The MERCURIUS™

BRB-SEQ INFO GUIDE

ALITHEA GENOMICS

Trusted by

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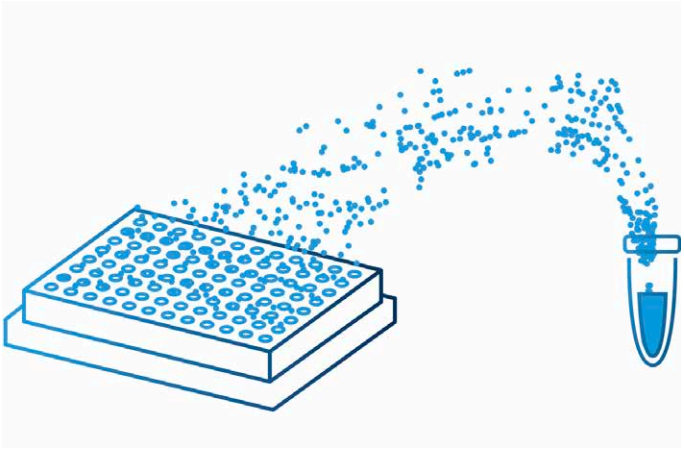
The MERCURIUS™

BRB-SEQ TECHNOLOGY

This technology unlocks the power of gene expression profiling by offering an unbiased RNA-seq procedure that is highly sensitive, massively multiplexed and extremely cost-effective. Compatible with Illumina®, AVITI™ and Ultima Genomics.



Massive sample multiplexing

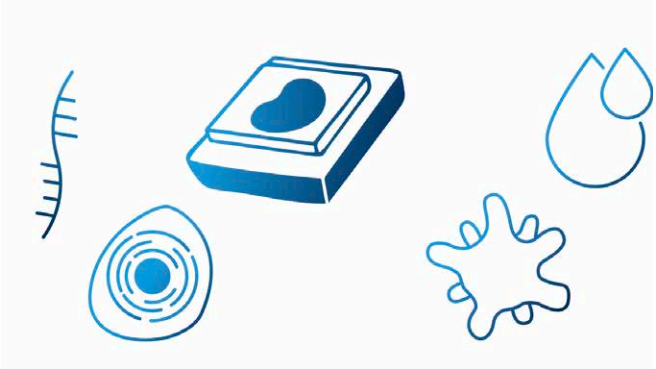
Up-to 384 samples are processed in one single tube

Our highly optimized sets of barcoded primers uniquely "tag" individual RNA samples during the first step of library preparation so that you can pool and process all samples together in a single tube early in the workflow.

