GO BEYOND RNA
ARRAYSTAR INC

Non-coding RNA and Epitranscriptomic Solutions

GlycoRNA Arrays *NEW !*
Cover Y-RNA/Y-RNA fragment, tRNA, tiRNA&tRF, pre-miRNA, miRNA & more

Downstream-of-Gene Transcript (DoG RNA) Arrays *NEW !*
Profile DoG RNAs and all their target RNA types simultaneously

R-loop Profiling *NEW !*
Profile the lncRNA/mRNA/circRNA organized R-loops in gene regulation by DRIPc-seq

Circular RNA Arrays
Accurately profile circular RNAs by highly specific circular junction probe design

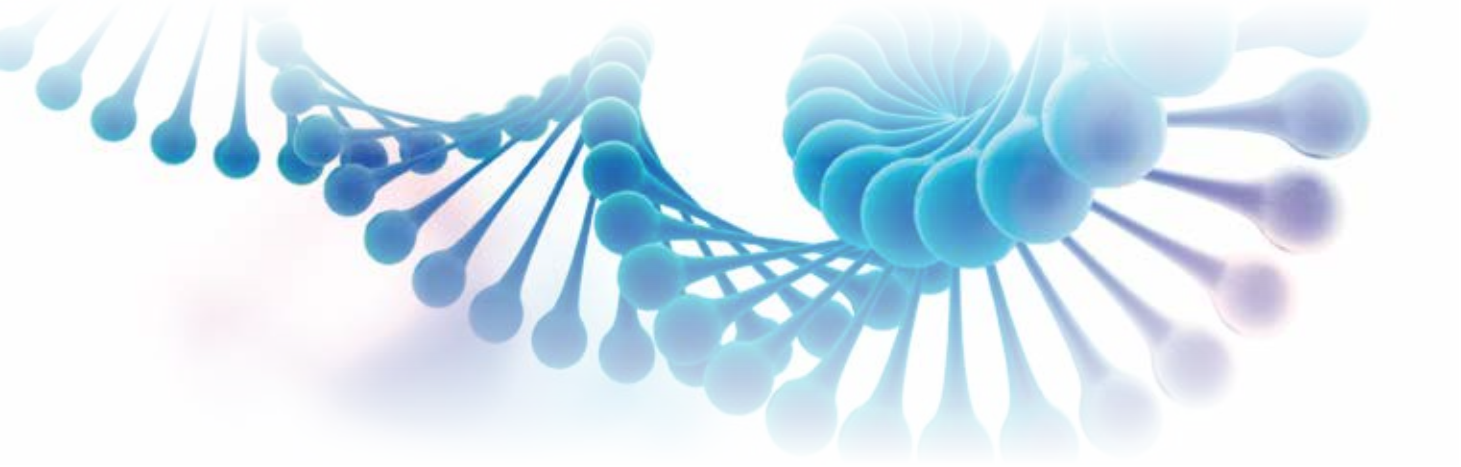
LncRNA Arrays
Overcome the limitations of RNA-seq for lncRNAs often at low abundance

Small RNA Arrays
Accurately profile miRNA, pre-miRNA, tRNA, tsRNA, and snoRNA simultaneously

Epitranscriptomic Arrays
Quantify the percentage of m6A modifications at the transcript specific level

m6A Single Nucleotide Arrays
Locate and quantify the exact m6A site at single nucleotide resolution

Small RNA Modification Arrays *NEW !*
Quantify o8G/m7G/m6A/Ψ/m5C in miRNAs, pre-miRNAs & tsRNAs



Go Beyond RNA

With the discoveries of novel gene regulatory activities beyond coding mRNAs and encoded proteins, a pursuit to uncover pivotal roles of ncRNAs has attracted intense scientific interest with alluring opportunities of finding new disease regulators, biomarkers, and therapeutic targets. Arraystar is taking the lead in supporting scientific endeavor into the once hidden yet exciting world of non-coding RNAs: lncRNAs, circular RNAs, microRNAs, tRNAs, tRFs, tiRNAs, snoRNAs and more.

As a newly unveiled layer of gene regulation, epitranscriptomic modifications of coding mRNAs and non-coding RNAs determine the molecular fates and profoundly impact cellular processes. Arraystar is in the best position to help your research into this omics dimension of not only mRNA, but also long and small ncRNA epitranscriptomics.

Our innovative products, in-depth expertise, and strong bioinformatics in these areas have supported 1700+ high impact publications since our 2009 inception. Arraystar will continue to take the industry lead to provide the best-in-class technologies and services for non-coding RNA and epitranscriptomic research, to explore new horizon, to open new opportunities, and to accelerate and advance your science of groundbreaking discoveries.

Arraystar Circular RNA Microarrays

Accurately profile circular RNAs by highly specific circular junction probe design

Highlights

- **The only commercially available circRNA microarrays.** Specifically designed for circRNA expression profiling. CircRNAs were comprehensively curated from the landmark publications and multiple data sources with stringent collection pipelines to produce the best circular RNA array contents.
- **Highly specific circular RNA signal detection.** Samples are treated with RNase R to specifically remove linear RNA in the total RNA samples. Circular junction sequence specific array probes ensure the most specific, accurate and reliable circRNA profiling, even in the presence of linear counterparts.
- **Detailed Annotation.** In addition to standard microarray data analysis, circRNAs specific information is further annotated with the target sites of conserved miRNAs with good mirSVR scores, to unravel their functional roles as miRNA sponges.
- **The preferred choice over RNA sequencing.** RNA-seq is currently inadequate for such task due to the particular properties of circular RNA.

Why Study Circular RNAs?

Circular RNA (circRNA) is a novel type of non-coding RNA covalently circularized in a closed loop, produced by RNA back splicing process. circRNAs are not known to translate proteins. With their extensive complementarity to linear RNA counterparts, stability against nucleases, resistance to miRNA-targeted degradation, high expression levels, enrichment in cytoplasm, and large number of miRNA binding sites, circRNAs have been increasingly recognized as exceptionally effective natural miRNA sponges and competing endogenous RNAs (ceRNAs) in gene regulation. Some intronic circular RNAs (ciRNAs) have been shown to enhance the host gene transcription [6]. Additionally, the tissue/developmental-stage-specific expression and long half-lives constitute an enormous advantage as a novel class of biomarkers.

To facilitate the analysis of circRNAs, Arraystar has pioneered the circRNA microarrays for human and mouse to systematically profile circRNAs under physiological and disease conditions.

circRNAs as microRNA Sponges

Circular RNAs can have multiple microRNA binding sites. For example, the physical interactions of ciRS-7 with miR-7 and gene silencing complex have been demonstrated by Photoactivatable-Ribonucleoside-Enhanced Crosslinking and Immunoprecipitation (PAR-CLIP) with AGO2 in the presence of miR-7, and by biotinylated miR-7 capture (Fig 1), showing ciRS-7 biochemically as a microRNA sponge.

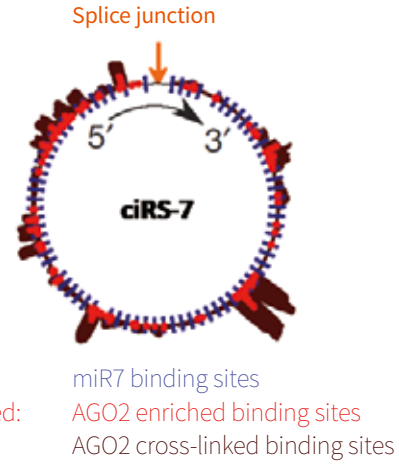


Figure 1. *ciRS-7, short for "circular RNA Sponge for miR7", has more than 70 copies of predicted miR-7 binding sites. It interacts with miR-7 and the catalytic component of RNA-induced silencing complex AGO2.*

circRNAs and RNA Binding Proteins

Circular RNAs may partner with very diverse RNA binding proteins (RBP) to perform wide range of molecular functions (Fig. 2). Circular RNAs may bind RBPs for subcellular delivery/localization (Fig. 3), sponge RBPs just like miRNAs, assemble different sets of RBP complexes, or act as a allosteric co-factor for enzymatic RBPs [8]. Antisense circular RNAs may form

direct base pairing with mRNAs to regulate the activity.

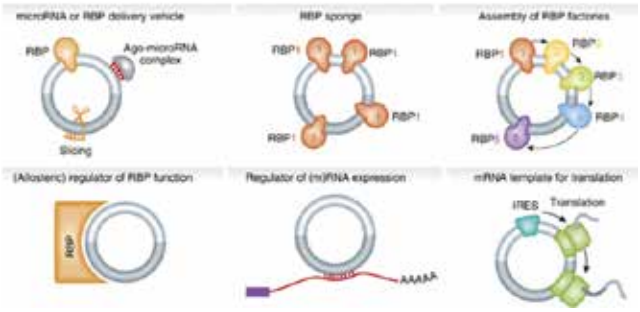


Figure 2. *Interplay of circular RNA with RNA binding proteins [8].*

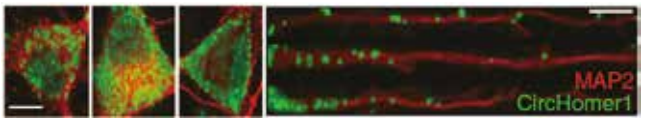


Figure 3. *Dynamic subcellular localization of circular RNAs in neuronal cell body and dendrites to regulate neuronal synaptic connections [7].*

CircRNAs in Biology and Disease

MicroRNAs may regulate up to 1/3 of all gene expression. circRNA regulation of microRNA activities can lead to biological phenotypes (Fig. 4). Disproportionately large number of circRNA targets are protein kinases, which are signal transduction mediators. Aberrant circRNA expression is involved in human diseases such as cancer, Alzheimer's disease and atherosclerosis. The higher specificity and stability of circRNA in diseases are desired properties in biomarker applications.

CircRNAs Are Stable due to Resistance to Exonuclease Degradation

Circular RNAs lack exposed 5' and 3' termini and are resistant to exonuclease degradation. Thus, circRNAs are stable and have much longer half-lives than their linear RNA counterparts (Fig. 5). The elevated abundance contributes to functioning as microRNA sponges. It also presents a good opportunity for biomarker applications.

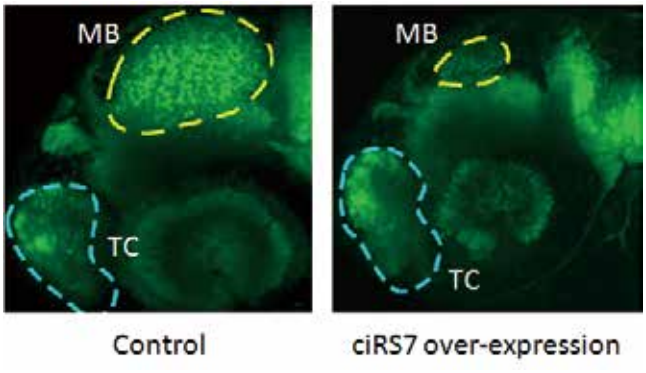


Figure 4. *ciRS-7 overexpression in embryonic brain leads to profound reduction of mid brain (MB) size (right), compared to the normal control (left). Co-overexpression of miR-7 ameliorates the effect. The telencephalons (TC) are relatively unaffected.*

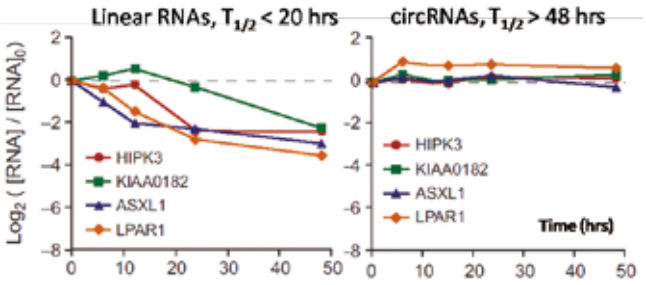


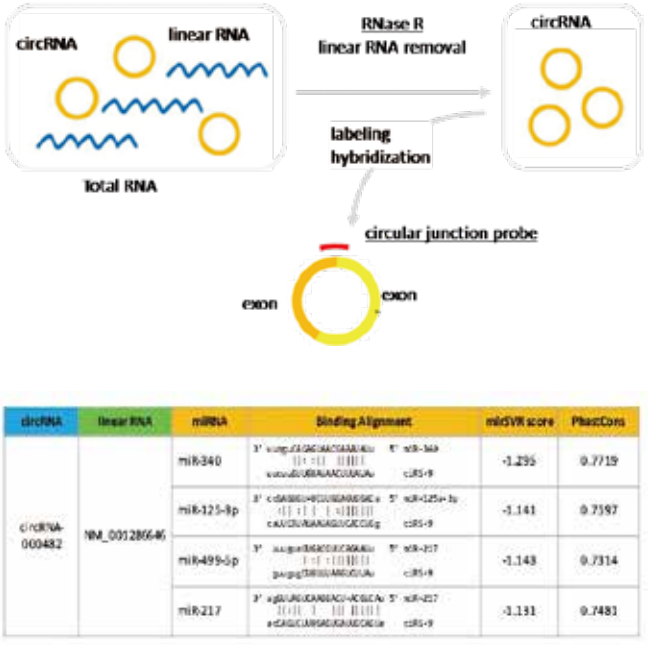
Figure 5. *Circular RNAs are stable and have half-lives more than 48 hours (right), compared to their linear RNA counterparts of less than 20 hours (left).*

Arraystar Circular RNA Microarrays

Arraystar circRNA Microarrays were the first and are currently the only commercially available technology for sensitive and reliable circRNA expression profiling. The microarrays use RNase R linear RNA removal and circular junction probes to achieve high specificity for circRNAs, even in the predominant presence of linear RNAs (Fig. 6, top). The profiling is complete with comprehensive, systematic and detailed annotation of circRNAs, including miRNA binding sites as microRNA sponges, to gain insight into circular RNA biology (Fig. 6, bottom).

