



# Method to analyze mutational and phenotypic profiles from single cell for clonal evolution

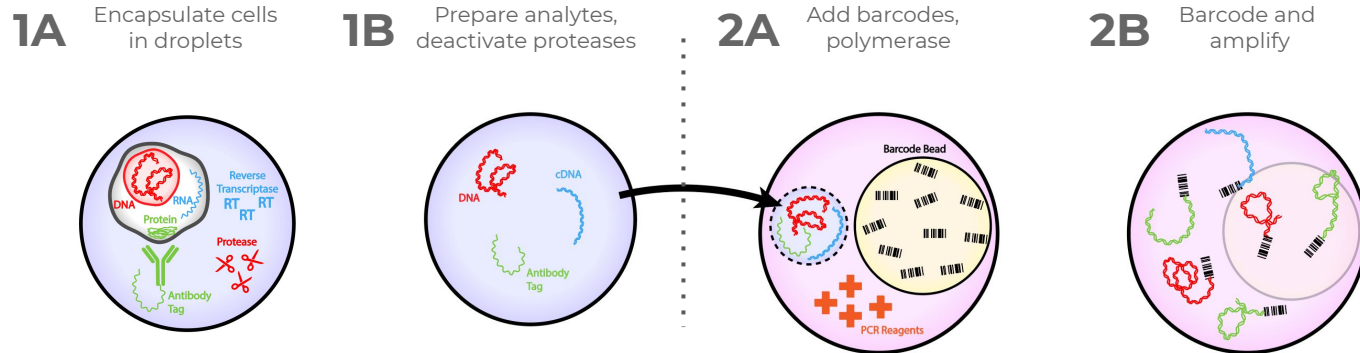
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<sup>1</sup>-Mission bio

# The Power of Single-cell Multi-Omics

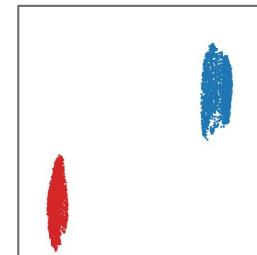
Single cell multiomics assays targeting RNA and Protein from the same cell provide a high-resolution view of the heterogeneity of the sample. However, both analytes target the phenotype of the cells and unambiguous inference that a cellular phenotype is caused by a genotype can only be achieved by their measurement from the same single cell. To address this gap, we have developed the Tapestri multi omics workflow to analyze the DNA and Protein information from the same cell.

