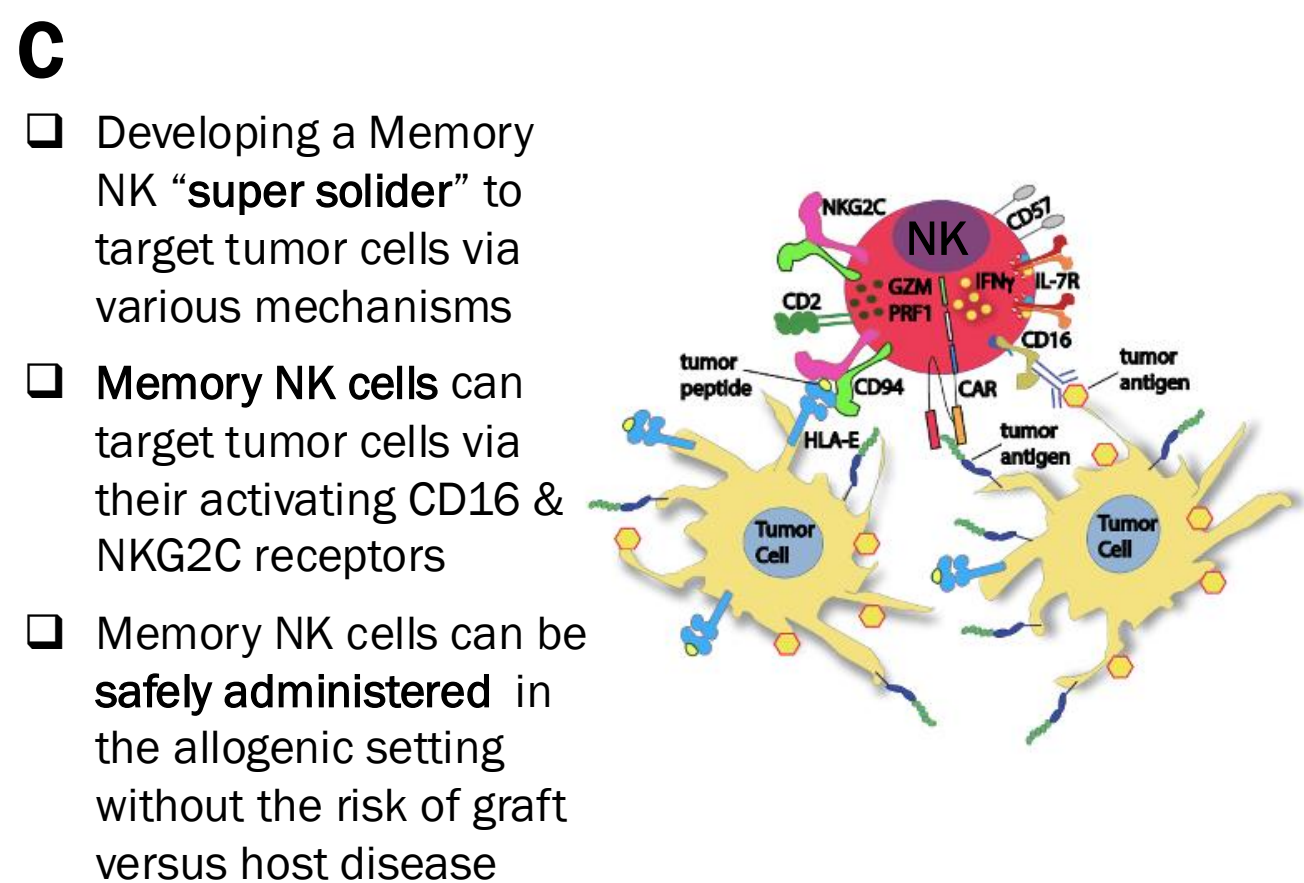
