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ASIA EDITION

Swift announces the highest throughput single-cell methyl-seq library preparation method

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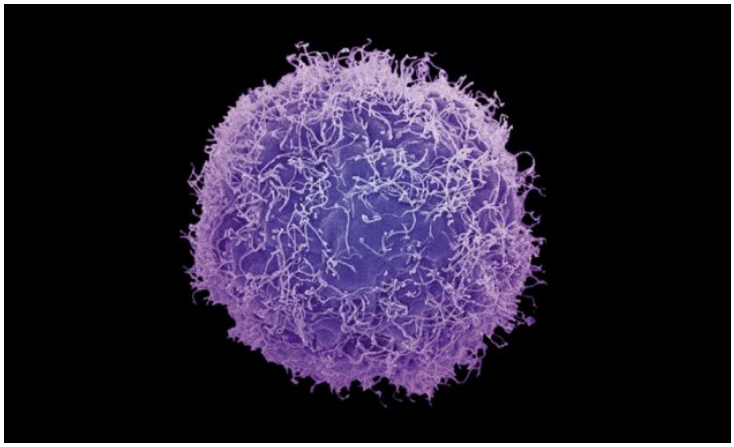
Study published in Science magazine demonstrates how epigenetic markers can identify cell subtypes and regulatory elements that drive cellular diversity



Singapore - Swift Biosciences, a leading provider of innovative library prep solutions for next-generation sequencing (NGS), 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 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."

The Accel-NGS Adaptase Module is now commercially available.