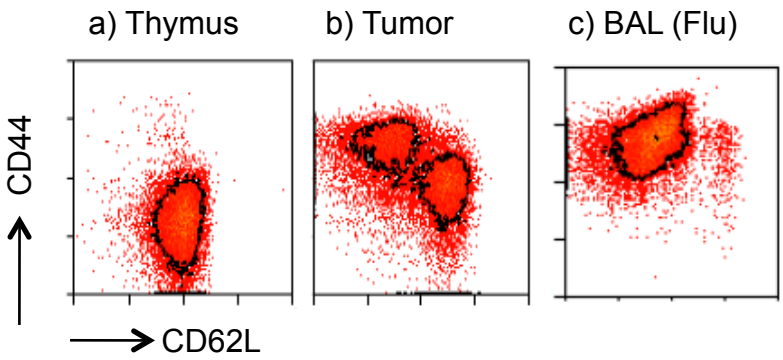
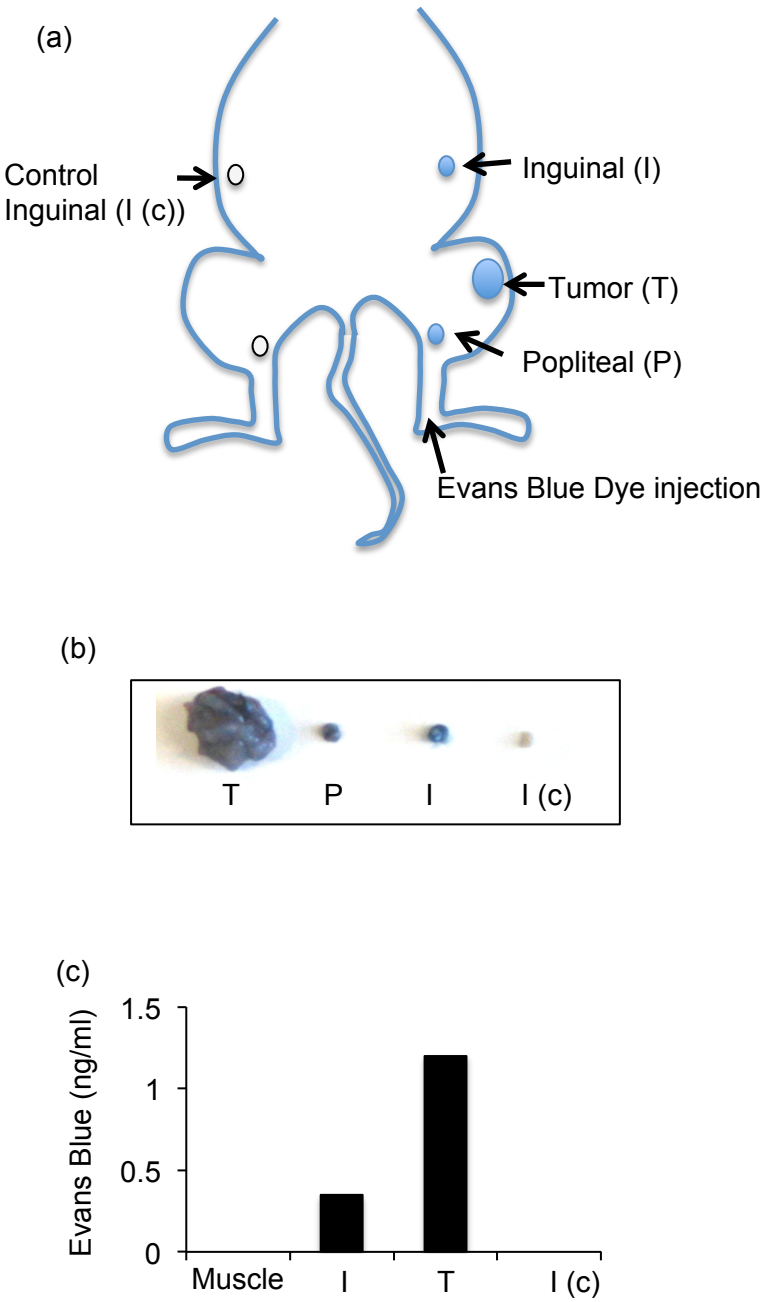


