

Increased Viral RNA Yields for the Earliest Detection of COVID-19 Outbreaks

Zymo Environ Water RNA Kit For SARS-CoV-2 Wastewater Surveillance



Highest RNA Concentration
Removes PCR Inhibitors
Eliminates Infection Risk

The Zymo Environ™ Water RNA Kit simplifies COVID-19 wastewater surveillance by increasing viral enrichment, inactivating pathogens, and improving limits of detection. The workflow yields highly concentrated, PCR inhibitor-free RNA ready for downstream applications including RT-qPCR, RT-ddPCR, and NGS.

Upgrade Your COVID-19 Wastewater Surveillance Today!

Visit www.zymoresearch.com/pages/zymo-environ-water-rna-kit



www.zymoresearch.com



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



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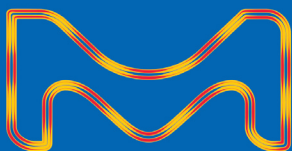
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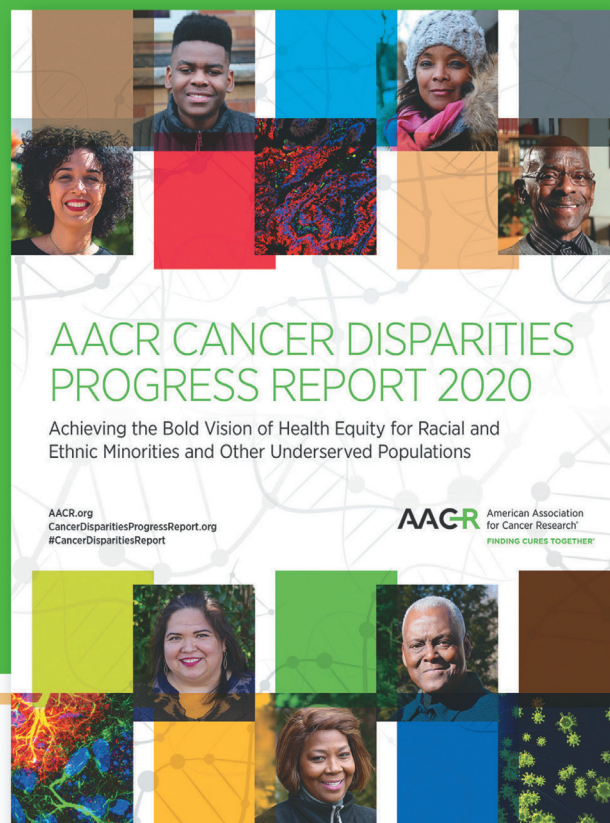


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DISCOVERY
SCIENCE
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AACR CANCER DISPARITIES PROGRESS REPORT 2020

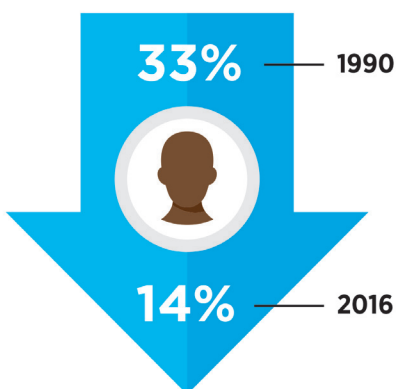
Achieving the Bold Vision of Health Equity for Racial and Ethnic Minorities and Other Underserved Populations



The American Association for Cancer Research is proud to announce the release of the inaugural *AACR Cancer Disparities Progress Report 2020*.

This report highlights the current disparities in the burden of cancer within the United States and the research that aims to mitigate these challenges. Some of the recent advances you will learn about include:

Decline in Disparity for Overall Cancer Death Rate between African Americans and Whites



The National Cancer Institute recently revised its eligibility criteria for cancer clinical trials to expand access for previously excluded patients.

Get your FREE copy of the full report by visiting

CancerDisparitiesProgressReport.org



so that you can learn about the many ways in which research is transforming lives.

