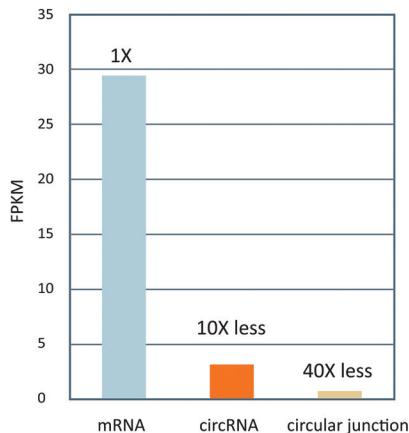


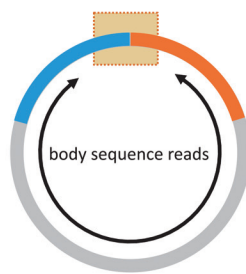
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Challenges of CircRNA Profiling



circular junction reads



Circular RNAs are expressed at $\sim 1/10$ the mRNA level. Circular junction reads (yellow box) accounting for only a fraction of the circular RNAs are even less, at $\sim 1/40$ of mRNA level.

Example: hsa_circ_0054254

circRNA study	Sample	circular junction reads
Rybak2015	frontal_cortex	3
	parietal_lobe	7
	diencephalon	2
Salzman2013	K562	3
	Gm12878	13
	Sknshra	1
	H1hesc	3
	Helas3	2
	Huvec	0
	A549	3
	Ag04450	1

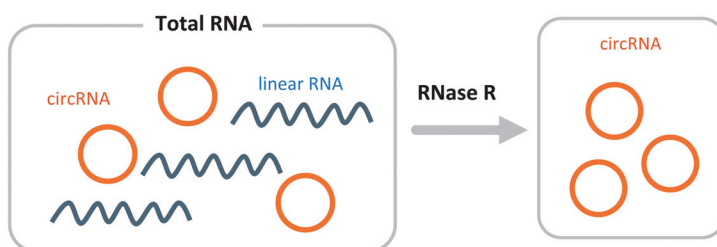
Only a few circular junction counts could be observed in deep sequencing, far below the limit of quantification [Szabo and Salzman (2016) Nat. Rev. Genet. PMID: 27739534].

Arraystar circRNA Arrays Power 500+ Publications

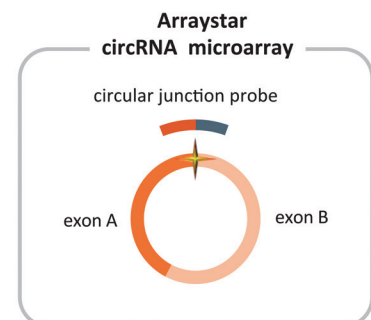


[View the publications](#)

