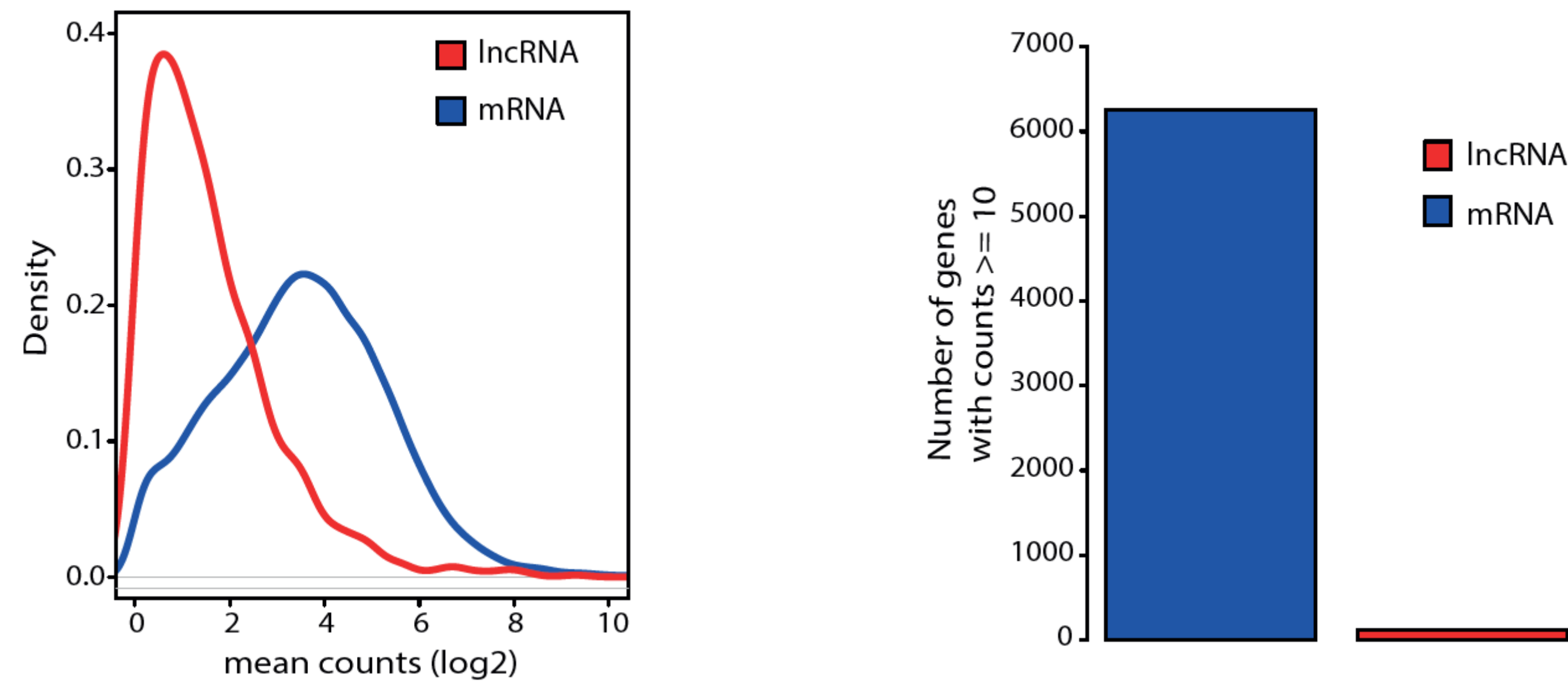


# A 3'-end capture sequencing method for high-throughput targeted gene expression profiling

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## Problem