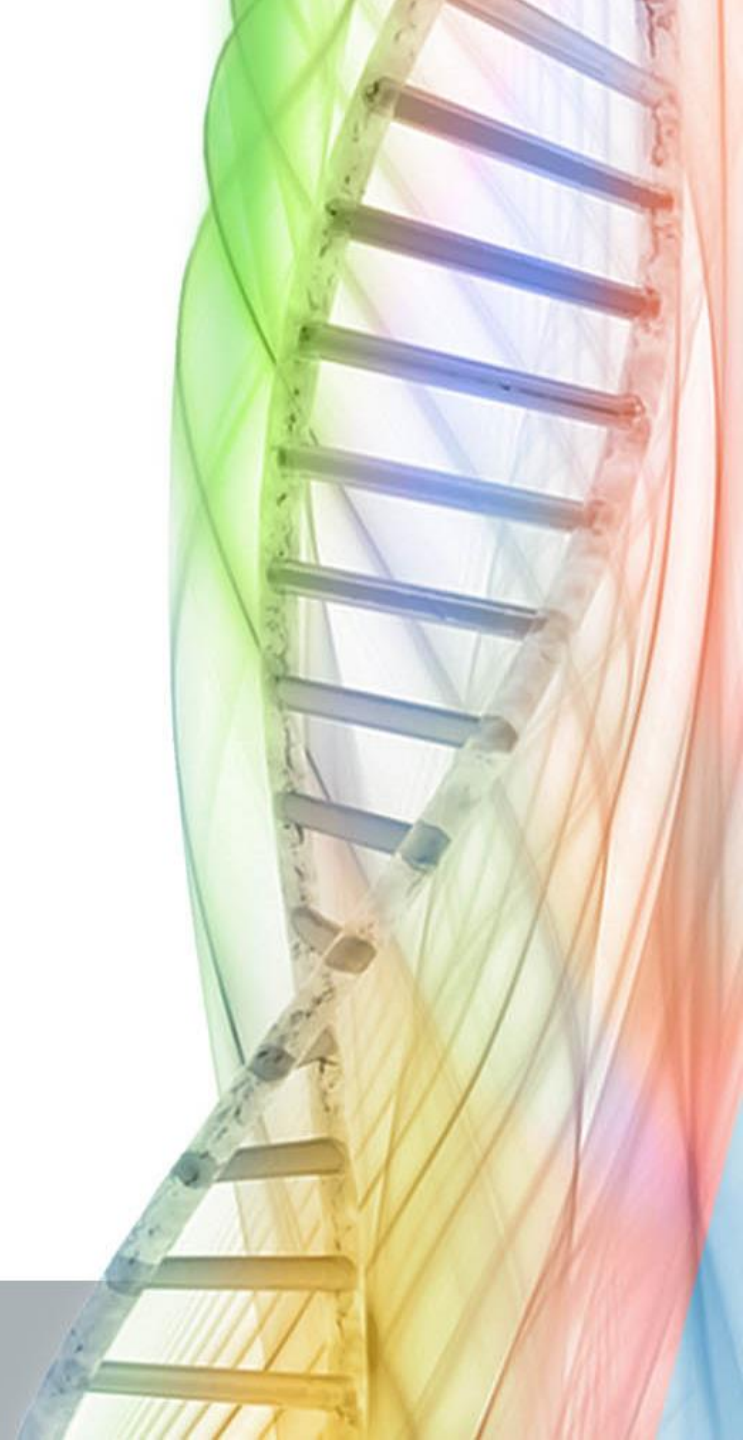


Partek Flow – Updates, New Features

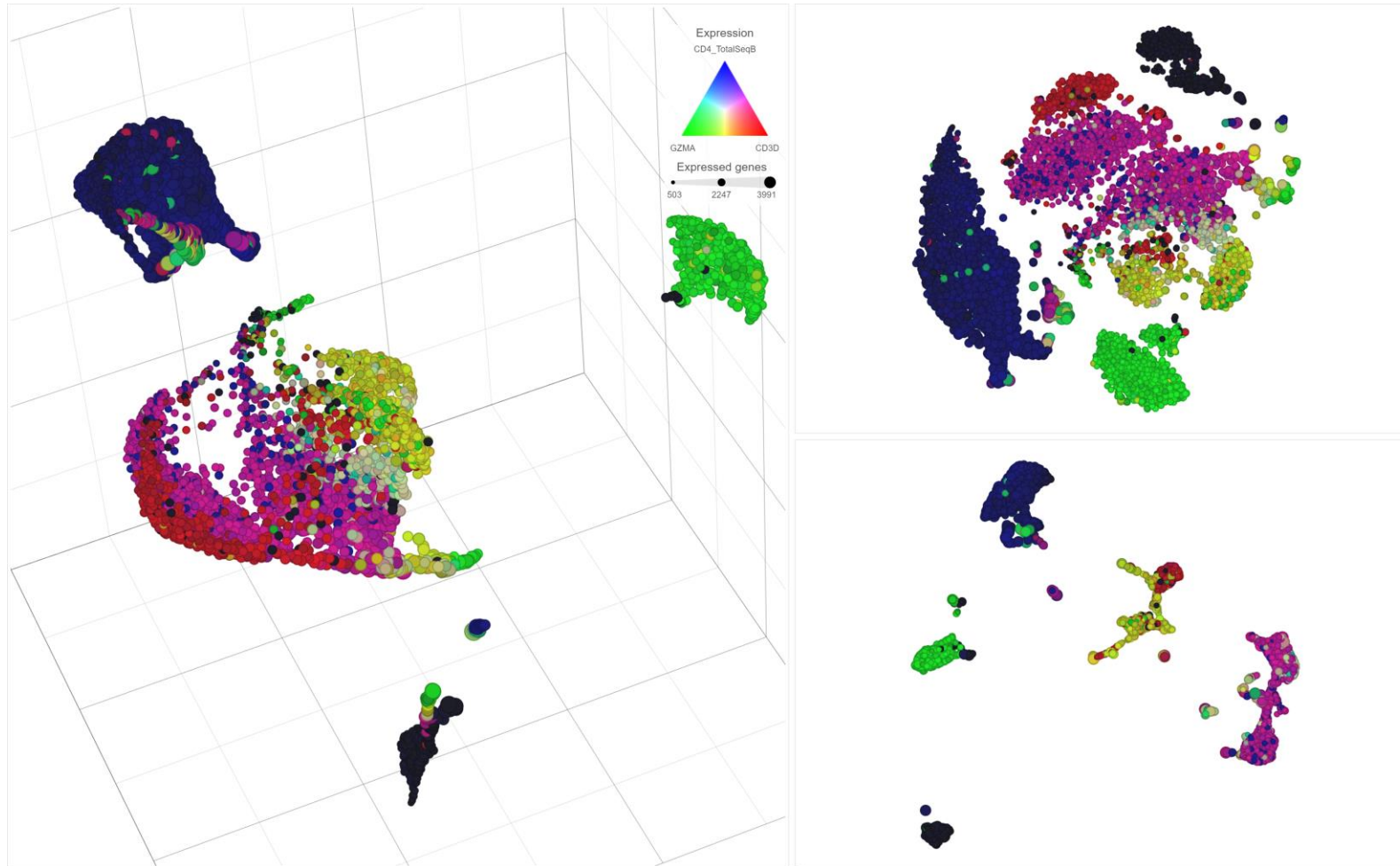
New and Updated Feature List

- Data Viewer
- Improvements and Additions to Single Cell Toolkit
 - Multi-Omics
 - Cell Hashing
 - Flow Cytometry & Mass Cytometry
 - Trajectory Analysis
 - Performance Optimizations
- ATAC-Seq / ChIP-Seq

