

# 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

### Reliable and consistent quality

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.



### 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.



Contact us: 1300 247 301

info@agrif.org.au

www.agrif.org.au/services

WEBNGS0915