statement

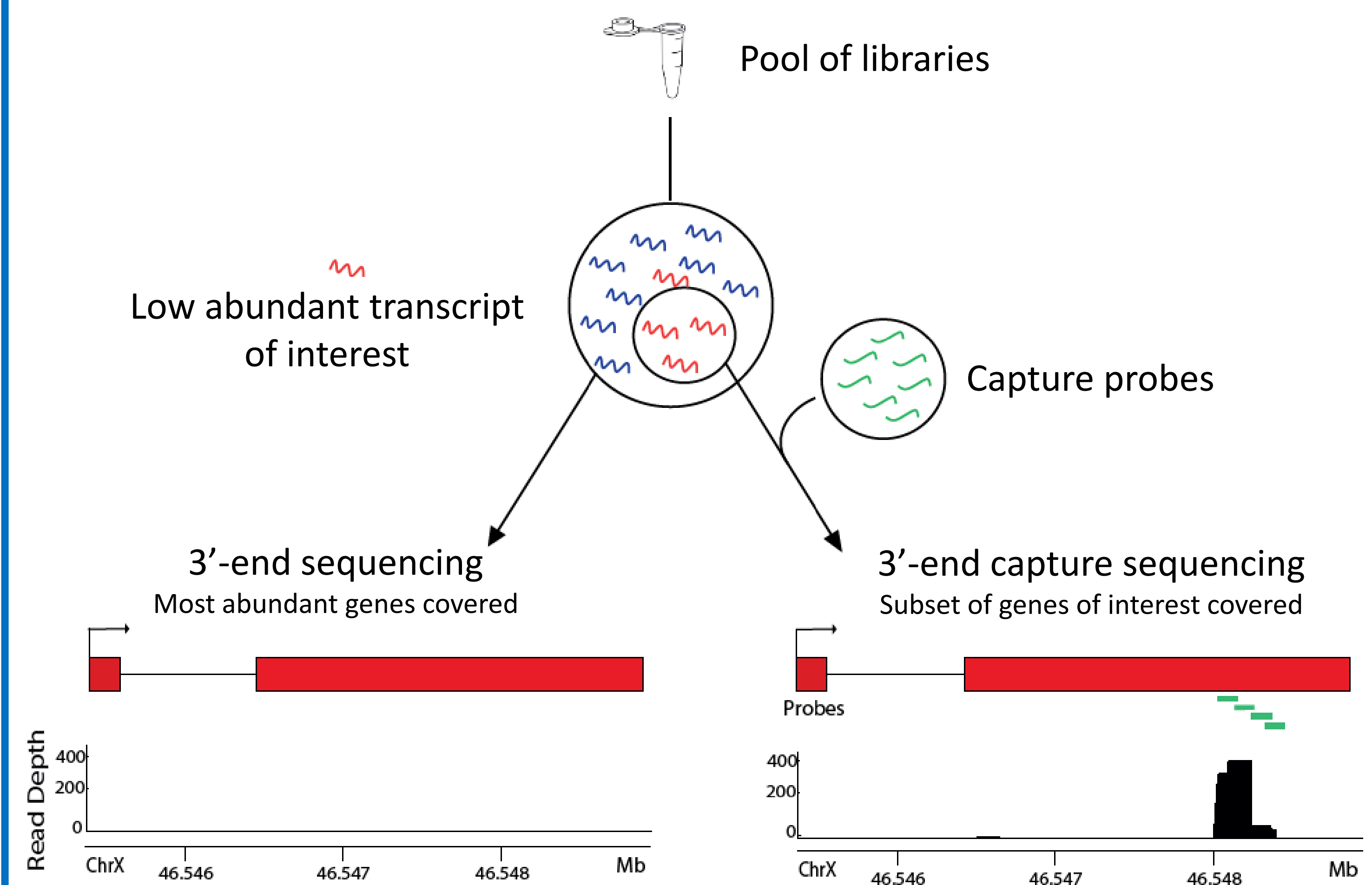
Most of the reads in RNA-sequencing are consumed by the most abundant genes, mostly messenger RNA (mRNA).



