

**Figure S1. NP309-specific memory CD4**<sup>+</sup> **T lymphocytes have a CD127**<sup>hi</sup> **Sca1**<sup>hi</sup> **Bcl2**<sup>hi</sup> **phenotype. (A)** The representative dot plots show NP309 tetramer binding in CD44<sup>hi</sup> CD62L<sup>lo</sup> CD4<sup>+</sup> T lymphocytes from uninfected versus LCMV-infected mice while the bar graph indicates the number (mean  $\pm$  S.D.) of NP309-tetramer<sup>+</sup> cells in each group (n=5 mice). **(B)** Dot plots showing CD127 and Sca1 expression in the indicated cell populations as well as a bar graph depicting the frequency (mean  $\pm$  S.D.) of each subpopulation among the same populations are displayed (n=5 mice). **(C)** The representative dot plots show CD127, Sca1, and Bcl2 expression in the indicated cell populations from uninfected and LCMV-infected animals while the bar graph indicates the frequency (mean  $\pm$  S.D.) of Bcl2<sup>hi</sup> fraction among CD127<sup>hi</sup> Sca1<sup>hi</sup> cells from the same populations (n=3-4 mice). Data are representative of 2 independent experiments performed. \*\* p<0.01, \*\*\* p<0.001.

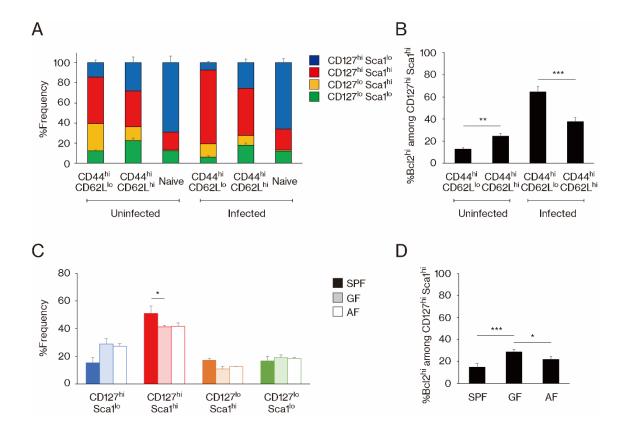


Figure S2. CD44<sup>hi</sup> CD62L<sup>hi</sup> CD4<sup>+</sup> T lymphocytes in uninfected SPF, GF, AF, and LCMV-infected mice. (A) The bar graph shows the frequency (mean  $\pm$  S.D.) of CD127<sup>hi</sup> Sca1<sup>lo</sup>, CD127<sup>hi</sup> Sca1<sup>hi</sup>, CD127<sup>lo</sup> Sca1<sup>hi</sup>, and CD127<sup>lo</sup> Sca1<sup>lo</sup> cells among the indicated CD4<sup>+</sup> T cell populations from uninfected SPF and infected mice (n=5 mice). (B) The bar graph indicates the Bcl2<sup>hi</sup> fraction (mean  $\pm$  S.D.) among CD127<sup>hi</sup> Sca1<sup>hi</sup> cells from CD44<sup>hi</sup> CD62L<sup>lo</sup> and CD44<sup>hi</sup> CD62L<sup>hi</sup> CD4<sup>+</sup> T cells in uninfected and LCMV-infected mice (n=3-4 mice). (C) The frequency (mean  $\pm$  S.D.) of the indicated subsets among total CD44<sup>hi</sup> CD62L<sup>hi</sup> CD4<sup>+</sup> T lymphocytes from SPF, GF, and AF mice (n=3-4 mice). (D) The Bcl2<sup>hi</sup> fraction (mean  $\pm$  S.D.) among CD127<sup>hi</sup> Sca1<sup>hi</sup> CD44<sup>hi</sup> CD62L<sup>hi</sup> CD4<sup>+</sup> T cells from SPF, GF, and AF animals (n=3-4 mice). Data are representative of 2 independent experiments performed. \* p<0.05, \*\*\* p<0.01, \*\*\*\* p<0.001.

