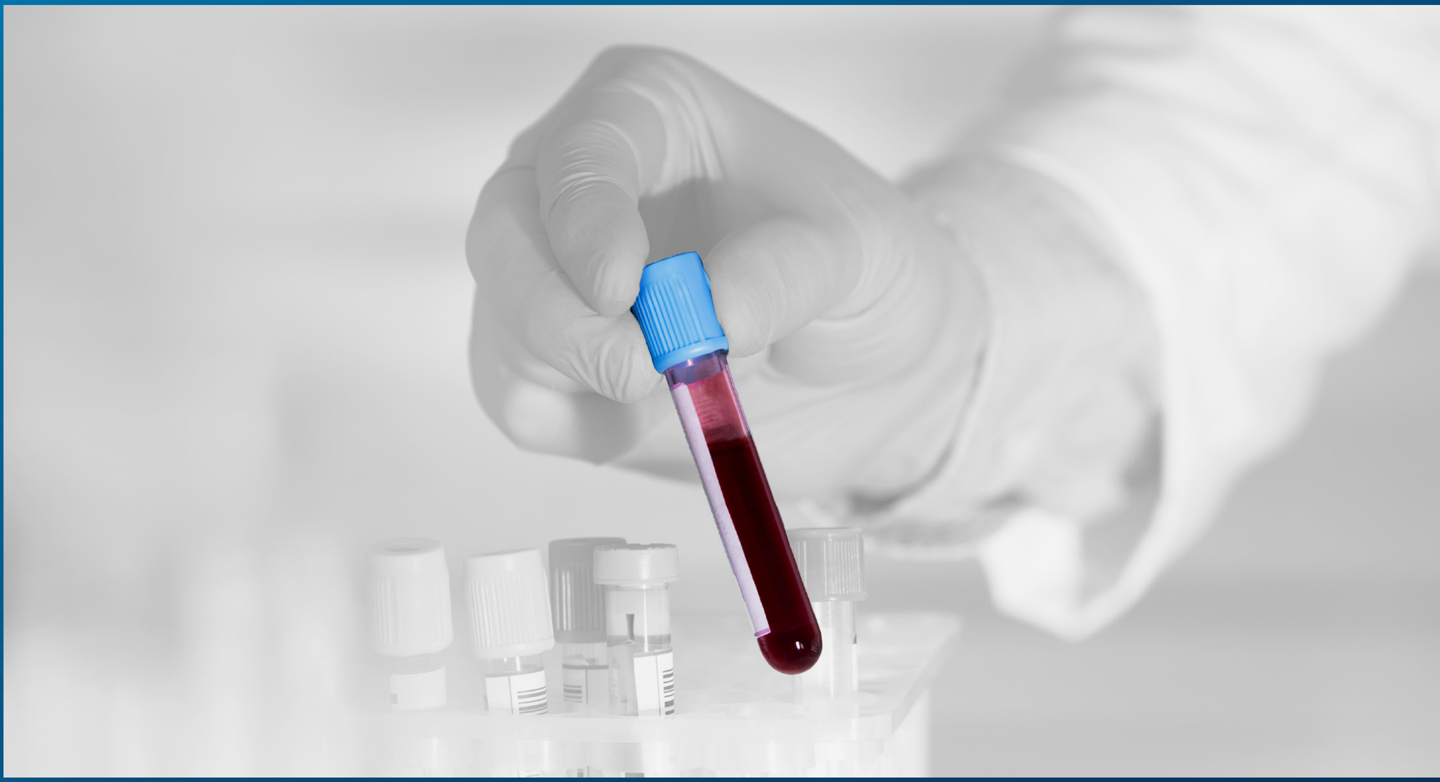
ALITHEA
GENOMICS

Large-scale RNA sequencing
For everyone

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



MERCURIUS™

Blood BRB-seq library preparation kits for Illumina®

The power of scalability with integrated globin depletion

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™ **Blood BRB-seq** library preparation kits for Illumina® contain all the oligos and enzymes needed to go from purified blood 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.

