

TRIZOL[®] IN

Direct-zol[™] RNA Purification

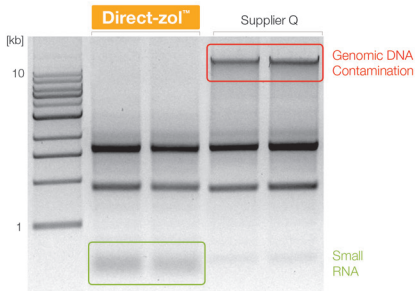


RNA OUT

Patented technology:
 Mix sample in TRIZOL[®], TRI Reagent[®], or similar.
 Add ethanol & load into the Zymo-Spin[™] column.
 No phase separation, no precipitation, no RNA loss.

7 minutes from TRIZOL[®] to purified RNA

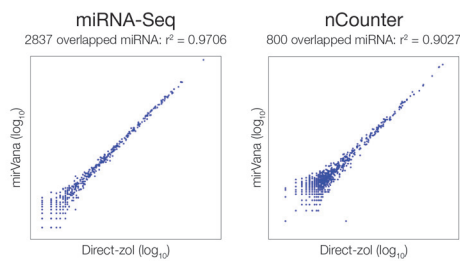
High-quality small & large RNA



High-quality small and large RNAs are effectively recovered using the Direct-zol[™] kit. RNA is DNA-free.

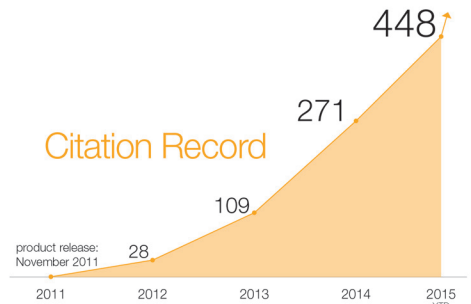
Samples available at zymoresearch.com/direct-zol or call (949) 679-1190

Non-biased miRNA recovery



The data show RNA purified from TRIZOL[®] samples using the Direct-zol[™] RNA MiniPrep compared to an unbiased method (miRvana[™], Ambion). Micro-RNA analysis was performed using miRNA-Seq (MiSeq[®], Illumina) and a direct hybridization assay (nCounter[®], Nanostring).

Highly cited



Product	Cat. No.	Size
NEW Direct-zol [™] RNA MiniPrep Plus	R2070, R2071* R2072, R2073*	50 Preps. (≤100 µg RNA) 200 Preps. (≤100 µg RNA)
Direct-zol [™] RNA MiniPrep	R2050, R2051* R2052, R2053*	50 Preps. (≤50 µg RNA) 200 Preps. (≤50 µg RNA)
NEW Direct-zol [™] RNA MicroPrep	R2060, R2061* R2062, R2063*	50 Preps. (≤10 µg RNA) 200 Preps. (≤10 µg RNA)

96-well spin plate & MagBead formats also available

* = Supplied with TRI Reagent[®]

TRIZOL[®] and TRI Reagent[®] are registered trademarks of Molecular Research Center, Inc.

U.S. Patent No. 9,051,563 B2 and other pending patents. Direct-zol[™] is a trademark of Zymo Research Corp.

