

CiteFuse enables multi-modal analysis of CITE-seq data

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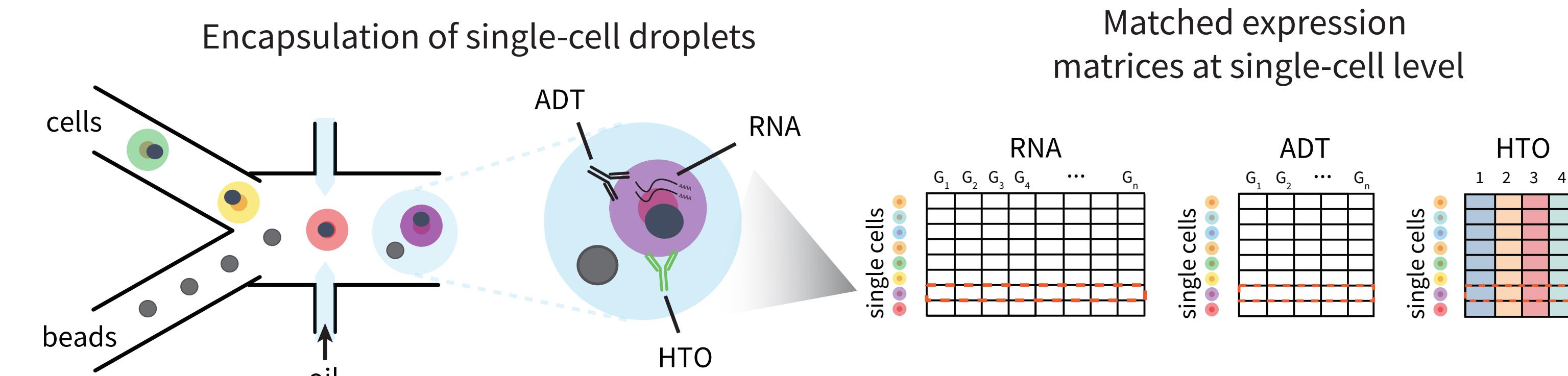
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The dawn of single-cell multi-omics

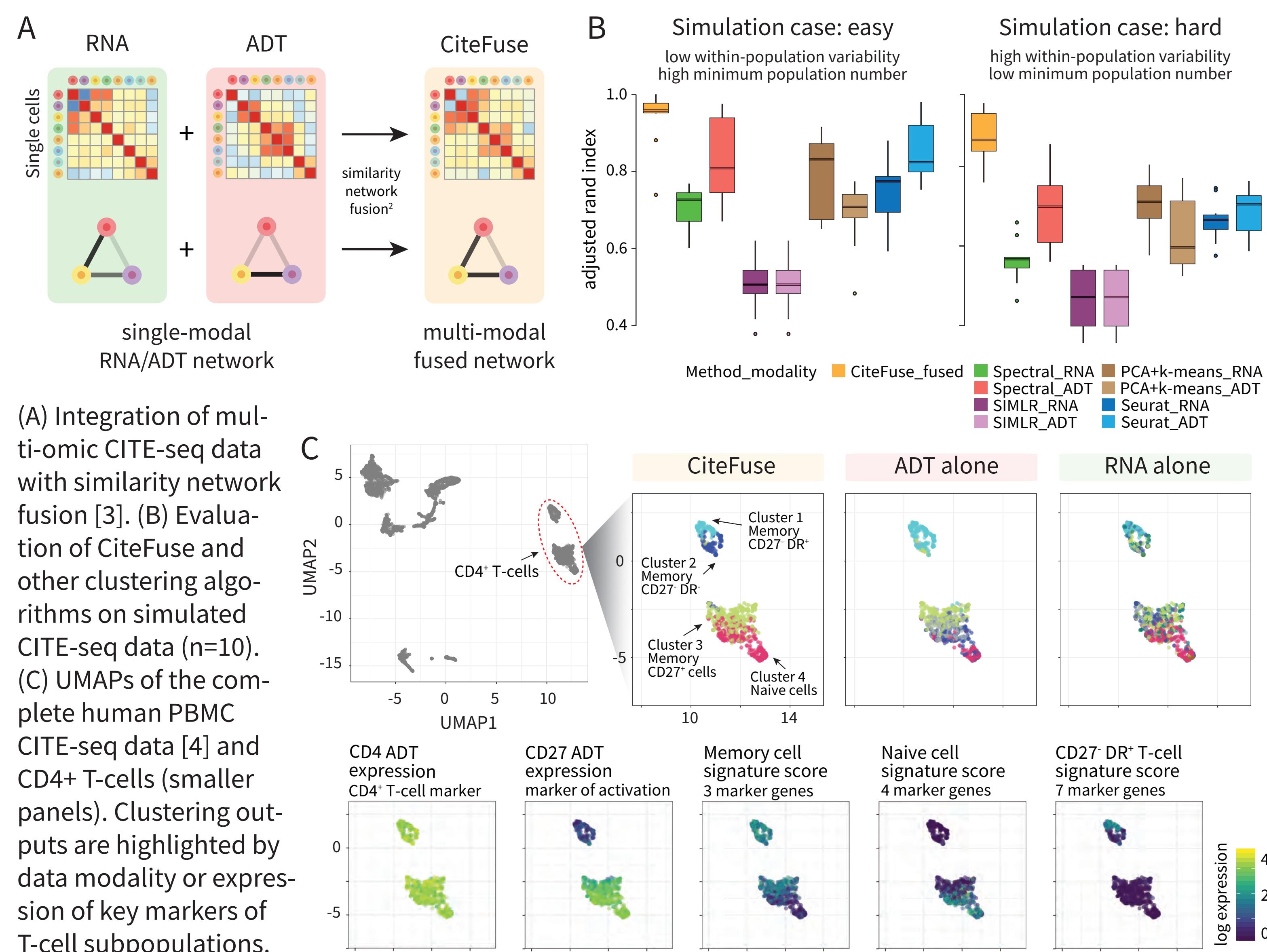
Single-cell technologies have transformed our understanding of cellular diversity and state by enabling high-throughput profiling of diverse information from individual cells [1]. Most of the technologies have focused on the measurement of a single modality. With fast-evolving technologies now measuring joint information from single cells, what more can we learn from multi-modal data?