## Aims

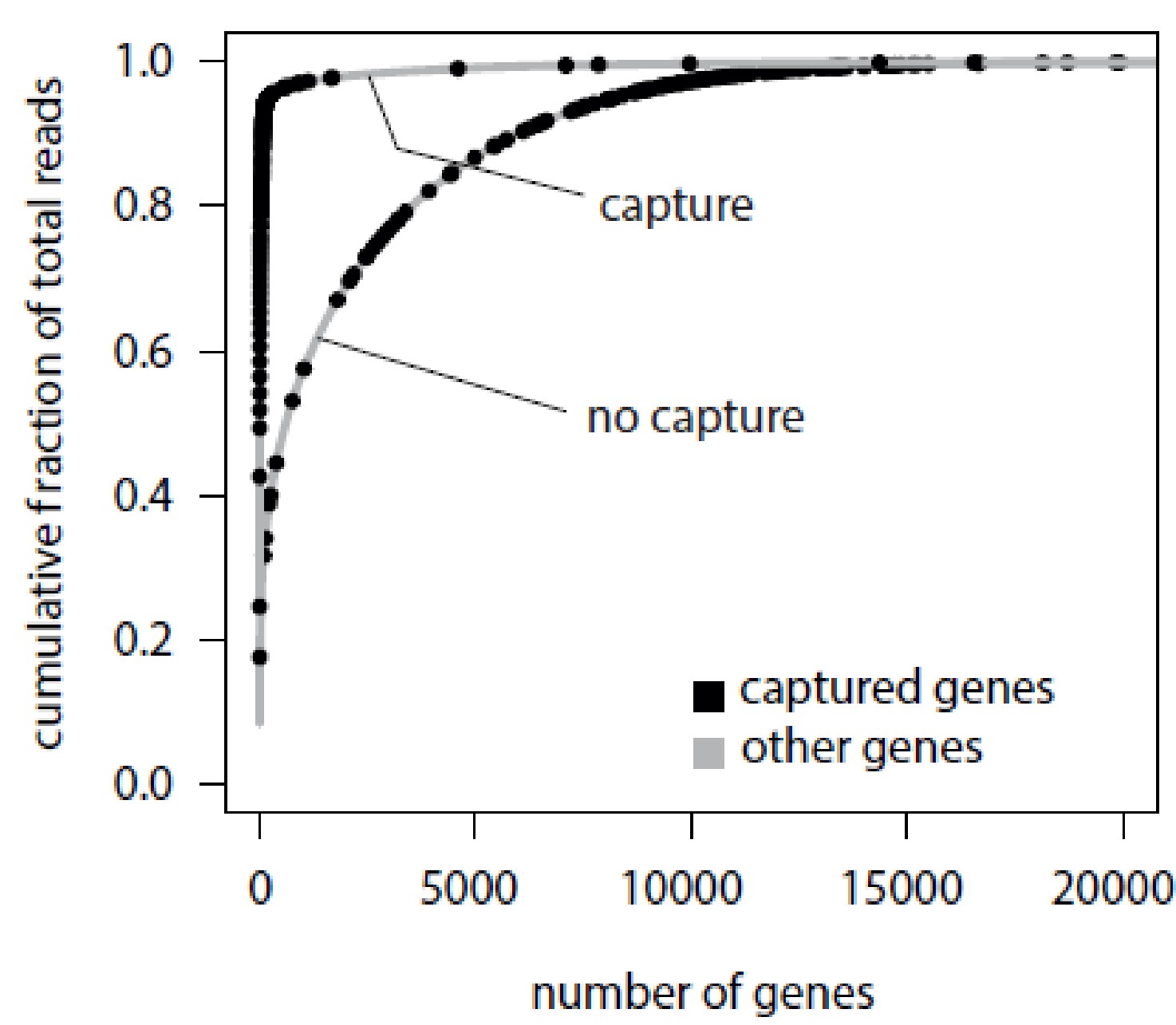
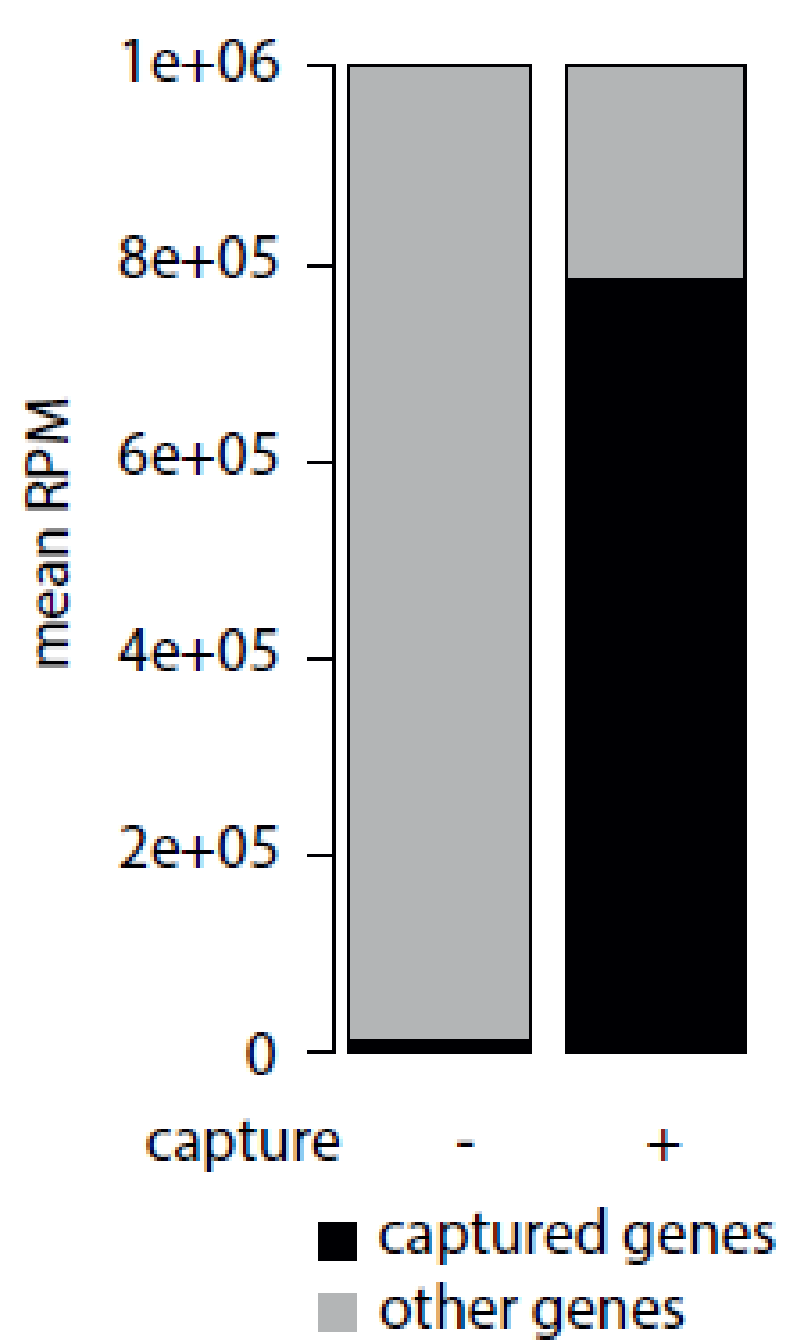
Develop a method to enrich low abundant genes, like long non-coding RNAs (lncRNAs), in 3'-end RNA-sequencing libraries.

