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#### [4] cytoTIL15 therapy controls allogeneic, HLA-matched melanoma PDX tumors in a MART-1-dependent manner

**Figure 2: Adoptive transfer of MART1-TCR transgenic TILs**

**Schematic of experimental timeline:**

- Day -14:** Serial transplant of  $10^6$  cells.
- Day -7:** Spike donor.
- Day 0:** Evaluation TILs.
- Day 1:** Unengineered TIL + IL2.
- Day 14:** cGMP manufacturing.
- Day 21:** cGMP manufacturing.
- Day 28:** cGMP manufacturing.
- Day 35:** cGMP manufacturing.
- Day 42:** cGMP manufacturing.

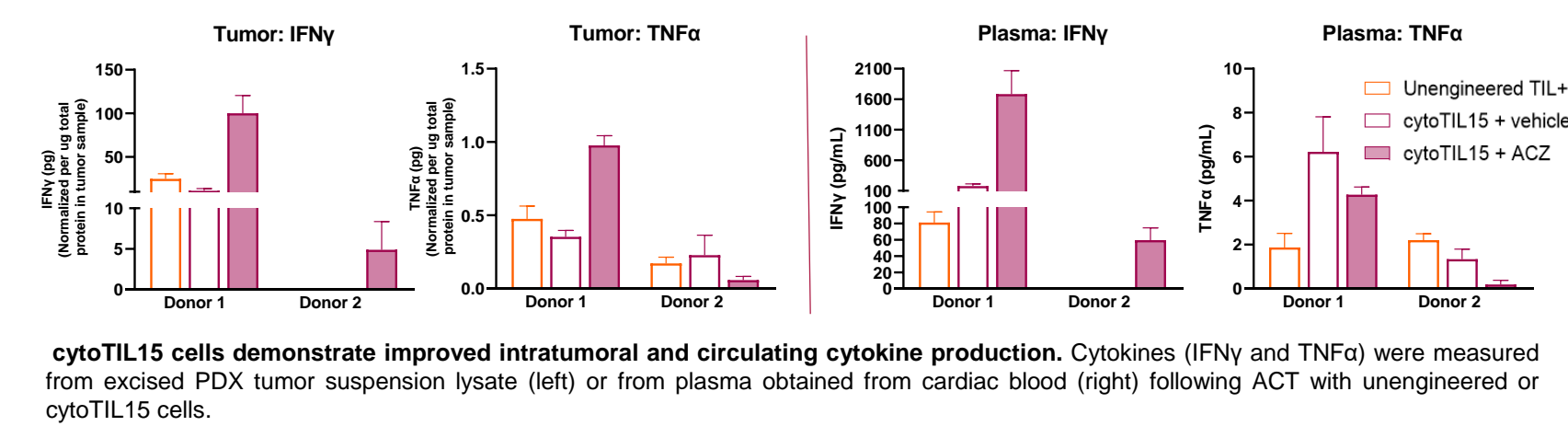
**Tumor Volume (mm<sup>3</sup>) vs Days post ACT:**

- (Donor 1) 1 CR:** Tumor volume increases over 42 days. Legend: No TILs (black), Unengineered + IL2 (orange), cytoTIL15 + ACZ (purple).
- (Donor 2) 2 CRs:** Tumor volume increases over 48 days. Legend: cytoTIL15 + ACZ (purple), Unengineered + IL2 (orange).
- (Donor 2) 3 CRs:** Tumor volume increases over 48 days. Legend: cytoTIL15 + ACZ (purple), Unengineered + IL2 (orange).

