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In **Announcement**

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Genome-in-a-Day

From the beginning, we designed BaseSpace to be a place where things moved quickly. We did this largely so that our customers and partners could easily deploy their own apps on the platform (more to come on that in a later post), but we also did it out of necessity to keep pace with the breakneck innovation from our sequencing systems. As many of you no doubt have seen, Illumina recently announced a new high-throughput sequencing instrument called the HiSeq2500, which will produce high quality, high coverage human genomes in a single day. This week, at the Advances in Genome Biology and Technology (AGBT) meeting, Illumina is releasing the first public dataset to be run on this new system, described in the Application Note here.

The Coriell sample NA18507 was prepared using a modified version of the TruSeq DNA sample prep protocol and sequenced at 40X depth in "rapid run" mode. It yielded >90% reads above Q30, for an output of ~135Gb. Bcl files generated by the HiSeq 2500 were converted to fastq's and aligned against human reference build hg19; BAM and variant calls were generated using CASAVA v1.8.2 and produced >95% dbSNP concordance. A few additional secondary build metrics:

Performance Parameter	
Build depth	39.8x
Total SNPs	4,529,962
Heterozygous:Homozygous ratio	1.82
Transition:Transversion ratio	2.03
Matching position in dbSNP132	95.03
Coverage of reference genome*	98.12
Omni1M genotype coverage	98.71

In keeping with our rapid deployment ethos, this week the results of this first

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