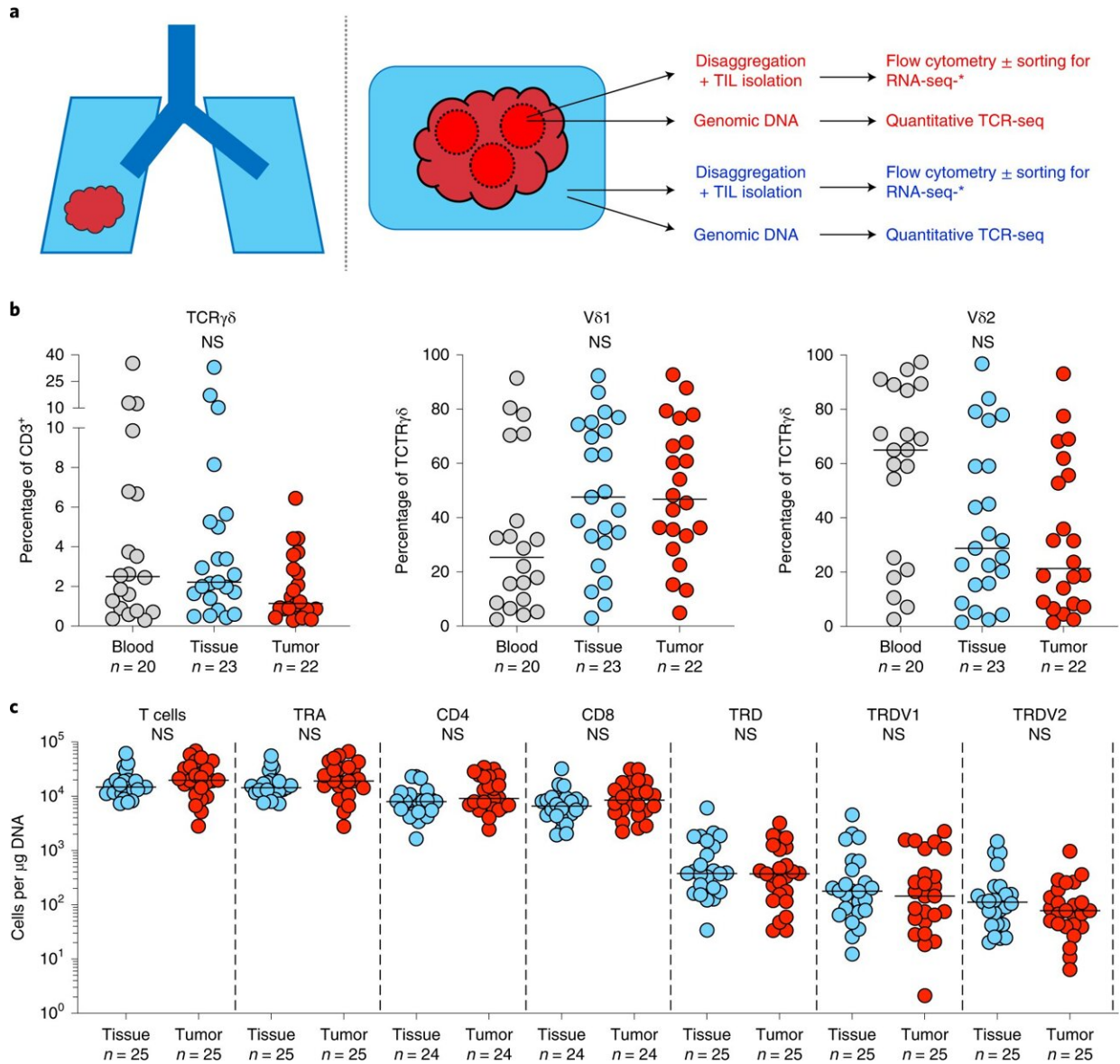


# Immune cell linked to better lung cancer survival

May 30 2022



Experimental design and  $\gamma\delta$  T cell composition in lung tissues and NSCLCs. a,

Overview of study design. Paired tumor regions (red) and NT lung tissues (blue) collected under the TRACERx Study were enzymatically digested to extract tissue/TILs. TILs were cryopreserved and thawed at a later date for flow cytometry  $\pm$  RNA-seq. In parallel, gDNA was extracted from undigested matched tumor regions and NT lung tissues and sent for subsequent quantitative TCR-seq. In addition, PBMCs were isolated from contemporaneous blood draws and cryopreserved before subsequent thaw for flow cytometry. b, Percentage of CD3<sup>+</sup> T cells staining for TCR $\gamma\delta$  (left) and percentage of TCR $\gamma\delta$  T cells staining for V $\delta$ 1 (middle) and V $\delta$ 2 (right) in PBMCs (blood), NT lung tissues (tissue) and tumors (tumor). Not all patients had paired samples. The bar represents the median. The Kruskal–Wallis test with post-hoc Dunn's test corrected for multiple testing was used. c, Absolute counts of total T cells,  $\alpha\beta$  T cells (TRA),  $\gamma\delta$  T cells (TRD) and V $\delta$ 1 (TRDV1) and V $\delta$ 2 (TRDV2) T cells per microgram of DNA determined by TCR-seq. Absolute counts of CD4<sup>+</sup>  $\alpha\beta$  T cells (CD4) and CD8<sup>+</sup>  $\alpha\beta$  T cells (CD8) were determined by mapping the proportion of CD3<sup>+</sup>/TCR $\gamma\delta$ <sup>-</sup> T cells staining for CD4 or CD8 in flow cytometry analysis of paired TILs. No significant differences were observed within demarcated T cell subsets between NT tissues and tumors. Samples with

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