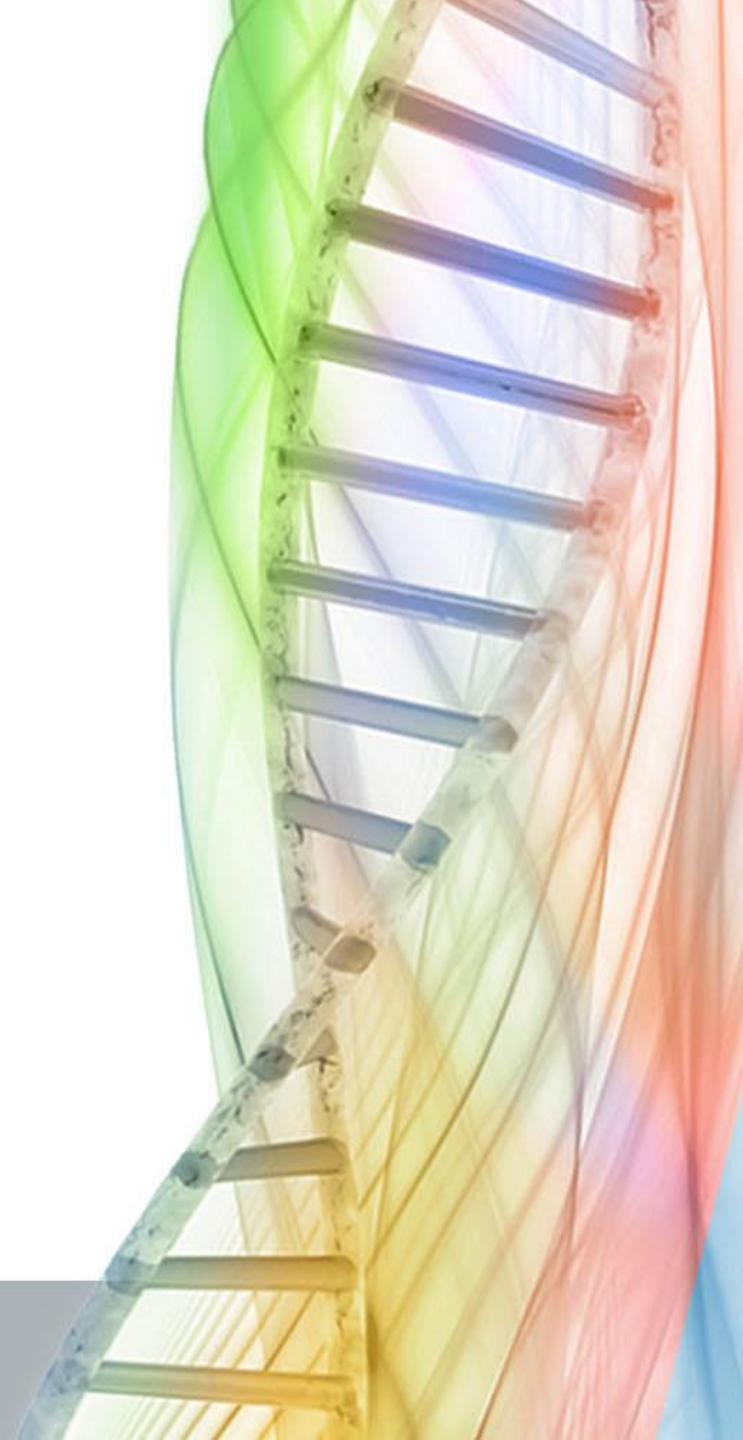
Data Viewer



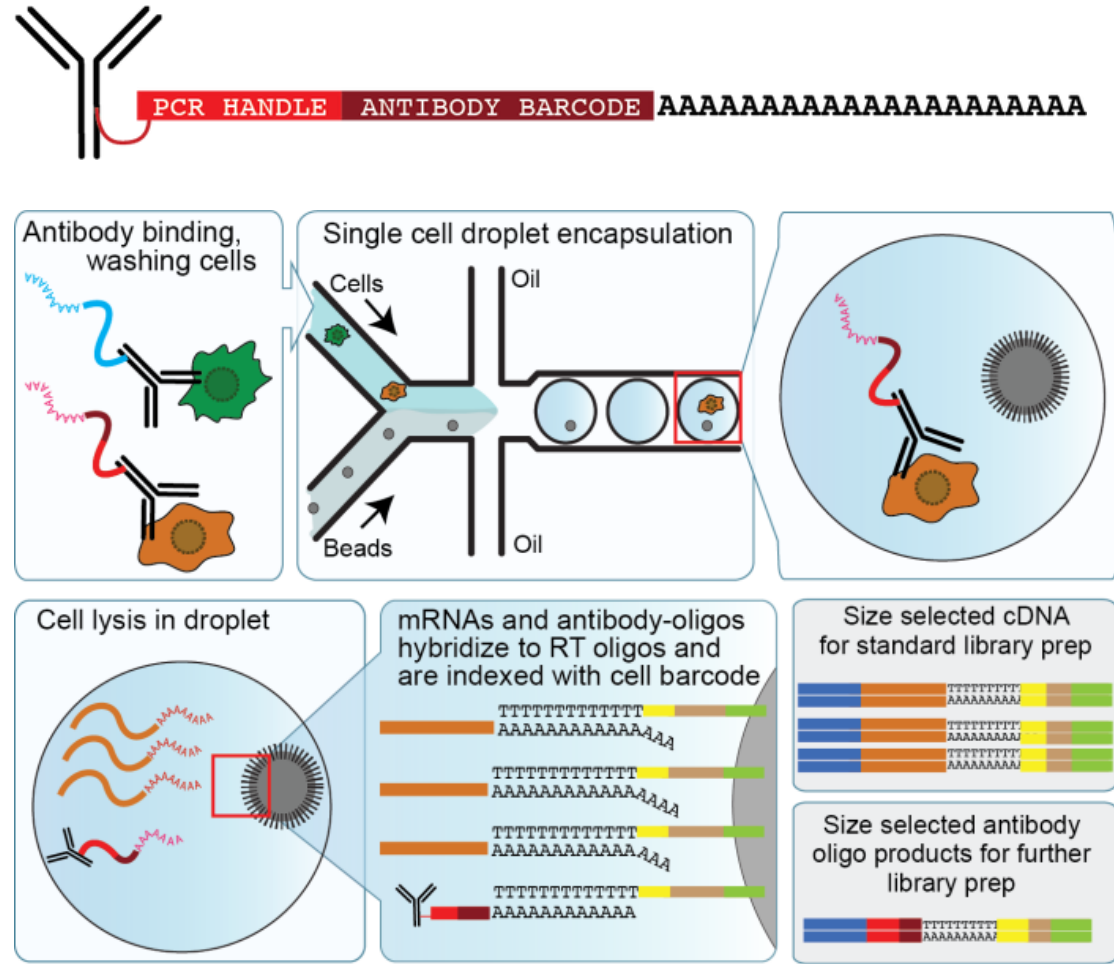
Data Viewer



Single Cell Multi-omics



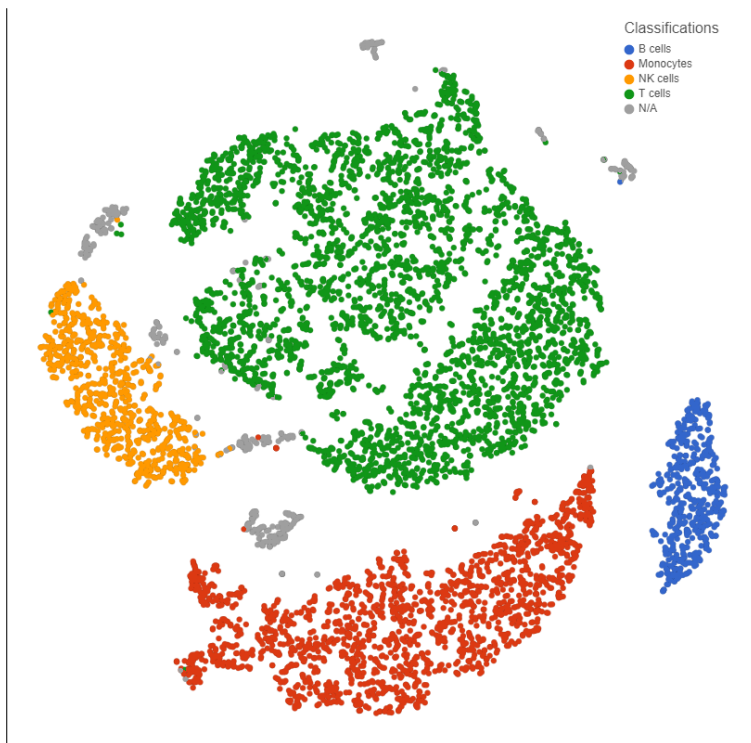
CITE-Seq / REAP-Seq / TotalSeq / Feature barcoding



