Integrated GENOMICS Cores

HIGH THROUGHPUT SEQUENCING FACILITY

Illumina Platform Comparison Table

	MiSeq		HiSeq		
Platform	**MiSeq**	**MiSeq NANO**	**HiSeq 2500**	**HiSeq 2500-v4**	**HiSeq 4000**
Nickname for system	**MiSeq**	**Nano**	**Rapid Run**	**V4 / High Output**	**4000**
Flowcells processed	1	1	1 or 2	1 or 2	1 or 2
Lanes/flowcell	1	1	2	8	8
Max PAIRED END Reads/Flowcell	50 million	2 million	600 million	3.2 billion	8.6-10 billion
Max SINGLE END Reads/Flowcell	25 M	1 M	300 M	1.6 B	4.3-5 B
Clusters/Flowcell	25 M	1 M	300 M	1.6 B	4.3-5 B
Note: each cluster produces one single read or one paired-end read (10K clusters produces 10K single reads or 20K paired end reads)					
Read Type Format Available	Single or Paired End	Single or Paired End	Single or Paired End	Single or Paired End	Single or Paired End
Read Length Available	50X, 100X, 150X, 250X, 300x, , Custom	50X, 100X, 150X, 250X, Custom	50X, 100X,150x,250x, Custom	50X, 100X, Custom	50x, 75x, 150x, Custom
Guaranteed read # / lane *unless indicated otherwise* (see note below)	15M , single end, v3	1M, single end	100M, single end	100M, single end	200M, single end
	30 M, Paired end, v3				
	8 M, single end, v2	2M, paired end	200M, paired end	150M, paired end	300-350, paired end
	16 M , paired end , v2				
Key applications	Small genome, amplicon, and targeted gene panel sequencing, confirming complex balanced pools	Minimal data required. QAQC check for library quality and pool balance	Production-scale genome, exome, transcriptome, sequencing, and more	Production-scale genome, exome, transcriptome, sequencing, and more	the same as HiSEQ2500 with longer read lengths and more reads

	NextSeq2000		
Platform	**P1**	**P2 Reagents**	**P3 Reagents**
Nickname for system	NextSeq P1	NextSeq P2	NextSeq P3

Flowcells processed	1	1	1
Lanes/flowcell	1	1	1
Max PAIRED END Reads/Flowcell	200 M	800 million	2.2 billion
Max SINGLE END Reads/Flowcell	100 M	400 M	1.1 B
Clusters/Flowcell	100 M	400 M	1.1 B
Read Type Format Available	Paired End	Paired End	Paired End*
	*some single end runs available upon request		
Read Length Available	150x, Custom	50x, 100x, 150x, Custom	50x*, 50x, 100x, 150x, Custom
	na	na	*1x50 available
Guaranteed Data Yield/ Flowcell	100M Clusters	400M clusters	1.1 B clusters
	200M Paired End Reads	800M paired end Reads	2.2 billion paired end Reads
Key applications	Small WGS, WES, scRNA-Seq	Small WGS, WES, scRNA-Seq	Small WGS, WES, scRNA-Seq, smallRNA/miRNA-Seq

Novaseq Standard Loading (one pool/FLOWCELL)				
Platform	**S Prime**	**NovaSeq 6000 S1**	**NovaSeq 6000 S2**	**NovaSeq 6000 S4**
Nickname for system	**SP**	**S1**	**S2**	**S4**
Flowcells processed	1 or 2	1 or 2	1 or 2	1 or 2
Depth	200-250 Gb (2x150bp)	400-500 Gb (2x150bp)	1000-1250 Gb (2x150bp)	2400-3000 Gb (2x150bp)
Run time	1 dy – 2 dy	1 dy – 2 dy	1 dy – 3 dy	1 dy –3 dy
Lanes/Flowcell	2	2	2	4
Max PAIRED END Reads/Flowcell	1600 million	3.2 billion	7.6 billion	20 billion
Max SINGLE END Reads/Flowcell	800 M	1.6 B	3.8 B	10 B
Max Clusters/Flowcell	800 M	1.6 B	3.8 B	10 B
Read Type Format	Paired End			

Read Type Format	*single end available upon request, S4/SE/50x			
Read Length Available*	50x, 150x, Custom	50x, 100x, 150x, Custom	50x, 100x, 150x, Custom	100x, 150x, Custom
Guaranteed read #/flowcell (see note below)	1.4 billion, paired end	3 billion, paired end	7 billion, paired end	17 billion, paired end.
Key applications	WGS model organisms, FAIRE/ChIP-seq large pools, metagenomics	Single Trio Human, 10X single cell, Chip-seq transcriptome	Production-scale genome, exome, transcriptome, sequencing, and more	Large production-scale genome, exome, transcriptome, sequencing, and more

Novaseq-XP Mode Loading (one pool/LANE)				
Platform	**NovaSeq 6000 SP XP**	**NovaSeq 6000 S1 XP**	**NovaSeq 6000 S2 XP**	**NovaSeq 6000 S4 XP**
Nickname for system	**SP-XP**	**S1- XP**	**S2-XP**	**S4-XP**
Platform	NovaSeq 6000 SP XP	NovaSeq 6000 S1 XP	NovaSeq 6000 S2 XP	NovaSeq 6000 S4 XP
Flowcells processed	1	1	1	1
Depth	125 Gb (2x150bp)	200-250 Gb (2x150bp)	500-625 (2x150bp)	600-750 Gb (2x150bp)
Run time	1 dy – 2 dy	1 dy- 2 dy	1 dy – 2 dy	1 dy – 2 dy
Lanes/Flowcell	2	2	2	4
Max PAIRED END Reads/LANE	800 million	1600 million	3.8 billion	5 billion
Max SINGLE END Reads/LANE	400 M	800 M	1.9 B	2.5 B
Max Clusters/LANE	400 M	800 M	1.9 B	2.5 B
Read Type Format	Paired End			
	*single end available upon request			
Read Length Available	50x, 150x, Custom	50x, 100x, 150x, Custom	50x, 100x, 150x, Custom	100x, 150x, Custom
Guaranteed read #/lane (see note below)	600 million, paired end	1.4 billion, paired end	3.2 billion, paired end	4.5 billion, paired end
Key applications	10X single cell, Chip-seq transcriptome	Single Trio Human, 10X single cell, Chip-seq transcriptome	genome, exome, transcriptome, ChIP-seq	genome, exome, transcriptome,

*** NOTE: Custom Cycles are typically possible if the entire flowcell is filled by the study. Please contact HTSF for confirmation.**

Read Number Guarantee :

The number of reads is only guaranteed for standardized libraries prepared and pooled by the HTSF. For novel library preparations, the HTSF may require a pilot to determine if we are capable to meet the goals. The pilot will typically be at the expense of the project. We can not guarantee the length for libraries and / or pools prepared by studies. *We will make every effort to have successful seq results,* but the number of reads per library, especially in the case of novel library preps or unbalanced pools may not meet the read per lane goals. Keep in mind that the above table refers to high diversity genomic DNA samples. For most other applications a 10% reduction in yield is to be expected.