# Identification of transcriptional signatures for cell types from single-cell RNA-Seq
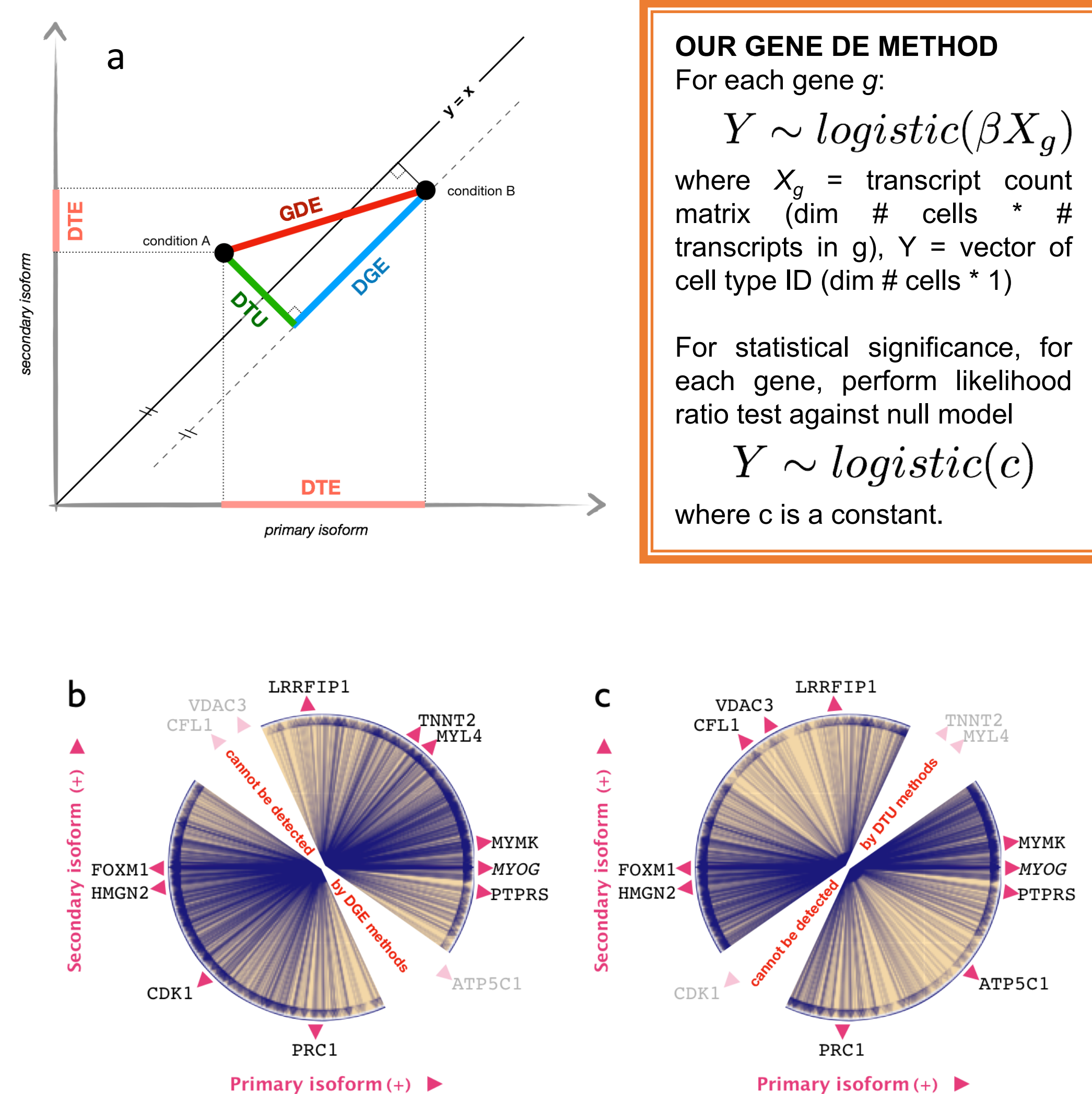
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*Authors contributed