Supplementary Figure 1

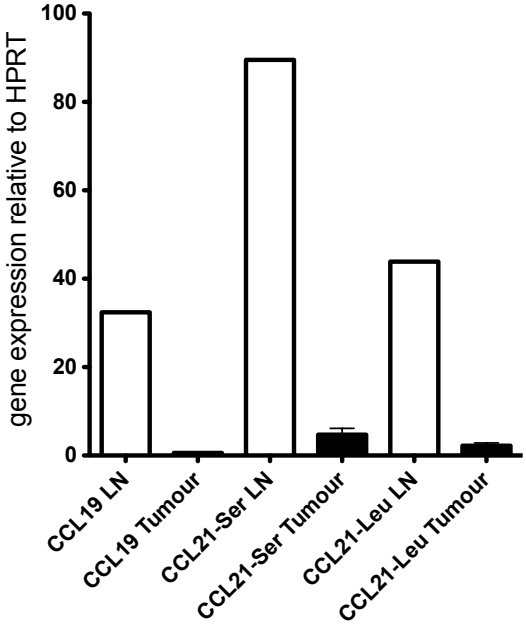
Cells from thymus (a), tumor (b) and BAL fluid (c) from influenza-infected mice were stained for CD4, CD44 and CD62L. Plots are gated on $CD4^+$ T cells.



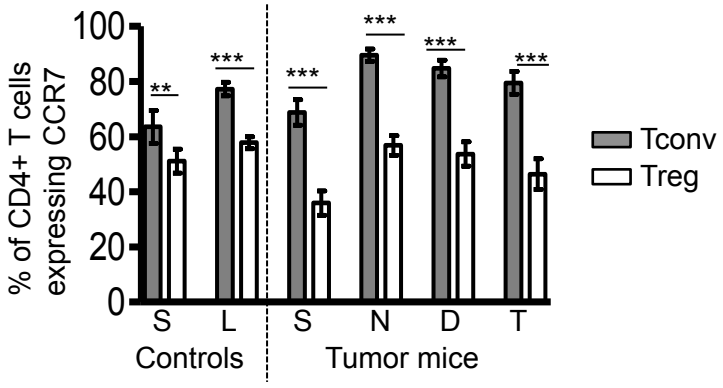
Supplementary Figure 2

80 μl of Evans Blue (1%) was injected into the base of the leg. Approximately 60 minutes later, dye accumulation was monitored in the tumor, inguinal and popliteal lymph nodes as shown in (a). Photographs were taken of the tumor and lymph nodes as shown in (b). The relative amount of Evans Blue extracted from the tumor, adjoining muscle and inguinal lymph nodes is shown in (c).

(a)