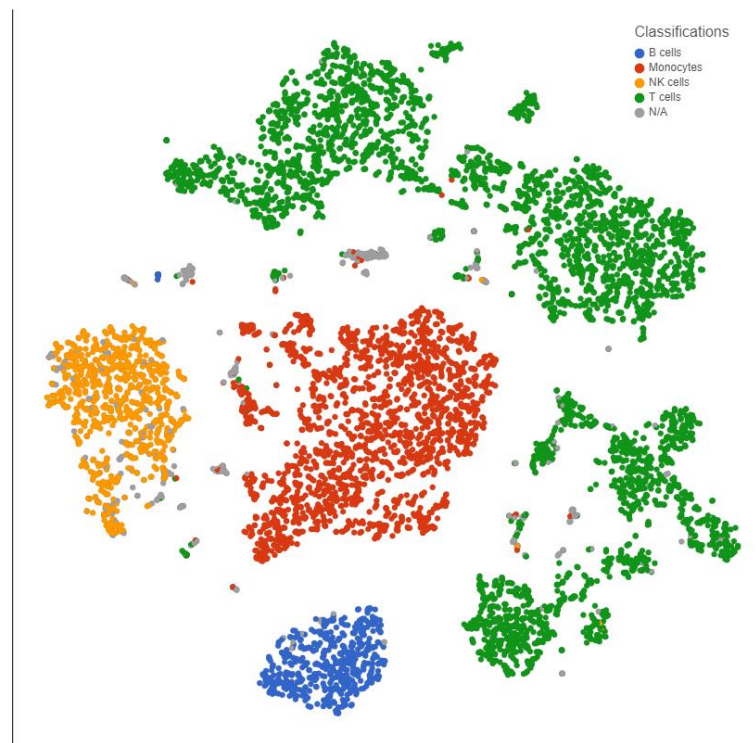
<https://cite-seq.com/>

Calculate t-SNE from mRNA, Protein, or Combined

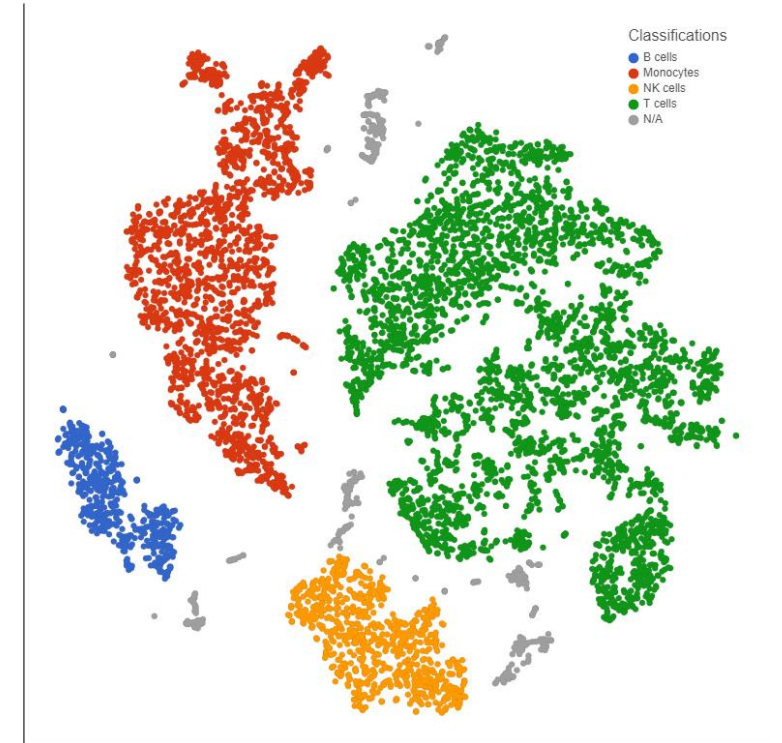
mRNA



Protein

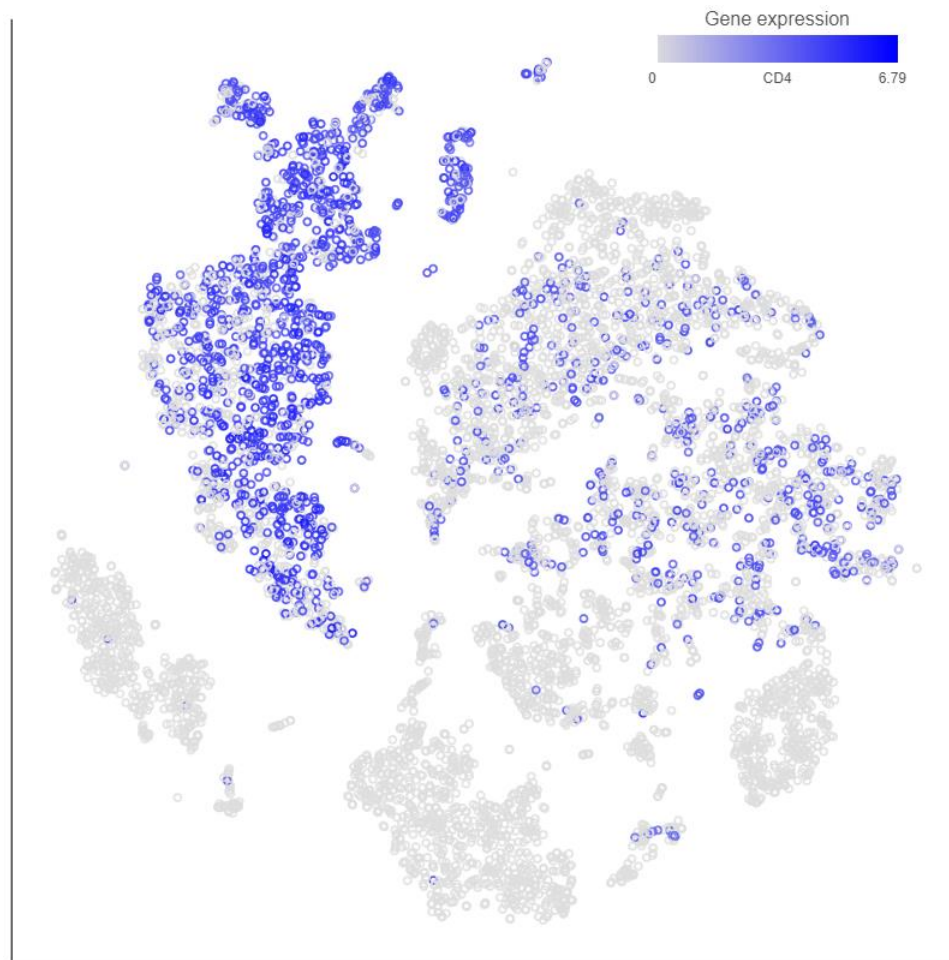


Combined

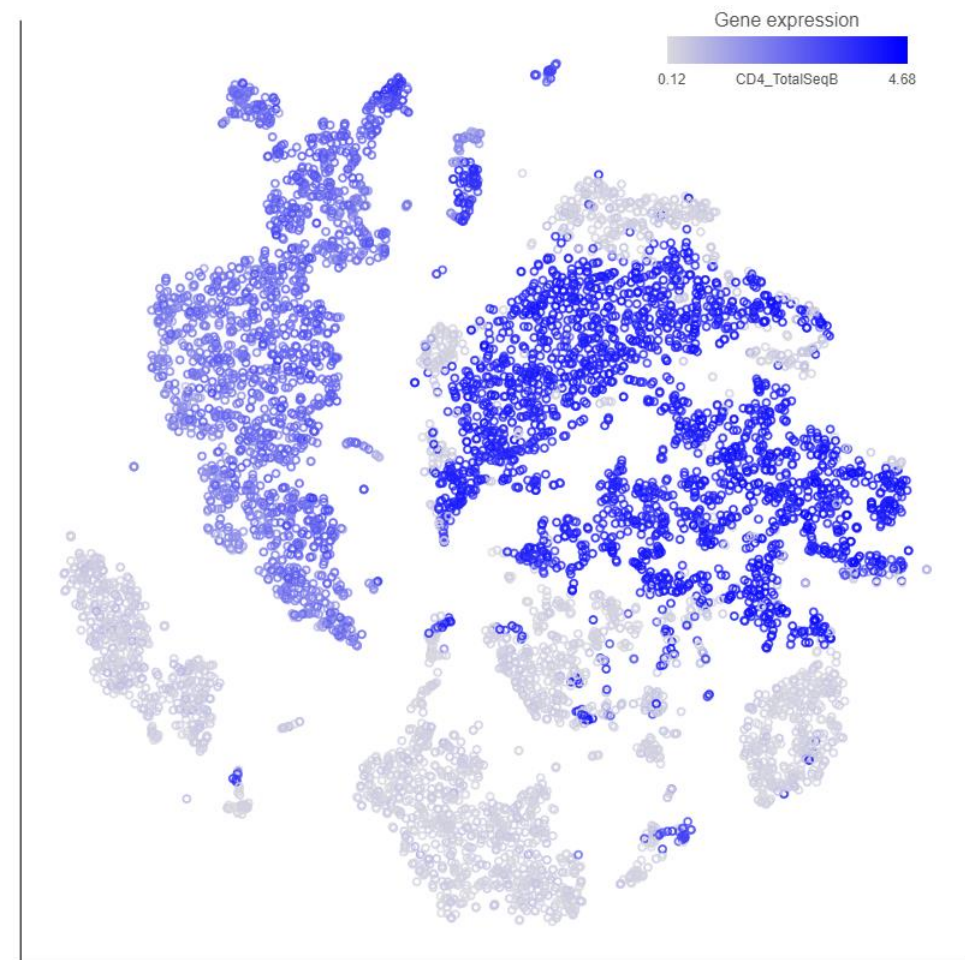


Integrate with mRNA data – Compare Protein and mRNA

CD4 mRNA

