

Study m6A Modifications Like Never Before

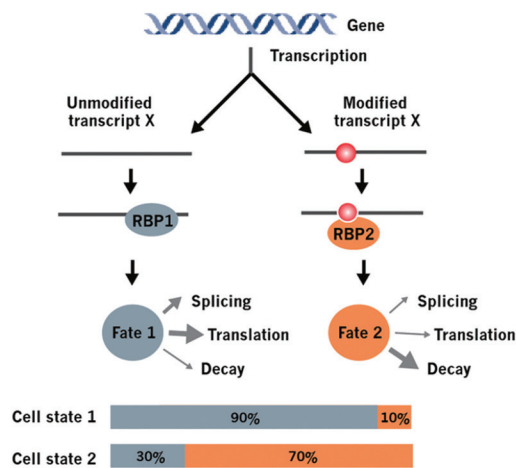


Fig. 1. m6A modified RNAs are immunoprecipitated and compared with the input RNAs in two-color channels of the Epitranscriptomic Array to accurately measure the modification percentage and abundance level for each transcript. The percentage of modification of “transcript a” RNA determines its different cell fates, e.g. for protein translation or RNA decay.

Epitranscriptomic Array

- Quantifying the percentage of modification for each transcript
- Coverage of mRNAs, lncRNAs, circRNAs and more
- RNA modifications at transcript-specific level
- Low sample amount, starting from 1 ug total RNA

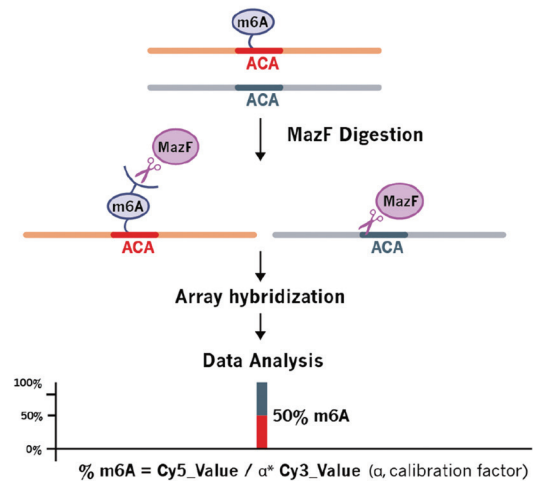


Fig. 2. Unmethylated (ACA) sites, but not methylated (m6ACA) sites, are cleaved by RNase MazF. The MazF treated and corresponding untreated sites are compared in two-color channels of the m6A Single Nucleotide Array to accurately quantify the m6A modification percentage, and abundance level at precise single nucleotide resolution.

m6A Single Nucleotide Array

- A new orthogonal methodology for m6A detection
- Single-Nucleotide resolution for m6A site location
- Quantifying the percentage of m6A site modification
- Reliable m6A site collection and systematic annotations
- Low sample amount, starting from 1 ug total RNA



