Illumina expands portfolio, 5/14

May 2014—Illumina is making available new products that can be applied directly to the discovery and translation of genomic variation in blood and tissue associated with cancer. The products complement Illumina's existing NGS and array portfolio and support streamlined workflows for cancer research and other applications using Illumina's NGS sequencers.

TruSeq RNA Access Library Prep Kits offer a solution for analyzing RNA isolated from formalin-fixed, paraffin-embedded tissues and other low-quality samples. Starting with as little as 10 ng total RNA, the kits deliver the discovery power of RNA sequencing at a reduced cost by focusing on the coding regions of the transcriptome.

TruSight Myeloid Sequencing Panel uses expert-curated content to offer accurate and cost-effective identification of somatic mutations in myeloid malignancies. It provides an assessment of 54 critical genes, including tumor suppressor genes and hotspots in oncogenes. This DNA-to-data solution offers a streamlined workflow and automated data analysis with somatic variant calling.

New BaseSpace Core Apps offer informatics support for the cancer market. The TopHat and Cufflinks Apps, as well as the RNA Express App, are designed to support transcriptome data analysis, including detection of fusion genes critical in cancer research. A Tumor Normal App delivers somatic variant calling of tumor and matched normal whole genome data sets based on the Strelka method. In addition, Illumina is developing apps to analyze data from its TruSight Tumor Sequencing Panel and TruSeq Amplicon–Cancer Panel, as well as an exome version of the Tumor Normal App that delivers variants (including copy number variations) based on Nextera Rapid Capture Enrichment data.

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