

SUPPLEMENTAL FIGURES

Preferential Homing of Tumor-specific and Functional CD8⁺ Stem Cell-like Memory T Cells to the Bone Marrow

Running title: Homing of T_{SCMs} to the bone marrow

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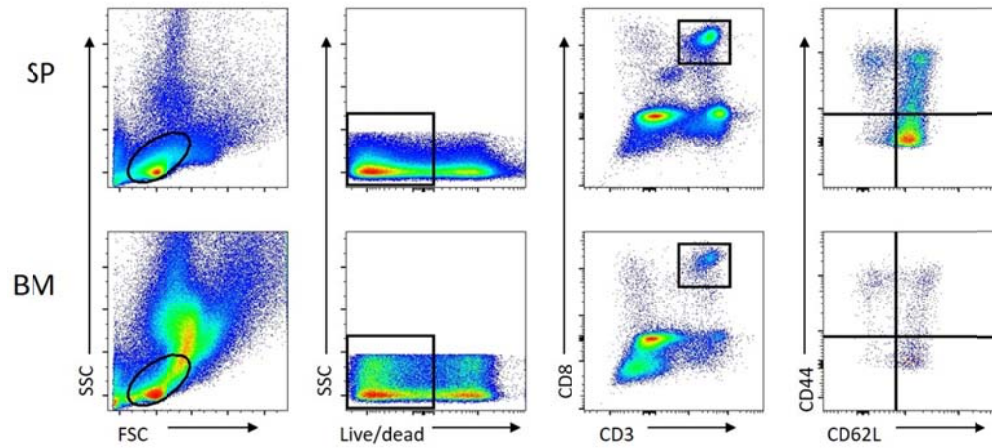


Figure S1 . Gating strategy for flow cytometric analysis of CD8⁺ T_{SCMS}

The expression levels of CD122 and Sca-1 were detected on the basis of the phenotype of naive CD8⁺ T cells to analyze CD8⁺ T_{SCMS}. The CD3⁺ CD8⁺ CD62⁺ CD44⁻ cells in C57BL/6 mice spleen (A) and bone marrow (B) were analyzed by flow cytometry. The forward scatter (FSC) and side scatter (SSC) show the properties of the cell size and density.

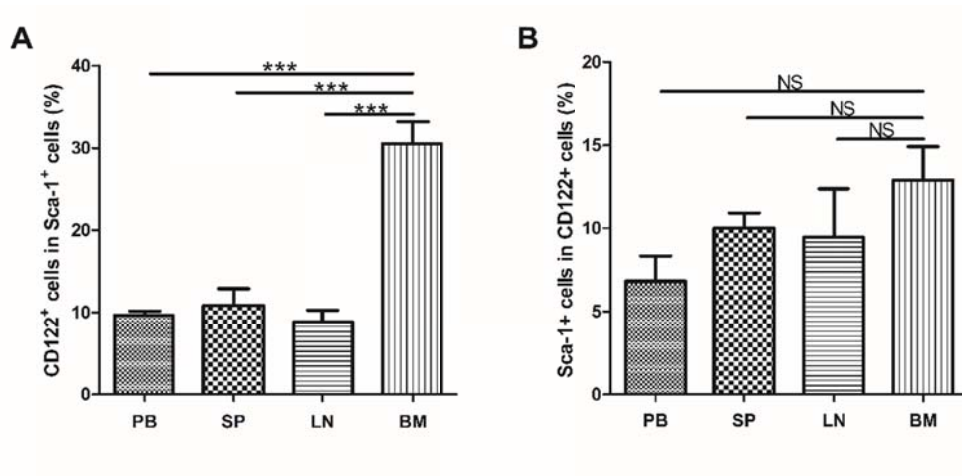


Figure S2. (A) The percentage of CD122⁺ cells in Sca-1⁺ cells and (B) the percentage of Sca-1⁺ cells in CD122⁺ cells in the organs, respectively.