equally, 1. UCLA-Caltech Medical Science Training Program   2. California Institute of Technology
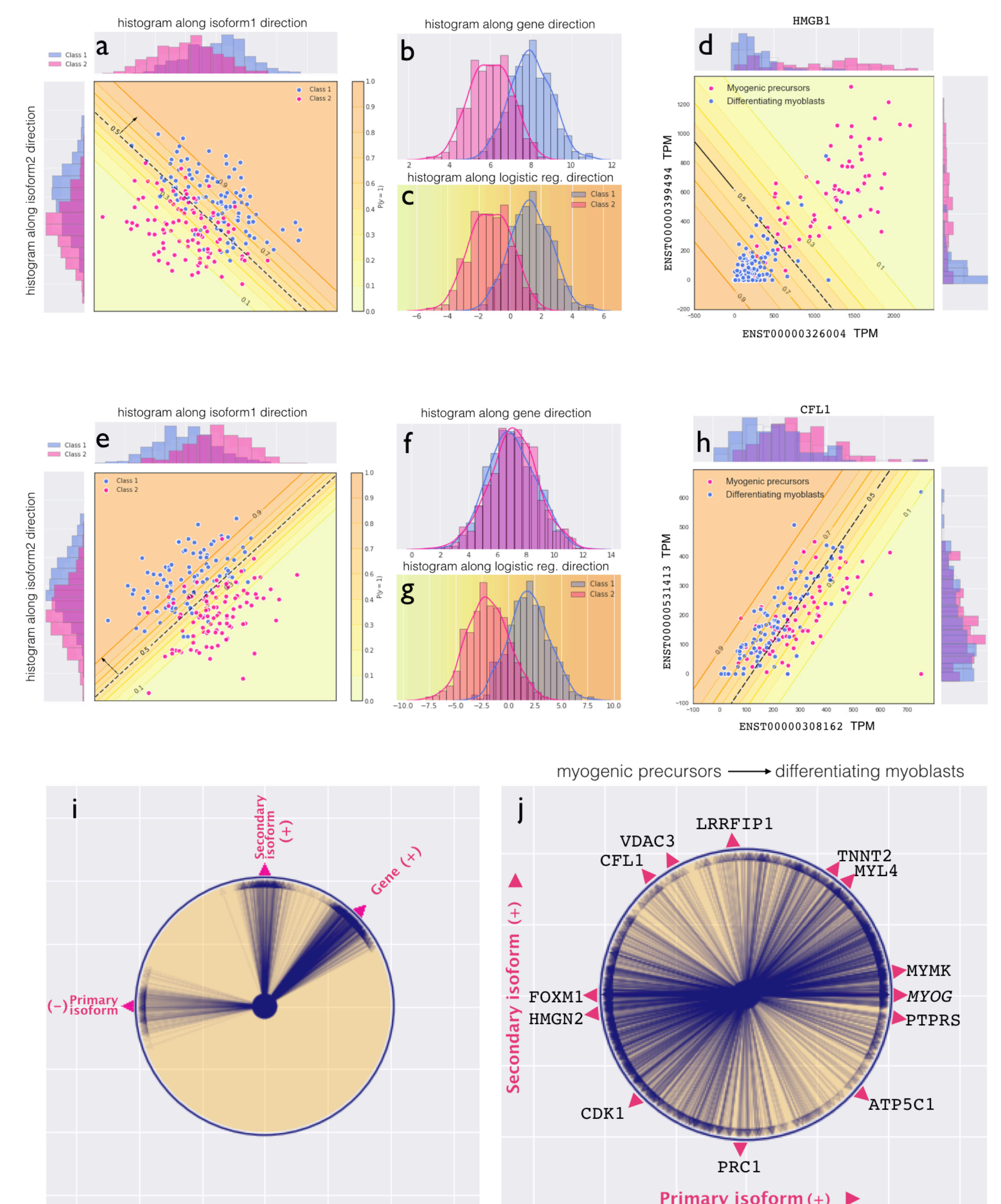3. UC Berkeley   4. Stanford University   5. University of Iceland

