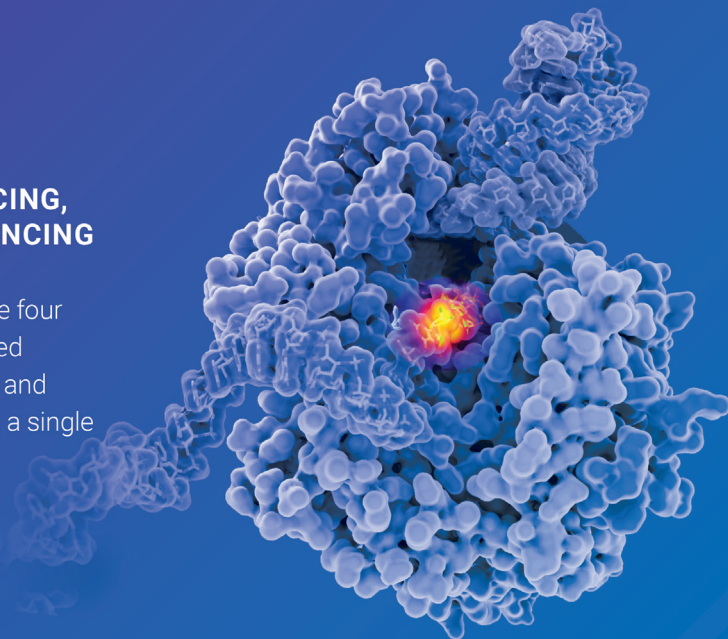




SAY GOODBYE TO BISULFITE SEQUENCING, AND HELLO TO PACBIO 5-BASE SEQUENCING

PacBio HiFi sequencing simultaneously calls the four DNA bases and 5-methyl cytosine from untreated genomic DNA. Achieve genome-wide detection and phasing of genetic and epigenetic variants from a single library prep with long and accurate reads.

**Get the most data from your samples
with PacBio HiFi 5-base sequencing.**



SCAN OR VISIT [PACB.COM/CSHLEPI22](https://pacb.com/CSHLEPI22)

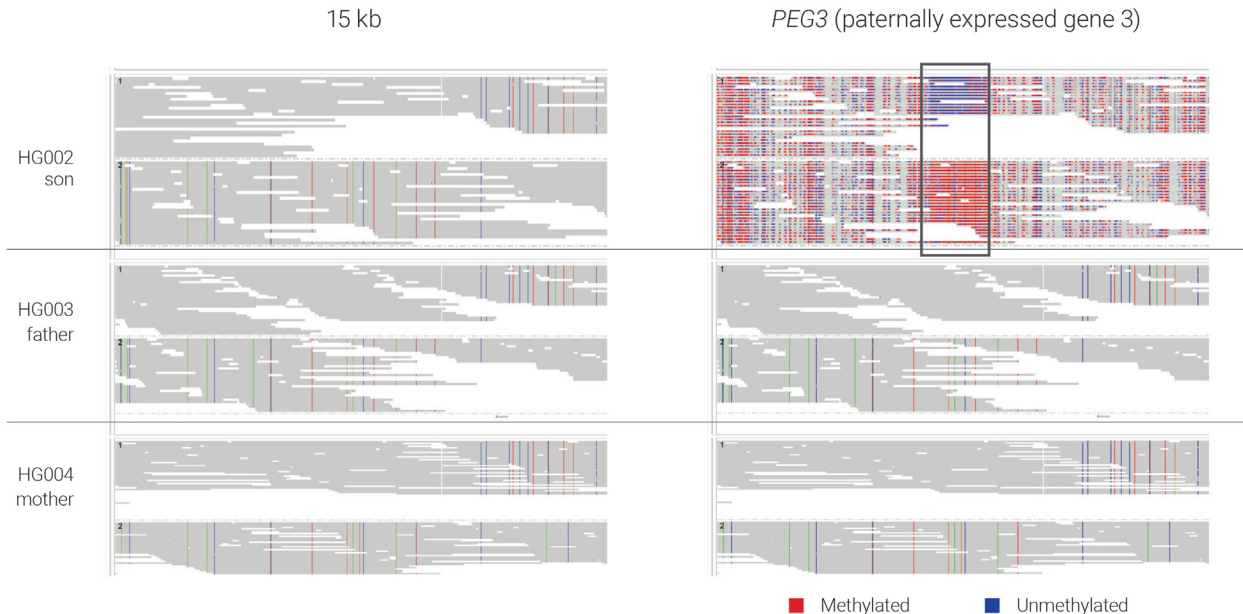
	Methylation microarrays	Short-read sequencing	Nanopore sequencing	HiFi 5-base sequencing
SNVs	⊗	✓	⊗	✓
Indels	⊗	✓	⊗	✓
SVs	⊗	⊗	✓	✓
Haplotype phasing	⊗	⊗	Limited	✓
Genome-wide	⊗	✓	✓	✓
5mC in CpG contexts	Limited	Requires special library preparation	Requires special data processing; conflated with basecalling	✓