The frequencies of CD122⁺ cells in CD3⁺ CD8⁺ CD4⁻ CD62L⁺ CD44⁻ Sca-1⁺ T cell

compartment (A), and the frequencies of Sca-1⁺ cells in CD3⁺ CD8⁺ CD4⁻ CD62L⁺ CD44⁻ CD122⁺ T cells (B) formulas as follow: CD122⁺ cells in Sca-1⁺ cells (%) = CD3⁺ CD8⁺ CD4⁻ CD62L⁺ CD44⁻ CD122⁺ Sca-1⁺ cells / CD3⁺ CD8⁺ CD4⁻ CD62L⁺ CD44⁻ Sca-1⁺ cells × 100%. Sca-1⁺ cells in CD122⁺ cells (%) = CD3⁺ CD8⁺ CD4⁻ CD62L⁺ CD44⁻ CD122⁺ Sca-1⁺ cells / CD3⁺ CD8⁺ CD4⁻ CD62L⁺ CD44⁻ CD122⁺ × 100%. Data are representative for three independent experiments (n=5). The data were shown as means ± SD, one-way ANOVA. * *P* < 0.05, ** *P* < 0.01, *** *P* < 0.001.

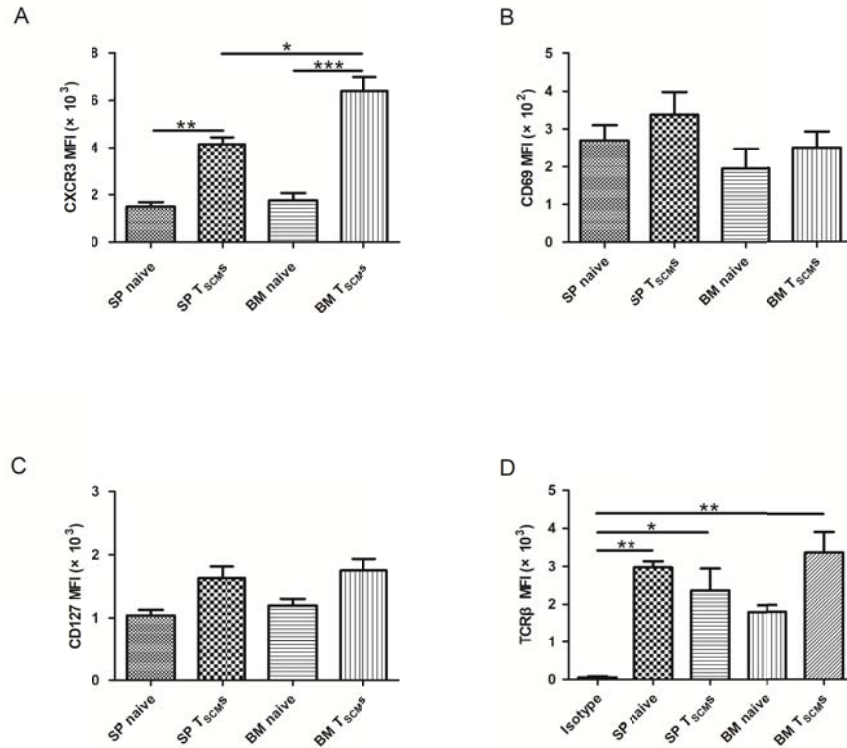


Figure S3. Flow cytometric analysis of SP naïve T cells, SP T_{SCMS}, BM naïve T cells and BM T_{SCMS}.

The MFI of a given molecule in different CD8⁺ T cell subsets was analyzed by flow cytometry. CD8⁺ T cell subsets were defined as follows: BM-resident T_{SCMS}, CD3⁺ CD8⁺ CD4⁻ CD44^{low} CD62L^{high} CD122^{high} Sca-1^{high}; BM- and SP-resident naïve T cells,

CD3⁺ CD8⁺ CD4⁻ CD44^{low} CD62L^{high} CD122^{low} Sca-1^{low}. Data are representative for five independent experiments (n=7), one-way ANOVA, **P* < 0.05, ***P* < 0.01, ****P* < 0.001..

