

Scalable, multimodal profiling of chromatin accessibility, protein levels and mitochondrial genotypes in single cells

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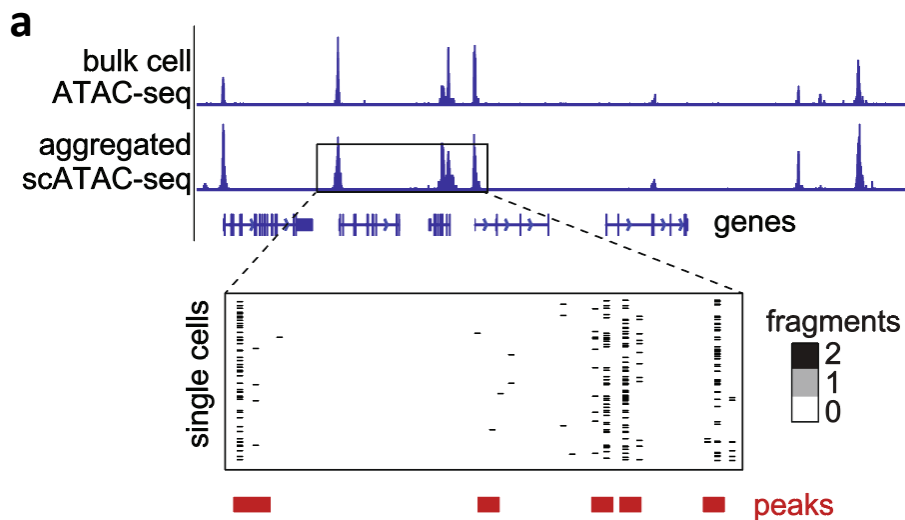
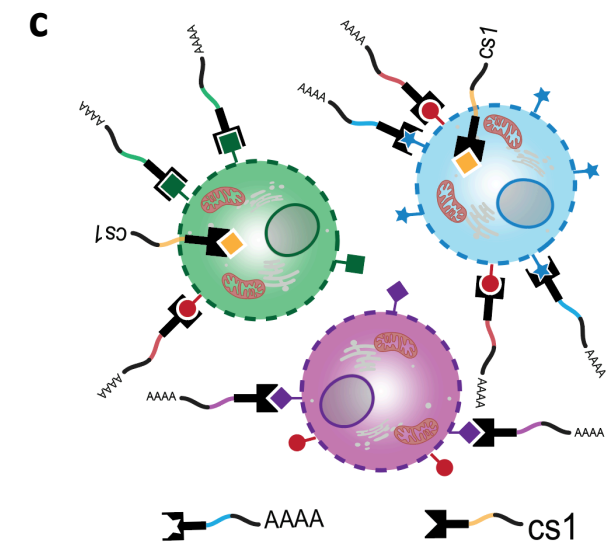
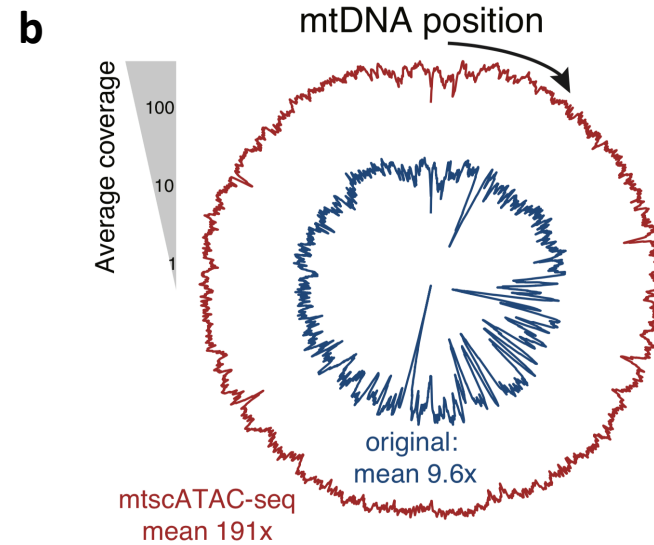


Figure adapted from Chen et al. *Genome Biology* 2019



Single cell Assay for Transposase-Accessible Chromatin by sequencing (**scATAC-seq**)

- Gene regulatory elements
- Transcription factor activity

Mitochondrial mtscATAC-seq

- Whole mtDNA genome sequencing
- Germline and somatic mutation detection for clonal tracing and mitochondrial disease studies

