

The MERCURIUS™

# DRUG-SEQ INFO GUIDE



ALITHEA  
GENOMICS

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The MERCURIUS™

# DRUG-SEQ TECHNOLOGY

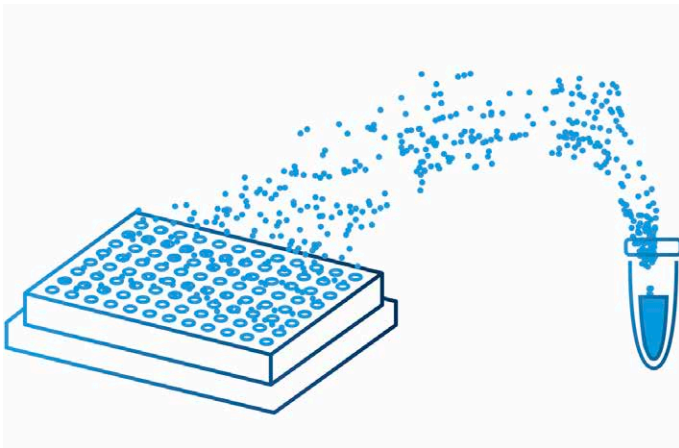
This technology boosts screening efforts based on gene expression profiling by offering an unbiased RNA-seq procedure that is highly sensitive, massively multiplexed and extremely cost-effective.

Compatible with Illumina®, AVITI™ and Ultima Genomics.

## Extraction-free

**Skip tedious RNA extraction step and go straight to library prep**

Cell lysis buffers are highly optimized for 2D cell cultures and organoid models to generate library preps efficiently without prior RNA isolation.

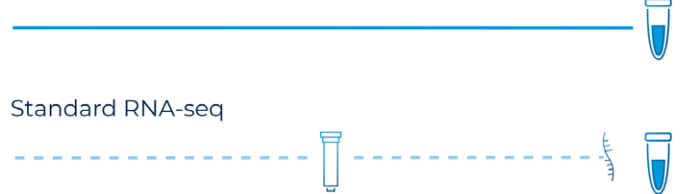


## Pre-amplification-free

**Improved protocol, leading to higher mapping and gene detection rates**

MERCURIUS™ DRUG-seq leverages a high-yield enzyme for reverse transcription. This streamlines the workflow and eliminates potential biases and duplication introduced with pre-amplification and template-switching oligos (TSO) used in the original DRUG-seq protocol while delivering superior performance.

