

## Background

### Problem

Throughput of single-cell experiments has not scaled, primarily due to high costs, making single-cell screens and profiling of rare cell populations or large patient cohorts prohibitively expensive.

### Solution

Here we increase the throughput of on-market systems by adding upstream combinatorial indexing technology using the ScaleBio™ scATAC pre-indexing kit, and with the stand-alone ScaleBio™ Single Cell RNA Sequencing Kit, which using three levels of indexing.

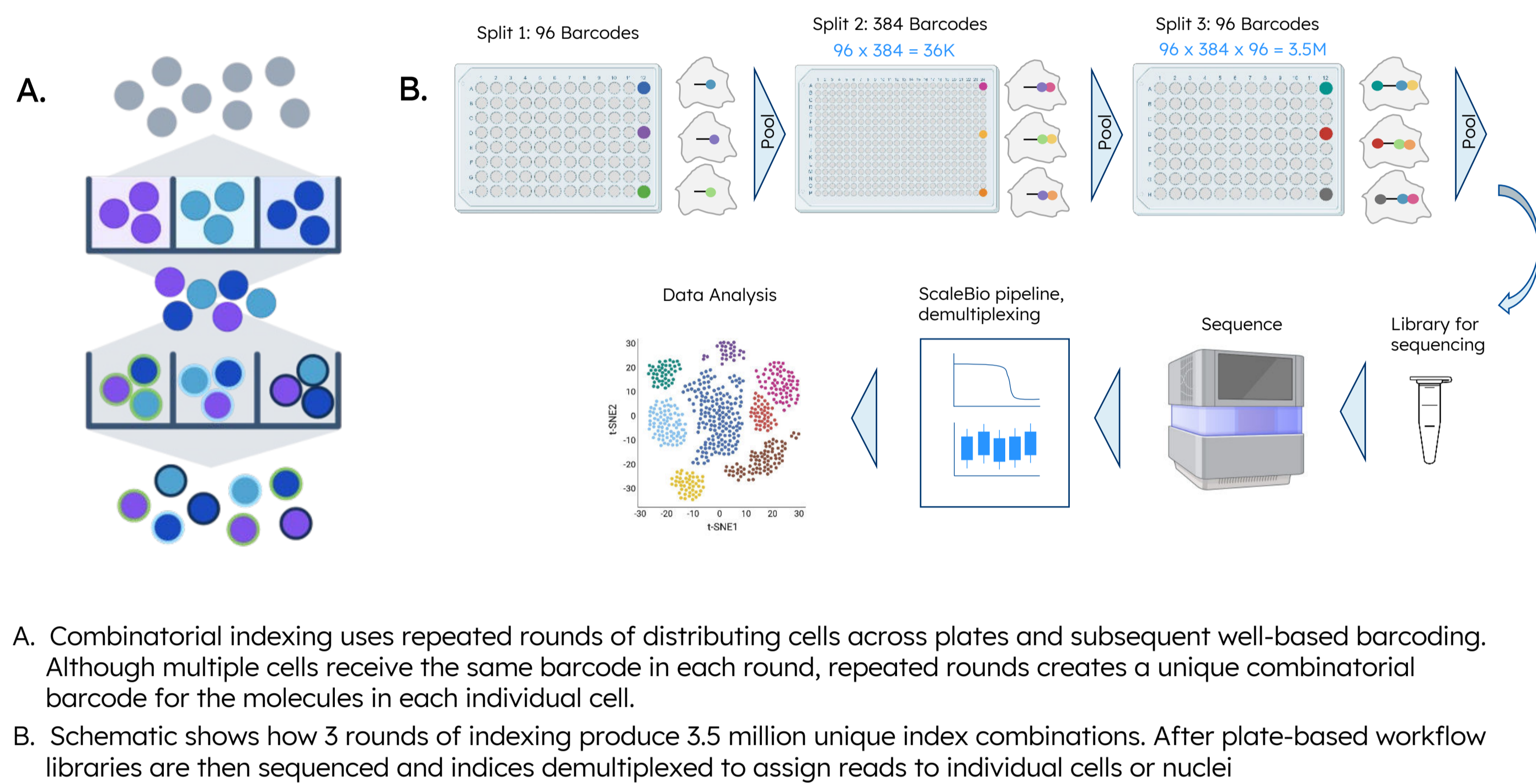
### Workflow

- **ATAC:** Nuclei from up to 24 samples are distributed across a plate for barcoded tagmentation. Nuclei can then be pooled and superloaded onto existing single-cell capture systems with up to 100,000 nuclei per channel while using the additional barcode to recover data from multiplets, maintaining a theoretical effective doublet rate of 3-5%.
- **RNA:** A 50:50 mix of human K562 and mouse 3T3 cells were processed through the 3-level scRNAseq workflow. Sequencing of these libraries demonstrates strong RNAseq metrics and low background and doublet rates. Similar observations could be made for PBMCs processed through this workflow, with major cell types easily identified.