HIFI SEQUENCING ENABLES SIMULTANEOUS PHASING OF READS INTO MATERNAL AND PATERNAL HAPLOTYPES AND DETECTION OF METHYLATION.

This directly reveals patterns of imprinting, where methylation status of a chromosome depends on whether it was inherited from a mother or father.

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Maternal imprinting at *PEG3* in a human trio. HiFi sequencing allows phasing of the haplotypes per sample; the trio identifies which allele is transmitted from which parent.

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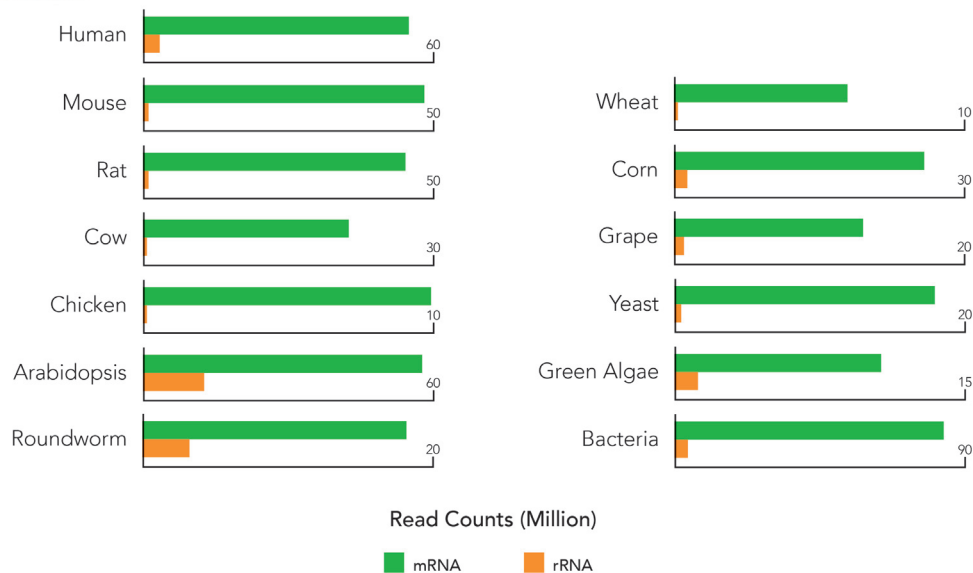
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The Zymo-Seq RiboFree® Kit Produces Dense Coverage of Protein Coding Genes. Classification of the STAR-aligned reads was based on Ensembl annotations and RepeatMasker rRNA tracks from UCSC genome browser when applicable.



