ALITHEA GENOMICS

RNA sequencing at scale.

Discover the unparalleled scalability of our multiplexed RNA-seq solutions and unleash the power of big RNA data

MERCURIUS™ **DRUG-seq** library preparation kits for Illumina®

Extraction-free protocol

Our MERCURIUS™ DRUG-seq technology enables the streamlined preparation of 3' mRNA-seq libraries of hundreds of RNA samples in a single tube.

Benefits

The Extraction-free **DRUG-seq** kits contain all the oligos and enzymes needed to go from 2D cell cultures to sequencing-ready DNA libraries.

Ideal for screening projects

More samples, more replicates. Robust results, significant discoveries.

Streamlined data pre-processing

Demultiplex and align your DRUG-seq data with our easy-to-use cloud-based platform.

No need for prior RNA extraction

An optimized lysis buffer for complete lysis and efficient reverse transcription.

Improved DRUG-seq protocol

Without pre-amplification, leading to higher mapping and gene detection rates.

One-day lab workflow

Convenient and short protocol from samples to sequencing-ready libraries in one day.

Experimental workflow at a glance

1. Cell Lysis and RNA solubilization

2. Reverse Transcription

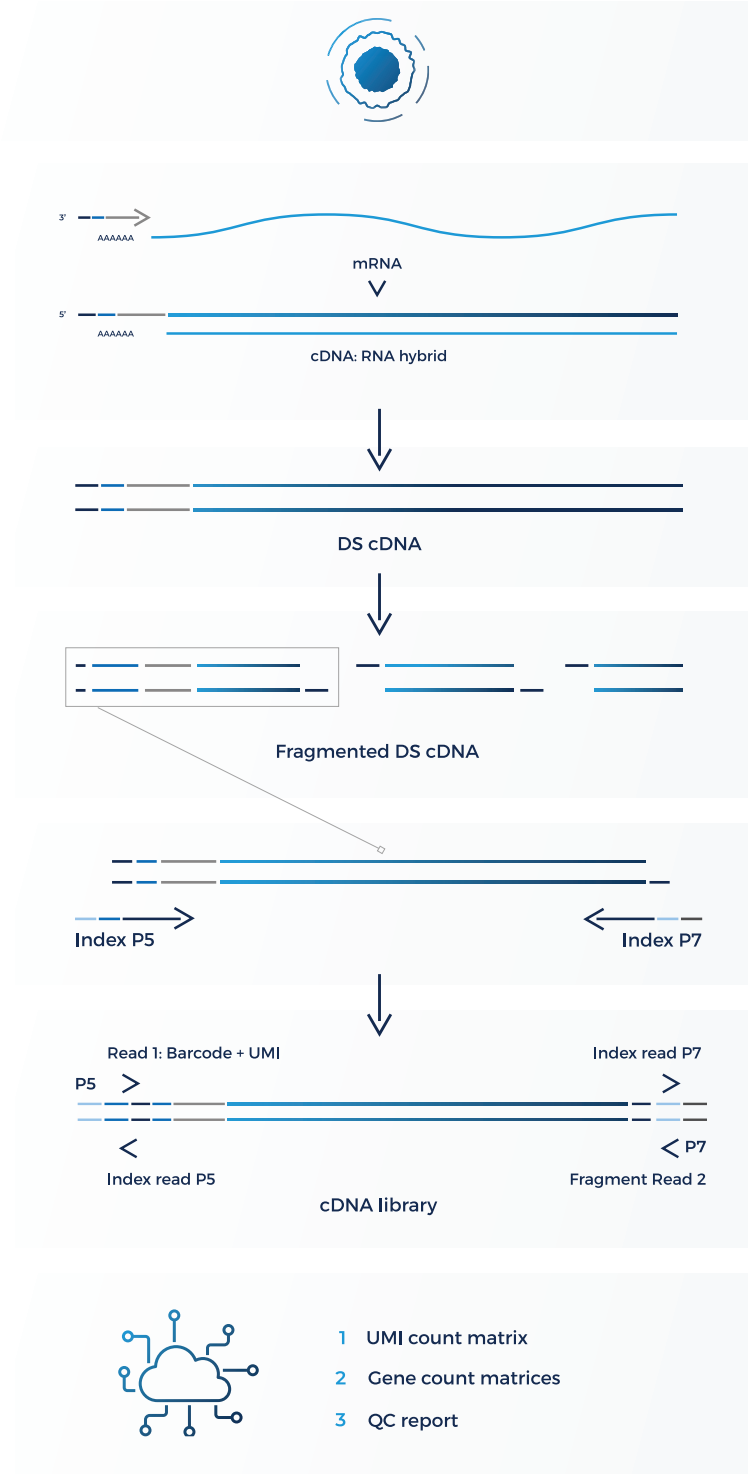
3. Second strand synthesis

4. Tagmentation

5. Library indexing and amplification

6. Library QC and sequencing

7. Sequencing data processing and analysis



The DRUG-seq workflow begins by adding a proprietary cell lysis buffer directly to pre-washed cells in the well plate. The lysates can then be used directly in reverse transcription reactions in which individual RNA samples are "tagged" with a specific DRUG-seq barcode and each RNA molecule is marked with a unique molecular identifier (UMI).