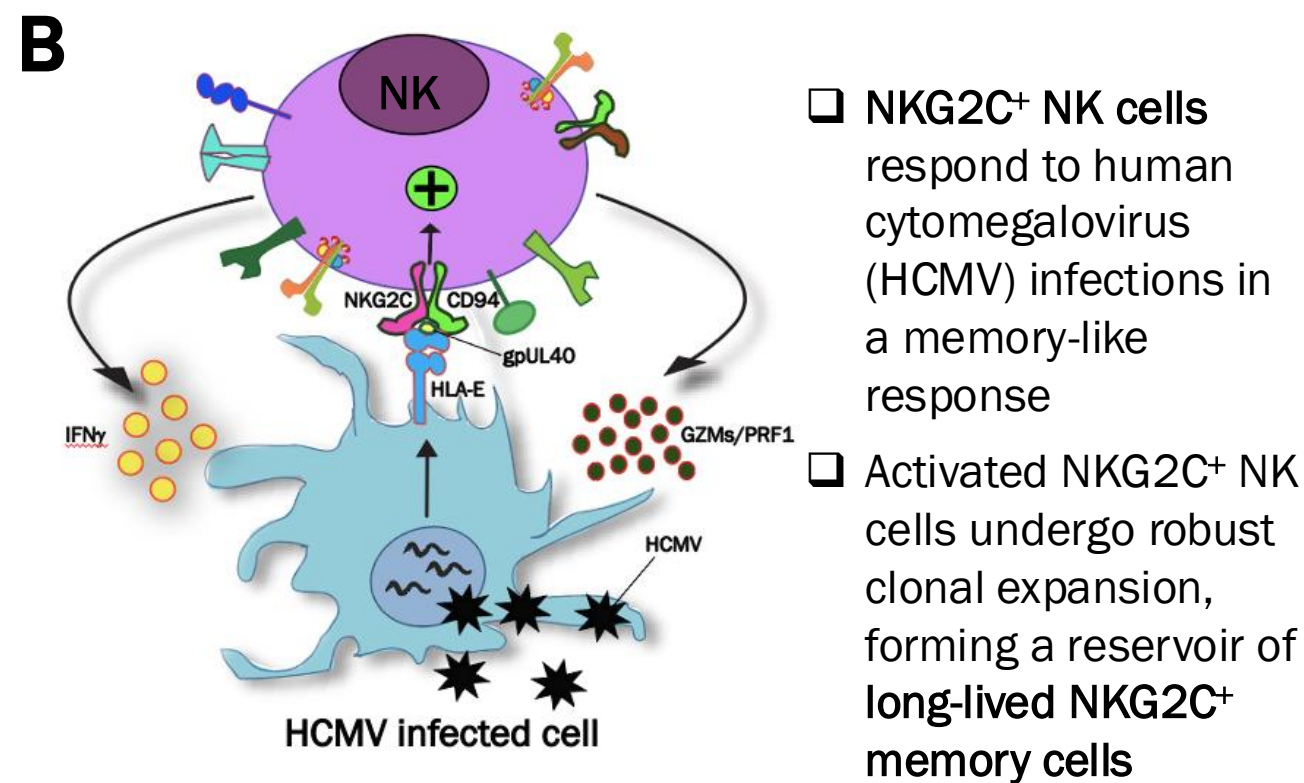
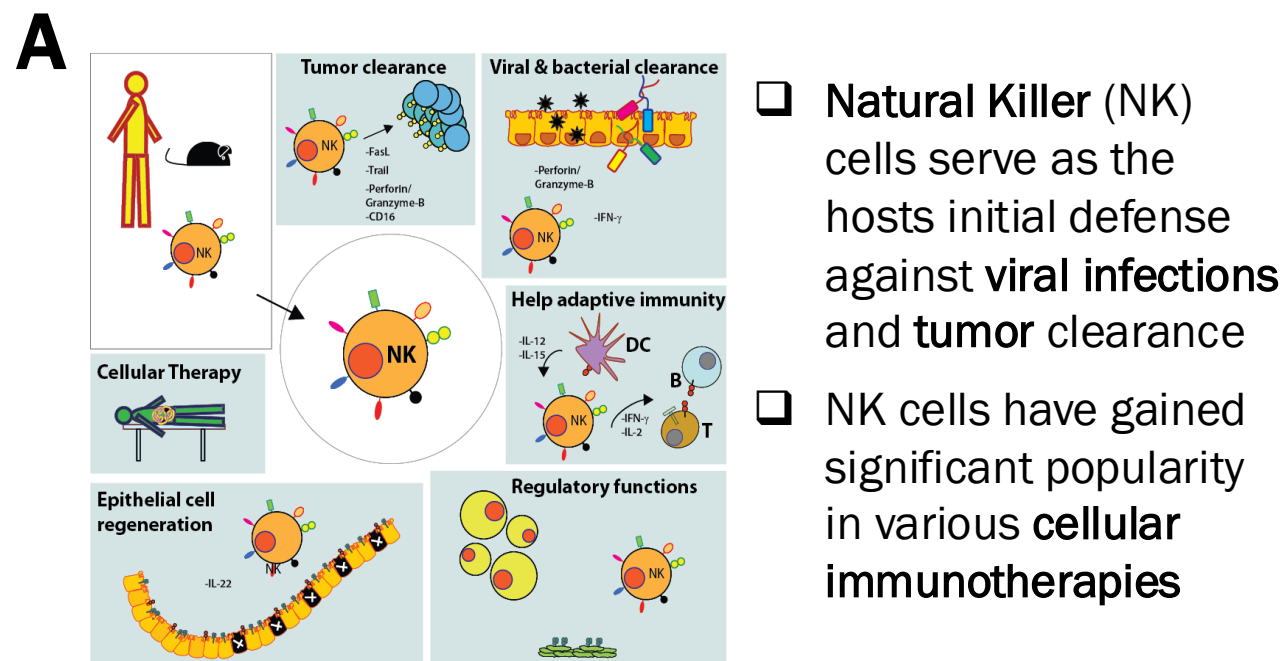