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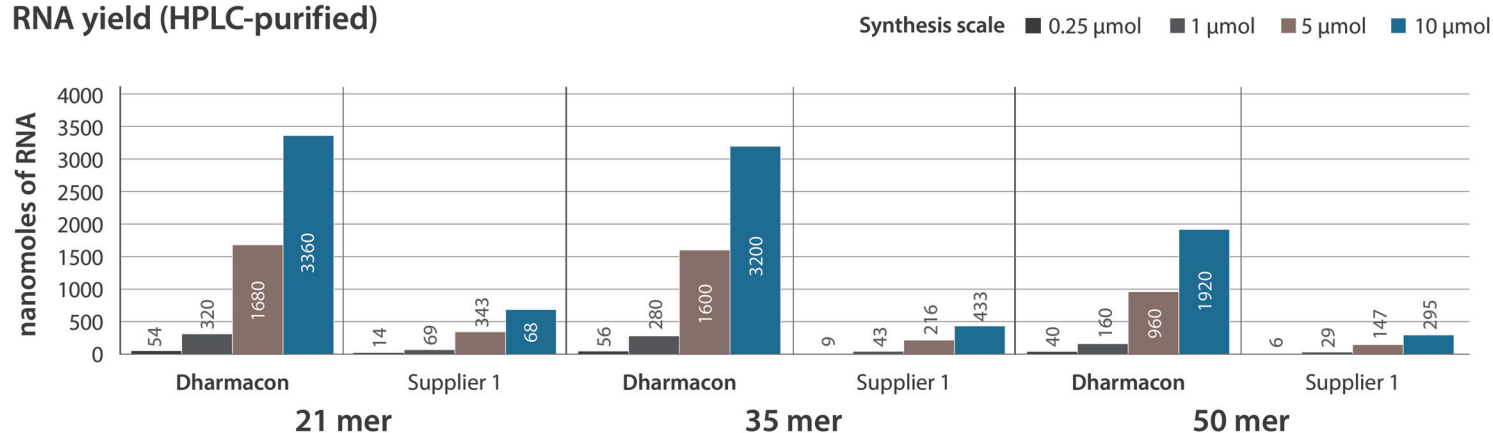
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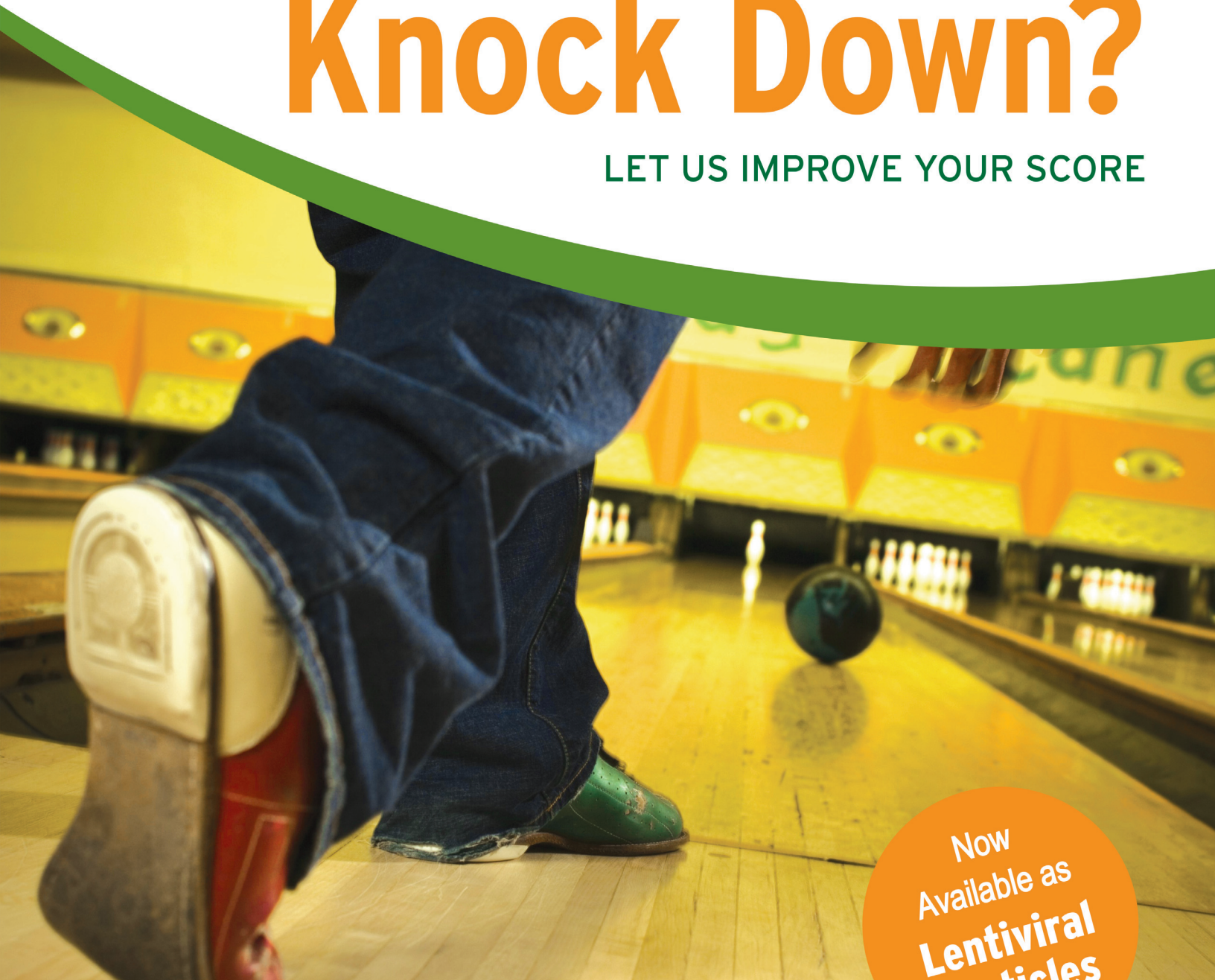
RNA yield (HPLC-purified)