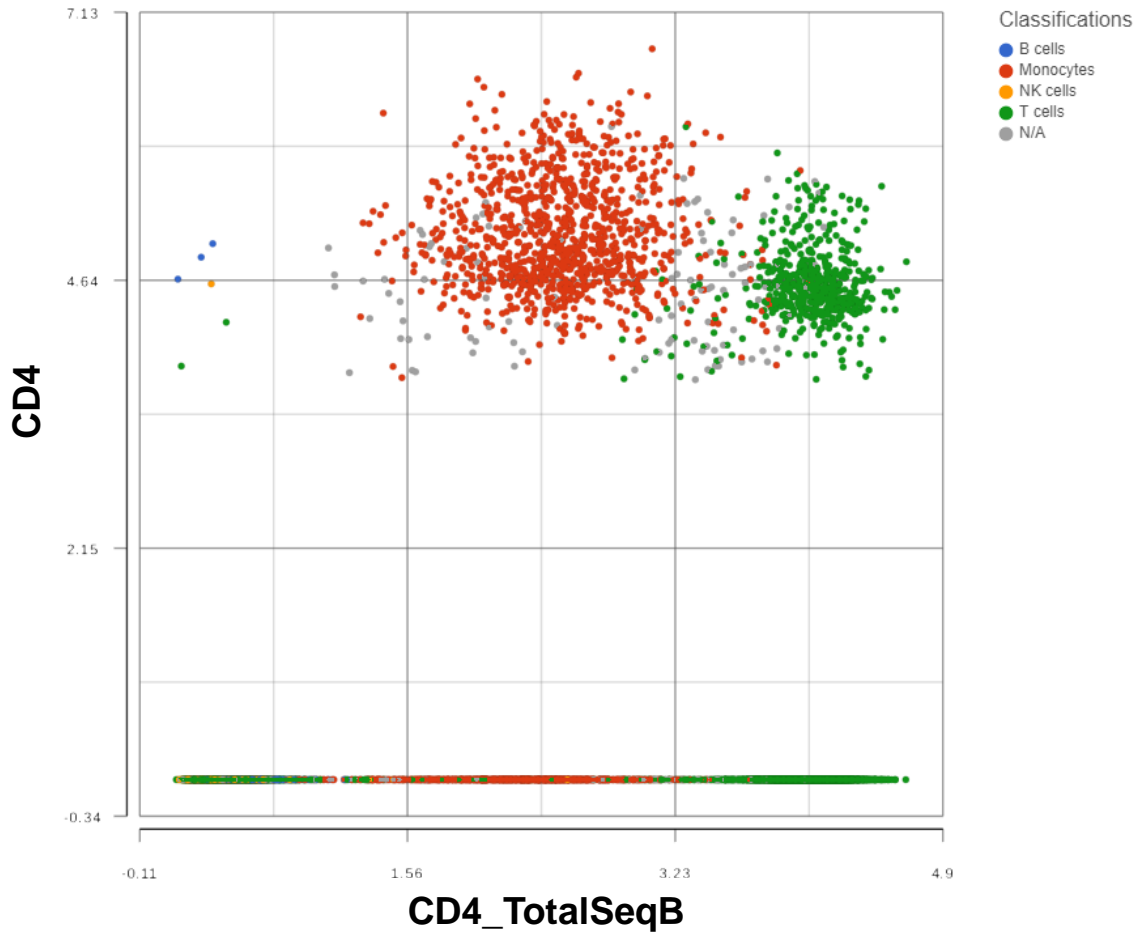


CD4 TotalSeq

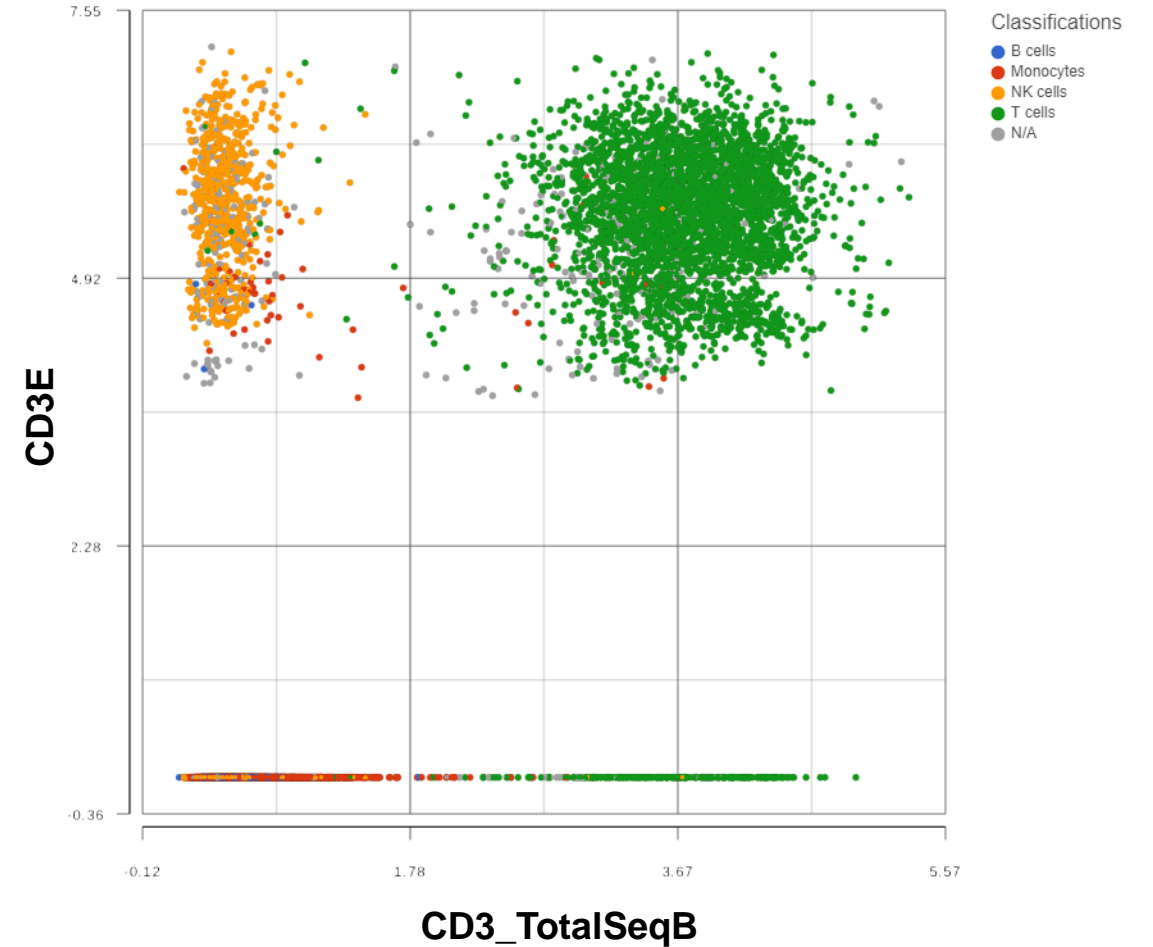


Integrate with mRNA data – Compare Protein and mRNA

CD4 Protein and mRNA



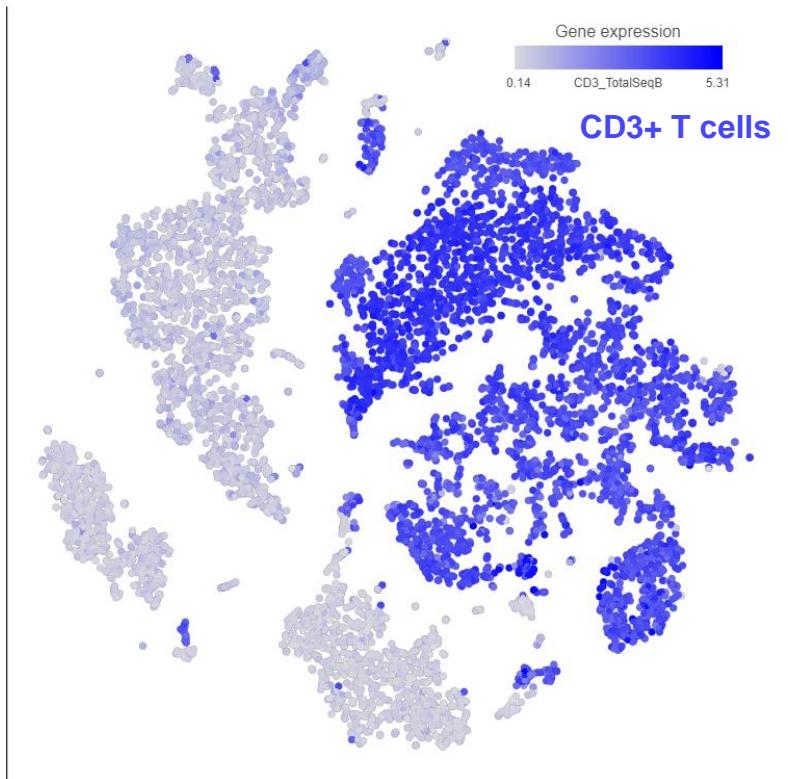
CD3 Protein and mRNA



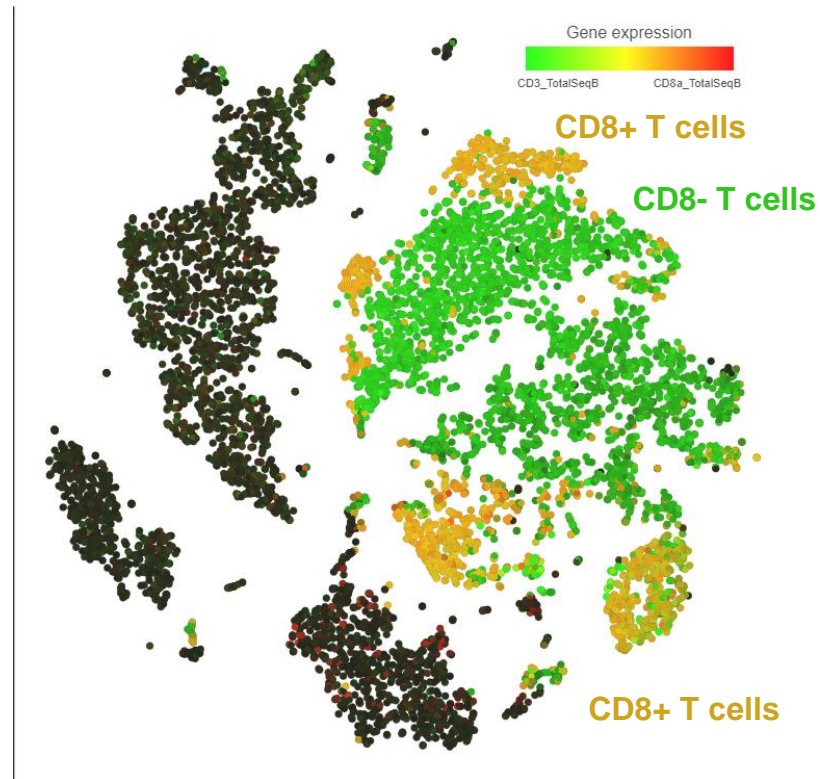
Integrate with mRNA Data – Identify Cell Types