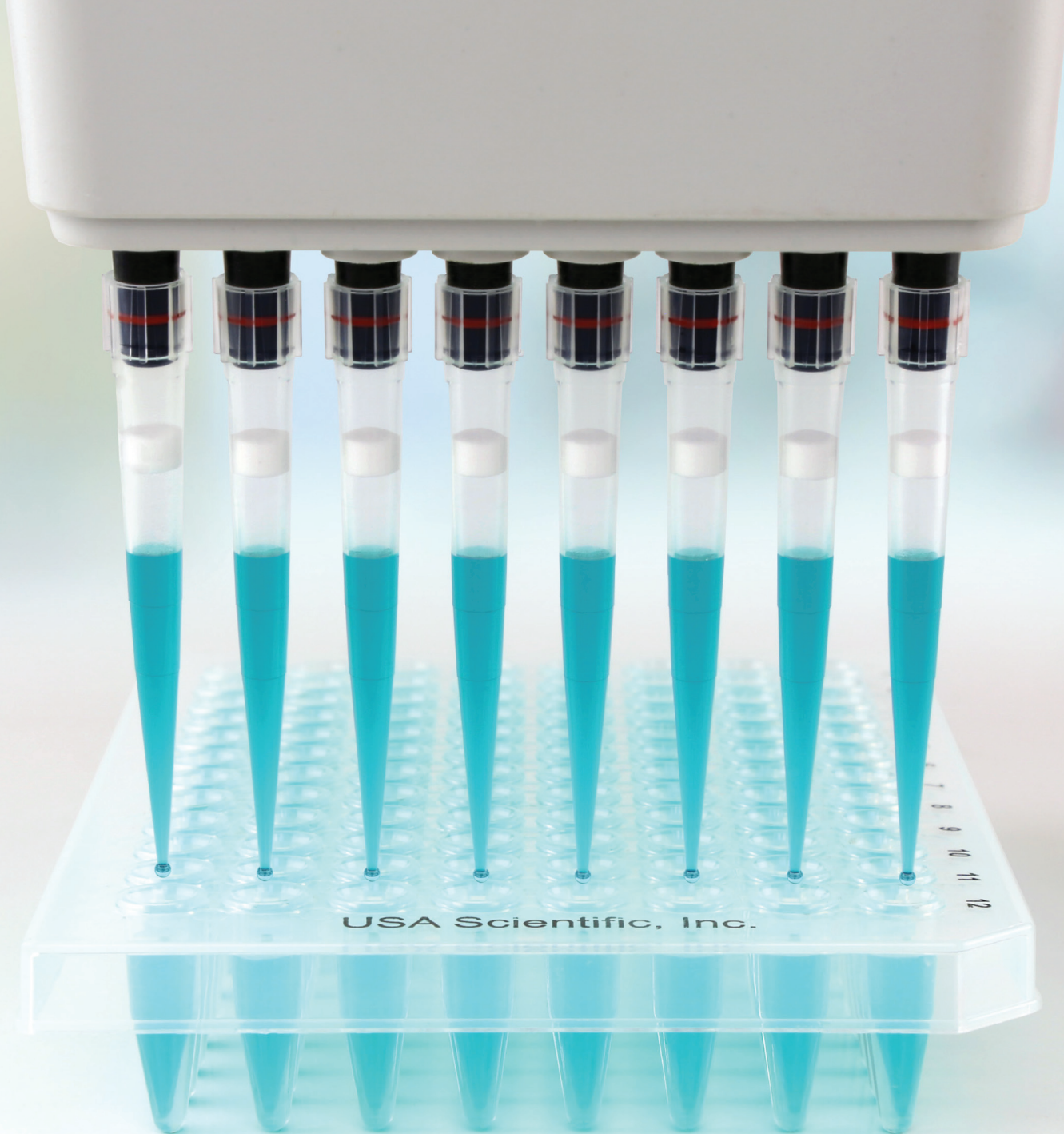
- Overcome the challenges of circRNA profiling by sequencing
- Unique circular junction array probes to specifically and accurately profile circRNAs
- Enhanced sensitivity and specificity by RNase R treatment to remove linear RNAs
- Easy and straight forward analysis with detailed annotations for circRNA biology



