

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 million	1.6 billion	3.8 billion	10 billion
Max Clusters /Flowcell	800 million	1.6 billion	3.8 billion	10 billion
Read Type Format	Paired End *single end available upon request			Paired End
Read Length Available*	50x, 150x, Custom Cycles	50x, 100x, 150x, Custom Cycles	50x, 100x, 150x, Custom Cycles	100x, 150x
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

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

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

**Read Number
Guarantee :**

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.