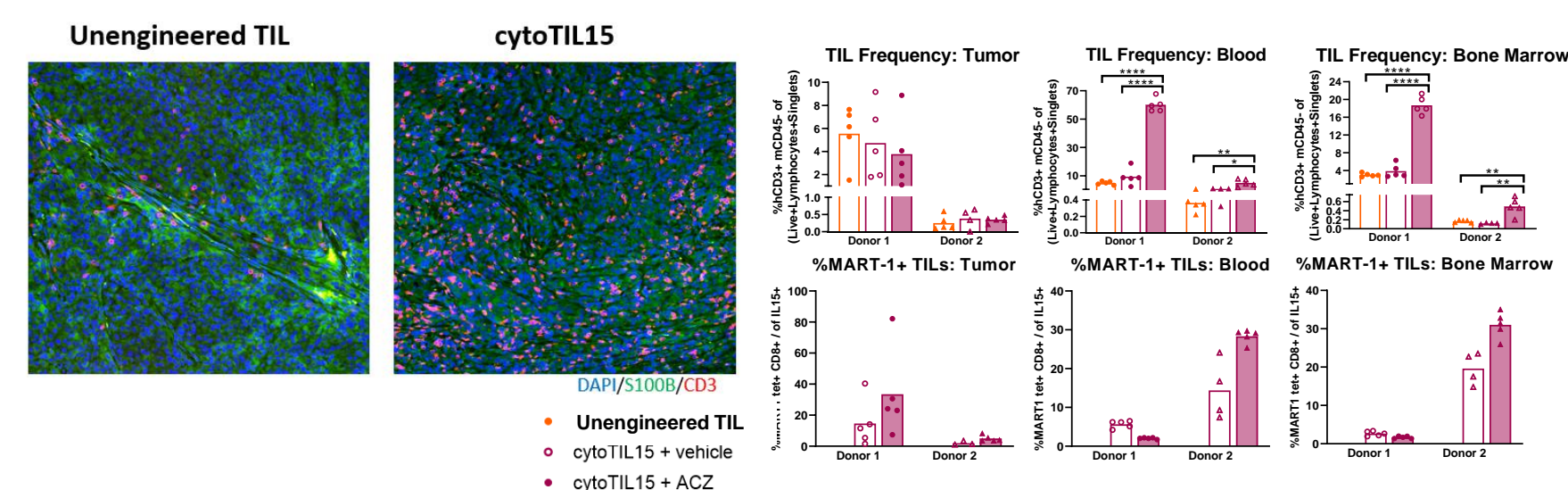
**MART1 TCR levels**

**cytoTIL15 therapy demonstrates superior tumor control *in vivo*, in an HLA-matched melanoma PDX model.** Top; MART1<sup>+</sup> melanoma tumor tissue was excised from the donor and implanted subcutaneously into female NSG mice. Serial passaging was performed *in vivo* to establish a PDX model, and animals were randomized on day-13 following PDX implant. On day 14 post-PDX implant, cytoTIL15 cells and unengineered TILs (expanded in REP with feeder cells +/- IL2 or ACZ for 14-days) from two HLA-matched and MART1-reactive donors were adoptively transferred fresh intravenously: cytoTIL15 cells (animals dosed with 200 mg/kg ACZ PO daily) demonstrated improved anti-tumor efficacy as compared to unengineered TILs (supported with 600,000 IU IL2 QD IP for 4 days). Bottom: Individual spider plots for each animal on study reveals that anti-tumor efficacy was associated with increased frequency of MART1-reactive TILs, as described in Figure 2. (n=8/arm \*p<0.05, \*\*\*p<0.001).