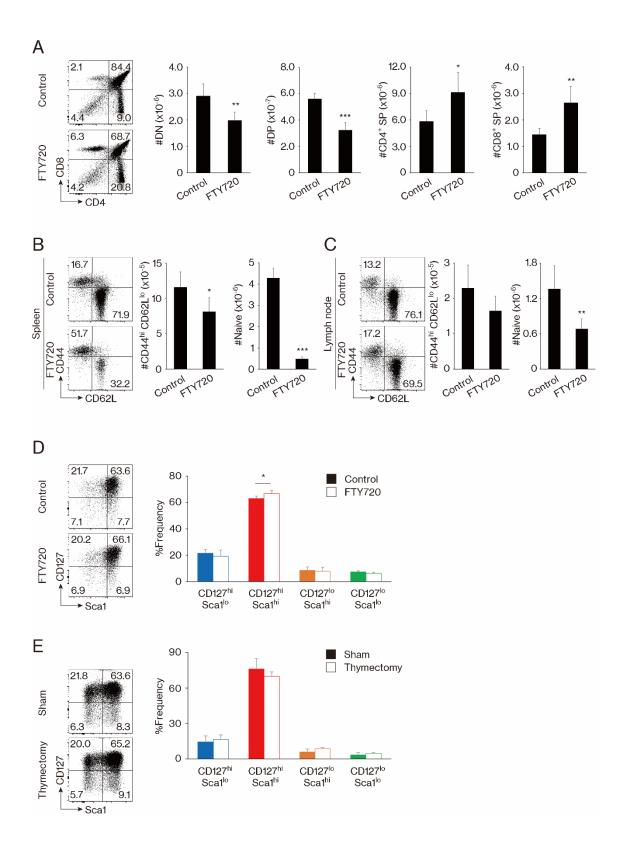


Figure S3. The four MP subpopulations in the periphery are maintained in the absence of thymic input. (A - D) Mice received FTY720 or control PBS and were

analyzed 2 weeks later. (A) Dot plots showing CD4 and CD8 expression in thymocytes from each group together with bar graphs indicating the number (mean  $\pm$  S.D.) of double-negative (DN), double-positive (DP), and CD4<sup>+</sup> and CD8<sup>+</sup> single-positive (SP) thymocytes (n=5 mice). (B, C) Dot plots displaying CD44 and CD62L expression in CD4<sup>+</sup> T lymphocytes in the (B) spleen and (C) lymph nodes as well as bar graphs depicting the number (mean  $\pm$  S.D.) of MP and naïve cells from each group (n=5 mice). (D) Dot plots showing CD127 and Sca1 levels in splenic MP CD4<sup>+</sup> T lymphocytes from each group and a bar graph indicating the frequency (mean  $\pm$  S.D.) of MP subpopulations among the total MP population (n=5 mice). Data are representative of 2 independent experiments. (E) Mice underwent adult-thymectomy or sham-operation and were analyzed for their MP T lymphocytes 2 weeks later. The representative dot plots display CD127 and Sca1 expression in MP cells from each group while the bar graph indicates the frequency (mean  $\pm$  S.D.) of MP subpopulations among total MP cells (n=4 mice). Data are pooled from 3 independent experiments performed. \* p<0.05, \*\* p<0.01, \*\*\* p<0.001.

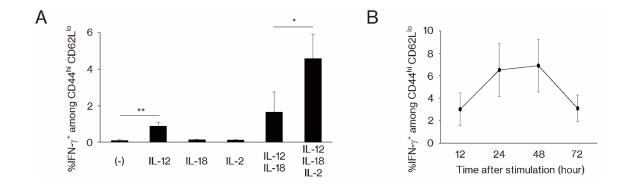
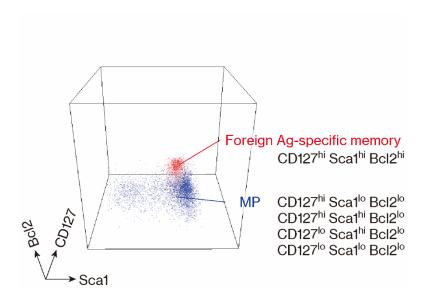


Figure S4. MP cells respond to IL-12, IL-18, and IL-2 and produce IFN- $\gamma$ . Total splenocytes were cultured (A) under the indicated conditions for 24 hours or (B) in the presence of IL-12, IL-18, and IL-2 for the indicated period. The graphs indicate the frequency (mean ± S.D.) of IFN- $\gamma$ <sup>+</sup> cells among MP CD4<sup>+</sup> T lymphocytes (n=4 mice). Data are representative of 2 independent experiments. \* p<0.05, \*\* p<0.01.