Study m6A Modifications Like Never Before

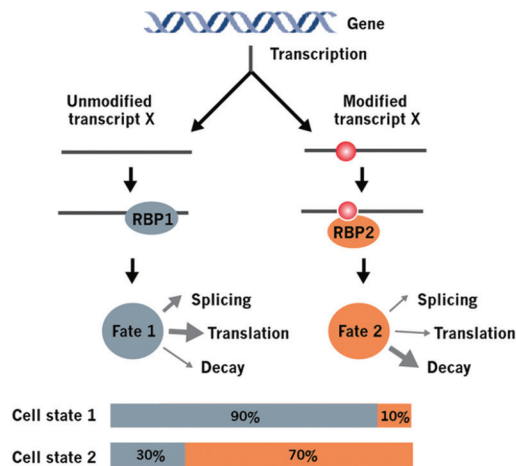


Fig. 1. m6A modified RNAs are immunoprecipitated and compared with the input RNAs in two-color channels of the Epitranscriptomic Array to accurately measure the modification percentage and abundance level for each transcript. The percentage of modification of “transcript a” RNA determines its different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

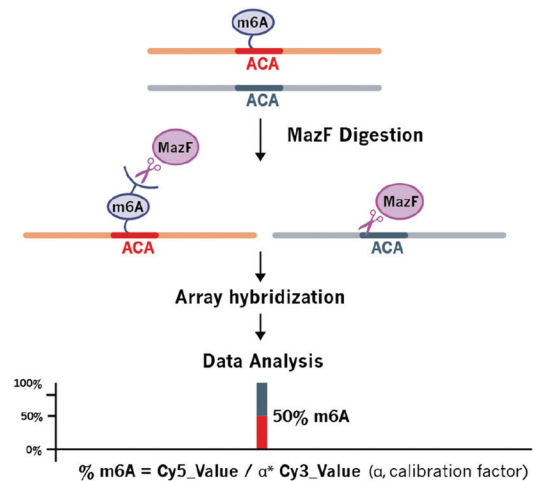


Fig. 2. Unmethylated (ACA) sites, but not methylated (m6ACA) sites, are cleaved by RNase MazF. The MazF treated and corresponding untreated sites are compared in two-color channels of the m6A Single Nucleotide Array to accurately quantify the m6A modification percentage, and abundance level at precise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

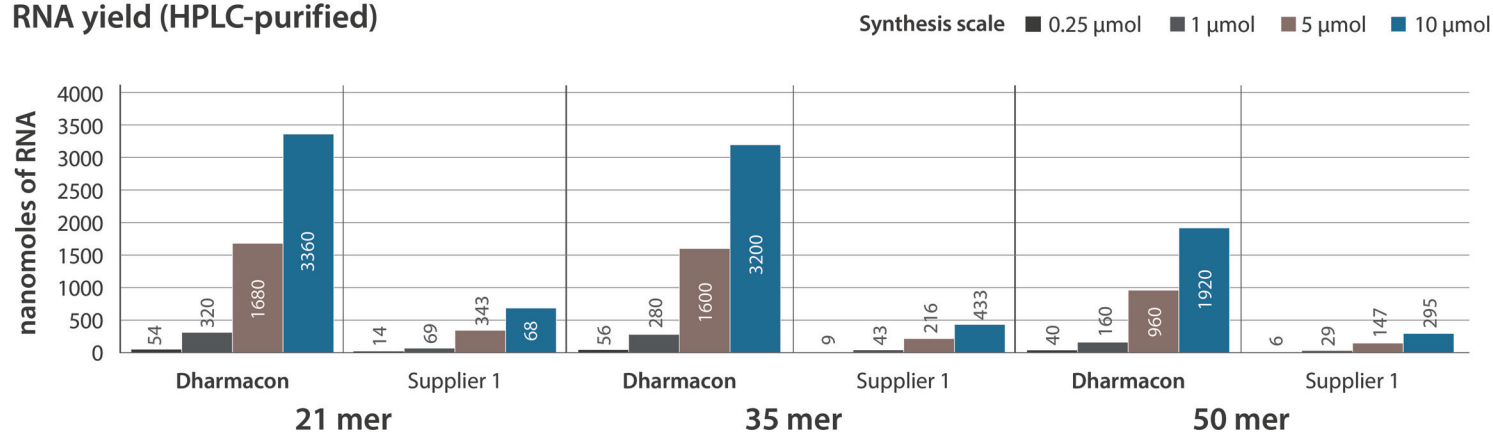
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Better RNA yields give you more for your money.

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.