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 |
| **Reads/FULL flowcell** | 25 million | 1 Million | 300 million | 1.6 bilion | 2-2.5 billion |
| **Read Type Format** | 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 | 50X, 100X, 150X, 250X | 50X, 100X,150x,250x | 50X, 100X | 50x, 75x, 150x |
| **Guaranteed read # / lane** *unless indcated 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 |

| **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 PE Reads/flowcell** | 1600 million | 3.2 billion | 7.6 billion | 20 billion |
| **Max Clusters/flowcell** | 800 million | 1.6 billion | 3.8 billion | 10 billion |
| **Read Type Format** | Paired End | | | Paired End |
| | *single end available upon request | | | |
| **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 |

| **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 PE Reads/LANE** | 800 million | 1600 million | 3.8 billion | 5 billion |
| **Max Clusters/LANE** | 400 milion | 800 million | 1.9 billion | 2.5 billion |
| **Read Type Format** | Paired End | | | Paired End |
| | *single end available upon request | | | |
| **Read Length Available** | 50x, 150x, Custom Cycles | 50x, 100x, 150x, Custom Cycles | 50x, 100x, 150x, Custom Cycles | 100x, 150x |
| **Guaranteed read #/lane(see note below)** | 600 million, paired end | 1.4 billion, paired end | 3.2 billion, paired end | 4 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.