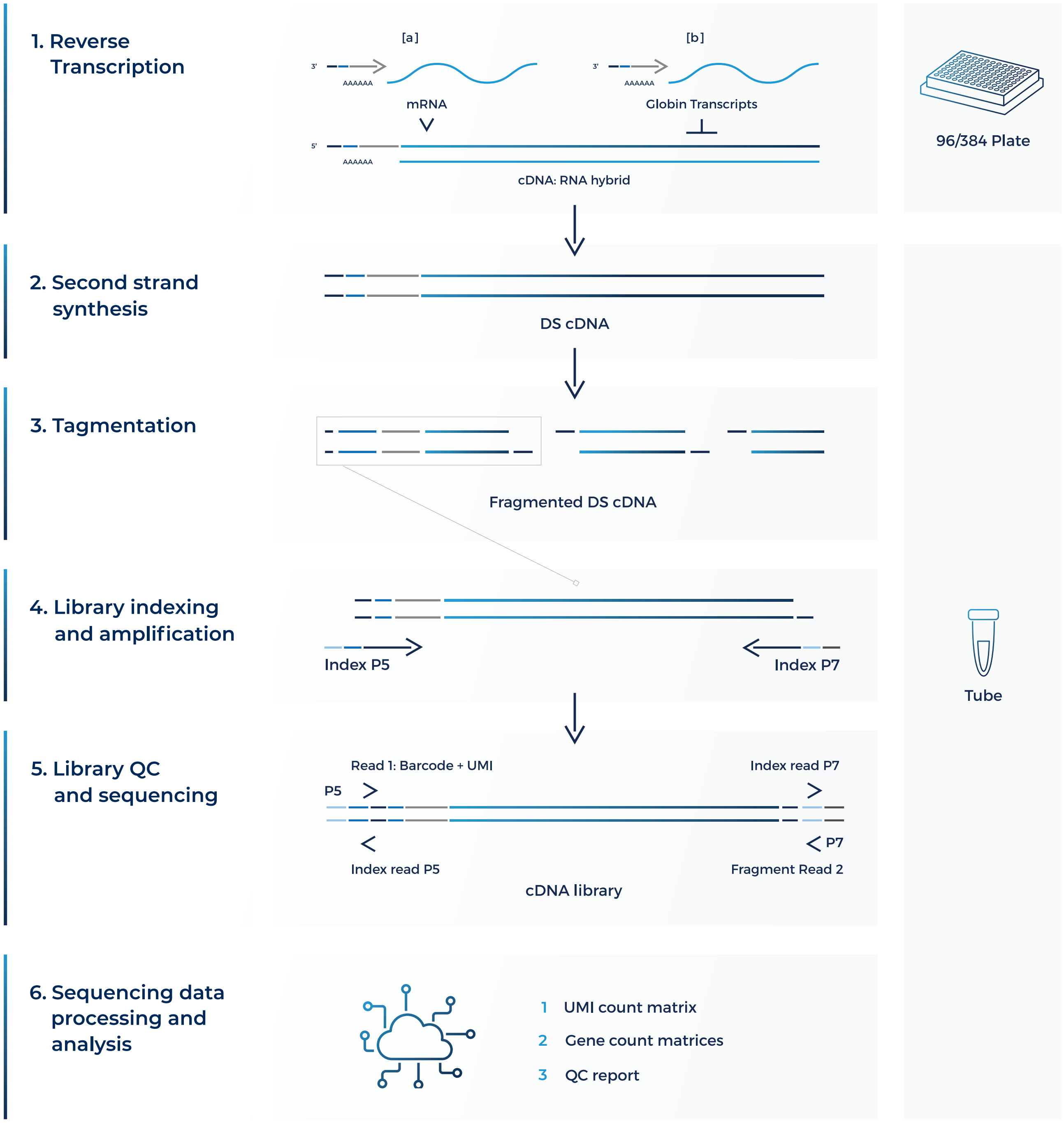
Integrated globin depletion

Seamlessly integrated globin depletion. No need to purchase additional kits.