Learn More about the fastest total RNA-Seq library prep kit at
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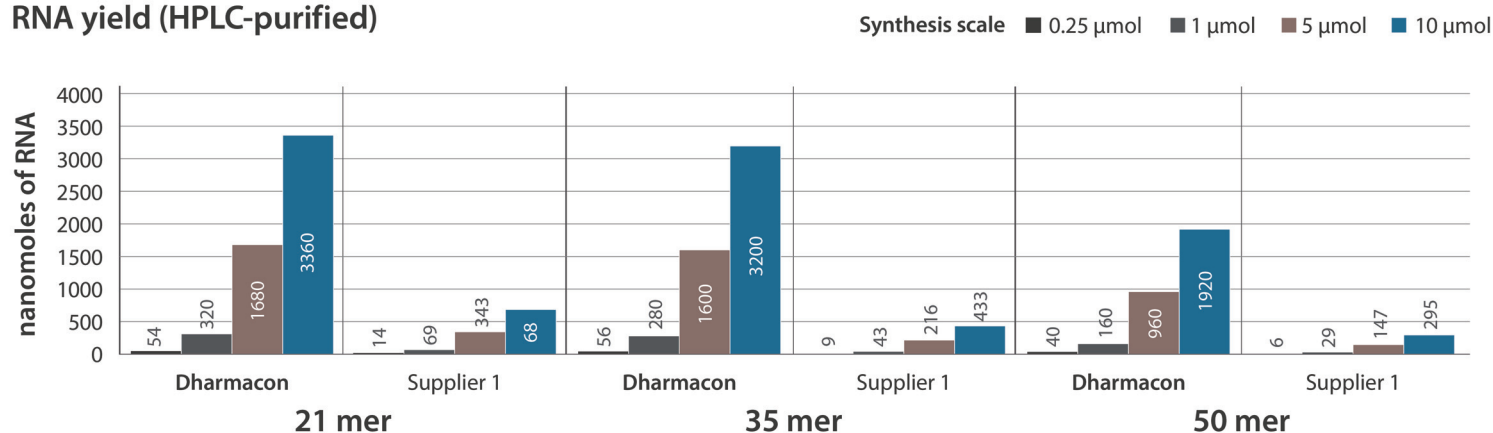
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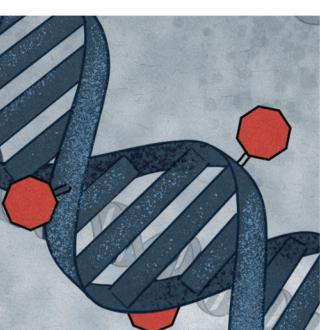
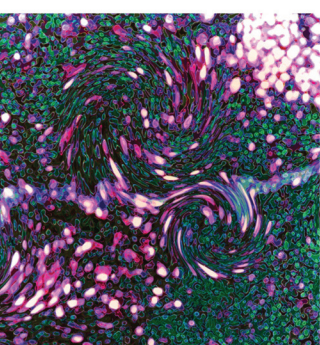
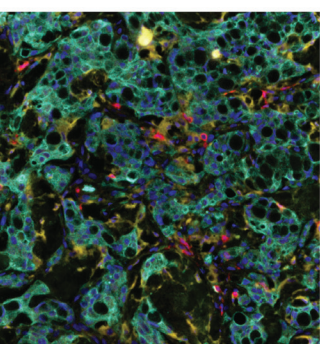
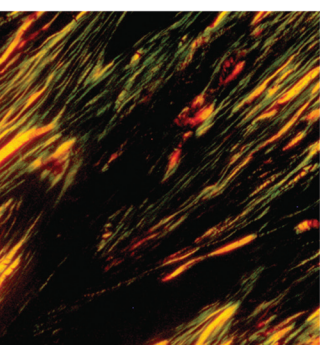
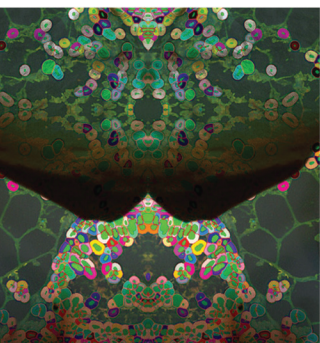
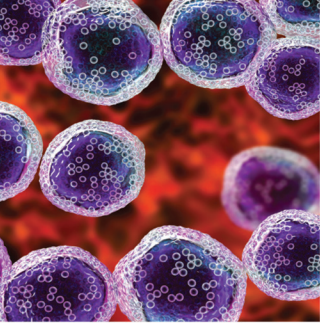
If your NMR, crystallography, or RNA binding study requires a non-standard chemical modification or a commercially unavailable modified nucleobase, we can help. For more than 20 years our chemists have utilized Dharmacon™ proprietary 2' ACE chemistry to synthesize RNA with superior yield and quality 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.