Overview of single cell RNA-seq workflows

Figure from Haque et al., 2017
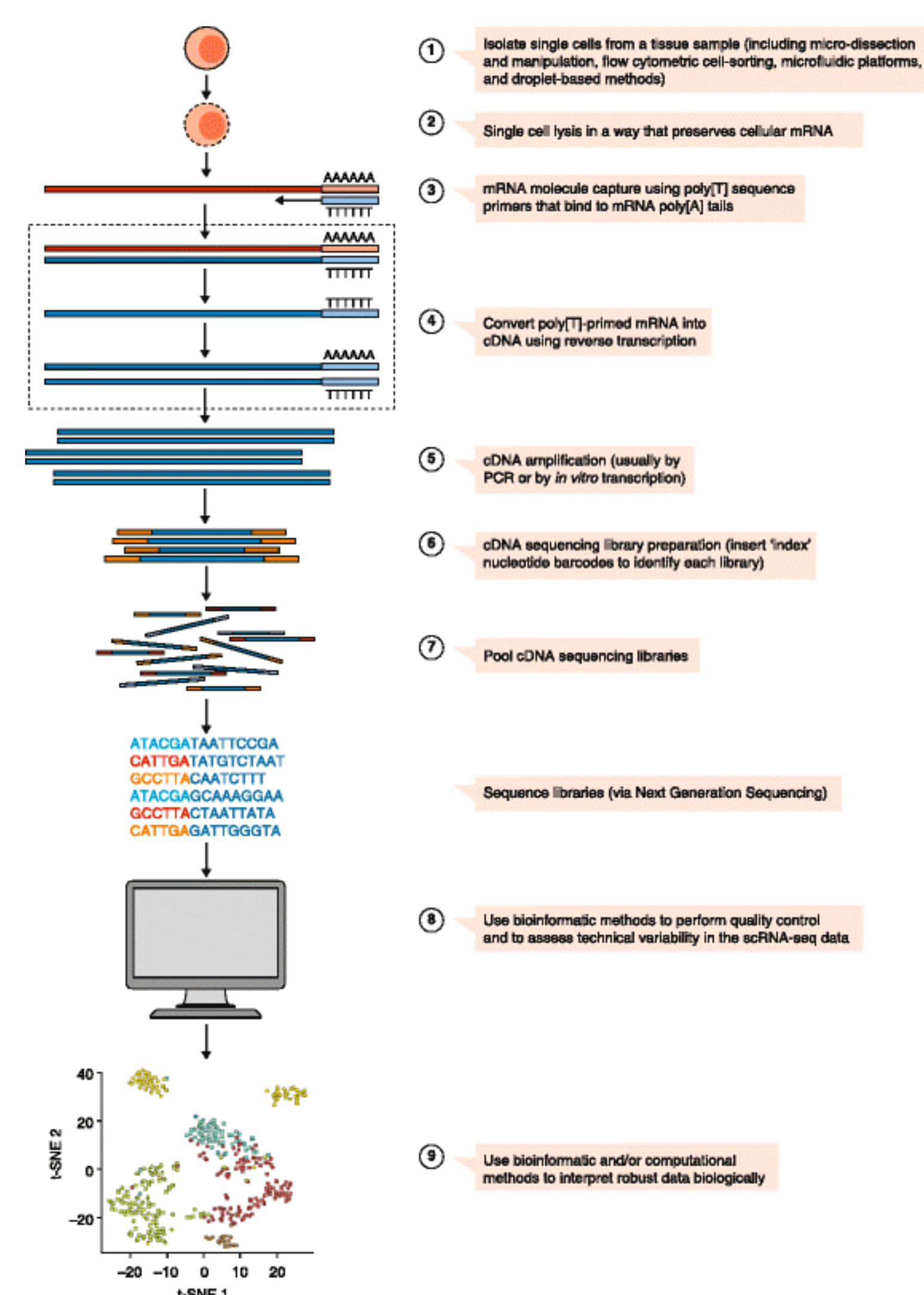
Traditional DE methods choose either a resolution of either genes or isoforms

OUR GENE DE METHOD
For each gene g:
$$Y \sim logistic(\beta X_g)$$
where X_g = transcript count matrix (dim # cells * # transcripts in g), Y = vector of cell type ID (dim # cells * 1)

For statistical significance, for each gene, perform likelihood ratio test against null model
$$Y \sim logistic(c)$$
where c is a constant.

