SeqLL Announces Publication of a New Single-Cell Epitranscriptomic Method Powered by SeqLL's tSMS® Platform

September 23, 2021

Method developed by leading researchers at the Bernstein Laboratory and SeqLL Inc.

Funding for the research and method development provided by the National Institutes of Health (NIH)

WOBURN, Mass., Sept. 23, 2021 (GLOBE NEWSWIRE) -- SeqLL Inc. ("SeqLL" or the "Company") (NASDAQ: SQL), a development-stage life sciences instrumentation and research services company engaged in the development of scientific assets and novel intellectual property across multiple "omics" fields, today announced the peer-reviewed publication of a new microscopy-based epitranscriptomic method powered by SeqLL's tSMS platform in the August issue of *Cell Report Methods*. The method was developed in collaboration with the laboratory of Bradley E. Bernstein, MD, PhD through grant R01-HG009269 from the National Institutes of Health (NIH) and the National Human Genome Research Institute (NHGRI).

The publication entitled: "*Systematic detection of m^{6}A-modified transcripts at single-molecule and single-cell resolution*" details a new microscopy-based approach to quantify epigenetically modified mRNA molecules in single cells and relates these findings to cellular phenotypes. The method employs nanoscale technology to compare cell surface markers, gene expression, total numbers of individual mRNA transcripts, and adenosine mRNA methylation (m6A) levels, all in the same cells allowing for the study of mRNA modifications in single cells. Current amplification-based technologies and methods use chemical modification of mRNA that can affect many cellular processes, and cannot be used on small samples or in single cells.

Kyung Lock Kim, Ph.D., postdoctoral researcher at Massachusetts General Hospital and lead author of the publication, said, "Our team developed this method to capture and directly interrogate RNA transcripts from thousands of single cells without PCR amplification or sample manipulation steps. Using RNA modification antibodies combined with SeqLL's tSMS single-molecule sequencing, we were able to resolve single cells and thereby measure surface markers, gene expression, and m ^{6}A levels in the same cells. Typically, epitranscriptome studies, including cancer research (e.g. AML and lung cancer), require a lot of sample input and are performed at bulk levels. However, this platform provides multifaceted information in single cell resolution, which will be helpful for cancer diagnosis and assessing its causality."

Daniel Jones, CEO, President and Co-Founder of SeqLL, added, "We are proud of the accomplishments of this team and are excited by the future work this platform will enable, particularly beyond this initial cancer research. Using this epitranscriptomic method to profile single cells, researchers will have the power to reveal insights into complex biological pathways beyond those that current methods allow. We look forward to many exciting discoveries using this new platform."

About tSMS
SeqLL's exclusive True Single Molecule Sequencing (tSMS) technology enables direct sequencing of millions of individual molecules. It does not involve PCR amplification at any stage of the process and offers simple, straight-forward Sample Prep protocols. It precisely reflects sample composition without bias and loss of diversity & rare species. True Single Molecule Sequencing is ideally suited for challenging applications, including low quantity, difficult or degraded samples, such as cell-free DNA, FFPE-isolated nucleic acids, ancient DNA and forensic samples. The tSMS platform offers maximum flexibility and avoids many of the challenges common for standard sequencing approaches.

About SeqLL
SeqLL Inc. ("SeqLL") is a development-stage life sciences instrumentation and research services company engaged in the development of scientific assets and novel intellectual property across multiple "omics" fields. The Company intends to leverage their expertise with True Single Molecule Sequencing ("tSMS ®") technology to enable researchers and clinicians to contribute major advancements to scientific research and development by accelerating one's understanding of the molecular mechanisms of disease and fundamental biological processes.

Forward Looking Statements
This press release contains certain forward-looking statements, including those related to the applicability and viability of the Company's new microscopy-based approach to quantifying epigenetically-modified mRNA molecules in single cells and other statements that are predictive in nature. Forward-looking statements are based on the Company's current expectations and assumptions. The Private Securities Litigation Reform Act of 1995 provides a safe-harbor for forward-looking statements. These statements may be identified by the use of forward-looking expressions, including, but not limited to, "expect," "anticipate," "intend," "plan," "believe," "estimate," "potential," "predict," "project," "should," "would" and similar expressions and the negatives of those terms. Prospective investors are cautioned not to place undue reliance on such forward-looking statements, which speak only as of the date of this presentation. The Company undertakes no obligation to publicly update any forward-looking statement, whether as a result of new information, future events or otherwise. Important factors that could cause actual results to differ materially from those in the forward-looking statements are set forth in the Company's filings with the Securities and Exchange Commission, including its registration statement on Form S-1, as amended from time to time, under the caption "Risk Factors."

Contacts:

Ashley R. Robinson
LifeSci Advisors, LLC
Tel: +1 (617) 430-7577
Email: arr@lifesciadvisors.com