**cytoTIL15 cells produce potent effector cytokines**

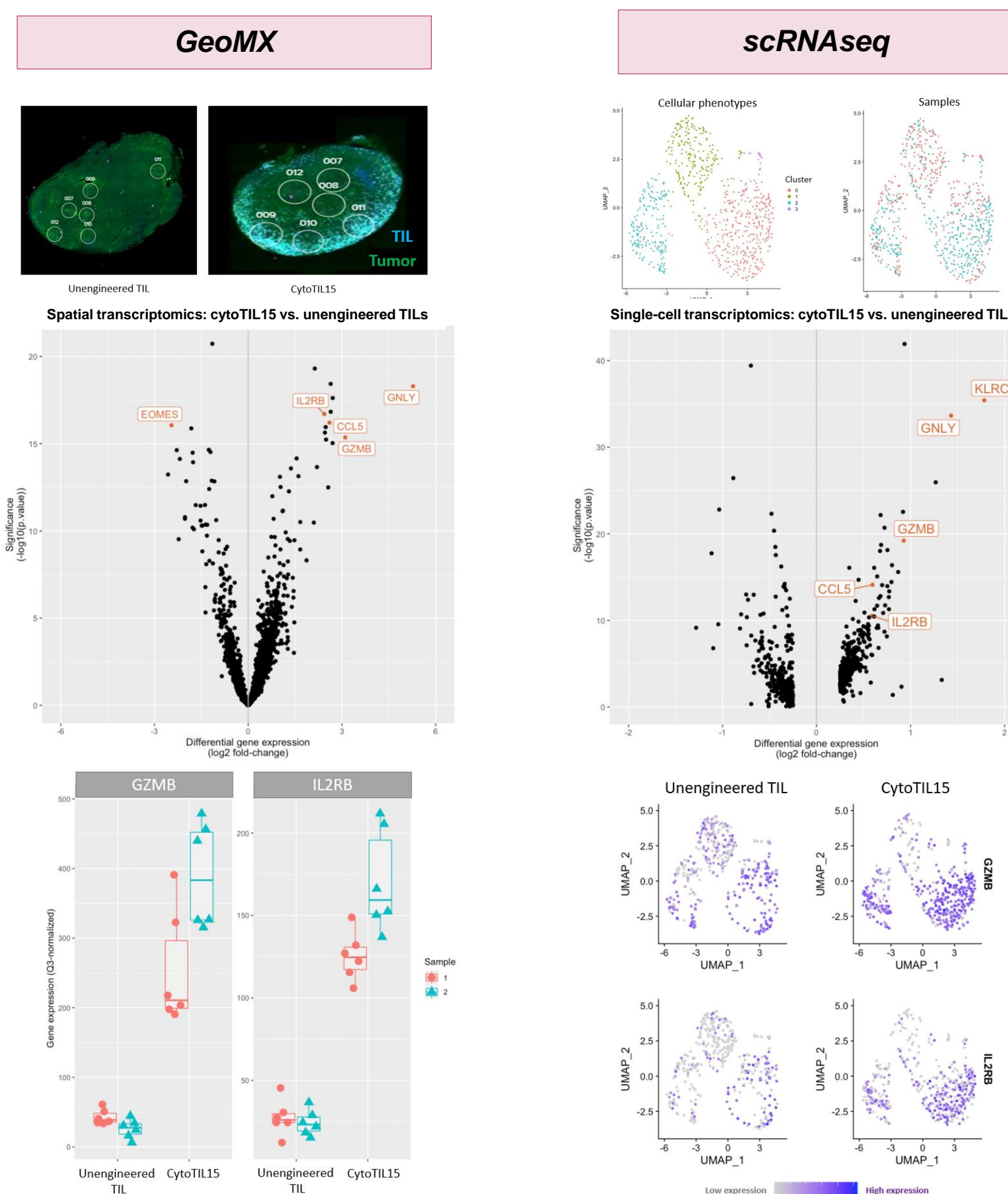


**[5] cytoTIL15 cells infiltrate into tumors, circulate and accumulate in bone marrow, and are enriched for MART-1 TCR**



**cytoT1L5 demonstrate enhanced infiltration and accumulation.** *Left:* Subcutaneous PDX tumors were harvested 20-days following ACT, with unengrafted TILs (+T1L2) or cytoT1L5 therapy. Tumors were formalin-fixed and paraffin-embedded, and immunofluorescence was performed to identify the TILs (CD3+, red color) infiltrating the tissue. *Right Top:* 14-days following ACT, PDX tumors, cardiac blood, and bone marrow were harvested, processed into single cell suspension, and stained and assessed via flow cytometry. Staining for the fraction of cells positive for anti-human CD3 and negative for anti-mouse CD45 revealed significant tumor infiltration by all TILs, and improved trafficking and accumulation into blood and bone marrow by cytoT1L5 therapy + ACZ (Fig. 1). *Right Bottom:* Flow cytometry analysis of TILs 15-days following ACT revealed TILs 15-days following ACT were MAA-reactive tetramer; MAA-reactive TILs enriched within all compartments, supporting the correlation of superior MAA-reactive TIL infiltration and improved anti-tumor efficacy, ( $n=5/\text{arm}$ ;  $p<0.05$ ,  $^{**}p<0.01$ ,  $^{***}p<0.0001$ ).

**GeoMX** **scRNAseq**



**cytOTIL15 demonstrates enrichment in genes associated with enhanced infiltration and anti-tumor effector function.** *Top:* Representative microscopy of digital spatial profiling revealing region of interest (ROI) selection for TIL (blue) and tumor (green) regions for PDX tumors treated with unengineered TILs or cytOTIL15 therapy. Similarly, representative unsupervised clustering of unengineered TIL- and cytOTIL15-therapy-treated tumors. *Middle:* Spatial and single-cell transcriptomics reveal a differential gene expression profile in cytOTIL15 cells vs. unengineered TILs, underscored by an enrichment in genes associated with pro-effector function and a favorable TIL phenotype such as IL2RB, GNLY, CCL5, GZMB, and KLRC1, and a decrease in exhaustion-associated genes such as EOMES. *Bottom:* GeoMx and scRNAseq reveal a significant ( $p < 0.05$ ) enrichment in GZMB and IL2RB occurring in infiltrating cytOTIL15 cells but not unengineered cells, which is associated with the distinct cluster profiles of each cell treatment.