Our method is sensitive to and reveals isoform dynamics

Simulations were used to evaluate our method
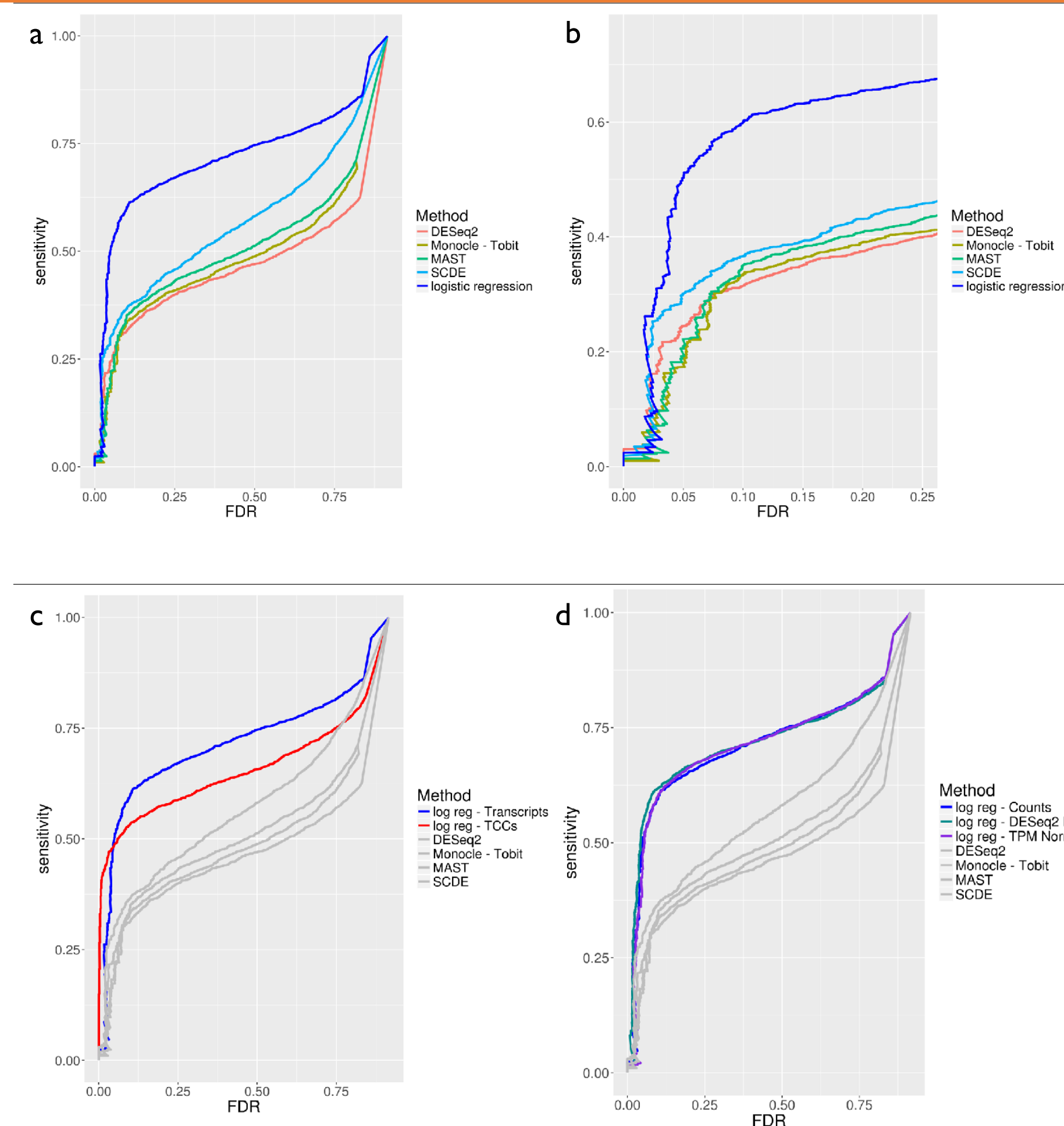
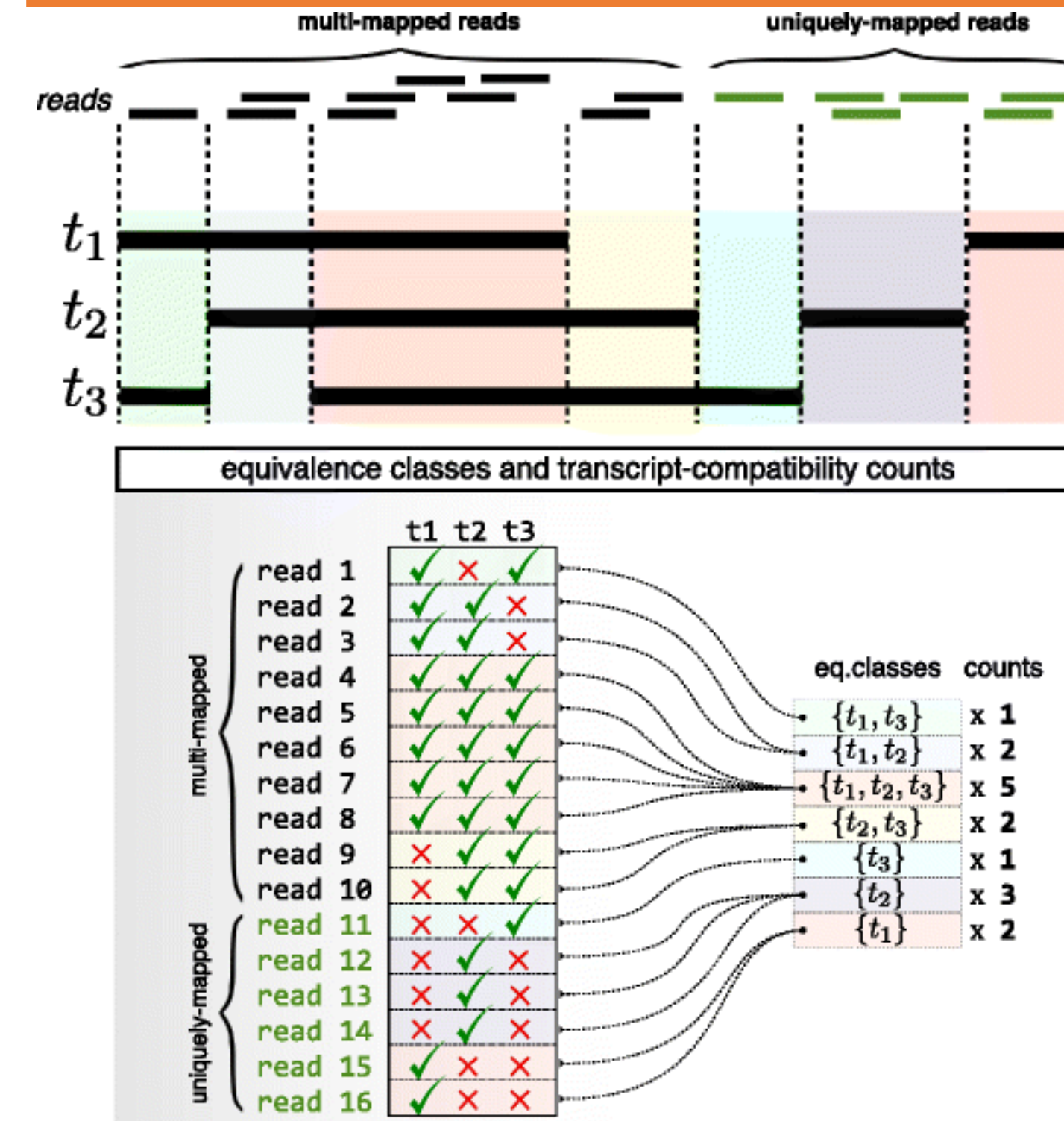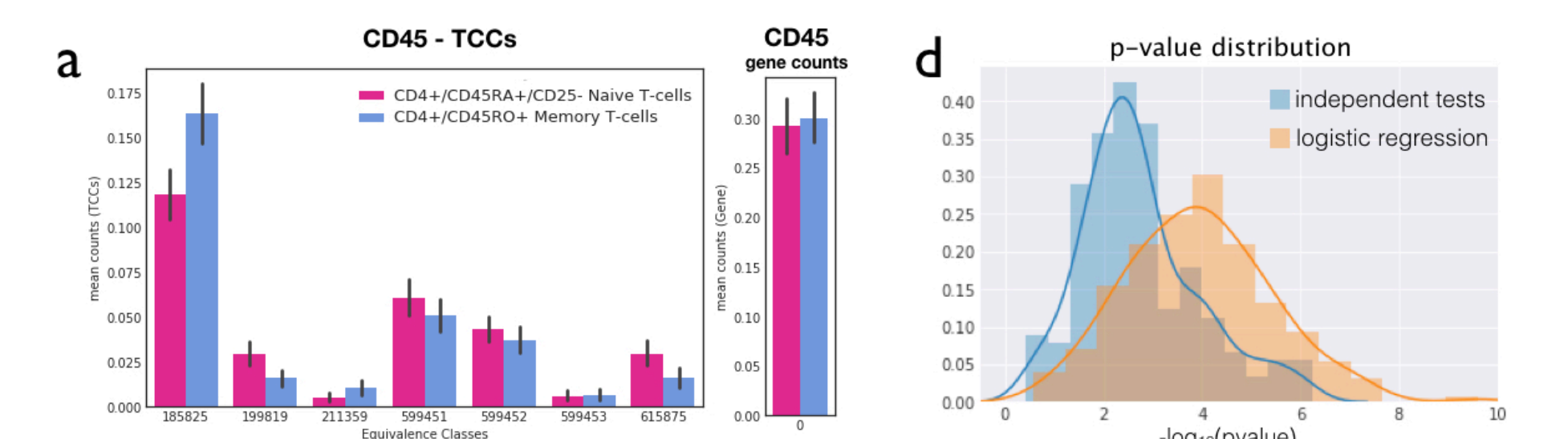