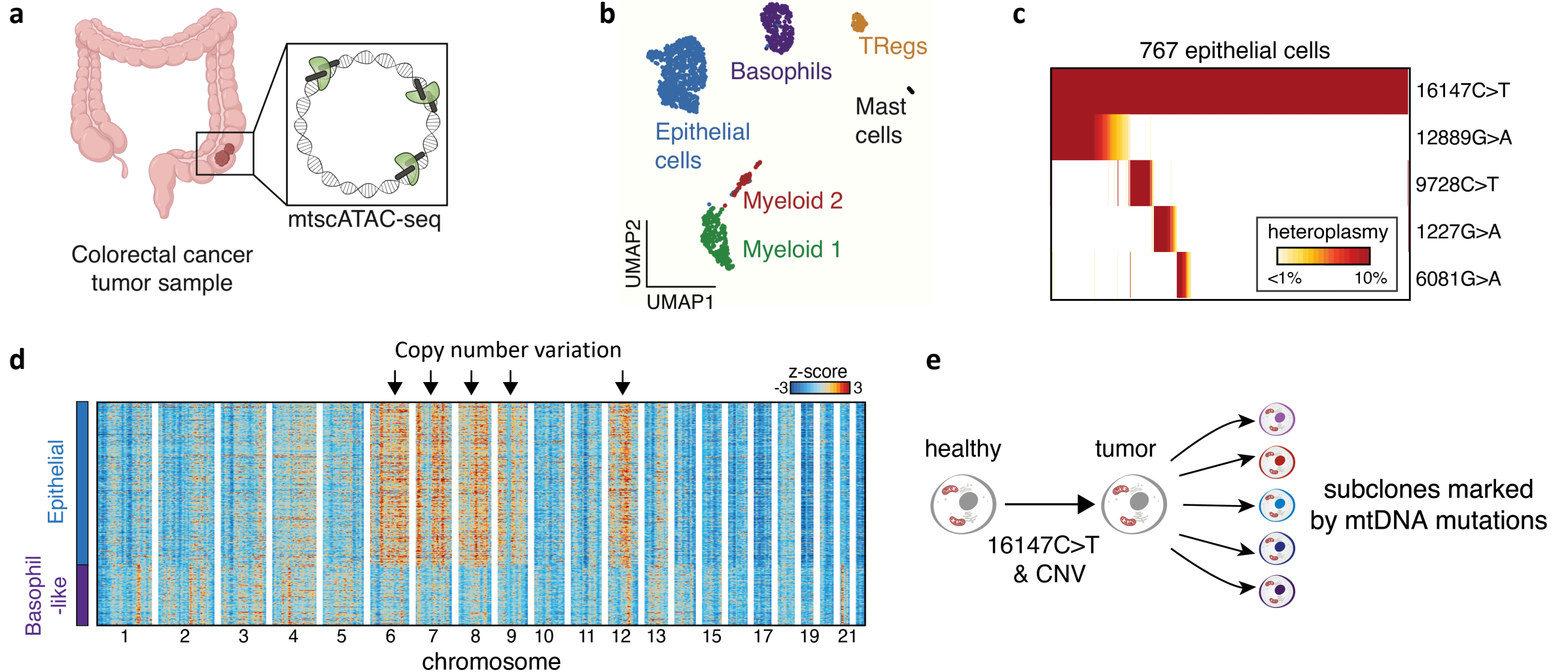
ATAC-seq with Surface Antigen Profiling by sequencing (ASAP-seq)

- Co-detection of surface and intracellular proteins

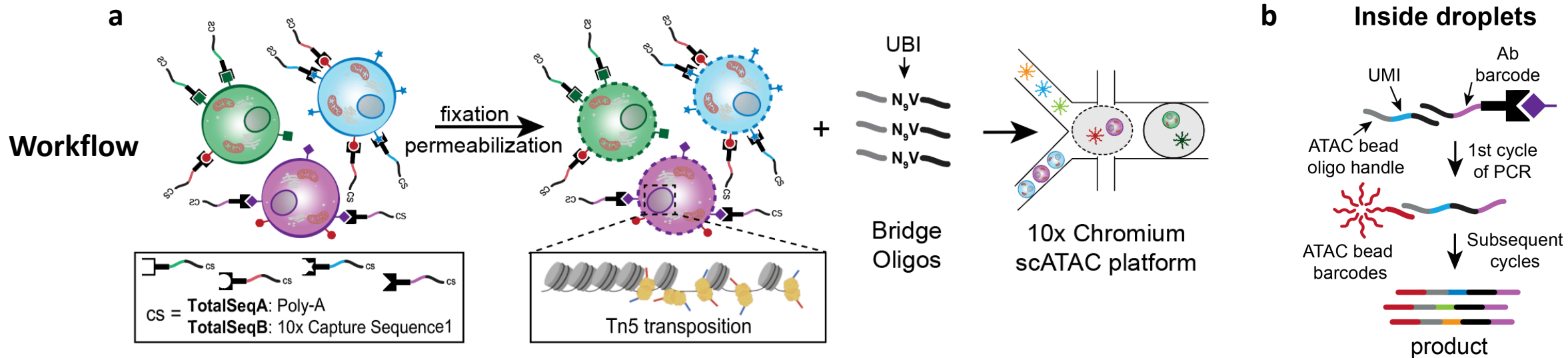
mtscATAC-seq → mitochondrial and nuclear mutations resolve clonal structures in human colorectal cancer

