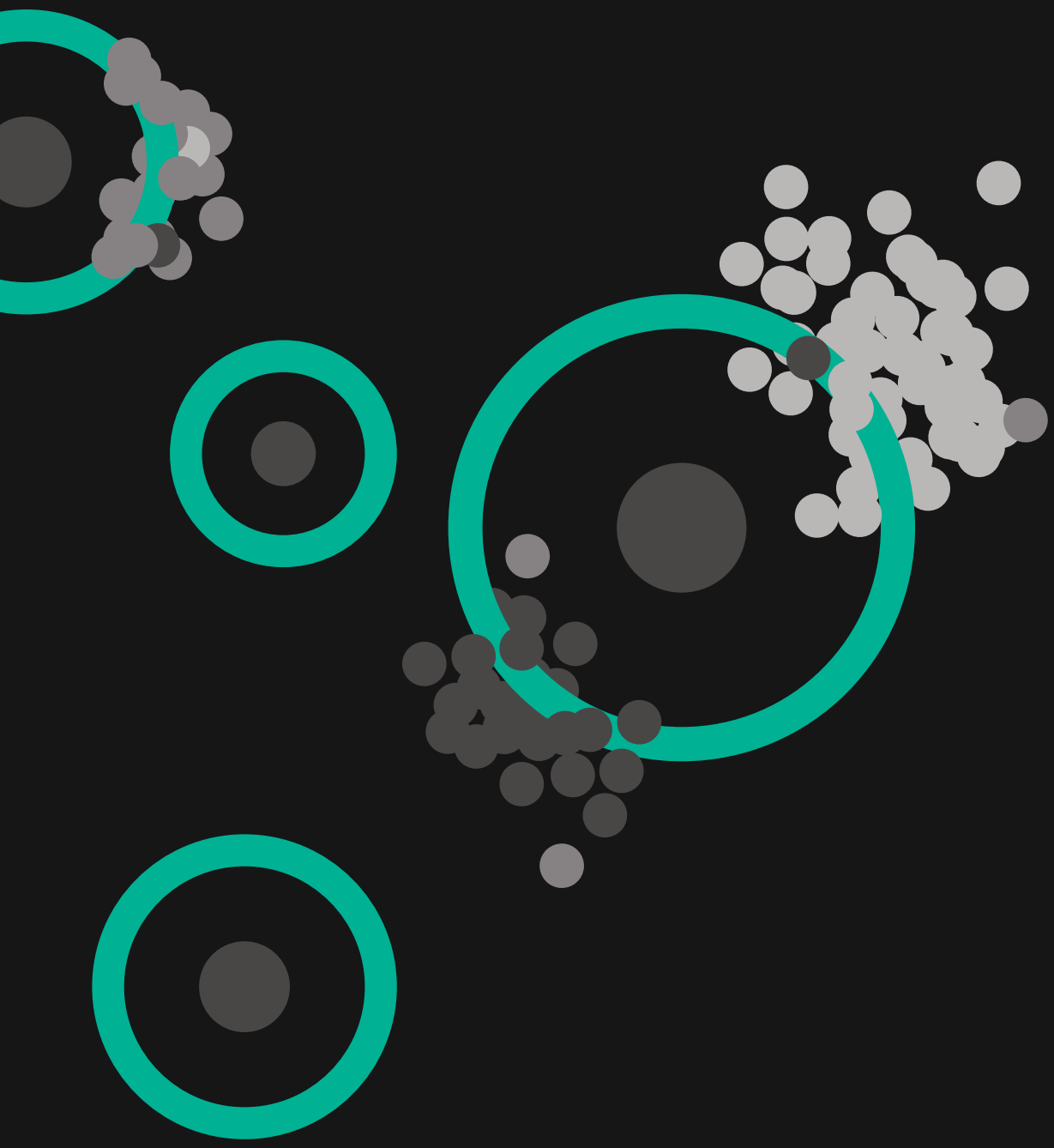
single cell RNA-Seq using the nadia instrument



dolomite bio

cost-effective scRNA-seq with exceptional gene capture rates

Single cell RNA-Seq enables the analysis of thousands of single cells in order to identify and monitor cellular expression patterns. Using the Drop-seq protocol, the Nadia instrument can dropletize up to 50,000 single cell libraries in under 20 minutes.

