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CONTACT: Darby Wagner
Lambert, Edwards & Associates
(616) 258-5779
dwagner@lambert-edwards.com

Swift Announces the Highest Throughput Single-Cell Methyl-Seq Library Preparation Method

Study published in Science magazine demonstrates how epigenetic markers can identify cell subtypes and regulatory elements that drive cellular diversity

(ANN ARBOR, Mich. – August 10, 2017) Swift Biosciences, a leading provider of innovative library prep solutions for next-generation sequencing (NGS), today announced the launch of a new single-cell methylation sequencing method based on its Accel-NGS® Adaptase™ technology, an efficient and robust NGS-prep solution for whole-genome bisulfite sequencing at single-cell resolution. This new method enables the efficient analysis of different methylated regions across thousands of cells from heterogeneous tissues, while also addressing applications, such as cell classification, regulation of cellular mechanisms in normal tissue, epigenetic alterations in disease states and evolutionary conservation of epigenomic regulation.

Methylation is a stable biomarker that can be used to identify cell types and the regulatory elements underlying cell function. When coupled with single-cell RNA expression studies, single-cell methylation can elucidate the regulatory elements, in turn controlling the unique expression profiles of individual cells and differences between cells. Additionally, recent clinical studies have uncovered methylation patterns in diseases—such as cancer—which identify tumor type, assess tumor burden in liquid biopsies, and correlate with disease progression, prognosis and drug response.

This method was recently described in the *Science* paper entitled "Single Cell Methylomes Identify Neuronal Subtypes and Regulatory Elements in Mammalian Cortex" by collaborators at the Salk Institute, University of California San Diego and Swift Biosciences. The workflow combines fluorescence-activated cell sorting-based isolation, bisulfite conversion and Swift's Accel-NGS Adaptase module with other commercially available components. The published results demonstrated a greater than two-fold increase in read-mapping rates as compared to other methods; thereby, significantly improving the data output per sequencing run while reducing the overall cost.

"This is one of many scientific collaboration in which Swift technologies is pushing the boundaries of science," said Timothy Harkins, president and CEO of Swift Biosciences and co-author on the paper. "We are excited about new insights into basic cellular processes, and the profound, future impact it will have on precision medicine."

"Our proprietary Adaptase technology constructs high-complexity NGS libraries from low-input, single-stranded DNA," said Laurie Kurihara, PhD, senior director of research and development and co-author on the paper. "Our single-cell workflow has fewer steps than other methods and

offers multiplexed, single-cell processing to provide greater productivity for high-throughput applications."

The Accel-NGS Adaptase Module is now commercially available.

About Swift Biosciences

Swift Biosciences is the NGS Library Prep company. Based in Ann Arbor, Michigan, the company develops novel library preparation solutions for emerging applications based on next-generation sequencing, including whole genome sequencing, targeted DNA sequencing, and epigenetic analysis. Swift Biosciences' products are designed to help customers analyze challenging biological samples faster, easier, and with greater sensitivity and accuracy, while being compatible with all leading instrumentation. Swift Biosciences is the first company to offer library preparation solutions on three major sequencing platforms, including Pacific Biosciences®, Illumina® and Ion Torrent™.

The company opened its doors in February 2010, and its product development enables new applications in multiple industries, including agrigenomics, pharmaceutical, academic, biotechnology, and oncology research fields.

For more information, visit SwiftBioSci.com and follow Swift Biosciences on Twitter @SwiftBioSci.

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