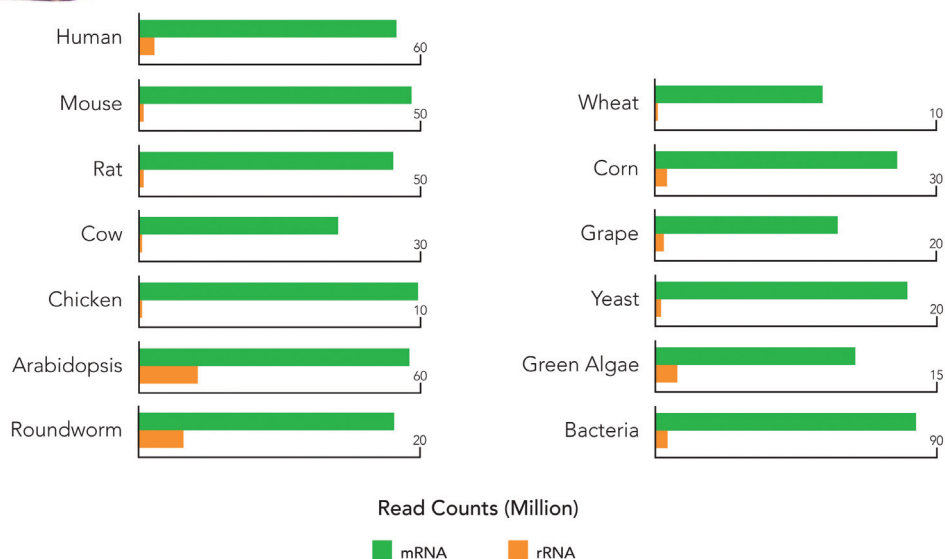


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The Zymo-Seq RiboFree® Kit Produces Dense Coverage of Protein Coding Genes. Classification of the STAR-aligned reads was based on Ensembl annotations and RepeatMasker rRNA tracks from UCSC genome browser when applicable.



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Arraystar Small RNA Modification Arrays

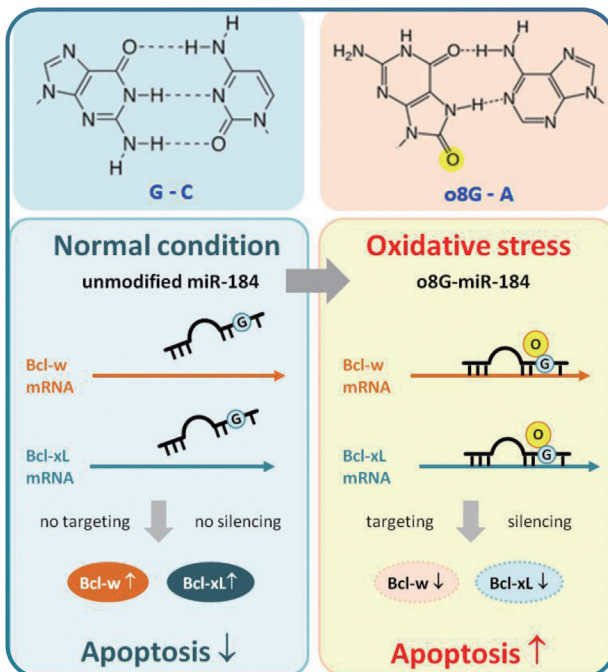
Quantifying Modifications in Small RNAs with High Sensitivity & Accuracy

- o8G/m7G/m6A/Ψ/m5C in miRNAs, pre-miRNAs & tsRNAs

Why Study Small RNA Modifications?

Small RNA modifications modulate the activities of small RNAs in diverse biological processes and play pivotal roles in pathological conditions. They can:

