

# NEXT GENERATION SEQUENCING

## LIBRARY PREPARATION

### DNA Libraries

#### Shotgun Library

For paired end and single end sequencing for genomes and long range PCR products (>5kb).

#### Exome Enrichment

Targeted re-sequencing of coding regions of the human or mouse genome. For screening the high value content of genomes economically.

#### Custom Capture

Design custom captures to sequence specific regions of interest to your research. For projects when you have a specific target in mind.

#### Mate-Pair Library

The preparation of long insert libraries from 2-17kb. Compatible with paired end sequencing.

#### ChIP-Seq

An optimised library preparation when only small amounts of DNA are available.

#### Library QC

We offer a service to quantify a library you have prepared yourself prior to sequencing with our qPCR and Bioanalyser.

### RNA Libraries

#### mRNA or stranded mRNA Library

Preparation of mRNA sequence libraries from total RNA via purification of PolyA RNA. For transcriptome analysis or gene expression quantification.

#### Whole Transcriptome Library

The preparation of a whole transcriptome library for analysis of the coding and non-coding RNA.

#### Small RNA Library

Incorporation of small RNA molecules, 19-35 nucleotides. Enables discovery and expression profiling of microRNAs and other small non-coding RNA in any organism.

In addition to next-generation sequencing, we provide a broad range of biomedical services

#### Gene Expression

- RNASeq and transcriptomes
- Expression Arrays

#### Applied Genomics

- Microbial identification
- Clinical data supply
- Assay development

#### Bioinformatics and Analysis

- Project design
- Secondary analysis

#### Sequencing

- Next-Generation sequencing
- Sanger sequencing
- Pyrosequencing

#### Genotyping

- GWAS and Cytogenomics Arrays
- Custom SNP
- Microsatellites
- Pyrosequencing

#### Epigenetics and Structural Genomics

- Whole human genome
- Targeted region quantification

#### Sample Preparation

- DNA extraction
- DNA purification

## Reliable and consistent quality

Providing quality genomic services is our top priority.

We operate to a unique set of quality standards: we are CPA, GLP/GCP accredited and we are also Agilent and Illumina CPro certified.

Our Next Generation services have been accredited to the ISO/IEC 17025:2005 standard by the National Association of Testing Authorities (NATA) so you can be sure to receive industry leading data quality and service, consistently.



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## PLATFORM SPECIFICATIONS

### Illumina HiSeq2500 High Output Mode

Read length	50 cycle SR	100 cycle SR	100 cycle PE	125 cycle PE
Unit	lane	lane	lane	lane
Guaranteed* yield (clusters)	200 million	200 million	200 million	200 million
Range of yield (clusters)	200-250 million	200-250 million	200-250 million	200-250 million
Range of yield (reads)	200-250 million	200-250 million	400-500 million	400-500 million
Output	10.0 – 12.5 Gb	20.0 – 25.0 Gb	40.0 – 50.0 Gb	50.0 – 62.5 Gb
Indexing Options	Up to 96	Up to 96	Up to 96	Up to 96

### Illumina HiSeq2500 Rapid Mode

Read length	50 cycle SR	100 cycle PE	150 cycle PE	250 cycle PE
Unit	lane	lane	lane	lane
Guaranteed* yield (clusters)	120 million	120 million	120 million	120 million
Range of yield (clusters)	120-150 million	120-150 million	120-150 million	120-150 million
Range of yield (reads)	120-150 million	240-300 million	240-300 million	240-300 million
Output	6.0 – 7.5 Gb	24.0 – 30.0 Gb	36.0 – 45.0 Gb	60.0 – 75.0 Gb
Indexing Options	Up to 96	Up to 96	Up to 96	Up to 96

### Illumina NextSeq 500

	Mid Output Flow Cell		High Output Flow Cell		
Read length	75 cycle PE	150 cycle PE	75 cycle SR	75 cycle PE	150 cycle PE
Unit	flow cell	flow cell	flow cell	flow cell	flow cell
Guaranteed* yield (clusters)	100 million	100 million	320 million	320 million	320 million
Range of yield (clusters)	100-150 million	100-150 million	320-400 million	320-400 million	320-400 million
Range of yield (reads)	200-300 million	200-300 million	320-400 million	640-800 million	640-800 million
Output	15.0 – 22.5 Gb	30.0 – 45.0 Gb	24.0 – 30.0 Gb	48.0 – 60.0 Gb	96 -120 Gb
Indexing Options	Up to 96	Up to 96	Up to 96	Up to 96	Up to 96

### Illumina MiSeq

Read length	50 cycle SR	150 cycle PE	250 cycle PE	75 cycle PE	300 cycle PE
Unit	flow cell	flow cell	flow cell	flow cell	flow cell
Guaranteed* yield (clusters)	10 million	10 million	10 million	20 million	20 million
Range of yield (clusters)	10-15 million	10-15 million	10-15 million	20-25 million	20-25 million
Range of yield (reads)	10-15 million	20-30 million	20-30 million	40-50 million	40-50 million
Output	0.5 – 0.75 Gb	3.0 – 4.5 Gb	5.0– 7.5 Gb	3.0 – 3.75 Gb	12.0-15.0 Gb
Indexing Options	Up to 96	Up to 96	Up to 96	Up to 96	Up to 96

SR= single read, PE= paired end. \*shotgun & RNA seq

#### Our funding partners

AGRF is a not-for-profit organisation supported by the Commonwealth Government infrastructure schemes administered through Bioplatforms Australia.

These schemes include NCRIS, EIF, Super Science Initiative CRIS and NCRIS 2.



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