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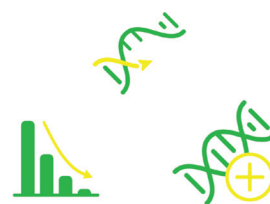


Infectious Samples, Tissue, Plants,
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Input Compatibility



RNA from TRIzol® in 7 Minutes



Reverse Transcriptase PCR
(RT-PCR)

Next-Gen Sequencing
(NGS)

Downstream Applications



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NGS library prep? We've got you covered.

For 13 years, NEB[®] has addressed library prep challenges by offering solutions that streamline workflows, minimize inputs, and improve library yield and quality. In fact, use of NEBNext[®] reagents has been cited in >20,000 publications.

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The NEBNext Ultra[™] II workflow, which lies at the heart of the NEBNext library prep solution, is available in a variety of streamlined and convenient kit formats. For added flexibility, NEBNext kits are easily scalable for automation on liquid

handling instrumentation. As a reagent manufacturer, NEB is ideally positioned to support your large volume and custom needs through our OEM & Customized Solutions group.

Our expertise, proven track record and depth of portfolio make NEBNext a preferred choice for high-quality sample preparation. We're ready to show you why it should be yours.



Interested in giving NEBNext a try? Learn more and request a sample at **NEBNext.com**.

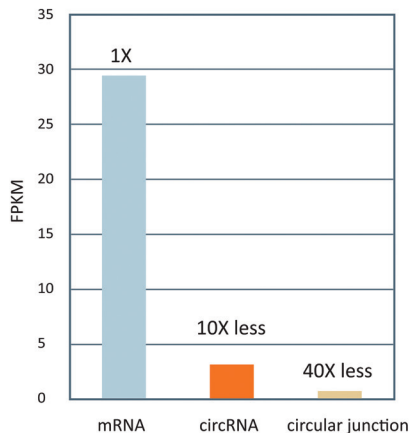
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be INSPIRED
drive DISCOVERY
stay GENUINE

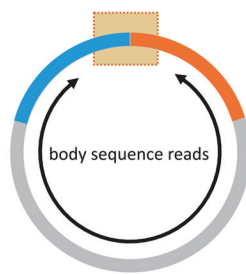
Dedicated to Non-coding RNAs Since 2009



Challenges of CircRNA Profiling



circular junction reads



Circular RNAs are expressed at $\sim 1/10$ the mRNA level. Circular junction reads (yellow box) accounting for only a fraction of the circular RNAs are even less, at $\sim 1/40$ of mRNA level.

Example: hsa_circ_0054254

circRNA study	Sample	circular junction reads
Rybak2015	frontal_cortex	3
	parietal_lobe	7
	diencephalon	2
Salzman2013	K562	3
	Gm12878	13
	Sknshra	1
	H1hesc	3
	Helas3	2
	Huvec	0
	A549	3
	Ag04450	1

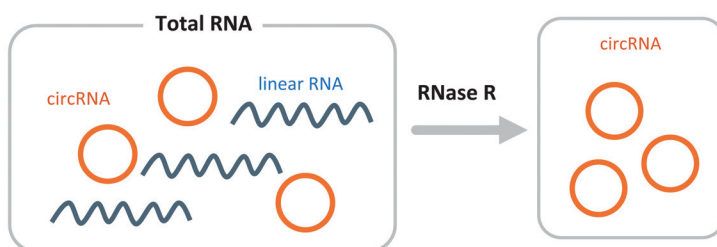
Only a few circular junction counts could be observed in deep sequencing, far below the limit of quantification [Szabo and Salzman (2016) Nat. Rev. Genet. PMID: 27739534].