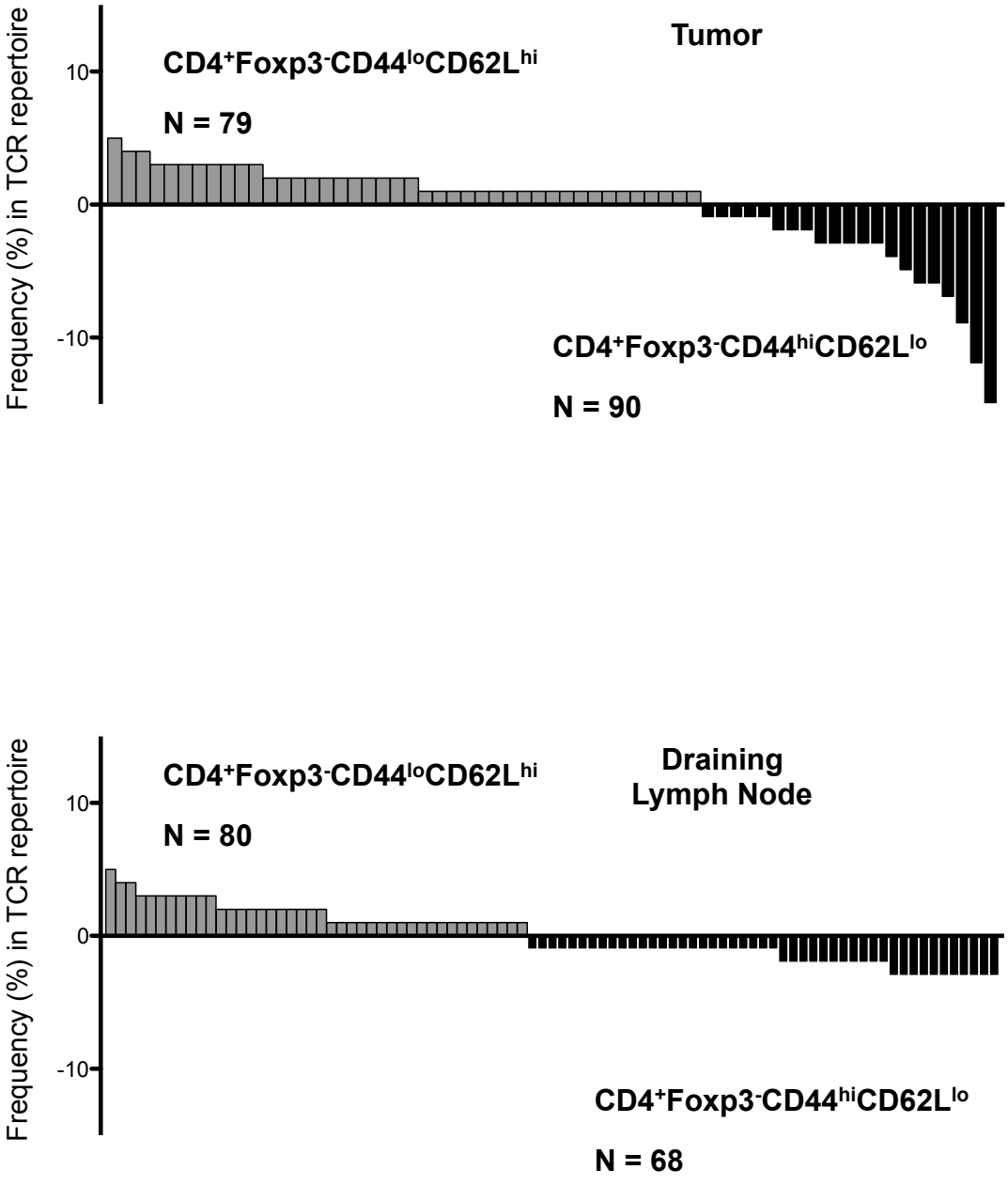


(b)



Supplementary Figure 3

Total RNA was extracted from spleens, tumors and lymph nodes and used for gene expression analysis of CCL19, CCL21-Ser and CCL21-Leu (a) . Gene expression is normalized to HPRT1 expression as an internal control within each tissue.
Single cell suspensions prepared from tumors, spleens and lymph nodes were stained for CCR7 and analysed by flow cytometry . Frequency of $CD4^+$ T cells expressing chemokine receptors in control (non-tumor-bearing) and tumor-bearing mice is shown (b). Shaded and clear bars represent Tconv and Treg, respectively. Letters S, L, N, D and T denote spleen, lymph node, non-draining lymph node, draining lymph node and tumor, respectively. P value interpretation: *** $p \leq 0.0009$; ** $p = 0.001 - 0.009$.



Supplementary Figure 4

Naïve and activated T cell populations from a tumor-bearing mouse were sorted by flow cytometry and analysed by TCR clonotyping. The CDR3 amino acid sequences were used to identify individual TCRs from the tumor and draining lymph node. Each graph displays the different TCR sequences observed (x axis) within the naïve (shaded & above) and activated (filled & below) T cell repertoires, and the frequency (y axis) of each sequence within that subset. The total number of TCR sequences analysed is displayed.