Figure S1. Endogenous IL-15 contributes to tumor control. $10^5$ MC38 colon carcinoma cells were administered SC to age-matched wt (grey, n=10) and IL-15 KO (red, n=10) mice. Tumor areas were calculated as length x width and plotted as mean ± SEM for each group over time.
Figure S2. Effects of hetIL-15 on TC-1 carcinomas. (A) Graph showing the TC-1 tumor growth in hetIL-15 treated and control mice. Tumor immune infiltrates from TC-1 carcinomas recovered from mice treated with either PBS or hetIL-15 were analyzed by flow cytometry to determine: (B) the frequency of tumor-infiltrating CD8+ T cells, (C) the percentage of dividing CD8+ T cells, (D) the expression of the survival factor Bcl-2 in the tumor-infiltrating CD8+ T cells. The count of tumor-infiltrating Tregs, CD8+ T cells/Treg ratio within the tumor and the percentage of CD8+ T cells expressing Granzyme B are shown in (E), (F) and (G) respectively.
Supplemental Figure 3

**Figure S3. Effects of hetIL-15 in spleens of MC38-bearing mice.** Spleen from MC38-bearing mice treated with either PBS or hetIL-15 were analyzed by flow cytometry to determine: (A) the absolute count of CD8+ T cells, (B) the percentage of dividing CD8+T cells, (C) the expression of the survival factor Bcl-2 in the CD8+ T cell subsets, (D) the absolute count of NK cells, (E) the percentage of dividing NK cells, (F) the percentage of CD8+T cells expressing Granzyme B, (G) the percentage of NK cells expressing Granzyme B. Splenic absolute count of XCR1+CD103+IRF8+ cDC1 in PBS- and hetIL-15-treated animals is shown in (H).
Figure S4. Top GO immune cell-function related pathways significantly enhanced in tumors by hetIL-15 treatment. Nanostring analysis identified up-regulation of genes representing immune-related pathway signatures in tumors by hetIL-15 treatment. Gene enrichment analysis on the GO database was performed on the top 150 analyzed genes (sorted by t-statistic).
Figure S5. CD11b⁺myeloid and B cells are distinct from cDC1 in tumor. (A) Flow cytometric analysis of CD64 expression by tumor infiltrating MHCII⁺CD11b\textsuperscript{high} (grey) and XCR1⁺CD103⁺IRF8⁺ cDC1 (blue). Expression of CD11c (B), XCR1 (C) and IRF8 (D) by B cells (grey) in comparison to XCR1⁺CD103⁺IRF8⁺ cDC1 (blue).