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PROTEIGENE

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dolomite
bio

RNA^{dia}

for single cell and single nucleus
sequencing on the Nadia platform

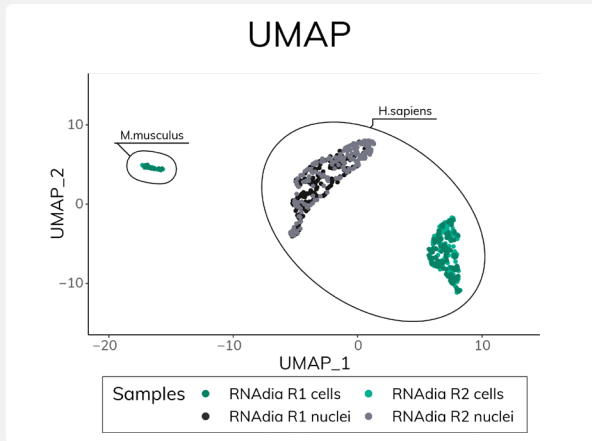


50% lower

reagent costs
compared to
competitors

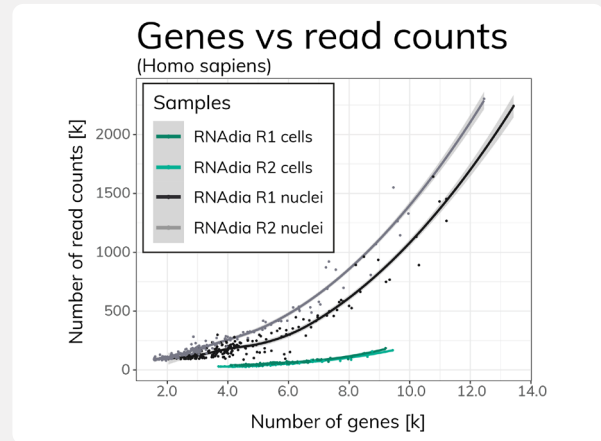


High quality



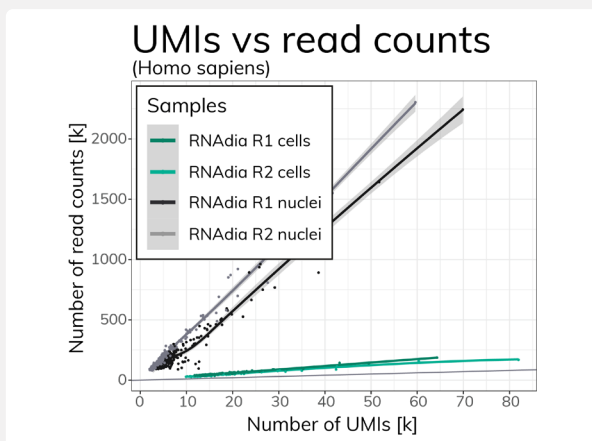
UMAP of RNAAdia cell and nuclei datasets

Mixed species datasets from cells (shades of green) and human datasets from nuclei (grey and black) were clustered in a two-dimensional space using UMAP. As expected, cells clustered into two distinct groups for human HEK293T and mouse 3T3 cell lines for cell datasets with a high overlap of the biological replicates. Human datasets from nuclei formed a distinct cluster with a high overlap of the cell replicates.



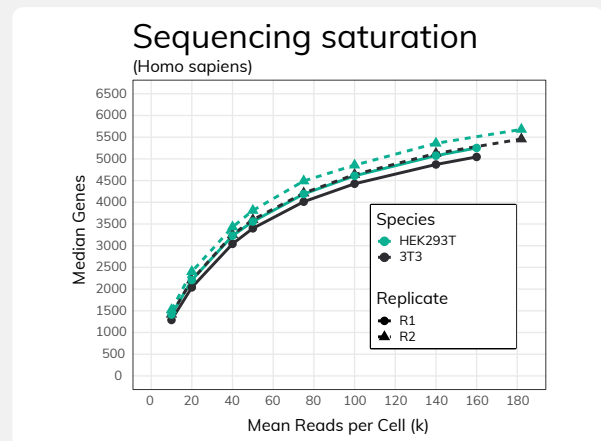
High gene capture for cells and nuclei

The number of detected genes was plotted against read depth across two biological replicates for both cell and nuclei datasets. Efficient gene capture was observed even at low sequencing depth, reducing cost for NGS analysis.



Efficient transcript capture for cells and nuclei

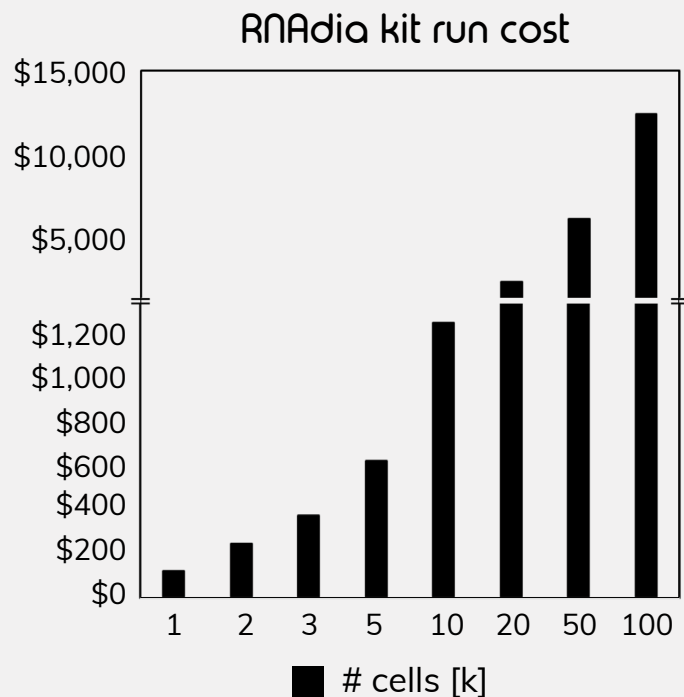
The number of detected UMIs (transcripts) was plotted against read depth across two biological replicates for both cell and nuclei datasets. Efficient UMI capture was observed even at low sequencing depth, reducing cost for NGS analysis.



Sequencing saturation plot

Median number of genes per cell as a function of the read depth per cell for RNAAdia libraries. Human HEK293T and mouse 3T3 cell lines were analyzed and were found to contain high RNA content compared to primary cell samples.

Low cost



Complete solution



Sample preparation

1



Single cell/nucleus library
construction on Nadia

2



Sequencing

3



Data analysis
& visualization

4

Following sample preparation, single cell libraries for sequencing of cellular transcripts are constructed on Nadia using the RNAia kit. The Nadia is an automated, microfluidic droplet-based platform for single cell research that encapsulates up to 8 samples, in parallel, in under 20 mins and captures over 50,000 cells in a single run. The RNAia kit allows for the construction of sequencing ready libraries. Those libraries are compatible with standard NGS short-read sequencing on Illumina sequencers, allowing analyses of thousands of transcriptional profiles of single cells in parallel. The resulting transcriptomic data can be analyzed using open-source pipelines or using our in-house service for data analysis. A similar workflow is available to process single nuclei.

Get in touch

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