Tel: (949) 679-1190 www.zymoresearch.com/direct-zol info@zymoresearch.com



A single cell – endless possibilities

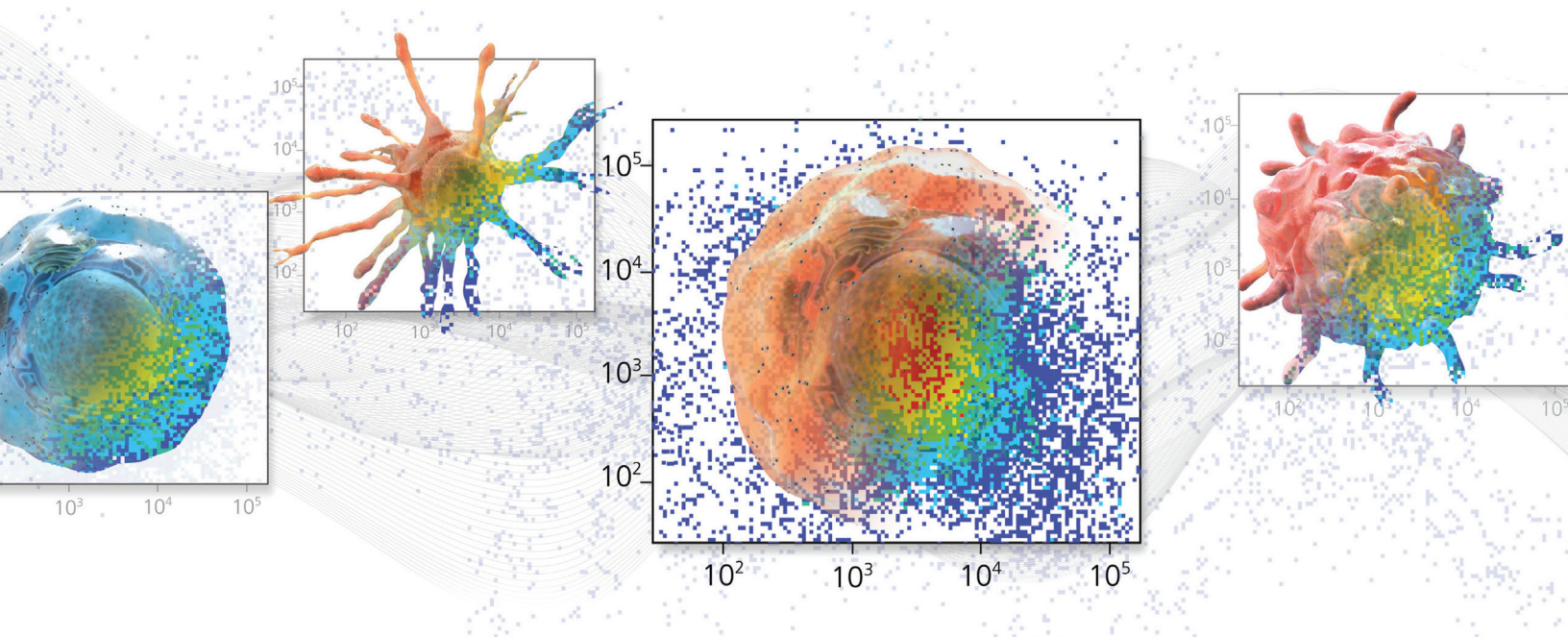
Generate sophisticated RNA libraries from a simple, single cell

Imagine a protocol that would allow you to examine the gene expression profile of a single cell. Recent advances in RNA sequencing technologies have revealed high heterogeneity in the profiles of individual cells – so any given cell can contain unique and critical information.

The protocol already exists: a PCR-free protocol that efficiently generates **RNA-seq libraries from a single cell** or even picogram amounts of RNA in just 6.5 to 7 hours. Using innovative multiple displacement amplification and efficient library adaptor ligation, this method prepares libraries that retain the unique transcriptional profile of a single cell with high fidelity and highly uniform coverage.

Discover how you can achieve whole transcriptome analyses from single cells at qiagen.com/Single-Cell-RNA