Dimensional Reduction with t-SNE

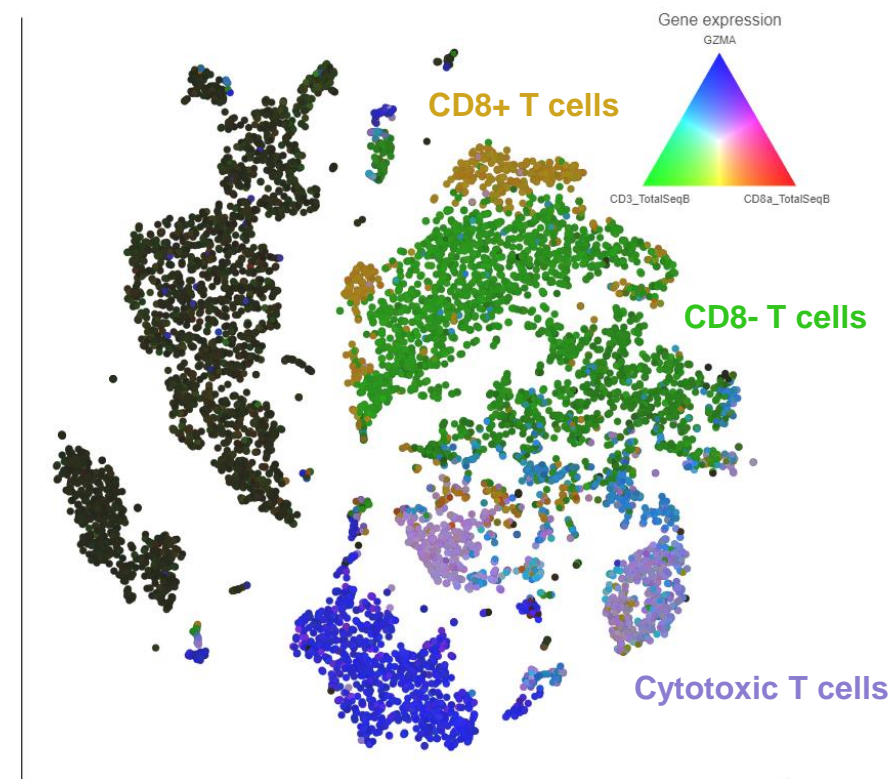
Overlay CD3 Protein



Add CD8 Protein

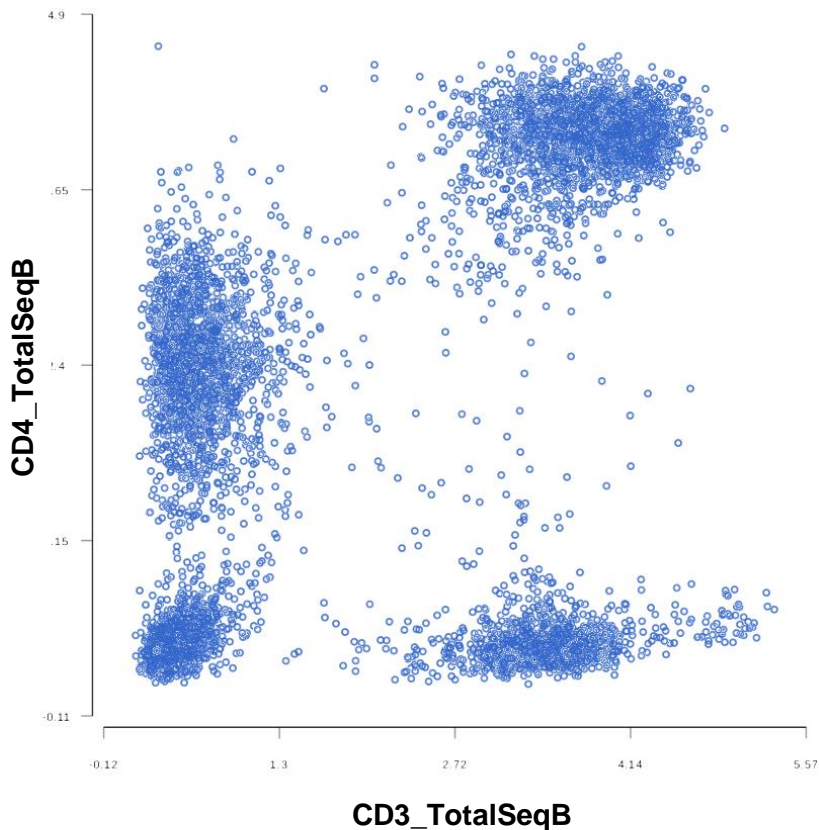


Add Cytotoxic Marker Gene

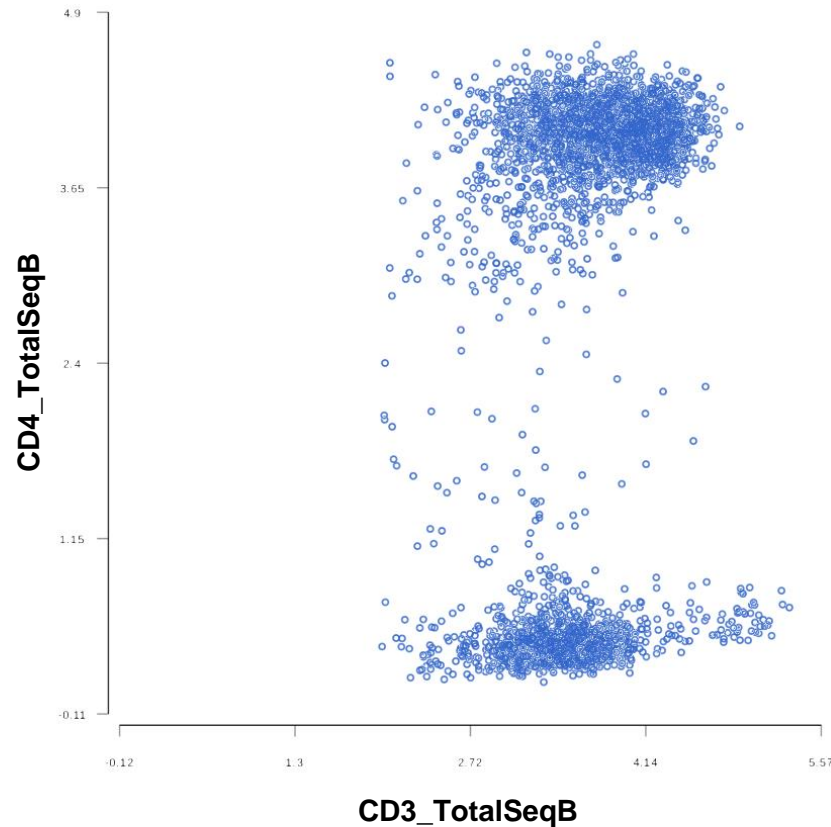


Integrate with mRNA Data – Identify Cell Types

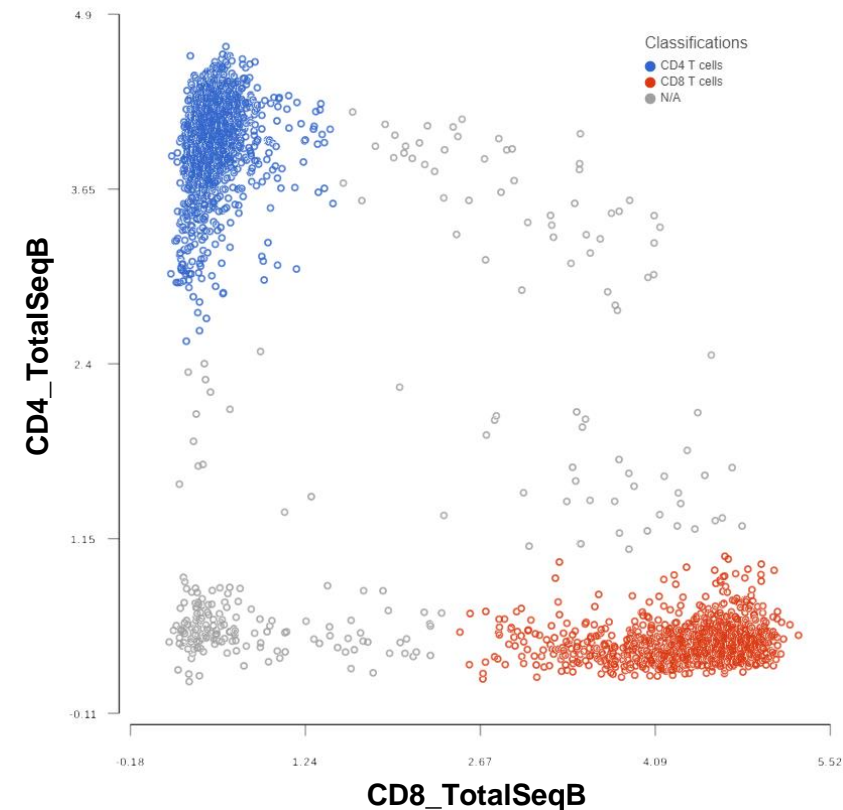
Visualize by Protein Markers