Alithea Genomics

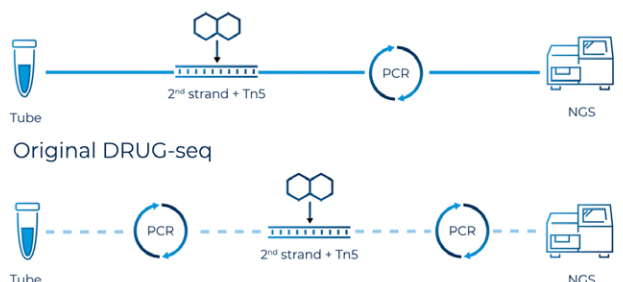


## Massive sample multiplexing

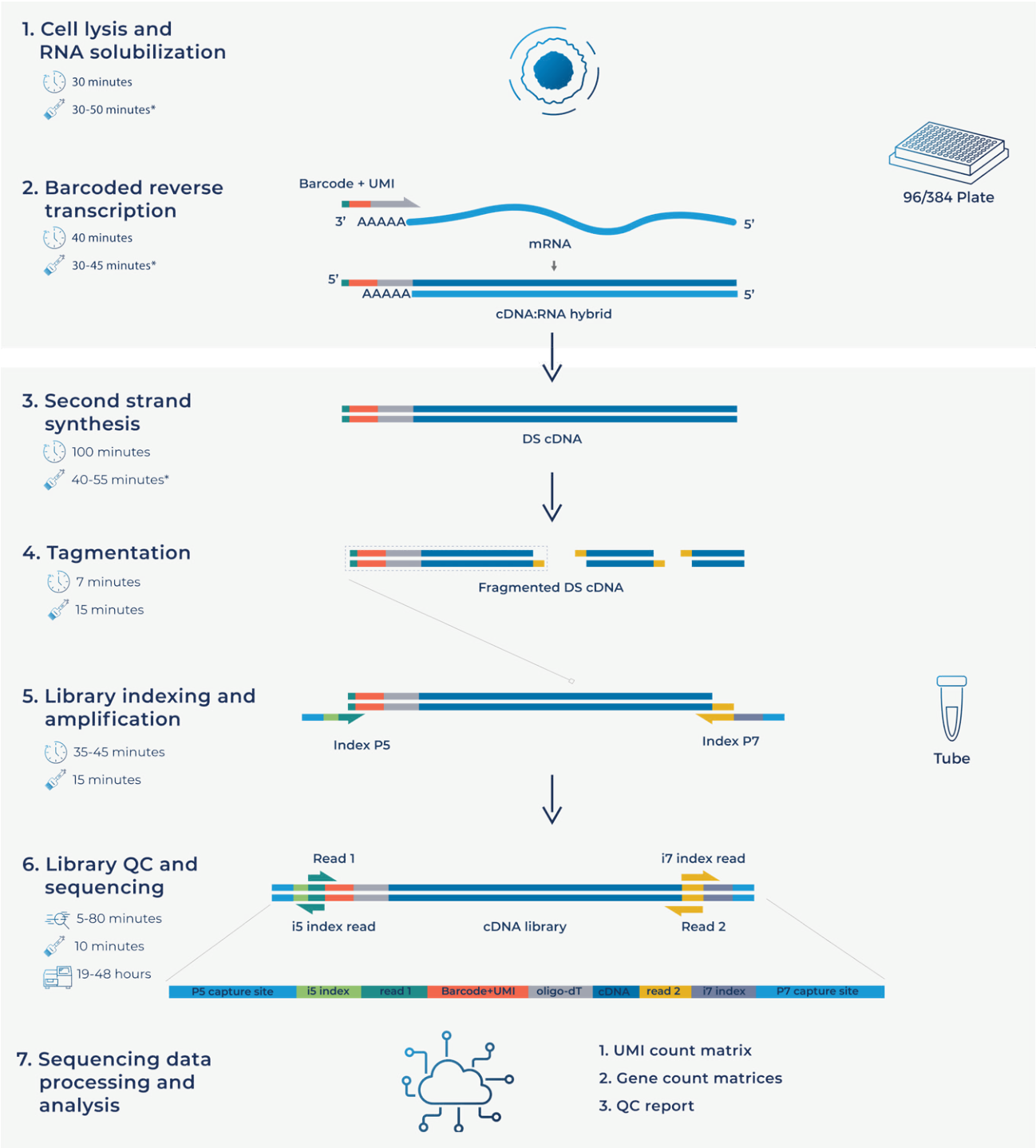
**Up-to 384 samples are processed in one single tube**

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.

MERCURIUS™ DRUG-seq



# Experimental workflow at a glance



The **DRUG-seq** workflow begins by adding the proprietary lysis buffer directly to pre-washed and frozen cells in 96- or 384-well-plates. The lysates can then be used directly in the DRUG-seq reverse transcription reaction, in which individual RNA samples are “tagged” with a specific 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.

# OUR KITS

The MERCURIUS™ DRUG-seq library preparation kits for Illumina®, AVITI™ and Ultima Genomics contain all the oligos and enzymes needed to go from cell and organoid lysates to sequencing-ready libraries.



## Ideal for screening projects

On thousands of samples in parallel and massively multiplexed. Compatible with 96, 384 and 1536 well-plate formats.



## No need for prior RNA extraction

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



## Pre-amplification free

No pre-amplification needed, leading to higher mapping and gene detection rates.