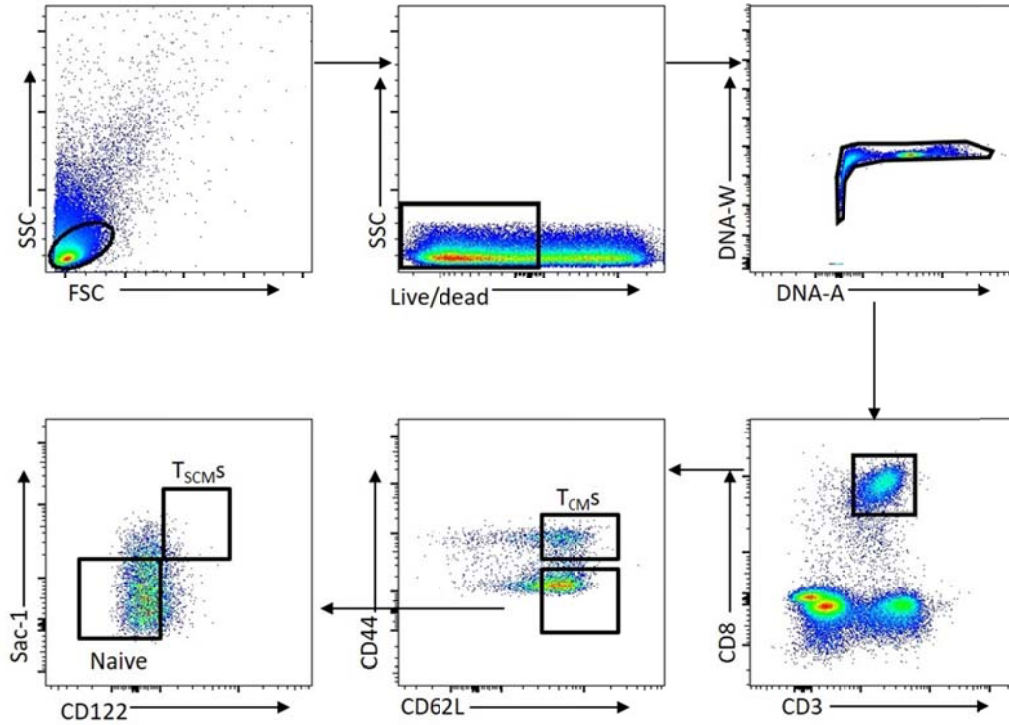


Figure S4. Gating strategy for flow cytometric analysis of DNA content in T-cell subsets.

The DNA content was tested by staining propidium iodide. The dot plots show the gating strategy of naïve T cells (CD3⁺ CD8⁺ CD44⁻ CD62L⁺ CD122⁻ Sca-1⁻) and T_{SCMS} (CD3⁺ CD8⁺ CD44⁻ CD62L⁺ CD122⁺ Sca-1⁺). The T_{CMS} were gated as CD3⁺ CD8⁺ CD44⁺ CD62L⁺ cells.

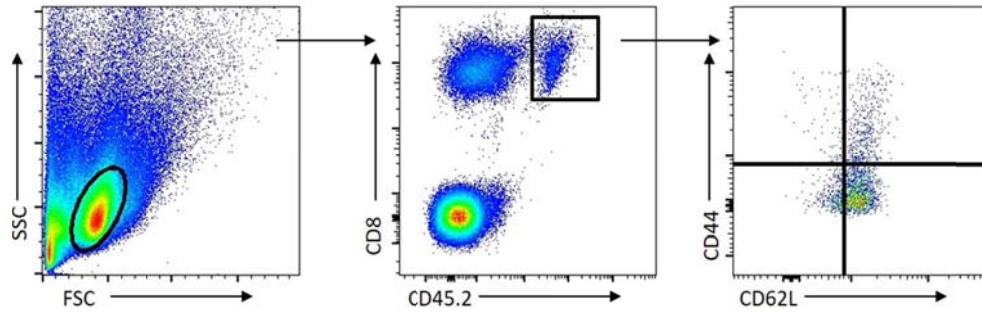


Figure S5. Gating strategy for the analysis of the in vivo activation of adoptive transfer OT I T cells.

The OT I mice $CD3^{+} CD4^{-} CD8^{+} CD44^{low} CD62L^{high}$ cells were sorted by flow cytometry and then the frequencies of $CD122^{high} Sca-1^{high}$ in $CD44^{low} CD62L^{high}$ T cells compartment was analyzed. Dot plots represent the strategy of flow cytometric analysis of adoptive transfer.

