Tumor-infiltrating mast cells are associated with resistance to anti PD 1 therapy.

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 Supplementary Figure 1. Vector maps. Schema of AVV8 (**a**) and pMV101 (**b**) DNA encoding hu-cytokine transgenes. pMV101 is a modified pVAX1 vector⁴⁸.

Supplementary Figure 2. Stability of Hu-mice. Representative examples of Hu-mice batches that received AAV8 and DNA plasmid encoded human cytokines as described in Figure 1 with longevity of 30 weeks or more after human CD34⁺ cell injections.

Human CD45: Mouse thymus

Mouse spleen

Supplementary Figure 3. Higher repopulation of human B-cells than T cells. Reconstituted humanized mice (n=45) as described in Figure 1 showed increased levels of B-cells than T cells (*p=0.000023) during early phase (8-10 weeks) of human lymphocyte reconstitution (**a**)**. b and c.** Human CD45⁺ cells in reconstituted mouse thymus and spleen. Human CD45⁺ cells (**brown staining**) are seen in lymphoid organs of mouse thymus (**b**) and spleen (**c**) as determined by IHC staining using anti-human CD45 antibody. All mice were euthanized by CO2 inhalation/cervical dislocation and organs harvested 24 weeks after CD34+ cell injections. Scale bars in both **3b** and $3c$ represents 250 μ m. Histology staining (b, c) was confirmed in repeat experiments (2x). One sided paired t-test was used for analysis when p values are provided. Source data are provided as a Source Data file.

Supplementary Fig. 4. Human immune subpopulation in spleen, thymus, lymph node, small intestines (SI) and lungs of humanized mice. a. Human macrophages in the spleen and SI. Representative section from mouse spleen and SI shows the presence of CD68⁺

monocyte/macrophage lineage cells **(left and right panels; scale bars: 200 m**). **b. Human CD4+ and CD8+ T-cell subpopulation in lymphoid organs.** Mouse spleen **(left panels; a)**, thymus **(middle panels)** and mesenteric lymph nodes **(right panels)** show presence of CD4+ (top panels) and CD8⁺ (bottom panels) T cells as determined by IHC staining using anti-human CD4 or CD8 antibodies. Scale bars in all the panels represent 200 μm. c. Human Tγ/δ cells. Reconstituted Hu-mice show presence of T γ/δ cells in the SI, liver, lymph node and spleen (right most panels; scale bars: $25 \mu m$) of mice that were treated with a bacterial metabolite HMBPP at 50 mg/kg (i.p.). Presence of T γ/δ cells were determined in an IHC staining by using mouse anti-human TCR γ/δ primary antibody followed by detection using secondary anti-mouse Qdot 625 antibody. Histology staining (a-c) was confirmed in repeat experiments (2x).

Supplementary Figure 5. Human $T\alpha/\beta$ **expression.** TCR sequence analysis of spleen and tumor cells obtained from Hu-mice melanoma model showed more diverse expression of T α/β chains in the spleen when compared to more restricted usage in tumors (**top panel**). TCR α/β chain expression showed high prevalence of several unique VJ clonotypes in tumors (**bottom panel**).

Supplementary Figure 6. Spleen T cells obtained from tumor challenged Hu-mice from 3 different batches of CD34⁺ donors (HLA-A1, -A-2 and -A3) react to melanoma-specific T**cell peptide antigens after** *in vitro* **stimulation. a. Schema of tumor cell challenge and cytokine PCR. b. Spleen T cells show reactivity to melanoma T-cell peptide antigens as measured by real time PCR.** Spleen T cells were stimulated *in vitro* for 72 h with various melanoma peptides (HLA A1 peptides, MAGE1: EADPTGHSY; MAGE3:EVDPIGKLY; TYR:KSDICTDEY; Flu: CTELKLSDY; HLA-A2 peptides, gp100₂₀₉₋₂₁₇ ITDQUPSV; gp100₂₈₀₋ 288 YLEPGPUTA; mod gp100: IMDQVPFSV; MART:AAGIGILTV; HLA-A3 peptides, NY-ESO: ELARRSLAQ and SLLMWITQC [pooled], gp100: LIYRRRLMK, Flu: ILRGSVAHK; all at a concentration of 25μ M) showed robust reactivity indicating sensitization to these antigens *in vivo* on tumor challenge. Assay was performed by real time PCR as described before² using standard Th1 cytokine primers (See Supplementary Table 3).

Supplementary Figure 7: Melanoma antigen-specific CDR3 (TCR) sequences are detected in TILs of Hu-mice. TCR sequences generated from TILs of two melanoma lesions (HLA-A2 matched to donor $CD34^+$ cells) or T cells from two spleens obtained from Hu-mice were clustered using the GLIPH algorithm (see method section) according to their local (**blue connections**) and global (**yellow connections**) similarity, which are likely to recognize a similar peptide/MHC complex. The TCRs are depicted as circles, the size indicating the abundance of the respective T-cell clonotype on a log scale. The origin, e.g. tumor 1 or 2 and spleen 1 or 2 is color coded. To predict the reactivity of the TCR clusters, virtual melanoma differentiation

antigens (MDA [MART-1 and gp100]), cancer testis antigens (CTA [MAGE A1 and NY-ESO-1]) were appended with fixed abundance values and depicted as squares (green, blue, cyan, and magenta, respectively). To determine specificity of CDR3 sequences virtual viral antigens (i.e., CMV and EBV) epitope/HLA-A2 reactive TCR were spiked in, which are depicted as colorcoded squares **(cyan and violet**, respectively) with fixed abundance values.

Supplementary Figure 8. Treatment with anti-PD-1 has no effect on aggressively growing melanoma tumor. In an established Hu-mice melanoma model (**see Fig. 2f**) anti-PD-1 treatment **(n=5)** was unable to restrict tumor growth of 451LU. Source data are provided as a Source Data file.

Supplementary Figure 9. Heterogeneous distribution of CD4⁺ and CD8⁺ T-cell distribution in tumors after anti-PD-1 therapy. Images of tumor sections were digitally quantified using NIS elements software and counts are from two different fields.

Supplementary Figure 10. Tumor-infiltrating immune cell types after immune-checkpoint therapy. CIBERSORT analysis of RNASeq from tumor tissues as in Figure 4a showed the presence of immune cell types including T- and B-cells, and monocytes/macrophages including mast cells. Some NK and DCs were also observed in the tumor tissues **(a**). **b-d**. Similarly, all 3 clinical trial datasets as in Figures 5b-d showed presence of other immune cell types. Size and the color of the closed circles indicates the abundance of each immune cell types in the tissues. Source data are provided as a Source Data file.

Supplementary Figure 11. Mast cells co-express CXCR3 after anti-PD-1 therapy. Increased levels of mast cells co-express CXCR3 after anti-PD-1 therapy, thus confirming their ability to migrate in response to increased CXCL-10 expression by tumor cells.

Supplementary Figure 12. Flow gating strategy. A representative example of flow strategy of Flow data in Fig.1b is described here. Immune cells labeled with antibody cocktail were analyzed by flow cytometry and acquired images are plotted using FlowJo software. Total lymphocytes are gated 1st (**top left panel)**, followed by gating for live cells **(top middle panel)**, and single cells (**top right panel**). From single cells, gating for mouse CD45⁺ cells (Y-axis) and human CD45⁺ cells (X-axis) are plotted (**bottom left panel**). CD3⁺ (2nd left panel), CD20⁺ (3rd **left panel**) and CD4⁺/CD8⁺ (**right most panel**) cells are all derived from human CD45⁺ gated region.

Supplementary Table 2.

Supplementary Table 3.