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

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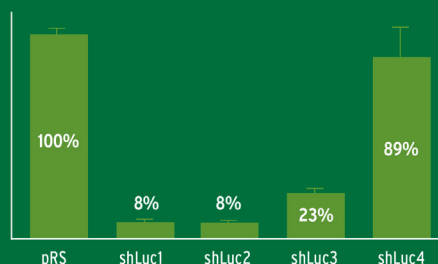


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A reporter construct expressing luciferase was co-transfected into HEK293 cells with 4 HuSH-29 luciferase constructs or empty pRS vector control. Forty-eight hours post-transfection, the cells were examined for gene expression knockdown.

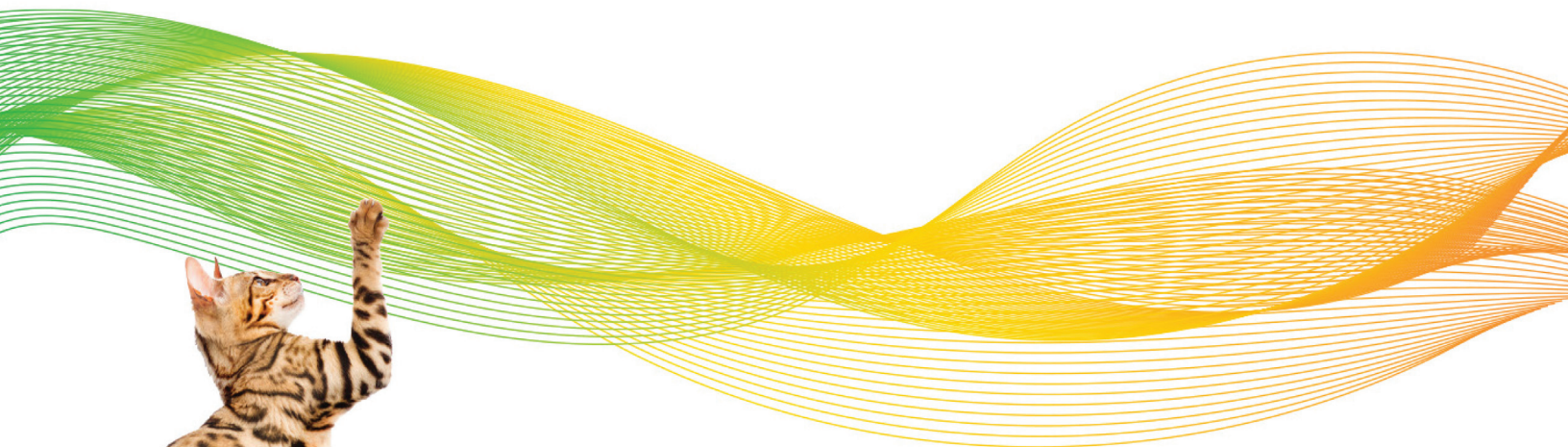
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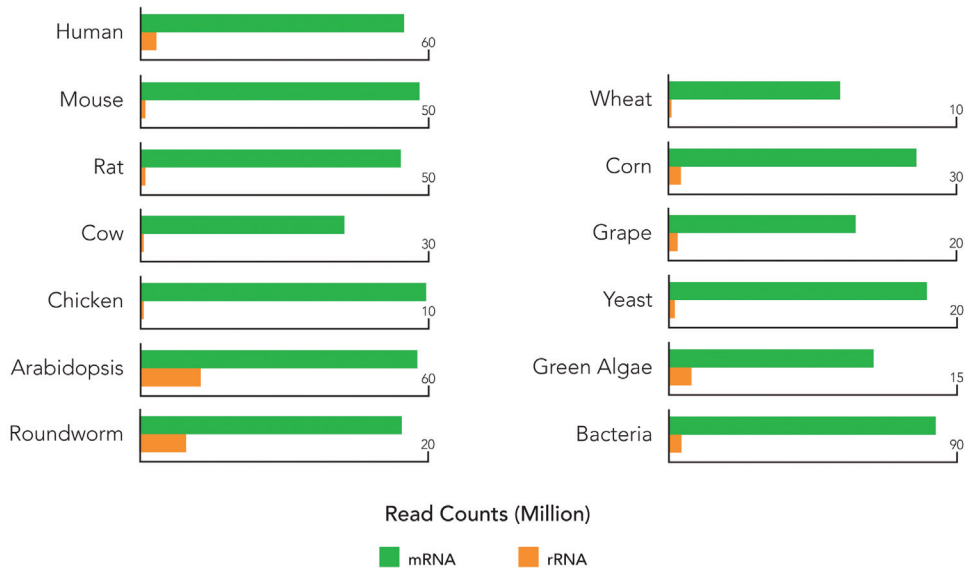