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2022 SCIENTIFIC CONFERENCES

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

Rethinking DCIS: An Opportunity for Prevention?

September 8-11, 2022 | Philadelphia, PA

Conference Cochairs: Lisa M. Coussens,
Laura J. Esserman, Kornelia Polyak,
and Jorge S. Reis-Filho

Pancreatic Cancer

September 13-16, 2022 | Boston, MA

Conference Cochairs: Andrew M. Lowy,
Marina Pasca di Magliano,
Robert H. Vonderheide, and Jen Jen Yeh

15th AACR Conference on The Science of Cancer Health Disparities in Racial/Ethnic Minorities and the Medically Underserved

September 16-19, 2022 | Philadelphia, PA

Conference Cochairs: Kevin L. Gardner,
K. Sean Kimbro, Martin Mendoza,
Camille C. R. Ragin, and Claradina Soto

Sixth CRI-ENCI-AACR International Cancer Immunotherapy Conference: Translating Science into Survival

September 28-October 1, 2022 | New York, NY

Conference Cochairs: Özlem Türeci,
E. John Wherry, and Jedd D. Wolchok

Colorectal Cancer

October 1-4, 2022 | Portland, OR

Conference Cochairs: Jiyoung Ahn,
Robert J. Coffey, and Scott Kopetz

Cancer Epigenomics

October 6-8, 2022 | Washington, D.C.

Conference Cochairs: Scott A. Armstrong,
Howard Y. Chang, Arul M. Chinnaiyan,
and Margaret A. Goodell

Tumor Immunology and Immunotherapy

October 21-24, 2022 | Boston, MA

Conference Cochairs: Thomas F. Gajewski,
Jennifer A. Wargo, and Jedd D. Wolchok

Innovation and Biomarkers in Cancer Drug Development (IBCD): A Joint Meeting Presented by the EORTC, NCI, EMA, and AACR

October 25, 2022 | Barcelona, Spain

Scientific Committee Cochairs: Roberto Salgado,
Tracy G. Lively, and David B. Solit