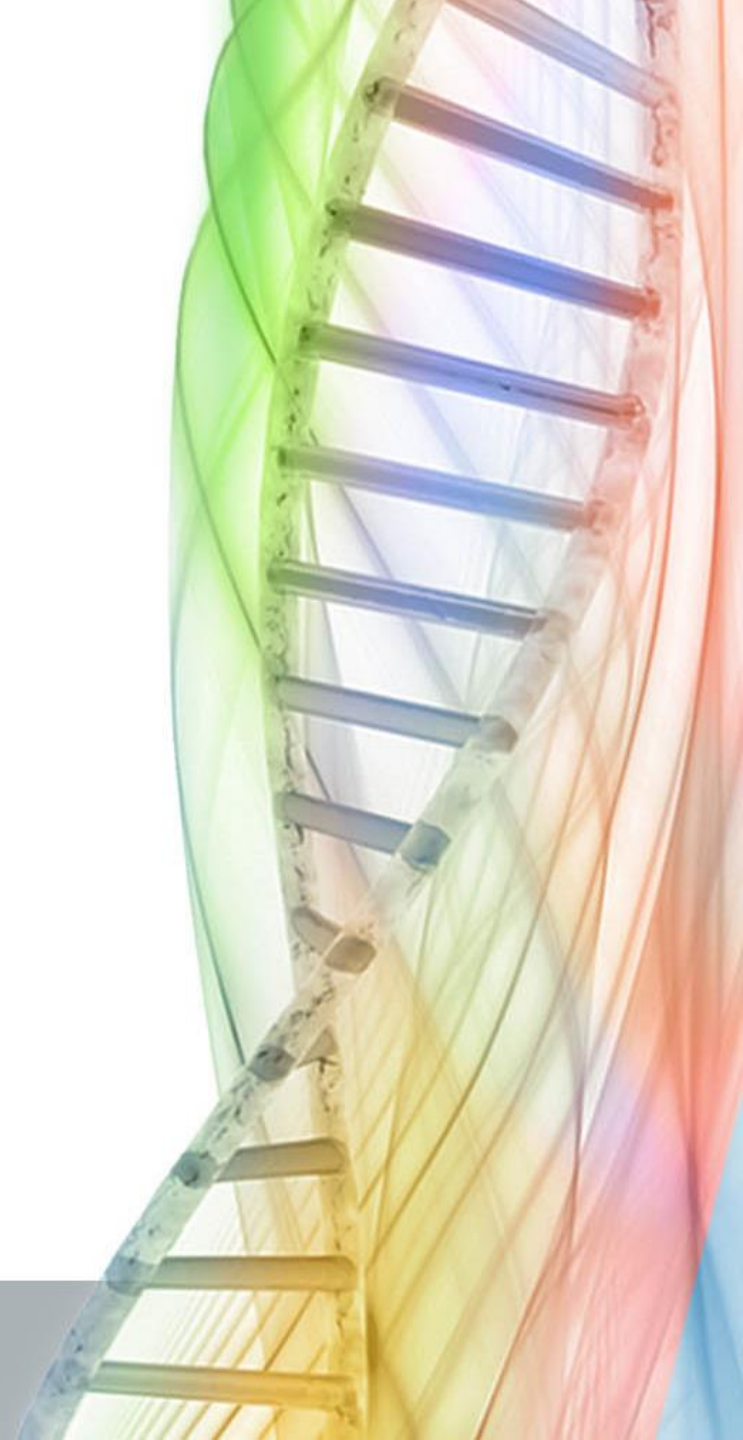
Filter to CD3+ Cells



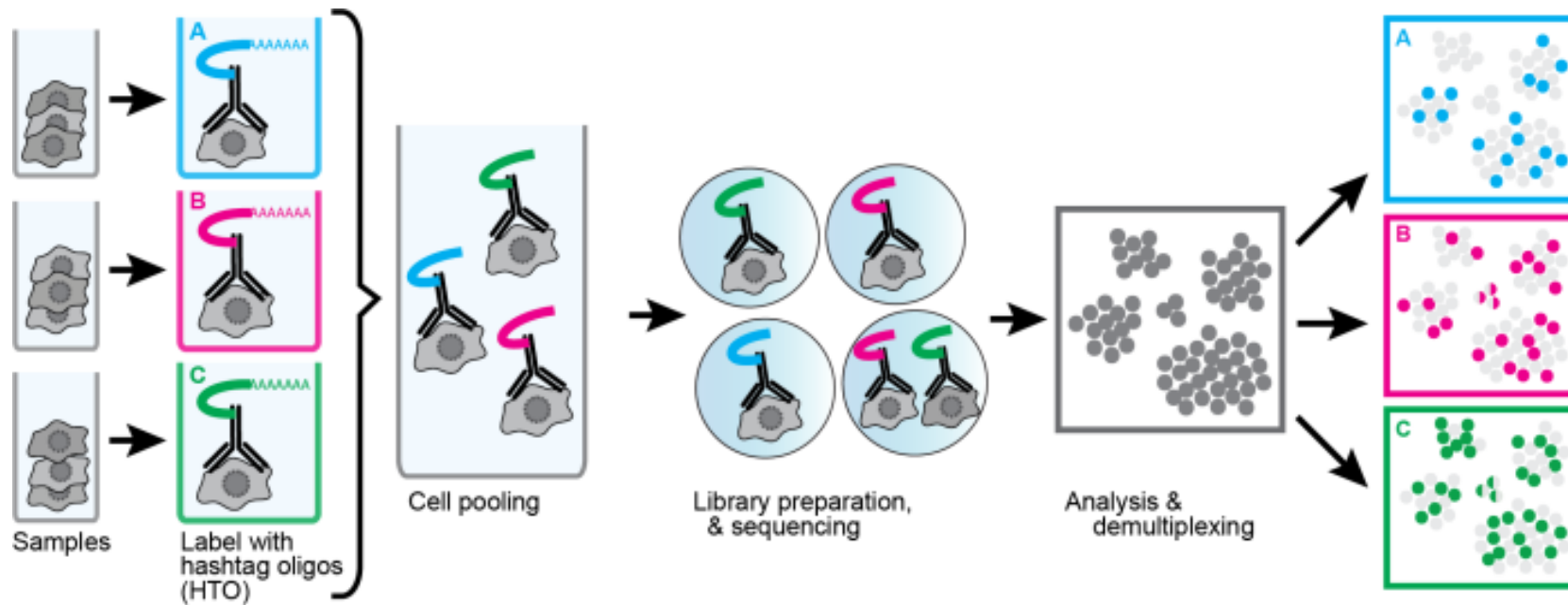
Classify CD4+ and CD8+ Cells



Cell Hashing



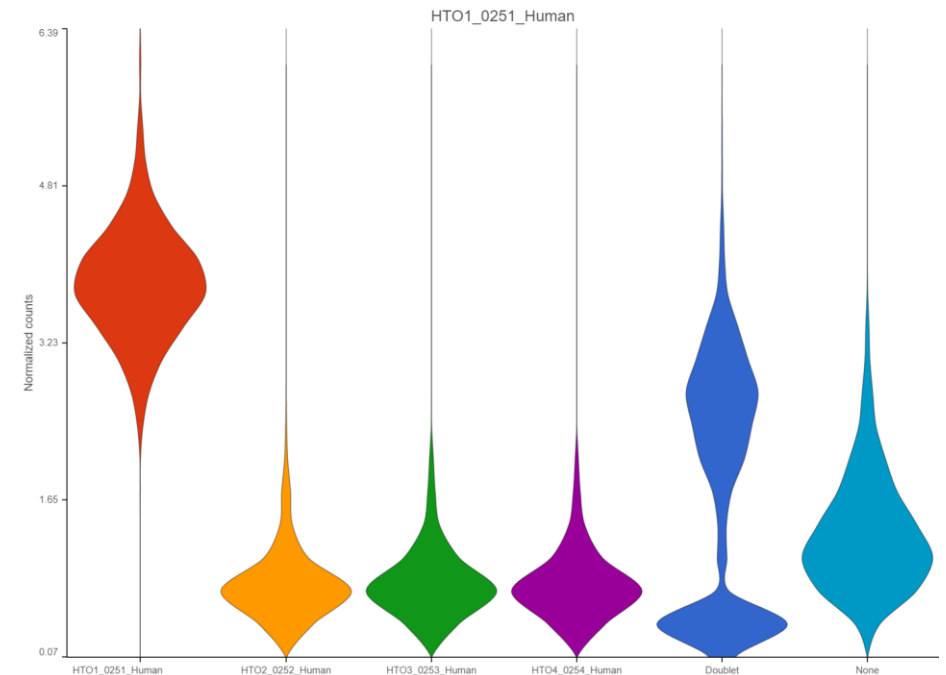
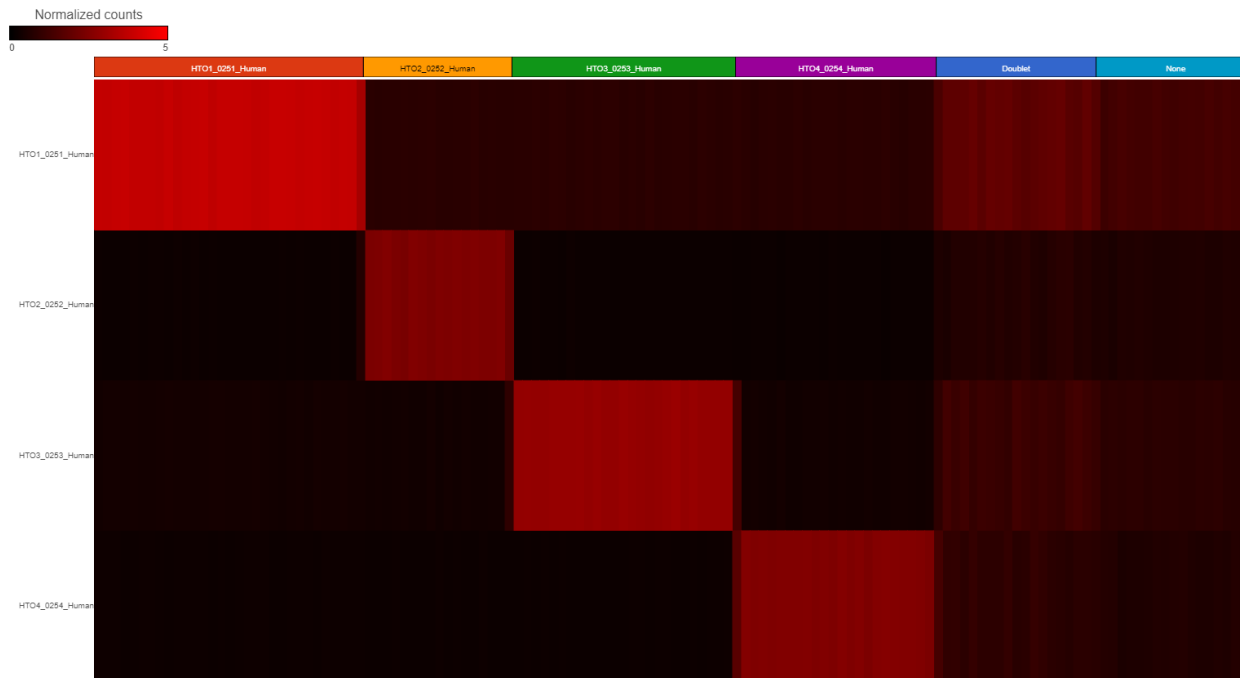
Intro to Cell Hashing



<https://cite-seq.com/cell-hashing/>

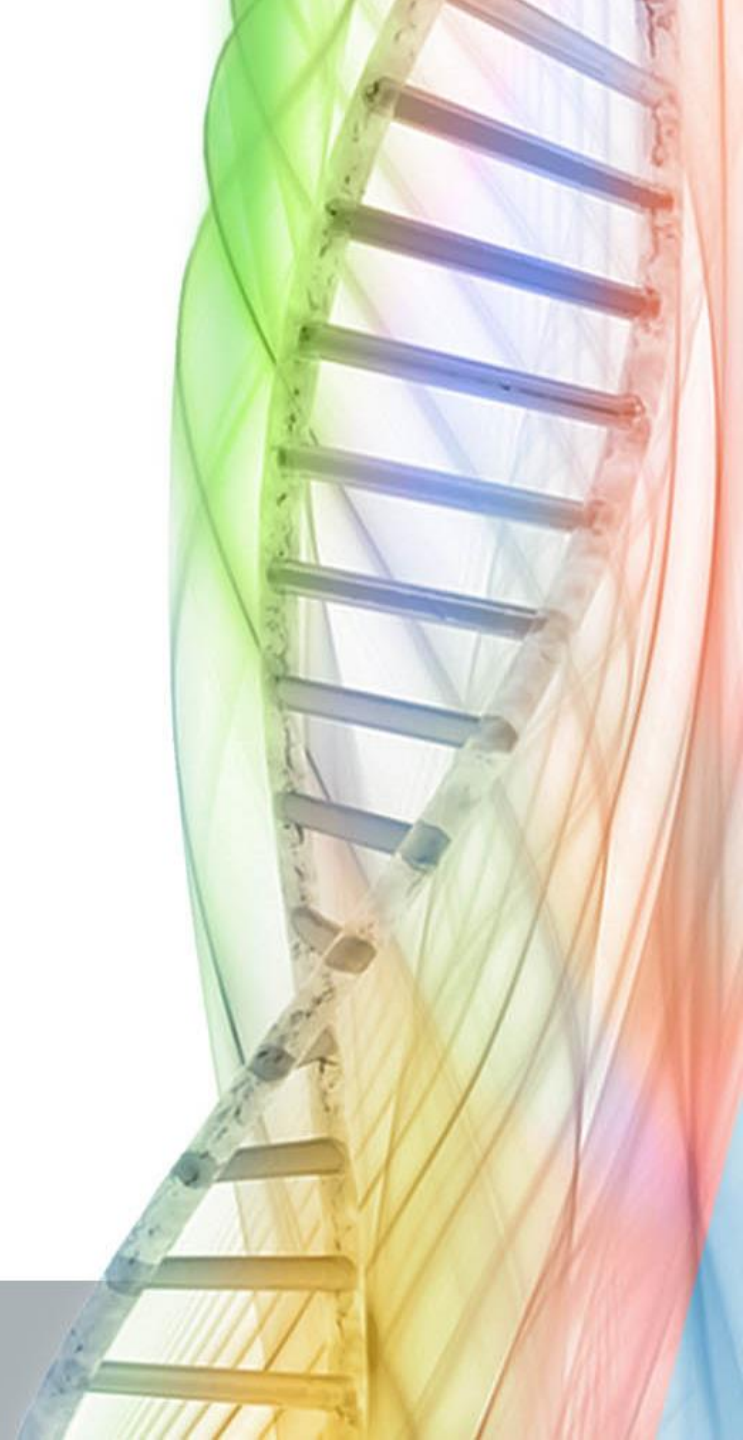
Automatically Demultiplex Your Cell Hashing Data