circRNA enrichment from total RNA by RNase R treatment



Unique circular junction probe for specific circRNA detection



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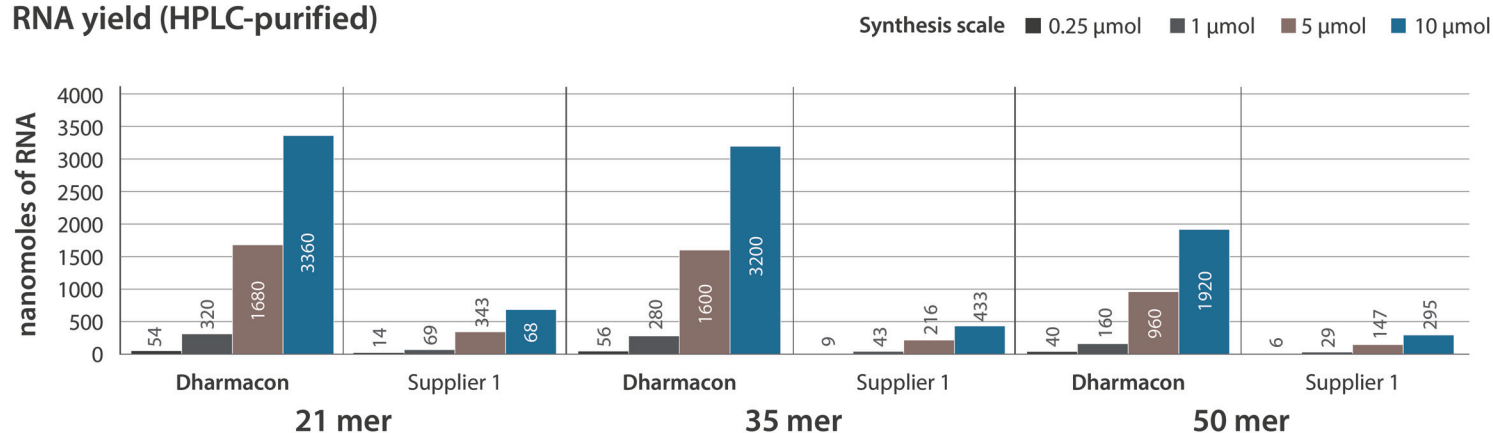
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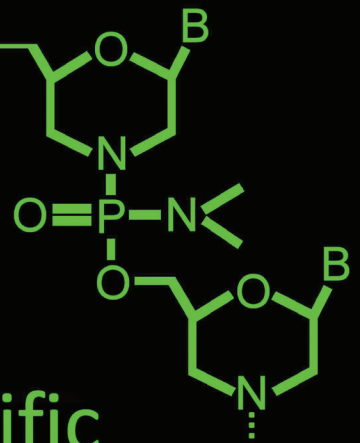
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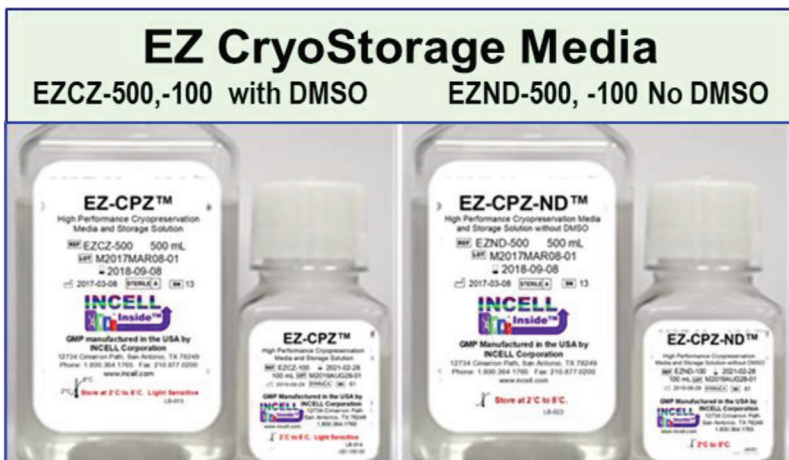
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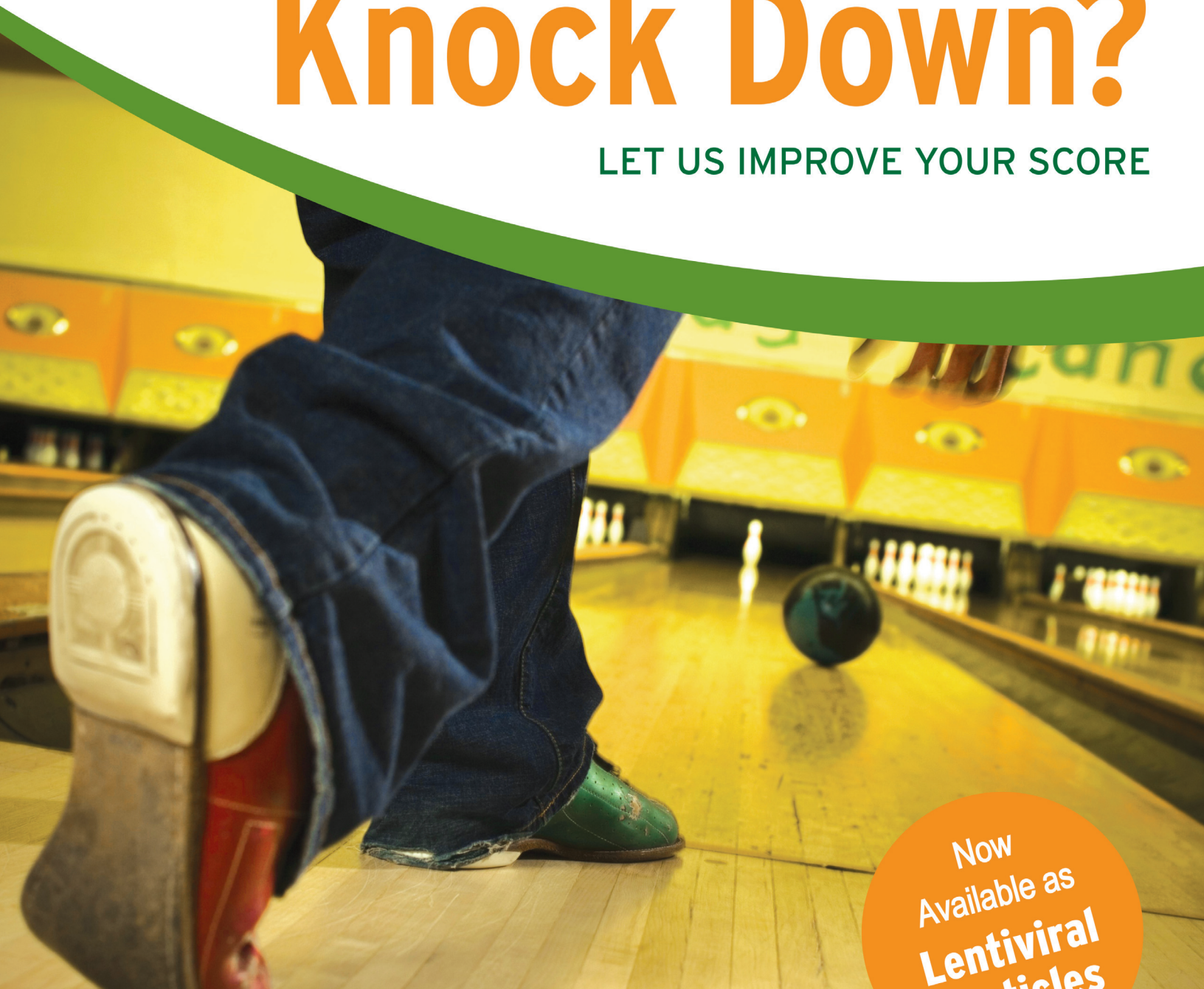


