



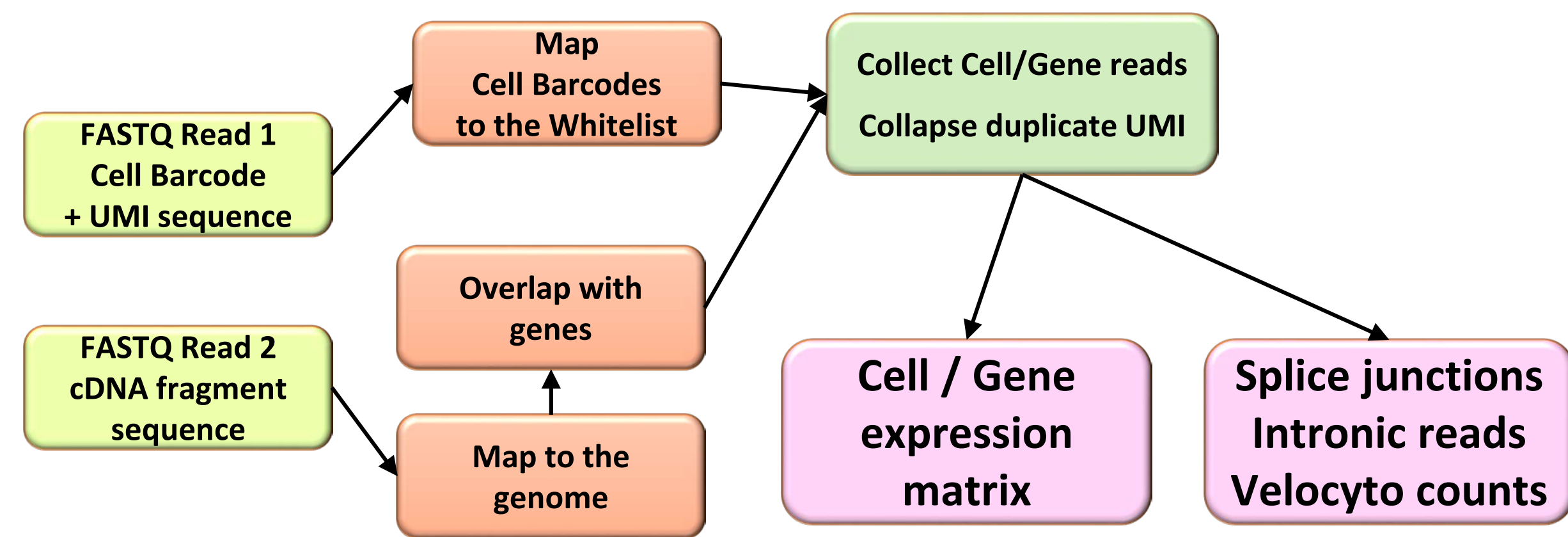
# STARsolo: single-cell RNA-seq analyses beyond gene expression.

