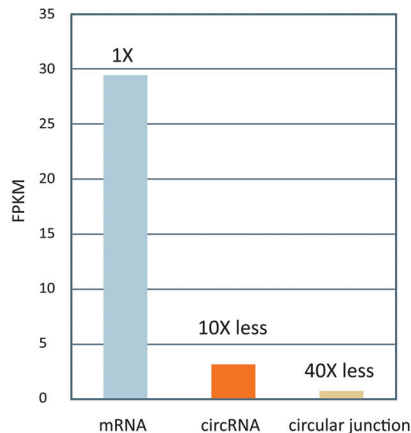


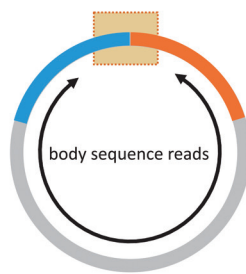
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## Challenges of CircRNA Profiling



circular junction reads



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                       |

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.

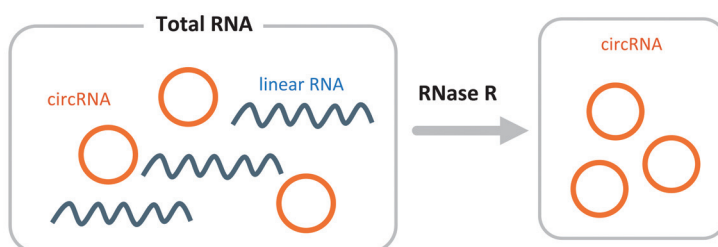
Only a few circular junction counts could be observed in deep sequencing, far below the limit of quantification [Szabo and Salzman (2016) Nat. Rev. Genet. PMID: 27739534].

## Arraystar circRNA Arrays Power 500+ Publications

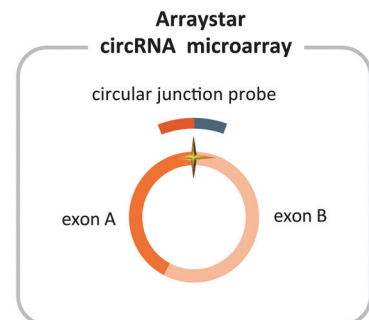


[View the publications](#)

- 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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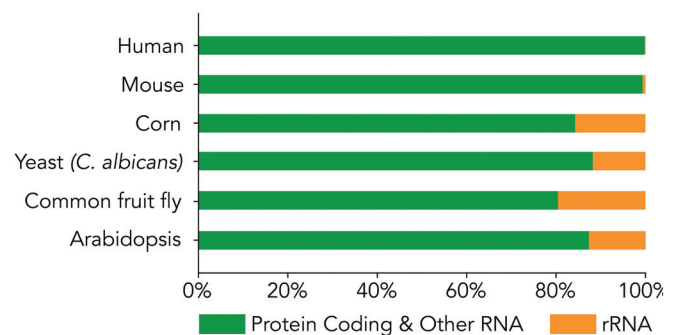
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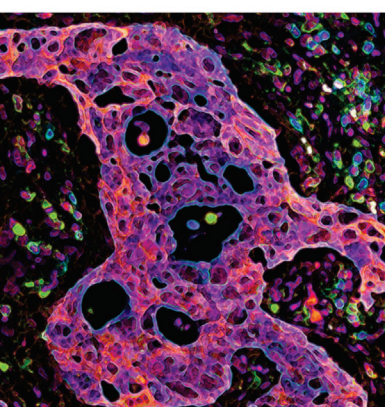
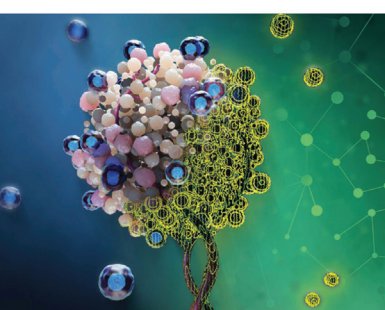
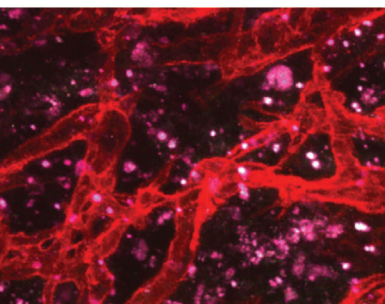
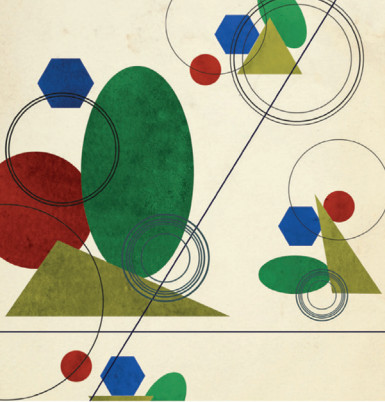
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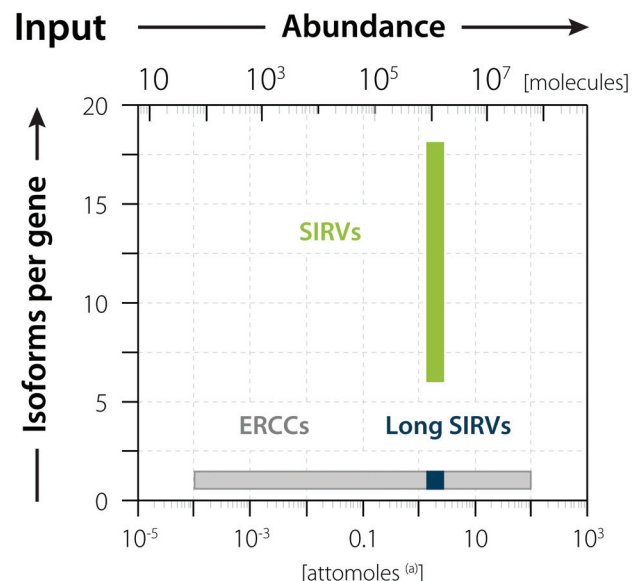


Figure 1 | Isoform and abundance complexity. The SIRV isoform and ERCC transcripts control for the two main dimensions of transcriptome complexity: isoforms and abundance. The Long SIRVs module additionally contains controls for length complexity.

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