**Figure S5. Foreign Ag-specific and MP CD4**<sup>+</sup> **T cells represent phenotypically distinct populations.** Foreign Ag-specific memory cells are CD127<sup>hi</sup> Sca1<sup>hi</sup> Bcl2<sup>hi</sup> (red) while MP cells are CD127<sup>lo-hi</sup> Sca1<sup>lo-hi</sup> Bcl2<sup>lo</sup> (blue). Among the latter, CD127<sup>hi</sup> Sca1<sup>hi</sup> cells represent the most mature MP subset with the Th1-type inflammatory potential.

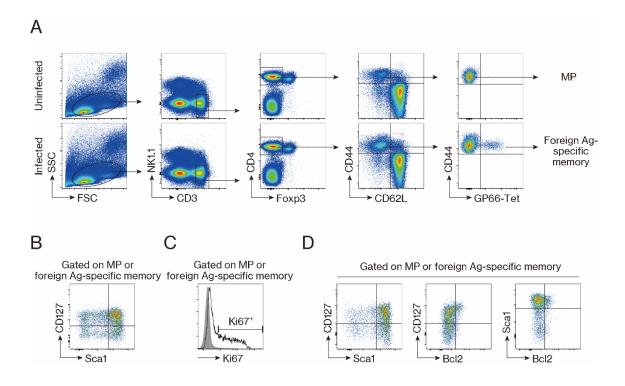


Figure S6. Gating strategy for flow cytometric analyses. (A) To detect MP and foreign Ag-specific memory CD4<sup>+</sup> T cells, total singlet cells were gated for CD3<sup>+</sup> NK1.1<sup>neg</sup> CD4<sup>+</sup> Foxp3<sup>neg</sup> CD44<sup>hi</sup> CD62L<sup>lo</sup> population. MP and foreign Ag-specific memory cells were then defined as tetramer<sup>neg</sup> cells from uninfected mice and tetramer<sup>+</sup> cells from LCMV-infected mice, respectively. (B) To analyze MP subsets, CD127 and Sca1 expression levels were measured in MP or foreign Ag-specific memory cells determined in (A). (C) For examination of proliferation status, Ki67 levels were measured in MP subsets as well as foreign Ag-specific memory cells using naïve cell population as a reference. (D) For detection of Bcl2, CD127, Sca1, and Bcl2 levels were simultaneously analyzed in MP and foreign Ag-specific memory cells. Bcl2<sup>hi</sup> fraction was determined as the frequency of Bcl2<sup>hi</sup> cells among CD127<sup>hi</sup> Sca1<sup>hi</sup> MP or foreign Ag-specific memory T lymphocyte populations.

Cell cycle	Cell cycle	Anti-anontosis
(positive regulators)	(negative regulators)	Anti-apoptosis
Aurka	Cdkn1a	Bcl2
Aurkb	Cdkn1b	Bcl2a1
Ccna2	Cdkn2a	Bcl2I1
Ccnb1	Cdkn2b	Bcl2l2
Ccnb2	Cdkn2c	Bcl2I10
Ccnd1	Cdkn2d	McI1
Ccnd2	Chek1	Naip1
Ccnd3	Chek2	Naip2
Ccne1	E2f4	Naip3
Cdc25a	E2f5	Naip4
Cdc25b	E2f6	Naip5
Cdc25c	E2f7	Naip6
Cdk1	E2f8	Naip7
Cdk2	Rb1	
Cdk4	Trp53	
Cdk6	Wee1	
E2f1		
E2f2		
E2f3		
Mdm2		
Plk1		
Plk3		
Plk4		
Tfdp1		
Tfdp2		

Table S1. T cell gene signatures.