

Genomic sequencing solutions, 3/17

March 2017—Illumina unveiled the NovaSeq series and announced the launch of the Illumina Bio-Rad Single-Cell Sequencing Solution at the J.P. Morgan Healthcare Conference in January.

NovaSeq, a scalable sequencing architecture expected one day to enable a \$100 genome, aims to open new horizons for more highly powered experiments at the depth required to discover rare genetic variants, according to a company statement. In addition to a single instrument capable of sequencing from three to 48 human whole genomes per run, the NovaSeq systems will open up new markets by making routine a wide range of applications from ultra-deep sequencing of matched tumor-normal pairs to large-scale variant discovery studies associated with complex diseases and low-pass sequencing of seed banks to select for specific traits.

The NovaSeq series includes the NovaSeq 5000 and 6000 systems, which feature automated onboard cluster generation, cartridge-based reagents, and streamlined workflows. With scalable throughput, users can perform sequencing applications requiring different levels of output by simultaneously running one or two flow cells from up to four different flow cell types. The system is for research use only; not for use in diagnostic procedures.

The Illumina Bio-Rad Single-Cell Sequencing Solution is a next-generation sequencing workflow for single-cell analysis, providing researchers the ability to investigate the coordinated contribution of individual cells in tissue function, disease progression, and therapeutic response.

The solution comprises the ddSEQ Single-Cell Isolator and SureCell WTA 3' library prep kit and delivers high-throughput sequencing of thousands of individual cells. Bio-Rad's droplet partitioning technology, Droplet Digital technology, is used to isolate and barcode single cells for downstream sequencing on many of Illumina's NGS instruments. The solution includes primary and secondary data analysis conducted via the BaseSpace Informatics Suite, Illumina's cloud-based genomics computing environment, and tertiary data analysis and visualization with SeqGeq from FlowJo LLC.

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