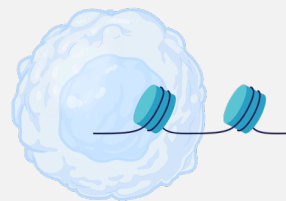




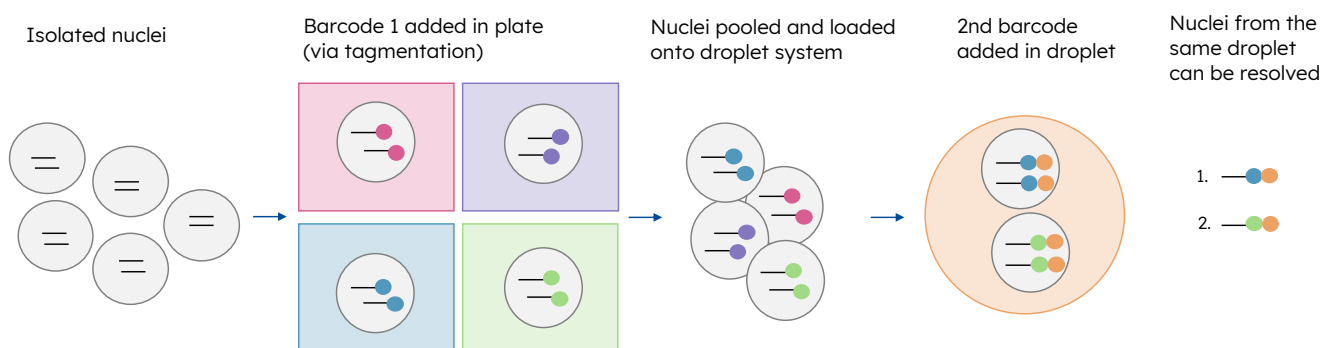
Single Cell ATACseq at SCALE.

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



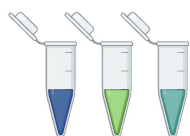
ScaleBio's scATAC Pre-Indexing Kit enables the high-throughput processing of up to 300,000 nuclei per run.

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.

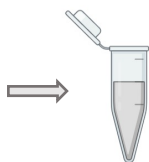


Pre-indexing workflow: 1.5 hours with 30 minutes of hands-on time

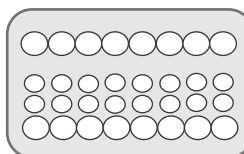
Nuclei loaded into each barcoded tagmentation well (x24)



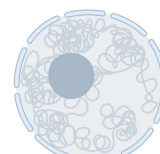
Pre-indexed nuclei are pooled



Up to 100,000 nuclei are loaded per channel



Recover 300,000 nuclei per run

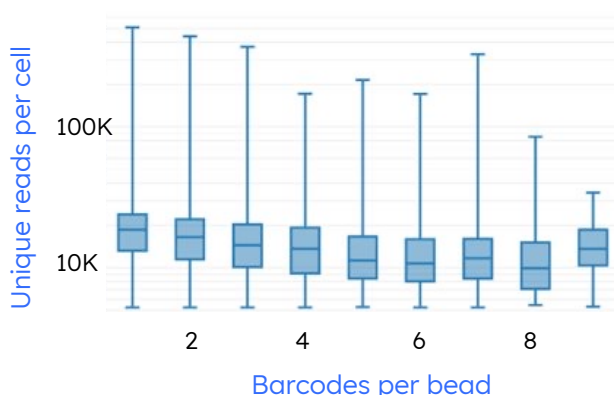
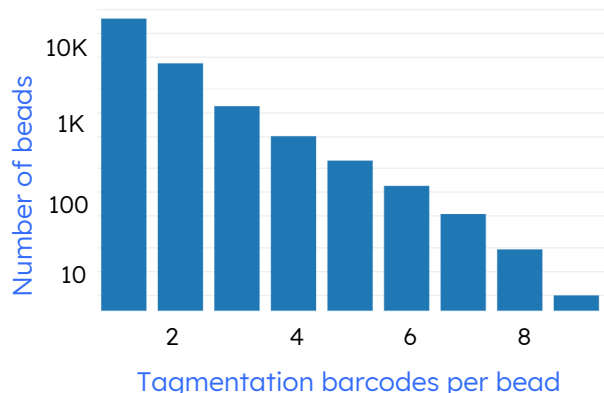


ScaleBio's bioinformatics pipeline resolves the combinatorial barcode, rescuing data from multiplets and *maintaining a 3-5% effective doublet rate.*

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



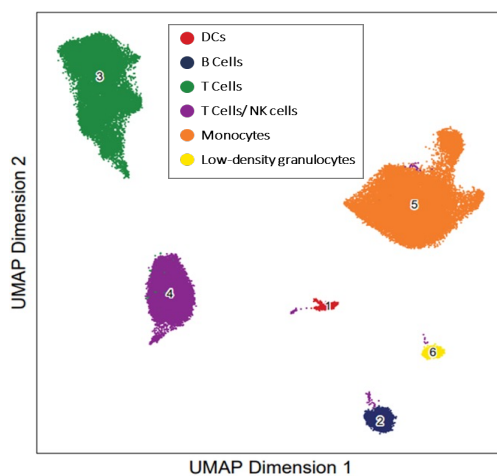
Even with extensive overloading, consistent reads per nuclei detected



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



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