Identifies Sample of Origin and Marks Doublets



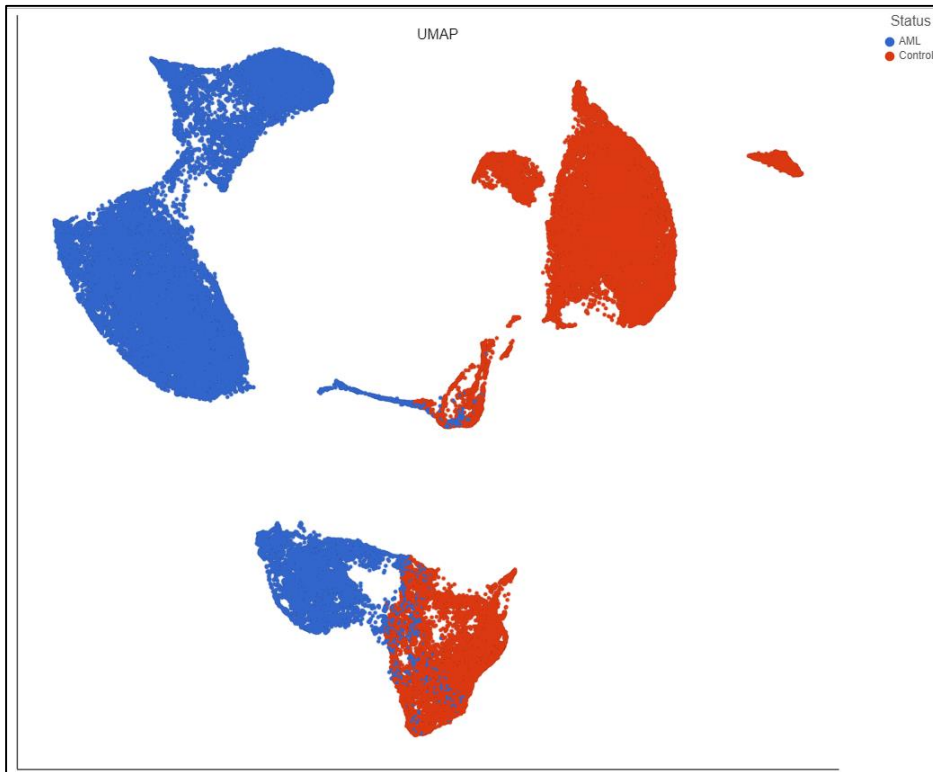
Filter to Singlets and then Perform Downstream Analysis with Sample of Origin Information