## Mission Bio 2-step workflow enables single-cell DNA, and protein detection



## DNA + Protein provides access to information not available through just a single analyte

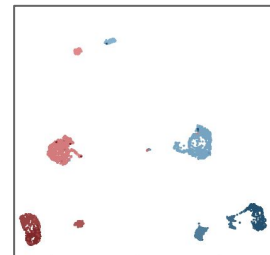
**DNA Only**  
2 PBMC Donors



**Protein Only**  
PBMC sub types



**DNA + Protein**  
PBMCs per donor



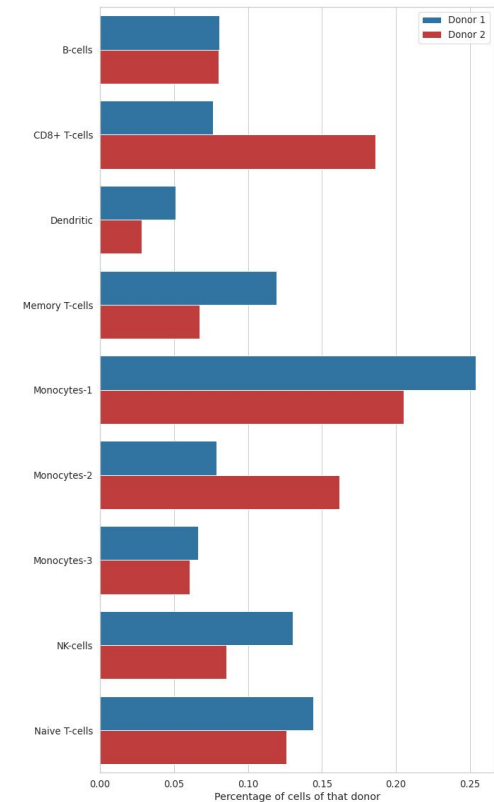
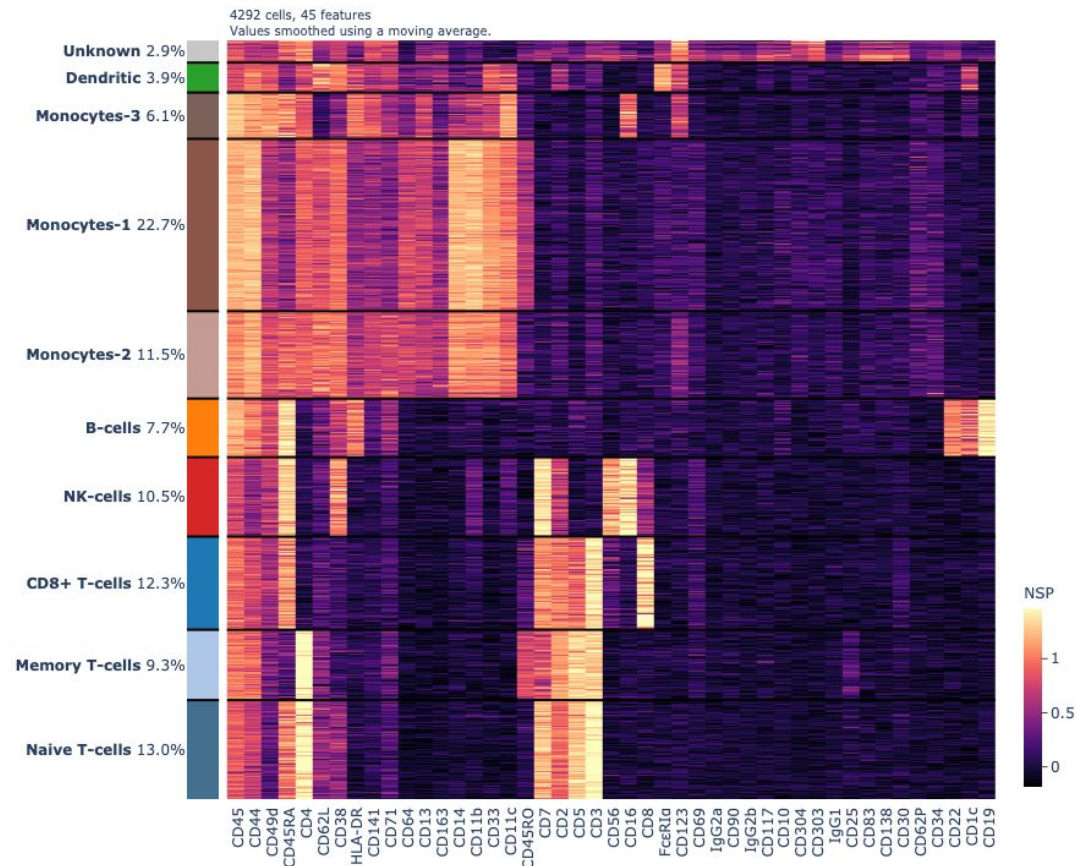
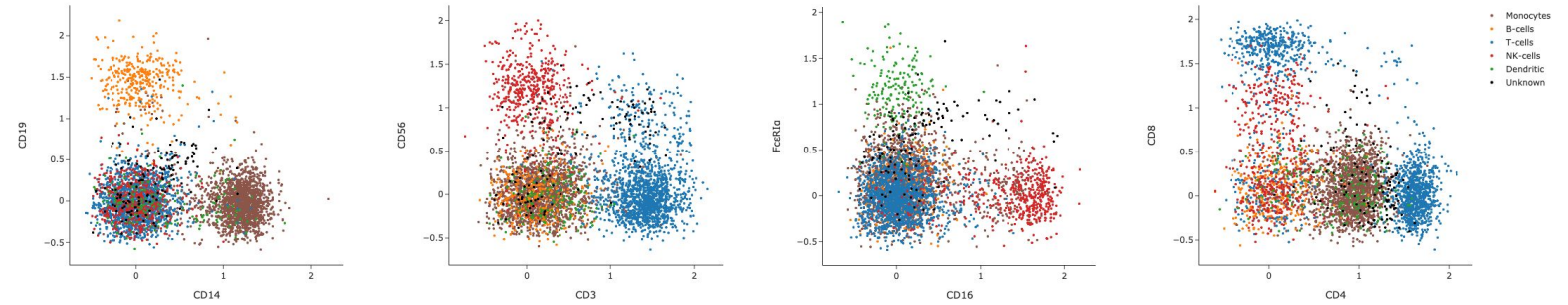


# Validating The Platform

We test this method on a model system with a two donor PBMC mixture titrated at a 50:50 ratio. Systemic artefacts such as read depth dependence of expression is corrected by normalization of the counts.

We can then identify two clones using the genetic variants and multiple cell types including the major populations such as T-cells, B-cells, Monocytes and NK-cells using the phenotypic expression.

Moreover, we are able to correlate the proportions of each PBMC cell type for the identified clones with that of the individual donors.



# Limit of Detection

We test this method on a model system with two donor PBMC, 2 cell lines mixture titrated at a 47:47:5:1 ratio with a 312 amplicon DNA panel and 45 plex antibody panel.

We filter cells using isotype controls from the antibody panel and mixed cell signatures using the DNA panel. We can identify 4 clones using the genetic variants. We can identify multiple cell types including the major populations such as T-cells, B-cells, Monocytes and NK-cells using the phenotypic expression in the PBMC donors.

The protein expression profile for the 1% and 5% population could also be identified distinctly from the PBMC cells.