Arraystar circRNA Arrays Power 500+ Publications

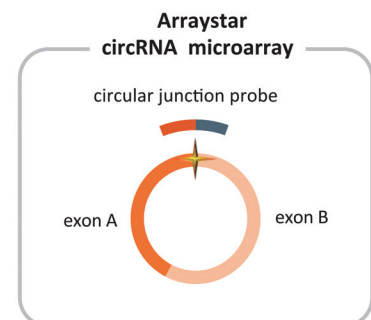


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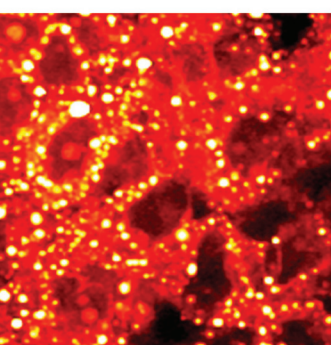
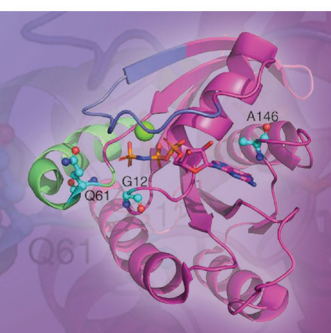
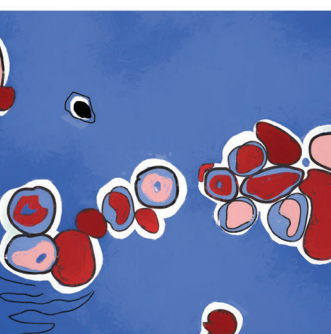
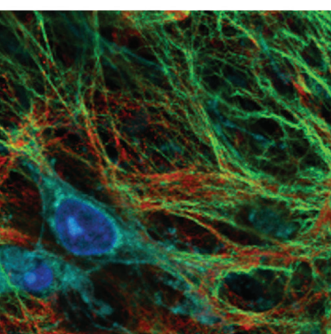
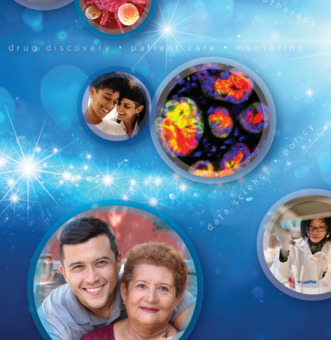
- Overcome the challenges of circRNA profiling by sequencing
- Unique circular junction array probes to specifically and accurately profile circRNAs
- Enhanced sensitivity and specificity by RNase R treatment to remove linear RNAs
- Easy and straight forward analysis with detailed annotations for circRNA biology



circRNA enrichment from total RNA by RNase R treatment



Unique circular junction probe for specific circRNA detection



AACR American Association
for Cancer Research®

2022 - 2023 SCIENTIFIC CONFERENCES

Presenting the most significant research on cancer etiology, prevention,
diagnosis, and treatment

San Antonio Breast Cancer Symposium

December 6-10, 2022 | San Antonio, TX

Codirectors: Carlos L. Arteaga and
Virginia G. Kaklamani

AACR-JCA Joint Conference Breakthroughs in Cancer Research – Translating Knowledge into Practice

December 10 – 14, 2022 | Maui, HI

Conference Cochairs: Antoni Ribas and
Masanori Hatakeyama

Acute Myeloid Leukemia and Myelodysplastic Syndrome

January 23-25, 2023 | Austin, TX

Conference Cochairs: Ravi Majeti, Maria (Ken)
Figueroa, and Ruben Mesa

Pediatric Hematologic Malignancies

February 19 - 22, 2023 | New Orleans, LA

Conference Cochairs: Terry J. Fry, Mignon
L. Loh, and Alejandro Gutierrez

Targeting RAS

March 5-8, 2023 | Philadelphia, PA

Conference Cochairs: Mariano Barbacid, Dafna
Bar-Sagi, Frank McCormick, and Deborah
K. Morrison

EACR-AACR Basic and Translational Research Conference: Immune Responses and DNA Repair: Cancer Fields Converging

March 15 - 17, 2023 | Florence, Italy

Scientific Program Committee Cochairs: Alberto
Bardelli, Michael B. Kastan, and Nicola Normanno

Advances in Prostate Cancer Research

March 15 - 18, 2023 | Denver, CO

Conference Cochairs: Cory Abate-Shen, Felix Y.
Feng, and Scott A. Tomlins

AACR Annual Meeting 2023

April 14-19, 2023 | Orlando, FL

Program Committee Chair: Robert H. Vonderheide

Advances in Kidney Cancer Research

June 24 - 27, 2023 | Austin, TX

Conference Cochairs: Othon Iliopoulos, M. Celeste
Simon, Cheryl Lyn Walker, and Qing Zhang

Molecular Biology in Clinical Oncology Workshop

July 16 - 22, 2023 | San Diego, CA

Workshop Director: Ross L. Levine
Workshop Codirectors: Christine M. Lovly, and
Jean Y. Tang

Integrative Molecular Epidemiology Workshop

July 24 - 28, 2023 | Boston, MA

Workshop Codirectors: Peter Kraft, Lorelei A.
Mucci, and Elizabeth A. Platz

The Science of Cancer Health Disparities in Racial/Ethnic Minorities and the Medically Underserved

September 29 - October 2, 2023 | Orlando, FL

Conference Cochairs: To be announced

Due to the nature of the COVID-19 pandemic, dates may be subject to change.