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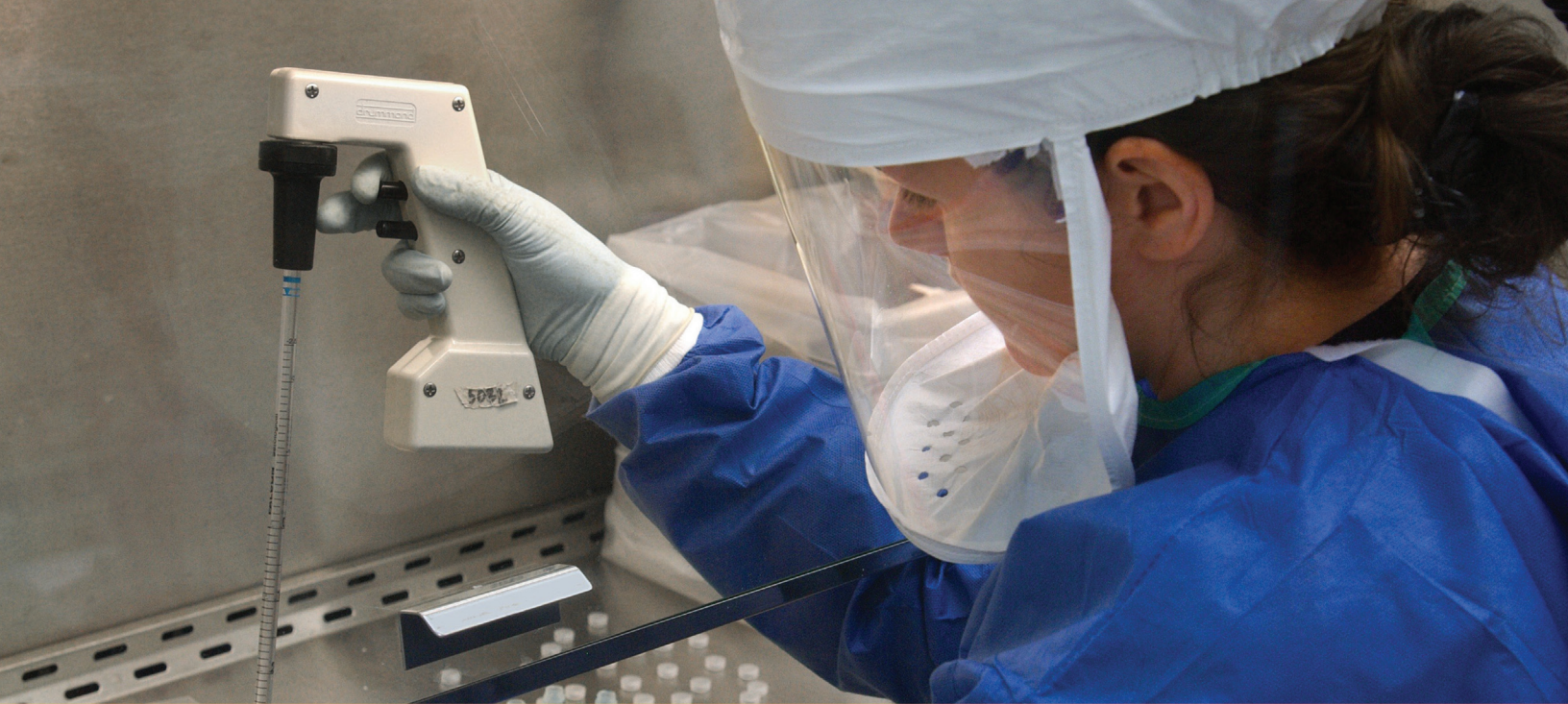
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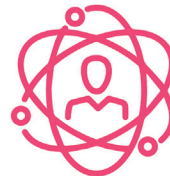
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