highlights

Low doublet rate
High reproducibility
Efficient gene capture
Low PCR duplication rate
Cost-effective single cell analysis

multiple applications

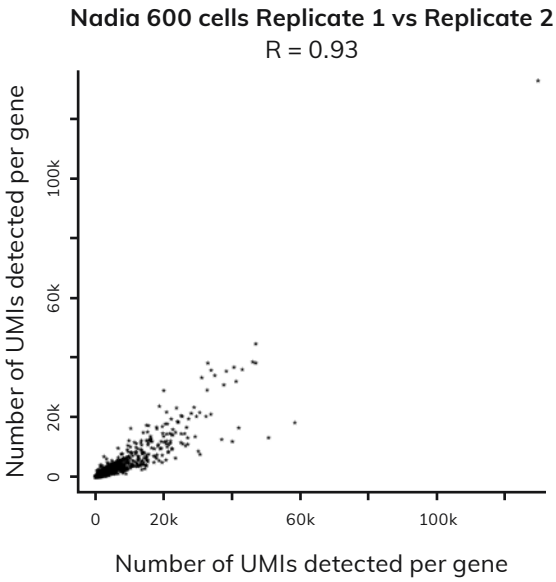
Cancer Biology
Immunology
Stem Cell
Neurobiology
Plant Biology

data sets

Dataset	NGS reads per cell	Median Genes	Median UMIs
Nadia 200 cells R 2	26,224	3,107	6,299
Nadia 600 cells R 1	121,975	5,525	23,233
Nadia 600 cells R 2	50,024	4,132	11,704
Macosko 1000 cells	124,161	4,868	16,295

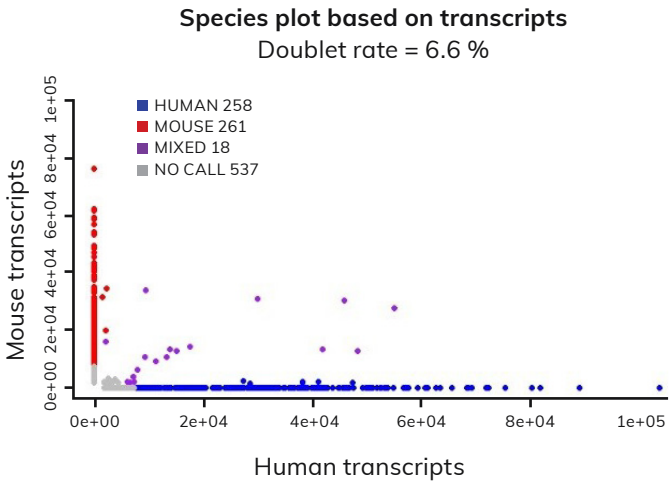
Three independently generated datasets on Nadia were compared to a datasets published by Macosko *et.al.* 2015. High numbers of genes and UMIs were detected even at low sequencing depths across all samples indicating cost-effective single cell analysis.