CITE-seq generates multi-modal data from the same cell

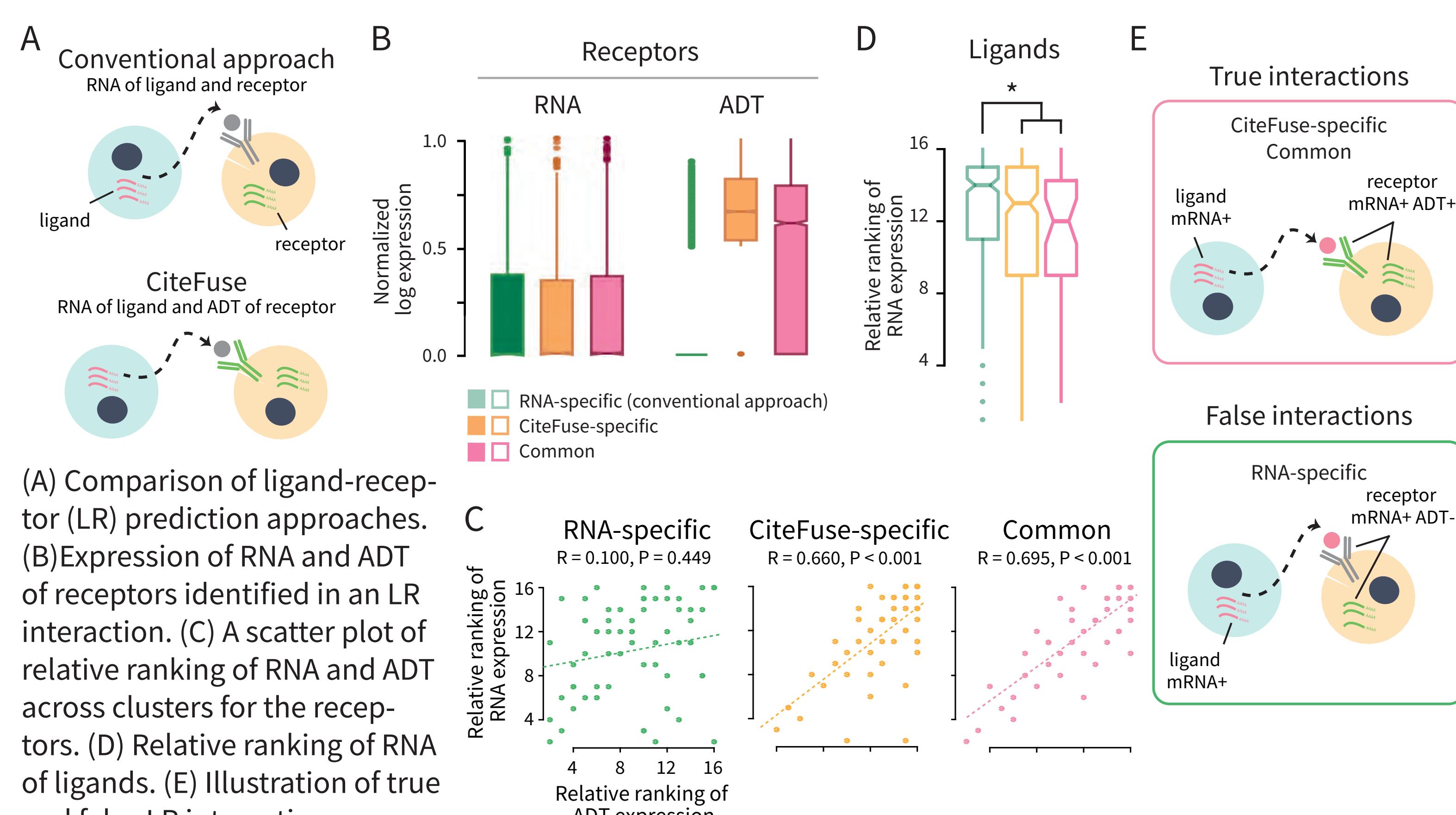


(A) A schematic of the micro-fluidic-based CITE-seq experiment [2] and the generation of matched RNA, antibody-derived tags (ADT), and hashtag oligonucleotide (HTO) expression matrices where rows indicate single cells and columns indicate RNA, ADTs, or HTOs, respectively.