Flow Cytometry & Mass Cytometry

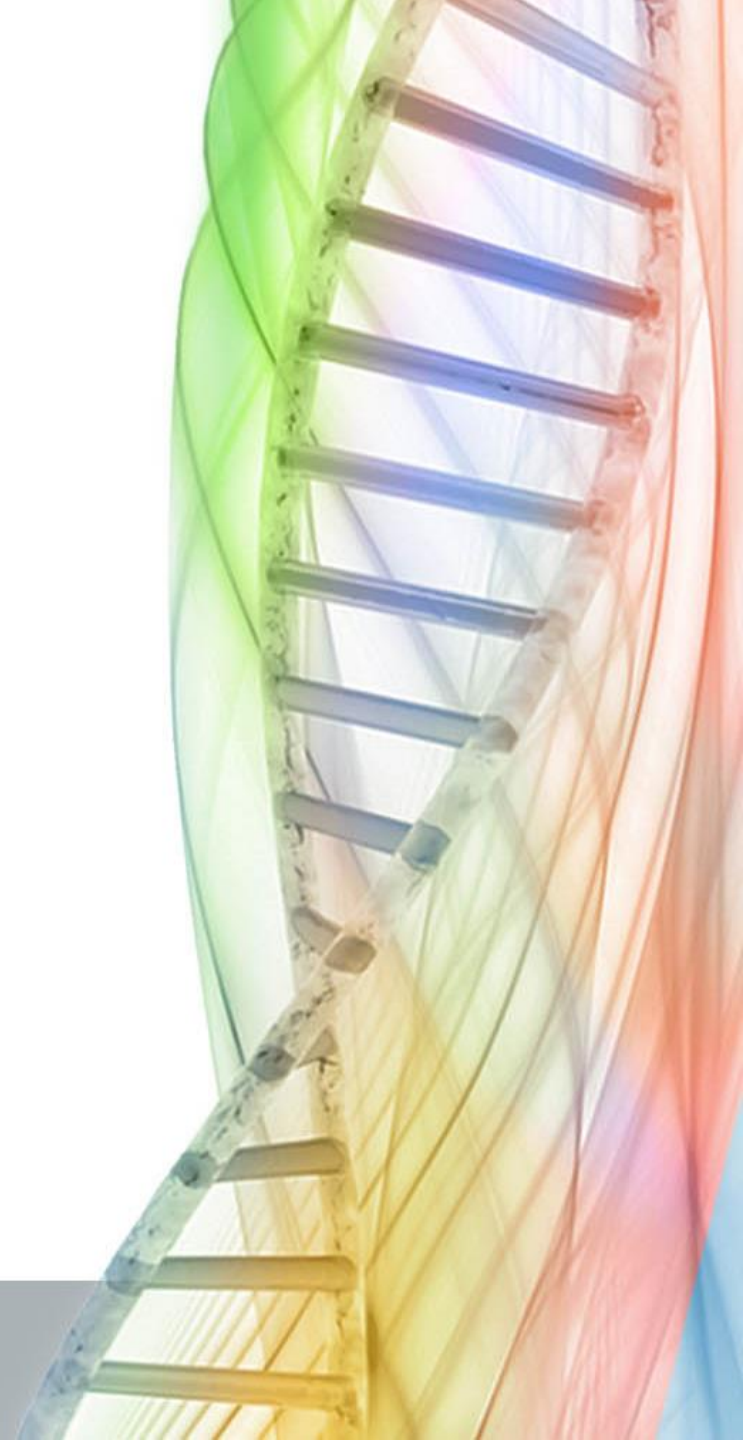


Flow Cytometry & Mass Cytometry

Import FCS2 and FCS3 files

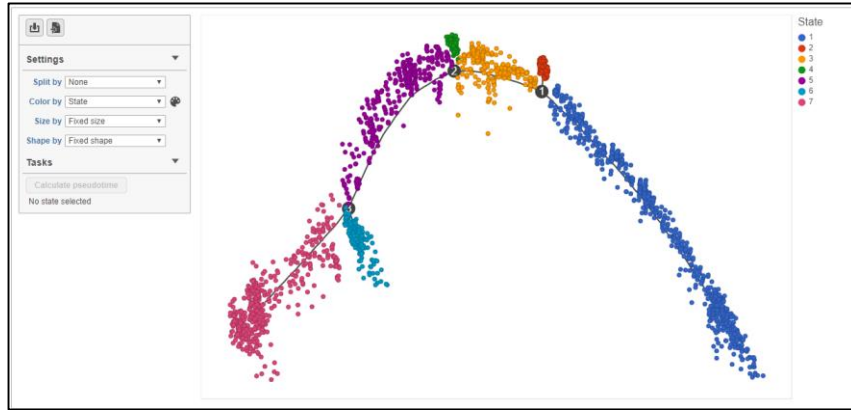


Trajectory Analysis

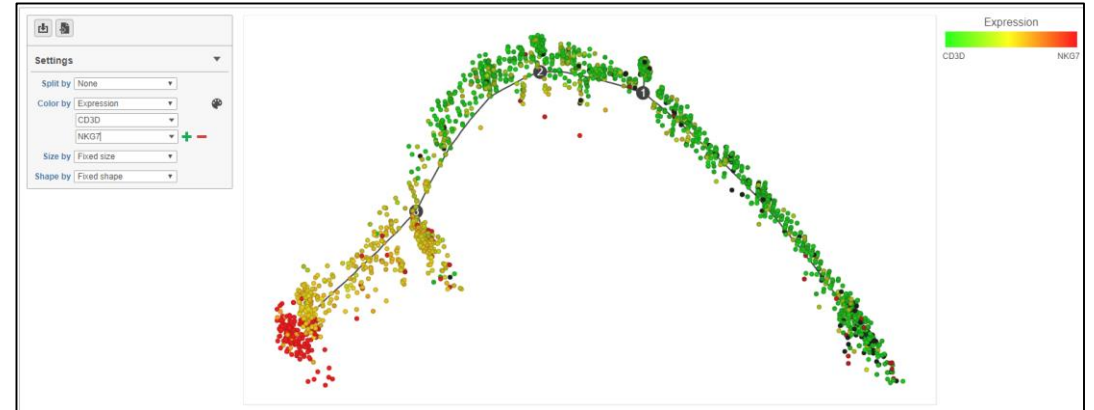


Build Trajectories and Calculate Pseudotime

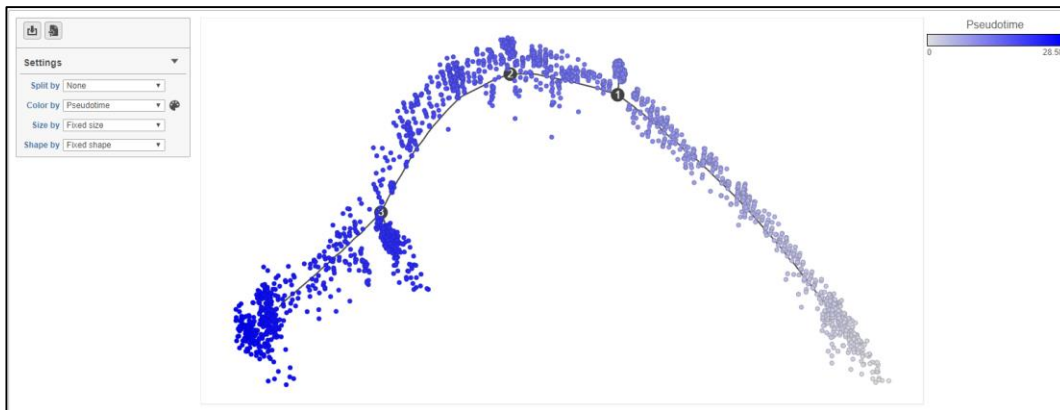
Calculate a Trajectory



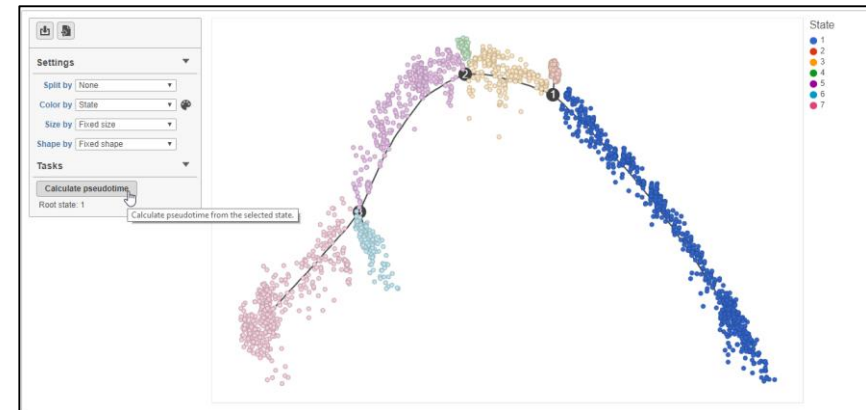
Overlay Expression Information



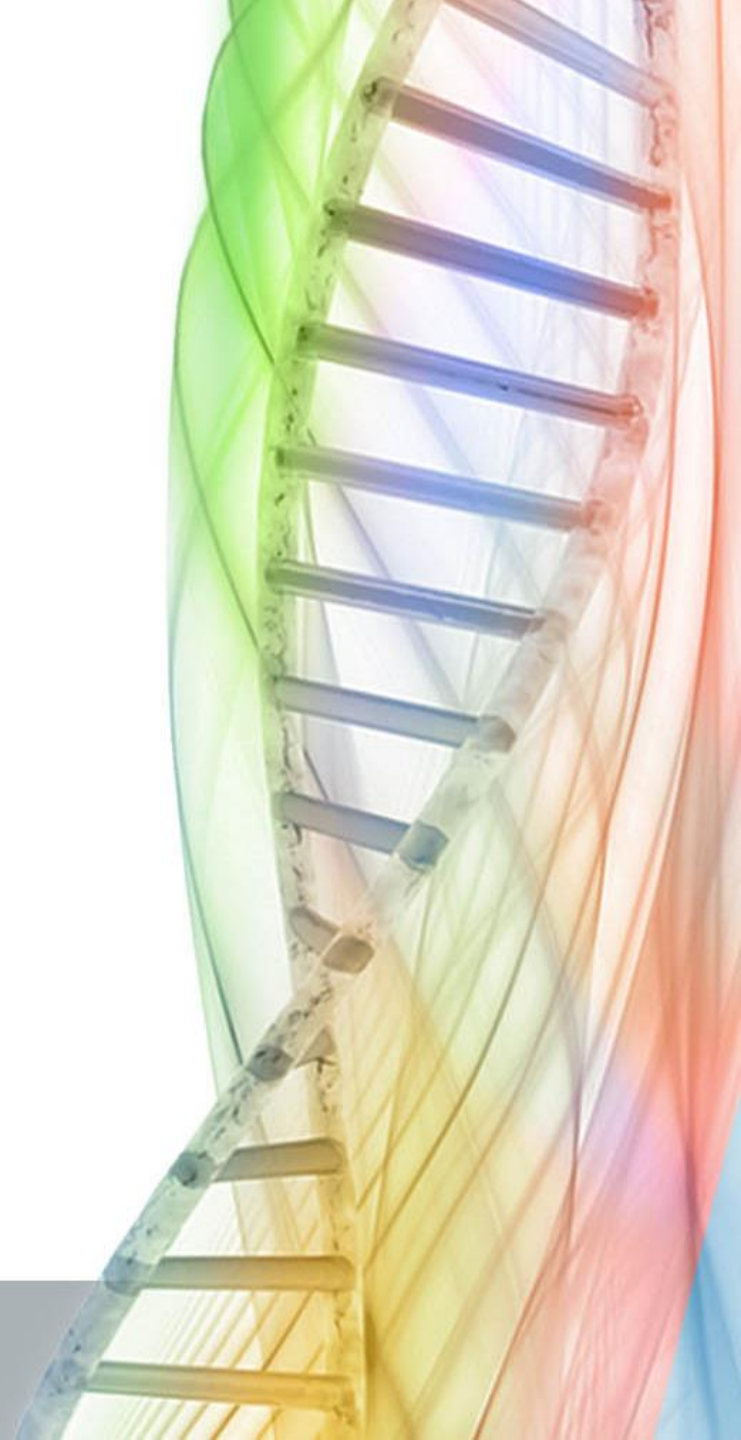
Calculate Pseudotime



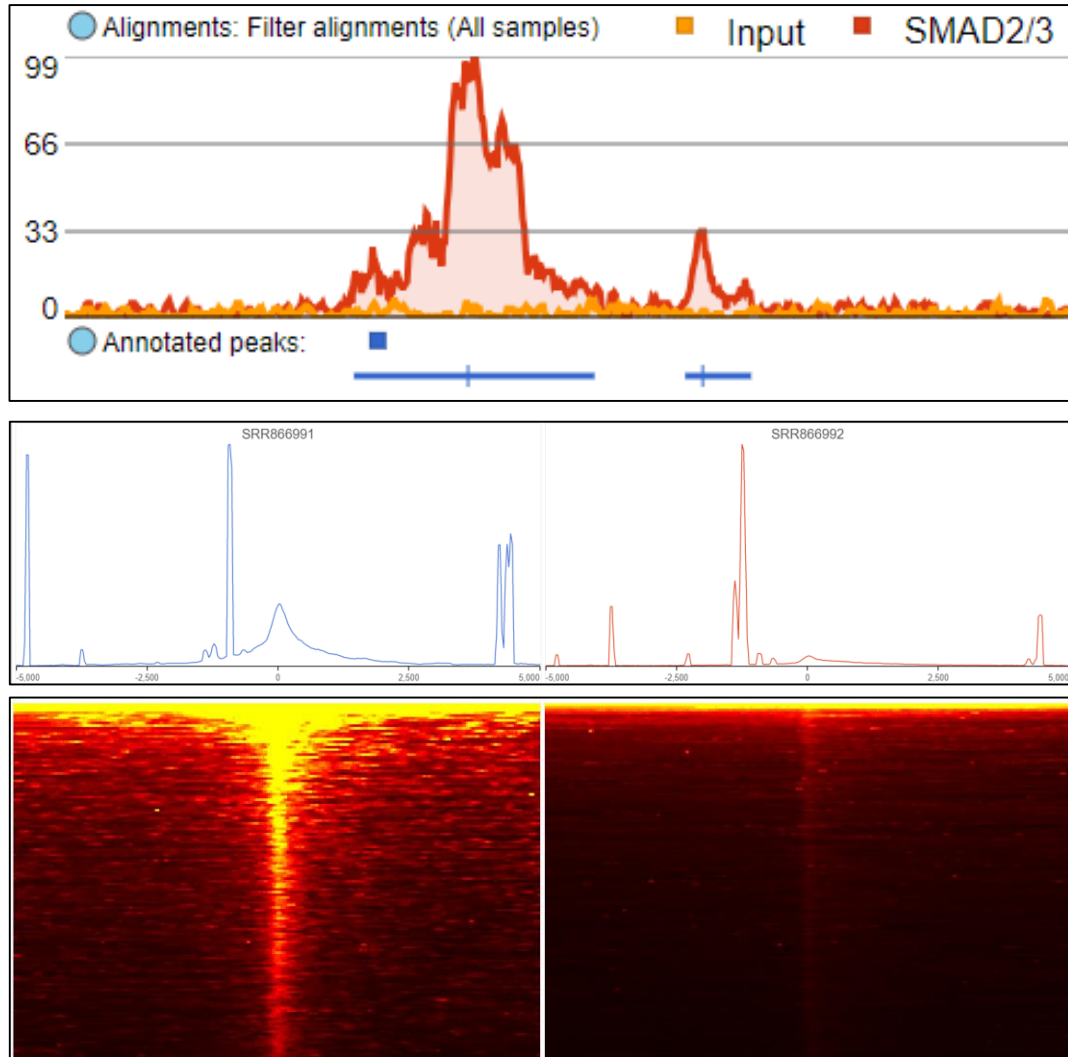
Choose a Root State



ATAC-Seq / ChIP-Seq



ATAC-Seq and ChIP-Seq



- Detect enriched regions with MACS2
- Annotate regions with gene section
- Visualize regions with TSS plot
- Analyze regions for motif enrichment
- Perform differential region analysis
- Integrate with RNA-Seq data