

Zymo Environ™ COVID-19 Wastewater Testing Service

Community-Wide Variant Tracking with a Single Sample



Affordable, Community-Wide COVID-19 Variant Surveillance

Detect and track concerning mutations associated with strains such as those found in Brazil, the UK, and South Africa



Track and monitor COVID-19 outbreaks in your community at scale, without the costs and resources needed for individual testing.



Forecast COVID-19 testing and vaccine distribution resources based on trends.



Viral surveillance in wastewater also accounts for asymptomatic cases, many of which would not typically receive a rRT-PCR test.



Viral RNA in wastewater can be found up to 10 days before symptomatic cases appear, giving you a head-start on controlling outbreaks.

Learn More and Get Custom Testing Solutions at

www.zymoresearch.com/pages/zymo-environ-covid-19-wastewater-testing-service



www.zymoresearch.com



info@zymoresearch.com



Toll Free: (888) 882-9682

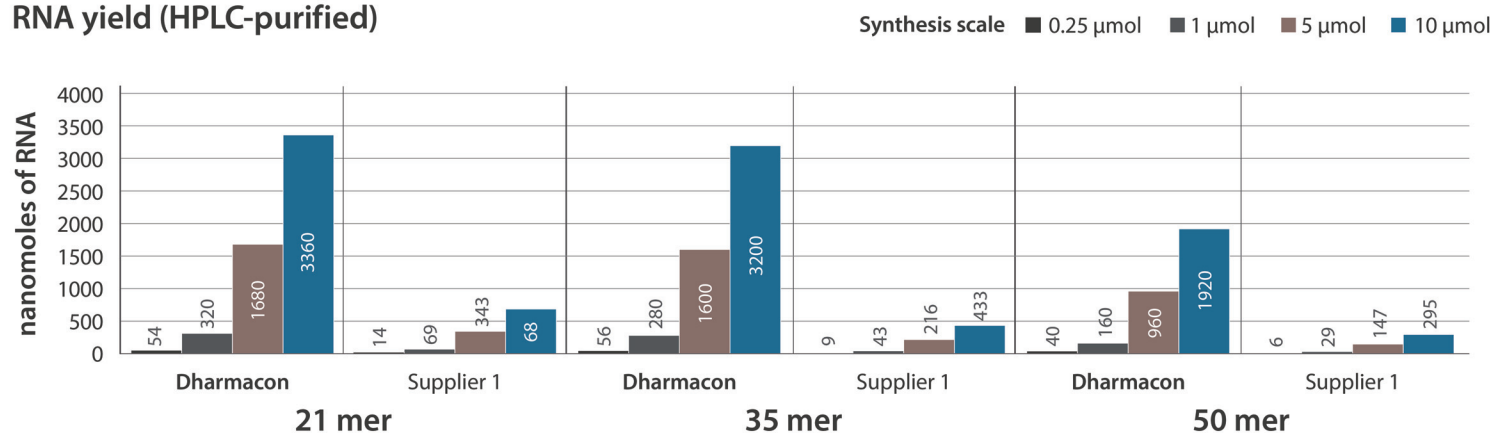


Meet your custom RNA requirements with our nearly limitless synthetic options.

If your NMR, crystallography, or RNA binding study requires a non-standard chemical modification or a commercially unavailable modified nucleobase, we can help. For more than 20 years our chemists have utilized Dharmacon™ proprietary 2' ACE chemistry to synthesize RNA with superior yield and quality giving you the flexibility you need.

Better RNA yields give you more for your money.

RNA yield (HPLC-purified)



The yield for RNA oligos of three different lengths was compared for all available synthesis scales between Dharmacon and a competitor.

Capture the entire transcriptome— in a single library.

Introducing the **new** SEQuoia Complete Stranded RNA Library Prep Kit for NGS.



It's new. It's different. And it's only from Bio-Rad.

The SEQuoia Complete Stranded RNA Library Prep kit gives you a truly holistic view of the transcriptome, capturing all types of RNAs (long, short, and everything in between) from all types of samples in less than 4 hours. With unparalleled uniformity of coverage, strandedness, and efficiency, what you will discover will definitely surprise you.

Are you ready for a new approach to transcriptomics?
Get the details at [bio-rad.com/SEQuoiaCompleteRNA](https://www.bio-rad.com/SEQuoiaCompleteRNA)

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Take CRISPR Beyond the Bench

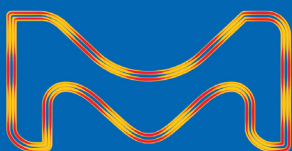
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Study m6A Modifications Like Never Before

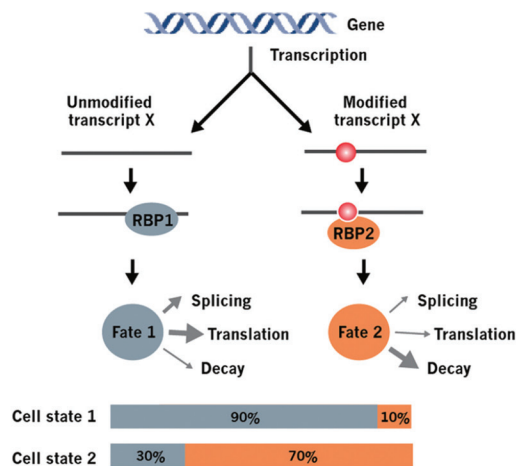


Fig. 1. m6A modified RNAs are immunoprecipitated and compared with the input RNAs in two-color channels of the Epitranscriptomic Array to accurately measure the modification percentage and abundance level for each transcript. The percentage of modification of “transcript a” RNA determines its different cell fates, e.g. for protein translation or RNA decay.

Epitranscriptomic Array

- Quantifying the percentage of modification for each transcript
- Coverage of mRNAs, lncRNAs, circRNAs and more
- RNA modifications at transcript-specific level
- Low sample amount, starting from 1 ug total RNA

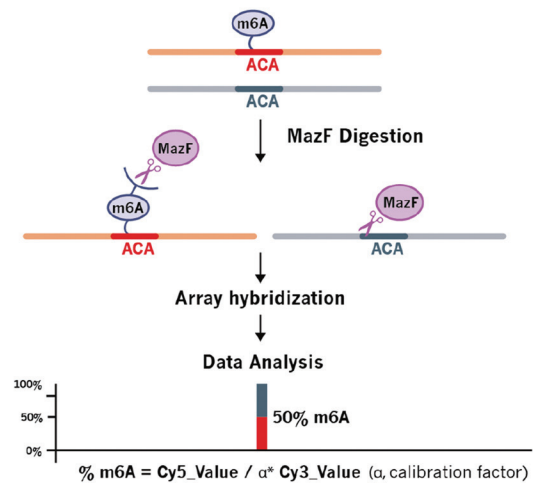


Fig. 2. Unmethylated (ACA) sites, but not methylated (m6ACA) sites, are cleaved by RNase MazF. The MazF treated and corresponding untreated sites are compared in two-color channels of the m6A Single Nucleotide Array to accurately quantify the m6A modification percentage, and abundance level at precise single nucleotide resolution.

m6A Single Nucleotide Array

- A new orthogonal methodology for m6A detection
- Single-Nucleotide resolution for m6A site location
- Quantifying the percentage of m6A site modification
- Reliable m6A site collection and systematic annotations
- Low sample amount, starting from 1 ug total RNA

To learn more: www.arraystar.com

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