DESKTOP WHOLE-GENOME SEQUENCER

The NextSeq 500 System delivers the power of high throughput sequencing with the load-and-go simplicity of a desktop sequencer, effectively transforming a broad range of high throughput applications into affordable, everyday research tools. Its push-button operation delivers a one-day turnaround for a number of popular sequencing applications, including one whole human genome and up to 16 exomes, up to 20 noninvasive prenatal testing samples, up to 20 transcriptomes, up to 48 gene expression samples, and up to 96 targeted panels. With its streamlined informatics, sequencing data can be run through a range of open -ource or commercial pipelines or instantly transferred, analyzed, and stored securely in BaseSpace or the new BaseSpace OnSite for researchers needing an on-premises solution. Users also have the flexibility to switch to lower throughput sequencing as needed, and while other platforms require several pieces of specialized equipment, the NextSeq 500 System integrates cluster generation and sequencing into a single instrument.

Illumina

For info: 800-809-4566 | www.illumina.com/nextseq

POST-BISULFITE DNA LIBRARY PREPARATION

The new EpiNext Post-Bisulfite DNA Library Preparation Kit is designed for constructing DNA libraries directly from bisulfite-treated DNA for whole genome bisulfite sequencing. Bisulfite conversion is an essential process of modifying DNA so that methylated cytosine bases can be detected via sequencing. Currently used whole genome bisulfite sequencing methods need rather large amounts of DNA (great than 1 µg) as input material, as well as requiring the need to first shear DNA and ligate adapters to DNA fragments prior to bisulfite conversion. The innovative technology developed by Epigentek allows bisulfite-treated DNA to be directly used for ligation, thereby eliminating the possibility of breaking adapter-ligated fragments, which can often occur in currently used next generation bisulfite sequencing methods. The commercial kit, based on this technology, has high sensitivity and efficiency, enabling input DNA to be as low as 1 ng, and could be used for precious or limited biological samples.

Epigentek

For info: 877-374-4368 | www.epigentek.com

GENE-EDITING KITS

The new GENASSIST range of gene-editing kits and reagents enable easier, robust implementation of CRISPR and rAAV gene editing experiments. The current GENASSIST offering comprises both off-the-shelf reagents for using CRISPR editing technology and a unique kit combination of these reagents to allow customers to generate their own CRISPR-ready cell lines that constitutively express Cas9-nickase. Using such cell lines provides a quick start for customers, enabling them to make further modifications to the cell line more efficiently than if they were starting fresh each time. Horizon is also launching a new service for the design, manufacture and most importantly validation of CRISPR RNA guides, in order to maximize the likelihood that gene editing will occur as expected. The new GENASSIST kits, combined with access to rAAV, ZFN, and CRISPR technologies, give researchers an invaluable suite of tools to determine the function of endogenous gene alterations and their effect on disease and therapeutic responses.

Horizon Discovery

For info: +44-(0)-1223-655580 | www.horizondiscovery.com

DNA LIBRARY KIT

The Accel-NGS 2S DNA Library Kit for Illumina Next Generation Sequencing (NGS) systems provides linear yields from inputs ranging from 10 pg to 1 µg. Polymerase chain reaction-free libraries can be produced from as little as 100 ng. Unlike other commercially available kits, exceptional quality and evenness of coverage are obtained even at very low levels of DNA input. The product is also is ideally suited for clinical samples such as FFPE tissues and plasma. Accel-NGS 2S enables NGS laboratories to stock and use a single kit for their varied DNA library needs, ranging from high molecular weight DNA to limited quantity, damaged FFPE samples. In addition to whole genome sequencing, Accel-NGS 2S is also compatible with the leading hybridization capture products and is suitable for ChIP-Seq. Built with usability in mind, the 2S protocol is readily automatable for those with high throughput applications. The wide dynamic range of input makes pre-library quantification optional, further streamlining workflow.

Swift Biosciences

For info: 734-330-2568 | www.swiftbiosci.com

NGS LIBRARY PREP KITS

Current methods used for epigenetic analysis of DNA methylation are deficient in differentiating 5-methylcytosine from 5-hydroxymethylcytosine. The new Pico Methyl-Seq Library Prep and RRHP 5-hmC Library Prep kits are designed for NGS-based, whole-genome analysis of 5-methylcytosine and genome-wide analysis of 5-hydroxymethylcytosine in DNA, respectively. These unique products feature streamlined workflows and include all the technologies required for consistent and robust library construction. Pico Methyl-Seq is a post-bisulfite library preparation method that can accommodate DNA inputs as low as 10 pg. Alternatively, RRHP allows for strand-specific, single-base profiling of 5-hmC from DNA inputs as low as 100 ng by utilizing a bisulfite-free, enzymatic-based method. When combined, both technologies will elucidate genomic-scale methylation and hydroxymethylation profiles for a particular DNA sample from any species.

Zymo Research Corporation

For info: 888-882-9682 | www.zymoresearch.com