Why Use Microarray Over RNA Sequencing for Circular RNA Profiling?

Circular RNAs as a population are typically present at much lower levels, at about 5~10% of linear RNAs. The cross circular junction sequences are even lower. At a typical RNA-seq depth, less than 5% of circRNAs (red circle) may be reliably quantified



circRNA	linear RNA	miRNA	Binding Alignment	miRSVR score	PhastCons
circRNA-000482	NM_001286646	miR-340		-1.295	0.7719
		miR-125-3p		-1.141	0.7197
		miR-499-5p		-1.143	0.7314
		miR-217		-1.191	0.7481

Figure 6. *Overview of circRNA microarray workflow (top) and detailed annotation of circRNA (bottom).*

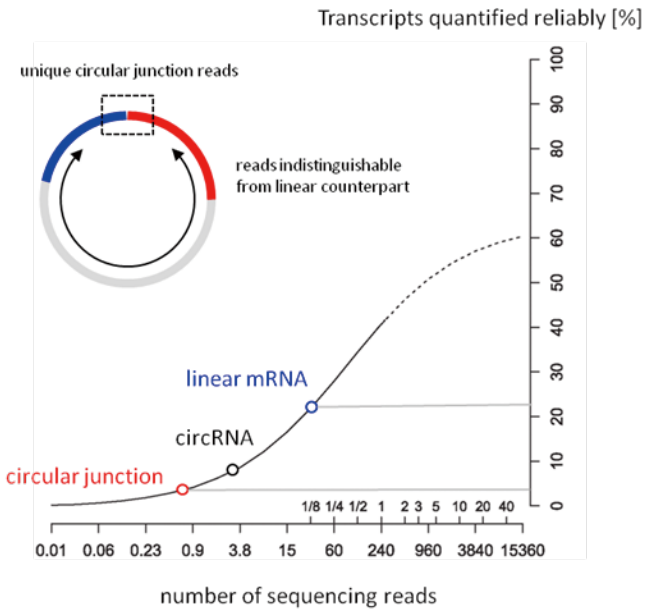


Figure 7. *RNA-seq quantification reliability vs read depth. Typical RNA-seq has a depth of < 30 mil reads for mRNAs (blue circle), which is < 0.5 mil for cross circular junction reads (red circle). Less than 5% circular junctions can be reliably quantified. Adopted from [9].*

(Fig. 7). Even at great sequencing depth of > 300 mil at high costs, the accuracy gains are only modest.

In practice, generic RNA-seq, mostly intended for mRNAs, are inadequate or simply unavailable as a provided service for circular RNA profiling. Circular RNA sequencing requires very deep sequencing depth and paired-end chemistry. Read mapping and data analysis require specialized database, de novo transcript assembly, special algorithms and complex computational pipeline. circRNA annotations such as microRNA binding as sponges are typically not included. Novel circular RNA discovery, a consideration of using RNA-seq, is actually not available for the above reasons.

On the other hand, circular RNA microarrays use circular junction probes, combined with enzymatic linear RNA removal, to interrogate circular RNAs highly specifically. Array hybridization is relatively independent of other high abundance RNAs. High sensitivity at one transcript per cell can be achieved. Overall, microarray is more efficient and robust in sample labeling than RNA sequencing library prep. At present, it is a mature technology that outperforms RNA-seq in circular RNA profiling.

Arraystar Circular RNA Microarray Specifications

	Human	Mouse
Total number of unique circRNAs	13,617	14,236
Probe Length	60nt	
Probe Region	Circular junctions of circRNAs	
Probe Specificity	Transcript specific	
CircRNA Enrichment	RNase R treatment	
Labeling Method	Labeling by random priming	
Salzman' s circRNAs (2013)	8,529	
Memczak' s circRNAs (2013)	1,601	1,750
Zhang' s ciRNAs (2013)	93	
Zhang' s circRNAs (2014)	4,980	
Jeck' s circRNAs (2013)	3,769	
Guo' s circRNAs (2014)	5,536	570
You' s circRNAs (2015)		13,300
Array Format	8x15K	

Circular RNA Research Roadmap

The differentially expressed circRNA candidates screened by circRNA microarrays are typically confirmed by an independent method such as by qPCR (Fig. 8). The validated circRNAs are further studied for biological functions, molecular mechanisms in gene regulation and biomarker applications (Fig. 9).

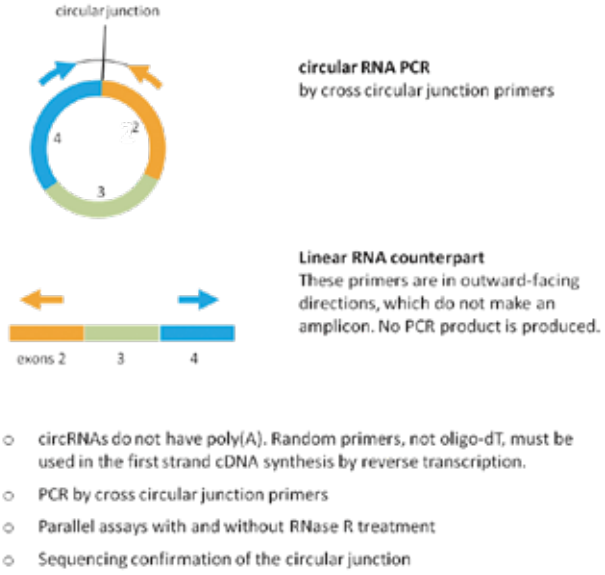


Figure 8. *qPCR validation of differentially expressed circRNAs screened by circRNA microarray. The concordance between qPCR and microarray for the differentially expressed circRNA is related to the magnitude of change (FC), p-value, as well as the abundance level.*

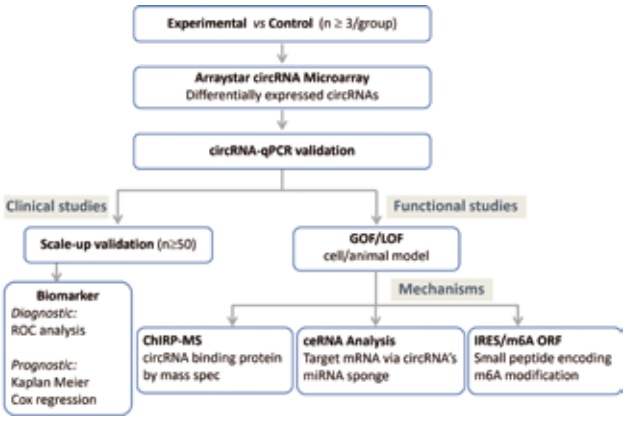


Figure 9. *Roadmap of circRNA expression profiling and follow-up studies.*

References

1. Guo, J. U., V. Agarwal, et al. (2014). Genome Biol 15(7): 409.

2. Jeck, W. R., J. A. Sorrentino, et al. (2013). RNA 19(2): 141-157.

3. Memczak, S., M. Jens, et al. (2013). Nature 495(7441): 333-338.

4. Salzman, J., R. E. Chen, et al. (2013). PLoS Genet 9(9): e1003777.

5. Zhang, X. O., H. B. Wang, et al. (2014). Cell 159(1): 134-147.

6. Zhang, Y., X. O. Zhang, et al. (2013). Mol Cell 51(6): 792-806.

7. You X. et. al. (2015) Nat Neurosci. 2015 Apr;18(4):603-10

8. Hentze and Preiss (2013) EMBO J 3;32(7):923-5.

Arraystar LncRNA Microarrays

Overcome the limitations of RNA-seq for lncRNAs often at low abundance

Highlights

- Most sensitive and best technology for lncRNA profiling, superior to RNA-seq
- Comprehensive and robust full-length lncRNA collection curated from all major latest databases and landmark publications
- Systematic and specialized lncRNA annotation, including genomic context, epigenomic context, completeness, subcellular localization, miRNA recognition site...
- Unambiguous, reliable, and accurate detection and quantification of lncRNA transcript isoforms otherwise difficult by RNA-seq
- Simultaneous lncRNA and mRNA profiling on the same array for co-expressional and correlational expression and regulation

Why Study LncRNAs?

LncRNAs are a major RNA class in the transcriptome [1], transcribed from genomic sites either in association with a protein coding gene nearby or in the intergenic regions as lincRNAs. They regulate gene expression by multiple mechanisms, either in cis or in trans, at transcriptional or post-transcriptional levels. LncRNAs play crucial roles in biological systems and diseases, contributing to understanding chromosomal inactivation, developmental programming, and diseases of unknown etiology. LncRNAs exhibit more cell type-specific expression than mRNAs, making them a class of higher specificity biomarker.

Arraystar LncRNA Microarrays

Arraystar LncRNA Arrays are designed to systematically profile lncRNAs along with the entire set of protein-coding mRNAs, providing:

Consolidated, comprehensive, robust, most up-to-date full-length lncRNA contents. Arraystar maintains high-quality lncRNA databases, sourcing lncRNAs from external data, scientific publications, and proprietary pipelines, and focusing on full-length lncRNAs with 5' and 3' end evidence [3-13]. The Array V5.0 includes 39,317 lncRNAs, categorized into two tiers: 8,393 Gold Standard LncRNAs (well-annotated and experimentally supported) and 30,924 Reliable LncRNAs (a comprehensive, high-confidence collection).

Systematic and functional annotation of LncRNAs. The LncRNA array package includes systematic and detailed annotations and analyses, providing genomic information, epigenomic context, subclassification, transcript model completeness, subcellular localization, miRNA recognition, conservation, tissue/cell specificity, and small peptide coding potentials, biological process, and disease association [14-30]. This rich source of information helps to unravel functional roles and molecular mechanisms of the LncRNAs.

Why Use Microarray Over RNA Sequencing for LncRNA Profiling?

LncRNAs often express and function at low abundance, buried in other classes of abundant RNAs (Fig. 1A), which cause serious limitations of RNA-seq for lncRNA profiling.

LncRNA quantification. At least hundreds of read counts are required for quantification by RNA-seq [31, 32]. Low lncRNA levels are unacceptably poor and not nearly sufficient for differential expression analysis, even with expensive deep coverage [2, 33] (Fig. 1B-D). Additionally, FPKM calculation in RNA-seq depends on accurate lncRNA transcript lengths, many of which are still lacking [1]. In contrast, LncRNA microarrays offer high sensitivity and accuracy for lncRNAs even at low abundance, as the array probes hybridize target RNAs at high affinity independently of other RNAs [35] (Fig. 1D).

LncRNA transcript isoforms. LncRNAs often have multiple isoforms with distinct functions, making transcript-specific profiling crucial. RNA-seq struggles with weak coverages, short read lengths, and inaccurate reconstruction of isoform transcript exon models, especially for non-predominant isoforms [2]. Arraystar LncRNA Microarrays use "transcript-specific" probes that hybridize to the splice junctions or exon sequences that are unique to each transcript isoform from

the same gene, achieving unambiguous and highly accurate isoform detection and quantification.

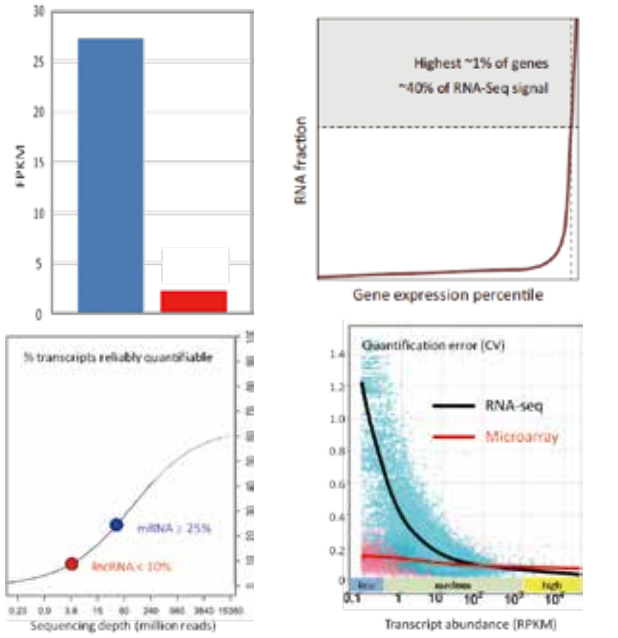
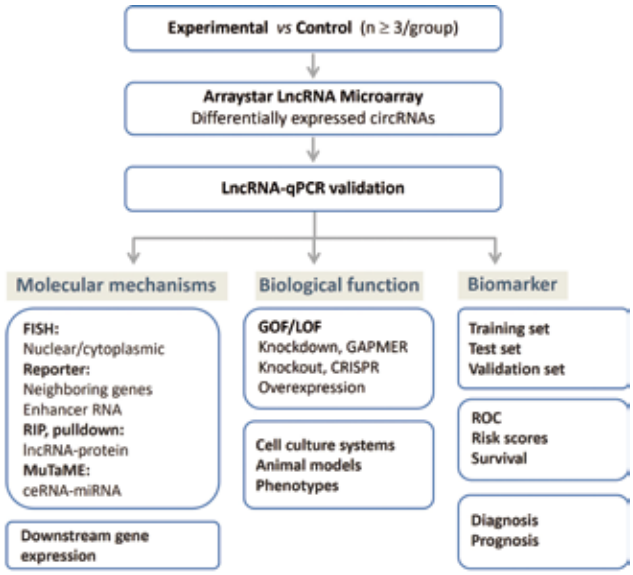


Fig 1. *(A) The median lncRNA expression level is ~10X lower than that of mRNAs [32]. (B) Top 1% of the highest expressed genes occupy ~40% of RNA-seq signal. Lowly expressed lncRNAs receive very little coverage [33]. (C) In 40 million reads, < 10% lncRNAs can be reliably quantified [34]. (D) While quantitative error becomes unacceptably high for RNA-seq when the RNA level is low, microarray continues to perform very well [35].*