excellence



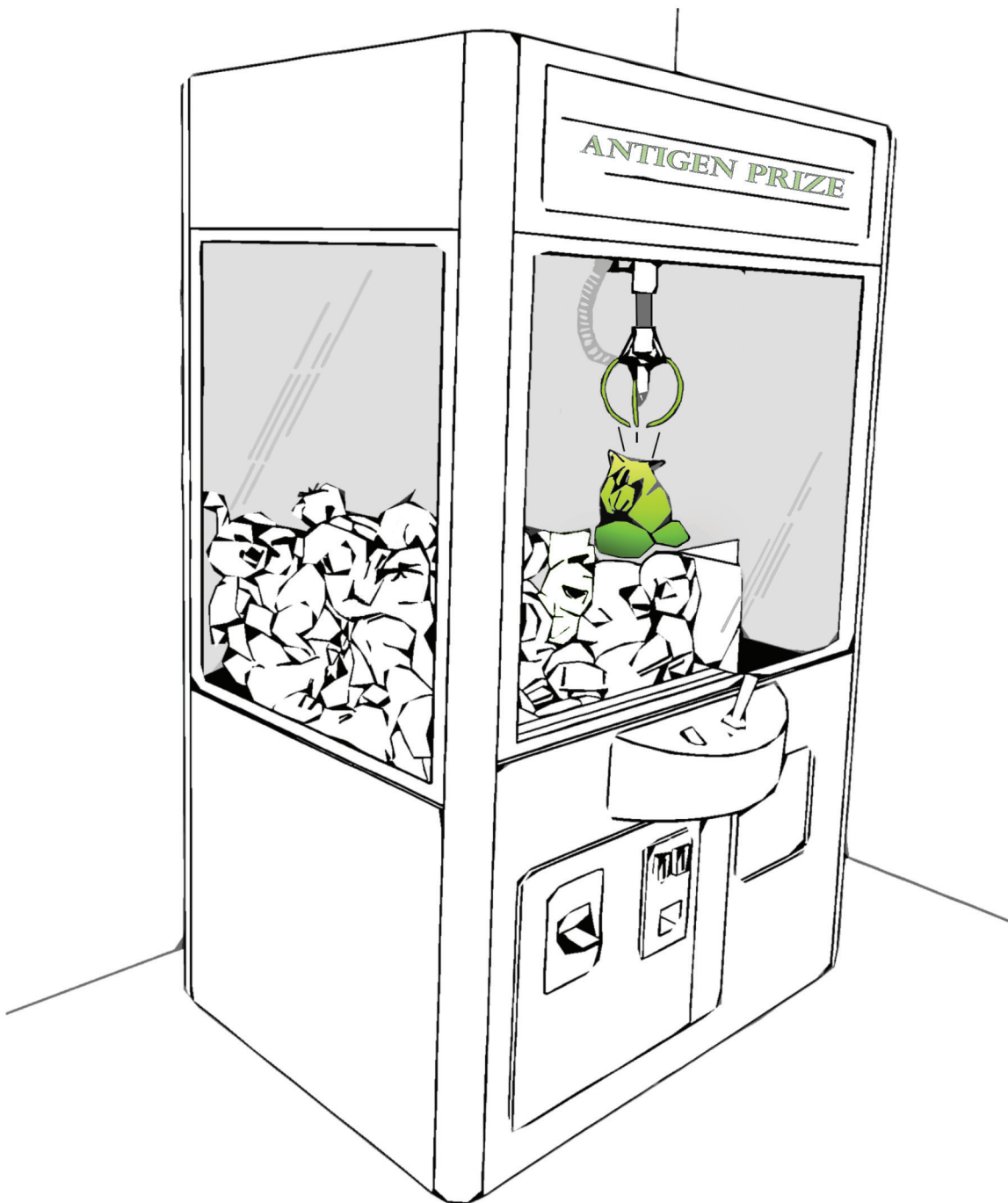
Millions of dots, each with a unique story

Every cell is a mystery waiting to be revealed. From phenotype, genomic expression, cytokine secretion, signaling activity or general health, flow cytometry is uniquely equipped to interrogate every facet of biology, all within a single cell. Let eBioscience flow cytometry reagents help you uncover the story that each cell contains within.

Don't settle for average. Real insight starts with single cells.

Learn more at www.affymetrix.com/single-cell-rna

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microRNA Array Services

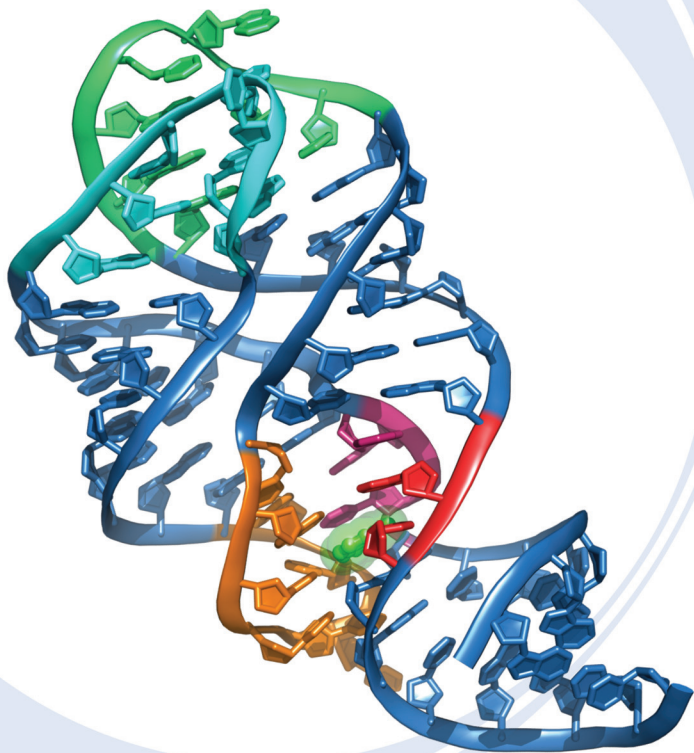
microRNA analysis using LNA™ micro-arrays performed by those who know the system best.

microRNA qPCR Services

Based on our powerful microRNA qPCR system. Ideal for validating your results or full profiling.