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

2. Second strand synthesis

3. Tagmentation

4. Library indexing and amplification

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 specific BRB-seq barcode and each RNA molecule is marked with a unique molecular identifier (UMI). In the Blood BRB-seq workflow, globin blockers are added to the reverse transcription reaction to prevent globin transcripts from being reverse transcribed.

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 the MERCURIUS™ **Blood BRB-seq** kit, which highlights the uniform distribution of the number of genes detected for each sample at three different counts per million (CPM) thresholds.

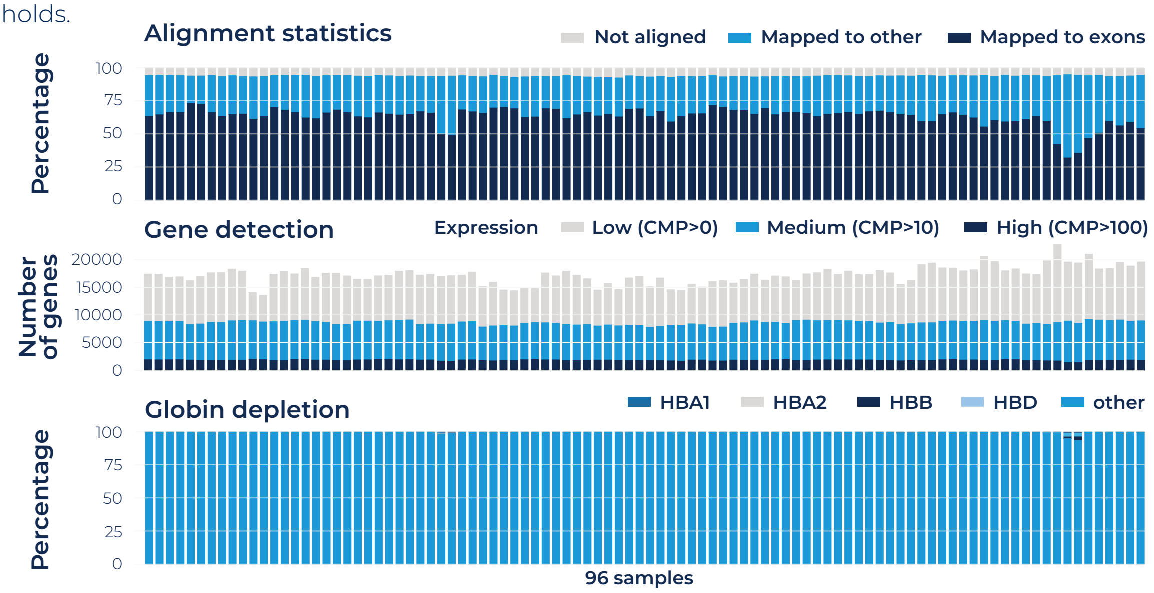


Figure. Sample plot generated from the MERCURIUS™ Blood BRB-seq cloud pre-processing platform (alitheagenomics.com/software) showing the number of detected genes for three counts per million (CPM) thresholds, as well as effective depletion of globin genes.. The library was sequenced at an average of 4.8 million reads per sample.

Related products	 Cat #10823	 Cat #11023	 Cat #10825	 Cat #11025
Total reactions how many library preps can be prepared in total with one kit	**96**	**384**	**384**	**1'536**
RNA multiplexing format how many samples can be pooled in one tube after RT	96	96	384	384
UDI pairs included corresponds to how many separate pools can be prepared with one kit	4	4	4	4
Globin blockers	Included	Included	Included	Included

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

Alithea Genomics is trusted by

EPFL
Johnson&Johnson
genesupport
Dana-Farber Cancer Institute
CHUV
LUDWIG CANCER RESEARCH
u^b UNIVERSITÄT BERN
UNIVERSITY OF CAMBRIDGE
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Stanford University

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