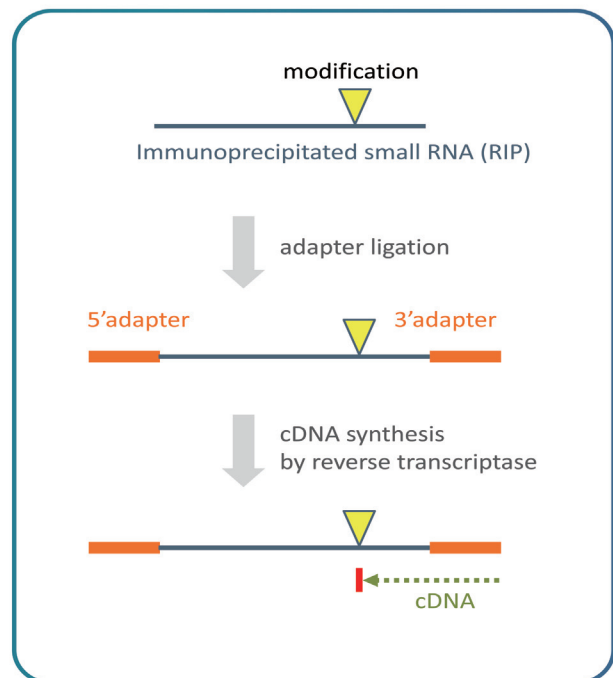
- Influence miRNA targeting
- Inhibit protein translation
- Serve as biomarkers



Oxidative modification of miR-184 enables it to target Bcl-xL and Bcl-w, based on Wang, J. X., et al. (2015) Mol Cell [PMID: 26028536]

Challenges to Quantify Small RNA Modifications Accurately

During small RNA MeRIP-sequencing library construction, the cDNA synthesis step is blocked by RNA modifications. It severely reduces the sequencing coverage and quantification accuracy.