LncRNA Research Roadmap



Arraystar LncRNA Microarray Specifications

	Human V5.0	Mouse V4.0	Rat V3.0
Total probes	60,491	60,641	38,352
Probe length	60 nt		
Probe region	Specific exon or splice junction along the entire length of the transcript		
Probe specificity	Transcript-specific		
mRNAs	21,174	22,692	27,770
LncRNAs	40,173	37,949	10,582
Gold Standard LncRNAs	8,393		
Reliable LncRNAs	30,924		
mRNA sources	RefSeq, UCSC, GENECODE, FANTOM5 CAT	Refseq, Known Gene, GENECODE	Refseq, Ensembl
LncRNA sources	FANTOM5 CAT, GENECODE, RefSeq, BIGTranscriptome, UCSC KnownGene, LncRNAdb, LncRNAWiki, RNAdb, NRED, CLS FL, NONCODE, MiTranscriptome	GENECODE, RefSeq, UCSC KnownGene, GenBank	RefSeq, Ensemb
Array format	8 × 60K	8 × 60K	4 × 44K

References

1. Uszczynska-Ratajczak, B., et al. (2018) Nat Rev Genet. [PMID: 29795125]
3. Guttman, M., et al. (2009) Nature. [PMID: 19182780]
4. Khalil, A. M., et al. (2009) Proc Natl Acad Sci U S A. [PMID: 19571010]
5. Hon, C. C., et al. (2017) Nature. [PMID: 28241135]
6. Lagarde, J., et al. (2017) Nat Genet. [PMID: 29106417]
7. Marques, A. C., et al. (2013) Genome Biol. [PMID: 24289259]
8. Alam, T., et al. (2014) PLoS One. [PMID: 25275320]
9. Mele, M., et al. (2017) Genome Res. [PMID: 27927715]
10. You, B. H., et al. (2017) Genome Res. [PMID: 28396519]
11. Wang, L., et al. (2013) Nucleic Acids Res. [PMID: 23335781]
12. Kong, L., et al. (2007) Nucleic Acids Res. [PMID: 17631615]
13. Lin, M. F., et al. (2011) Bioinformatics. [PMID: 21685081]
14. Kaewsapsak, P., et al. (2017) Elife. ([PMID: 29239719]
15. Mas-Ponte, D., et al. (2017) RNA. [PMID: 28386015]
16. Benoit Bouvrette, L. P., et al. (2018) RNA. [PMID: 29079635]
17. Salmena, L., et al. (2011) Cell. [PMID: 21802130]
18. Tay, Y., et al. (2011) Cell. [PMID: 22000013]
19. Chan, J. J. and Tay, Y. (2018) Int J Mol Sci. [PMID: 29702599]
20. Tay, Y., et al. (2014) Nature. [PMID: 24429633]
29. Bao, Z., et al. (2019) Nucleic Acids Res. [PMID: 30285109]
30. Chen, G., et al. (2013) Nucleic Acids Res. [PMID: 23175614]
31. Anders, S. and Huber, W. (2010) Genome Biol. [PMID: 20979621]
32. Derrien, T., et al. (2012) Genome Res. [PMID: 22955988]
33. Ira W. Deveson., et al. (2017) Trends in Genetics. [PMID: 28535931]
34. Labaj, P. P., et al. (2011) Bioinformatics. [PMID: 21685096]
35. Zhang, X., et al. (2010) Endocrinology. [PMID: 20032057]

Arraystar Small RNA Microarrays

Accurately profile miRNAs, pre-miRNAs, tRNAs, tsRNAs, and snoRNAs simultaneously

Highlights

- Simultaneously profile the major small RNA classes: miRNA, pre-miRNA, tRNA, tsRNA, and snoRNA
- Raise the bar of small RNA profiling to high sensitivity, specificity and accuracy by direct end-labeling and smart probe design.
- Direct and simplified procedures to overcome biases from RNA modifications, RNA fold hindrance, reverse transcription blocks, PCR amplifications, and analysis inaccuracy in small RNA-seq.
- Required RNA sample amounts starting as low as 100 ng, opening up many research opportunities.
- Tolerant for RNA samples at lower qualities: e.g. degraded RNAs, serum/plasma/biofluid RNAs, FFPE RNAs.

Biomarker Potentials of tRNAs and tsRNAs

Small RNAs such as microRNAs have been popularly explored as biomarkers. tRNA and tsRNA populations are now emerging as new classes of biomarkers with greater potentials, owing to their many desired characteristics. The high stability and abundance of tRNA and tsRNA in body fluids (Fig. 1)[1-6] , the involvement in pathological processes, the demonstrated differential expression in solid tumors and hematological malignancies, and their power to discriminate cancer patients from healthy controls open the prospect for development of tRNAs and tsRNA-based biomarker tests. For example, the tRF profiles have been shown to discriminate triple-negative, triple positive breast cancer cells from the normal controls in unsupervised clustering [7] (Fig. 2). The ratio of tsRNAs has also been demonstrated as a good indicator of cancer progression-free survival and a candidate prognostic marker [4].

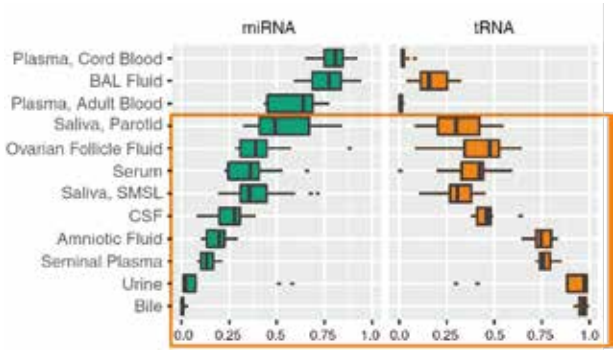


Figure 1. *Relative proportions of miRNA vs tRNA in biofluids, where many biofluids have tRNA contents much higher than miRNA [1,2].*

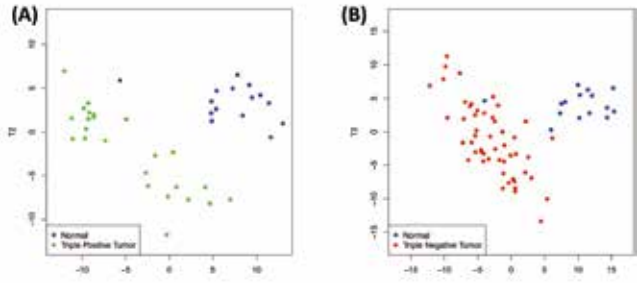


Figure 2. *tRF profiles discriminate triple- positive (A), triple-negative breast cancer cells (B) from the normal controls in unsupervised clustering[7].*

Arraystar Small RNA Array, with the low requirements of RNA amount and quality, opens up opportunities for tRNA/tsRNA biomarker research projects where the samples are rare or of limited supply.

Arraystar Small RNA Microarrays

Arraystar Small RNA Array, combining direct end-labeling and smart probe design microarray technologies, is designed as a practical and effective solution to profile the full spectrum of small RNAs at high sensitivity and accuracy yet at much less input RNA amounts.

Raising the bar of small RNA profiling for high sensitivity, specificity and accuracy

By end-direct labeling, the small RNAs are ligated with pCp-Cy3 onto the 3'-ends by T4 RNA ligase, and one RNA molecule is labeled with one Cy3 label. This method eliminates biases from cDNA synthesis by reverse transcription due to RNA modification interference and RNA folding hindrance as in small RNA-seq; avoids distortions from PCR amplification cycles as in required small RNA-seq library amplification; uses DMSO to reduce the RNA structure and sequence context differences among small RNAs. All these help to preserve the fidelity of native small RNA levels and achieve the unbiased high quantification accuracy better than RNA-seq or even qPCR.

The smart probe design incorporates 5'-hairpin structure and normalized sequence targeting region to specifically distinguish small RNAs with only 1~2 nucleotide differences. Moreover, the high affinity probe hybridization ensures very high sensitivity even for small RNAs at low abundance.

Low RNA sample amount requirements

Arraystar Small RNA Microarray requires as little as 100 ng total RNA, which is magnitudes lower than what small RNA-seq requires. As its direct end labeling chemistry does not require RNA pretreatments that often cause RNA loss, the microarray significantly reduces the demand for input RNA amounts especially for heavily modified RNA biotypes (e.g. tRNA and tsRNA). The low sample amount requirement opens up opportunities for research projects where the samples are rare or of limited supply.

Tolerant for RNA samples at lower qualities

The direct end-labeling is relatively insensitive to nucleotide damage in the substrate RNA sequence as it does not rely on cDNA copying by reverse transcription. Furthermore, whereas the microarray probes are unaffected by unrelated sequence presence, RNA fragments from the abundant rRNAs in degraded RNA samples can contaminate small RNAs in the size range, depressing small RNA coverage in small RNA-seq.

For these reasons, Small RNA Array is particularly advantageous for preserved or chemically treated samples or degraded samples. e.g. serum/plasma/biofluid/FFPE RNAs.

Simultaneous profiling of multiple small RNA classes

Profiling different small RNA classes by sequencing requires separate sequencing methods and experiments: miRNA-seq, tRNA-seq, tsRNA-seq, and regular RNA-seq for longer snoRNA and small RNA precursors. Arraystar Small RNA microarrays use unified labeling chemistry to hybridize to the probes in one array for all major small RNA classes.

Rich Small RNA Analyses and Annotations

For each small RNA class, the data analyses include profiling measurement values, statistical computations, informative annotations, and publication quality graphics.

Differential expression analysis (tsRNA and tRNA as examples)

tsRNA					
tsRNA_type	tsRNA-sequence	tsRNA-length	tsRNA-precursor	Level	Molecular mechanism
3' tiRNA	ATTCAAAGGTTCCGGGTTCGAGTCCCGGCGGAGTCGCCA	39	tRNA-Arg-TCT-1	Potential	Cytotoxicity to neurons
3' tiRNA	ATGCCGAGGTTGTGAGTTCAAGCCTCACCTGGAGCACCA	39	tRNA-Ile-TAT-3	Potential	Cytotoxicity to neurons

tsRNA_type: tsRNA type (tRF-5, tRF-3, tRF-1, 5-Leader, 5-tiRNA, 3-tiRNA, and i-tRF).

tsRNA-sequence: tsRNA sequence.

tsRNA-length: tsRNA length.

tsRNA-precursor: Symbol for the tsRNA precursor.

Level: Confidence level for the tsRNA

Functional - Documented with characterized biological functions or disease association;

Reliable - Recorded in tRFdb or reported by literatures, but without further studies;

Potential - Predicted by Arraystar based on RNA fragment lengths and cleavage positions in the tRNA.

Mechanism: The molecular mechanism of tsRNA.

Sequence: Sequence of the tRNA isodecoder.

Gene name: Gene name of the isodecoder tRNA.

GenomeLocus: Genome locus of the tRNA isodecoder.

tRNA promoter Locus: Genome locus of the tRNA isodecoder promoter. TRNA promoter - tRNA promoters which include a tRNA gene plus 100 base pairs of upstream sequence. (PMC6108506).

pre-tRNA locus: Genome locus of the tRNA isodecoder precursor. pre-tRNA - precursor tRNA which include a tRNA gene plus 100 base pairs of upstream sequence and a 3'trailer.

tRNA neighboring gene: The nearest gene name of the tRNA isodecoder.

tRNA					
tRNA-Sequence	Gene name	GenomeLocus	tRNA promoter locus	pre-tRNA locus	tRNA neighbouring gene
GGGGGTAT AGCTCAG… …	tRNA-Ala-AGC-1-1	chr6: 28795963-28796035:-	chr6: 28795963-28796135:-	chr6: 28795952-28796135:-	XXbac-BPG308K3.5
GGGGAATT AGCTCAA… …	tRNA-Ala-AGC-10-1	chr6: 26687256-26687329:+	chr6: 26687156-26687329:+	chr6: 26687156-26687342:+	RP11-457M11.7

Hierarchical clustering

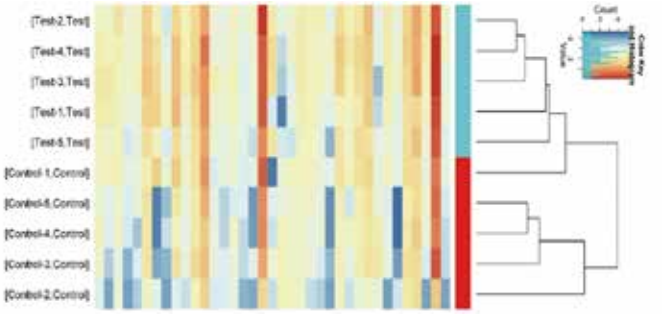


Figure 4. *Hierarchical clustering heatmap of differentially expressed miRNAs.*

Arraystar Small RNA Microarray Specifications

	Human	Mouse	Rat
Total probes	14,707	14,895	14,238
miRNAs	2,627 (1,318 5-p-miRNAs ; 1,309 3-p-miRNAs)	1,949 (966 5-p-miRNAs; 983 3-p-miRNAs)	749 (355 5-p-miRNAs; 394 3-p-miRNAs)
tsRNAs	4,254	1,809	1,135
pre-miRNAs	1,745	1,122	448
mature tRNAs	346	270	197
snoRNAs	955	1,323	1,486
Small RNA sources	miRNA: miRBase tsRNA: tRFdb, MINTbase, GtRNADb pre-miRNA: miRBase tRNA: GtRNADb, ENSEMBL snoRNA: ENSEMBL Scientific publications		
Array Format	8 x 15K		

References

1. Godoy P.M. et al. (2018) Cell Rep [PMID: 30380423]
2. Schageman J. et al. (2013) Biomed Res Int [PMID: 24205503]
3. Quek C. et al. (2017) RNA Biol [PMID: 28005467]
4. Olvedy M. et al. (2016) Oncotarget [PMID: 27015120]
5. Dhahbi J.M. et al. (2013) BMC Genomics 14:298 [PMID: 23638709]
6. Schageman J. et al. (2013) Biomed Res Int 2013:253957 [PMID: 24205503]
7. Telonis A.G. et al. (2015) Oncotarget 6(28):24797-822 [PMID: 26325506]

Arraystar Epitranscriptomic Microarrays

Quantify the percentage of m6A/m5C modifications at the transcript specific level

Highlights

Arraystar Epitranscriptomic Microarrays have unique advantages over MeRIP-seq (Table 1).

