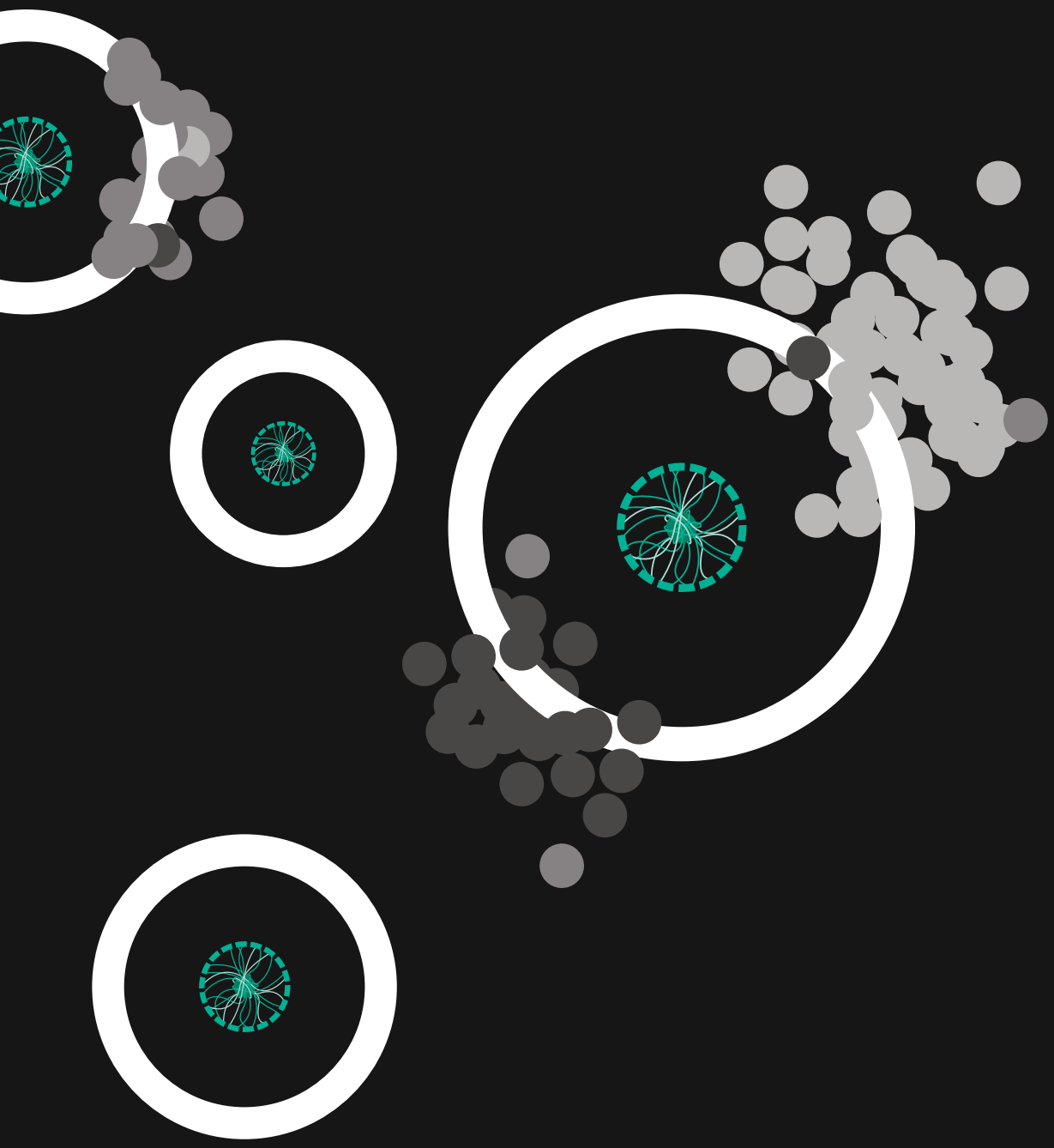
Single nuclei RNA-Seq using the Nadia Instrument



dolomite bio

sNuc-Seq on Nadia

Single nuclei RNA-Seq allows researchers to profile gene expression in difficult to isolate cells as well as archived tissue. To enable this application, Dolomite Bio has established high throughput sNuc-Seq on the Nadia Instrument.