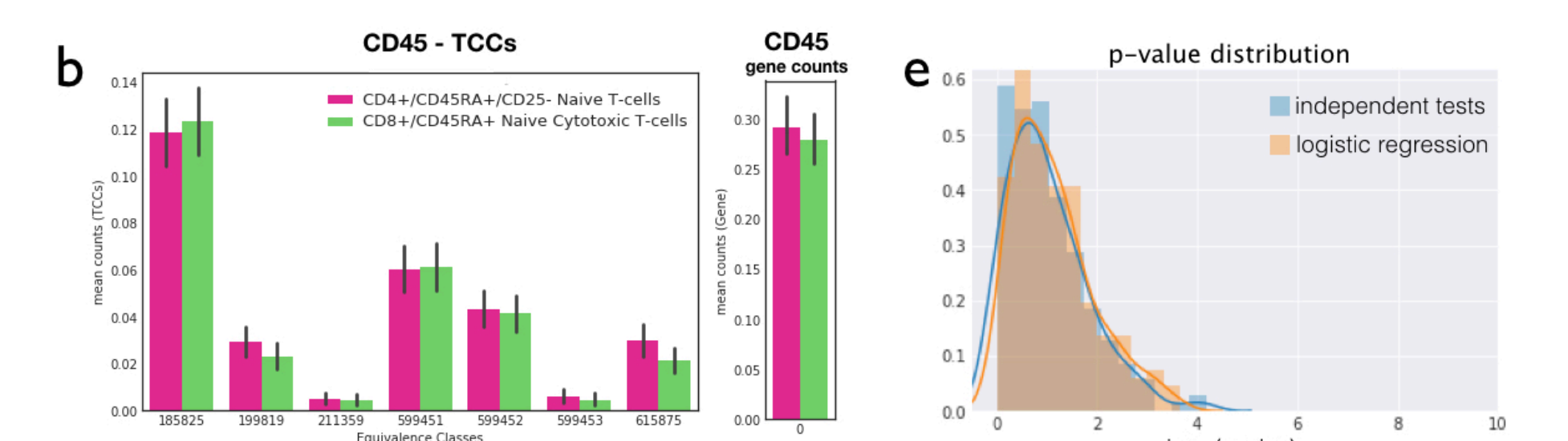## Transcript compatibility counts preserve isoform information