- A single Epitranscriptomic Microarray to simultaneously profile what gene transcripts are modified, differential modification between conditions, and very importantly, the percentage of modification for each transcript
- Excellent coverage for coding and noncoding RNA classes, even for lncRNAs and circRNAs that are difficult by MeRIP-seq
- rRNA depletion not required. Faster, simpler than MeRIP-seq
- Low demand for sample amounts, starting from as little as 1 μg total RNA
- Suitable for more sample types, such as degraded FFPE, and serum/plasma/whole blood samples

	Epitranscriptomic Microarray	MeRIP-seq
RNA amount	⩾ 1μg total RNA	⩾ 120 μg total RNA
%Modification	Yes	No
RNA biotypes	mRNA, lncRNA, circRNA, pre-miRNA, pri-miRNA, snoRNA, snRNA	Poly(A+) mRNA and lncRNA
Transcript isoform-specific	Excellent	Poor
RNA sample sources	Cell lines, tissues, low or degraded samples (FFPE, serum, plasma)	Cell lines, tissues in large quantity
mRNA isolation or rRNA removal	Not required	Required (large RNA amount scale-up)

Why Quantify RNA Modifications at the Transcript Specific Level?

RNA modifications, such as m6A, m1A, m5C, and pseudouridine, together form the epitranscriptome and collectively encode a new layer of gene expression regulation. m6A, the most abundant internal modification in mRNAs and lncRNAs, impacts all aspects of post-transcriptional mRNA/lncRNA metabolism and functions [1]. In addi-tion to mRNA, m6A also functions in noncoding RNAs, such as cap-independent translation initiation of circRNA[2] and pri-miRNA processing[3]

The potential effects of RNA modifications depend on not only which gene transcripts, but also the percentage of transcripts that are modified. However, current transcriptome-wide RNA modification profiling methods deal mostly with mapping the modification sites but are unable to quantify the percentage of modified RNA for that transcript. The lack of such stoichiometric information has been a major concern for scientists [1,4]

Arraystar Epitranscriptomic Microarrays

Arraystar Epitranscriptomic two-color channel microarrays work with RNA modification immunoprecipitation to quantify the percentage of RNA that is modified for each transcript isoform. The microarrays cover the epitranscriptomes of mRNA, lncRNA, circRNA, pre-miRNA, pri-miRNA, snoRNA, and snRNA classes.

Quantifying the percentage of modification

The modified vs unmodified fractions of the same RNA transcript, which differ only in the structures or the bound readers, can assume different fates, functions and biological outcomes [4] (Fig. 1). While MeRIP-seq is used to map the modification sites, it does not quantify the relative fraction of modified RNA for a given transcript. Arraystar Epitranscriptomic Microarrays have the power to quantify the percentage by measuring the modified and unmodified transcripts in two color channels on the same array (Fig. 2), while simultaneously profile what gene transcripts are modified and the differential modification between conditions.

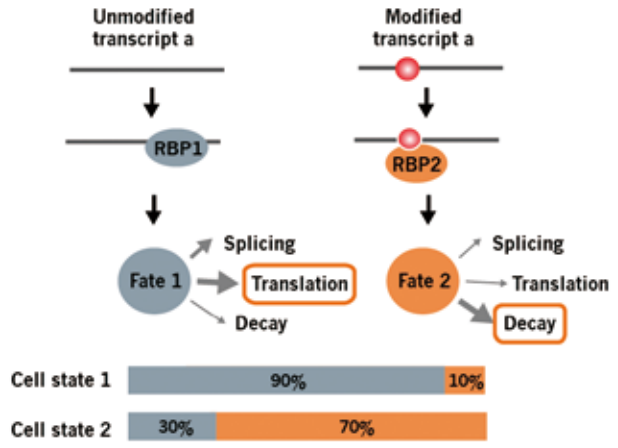


Figure. 1. *The changing modification stoichiometry generates functional diversity from the same RNA transcript. The percentage of modified RNA "transcript a" can be very low under one cellular condition (e.g. Cell state 1), but change to high (e.g. Cell state 2) under another cellular condition. By causing RNA structural changes and direct recruitment of modification reader proteins, the modified "transcript a" acquires a different fate, for example, from protein translation to increased RNA decay.*

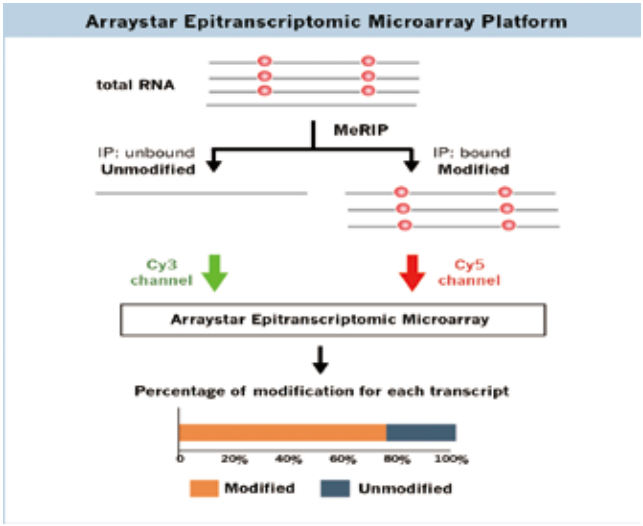


Figure 2. *Arraystar Epitranscriptomic Microarray measures Cy5 labeled modified RNA and Cy3 labeled unmodified RNA in two-color channels on the same array, such that the percentage of modification for each transcript can be measured.*

Covering coding and noncoding epitranscriptomes

The high sensitivity and accuracy of the microarrays are excellent even for RNA types (e.g. lncRNAs and circRNAs) otherwise technically difficult for MeRIP-seq.

• *Arraystar mRNA&lncRNA Epitranscriptomic Microarrays: For mRNA, lncRNA, and mid-sized noncoding RNA classes of pre-miRNA, pri-miRNA, snoRNA, and snRNA.*

• *Arraystar circRNA Epitranscriptomic Microarrays: For circular RNA*

Transcript isoform specific profiling

Alternatively spliced transcript isoforms can have distinct tissue-specific expression and biological functions. For example, TRIM9 short isoform (NM_052978), but not the long isoform (NM_015163), promotes virus-induced interferon production [5]. The percentages of modified transcript isoforms have been associated with biological functions and diseases. Unfortunately, MeRIP-seq performs poorly at transcript-specific level due to required deep sequencing coverage, short read assembly, and quantification inaccuracy.

Arraystar Epitranscriptomic Microarrays use specific exon or splice junction probes to unambiguously, reliably and accurately profile the RNA modification in each individual transcript isoform, defining a new level of epitranscriptomic details.

Low sample amount requirements

Many biological samples are of limited supplies. Current MeRIP-seq requires a massive amount of total RNA (>= 120 µg). Arraystar Epitranscriptomic Microarrays use as little as is 1 µg total RNA, opening up broad opportunities for research projects.

Arraystar Epitranscriptomic Microarray Specifications

Epitranscriptomic Array Services	Array Contents
Human mRNA&lncRNA Epitranscriptomic Array (m6A/m5C)	44,122 mRNAs; 12,496 lncRNAs; 3,813 Mid-size ncRNAs
Mouse mRNA&lncRNA Epitranscriptomic Array (m6A/m5C)	48,161 mRNAs; 8,393lncRNAs; 4,087 Mid-size ncRNAs
Rat mRNA&lncRNA Epitranscriptomic Array (m6A/m5C)	27,770 mRNAs; 10,582 lncRNAs; 2,505 Mid-size ncRNAs
Human circRNA Epitranscriptomic Array (m6A/m5C)	13,617 circular RNAs
Mouse circRNA Epitranscriptomic Array (m6A/m5C)	14,236 circular RNAs
Rat circRNA Epitranscriptomic Array (m6A/m5C)	14,145 circular RNAs

References

1. Gilbert W.V. et al. (2016) Science [PMID: 27313037]
2. Yang Y. et al. (2017) Cell Res. [PMID: 28281539]
3. Alarcón C.R. et al. (2015) Cell [PMID: 26321680]
4. Lewis C.J. et al. (2017) Nat. Rev. Mol. Cell Biol. [PMID: 28144031]
5. Qin Y. et al. (2016) Cell Res. [PMID: 26915459]

Arraystar m6A Single Nucleotide Microarrays

Locate and quantify the exact m6A sites at single nucleotide resolution

Highlights

Arraystar m6A Single Nucleotide Microarrays add invaluable benefits which are lacking for conventional m6A-seq analysis:

- Systematic m6A profiling independent of m6A-antibody immunoprecipitation based approaches.
- Precise detection of m6ACA at single nucleotide resolution.
- Quantifying m6A modification stoichiometry and abundance.
- Low demand for sample amounts, as low as 1 ug total RNA.
- Specialized pipeline to collect and annotate the quantifiable Single -m6ACA sites.

Why Study Single-m6A sites?

The single-m6A modifications are often related to molecular functions in mRNA translation initiation or translation elongation dynamics. They also regulate noncoding RNA decay and activities.

Single-m6A site in 5' UTR for cap-independent translation initiation of Hsp70 mRNA

A single-base m6A modification at in the 5' UTR of Hsp70 mRNA is necessary and sufficient to promote its noncanonical cap-independent translation (Fig. 1) [18]. Under stress conditions, nuclear localized YTHDF2 reader protein protects the m6A from demethylation by FTO. Translation initiation factor (eIF3) can directly bind to the m6A and initiate the internal translation, thereby allowing cap-independent translation of HSP70 when the global cap-dependent translation is shutting down in the stressed cells.

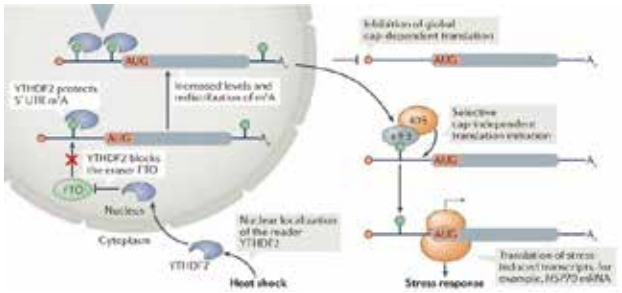


Figure 1. *Molecular mechanism of cap-independent translation of HSP70 mRNA under heat shock stress by a single-base m6A modification [18, 19].*

Single-m6A site in mRNA CDS affects mRNA translation dynamics

A single-base m6A modification in mRNA coding sequence (CDS) can affect the translation elongation dynamics [20]. An m6A in a codon can slow down the cognate-tRNA decoding and also act as a barrier/controller for tRNA accommodation and translation elongation. The m6A stalled translation may produce truncated proteins and have chain effects on co-translational protein folding, chaperoning, and localization signal recognition, all of which can potentially drive the protein for different fates or activities [21]. Conceivably, if m6A recodes a codon for another amino acid, it could lead to protein variants with an deviant function and substantial biological consequence even at low occupancy [20](Fig. 2).

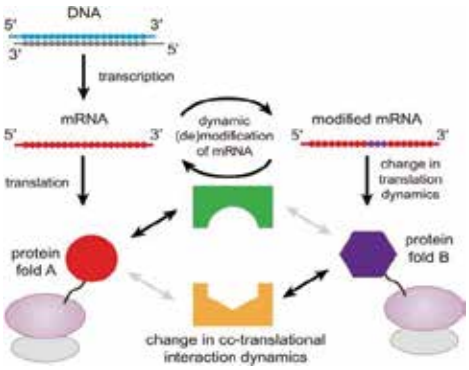


Figure 2. *The changed translation elongation dynamics can influence co-translational nascent protein folding or interaction with other partnering factors [20].*

Single-m6A site regulating lncRNA decay

Single-base m6A sites (A917, A1025 and A1056) in linc1281 are required to decoy let-7 family miRNAs (Fig. 3) [22]. By sequestering these pluripotency-related miRNAs, the m6A modified linc1281 ensures the cells of mESC identity.

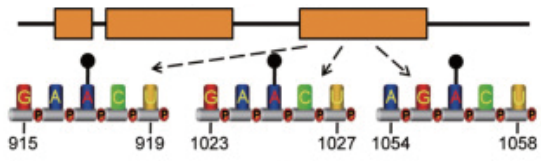


Figure 3. *m6A methylation of single-m6A sites in the last exon of linc1281 is required for the lncRNA to bind let-7 miRNAs and act as a competing endogenous RNA (ceRNA) to regulate mESC differentiation [22].*

Arraystar m6A Single Nucleotide Microarrays

Arraystar has developed m6A single nucleotide resolution arrays that precisely locate the m6A modification at exact adenosine and quantify the stoichiometry of m6A modification fractions.

An orthogonal methodology for m6A detection

Due to the m6A-antibody cross-reactivity with other related modifications (e.g. m6Am)[1, 7-9], the assay specificity to m6A modification is limited. Also, in the absence of an orthogonal technique as an independent reference, the sensitivity of m6A-antibody based m6A profiling has not been systematically evaluated. For the first time, the microarrays based on methyl-sensitive MazF RNase now allow systematic m6A profiling independent of m6A-antibody immunoprecipitation based approaches such as MeRIP or miCLIP.

Single-nucleotide resolution for m6A site location

RNase MazF cleaves single stranded RNA 5' immediate to unmethylated (ACA) sequence, but not methylated (m6ACA) (Fig. 4) [1, 10]. The MazF digested RNA fragments with cleaved (ACA) and uncleaved m6ACA are labeled with Cy5 color, whereas the input RNA fragments without MazF digestion are separately labeled with Cy3 color. These RNAs are then combined and hybridized with Arraystar m6A Single Nucleotide Resolution Arrays, to quantify the m6A modification stoichiometry and abundance for each site (Fig. 5).