Ash Blibaum, Jonathan Werner, and Alexander Dobin

Cold Spring Harbor Laboratory



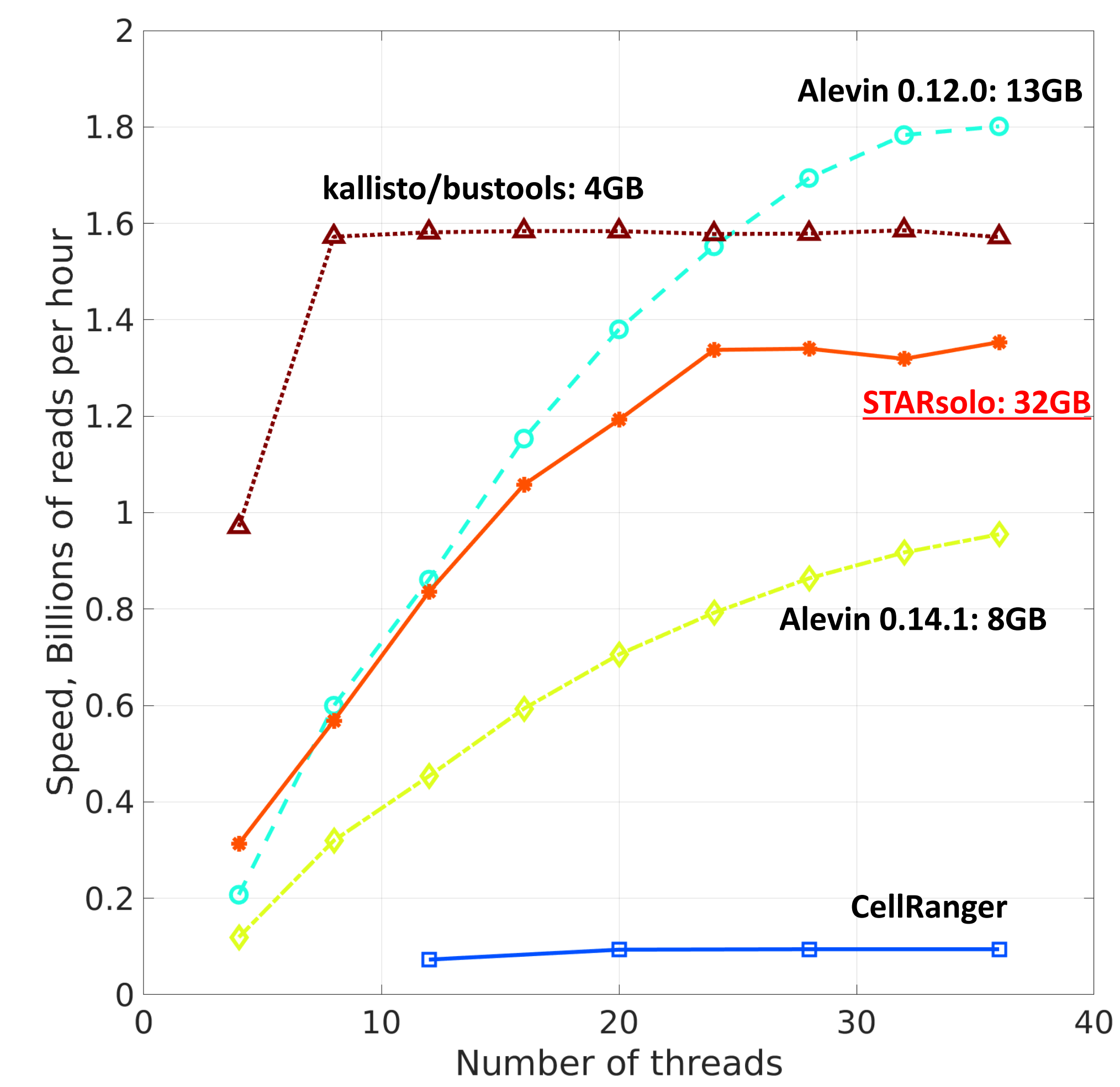
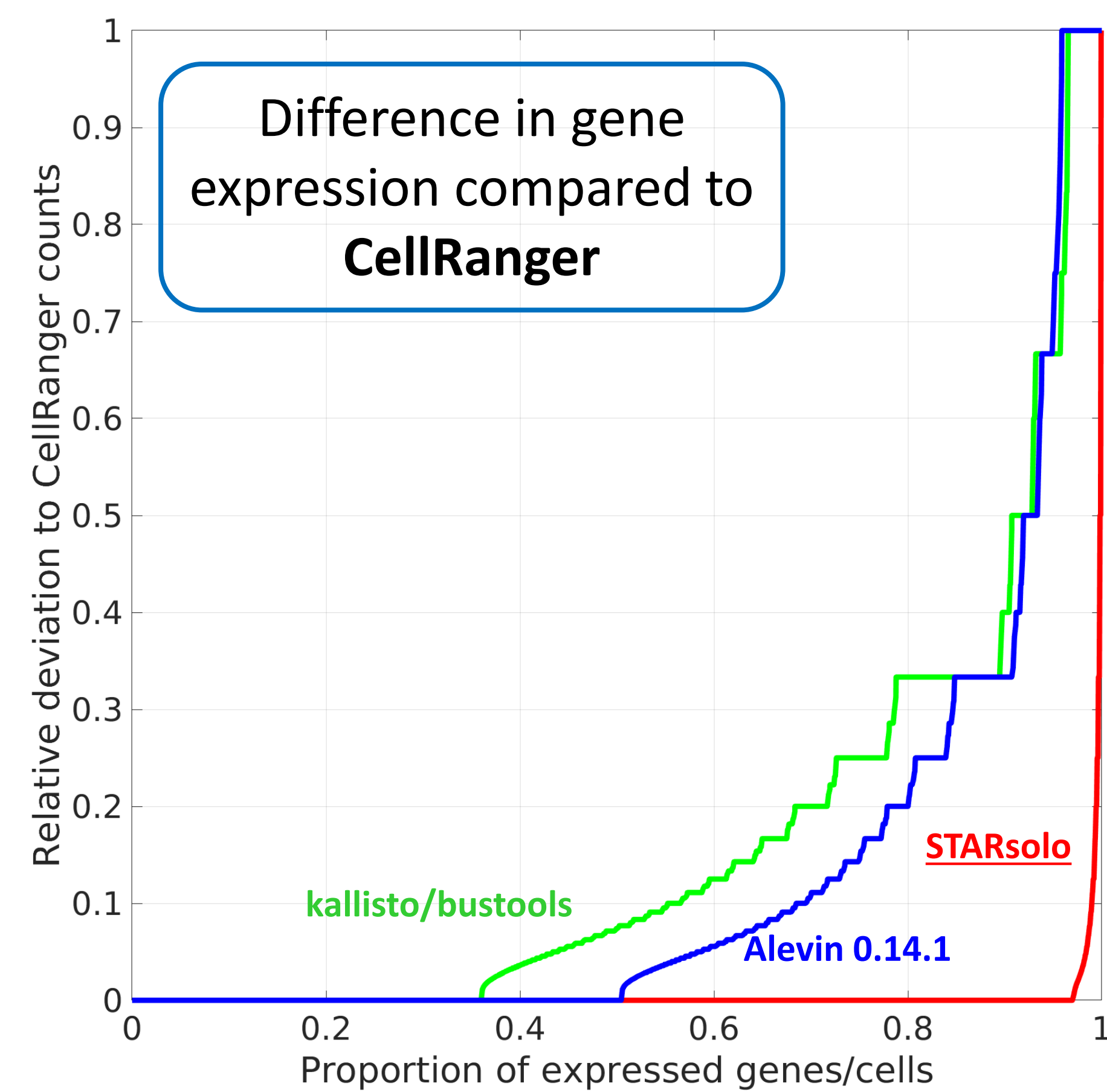