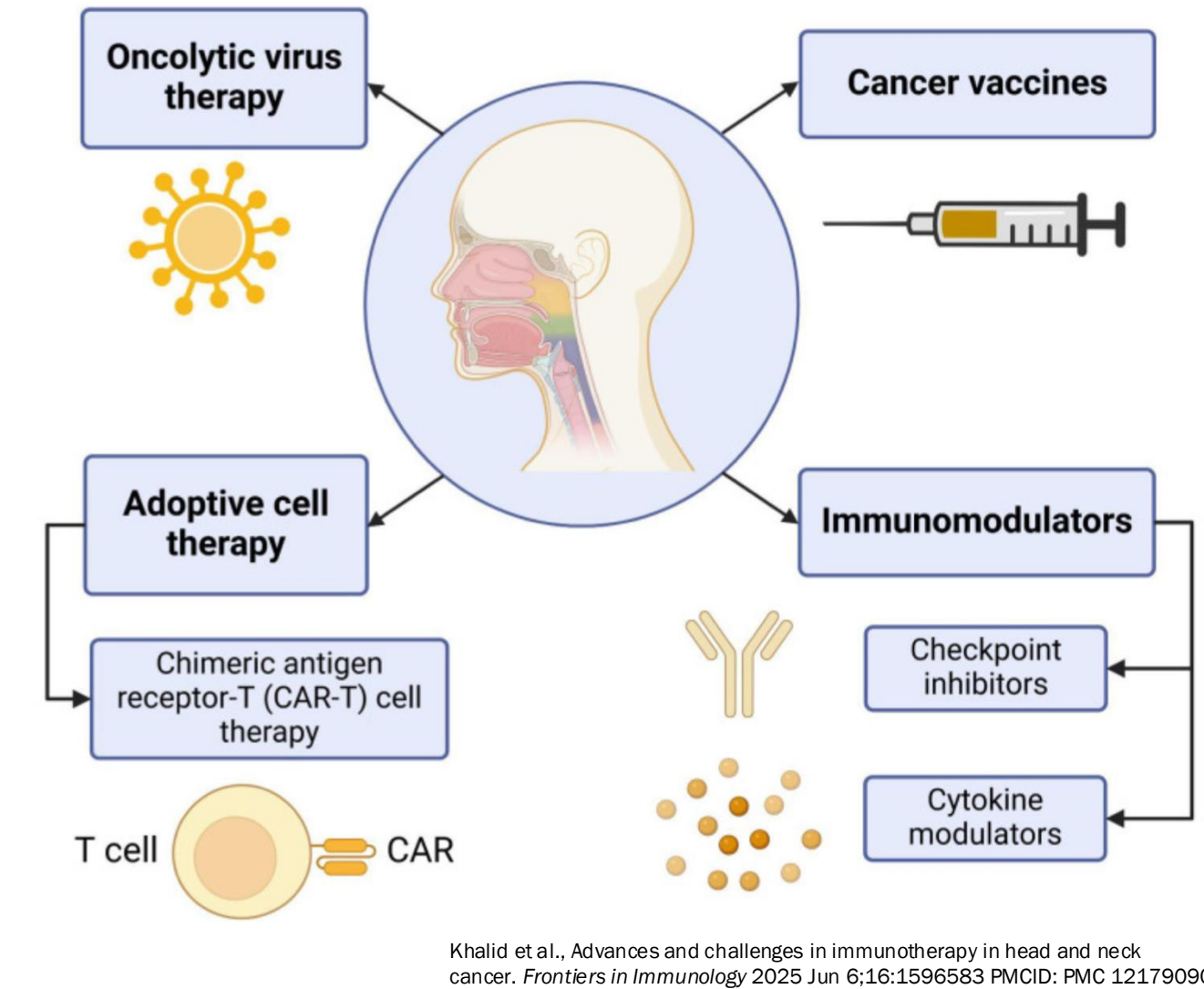


