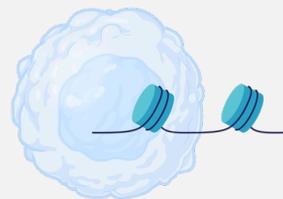




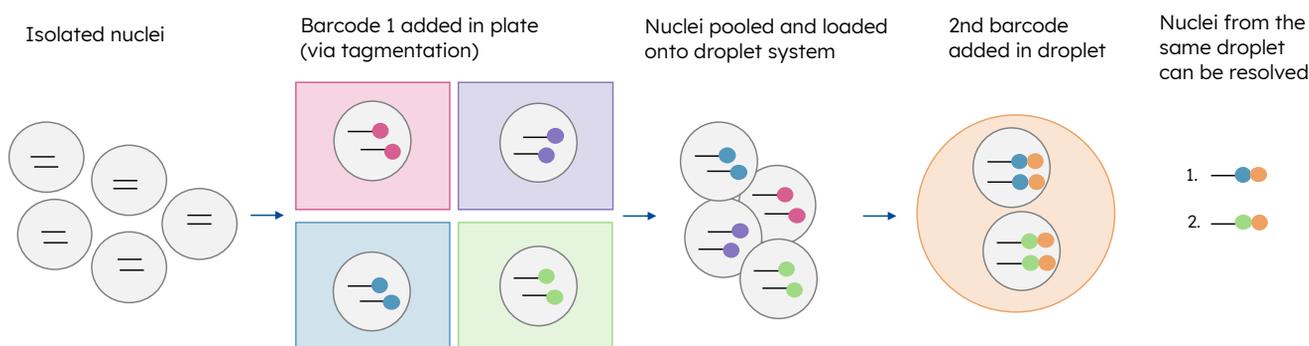
# Single Cell ATACseq at SCALE.

Process up to 300,000 nuclei per run with the ScaleBio scATAC Pre-Indexing Kit.



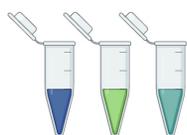
ScaleBio's scATAC Pre-Indexing Kit enables the high-throughput processing of up to 300,000 nuclei per run.

Upfront barcoding of isolated nuclei enables superloading of existing droplet systems, allowing for a 10-fold increase in throughput at a significant reduction in cost.

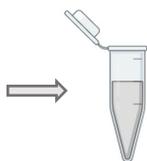


## Pre-indexing workflow: 1.5 hours with 30 minutes of hands-on time

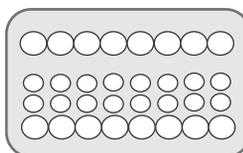
Nuclei loaded into each barcoded tagmentation well (x24)



Pre-indexed nuclei are pooled



Up to 100,000 nuclei are loaded per channel



Recover 300,000 nuclei per run



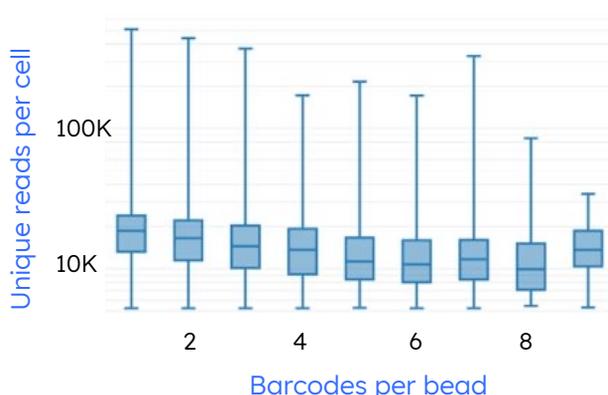
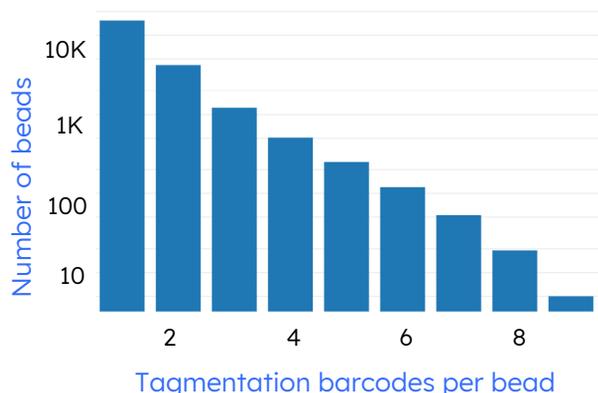
ScaleBio's bioinformatics pipeline resolves the combinatorial barcode, rescuing data from multiplets and *maintaining a 3-5% effective doublet rate.*

### Throughput

Nuclei loaded into Scale plate	1.2M
Recovery after tagmentation plate	~600K
Nuclei loaded into on-market system	600K
Recovery from sequencing	~300K



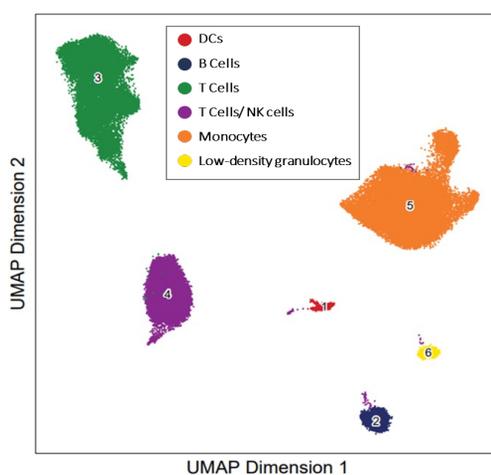
Even with extensive overloading, consistent reads per nuclei detected



## High nuclei recovery, low background, and clean cell type identification

Human PBMCs show distinct phenotypic clusters

Metric	Value
Total Reads	4,341,281,402
Aligned passing reads	92.2%
Mitochondrial reads	3.6%
Nuclei above threshold	70,496
% reads in nucleus	62.1%
Mean reads per nucleus	35,259
Median unique reads per nucleus	16,744
Saturation in nucleus	48%



## SCALE your projects and expand your research

Achieve the benefits of combinatorial indexing technology with ScaleBio



Scalable sample indexing



Cost-effective library preparation



Scalable sample throughput



Instrument agnostic and compatible