Figure from Ntranos et al., 2017

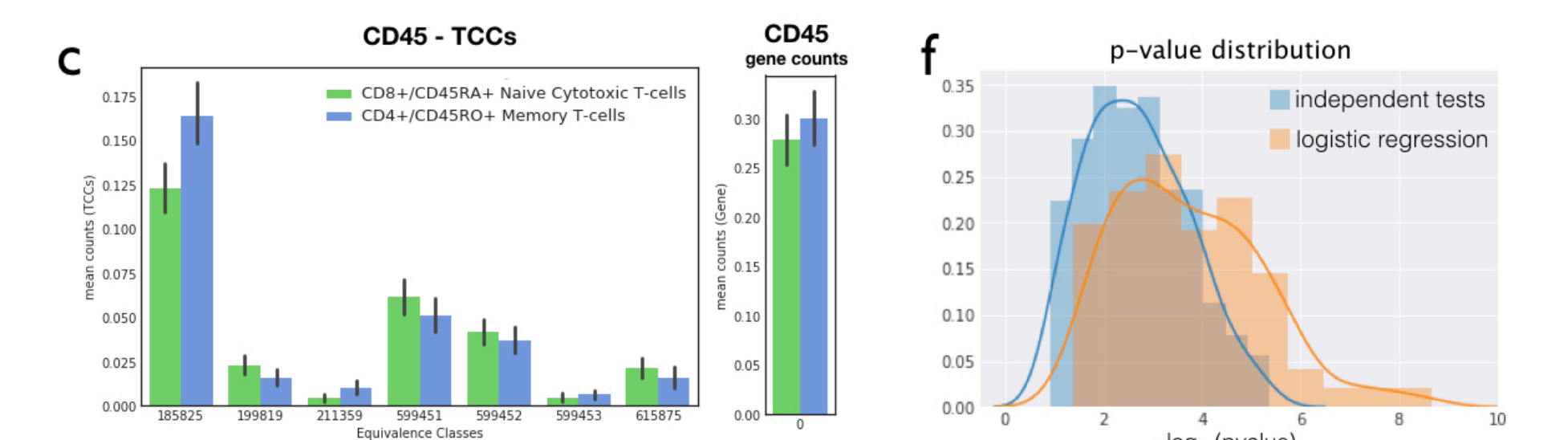## Marker of memory v. naïve T cells found using purified cell types

Naïve T-cells (CD4+/CD45RA+/CD25-) vs Memory T-cells (CD4+/CD45RO+)