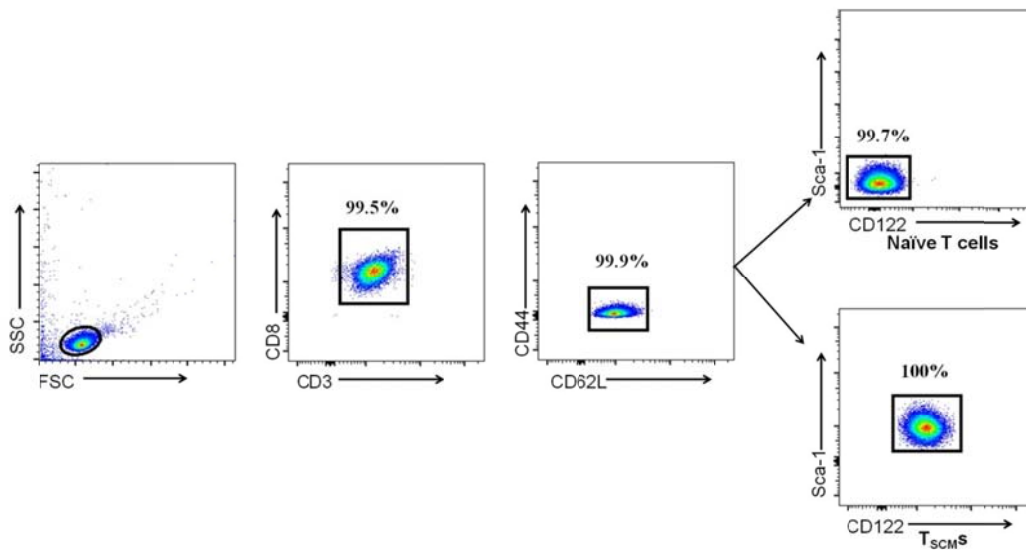


Figure S6. The purity of naïve T cells ($CD3^{+} CD8^{+} CD44^{low} CD62L^{high} Sca-1^{low} CD122^{low}$) and T_{SCMs} ($CD3^{+} CD8^{+} CD44^{low} CD62L^{high} Sca-1^{high} CD122^{high}$) after sorted by flow cytometry.

The $CD3^{+} CD8^{+} CD62L^{+} CD44^{-} Sca-1^{high} CD122^{high}$ cells and $CD3^{+} CD8^{+} CD44^{low} CD62L^{high} Sca-1^{low} CD122^{low}$ cells were sorted. Numbers in dot plots show the purities of $CD3^{+} CD8^{+} CD44^{low} CD62L^{high} Sca-1^{high} CD122^{high}$ cells and $CD3^{+} CD8^{+} CD44^{low} CD62L^{high} Sca-1^{low} CD122^{low}$ cells which were sorted by flow cytometry. Data are representative for three independent experiments (n=5).

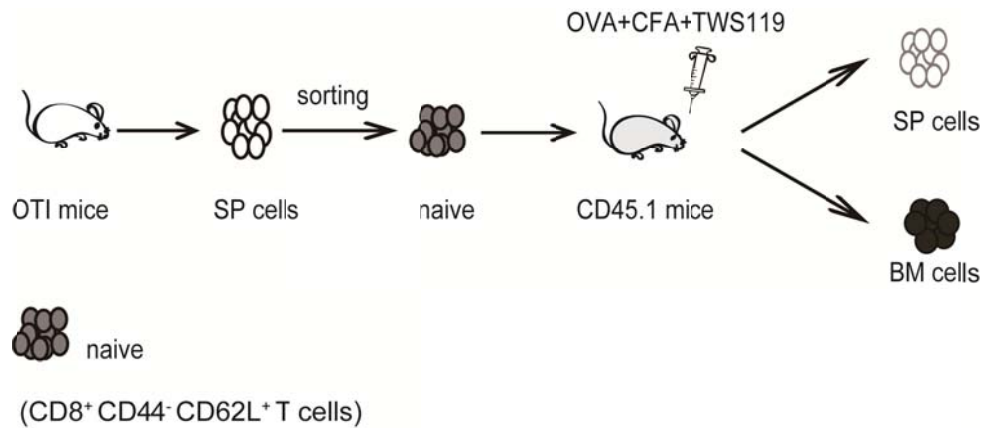


Fig S7. The strategy for testing frequency of in-vivo generated $CD8^{+} T_{SCMs}$ with TWS119.

The 2×10^6 OT-I naïve $CD8^{+}$ T cells were adoptively transferred into congenic CD45.1 mice and then injected i.p. 500 μ g per mice ovalbumin (OVA) (Sigma) with complete Freund's adjuvant (CFA) (Sigma). Mice received four doses per day of TWS119 at 40 mg/kg from day 0 to day 3. Six days after injection, mice with or without the treatment of TWS119 were sacrificed for further analysis.