EORTC-NCI-AACR Molecular Targets and Cancer Therapeutics Symposium

October 26-28, 2022 | Barcelona, Spain

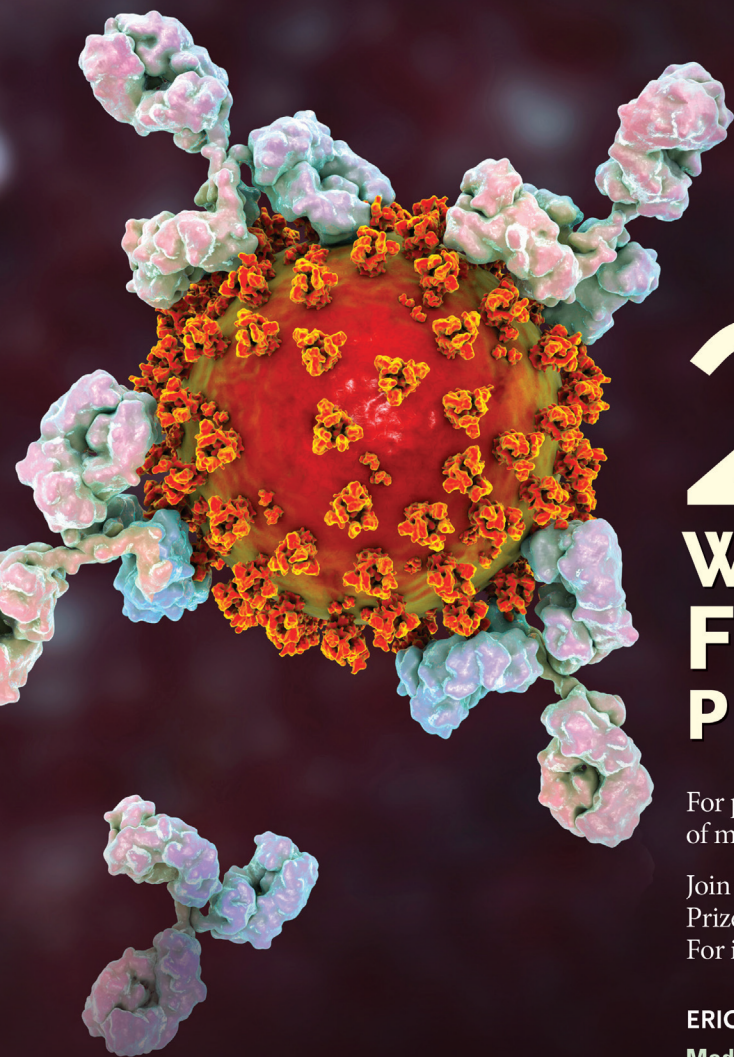
Scientific Committee Cochairs: Ruth Plummer,
James L. Gulley, and Lillian L. Siu

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

Learn more and register at
[AACR.org/Calendar](https://aacr.org/calendar)

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2022 WARREN ALPERT FOUNDATION PRIZE RECIPIENTS

For pioneering work leading to the discovery and development of mRNA vaccines.

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BioNTech SE

KATALIN KARIKÓ, PhD
BioNTech SE

DREW WEISSMAN, MD, PhD
University of Pennsylvania

UGUR ŞAHİN, MD
BioNTech SE

CALL FOR NOMINATIONS FOR THE 2023 PRIZE

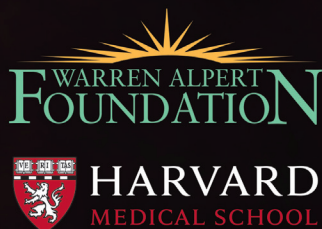
The Warren Alpert Foundation's Scientific Advisory Board, comprising internationally renowned biomedical scientists and chaired by the Dean of Harvard Medical School, invites your nominations for the 2023 Warren Alpert Foundation Prize.

Nominations should be made for scientific achievements that have led to the prevention, cure, or treatment of human disorders or for research that holds great promise to change our ability to treat disease.

Nominations are accepted from academic institutions, centers of research, government, or other biomedical institutions from around the world.

Nomination Deadline: November 7, 2022

For more information, visit www.warrenalpert.org





For more information
and additional resources,
please visit our website.



The diagram illustrates the workflow for CORALL and Conventional WTS (Whole Transcriptome Sequencing) over time. The CORALL workflow is shown in dark blue chevron boxes, while the Conventional WTS workflow is shown in light gray chevron boxes. A timeline at the top indicates a total duration of approximately 4.5 hours for CORALL and approximately 6 hours for Conventional WTS.

CORALL Workflow:

- First Strand Synthesis
- Clean-up
- UMI-Linker Ligation
- Clean-up
- PCR
- Clean-up

Conventional WTS Workflow:

- RNA Fragmentation
- First Strand Synthesis
- Second Strand Synthesis
- Clean-up
- End Repair
- Adapter Ligation
- Clean-up
- PCR
- Clean-up

The CORALL workflow is significantly shorter and more streamlined than the Conventional WTS workflow, which includes additional steps like RNA Fragmentation, Second Strand Synthesis, End Repair, and Adapter Ligation.

CORALL RNA-Seq V2 supports the widest input range (1 ng - 1000 ng) with excellent performance for low input RNA. The highly sensitive protocol delivers exceptional results for difficult samples, such as FFPE RNA.



SKIP the SYNTHESIS —And the Hassle.

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