ALITHEA GENOMICS

RNA sequencing at scale.

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

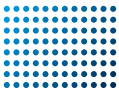
MERCURIUS™ **BRB-seq** library preparation kits for Illumina®

RNA-seq at scale for purified RNA samples

Our bulk RNA barcoding and sequencing (BRB-seq) technology enables the streamlined preparation of 3' mRNA-seq libraries of hundreds of RNA samples in a single tube.

Benefits

The MERCURIUS™ **BRB-seq** library preparation kits for Illumina® contain all the oligos and enzymes needed to go from purified RNA to sequencing-ready DNA libraries.



Bulk RNA sequencing at scale

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

Streamlined data pre-processing

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

BRB-seq as a flexible solution

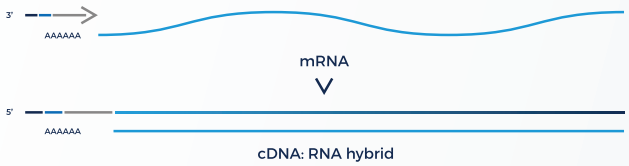
For projects of all sizes, from a few samples to up-to 384 samples in one single tube.

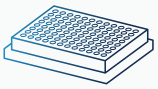
One-day lab workflow

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

Experimental workflow at a glance

1. Reverse Transcription



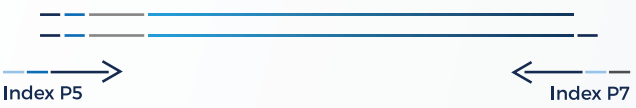


96/384 Plate

2. Second strand synthesis

3. Tagmentation

4. Library indexing and amplification



Tube

5. Library QC and sequencing

6. Sequencing data processing and analysis

1 UMI count matrix
2 Gene count matrices
3 QC report

The standard **BRB-seq** workflow begins with an optimized reverse transcription reaction, in which individual RNA samples are "tagged" with a sample specific BRB-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 performing MERCURIUS™ **BRB-seq** on 384 purified RNA samples from mouse liver tissue and sequenced at 1M reads/sample on an Illumina sequencer.

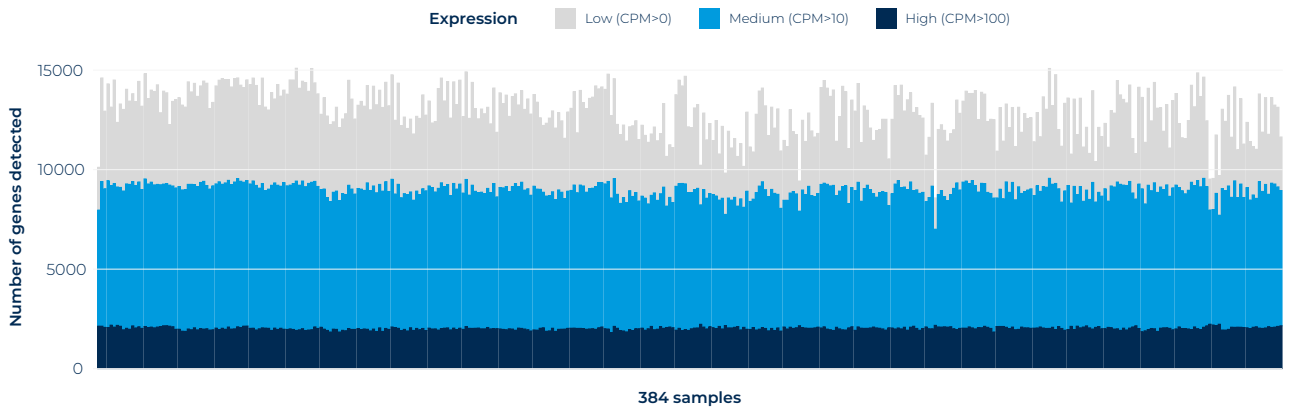


Figure. Sample plot generated from the MERCURIUS™ BRB-seq cloud pre-processing platform (alitheagenomics.com/software) showing the number of detected genes for three counts per million (CPM) thresholds. The library was sequenced at an average of 1 million reads per sample.

	Cat #10813	Cat #11013	Cat #10814	Cat #11014	Cat #12014	Cat #13014
Total reactions how many library preps can be prepared in total with one kit	**96**	**384**	**384**	**1'536**	**6'114**	**24'576**
RNA 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

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

Alithea Genomics is trusted by

BAYER · Johnson & Johnson · Roche · Dana-Farber Cancer Institute · CHUV · LUDWIG CANCER RESEARCH · syngenta · UNIVERSITY OF CAMBRIDGE · FIRALIS · Stanford University

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