Somatic mitochondrial mutations and copy number variants detected from mtscATAC-seq data

- Combined detection of different types of somatic variants presents a powerful means to better resolve subclonal structures and associated clonal phenotypes and evolutionary processes in malignancies

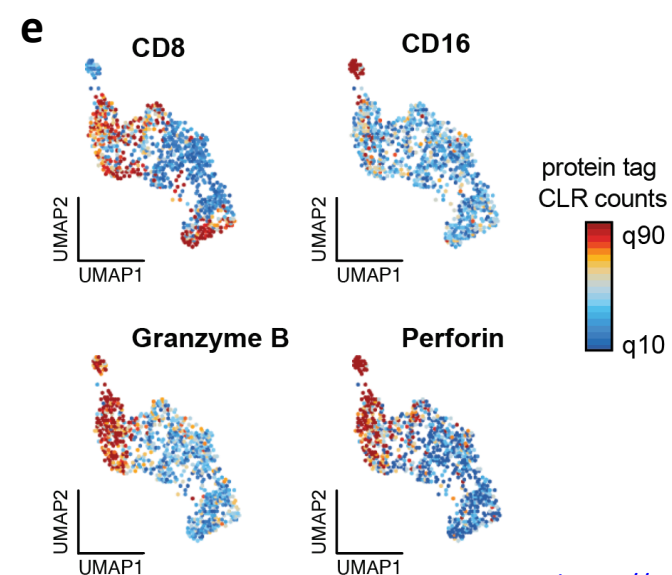
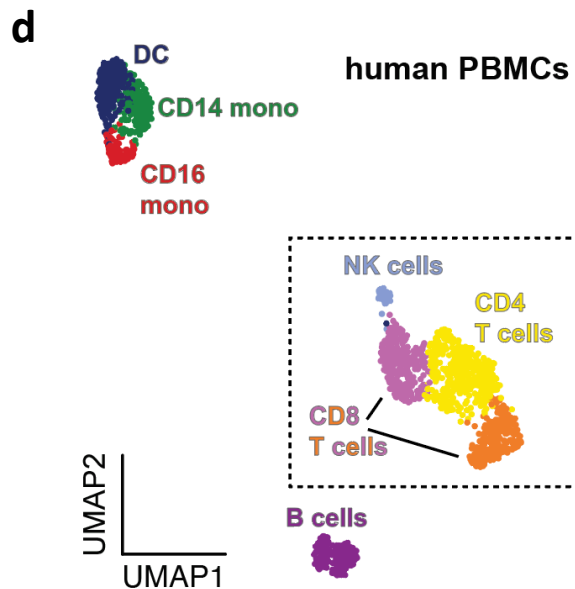
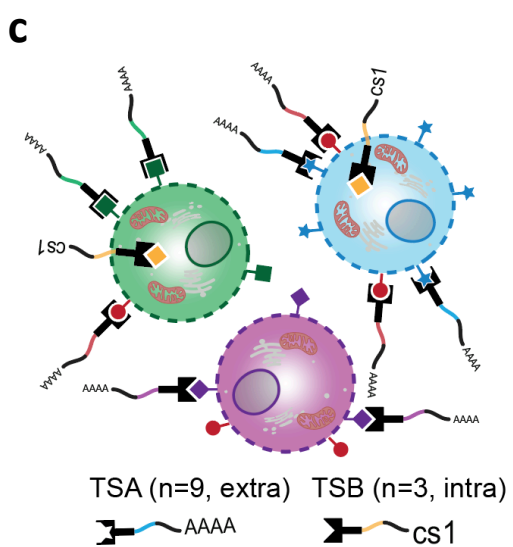