## Method

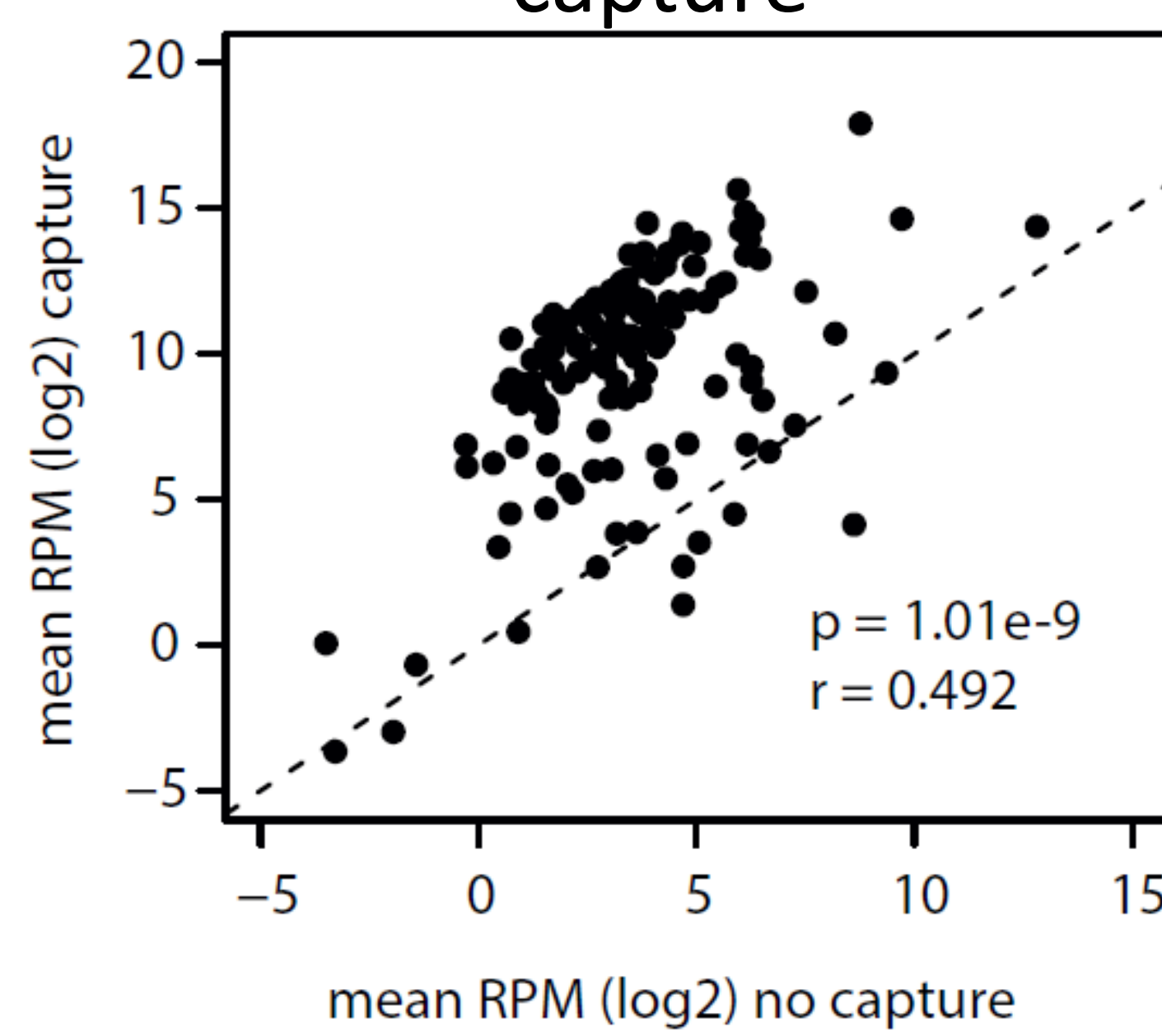


## Results