CiteFuse gains information from multi-modal analysis



CiteFuse facilitates prediction of accurate ligand-receptor interactions

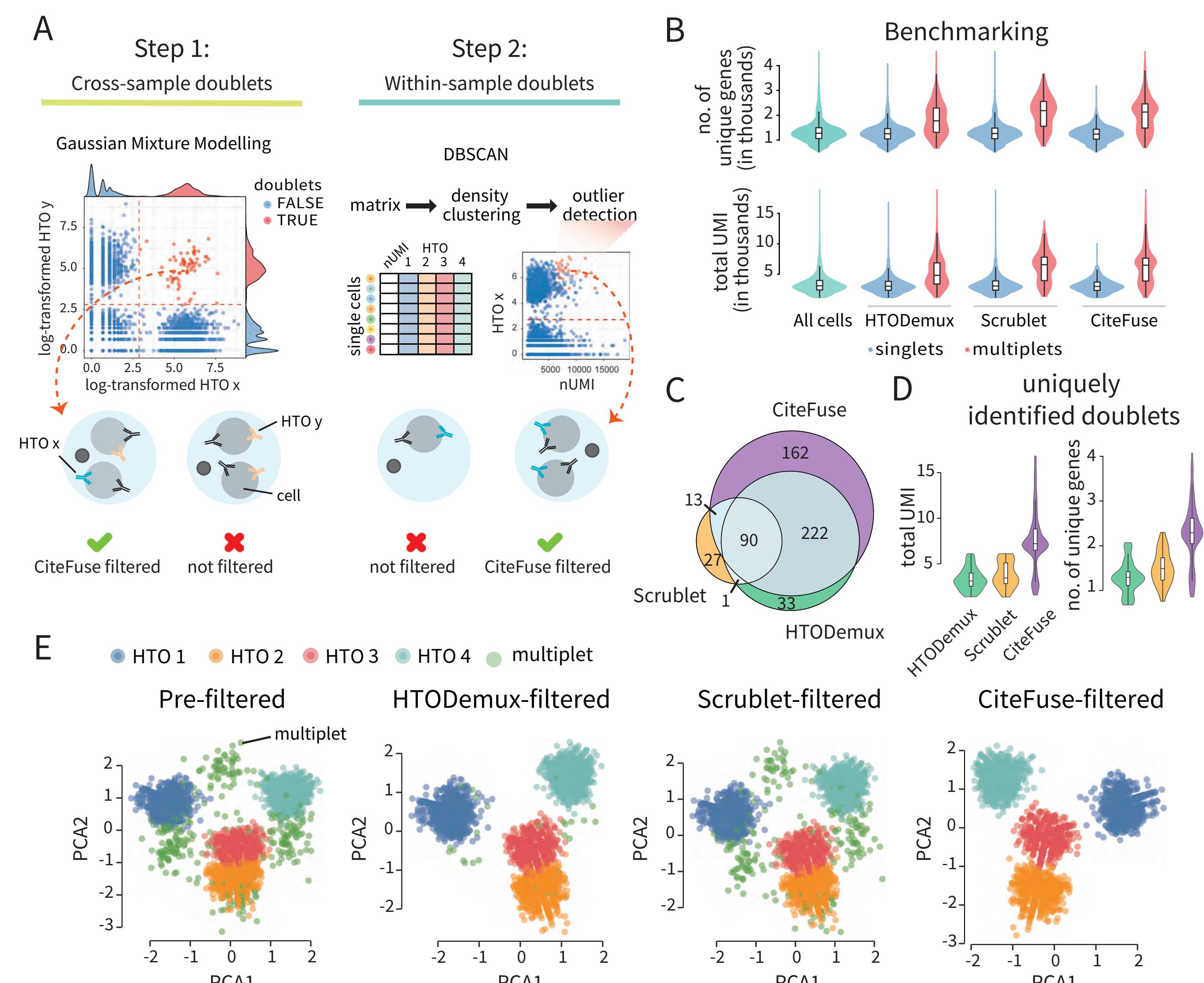


Acknowledgements and References

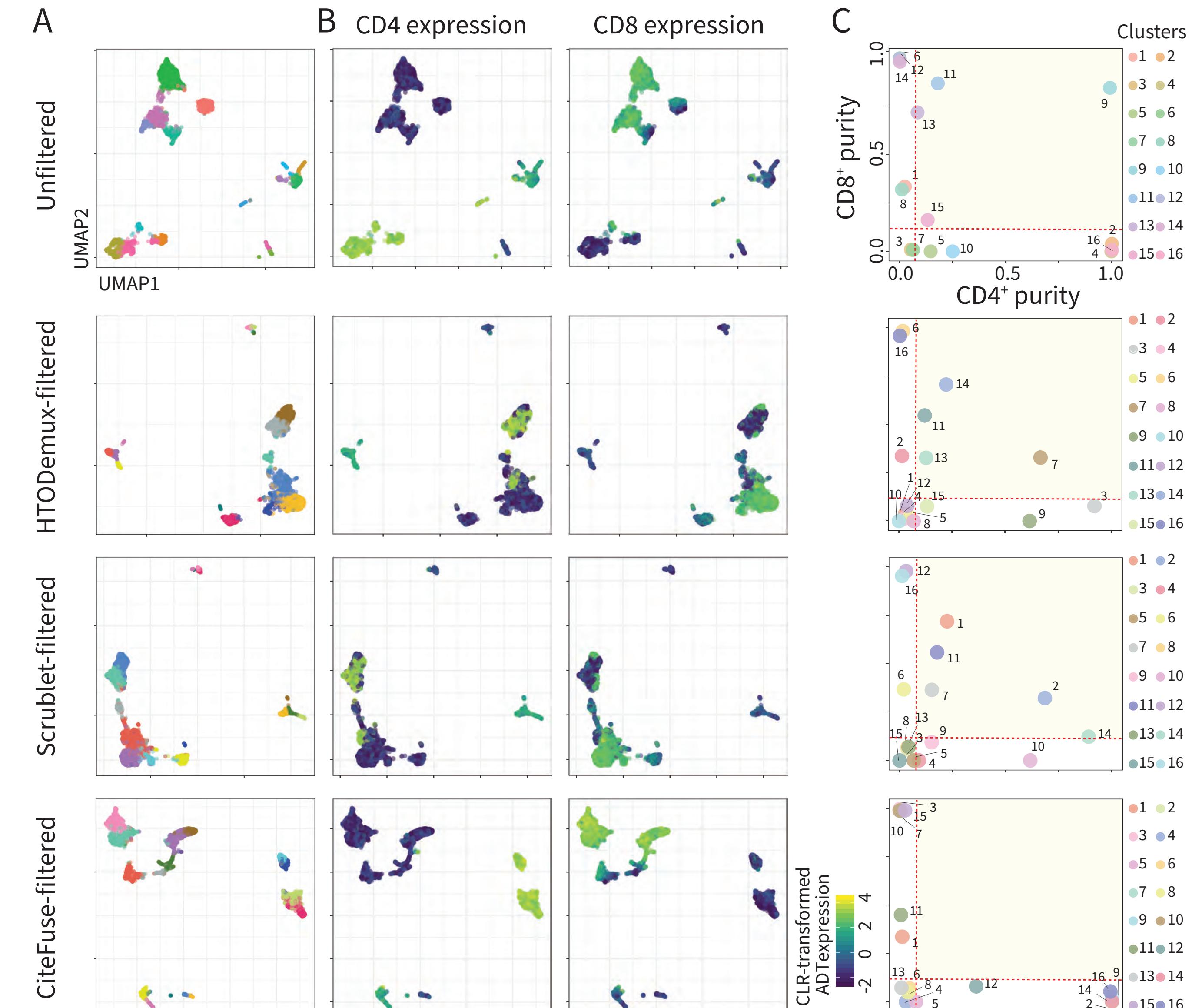
- [1] Stuart and Satija (2019) *Nature Review Genetics* [2] Stoeckius et al. (2017) *Nature Methods* [3] Wang et al. (2014) *Nature Methods* [4] Mimitou et al. (2019) *Nature Methods* [5] Stoeckius et al. (2019) *Genome Biology* [6] Wolock et al. (2019) *Cell Systems*

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A stepwise doublet detection method filters both within- and cross-sample doublets



CiteFuse-filtered dataset best preserves the separation between CD4⁺ and CD8⁺ T-cells



Take home messages for CiteFuse

- CiteFuse gains information from multi-modal integration of CITE-seq data
- Doublet detection approach in CiteFuse effectively removes both within- and cross-sample doublets
- CiteFuse facilitates accurate ligand-receptor interaction prediction



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