Highlights

High gene capture
Low doublet rate
High correlation between sNuc-Seq and scRNA-Seq
Cost-effective single nuclei analysis
High purity of isolated nuclei

Multiple applications

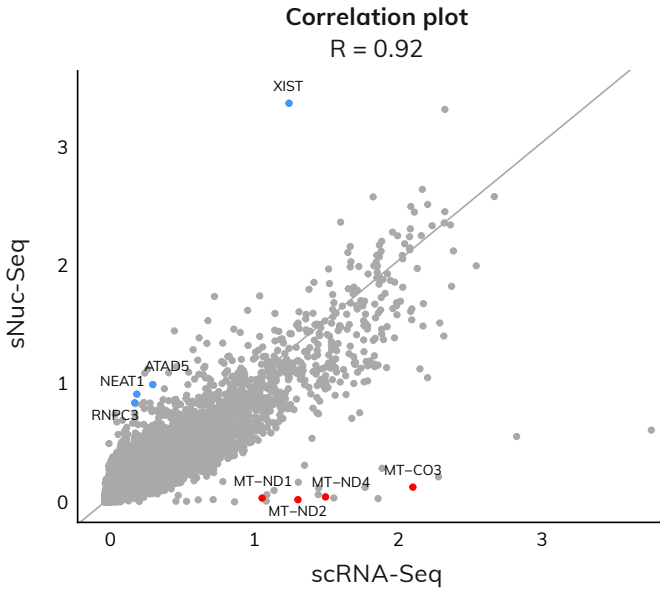
Archived Tissue
Neurobiology
Plant Biology
Cancer Biology

Data sets

Dataset	NGS reads per nuclei	Median Genes	Median UMIs
Nadia in-house R1	86,761	2,420	4,397
Nadia in-house R2	88,348	1,714	2,804
Nadia external R3	86,967	2,041	3,546
Habib R1	54,424	1,226	1,831
Habib R2	50,580	1,528	2,352

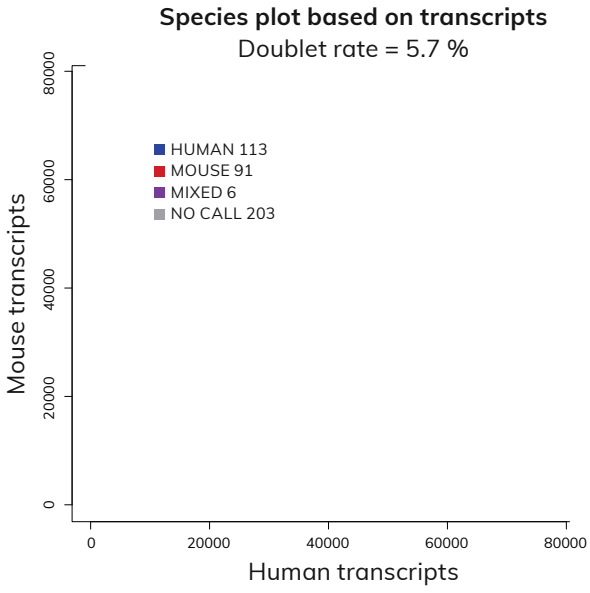
Three independent sNuc-Seq datasets were generated in-house and externally on Nadia and compared to data published by Habib *et al.* 2017. Numbers of genes and UMIs detected were comparable across datasets.

High correlation between sNuc-Seq and scRNA-Seq

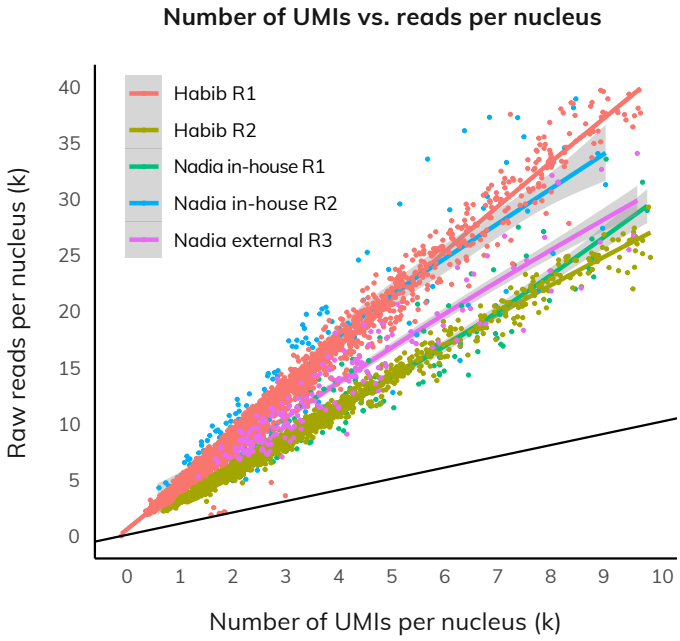


A high correlation between average gene expression of single nuclei and single cells can be observed. Marker genes specifically enriched in cells (red) and nuclei (blue) can clearly be distinguished.

Single nuclei sequencing with low doublet rate



Species mixing experiments were performed to estimate the doublet rate and level of cross-contamination. The Barnyard-plot shows the number of human and mouse transcripts associated with a nuleus, indicating truly single nuclei data.