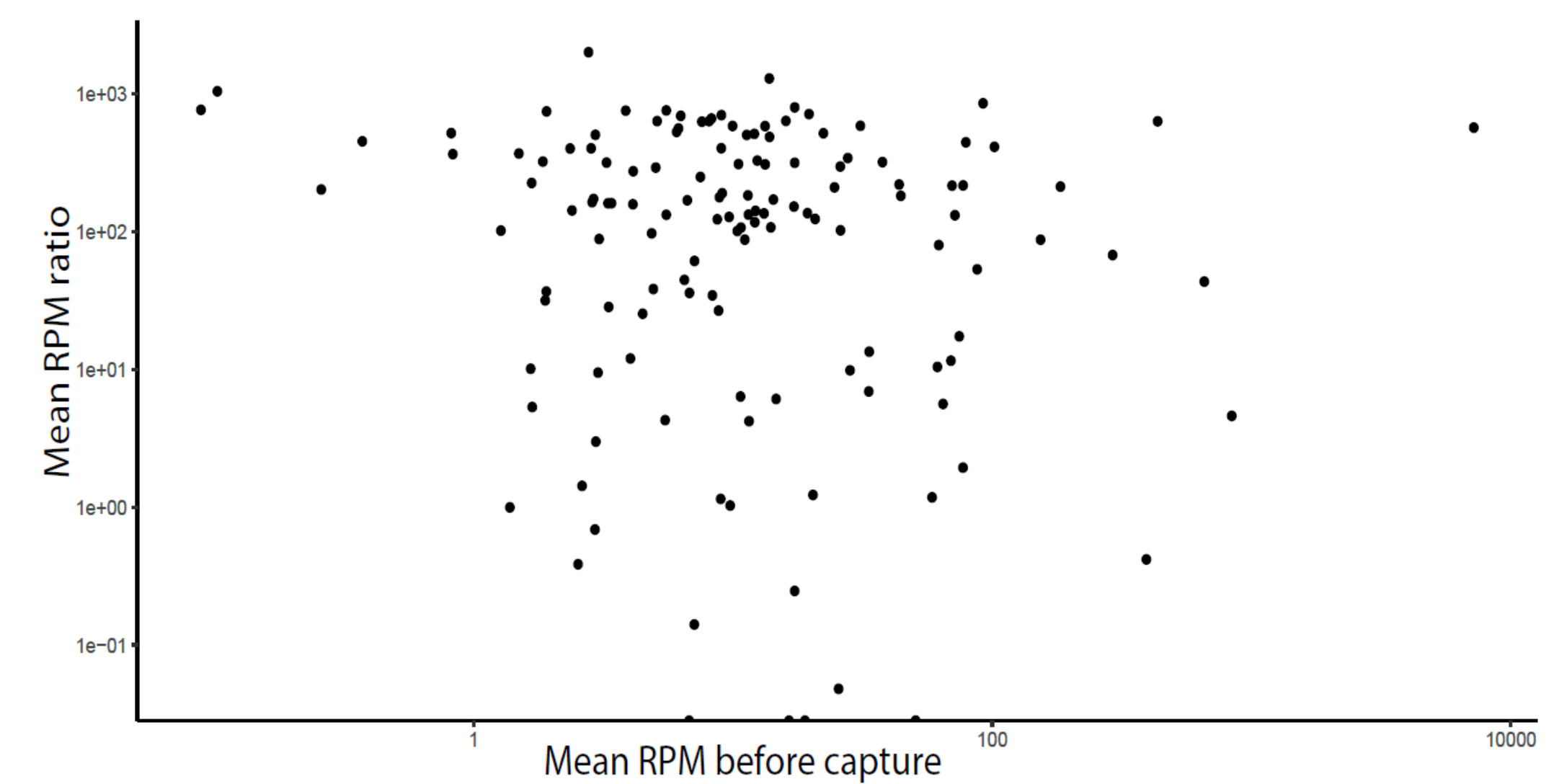
80% of reads are allocated to targets upon capture