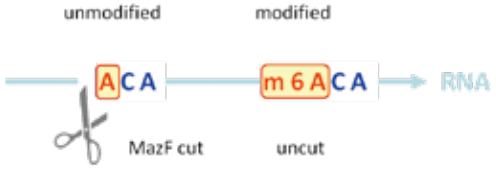


Figure 4. *MazF enzyme cuts at unmethylated (ACA) sequence but not methylated (m6ACA).*

m6A modification stoichiometry

The m6A stoichiometry, i.e. the fraction of m6A modification at that site, is critical for understanding its functional significance, answering questions about the m6A writing/reading/erasing, regulation, the dynamics in response to stimuli [3, 11, 12], and prioritizing the m6A sites for study. The fraction or percentage of m6A modification can be quantified by the two-color channel intensities at each site, addressing the long-standing unfulfilled needs in determining the dynamic m6A status.

Low RNA sample amount requirement

The microarrays use as low as 1 µg total RNA. The highly sensitive and specific MazF enzymatically works well even on extremely low RNA amounts at nanogram or picogram level. m6A profiling can now be performed on rare samples, precious pathological specimens, particular histological sites, low yield sorted cells, or small animal models.

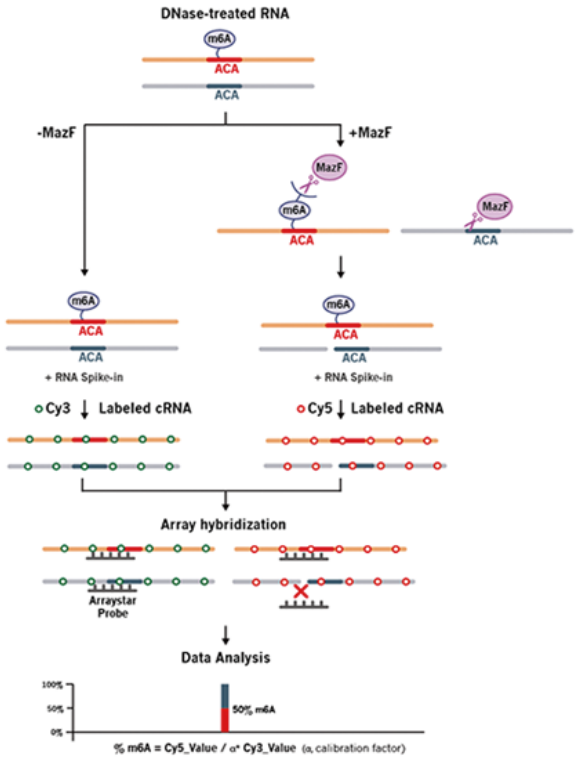


Figure 5. *The workflow of Arraystar m6A Single Nucleotide Resolution Array.*

Reliable collection and systematic annotations

Most m6A modifications occur in m6A motifs having a core (ACA) sequence, collectively referred to as m6ACA sites. For reliable collection of m6ACA sites, we have established a pipeline to discover all m6ACA sites that are quantifiable by

array probes. An ACA site without another ACA present within 40 nt can be uniquely detected by a probe and is defined as quantifiable Single-ACA site. Multiple ACA sites closely located within a 20-nt region can be collectively detected by a probe and is defined as quantifiable Poly-ACA site. Additionally, when multiple Single-(ACA) or Poly-(ACA) are contained within a 500 nt region and the distance between them is < 100nt, they are merged as one Clustered-ACA region (Fig 6), which can be analyzed by integrating the signals from the individual probes of constituent Single- and Poly-ACA sites. Not all ACA sequences in the RNAs are modified by m6A. All quantifiable ACA sites are further mapped to the cataloged m6A sites in the miCLIP dataset[13-16] and the m6A consensus near the m6A-seq peak summits[17], which defines a high and ultra-high confidence Single-, Poly-, and Clustered-m6ACA sets.

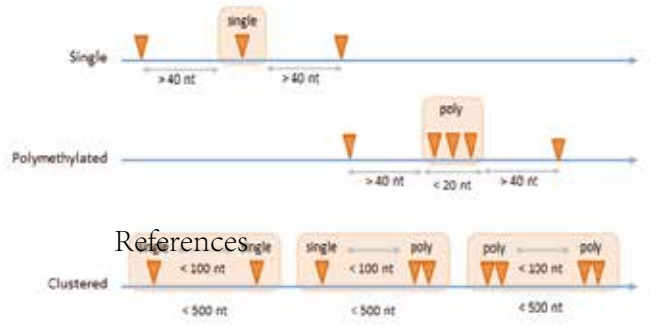


Figure 6. *The collection pipeline of quantifiable Single-, Poly-, and Clustered-m6ACA sites.*

Why use m6A Single Nucleotide Microarray over MeRIP-sequencing

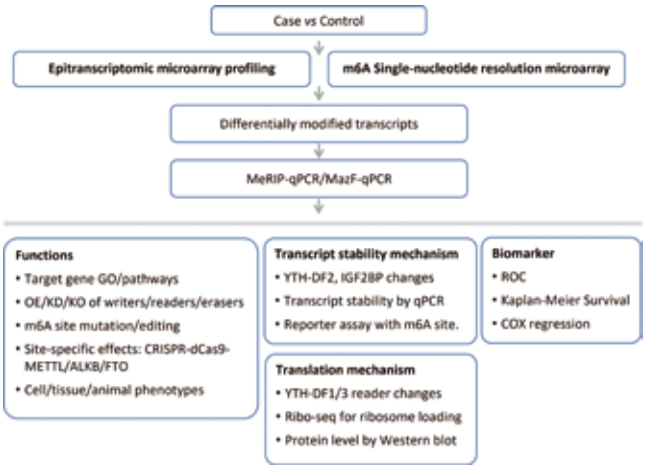
Profiling m6A at single nucleotide resolution has been challenging. Conventional methods such as m6A/MeRIP-seq have helped to make the analysis of m6A epitranscriptomics possible [1-5], but they cannot precisely identify which adenosines in a MeRIP-seq peak are actually modified, nor can they quantify the modification fraction for each site [6].

	m6A Arrays	MeRIP-Seq
Quantification	• m6A stoichiometry as %Modified • m6A RNA abundance • Differential analysis of both %Modified and abundance	• Lack of modification stoichiometry • Differential analysis of abundance only
m6A-site resolution	Single-nucleotide	~ 100 nt
Starting RNA amount	>= 1 µg total RNA	>= 120 µg total RNA
Poly(A) selection or rRNA removal	Not required	Required (scale-up needed)
RNA integrity demand	Tolerant	High

m6A Single Nucleotide Microarray Specifications

Array Name	Species	Size	Contents
m6A Single Nucleotide Array	Human Mouse Rat	8 x 15K	~14K probes targeting Single- or Poly- m6A sites.

m6A Epitranscriptomics Research Roadmap



References

1. Garcia-Campos M A, Edelheit S, Toth U, et al. Cell, 2019,178(3):731-747.
2. Knuckles P, Buhler M. FEBS Lett, 2018,592(17):2845-2859.
3. Schwartz S. RNA, 2016,22(2):169-174.
4. Meyer K D, Jaffrey S R. Annu Rev Cell Dev Biol, 2017,33:319-342.
5. Yue Y, Liu J, He C. Genes Dev, 2015,29(13):1343-1355.
6. Liu N, Parisien M, Dai Q, et al. RNA, 2013,19(12):1848-1856.
7. Dominissini D, Moshitch-Moshkovitz S, Schwartz S, et al. Nature, 2012,485(7397):201-206.
8. Schwartz S, Bernstein D A, Mumbach M R, et al. Cell, 2014,159(1):148-162.
9. Linder B, Grozhik A V, Olarerin-George A O, et al. Nat Methods, 2015,12(8):767-772.
10. Imanishi M, Tsuji S, Suda A, et al. Chem Commun (Camb), 2017,53(96):12930-12933.
11. Grozhik A V, Jaffrey S R. Nat Chem Biol, 2018,14(3):215-225.
12. Meyer K D, Jaffrey S R. Nat Rev Mol Cell Biol, 2014,15(5):313-326.
13. Linder B. et al. (2015) [PMID: 26121403]
14. Ke S. et al. (2015) [26404942]
15. Chen K. et al. (2015) [25491922]
16. Kai X. et al. (2017) [28809392]
17. Schraga Schwartz, et al. (2013) [24269006]
18. Zhou, J., et al. (2015) " Nature 526(7574):591-4 [PMID: 26458103]
19. Kathrin Leppek, et al. (2018) [PMID: 29165424]
20. Choi, J., et al. (2016) " Nat Struct Mol Biol 23(2):110-5 [PMID: 26751643]
21. Kim, S. J., et al. (2015) Science 348(6233):444-8 [PMID: 25908822]
22. Yang, D., et al. (2018) Nucleic Acids Res 46(8):3906-3920 [PMID: 29529255]

Arraystar Small RNA Modification Arrays

8G/m7G/m6A/Ψ/m5C in miRNAs, pre-miRNAs & tsRNAs

Highlights

- Detecting and quantifying a variety of small RNA modifications
- Coverage of multiple small RNA classes
- Gold standard for accurate quantification of modified small RNAs
- High sensitivity for modified small RNAs at lower levels
- Low sample amount required, starting from as little as 1 ug total RNA

Why Study Small RNA Modifications?

Small RNAs, including microRNAs (miRNAs) and tRNA-derived small RNAs (tsRNAs, i.e. tRFs and tiRNAs), harbor a diversity of RNA modifications. RNA modifications such as 5-methylcytidine (m5C), 7-methylguanosine (m7G), 8-oxoguanine(O8G), pseudouridine (Ψ) and m6A-methylation (m6A) modulate the activities of small RNAs in diverse biological processes and play pivotal roles in pathological conditions.

Small RNA modifications influence miRNA targeting

Modifications in the seed regions of miRNAs are known to alter the miRNA-mRNA base pairing and targeting specificity, having profound biological consequences [4-6]. For example, Reactive Oxygen Species (ROS) can convert guanine (G) to 8-oxoguanine (O8G) in miRNAs. O8G base pairs with adenine (A) instead of unmodified G pairing with C. Thus, O8G modification in the seed region of a miRNA alters the mRNA targeting through O8G•A base pairing (Fig. 1, Top). When modified with o8G, miR-184 binds its new mRNA targets BCL-XL and BCL-W and suppresses their translation, resulting in increased cardiomyocyte cell death (Fig. 1, Bottom)[1]. In another example, introducing o8G in the seed region of miR-1 alone is sufficient to cause cardiac hypertrophy in mice [2]. Therefore, modifications installed in response to pathophysiological conditions can serve as an epitranscriptional mechanism to coordinate the gene expression [2].

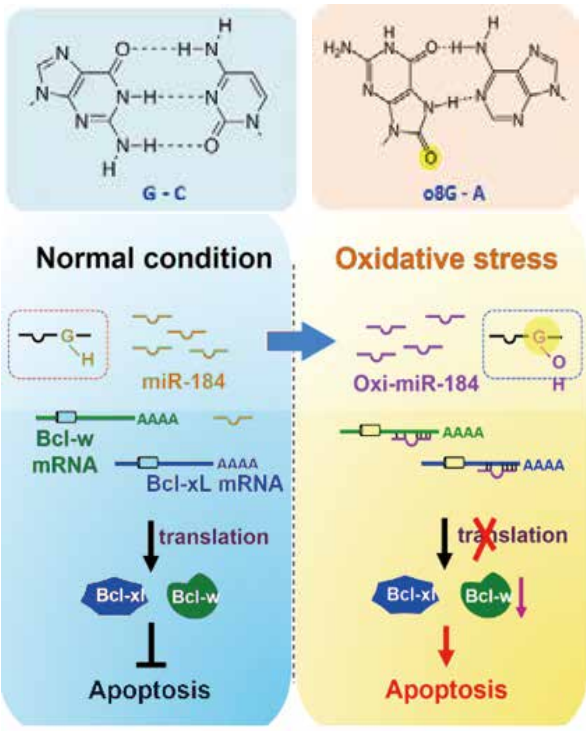


Fig.1. *Top: o8G modification converts G-C pairing to altered G-A pairing. Bottom: Under oxidative stress, miR-178 is o8G modified and re-targets anti-apoptotic Bcl mRNAs, causing apoptosis [1].*

Small RNA modifications inhibit protein translation

Modified small RNAs can decoy RNA binding proteins (RBP), thereby displacing the RBP from mRNAs, inhibiting its binding to the target mRNAs, and suppressing the translation. For example, the 5' terminal oligoguanine (TOG) in tsRNAs can either have an unmodified uridine (U8) or pseudouridine (Ψ8) modified by PUS7 at the 8th position. The U8/Ψ8 status determines the different binding affinities with polyadenylate-binding protein 1 (PABPC1) as a translational initiation factor. Ψ8-TOG-5'tsRNAs bind more tightly to PABPC1, displace it from mRNAs, and inhibit the translation, whereas U8-TOG-5' tsRNAs do not (Fig. 2)[3].