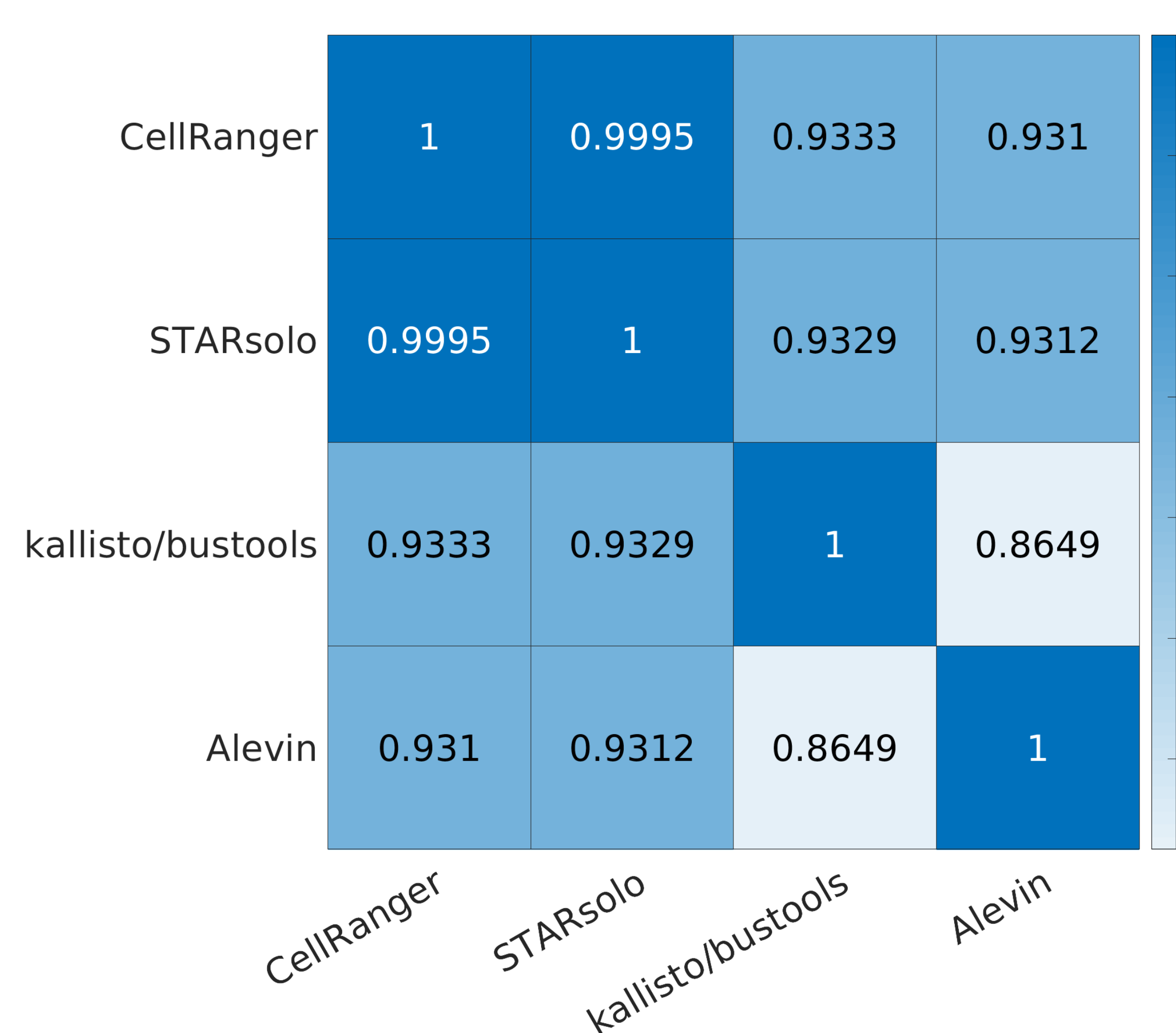
## STARsolo algorithm