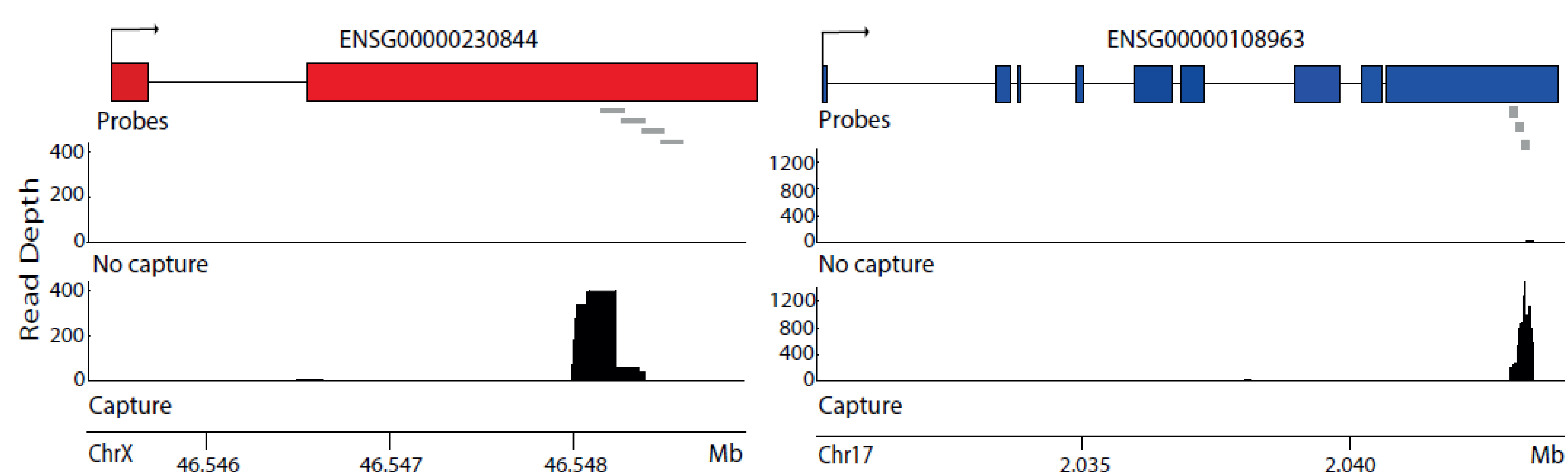
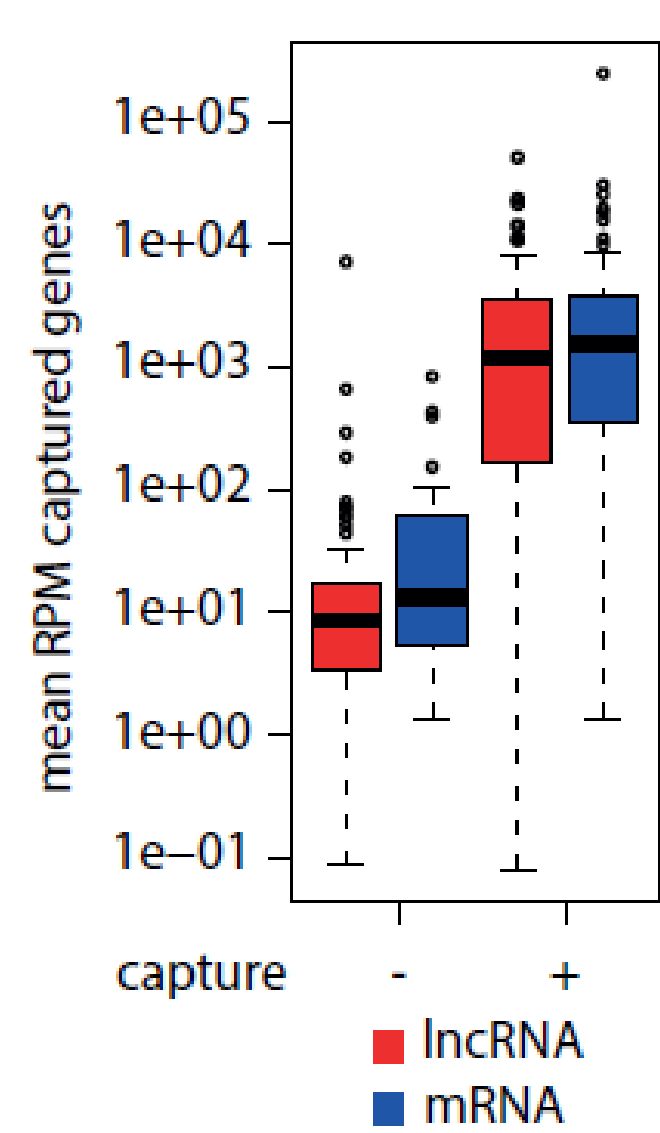
Good correlation of gene expression before and after capture