BACKGROUND

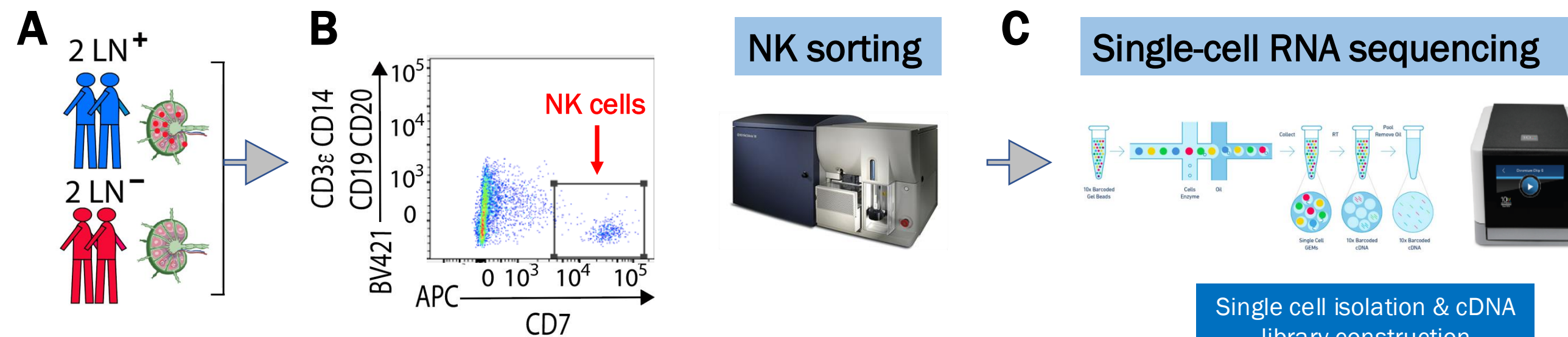


KNOWLEDGE GAPS

Novel immunotherapy agents for head and neck cancers

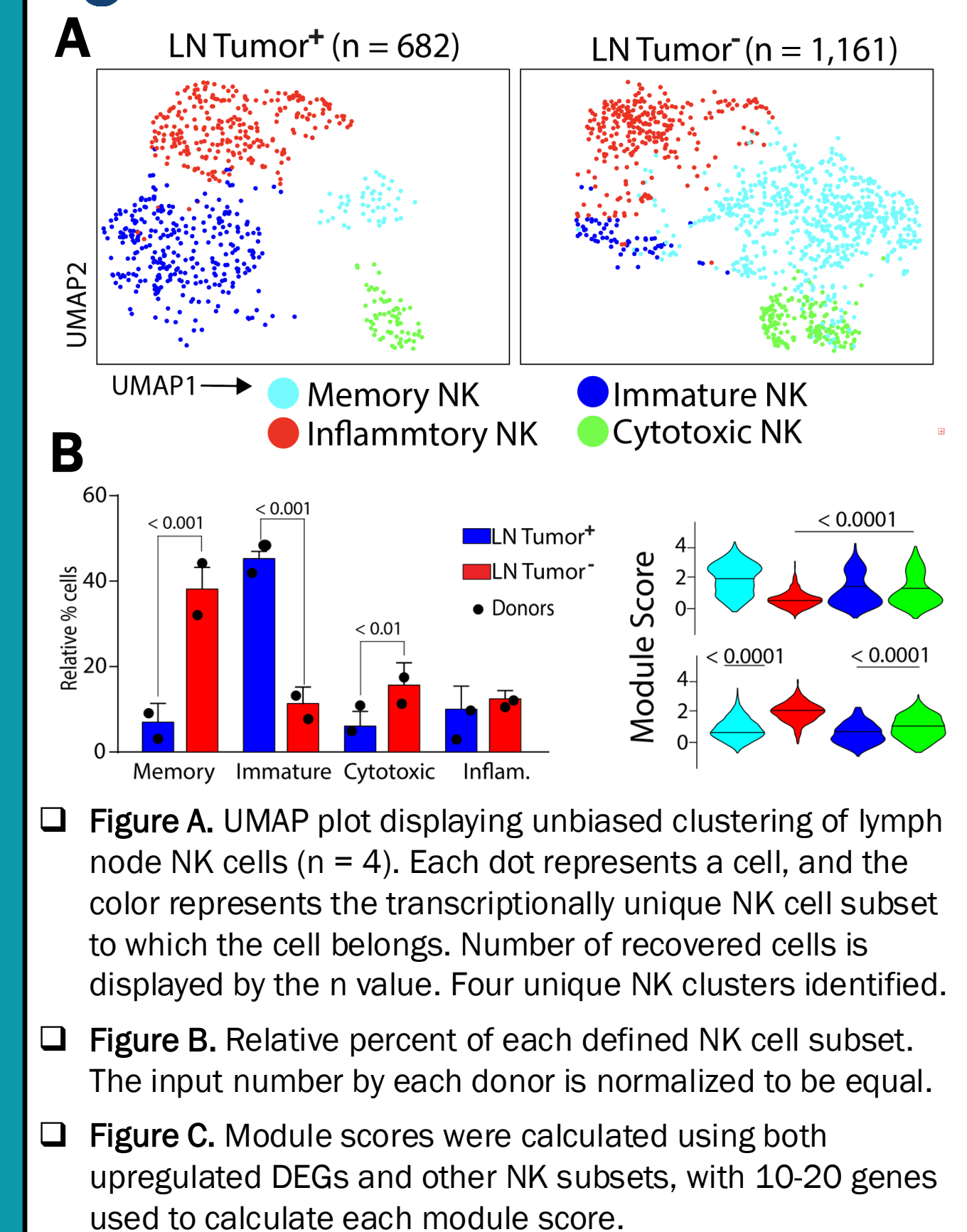


METHODS



- Figure A:** Lymph node specimens were obtained from four adult patients with primary head and neck squamous cell carcinoma at the Department of Otolaryngology, Medical College of Wisconsin. Two patients had positive lymph nodes (LN⁺) and two had negative lymph nodes (LN⁻).
- Figure B:** Lymph node specimens were processed into single-cell suspensions, and CD7⁺ NK cells were isolated and sorted using the gating strategy CD3ε/CD14/CD19/CD20⁻ CD7⁺ to capture all NK cells, including early progenitor cells.
- Figure C:** NK cells (CD3ε/CD14/CD19/CD20⁻ CD7⁺) from lymph node specimens were then utilized to perform single-cell RNA sequencing via the 10x genomic protocol. Sequencing data were aligned with the Cell Ranger pipeline and analyzed using multiple bioinformatic tools to assess transcriptional profiles.

RESULTS



Future directions

Our future work will focus on expanding the sample size and validating our scRNA-seq findings at the protein level. In addition, we plan to perform ChIP-seq and ATAC-seq on Memory NK cell population to further elucidate the epigenetic mechanisms regulating their function and anti-tumor response.

Acknowledgements

This work was supported in part by the National Center for Advancing Translational Sciences, National Institutes of Health, Grant Number TL1 TR001437. NIH grants R01 A1064828, R01 AI102893; NCI grant R01 CA179363 (S.M.), and Nicholas Family Foundation. We thank the MCW Department of Otolaryngology for providing travel funds. The content is solely the responsibility of the author(s) and does not necessarily represent the official views of the NIH.