

ILLUMINA SEQUENCING INSTRUMENTS STATISTICS

| Sequencer | Maximum output 2x150 bp reads | Maximum # reads |
|-------------------------|----------------------------------|--------------------|
| Bench Top | | |
| iSeq 100 | 1.2 Gb | 4 million |
| MiniSeq | 7.5 Gb | 25 million |
| Production Scale | | |
| MiSeq | 15 Gb | 25 million |
| NextSeq 550 | 120 Gb | 400 million |
| NextSeq 2000 | 300 Gb | 1 billion |

| Sequencing Center | | | Human Genomes per run (30x) | Human Exomes per run (100x) | Human Transcriptomes per run (50M reads) |
|--------------------------|---------|-------------|--------------------------------|--------------------------------|---|
| NovaSeq 6000 SP Flowcell | 250 Gb | 1.6 billion | 4 | 40 | 32 |
| NovaSeq 6000 S1 Flowcell | 500 Gb | 3.2 billion | 8 | 80 | 64 |
| NovaSeq 6000 S2 Flowcell | 1250 Gb | 8.2 billion | 20 | 200 | 164 |
| NovaSeq 6000 S4 Flowcell | 3000 Gb | 20 billion | 48 | 500 | 400 |

Real World Data With S4 Flowcell

Common Bean Genome = ~550 Mb

One lane of S4 flow cell

**Experience shows: = 52 genomes

**Expected result: = 72 genomes

Why the difference

**Human estimates are optimized

**Real world experience with other species are not optimized