High reproducibility with nadia

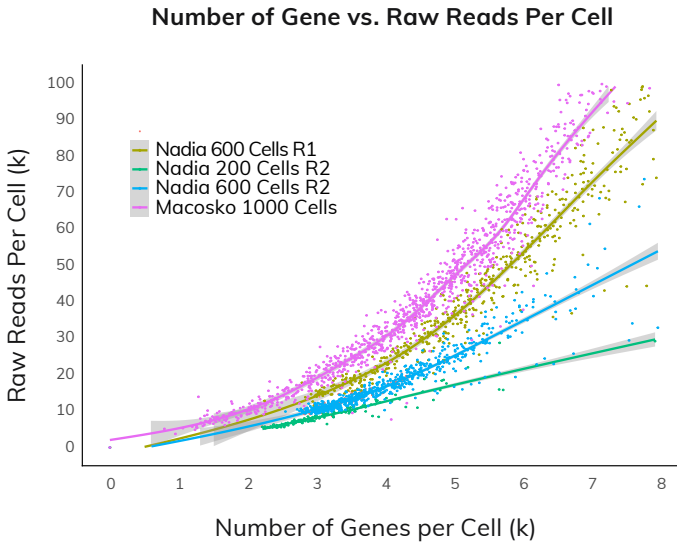


This plot shows the correlation of two datasets from different users generated on different days on the Nadia instrument. Both datasets show high concordance between individual experiments as well as different users.

Single cell 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 cell, indicating truly single cell data. Values obtained confirm the high quality of the samples and the downstream preparation of the single cell library.

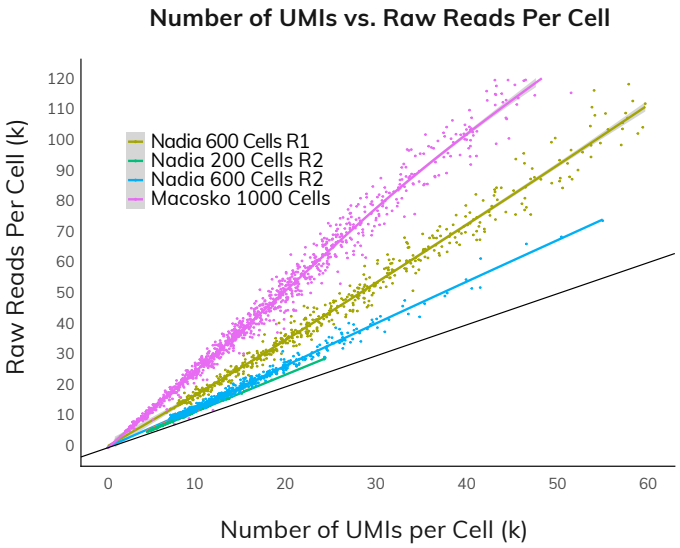


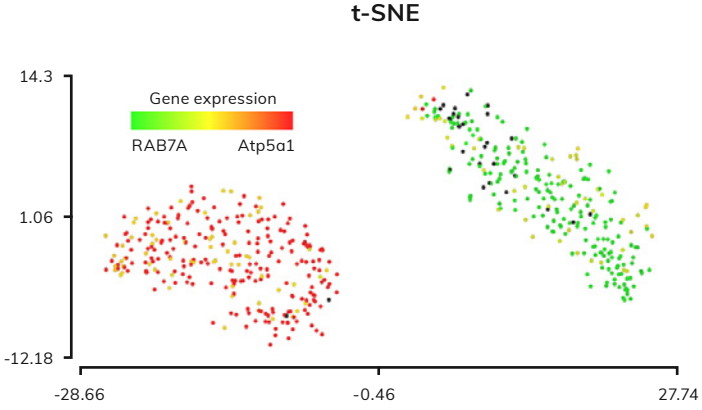
Efficient gene capture at low sequencing depth for cost effective single cell analysis

The number of detected genes was compared to the read depth across all samples. Efficient gene capture was observed even at low sequencing depth, reducing cost for NGS analysis.

Low PCR duplication rate for Drop-seq to reduce sequencing cost

The number of detected UMIs was compared to the read depth per cell across samples. 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.





t-SNE plot of a nadia mixed species dataset

The mixed species dataset was clustered in a two-dimensional space using t-SNE in Partek Flow. As expected, cells clustered into two distinct groups. Cell groups were coloured by the marker genes Atp5a1 for mouse and RAP7A for human cells.

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