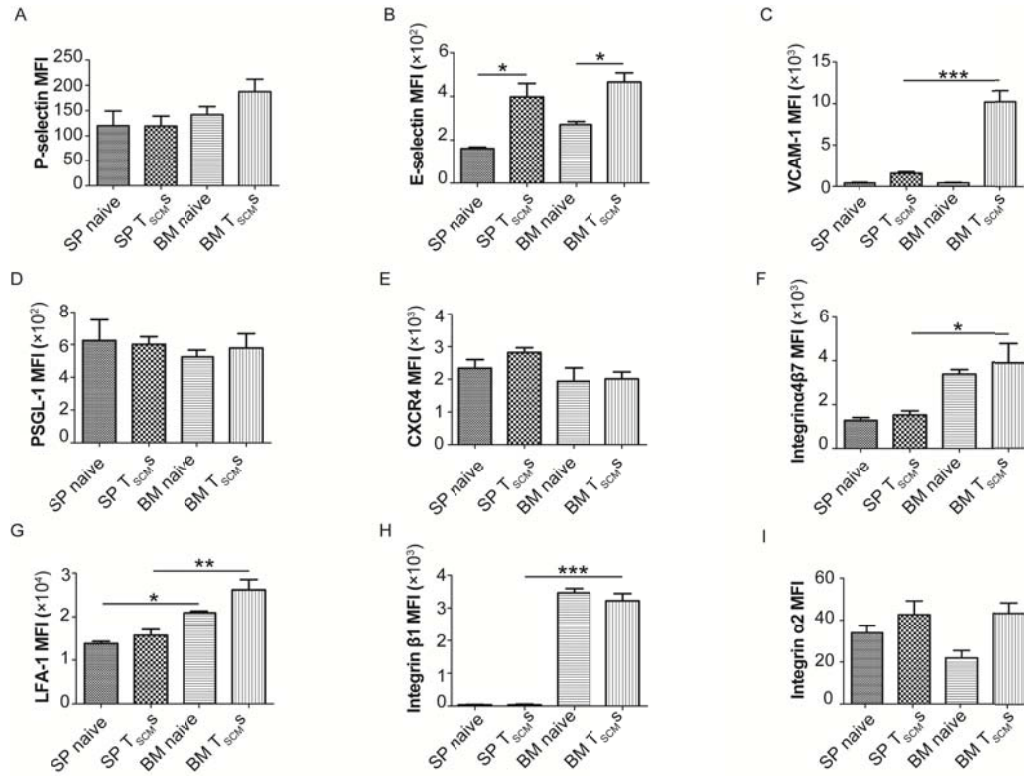


Figure S8. Expression levels of adhesion molecules on the surface of T_{SCMS}.

The MFI of a given adhesion molecule in different CD8⁺ T cell subsets was analyzed by flow cytometry. CD8⁺ T cell subsets were defined as follows: BM-resident T_{SCMS}, CD3⁺ CD8⁺ CD4⁻ CD44^{low} CD62L^{high} CD122^{high} Sca-1^{high}, BM- and SP-resident naïve T cells, CD3⁺ CD8⁺ CD4⁻ CD44^{low} CD62L^{high} CD122^{low} Sca-1^{low}. Data are representative for three independent experiments (n=6), one-way ANOVA, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Table 1

Primer sequences for qRT-PCR.

<i>Ccr2</i> forward	ATGGAAGACAATAATATGTTACC
<i>Ccr2</i> reverse	ATGACAAGGCTCACCATC
<i>Tcf7</i> forward	GTACATGGAGAAGCCGAGGG
<i>Tcf7</i> reverse	ACTCTGGAAGTTTGTCCGGG
<i>Tcf7</i> RT	ACCTCCTAGGCCAATAGGGAGGTCCAGCCA
<i>Klf7</i> forward	CGTTGAAACTGGTGGCCAAG
<i>Klf7</i> reverse	ATAAACTTTCCGGCACCCGT
<i>Lef1</i> forward	AGCACGGAAAGAGAGACAGC
<i>Lef1</i> reverse	GCTGTCAATTCTGGGACCTGT
Mouse beta catenin forward	CGCCGCTTATAAATCGCTCC
Mouse beta catenin reverse	TTCACAGGACACGAGCTGAC
<i>Ccr5</i> forward	GTTGTTTTGGAGAACGCCCC
<i>Ccr5</i> reverse	CAACACTGCTCCGAAACTGC
<i>CD122</i> forward	TTGTCTGCTACCTAAGCTGCG
<i>CD122</i> reverse	GGCTCCAGGGAAGAGCTATG
<i>CD44</i> forward	AAAAAGCCATGCAGCAGCTC
<i>CD44</i> reverse	TTGCCTCTTGGGTGGTGTTC
<i>Ly6a</i> forward	CCACATCTGACAGAACTTGCC
<i>Ly6a</i> reverse	GCTGCACAGATAAAACCTAGCAG
Mouse <i>GAPDH</i> forward	GGACCTCATGGCCTACATGG
Mouse <i>GAPDH</i> reverse	TAGGGCCTCTCTTGCTCAGT