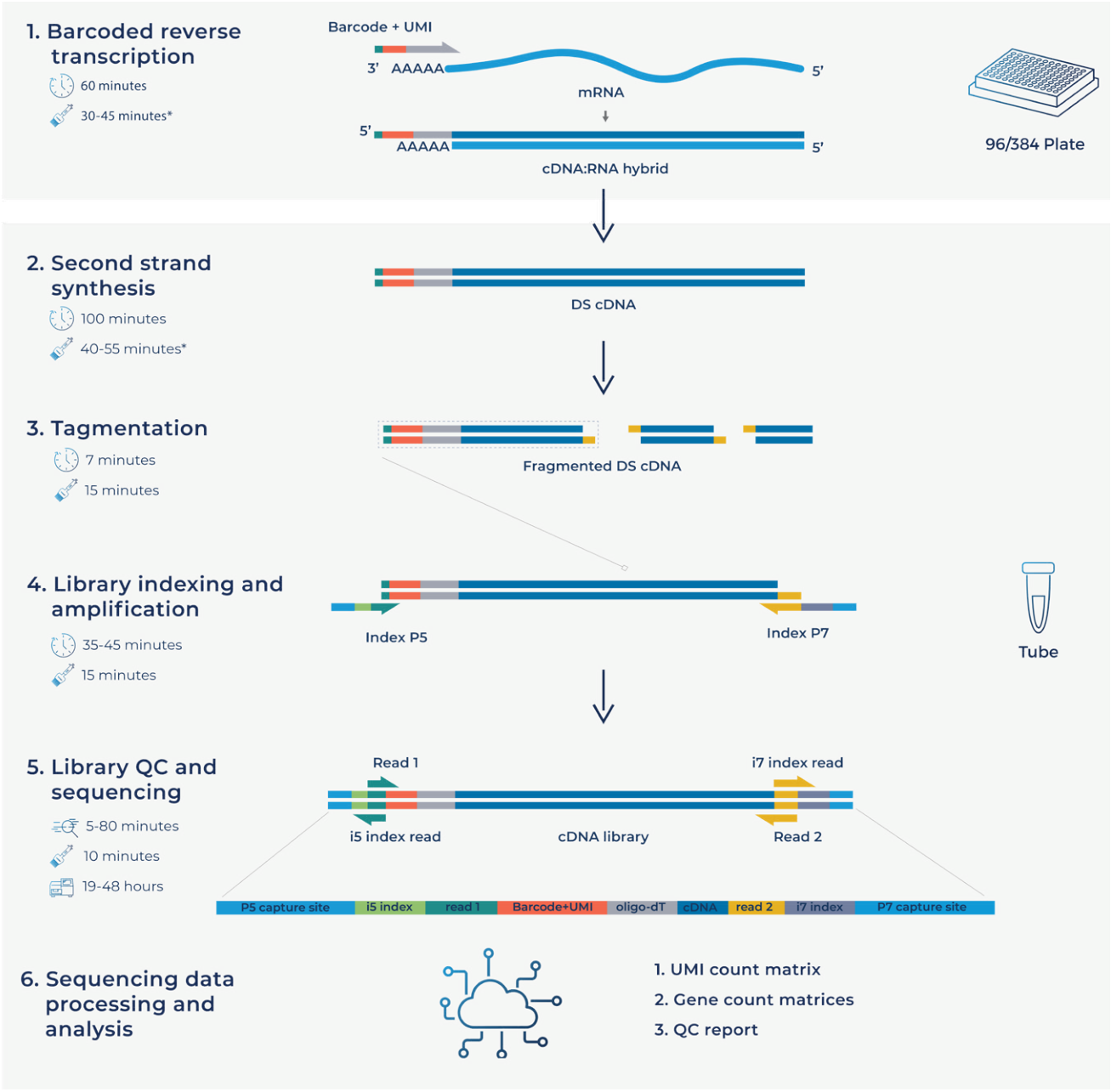
Compatibility with diverse sample types

From purified RNA to whole blood samples

Our solutions accommodate a wide range of inputs.



Experimental workflow at a glance



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).

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

OUR KITS

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

Scalable bulk RNA sequencing

Perform up-to 384 RNA-seq library preps in a single tube. High quality, high cost-effectiveness.

Unbiased whole transcriptome screening

No need for prior target selection.

Fewer pipetting operations

Our massive sample mutiplexing capabilities reduce manual labor and sample handling risks.

One-day lab work

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

DISCOVER OUR KITS

Cat. number	**Total preps** How many samples can be prepared in total with one kit	**RNA and plate multiplexing format** How many samples can be pooled in one tube after RT	**Barcoded oligo-dT plates included**	**UDI pairs included** Corresponds to how many separate pools can be prepared with one kit
#10813	96	96	1	4
#11013	384	96	4	4
#10814	384	384	1	4
#11014	1,536	384	4	4

OUR SERVICE

By leveraging BRB-seq, we not only provide to industrial and academic clients high quality RNA-seq data, but we also do so with the highest affordability and shortest turnaround times on the market.

Scalable bulk RNA sequencing

Perform up-to 384 RNA-seq library preps in a single tube. High quality, high cost-effectiveness.

Unbiased whole transcriptome screening

No need for prior target selection.

Ultra scalable and ultra low-cost

The more samples are processed together, the lower the cost per sample.

Flexible service

Library prep only or end-to-end service, including data pre-processing and downstream analysis.

WHAT WE OFFER

The MERCURIUS™ BRB-seq service - for purified RNA samples, offers a convenient and streamlined solution for transcriptomics projects of any size.