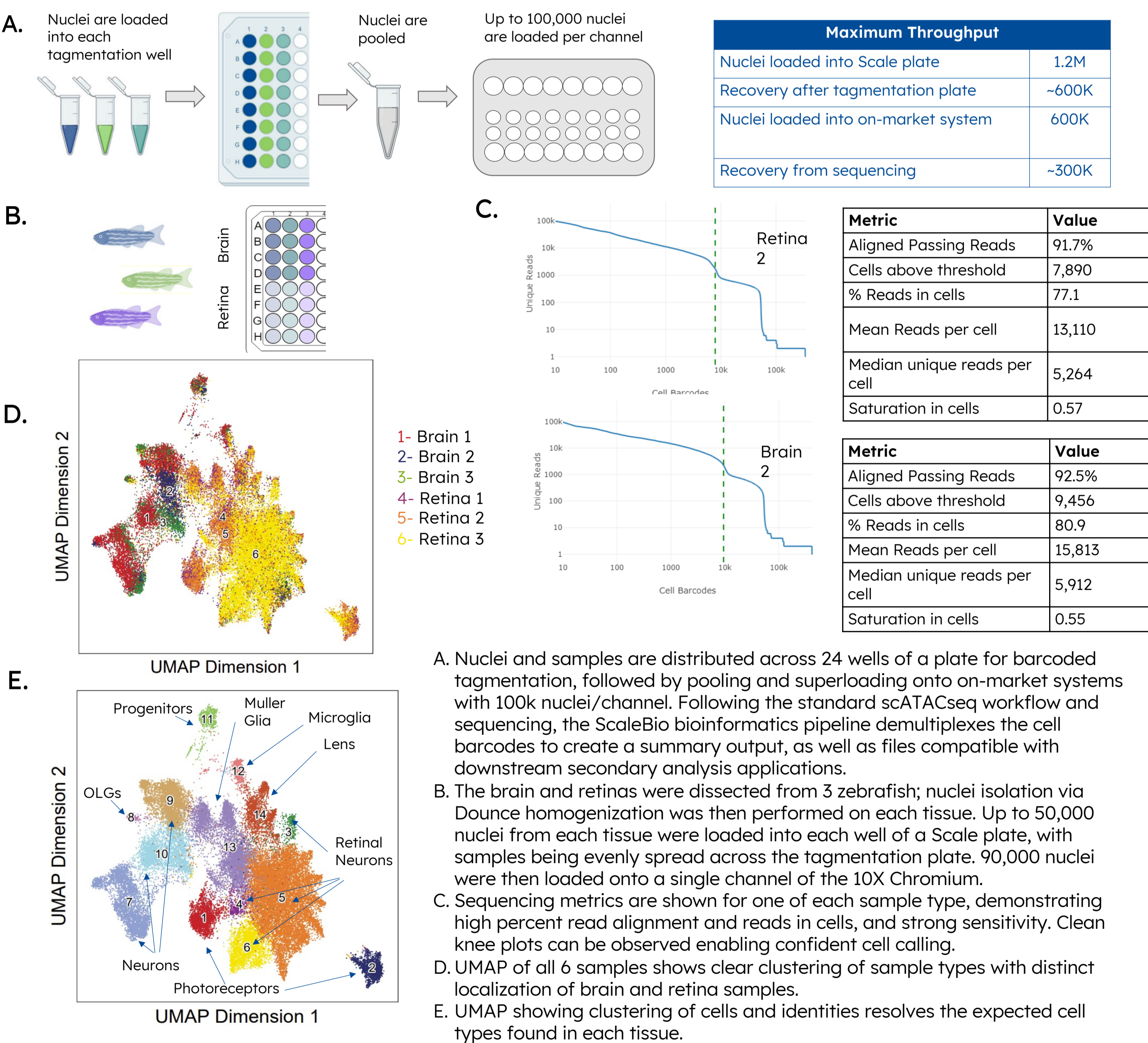
### Results

Combinatorial indexing can be effectively applied to single cell applications to increase throughput while decreasing cost.