All samples are subsequently pooled into one single tube and purified. Library amplification is performed with unique dual indexes to maximize the efficiency of library demultiplexing during next-generation sequencing.

Large-scale transcriptomics made possible

Below is a sample result obtained using a MERCURIUS™ **DRUG-seq kit**, which highlights the uniform distribution of the number of genes detected for each sample at three different counts per million (CPM) thresholds.

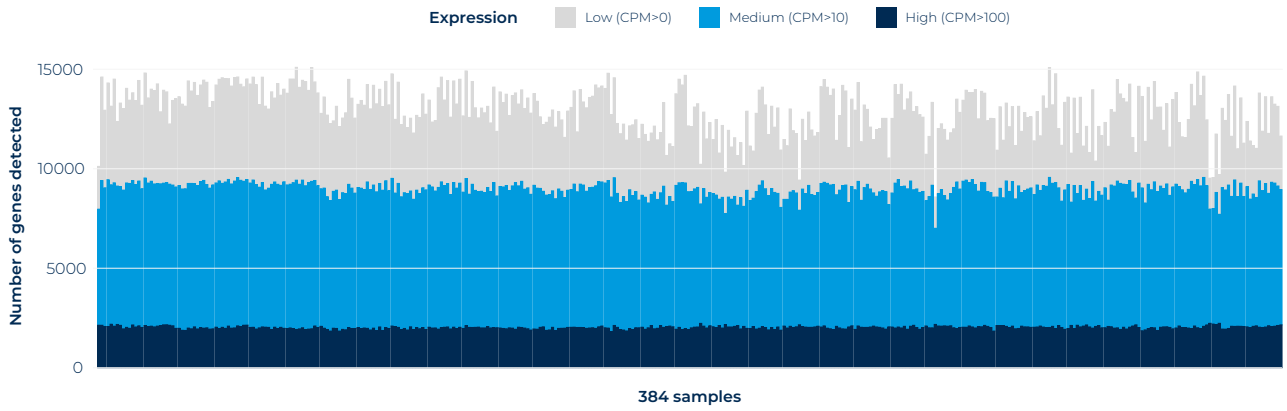


Figure. Sample plot generated from the MERCURIUS™ DRUG-seq kit pipeline showing the number of detected genes for three counts per million (CPM) thresholds (i.e., a gene is considered 'detected' only if the number of attributed reads is greater than the CPM threshold). The library was sequenced at an average of 1.5 million reads per sample (n = 384 samples).

Related products

	Cat #10841	Cat #11041	Cat #10851	Cat #11051	Cat #12051	Cat #13051
Total reactions how many library preps can be prepared in total with one kit	**96**	**384**	**384**	**1'536**	**6'144**	**24'576**
RNA and plate multiplexing format how many samples can be pooled in one tube after RT	96	96	384	384	384	384
UDI pairs included corresponds to how many separate pools can be prepared with one kit	4	4	4	4	16	16
Lysis buffer	Included	Included	Included	Included	Included	Included

For more reactions, higher multiplexing and more UDIs inquire today.

Alithea Genomics is trusted by

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