PACKAGE 1

MERCURIUS™

BRB-seq Library Prep

+

Next Gen Sequencing

+

Data pre-processing

PACKAGE 2

MERCURIUS™

BRB-seq Library Prep

+

Next Gen Sequencing

+

Data pre-processing

+

Downstream analysis

PERFORMANCE

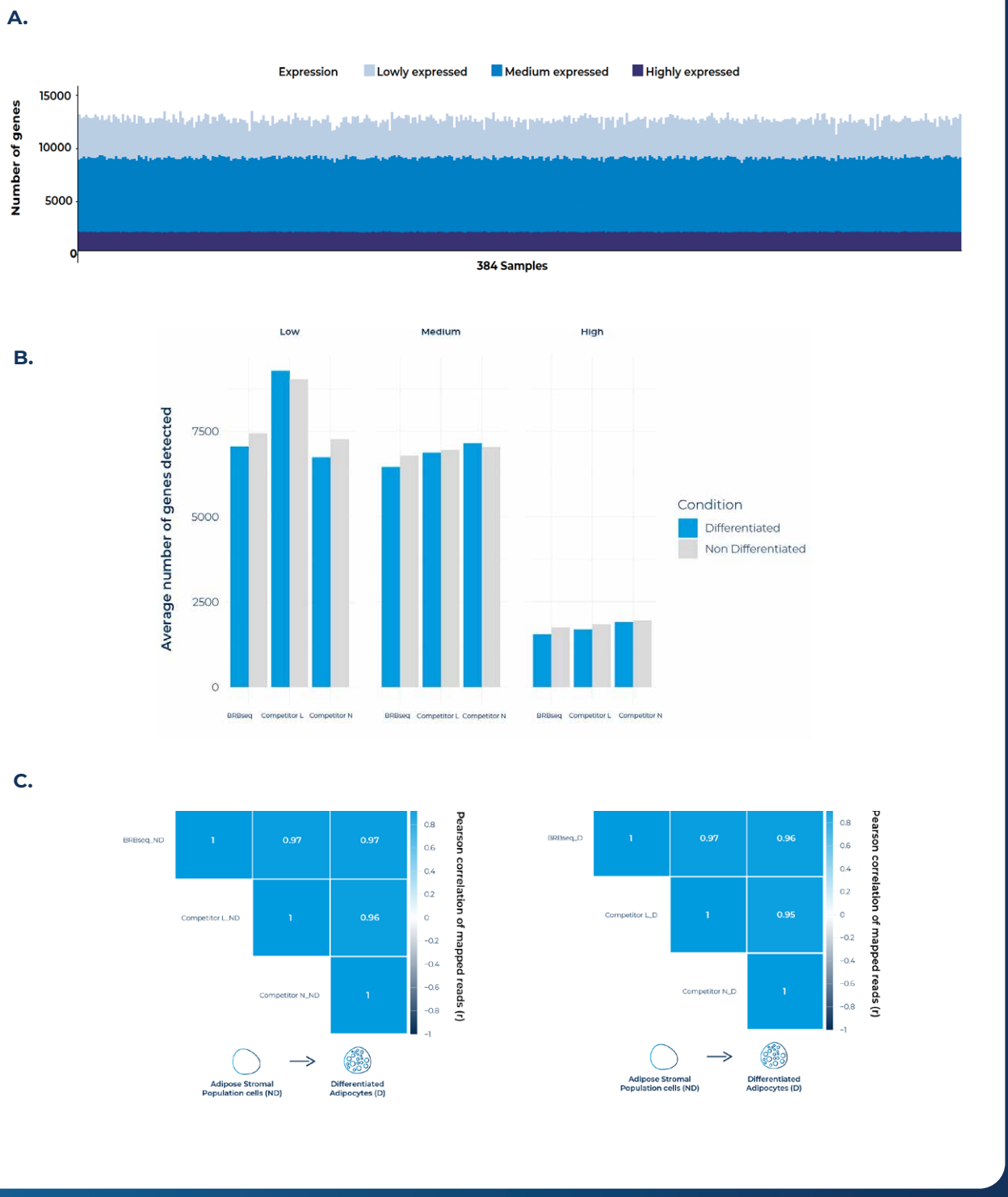


Figure. A Distribution of the number of detected genes across 384 samples prepared with the MERCURIUS™ BRB-seq library preparation kit. The library was sequenced at an average of 1 million reads.. **B.** Number of detected genes for the non-differentiated and differentiated Adipose Stromal Population Cells between BRB-seq and two other commercial kits. The expressed genes are split into three categories: Lowly Expressed (left, 0 < CPM < 10), Mid expressed (middle, 10 < CPM < 100), and Highly expressed (right, CPM > 100). **C.** Genome-wide Pearson correlation of mapped reads for the non-differentiated (ND) and differentiated (D) Adipose Stromal Population Cells between BRB-seq and two other commercial kits. A high correlation was observed both within technical replicates and across different library prep kits. All replicates were prepared from the same RNA sample and the sequencing depth was 3M reads/sample.