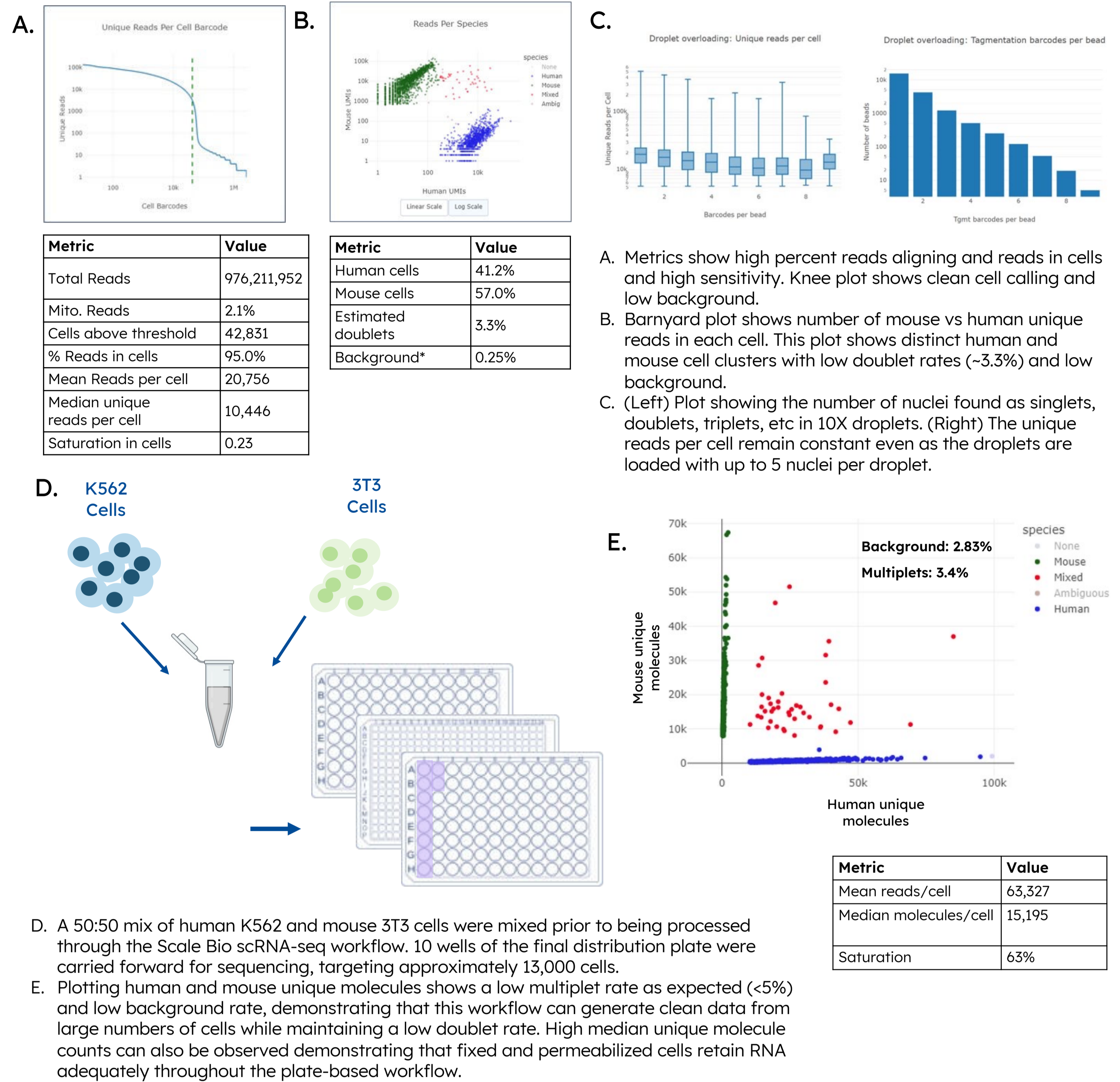
**Figure 1: Combinatorial indexing technology can be used to increase single cell sequencing throughput, while decreasing cost.**