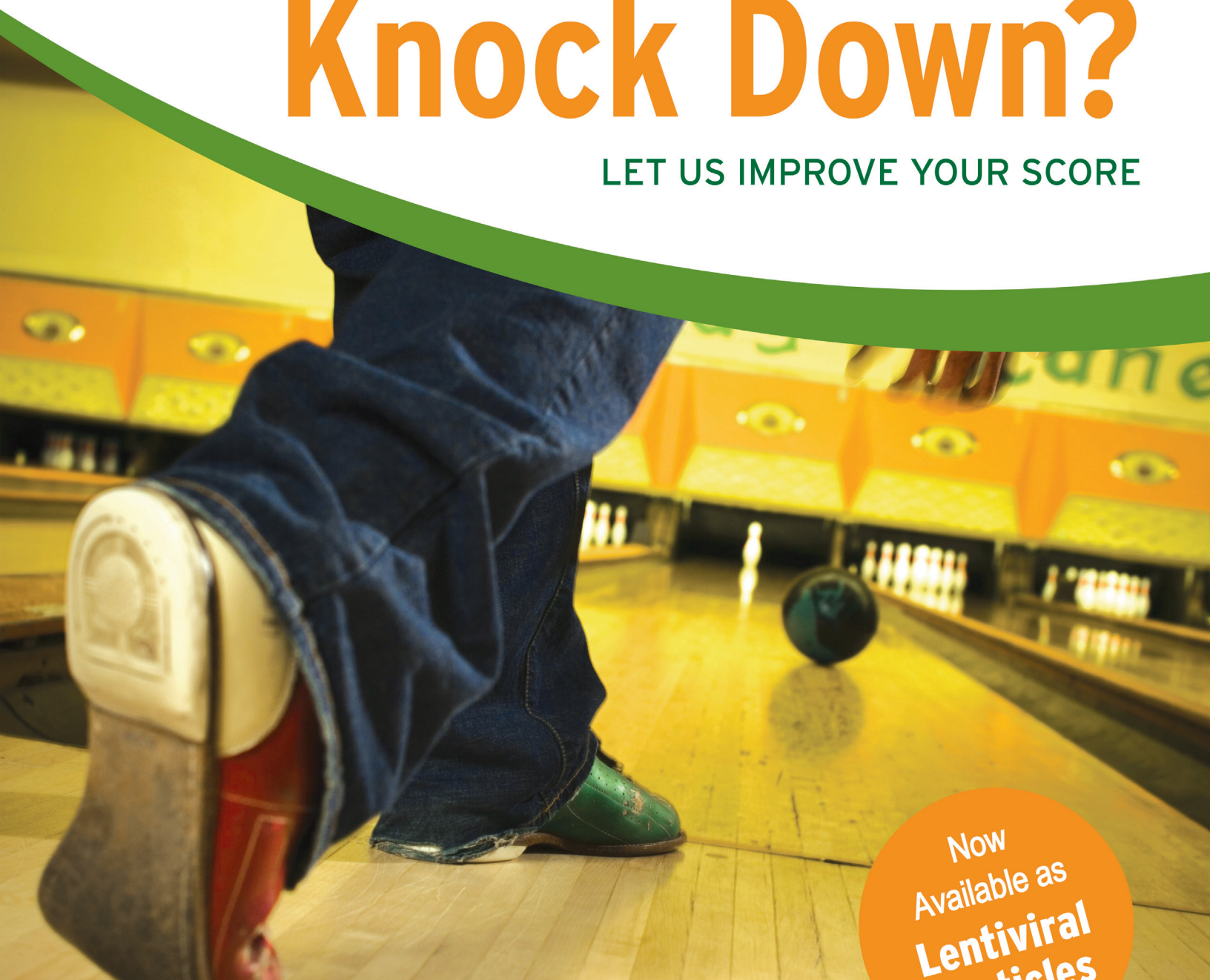


Non-Sequencing Based Solution: Small RNA Modification Arrays

- Gold standard for accurate quantification of modified small RNAs.
- One step direct labeling that eliminates the problems of RNA modifications blocking cDNA synthesis during RNA-seq library prep.
- No PCR to distort native RNA levels.
- Low sample amount requirements.
- Array coverage of multiple small RNA classes, including miRNAs, pre-miRNAs, and tsRNAs.

Looking for that Perfect Knock Down?

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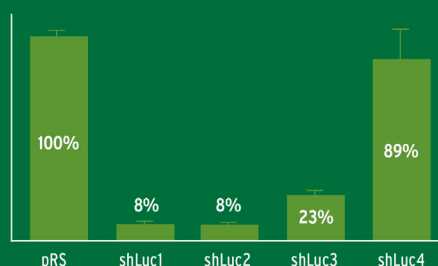


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HuSH-29 Validation



A reporter construct expressing luciferase was co-transfected into HEK293 cells with 4 HuSH-29 luciferase constructs or empty pRS vector control. Forty-eight hours post-transfection, the cells were examined for gene expression knockdown.

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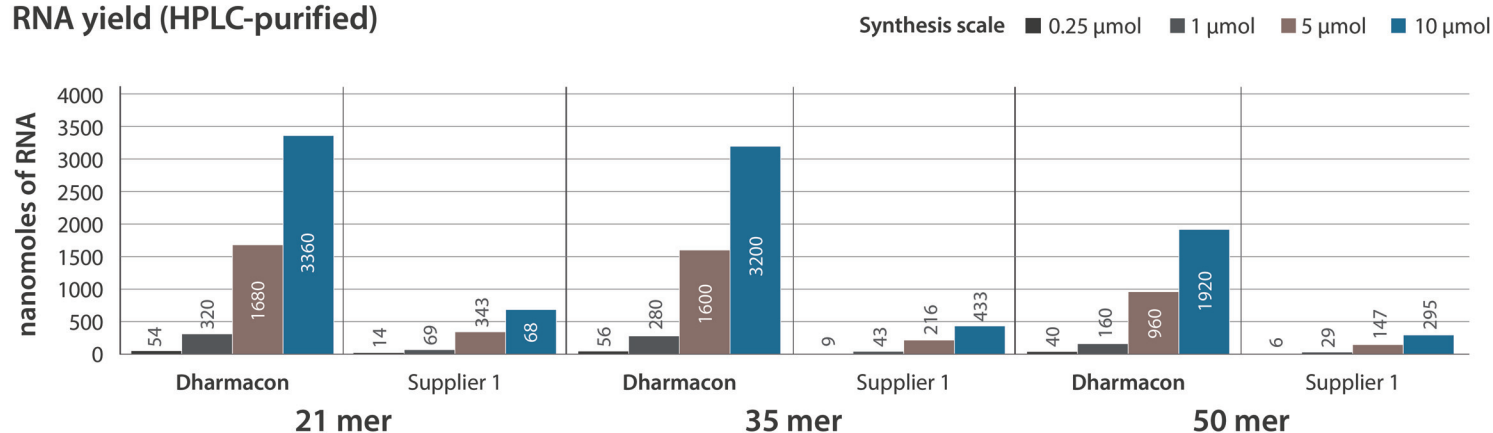
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RNA yield (HPLC-purified)



The yield for RNA oligos of three different lengths was compared for all available synthesis scales between Dharmacon and a competitor.