

- Advice on experimental design as it pertains to downstream bioinformatics analyses
- Post-production QC of sequencing and array data
- Assistance with genome/transcriptome assembly/mapping
- 16S/COI OTU calling
- Setup and running of custom/batch BLAST searches
- Educational training, upskilling & custom workshops

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