## STARsolo advantages

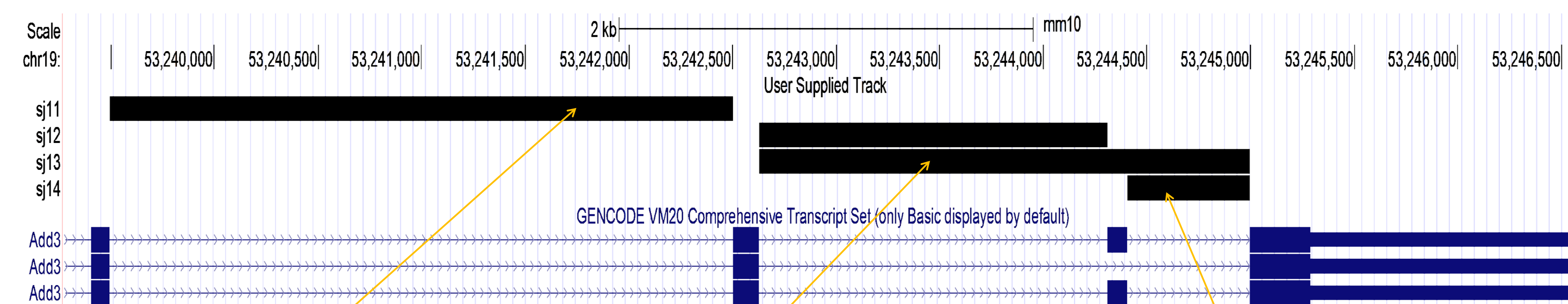
- Gene/cell counts are nearly identical to CellRanger's drop-in replacement for unfiltered gene/cell count matrix
  - STAR ... --soloType Droplet --soloCBwhitelist whitelist.txt
- 10X faster than CellRanger only 10% overhead over mapping to genome
- Maps (not pseudomaps) to the genome (not transcriptome) intronic reads, novel isoforms, etc
- Open source (MIT) open to implementing other features manuscript in preparation
- Outputs other transcriptomic features
  - splice junctions: annotated and novel
  - intronic reads: for single-nucleus RNA-seq
  - isoforms quantification: STARsolo-Quant
  - velocity (LaManno et al) spliced/unspliced counts
  - Coming soon: novel polyA-sites, promoters (5' protocol) fusions
- Support other protocols
  - Drop-seq, SeqWell, etc: no whitelist
  - inDrop, other complex barcodes
  - Coming soon: Smart-seq, Split-seq, sci-RNA-seq

