TATAA Newsletter 2018-06-27

tataabiocenter

New Method for Quantification of Nascent RNA Using Metabolic Labeling and RNA-Seq

SLAMseq Metabolic RNA Labeling Kit

The fastest labeling method, which does not require pull-down or biochemical isolation

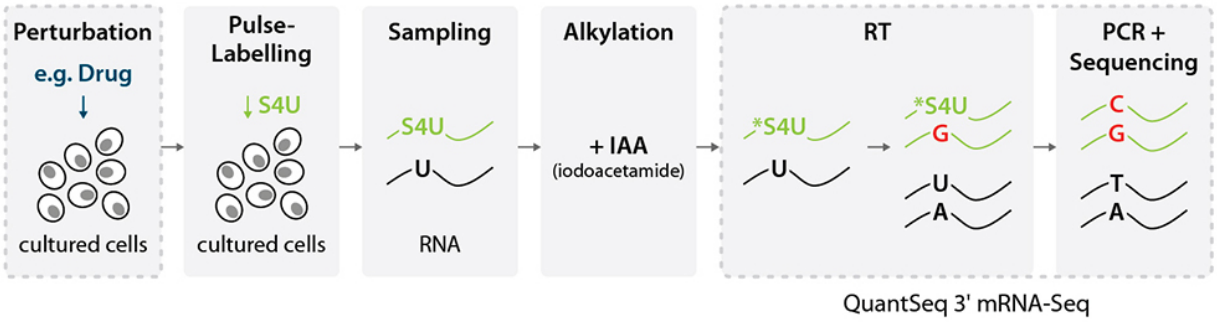
- Measure nascent RNA expression and transcript stability
- Enhance the temporal resolution of differential expression
- Analyze transcriptome-wide kinetics of RNA synthesis and turnover
- Identify primary and secondary transcriptional targets
- Use in combination with QuantSeq 3’ mRNA-Seq for cost- and time-effective, high-throughput time-resolved sequencing
- Analyze the data on the automated and user-friendly SLAMseq-QuantSeq data analysis pipeline SLAMdunk

The new transcriptome-wide, quantitative, fast, and reliable SLAMseq (thiol (SH)-Linked Alkylation for the Metabolic Sequencing of RNA) labeling method enables very straightforward, time-resolved measurement of newly-synthesized and existing RNA. Learn more about SLAMseq.

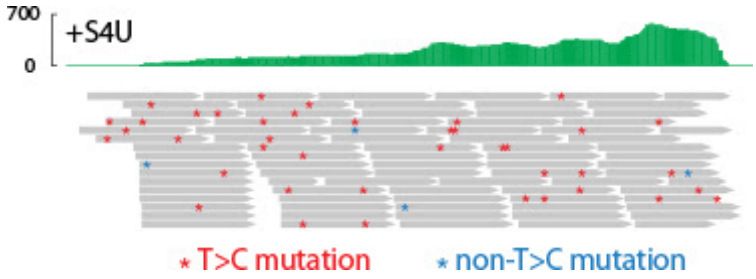
Total RNA from SLAMseq experiments can be used as direct input for Lexogen's QuantSeq 3’ mRNA-Seq Library Prep. QuantSeq generates stranded libraries that require 10x less reads than standard RNA-Seq. This enables samples from more complex experiments to be multiplexed together in a single sequencing lane or run.

Thus, both technical and biological replicates can be included in SLAMseq experiments at minimum costs. Learn more about QuantSeq.

SLAMseq Workflow

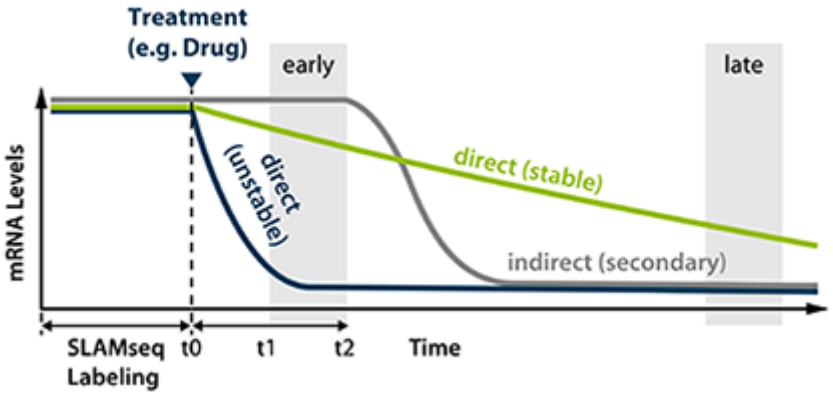


SLAMseq Read Coverage



A study recently published in Science *(Muhar, M et al. (2018) SLAM-seq defines direct gene-regulatory functions of the BRD4-MYC axis, DOI:10.1126/science.aao2793)* demonstrates how unique qualities of SLAMseq and QuantSeq were leveraged to determine direct transcription targets of cancer genes in response to drug treatment.

Primary and Secondary Drug Target Responses in SLAMseq Experiments



"Combining chemical-genetic protein degradation and SLAMseq allowed us to do an experiment we have long been dreaming of: Eliminate a transcription factor within 30 minutes and directly measure changes in transcriptional output. We used it to answer long-standing questions about MYC and BRD4, but our approach can be applied to study direct transcription targets of any gene or pathway," says Johannes Zuber, a group leader at the Research Institute of Molecular Pathology (IMP), who headed the study.

News

Want to learn about Molecular microbiological identification and typing?

Dr Mikael Kubistas webinar “Normalization of qPCR data”

Application now open for EMBL Course: Liquid Biopsies

Webinar “AR-V7 Key in Tx of mCRPC” by Andrew Armstrong, MD, presented at ASCO

Services - better results, faster	High-quality products	Hands-on trainings