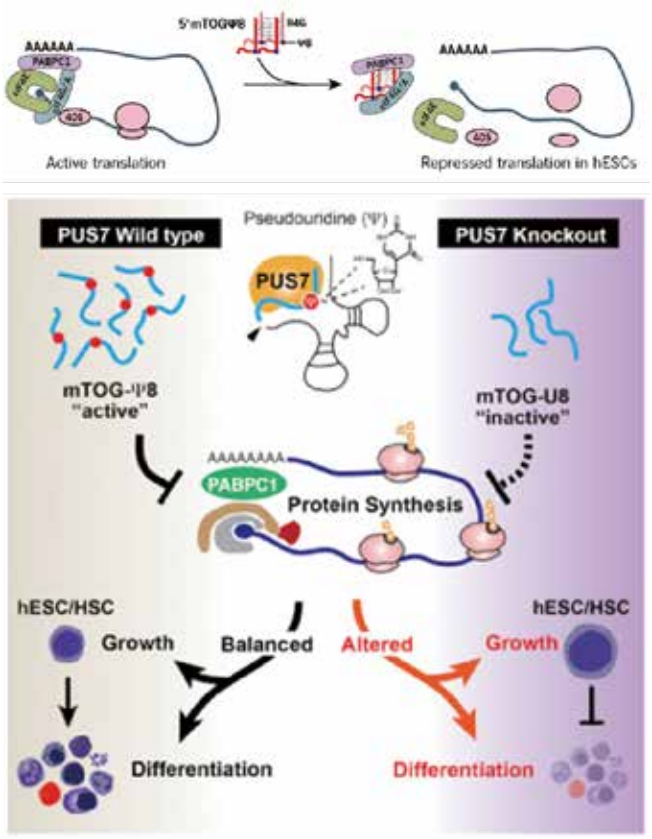


***Fig. 2**. 5'TOG-tsRNAs with Ψ modification at position 8 decoy and displace PABPC1 from the translation initiation complex, thereby repressing the translation of capped mRNAs [3]*

Small RNA modifications as biomarkers

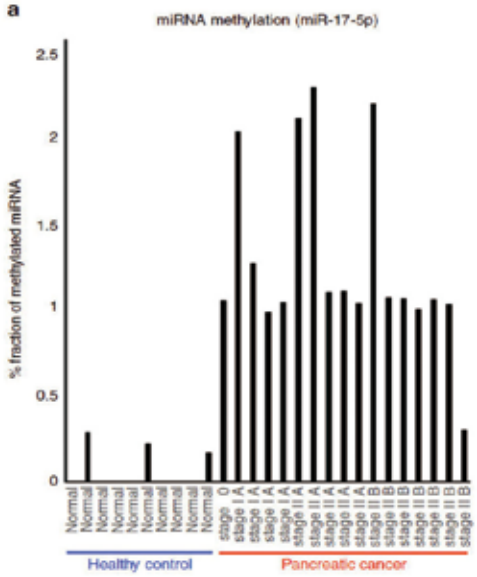


***Fig. 3.** m6A methylation of serum miR17-5p displays superior diagnostic value in pancreatic cancer [4].*

The associations of small RNA modifications with diseases offer opportunities for a new class of epitranscriptional biomarkers for potentially superior diagnostic/prognostic performance [4]. For example, o8G oxidation of miRNAs coordinates redox-mediated gene expression and is correlated with pathophysiological conditions of cardiomyocytes [2]. Overall, m6A modification of miRNA is significantly increased in cancers compared with normal tissues. For example, m6A modified miR-17-5p level in serum indicates early pancreatic cancer with extremely high sensitivity and specificity (Fig.3) [4].

What Are the Challenges to Quantify Small RNA Modifications Accurately?

Although sequencing has been used for small RNA profiling, the influence of RNA modifications on the sequencing quantification has largely been ignored. Various RNA modifications, such as m1A, m3C and m1G, do interfere with and block the reverse transcription reaction during sequencing library construction, thereby making accurate quantification of small RNAs and especially their modifications impossible (Fig.4). For example, small RNA-seq is mostly biased toward 18-nt 3'-tsRNA rather than the more predominant 22-nt isoforms seen by northern blot. This is due to the presence of m1A in the TUC loop, which blocks reverse transcriptase from proceeding. Most of the past small RNA sequencing data were obtained using the library construction methods above without regards to the modifications, which could mislead the interpretation.

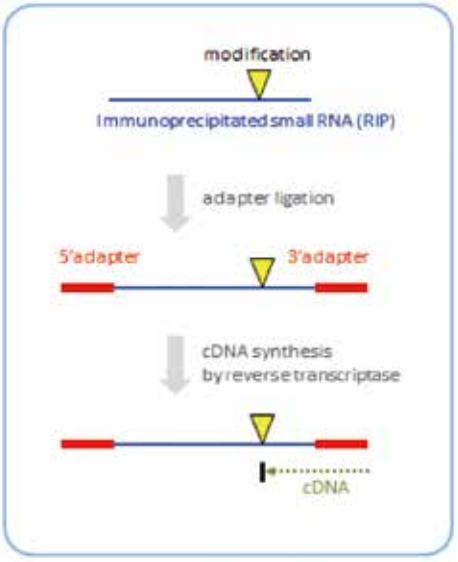


***Fig.4.** Small RNA MeRIP-seq limitation: cDNA synthesis during sequencing library construction is blocked by RNA modifications.*

Also, small RNA profiling by small RNA-seq requires multiple PCR amplification steps, which incurs significant quantification bias/inaccuracies. The situation therefore necessitates the use of independent, orthogonal methodologies.

In practice, most sequencing based methods for modification profiling require large amount of input total RNAs (> 100 ug), precluding many studies with only limited sample amounts.

Furthermore, small RNA-seq commonly uses Reads Per Million RNA reads (RPM) for normalization and to represent the relative RNA abundances in the sample. However, RPM depends on the composition of the small RNA population in a sample. A change in one small RNA's RPM will adjust all the other small RNAs' values even their actual absolute expression levels are not changed.

In order to identify and quantify the full spectrum of modified-small RNAs with high sensitivity and accurate stoichiometry, there is a need for overcoming the limitations of the sequencing-based approaches and developing non-sequencing based methods.

The Non-Sequencing Based Solution – Small RNA Modification Arrays

Arraystar Small RNA Modification Arrays are designed to quantify a choice of o8G, m7G, m6A, Ψ, or m5C modifications in miRNAs, pre-miRNAs, and tsRNAs on a single array. Combined with RNA immunoprecipitation (RIP), the arrays simultaneously measure the modified and unmodified small RNA levels in two-color channels on the same array, providing the key information to study regulatory impacts of the modification in small RNAs.

Gold standard for accurate quantification of modified small RNAs

The arrays use direct RNA end labeling to ensures high fidelity of quantification, without the problems of RNA modifications blocking cDNA synthesis during RNA-seq library prep (Fig. 5). Here, the 3’ -end of the RNAs are ligated with cytidine-5'-phosphate labeled with Cy5 (for modified IP-RNA) or Cy3 (for unmodified supernatant RNA) by T4 RNA ligase in one step ligation. No problematic reverse transcription or PCR amplification are used. Such directly labeled RNAs most faithfully represent the RNA abundance levels.

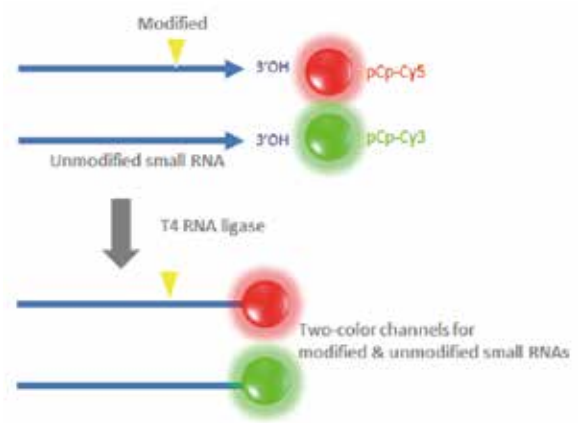


Fig. 5. *One-step direct RNA end labeling of modified and unmodified RNAs by cytidine-5'-phosphate Cy5 or Cy3 labels in separate two-color channels, to achieve the most faithful quantification accuracy.*

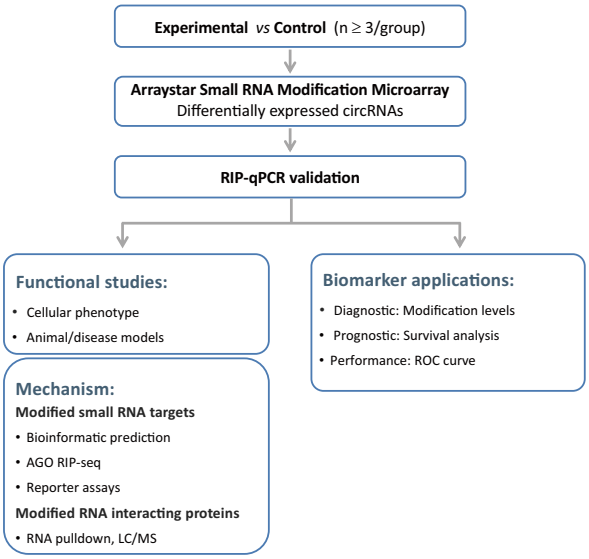
Low sample amount requirements

Very often, many biological samples are of limited supplies. Arraystar Small RNA Modification Microarrays use as little as 1 ug total RNA, opening up opportunities for broad research projects.

Array coverage of multiple small RNA classes

	Human	Mouse
miRNAs	2,628 (1,319 5-p-miRNAs & 1,309 3-p-miRNAs)	1,949 (966 5-p-miRNAs & 983 3-p-miRNAs)
pre-miRNAs	1,745	1,122
tsRNAs	5,128	1,809
Small RNA sources	miRNA: miRBase (v22) pre-miRNA: miRBase (v22) tsRNA: tRFdb, GtRNADb (18.1 2019.08) Literatures: Scientific publications (up to 2019)	

Research Roadmap for Small RNA Modification Profiling



References

[1] Wang, J. X., et al. (2015) "Oxidative Modification of miR-184 Enables It to Target Bcl-xL and Bcl-w" Mol Cell 59(1):50-61 [PMID: 26028536]

[2] Seok, H., et al. (2020) "Position-specific oxidation of miR-1 encodes cardiac hypertrophy" Nature 584(7820):279-285 [PMID: 32760005]

[3] Guzzi, N., et al. (2018) "Pseudouridylation of tRNA-Derived Fragments Steers Translational Control in Stem Cells" Cell 173(5):1204-1216 e26 [PMID: 29628141]

[4] Konno, M., et al. (2019) "Distinct methylation levels of mature microRNAs in gastrointestinal cancers" Nat Commun 10(1):3888 [PMID: 31467274

Arraystar GlycoRNA Array

Discover the Pivotal Roles of Glycosylated RNAs in Cancer and Disease

Highlights

- **Unprecedented scientific and medical opportunities.** The newly discovered glycoRNAs now join the ranks of biologically, clinically, and pharmaceutically important glycoproteins and glycolipids.
- **Comprehensive glycoRNA profiling.** One array simultaneously covers all classes of glycosylated Y-RNA, pre-miRNA, tRNA, rRNA, snoRNA, snRNA and their fragments.
- **Discovery of novel glycoRNAs.** Previously unknown glycoRNAs can be detected for glycosylation comprehensively on the Array.
- **Suitable for all sample types.** Chosen glycoRNA capture method detects glycoRNAs for any sample types: living or non-living cells, tissues, biofluids.
- **High sensitivity and reliability.** Direct glycoRNA end labeling bypasses challenges of RNA modification/ folding, and distorted PCR in small RNA sequencing

What Are GlycoRNAs?

While only lipids and proteins have long been believed to be modified with sugars, RNAs were not thought to be glycosylated. In 2021 in Nobel laureate Bertozzi lab, mammalian small noncoding RNAs were discovered to link with sialylated glycans, challenging the old beliefs and making significant advancement in the RNA and glycobiology fields [1].

GlycoRNAs are primarily glycosylated small non-coding RNAs, including small nuclear RNAs (snRNAs), ribosomal RNAs (rRNAs), small nucleolar RNAs (snoRNAs), transfer RNAs (tRNAs), Y-RNAs, and miRNAs [1, 2]. They may have molecular functions fundamentally different from their un-glycosylated counterparts.

Why Study GlycoRNAs?

GlycoRNAs are predominantly located on the cell surface [1], which suggests their role in mediating extracellular interactions. Particularly, GlycoRNAs bind to the sialic acid-binding immunoglobulin-like lectin (Siglec) receptor family, participating in cell adhesion, signaling, and immune response modulation [1]. Moreover, as the ligands for Siglec receptor family are largely unknown, newfound glycoRNAs could be the long sought-after ligands [3, 4].

Aberrant protein and lipid glycosylation has long been established hallmarks of various human diseases. Similarly, glycoRNAs have the potential for disrupted glycan networks in diseases. GlycoRNAs have been found involved in breast [5] and pancreatic cancers [2, 6], autoimmune, atherosclerosis and cardiovascular diseases [7, 8], stoke [9], inflammatory lung diseases [10], and immunomodulation [11](Fig. 1).

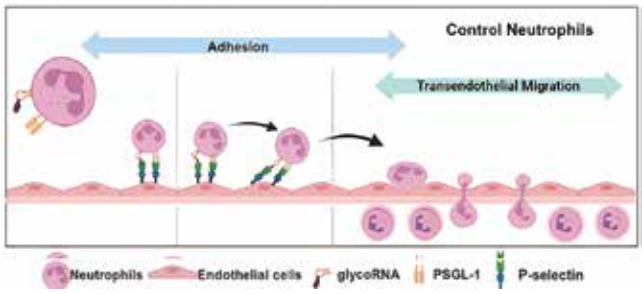


Fig.1. *GlycoRNAs on the neutrophil surface control neutrophil recruitment in immune modulation [11].*

As a new avenue for therapeutic research, modifications to glycoRNA glycans could influence responsiveness to immunotherapies. Antisense targeting the RNA moieties is amenable to rational drug design and can be highly selective. Notably, large molecule drug can react with glycoRNA targets without the difficulties to enter the cells. For biomarker applications, the glycan and RNA moieties have the biochemical properties for both immunochemical and sequence based detection methods, allowing highly sensitive and specific diagnosis and prognosis of diseases [12, 13].

GlycoRNAs hold transformative potential in transcriptomics, epitranscriptomics, RNA biology, glycobiology, cell biology, biochemistry, signal transduction, immunology, fundamental biology, and biomedical/clinical sciences.