Learn more and register at
AACR.org/Calendar

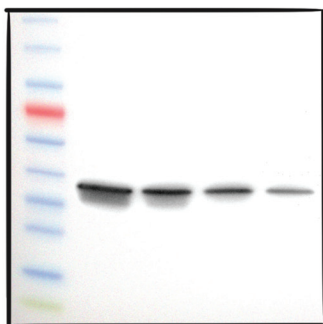
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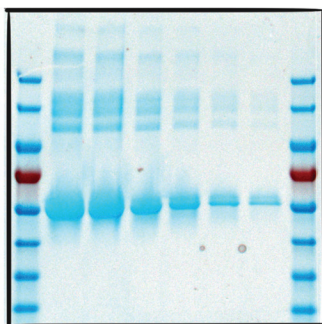
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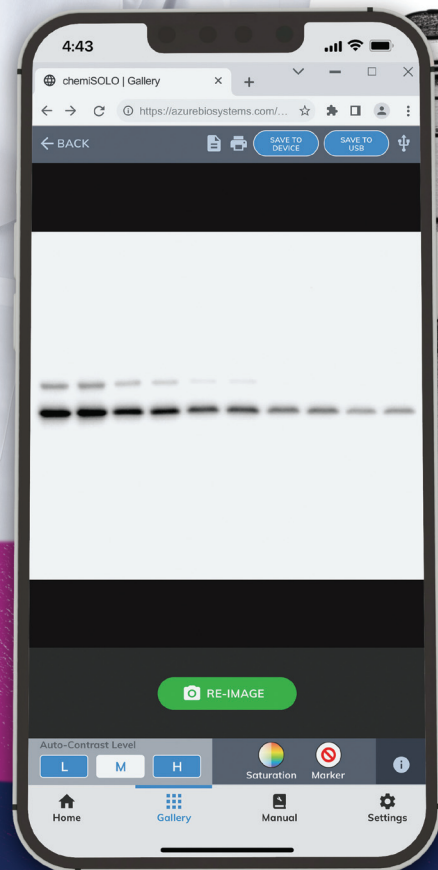
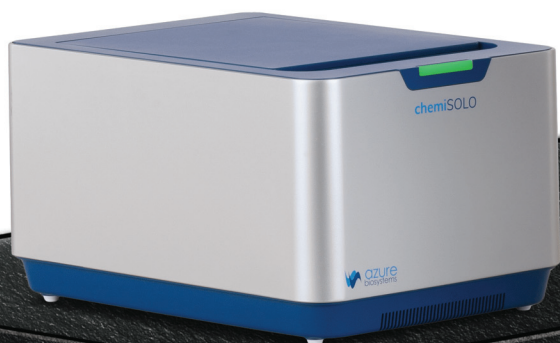
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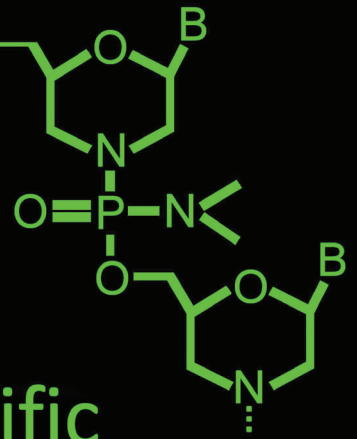
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CORALL RNA-Seq V2!

For whole blood sequencing experiments that are not in vein!

Increase Gene Detection from Blood Samples

Get the best sequencing results with convenient CORALL V2 workflows for whole blood samples!

Whole Transcriptome Blood RNA-Seq

CORALL RNA-Seq V2 combined with simultaneous rRNA and globin depletion provides a highly convenient workflow for processing whole blood samples and significantly increases gene detection (Fig 1).

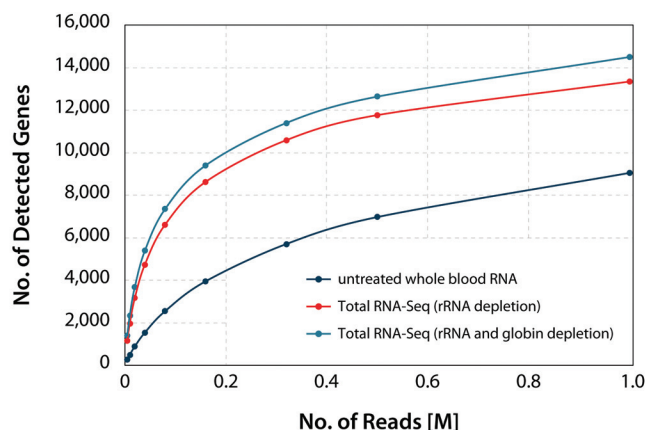


Figure 1 | Increased gene detection for CORALL Total RNA-Seq with rRNA and globin depletion (Cat. No. 186). Number of detected genes as a function of the number of reads uniquely mapping to exons.

mRNA-Seq Workflow from Whole Blood

Sequence what matters most by combining CORALL mRNA-Seq with rRNA and globin depletion to free up sequencing space for your mRNAs of interest (Fig. 2).

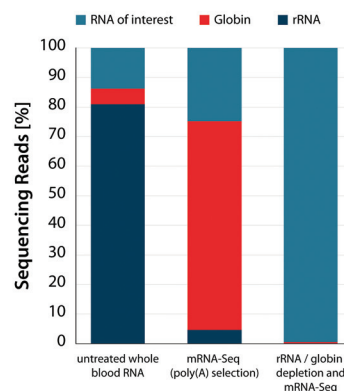


Figure 2 | CORALL mRNA-Seq V2 with an additional rRNA and globin depletion step (Cat. No. 186 + Cat. No. 157) efficiently removes globin mRNA from human whole blood RNA for mRNA-Seq applications.



Interested to learn more?

Check the product page for more information!

Benefits:

- Unlock the potential of whole blood RNA-Seq.
- Optimize your workflow, increase gene detection.
- Save time with a fully automatable workflow.