

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™
Plant BRB-seq library
preparation kits for Illumina®

RNA-seq at scale for plant purified RNA

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



Validated on plant samples

The production process and kit composition are optimized and QC'ed with plant RNA.



Bulk RNA sequencing at scale

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



BRB-seq as a flexible solution

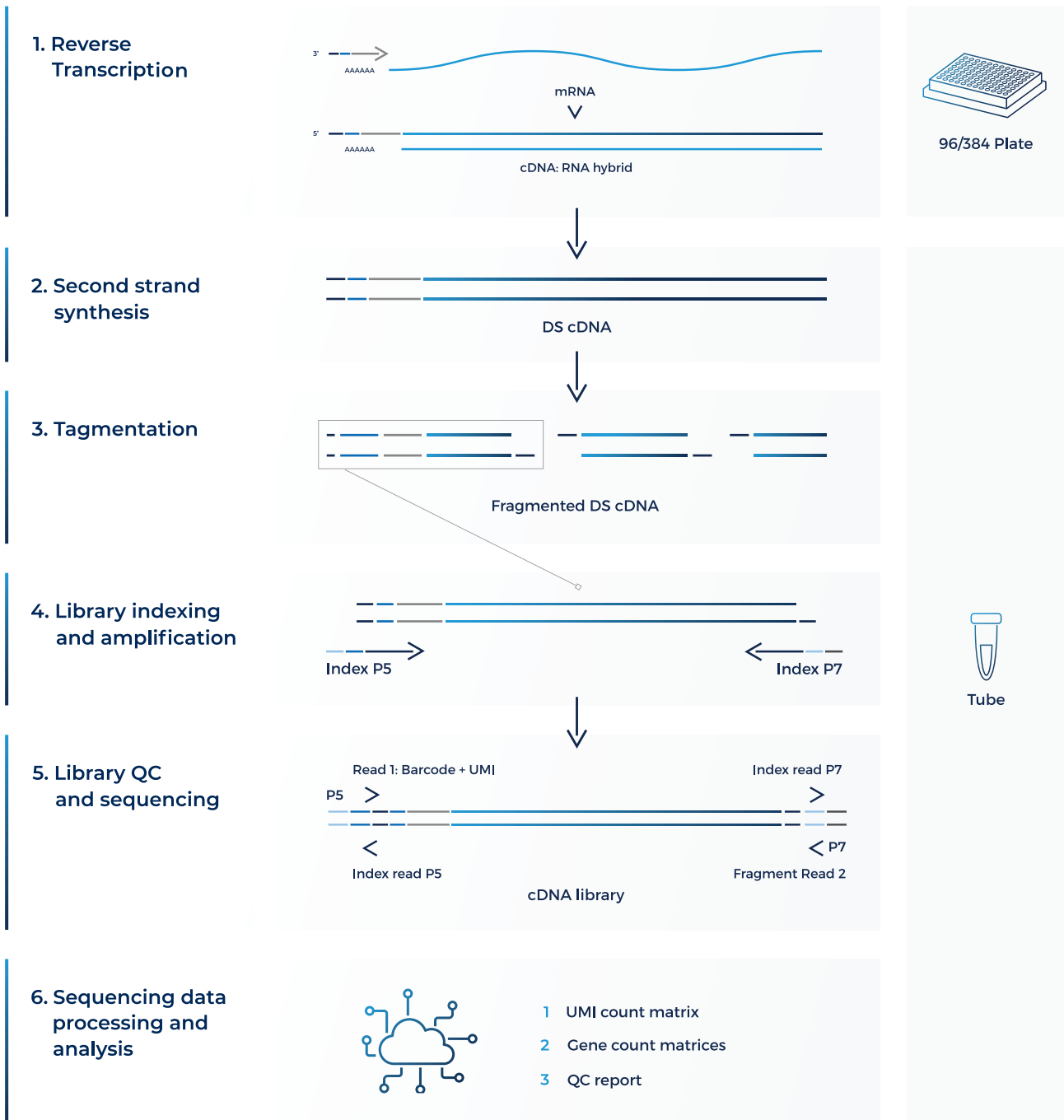
For projects of all sizes, from a few samples to up-to 384 samples in one single tube.



One-day lab workflow

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

Experimental workflow at a glance



The **Plant 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™ **Plant BRB-seq** on 96 purified plant RNA samples from *Arabidopsis* and sequenced at 3M reads/sample on an Illumina sequencer.

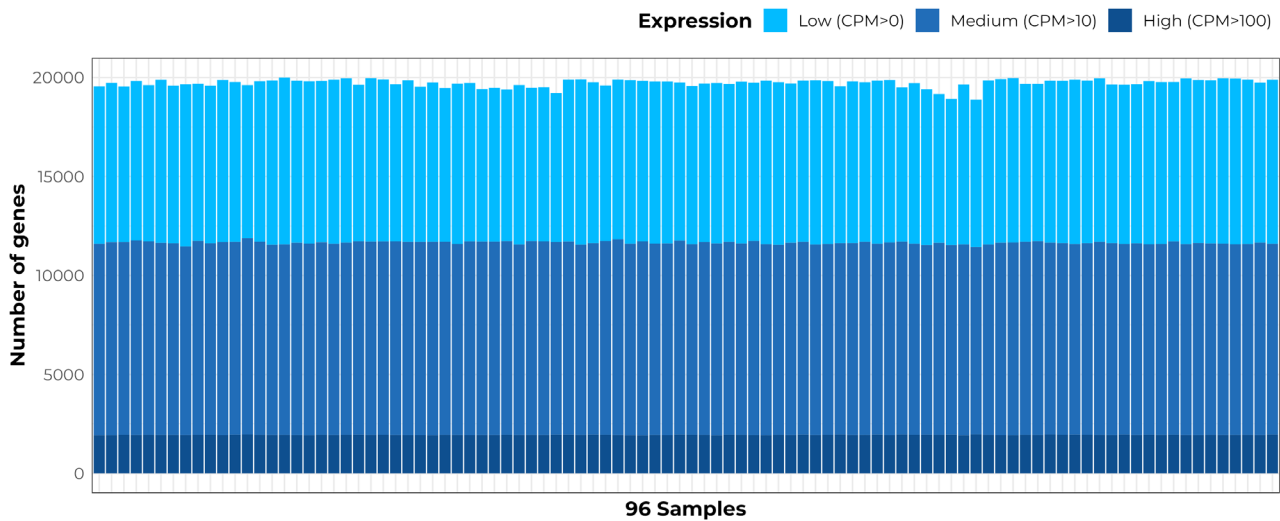


Figure. Sample plot generated from the MERCURIUS™ Plant BRB-seq cloud pre-processing platform (alitheagenomics.com/software) showing the number of detected genes for three counts per million (CPM) thresholds. The library was sequenced at an average of 3 million reads per sample.



Cat #10713 Cat #11713 Cat #10714 Cat #11714 Cat #12714 Cat #13714

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



Reach out to us



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