Using Partek Flow for effortless analysis of nadia-derived single cell data
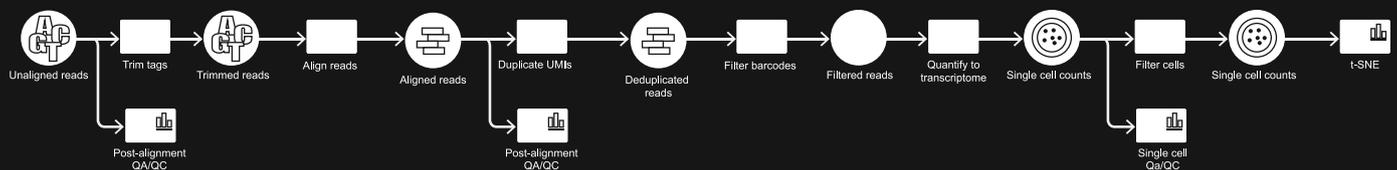
nadia

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Analysis of Nadia-derived single cell data without prior bioinformatics experience using Partek Flow
Partek Flow is an easy-to-use software solution for the analysis and visualization of single cell NGS data. The software includes all necessary bioinformatics tools to analyze NGS data starting with FASTQ files. With this solution, Nadia-derived single cell data can be studied easily to provide scientists with a comprehensive understanding of their single cell sample.
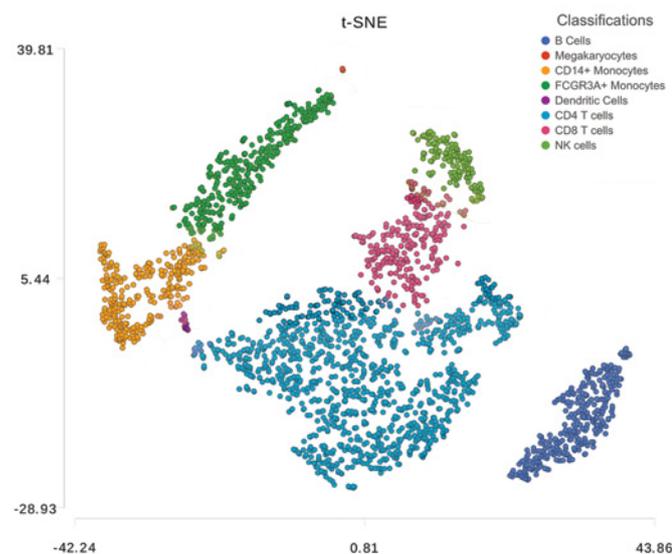
nadia pipeline in Partek Flow

After sequencing, Nadia derived single cell data is analyzed through Partek Flow to create user-defined data plots. Complex upstream data processing steps including sequence alignment, tag trimming, de-duplication, barcode identification and transcriptome quantification are automated within the software workflow.

- **Import data -** Start with FASTQ, BAM, or count matrix files, from single or multiple samples

- **Trim tags** – Automatically remove cell barcodes and UMIs

- **Align reads** - Align to the reference genome using industry standard RNA aligners

- **Deduplicate UMIs** - Remove PCR duplicates

- **Post-alignment QA/QC** - Filter to include only high-quality single cells

- **Quantify to transcriptome** - Generate a single-cell expression count matrix against an annotation model of your choice

- **Perform downstream single cell RNA-seq analysis** - including QA/QC, filtering, normalization, clustering, sub-population classification, biomarker discovery and more
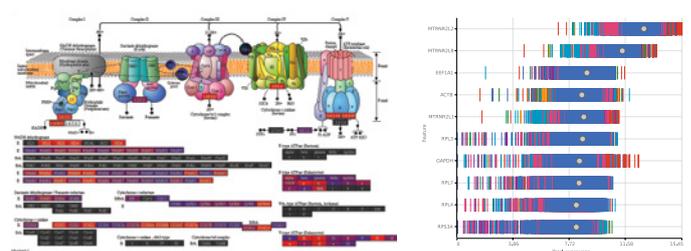

Unaligned reads → Trim tags → Trimmed reads → Align reads → Aligned reads → Duplicate UMIs → Deduplicated reads → Filter barcodes → Filtered reads → Quantify to transcriptome → Single cell counts → Filter cells → Single cell counts → t-SNE

Post-alignment QA/QC — Post-alignment QA/QC — Single cell Qa/QC

Discovery of cellular heterogeneity and unique cell types with Partek Flow

A

Nadia single cell data is visualized with a range of intuitive tools to fully understand all regulatory processes within a single cell sample. With the use of t-SNE plots, for example, single cell data can be examined to identify differences in expression levels within a sample for cell type or cluster classification. Other tools such as pathway diagrams help determine differentially regulated cellular pathways.

A: Visualization of single-cell data with 3D t-SNE or PCA, B: Visualization of pathways diagrams from the KEGG database, C: Identification of the most highly expressed genes in single cells

B

C