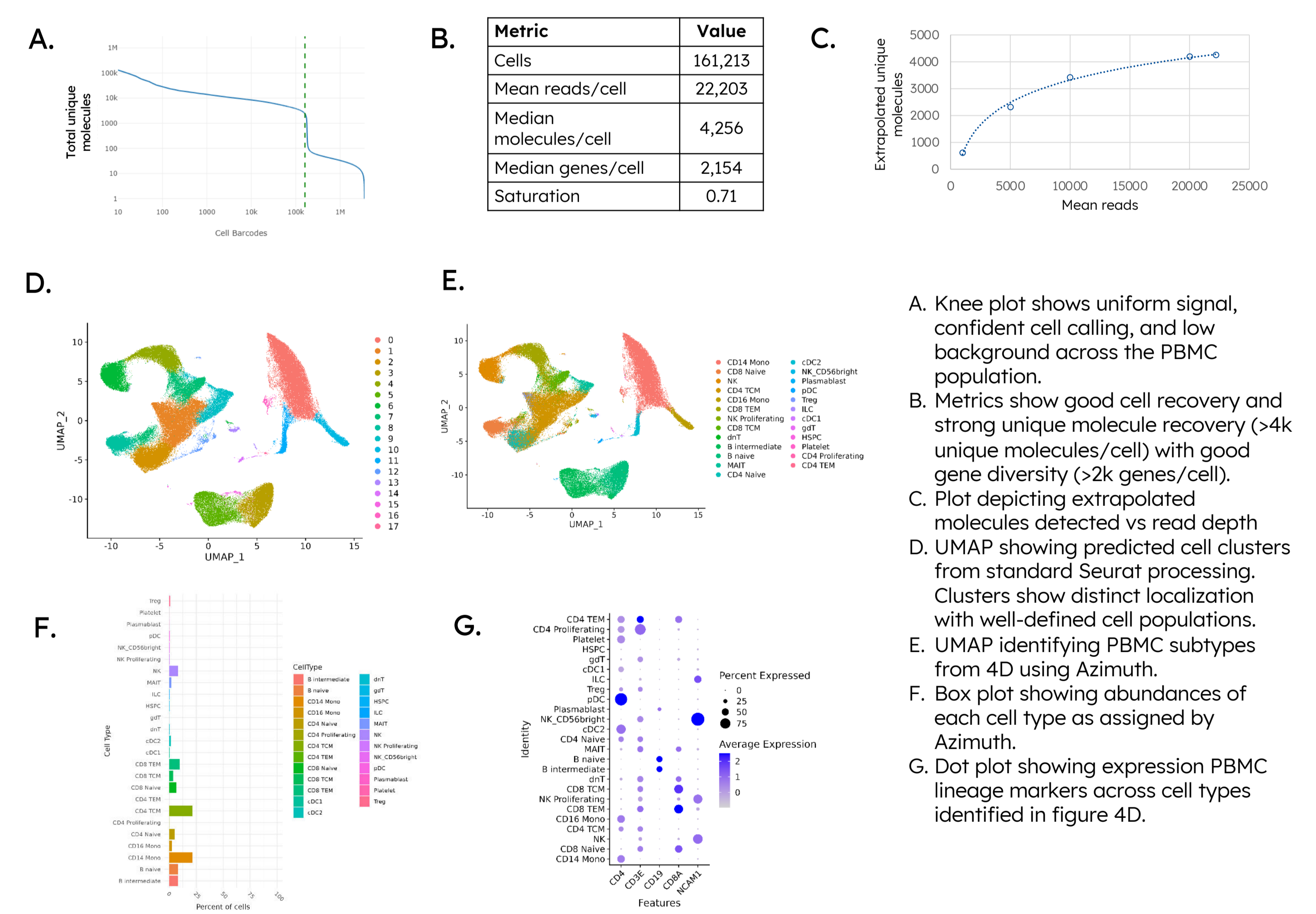
**Figure 3: ScaleBio ATACseq pre-indexing workflow produces good cell recovery, strong ATAC metrics, and successful cell-type identification with zebrafish brain and retina.**



**Figure 2: ScaleBio scATAC and scRNA-seq workflows produce high quality data with low background and multiplet rate**



**Figure 4: ScaleBio scRNA-seq kit produces high quality data with high cell recovery, UMI, and gene counts**



## Conclusions

- The ScaleBio™ scATAC pre-indexing kit can be used to increase throughput of existing scATACseq methods by enabling superloading of a 10X lane while maintaining low effective doublet rates and background and high sensitivity, nuclei recovery, and cell-type resolution.
- The ScaleBio™ Single Cell RNA Sequencing Kit shows strong cell recovery with high sensitivity and low background. Data from PBMCs shows that the kit can recover the expected major cell populations from PBMCs.