## Benchmarking: 10X Genomics dataset: 4k Pan T Cells from a Healthy Donor

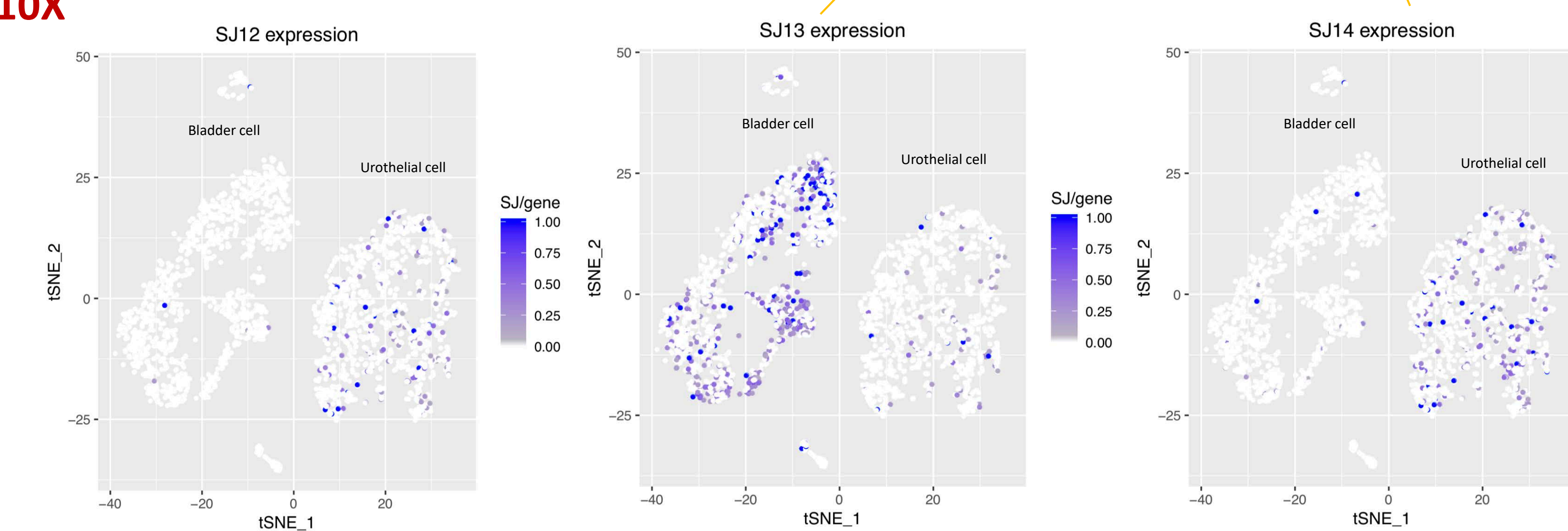


## Alternative splicing: HCA Tabula Muris datasets

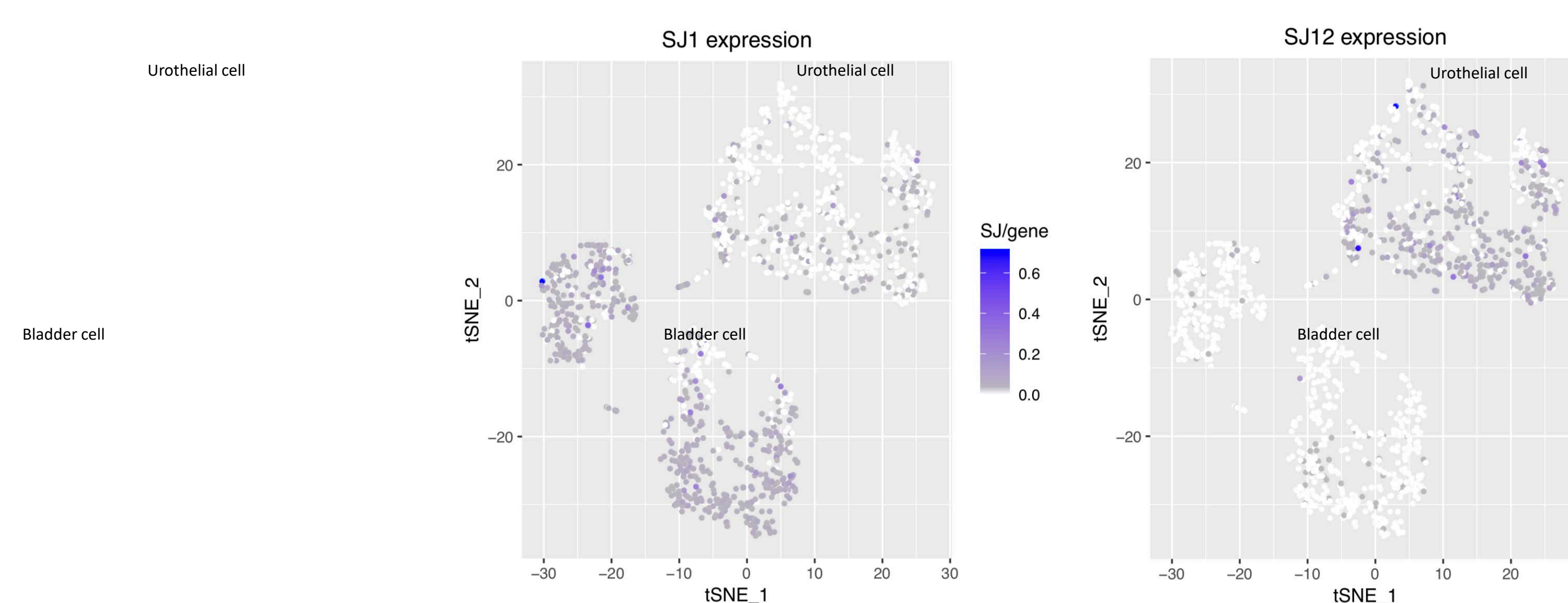
Example: Gene Add3: Adductin gamma: membrane skeletal protein involved in spectrin-actin network assembly



10X



Smart-seq



## Novel splicing: 10X 9k Mouse Brain Cells