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Complete kit for isolating poly (A)⁺ mRNA from your samples using magnetic beads.

CATALOG # | 10760013

MagneZoom™ Oligo (dT)₂₅

Magnetic beads for isolating poly (A)⁺ mRNA.

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microRNA Purification Kit

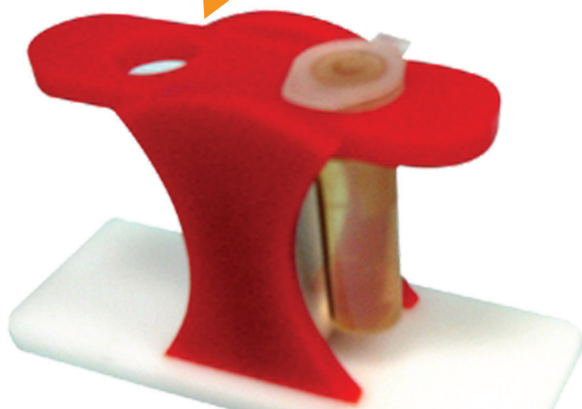
Isolate all small RNAs from your sample including miRNA, siRNA, tRNAs and 5S rRNA.

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MagneZoom™ Paramagnetic Beads Station

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- H minus Moloney Murine Leukemia Virus (M-MLV) Reverse Transcriptase is a recombinant M-MLV reverse transcriptase. RNase H activity has been eliminated by a point mutation in the RNase H domain of M-MLV RTase, ensuring high yields.
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RNasin is a ribonuclease inhibitor extracted from human placenta with a molecular weight 51 kDa. It inhibits the activity of RNase by specifically binding up to RNase with a non-covalent bond. RNasin, free of RNase or Nickase, can maintain its activity at pH from 5 to 8, and the highest one at pH7.8.

AACR Annual Meeting

American Association
for Cancer Research

2016 • NEW ORLEANS

APRIL 16-20, 2016
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For more information visit
www.AACR.org/AACR2016

Delivering
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Join us in New Orleans

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You are invited to stretch your boundaries, form collaborations, attend sessions outside of your own area of expertise, and learn how to apply exciting new concepts, tools, and techniques to your own research.

Get your fill of ground-breaking cancer science each day, and then enjoy the great sounds, food, and culture that is New Orleans.

If you can only attend one cancer science meeting this year, the AACR's Annual Meeting is it!

Submit your abstract by **December 1, 2015!**

Be sure to register early to take advantage of reduced rates!

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Join the AACR and enjoy substantially reduced registration rates, the privilege of sponsoring an abstract for the Annual Meeting and Special Conferences, funding and award opportunities, and much more.

We look forward to seeing you in New Orleans!

2016 Keystone Symposia RNA Conferences

Small RNA Silencing: Little Guides, Big Biology

Scientific Organizers: Phillip D. Zamore, Yukihide Tomari and Mihaela Zavolan
January 24–28, 2016 | Keystone Resort | Keystone, Colorado | USA

www.keystonesymposia.org/16A6

Deadlines: Discounted Registration – Nov 23, 2015

Plant Epigenetics: From Genotype to Phenotype

Scientific Organizers: Scott D. Michaels, Doris Wagner and Nathan M. Springer
February 15–19, 2016 | Sagebrush Inn & Suites | Taos, New Mexico | USA

www.keystonesymposia.org/16B1

Deadlines: Abstract – Nov 16, 2015; Discounted Registration – Dec 15, 2015

Noncoding RNAs in Health and Disease

Scientific Organizers: Ramin Shiekhattar and Roberto Bonasio
February 21–24, 2016 | Santa Fe Community Convention Center | Santa Fe, New Mexico | USA

www.keystonesymposia.org/16Q5

Deadlines: Abstract – Nov 18, 2015; Discounted Registration – Dec 18, 2015

Chromatin and Epigenetics

Scientific Organizers: Luciano Di Croce and Yang Shi
March 20–24, 2016 | Whistler Conference Centre | Whistler, British Columbia | Canada

www.keystonesymposia.org/16C2

Deadlines: Discounted Abstract/Scholarship – Nov 18, 2015; Abstract – Dec 16, 2015; Discounted Registration – Jan 20, 2016