ASAP-seq enables co-detection of surface markers and intracellular proteins

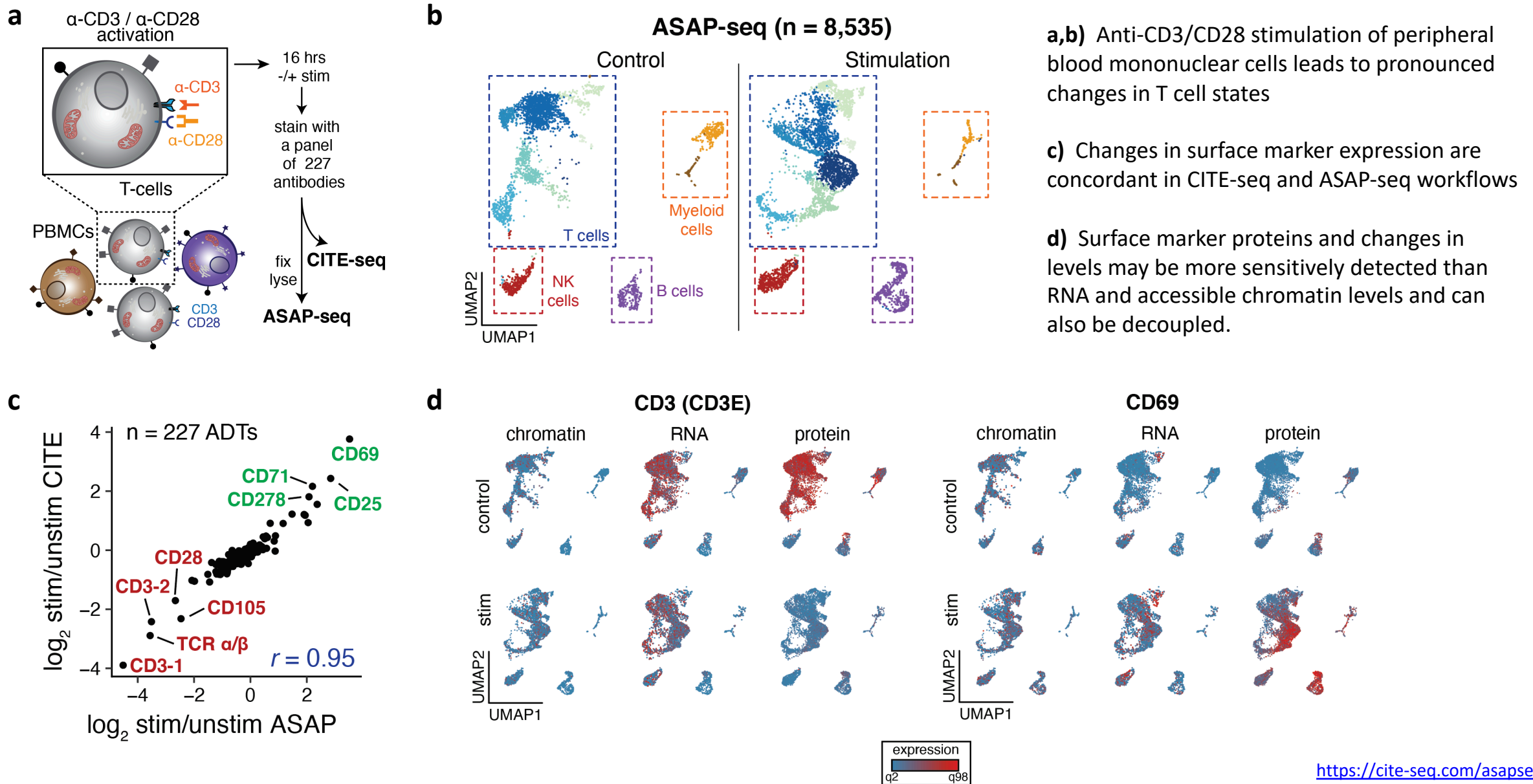


Intracellular staining

- Use of different oligo handles
- Specific staining of Granzyme B and Perforin in NK and cytotoxic T cells



Combined CITE- & ASAP-seq of anti-CD3/CD28 stimulated human PBMCs



a,b) Anti-CD3/CD28 stimulation of peripheral blood mononuclear cells leads to pronounced changes in T cell states

c) Changes in surface marker expression are concordant in CITE-seq and ASAP-seq workflows

d) Surface marker proteins and changes in levels may be more sensitively detected than RNA and accessible chromatin levels and can also be decoupled.