## One-day lab work

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

# DISCOVER OUR KITS

Cat. number	Total preps <small>How many samples can be prepared in total with one kit</small>	RNA and plate multiplexing format <small>How many samples can be pooled in one tube after RT</small>	Barcoded oligo-dT plates included	UDI pairs included <small>Corresponds to how many separate pools can be prepared with one kit</small>
#10841	96	96	1	4
#11041	384	96	4	4
#10851	384	384	1	4
#11051	1,536	384	4	4

# OUR SERVICE

The MERCURIUS™ DRUG-seq service boosts screening efforts based on gene expression profiling by offering a unique RNA-seq procedure that is highly sensitive, extraction-free, massively multiplexed and extremely cost-effective.



## Ideal for screening projects

On thousands of samples in parallel and massively multiplexed. Compatible with 96, 384 and 1536 well-plate formats.



## Ultra scalable and ultra low-cost

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



## Unbiased whole transcriptome screening

No need for prior target selection.



## Flexible service

Library prep only or end-to-end service, including cell culture and treatment, Cell Painting, NGS and downstream analysis.

# WHAT WE OFFER

A Transformative Tool for High Throughput Toxicology Screening for Environmental and Pharmaceutical Compounds.

## PACKAGE 1



MERCURIUS™

**DRUG-seq Library Prep  
and NGS**

## PACKAGE 2



MERCURIUS™

**Cell Culture & Treatment  
+  
DRUG-seq Library Prep  
and NGS**

## PACKAGE 3



MERCURIUS™

**Cell Culture & Treatment  
+  
Cell Painting  
+  
DRUG-seq Library Prep  
and NGS**

# HOW IT WORKS

## PACKAGE 1

Client ships frozen plates



## PACKAGE 2 & 3

Client defines cell model and treatment



Cell culture and treatment



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### PACKAGE 3 ONLY

Cell Painting assay



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Library prep and QC, followed by sequencing



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Downstream data analysis and reporting



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# CASE STUDY

Large-scale analysis of synergistic / antagonistic compound combinations effects.

In collaboration with

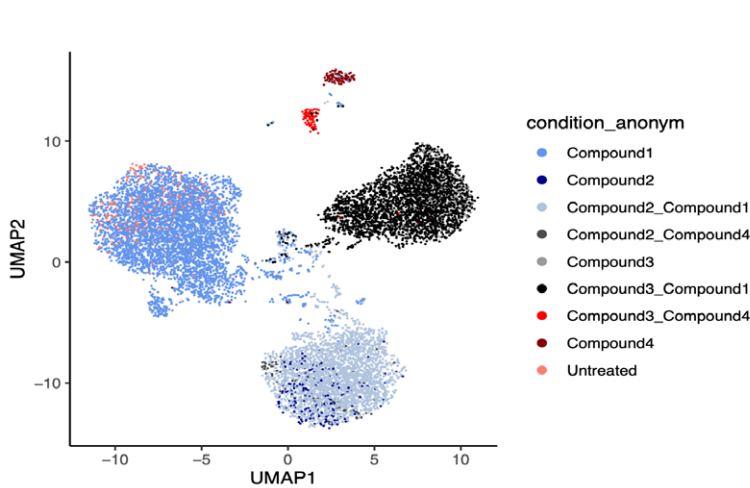
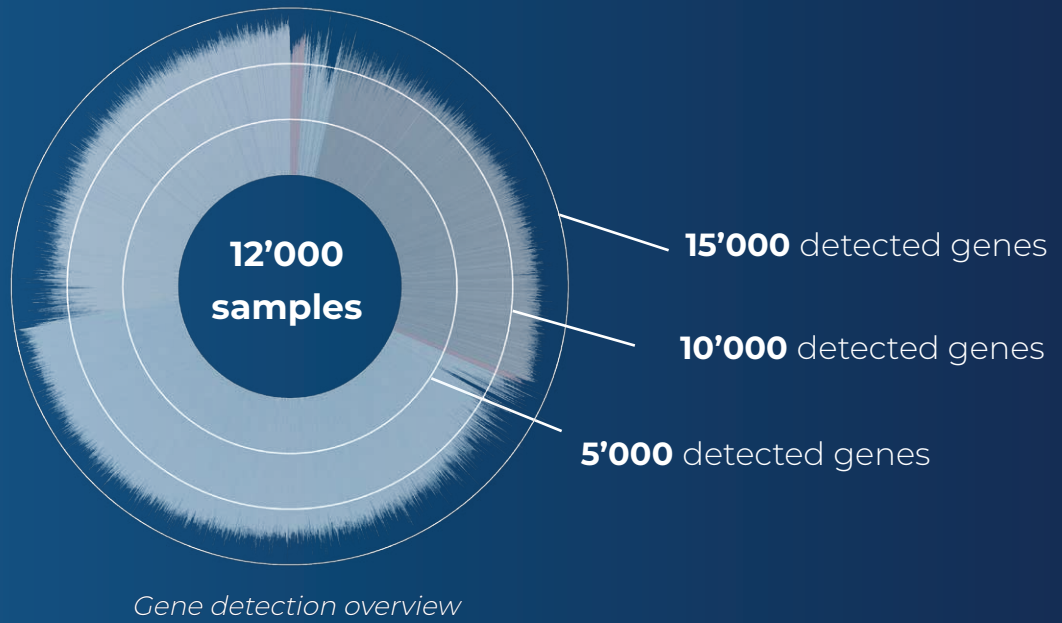