Heart Failure: Genetics, Genomics and Epigenetics

Scientific Organizers: Stuart A. Cook, Christine E. Seidman and Yigal M. Pinto
April 3–7, 2016 | Snowbird Resort | Snowbird, Utah | USA

www.keystonesymposia.org/16Z1

Deadlines: Discounted Abstract/Scholarship – Dec 3, 2015; Abstract – Jan 7, 2016; Discounted Registration – Feb 4, 2016

Epigenetic and Metabolic Regulation of Aging and Aging-Related Diseases

Scientific Organizers: Anne Brunet, David M. Sabatini and Shelley L. Berger
May 1–5, 2016 | Hilton Santa Fe Historic Plaza | Santa Fe, New Mexico | USA

www.keystonesymposia.org/16E1

Deadlines: Discounted Abstract/Scholarship – Jan 5, 2016; Abstract – Feb 2, 2016; Discounted Registration – Mar 1, 2016

Positive-Strand RNA Viruses

Scientific Organizers: Raul Andino and Peter D. Nagy
May 1–5, 2016 | Hyatt Regency Austin | Austin, Texas | USA

www.keystonesymposia.org/16N1

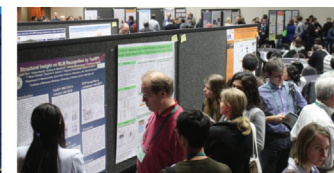
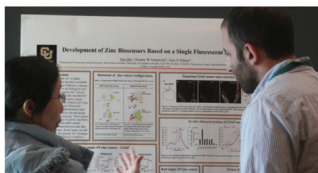
Deadlines: Discounted Abstract/Scholarship – Jan 6, 2016; Abstract – Feb 3, 2016; Discounted Registration – Mar 2, 2016

Nucleic Acid Sensing Pathways: Innate Immunity, Immunobiology and Therapeutics

Scientific Organizers: Thomas Tuschl, Veit Hornung and Karl-Peter Hopfner
May 8–12, 2016 | Maritim Hotel & Conference Center | Dresden | Germany

www.keystonesymposia.org/16E2

Deadlines: Discounted Abstract/Scholarship – Jan 7, 2016; Abstract – Feb 9, 2016; Discounted Registration – Mar 8, 2016



Submit an abstract to participate fully in the conference via poster presentation and possible selection for a short talk. Scholarships are available for graduate students and postdoctoral fellows. For full details on these and other related conferences, please visit www.keystonesymposia.org/meetings.

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GE Healthcare

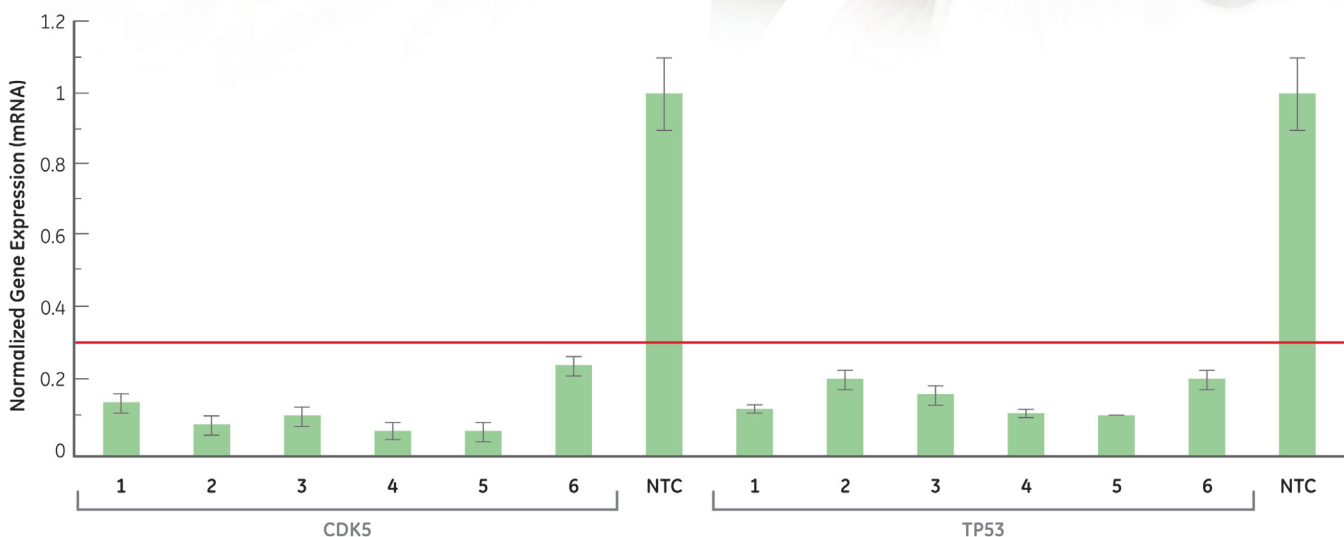
Flexible, guaranteed shRNA from Dharmacon