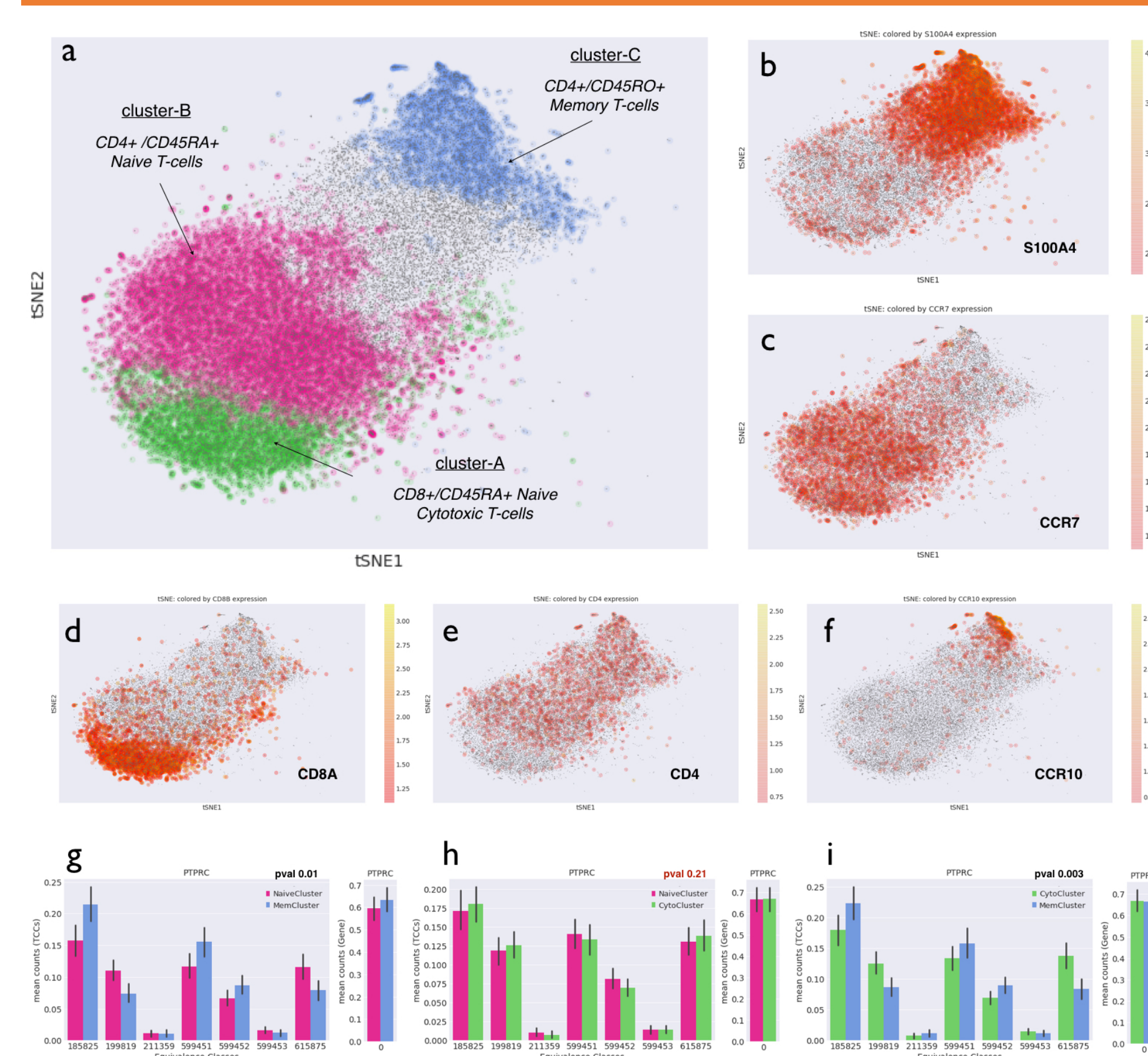Naïve T-cells (CD4+/CD45RA+/CD25-) vs Naïve Cytotoxic T-cells (CD8+/CD45RA+)

Naïve Cytotoxic T-cells (CD8+/CD45RA+) vs Memory T-cells (CD4+/CD45RO+)

kallisto pseudobam can be used to visualize and interpret TCC results

De novo analysis of 10x PBMC data recapitulates discovery in purified cell types

References

1. Haque et al., A practical guide to single-cell RNA-sequencing for biomedical research and clinical applications, *Genome Medicine*, 2017.
2. Yi et al., Gene-level differential analysis at transcript-level resolution, *Genome Biology*, 2017.
3. Bray et al., Near-optimal probabilistic RNA-seq quantification, *Nature Biotechnology*, 2017.
4. Ntranos et al., Fast and accurate single-cell RNA-seq analysis by clustering of transcript-compatibility counts, *Genome Biology*, 2017.
5. Zheng et al., Massively parallel digital transcriptional profiling of single cells, *Nature communications,* 2017.

Acknowledgements