**3'840**  
Compound combinations

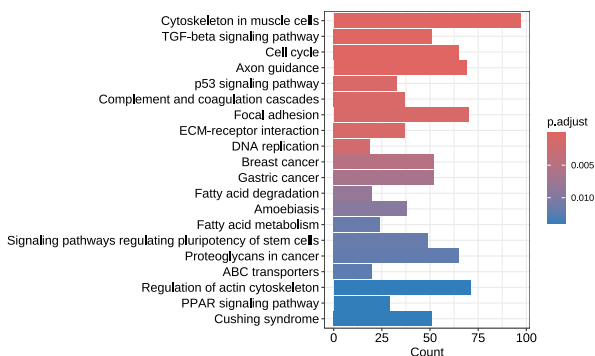
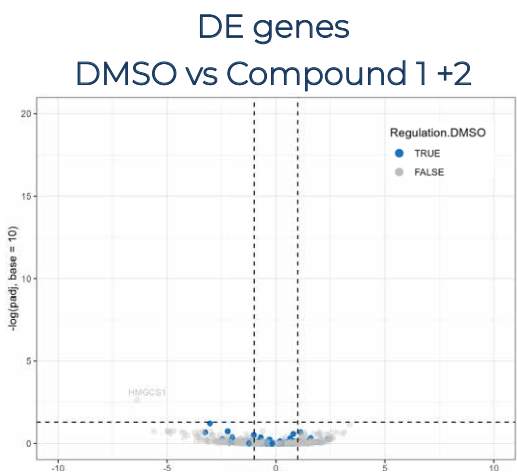
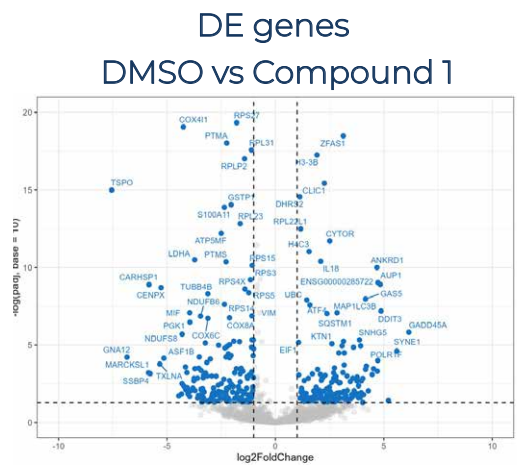
**12'000**  
Samples

**12'000**  
Genes / sample  
1M reads/sample

**7 days**  
Samples-to-data



*Analysis of top DE genes reveals signature of drug response in combinatorial treatment context.*



*DRUG-seq enables detailed pathway analysis of biological processes.*

*DRUG-seq can detect potential synergistic / antagonistic effect of drug combinations.*