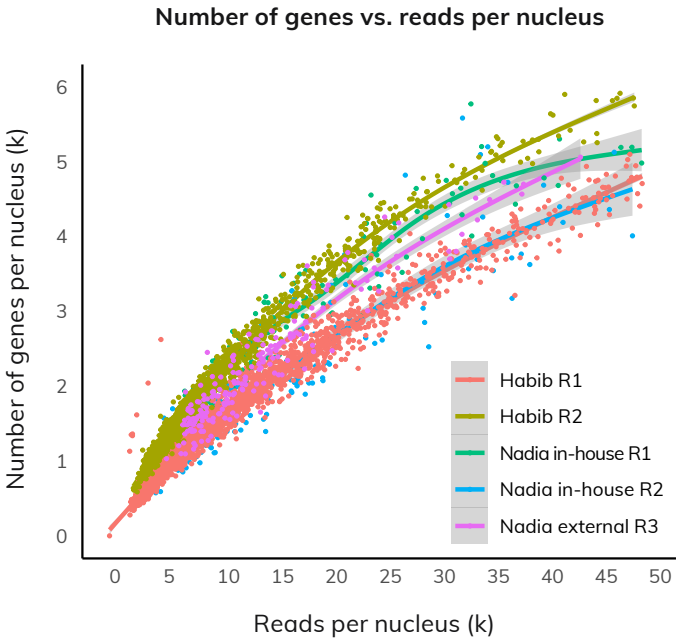


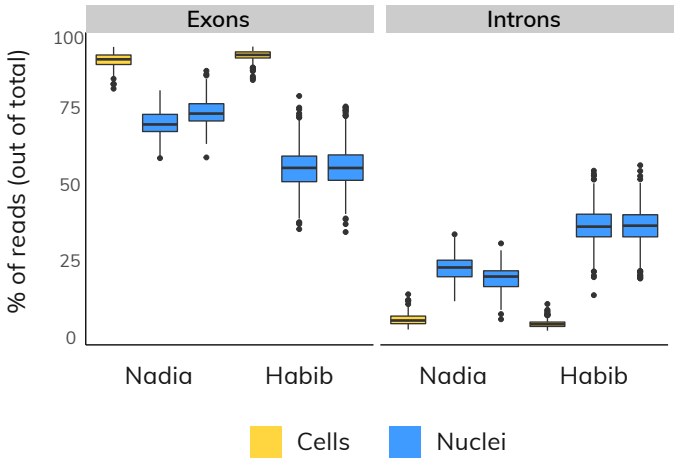
Low PCR duplication rate for cost-effective NGS analysis

On average, 3,500 UMIs (transcripts) were detected per nucleus. The black line represents the ideal ratio of 1 UMI per 1 read, indicating no PCR duplicates. All datasets align closely to this threshold highlighting a low duplication rate during PCR amplification.

Efficient gene capture for cost-effective single nuclei analysis

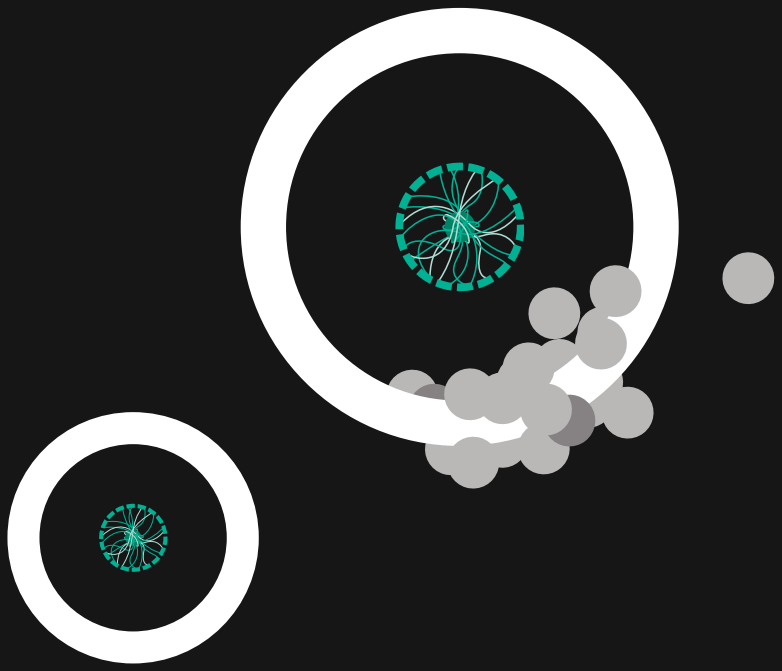
On average, ~2,000 genes were captured per nucleus. These values were consistent across all generated datasets and are similar to previously published data by Habib *et al.* 2017.





Ratio of intronic to exonic reads reflect the enrichment of nascent transcripts in the nucleus

When comparing scRNA-Seq and sNuc-Seq data, the percentage of exonic reads in cells (yellow) attributed to ~ 90% of the total reads, as opposed to nuclei, where exons contributed to only ~ 50-60% of all reads. In contrast, as expected the percentage of intronic reads observed for cells was <10% compared to up to 40% in nuclei.



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