How to Study GlycoRNAs

Arraystar GlycoRNA Array uses glycoRNA capture by lectin (WGA) affinity binding that works on regularly purified RNA samples from any sources (e.g. cells, tissues, biofluids), without the limitation of cultured living cell metabolic labeling. The captured glycoRNAs are detected by microarray to quantify and profile the glycoRNA expression. The integration of these two advanced techniques leverages the strengths of both methods for high specificity, sensitivity, and accuracy.

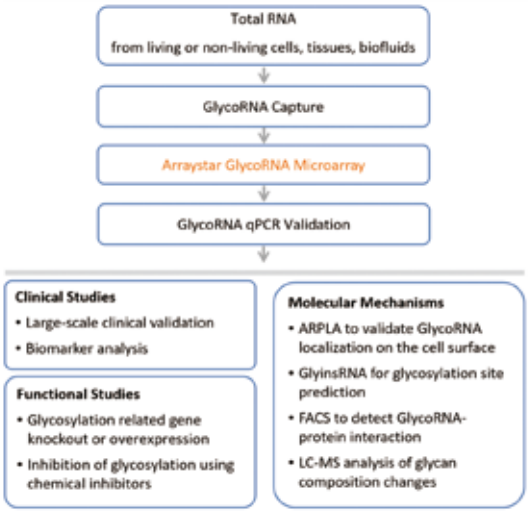
The array covers a wide range of glycosylated small RNA classes, including Y-RNAs/Y-RNA fragments, tRNAs, tsRNAs (tiRNAs & tRFs), pre-miRNAs, miRNAs, snRNAs/snRNA fragments, snoRNAs/snoRNA fragments, and rRNAs/rRNA fragments.

Using this cutting edge approach, researchers can gain comprehensive glycoRNA expression details to discover and understand this new class of RNA molecules in gene regulation, cellular functions and human diseases.

Overcoming the Limitations of Sequencing

For glycoRNA microarray, glycoRNAs are directly end-labeled by simple Cy3C ligation, without the problems of RNA modifications and RNA folding that hinder and block reverse transcription as required in RNA sequencing library construction. PCR amplification, which can introduce bias and distortion greatly, is no longer needed. Now all classes of glycoRNAs, particularly the heavily modified tRNAs and tsRNAs, can be profiled simultaneously on one array with unbiased, accurate, and sensitive quantification, effectively overcoming the limitations of sequencing.

GlycoRNA Research Roadmap



Arraystar GlycoRNA Array Specifications

Probe design	Small RNA specific sequence with 5'hairpin cap and 3'spacer			
Probe-binding sites	miRNA/5'tsRNA: 3'-sequence 3'tsRNA/Y-RNA/snRNA/snoRNA/rRNA-derived fragment: Any segment in the full-length sequence pre-miRNA: Loop region of the pre-miRNA tRNA: Anti-codon loop sequence of the mature tRNA Y-RNA/snoRNA/snRNA/rRNA: Specific sequence within the entire length of the RNA			
Probe specificity	Specific for the small RNAs			
Array Format	8x15K			
Coverage of small RNA classes				
	Human	Mouse	Rat	Sources
Total number of distinct probes	7,646	7,420	5,312	
YsRNA (Y-RNA-derived small RNA)	10	5	7	Human: Literatures Mouse and Rat: Predicted
snsRNA (snRNA-derived small RNA)	4	35	35	
sdRNA (snoRNA-derived small RNA)	289	1,334	1,464	
rRF (rRNA-derived small RNA)	210	479	280	Human: MINTbase(V1) Mouse and Rat: Predicted
miRNA	2,627	1,949	749	miRBase(v22)
tsRNA (tRNA-derived small RNAs)	1,432	910	653	tRFdb, MINTbase, GtRNADb (v18.1, 2019.08) Literatures up to 2019
pre-miRNA	1,745	1,122	448	miRBase(v22)
mature-tRNA	338	267	195	GtRNAdb (v18.1, 2019.08) ENSEMBL (v99)
snoRNA	955	1,297	1,464	ENSEMBL (v99)
Y-RNA	4	2	3	RNAcentral (V24) RefSeq (2024.08)
snRNA	27	15	9	
rRNA	5	5	5	

References

[1] Flynn, R. A., et al. (2021) Cell [PMID:34004145]

[2] Li, J., et al. (2024) bioRxiv [doi:10.1101/2024.06.18.599663]

[3] Disney, M. D. (2021) Cell [PMID:34115968]

[4] Clyde, D. (2021) Nat Rev Genet [PMID:34168329]

[5] Ma, Y., et al. (2024) Nat Biotechnol [PMID:37217750]

[6] Li, J., et al. (2023) Anal Chem [PMID:37524653]

[7] Driedonks, T. A. P., et al. (2018) Front Immunol [PMID:30697216]

[8] Hizir, Z., et al. (2017) Cell Death Dis [PMID:28055017]

[9] Chokkalla, A. K., et al. (2023) J Cereb Blood Flow Metab [PMID:36644904]

[10] Abledu, J. K., et al. (2024) bioRxiv

[11] Zhang, N., et al. (2024) Cell [PMID:38262409]

[12] Angata, K., et al. (2020) Front Oncol [PMID:32850363]

[13] Nishimura, S. (2011) Adv Carbohydr Chem Biochem [PMID:21763513]

Downstream-of-Gene Transcript Array

One Array to Profile DoG RNAs & All Their Target RNAs Accurately

Highlights

- Designed to profile and study DoG RNAs having important biological and disease functions.
- One array to detect DoG RNAs and all their regulatory targets: sense-overlapping lncRNA/circRNAs, DoG-derived chimera RNAs and circular RNAs, and anti-sense overlapping mRNAs/lncRNAs.
- Accurate and sensitive probes specific to the unique splice junctions for detection and quantification, without the difficult computational and bioinformatic analyses otherwise required by sequencing.
- High sensitivity, good for DoG-derived circular RNAs and chimera RNAs often at low abundance.

What Are DoG RNAs?

Downstream-of-gene (DoG) RNAs are RNAs transcribed beyond the polyadenylation signal (PAS) at the transcription end site and are continuous with upstream RNAs[1]. They are typically 5–200 kb long and occur in about 10% of host genes[1], often overlapping with downstream transcription units called read-in genes [2, 3] (Fig. 1).

DoG RNAs result from transcription termination failure[4]. Normal transcription termination requires coordinated slowing, pausing, and dislodging of RNA polymerase II and 3' end cleavage of the transcript. Disruption in these steps, due to stresses like osmotic shock[5], heat[6], viral infections[3, 7], or cancer mutations[2], leads to read-through transcription.

Why Study DoG RNAs?

The functions of DoG RNAs and their transcription processes are currently the focus of active research, as highlighted below.

Transcriptional interference in cell senescence

In senescent cells, a family of senescence-triggered antisense read-through RNAs (START RNAs) are induced as DoG RNAs[8].

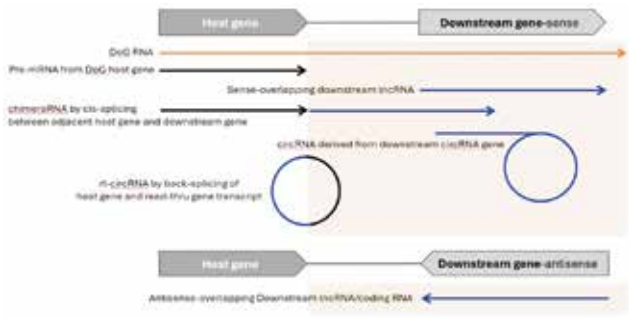


Fig. 1. *DoG RNAs and its downstream genes.*

Importantly, START RNAs act as antisense RNAs to repress the expression of their corresponding sense RNAs.

Genome 3D organization during viral infection

NS1 Influenza A viral protein can induce read-through transcription of highly active host genes, causing displacement of cohesin from the host chromatin, elimination of chromatin loops, and decompaction of chromatin in the read-through regions[7].

Cancers and diseases

DoG-derived chimeric RNAs are recurrently detected in different tumors, e.g. chimeraRNA CTSC-RAB38 in 20% of the TCGA cancer samples[2], CHFR-GOLGA3 in bladder cancer[9], and DoG derived lncRNA SLC45A3-ELK4 in prostate cancer to control the cancer cell proliferation and cancer progression[10].

Regulatory DoG-derived circRNAs and rt-circRNAs

Some DoG RNAs can be circularized to form Read-through circRNAs (rt-circRNAs)(Fig. 1)[11, 12]. DoG derived circular RNAs may regulate gene expression and diseases similar to other circRNAs.

Regulation of DoG RNA expression

DoG gene expression can be controlled by epigenetic regulation, e.g. histone H3K36 trimethylation[2, 13, 14] and histone variant H2A.Z[8]; by epitranscriptomic RNA

modifications[15-17]; and by R-loops[18].

How to Study DoG RNAs?

Arraystar Downstream-of-Gene Transcript (DoG RNA) Microarray is designed to simultaneously detect and quantify DoG RNAs, pre-mRNAs of the host genes, and downstream overlapping transcripts as their potential regulatory targets at high accuracy and specificity.

Compared to sequencing, DoG RNA profiling by microarray is simpler, more sensitive, and accurate. While sequencing requires complex analyses and specialized computational pipelines due to the diverse RNA types, the microarrays utilize probe designs to target unique splice junctions with high sensitivity, even for low-abundance circRNAs and rt-circRNAs (Fig. 2). Sequencing would require costly, deep coverage that remains inadequate. For DoG RNA profiling, the Arraystar DoG RNA microarray offers a unique tailored solution.

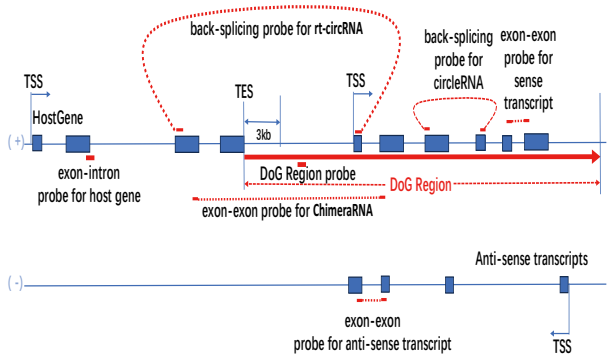
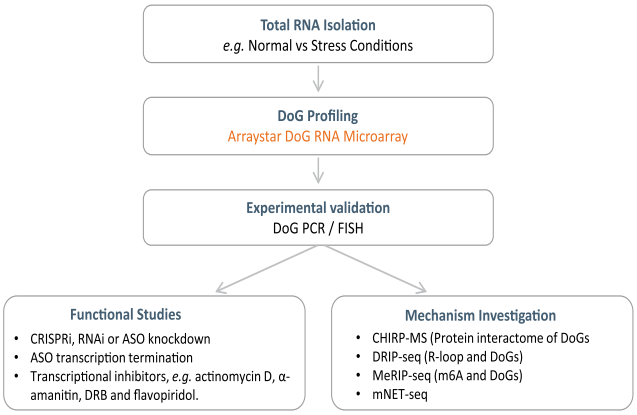


Fig. 2. *Arraystar DoG RNA Microarray probe design*

Arraystar Human DoG RNA Microarray Specifications

DoGs	4,460
DoG gene pre-mRNAs	4,460
Downstream lncRNAs (Sense)	480
Downstream circRNAs	1,546
chimeraRNAs	539
rt-circRNAs	356
Downstream antisense transcripts	1,866
Drosophila spike-in controls	1,000
DoG and downstream transcripts Sources	**DoGs:** Scientific publications **Host genes:** GENCODE human V44 **Downstream coding/non-coding RNAs:** GENCODE human V44 **Downstream circular RNAs:** circBase **Downstream chimeraRNAs:** FusionGDB2, GENCODE human V44,and scientific publications **Downstream rt-circRNAs:** scientific publications **Drosophila RNAs:** ENSEMBL BDGP6.46
Array Format	8 x 15K

DoG RNA Research Roadmap



References

[1] Mol Cell (2015)[PMID:26190259]

[2] Elife (2015)[PMID:26575290]

[3] Nat Commun (2015)[PMID:25989971]

[4] Trends Biochem Sci (2022)[PMID:34489151]

[5] Mol Cell (2021)[PMID:33400923]

[6] Mol Cell (2022)[PMID:35114099]

[7] Cell (2018)[PMID:30146161]

[8] Cell Rep (2017)[PMID:29186682]

[9] Int J Biochem Cell Biol (2019)[PMID:30818082]

[10] Cancer Lett (2017)[PMID:28716526]

[11] Cell (2019)[PMID:30735636]

[12] RNA Biol (2020)[PMID:32783578]

[13] Nature (2009)[PMID:19136943]

[14] Proc Natl Acad Sci U S A (2011)[PMID:21571633]

[15] Science (2018)[PMID:30262497]

[16] Trends Biotechnol (2021)[PMID:32620324]

[17] Life Sci Alliance (2019)[PMID:31142640]

[18] Mol Cell (2024)[PMID:38569554]

Arraystar R-loop Profiling by DRIPc-seq

Profiling the lncRNA/mRNA/circRNA organized R-loops in gene regulation

Highlights

- Powerful profiling: To study R-loops as a new player in gene regulation in the genome.
- Strand specificity: To identify lncRNAs/mRNAs in the R-loops, precise locations, and strand directions in the reference genome.
- High reliability: Well established optimal experimental procedures to produce best possible results.
- Flexibility: For any species with a reference genome.
- Rigorous quality: The positive and negative controls ensure DRIPc-seq library quality.
- Results: Provided with rich annotation, genome browser tracks, and publication-ready graphics.