Using our most advanced shRNA design algorithm coupled with a suite of configurable vector options, SMARTvector™ Lentiviral shRNA and SMARTvector Inducible Lentiviral shRNA collections ensure you get stronger, more consistent knockdown while minimizing off-target effects and toxicity. Increase your probability of success and take control of your experiments with SMARTvector shRNAs.

For RNAi, gene editing, and gene expression tools, count on Dharmacon.



SMARTvector Lentiviral shRNA delivers strong and consistent knockdown



Stronger, more consistent knockdown

A549 cells seeded at 7500 cells/well were transduced with Dharmacon SMARTvector Lentiviral shRNA particles targeting CDK5 and TP53. Both genes were targeted with six different shRNA constructs using the mCMV-promoter at an MOI of 20. mRNA knockdown was assessed 72 hours post-transduction using QuantiGene branched DNA assay (Panomics, Inc.) and normalized to SMARTvector Non-targeting Control. The red line indicates 70% mRNA knockdown.

Sequence Exosome RNAs

Exosomes are 60 - 150 nm membrane signaling vesicles secreted by most cell types in vivo and in vitro. Exosomes are found in blood, urine, amniotic fluid, malignant ascite fluids and contain distinct subsets of microRNAs, mRNAs, lincRNAs and other ncRNAs. The identity and abundance of these RNAs has been shown to be a valuable approach to discover sequence signatures for the diagnosis and prognosis of disease. SBI's Exo-NGS service provides the exosome researcher with a comprehensive, expert service to isolate and identify exosome-associated RNA biomarkers.

Compare exo-RNA sequence profiles across patient samples.

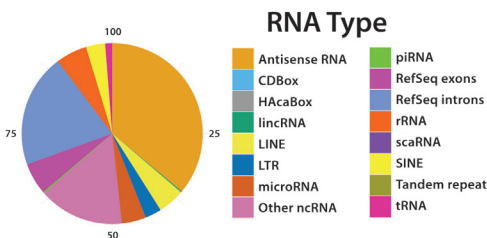
Building Exosome RNA NGS Libraries

- ▶ Exosomes isolated from samples
- ▶ Exo-RNAs purified with chromatography
- ▶ Illumina bar-codes added and amplified
- ▶ Library size-selection and PAGE purification
- ▶ High sensitivity library QC with Bioanalyzer
- ▶ Multiplexed HiSeq NGS for enhanced read depth

Primary Data Deliverables

- Raw sequencing reads in FASTA format
- Sequencing read quality values
- Analyzed Data – Small RNA Workflow
- Relative abundance of each RNA type
- Table of counts of mature microRNAs
- Differential expression heatmaps

RNA Type Charts

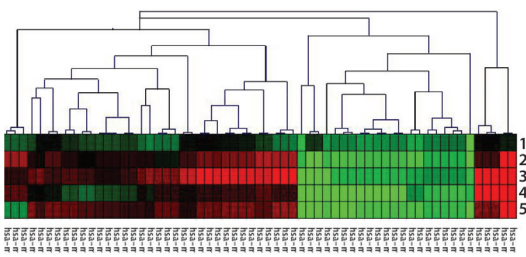


Custom Genome Browser with Your Data



- ▶ Sequencing data uploaded
- ▶ Access to public databases
- ▶ Analyze with accepted analytics
- ▶ Visualize your data automatically
- ▶ Compare to known ENCODE data

Expression Heatmaps



Put your data into context.
www.systembio.com/exo-ngs

CONTACT SBI: services@systembio.com
650-968-2200