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We're accelerating the pace of sequencing again, with the new TruSeq™ v3 reagent kits and software. HiSeq sequencers will be even more powerful— letting you sequence up to 600 Gb of high-quality data in a single run.

- Software – Improved image analysis increases data yield at high cluster density
- Reagents – Greater coverage uniformity, enabling high performance at significantly increased cluster densities

HiSeq Systems Performance
TruSeq v3 Cluster Generation, v3 SBS Kits, and HCS 1.4

	HiSeq 2000	HiSeq 1000	HiScan SQ
Output	Up to 600 Gb	Up to 300 Gb	Up to 150 Gb
Reads per run	Up to 6 Billion Paired-end	Up to 3 Billion Paired-end	Up to 1.5 Billion Paired-end
Performance	> 80% above Q30 at 2 x 100 bp		

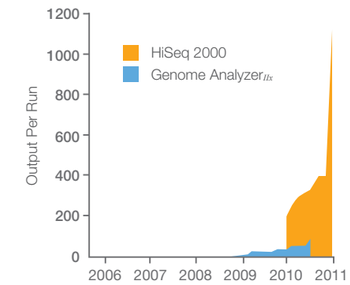
Pushing the envelope. 1,000-fold improvement in just four years.

Sequencing Run Parameters

Run form at: 2 x 150 bp	
Output per run	1.13 Tb
Output per day	81 Gb

Over the last few years we've scaled from targeting 1 Gb on the Genome Analyzer, to generating in excess of 1 Tb* internally on the HiSeq 2000.

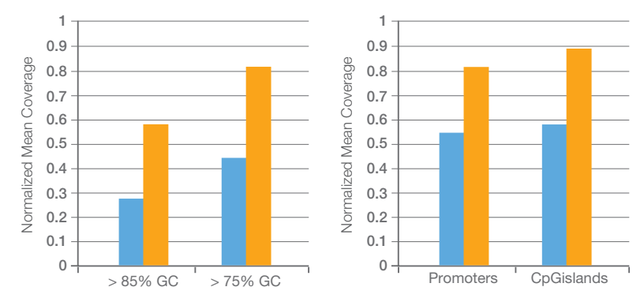
* R&D configuration not supported at launch



Driving the highest data quality.

Every Illumina sequencer is powered by TruSeq—the technology that delivers the most accurate human genome at any coverage.

- Highest coverage uniformity and lowest number of gaps
  — Lowest risk of missing variants
- Best raw accuracy based on verifiable data
- Highest percentage and yield of error-free reads
- Most sensitive and specific SNP and indel detection



TruSeq v3 cluster generation chemistry improves Illumina's industry-leading coverage uniformity, providing better coverage of GC-rich regions and maintaining coverage uniformity at higher cluster densities. This chart shows improvements in coverage of GC-rich regions at cluster densities previously unsupported due to density dependent bias.

Making sequencing easier.

TruSeq sequencing reagents and Illumina's proprietary Nextera™ library preparation provide a streamlined workflow that is economical and scalable, delivering industry-leading accuracy for sequencing studies. Driving down the cost of genome and transcriptome sequencing. Accelerating the time to discovery.