Introduction

R-loop is a RNA:DNA three-stranded hybrid structure formed between LncRNA/mRNA/CircRNA strand and the template DNA strand by base pairing, leaving the non-template DNA strand unpaired and displaced in the loop (Fig.1) [1]. R-loops are widely distributed, occurring in 5% of the mammalian genomes [2,3]. R-loops are often located in the CpG islands of the promoters or transcription stop sites. High GC skews (G enrichment over C in the downstream of TSS non-template strand), G-quadruplexes, DNA gaps and DNA/RNA modifications contribute the formation of R-loops [4]. R-loops have important biological functions in gene regulation, DNA replication, and DNA/histone modifications.

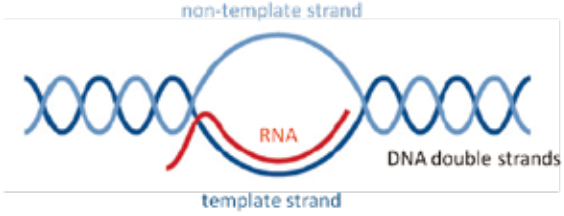


Fig. 1. *R-loop structure[5].*

LncRNA Organized R-loops impact transcription

R-loops can form between a lncRNA strand and the DNA in the loop. For example, TCF21 is a tumor suppressor in many cancers. TARID (TCF21 antisense RNA inducing demethylation) is a head-to-head antisense lncRNA of TCF21 gene and forms R-loop in the promoter region (Fig. 2). The R-loop is recognized by GADD45a, which recruits demethylase TET1, removes DNA methylation, increases TCF21 mRNA transcription, and regulates the cell cycles [6].

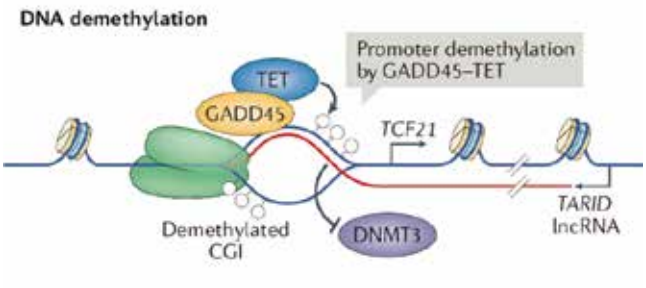


Fig. 2. *Antisense lncRNA-TARID forms R-loop to regulate TCF21 promoter demethylation and TCF21 mRNA transcription [4,6].*

mRNA Organized R-loops Regulate DNA Methylation Transcription

Normally, the R-loop at BAMBI (a negative regulator of TGF) gene promoter facilitates more transcription. However in amyotrophic lateral sclerosis (ALS4), senataxin mutation reduces R-loop and increases the DNA methylation at the BAMBI promoter, leading to BAMBI transcription repression, TGF signal transduction upregulation, and ALS progression [7].

DRIPc-seq for R-loop Profiling

Arraystar DRIPc-seq (DNA–RNA immunoprecipitation followed by cDNA conversion coupled to high-throughput sequencing) profiles lncRNA/mRNA organized R-loop distribution in the genome. Compared with traditional DRIP-seq that sequences the DNA fragments in the R-loops, the upgraded DRIPc-seq sequences the RNAs in the R-loops, which has the additional ability to determine the RNA strand directions, template/non-

template DNA information, and semiquantification.

In the DRIPc-seq, S9.6 antibody is used to highly specifically immunoprecipitate the R-loops. The RNA strands in the R-loops are sequenced (Fig. 3). The DRIPc-seq data are bioinformatically analyzed to gain biological and functional insights (Fig. 4).

Along with LncRNA Array, MeDIP-seq, or ChIP-seq, DRIPc-seq provides valuable functional insights in epigenetic and transcriptional regulation by R-loops.

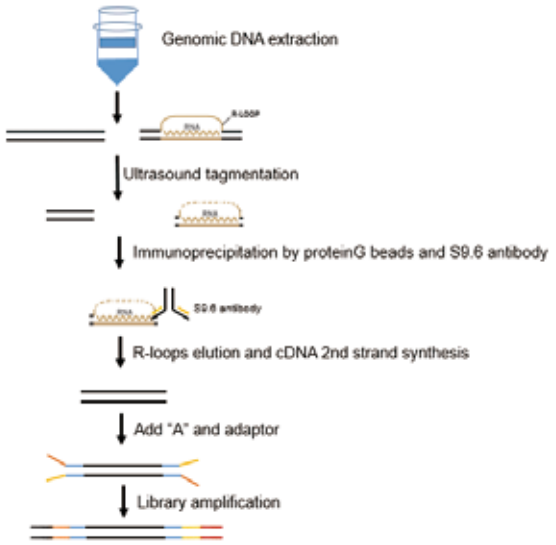


Fig. 3. *DRIPc-Seq workflow.*

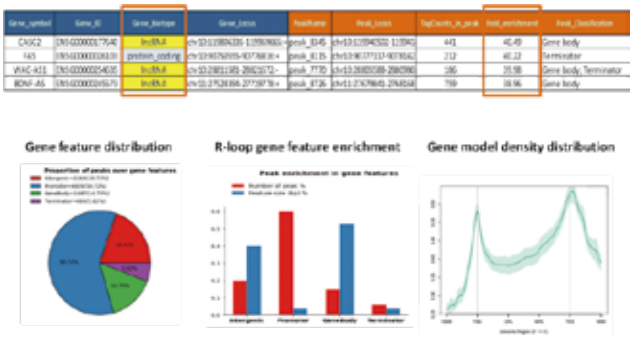
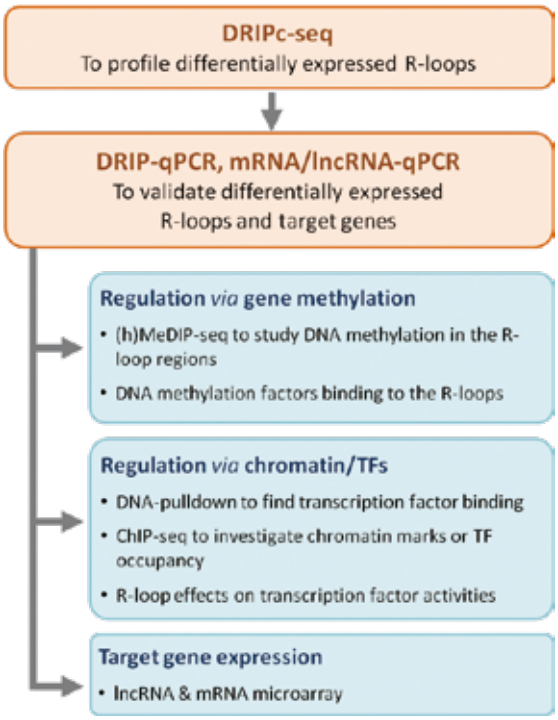


Fig. 4. *DRIPc-seq R-loop peak analysis, annotation, and gene feature distribution.*

R-loop Research Roadmap Ahead

With the wealth of information obtained from R-loop profiling by DRIPc-seq, the differentially expressed R-loops can be confirmed by DRIPc-qPCR, and the R-loop associated gene expression by mRNA/lncRNA-qPCR. As a research roadmap ahead, DNA methylation mediated by R-loops can be studied MeDIP-seq or chromatin changes or transcription factor bindings by ChIP-seq analysis, which can provide integrative view of R-loop regulatory effects by the epigenomic changes. Finally lncRNA/mRNA microarray can be used to measure the outcomes of target gene expression under the R-loop regulation.



References

[1] Hamperl S. and Cimprich KA. (2014) The contribution of co-transcriptional RNA:DNA hybrid structures to DNA damage and genome instability. DNA Repair (Amst) 19:84-94 [PMID:24746923]

[2] Sanz LA. et al (2016) Prevalent, Dynamic, and Conserved R-Loop Structures Associate with Specific Epigenomic Signatures in Mammals. Mol Cell 63(1):167-78 [PMID:27373332]

[3] Li M. and Klungland A. (2020) Modifications and interactions at the R-loop. DNA Repair (Amst) 96:102958 [PMID:32961406]

[4] Niehrs C. and Luke B. (2020) Regulatory R-loops as facilitators of gene expression and genome stability. Nat Rev Mol Cell Biol 21(3):167-178 [PMID:32005969]

[5] Hegazy YA. et al (2020) The balancing act of R-loop biology: The good, the bad, and the ugly. J Biol Chem 295(4):905-913 [PMID:31843970]

[6] Arab K. et al (2019) GADD45A binds R-loops and recruits TET1 to CpG island promoters. Nat Genet 51(2):217-223 [PMID:30617255]

[7] Grunseich C. et al (2018) Senataxin Mutation Reveals How R-Loops Promote Transcription by Blocking DNA Methylation at Gene Promoters. Mol Cell 69(3):426-437.e7 [PMID:29395064]

Selected Publications

Arraystar Epitranscriptomic Microarray

mRNA&LncRNA

Multigenerational paternal obesity enhances the susceptibility to male subfertility in offspring via Wt1 N6-methyladenosine modification. Xiong Y W, et al. ***Nature Communications,*** 2024

Increased PTCHD4 expression via m6A modification of PTCHD4 mRNA promotes senescent cell survival. Rossi M, et al. ***Nucleic acids research***, 2024

Circular RNA

METTL14-mediated m6A modification of circORC5 suppresses gastric cancer progression by regulating miR-30c-2-3p/AKT1S1 axis. Fan H N, et al. ***Molecular Cancer,*** 2022

Arraystar Small RNA Modification Microarray

o8G Site-Specifically Modified tRF-1-AspGTC: A Novel Therapeutic Target and Biomarker for Pulmonary Hypertension. Zhang J, et al. ***Circulation Research,*** 2024

A Novel tsRNA, m7G-3′ tiRNA Lys TTT, Promotes Bladder Cancer Malignancy Via Regulating ANXA2 Phosphorylation. Ying X, et al. ***Advanced Science,*** 2024

Arraystar CircRNA Microarray

Circular RNA circPHLPP2 promotes tumor growth and anti-PD-1 resistance through binding ILF3 to regulate IL36γ transcription in colorectal cancer. Hu Y, et al. ***Molecular Cancer,*** 2024

CircPDIA3/miR-449a/XBP1 feedback loop curbs pyroptosis by inhibiting palmitoylation of the GSDME-C domain to induce chemoresistance of colorectal cancer. Lin J, et al. ***Drug Resistance Updates,*** 2024

Arraystar LncRNA Microarray

A novel lncRNA ROPM-mediated lipid metabolism governs breast cancer stem cell properties. Liu S, et al. ***Journal of Hematology & Oncology,*** 2024

LncRNA evf-2 Exacerbates Podocyte Injury in Diabetic Nephropathy by Inducing Cell Cycle Re-entry and Inflammation Through Distinct Mechanisms Triggered by hnRNPU. Zhang C, et al. ***Advanced Science***, 2024

Arraystar Small RNA Microarray

P1.02D.02 Tumor-Derived Exosomal tsRNA 3' tiRNA-AlaCGC Promotes Immune Tolerance by Inducing Fibroblast Senescence in LUAD. Zhang Y, et al. ***Journal of Thoracic Oncology,*** 2024

tRNA Sequencing

Threonine fuels glioblastoma through YRDC-mediated codon-biased translational reprogramming. Wu X, et al. ***Nature Cancer,*** 2024

NuRNA™ Central Metabolism PCR Array

Fatty Acid Oxidation Supports Lymph Node Metastasis of Cervical Cancer via Acetyl-CoA-Mediated Stemness. Yuan L, et al. ***Advanced Science,*** 2024

nrStar ™ Functional LncRNA PCR Array

OP0084 the role of mechanical strain-induced hotair lncrna downregulation in the pathophysiology of rheumatoid arthritis. Meier F, et al. ***Annals of the Rheumatic Diseases***, 2024

rtStar ™ tRNA Pretreatment & First-Strand cDNA Synthesis kit (CAT# AS-FS-004)

Valine aminoacyl-tRNA synthetase promotes therapy resistance in melanoma. El-Hachem N, et al. ***Nature Cell Biology,*** 2024

Chemotherapeutic agents and leucine deprivation induce codon-biased aberrant protein production in cancer. Adva Kochavi, et al. ***Nucleic Acids Research,*** 2024

Nucleotidyltransferase toxin MenT extends aminoacyl acceptor ends of serine tRNAs to control Mycobacterium tuberculosis growth. Xu X, et al. ***Nature Communications,*** 2024

One-stop Shop for All the Services You Need

Microarray Solutions

- Epitranscriptomic Array Service
- m6A Single Nucleotide Array Service
- Small RNA Modification Array Service ***NEW !***
- Circular RNA Array Service
- LncRNA Array Service
- Downstream-of-Gene Transcript (DoG RNA) Array Service ***NEW !***
- Super-enhancer LncRNA Array Service
- T-UCR Array Service
- GlycoRNA Array Service ***NEW !***
- Small RNA Array Service
- piRNA Array Service

Next-Gen Sequencing Solutions

- RNA Sequencing
- miRNA Sequencing
- tRNA Sequencing
- tRF&tiRNA Sequencing
- eccDNA Sequencing ***NEW !***
- DRIPc-sequencing ***NEW !***
- MeRIP-sequencing
- (h)MeDIP-sequencing with LncRNA Promoter Analysis
- ChIP-sequencing

ncRNA PCR Arrays

- nrStar ™ Functional LncRNA PCR Arrays
- miRStar ™ Canonical Conserved microRNA PCR Array
- nrStar ™ tRNA PCR Arrays
- nrStar ™ tRF & tiRNA PCR Arrays
- nrStar ™ snoRNA PCR Arrays

mRNA PCR Arrays

- NuRNA ™ tRNA Modification Enzymes PCR Array
- NuRNA ™ Small RNA Biogenesis Proteins PCR Array
- NuRNA ™ Epitranscriptomics PCR Array
- NuRNA ™ Central Metabolism PCR Array

GO BEYOND RNA
ARRAYSTAR INC

Contact Us

Call: 888-416-6343
Email: info@arraystar.com
www.arraystar.com