Capture efficiency is independent of initial transcript abundance

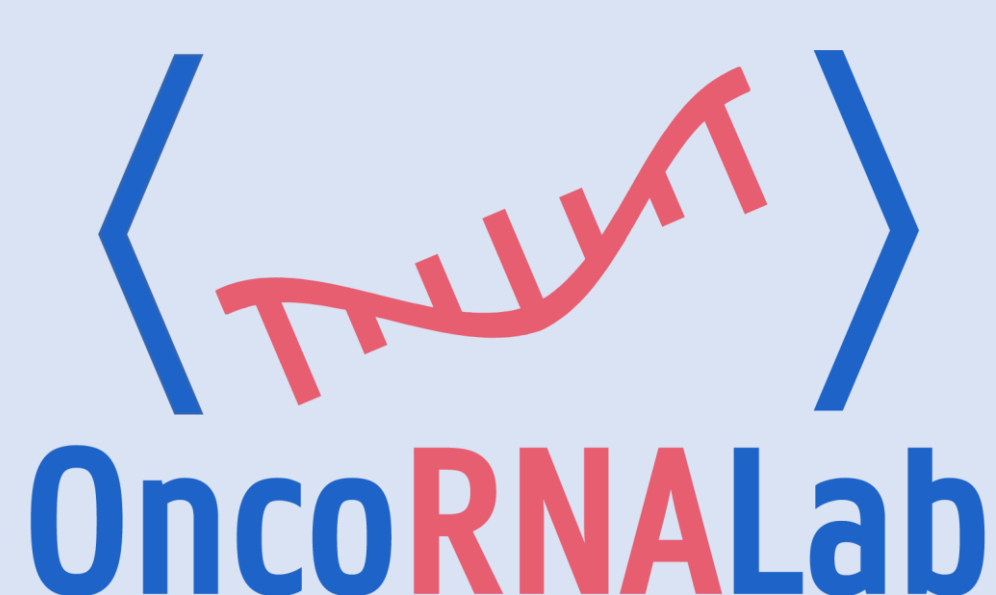


Capture provides a 100-fold coverage enrichment, independent of target biotype



## Contact

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## Conclusions

- 3'-end capture sequencing efficiently enriches low abundant targeted isoforms
- Capture efficiency is similar for coding and non-coding genes
- Targeted 3'-end capture sequencing enables a 100-fold sequencing depth reduction, and thus a reduction in sequencing costs
- Capture sequencing maintains inter-gene and inter-sample gene abundance differences