The diagram illustrates the functional outcomes of cytoTIL15™ treatment. It is structured into three main sections: T cell Functionality, cytoTIL15™, and IL15 Functionality.

- T cell Functionality:** This section, highlighted with a red header, lists three key outcomes, each preceded by a red checkmark icon:
  - TCR Diversity
  - T cell Polyfunctionality
  - Tumor Reactivity
- cytoTIL15™:** The central element of the diagram, representing the treatment itself.
- IL15 Functionality:** This section, highlighted with an orange header, lists four key outcomes, each preceded by an orange checkmark icon:
  - Memory phenotype
  - Increase Persistence
  - Increased Potency
  - ACZ-controlled activity in vivo

Arrows indicate a flow from T cell Functionality to cytoTIL15™, and from cytoTIL15™ to IL15 Functionality.

- cytoTIL15 administered without IL2 show superior *in vivo* persistence compared to IL2 dependent TIL
- cytoTIL15 therapy demonstrates superior tumor control in allogeneic, HLA-matched melanoma PDX model
- cytoTIL15 cells expand and infiltrate into PDX tumors and produce IFN $\gamma$  and TNF $\alpha$
- Anti-tumor efficacy of cytoTIL15 in allogeneic PDX model is associated with reactivity to conserved melanoma associated antigen MART-1
- Anti-MART-1 cytoTIL15 display increased expression of TCF-1, which in melanoma patients has been associated with responses to immune checkpoint blockade, as well as progression free survival (PFS) and overall survival (OS)
- cytoTIL15 cells show a distinct profile of RNA expression consistent with their increased persistence and anti-tumor efficacy (*e.g.*, IL2RB, GNLY, CCL5, GZMB, and KLRC1)
- The University of Texas MD Anderson Cancer Center is currently enrolling patients in a Phase 1 clinical trial of OBX-115, which is being evaluated in patients with metastatic melanoma (NCT05470283).

Figure 1 consists of four pie charts (A, B, C, D) and a legend. The legend lists 28 V gene families with corresponding color codes: VJ5.3 (green), VJ3 (blue), VJ7.1 (orange), VJ16 (purple), VJ17 (black), VJ19 (brown), VJ20 (dark brown), VJ5.1 (dark blue), VJ18 (dark red), VJ8 (red), VJ13.6 (dark green), VJ13.1 (light green), VJ12 (light green), VJ2 (light blue), VJ5.2 (light blue), VJ21.3 (light blue), VJ1 (yellow), VJ23 (grey), VJ14 (grey), VJ22 (yellow), VJ11 (blue), VJ7.2 (orange), VJ4 (red), and VJ13.2 (purple).

(A) Tumor Digest: A pie chart showing the distribution of V gene families in Tumor Digest. The chart is divided into 28 segments, with colors corresponding to the V gene families in the legend. The segments are arranged in a circular pattern, with colors transitioning from green at the top to purple at the bottom.

(B) PreREP: A pie chart showing the distribution of V gene families in PreREP. The chart is divided into 28 segments, with colors corresponding to the V gene families in the legend. The segments are arranged in a circular pattern, with colors transitioning from green at the top to purple at the bottom.

(C) Conventional TILs: A pie chart showing the distribution of V gene families in Conventional TILs. The chart is divided into 28 segments, with colors corresponding to the V gene families in the legend. The segments are arranged in a circular pattern, with colors transitioning from green at the top to purple at the bottom.

(D) cytoTIL 15: A pie chart showing the distribution of V gene families in cytoTIL 15. The chart is divided into 28 segments, with colors corresponding to the V gene families in the legend. The segments are arranged in a circular pattern, with colors transitioning from green at the top to purple at the bottom.

Flow cytometry for 24 TCR Vβ families (~70% of total TCR repertoire) in fresh post-REP.  
Data pooled from 3 donors