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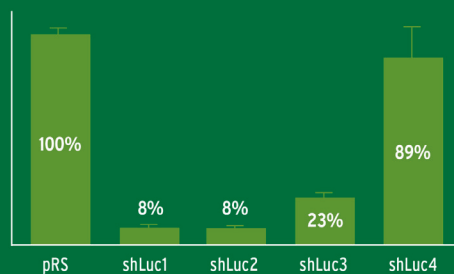


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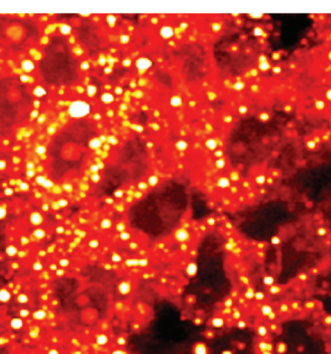
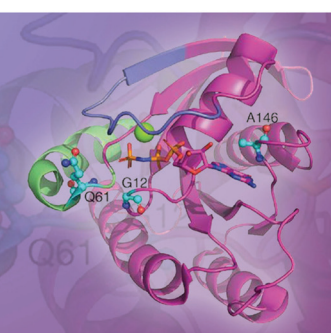
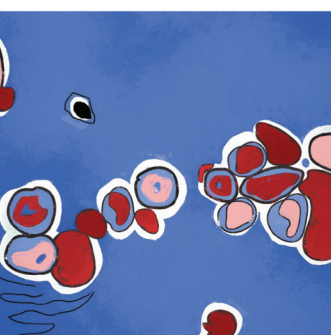
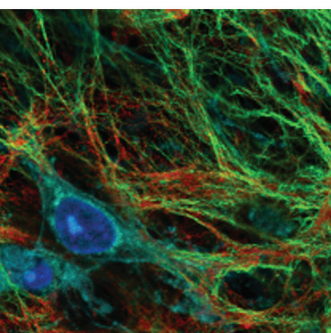
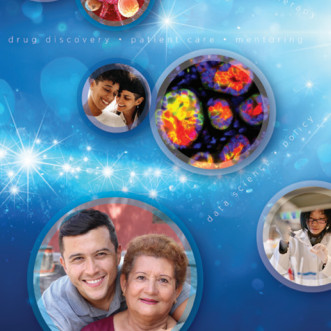
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A reporter construct expressing luciferase was co-transfected into HEK293 cells with 4 HuSH-29 luciferase constructs or empty pRS vector control. Forty-eight hours post-transfection, the cells were examined for gene expression knockdown.

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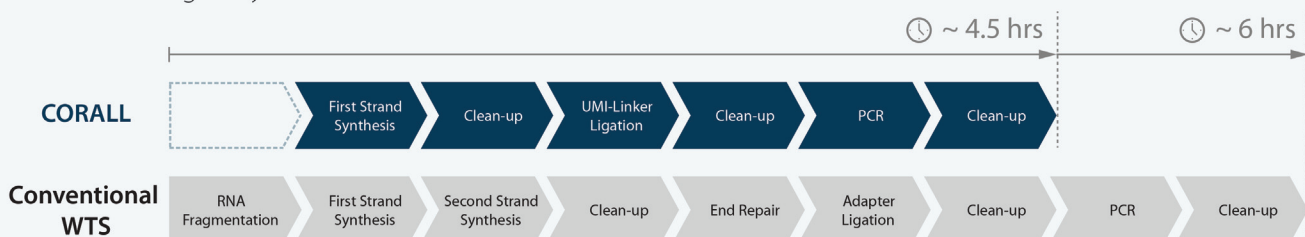
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