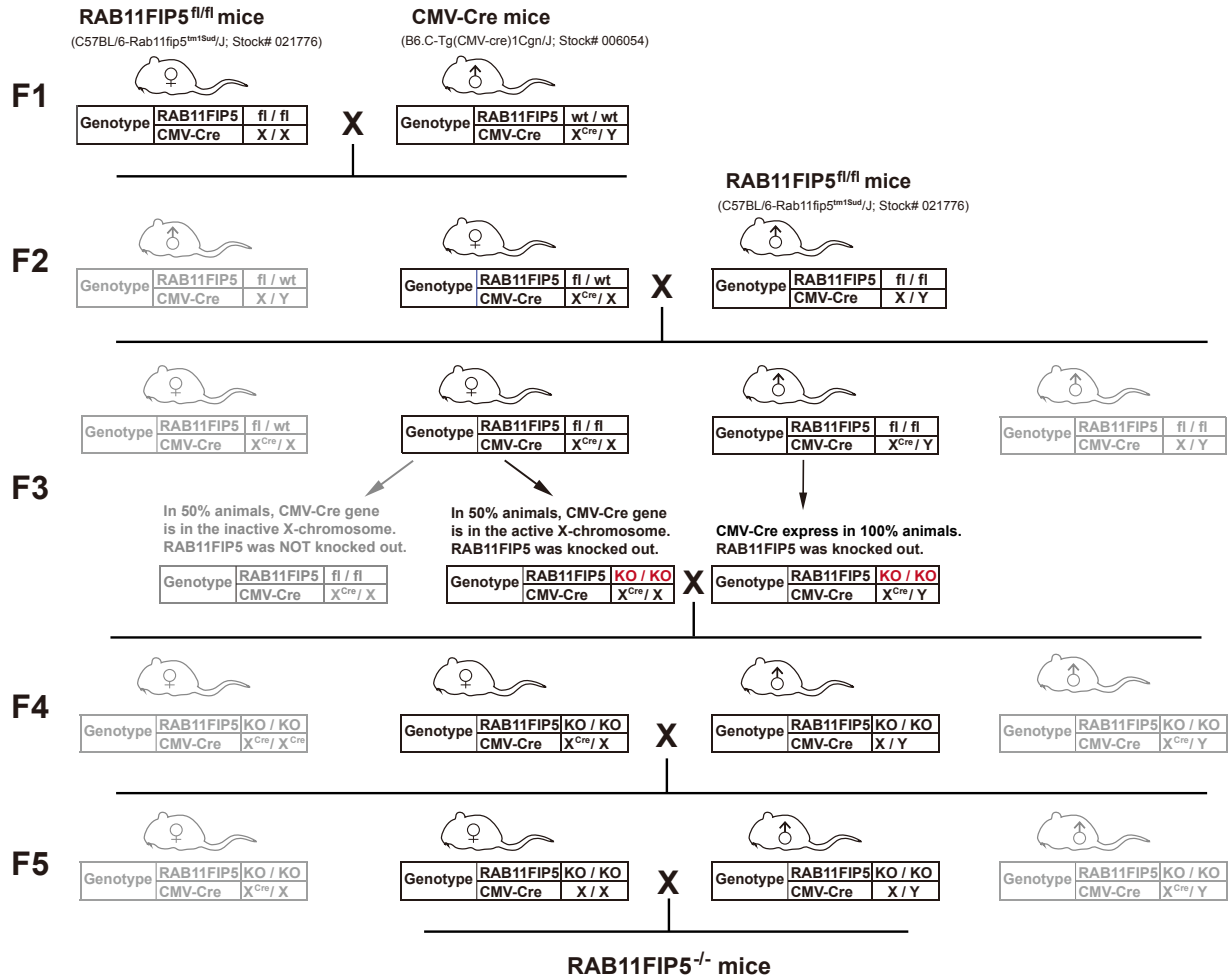
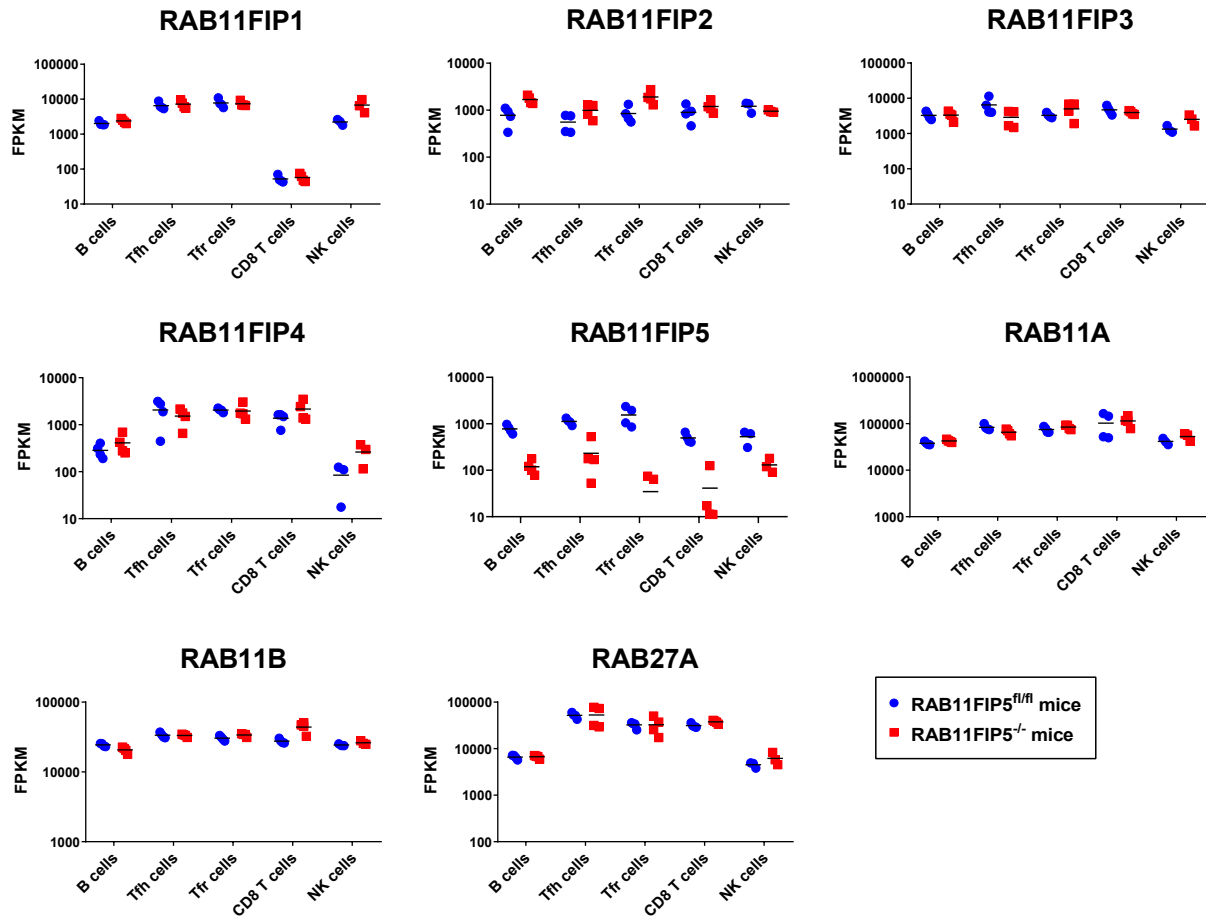


1 SUPPLEMENTAL FIGURES
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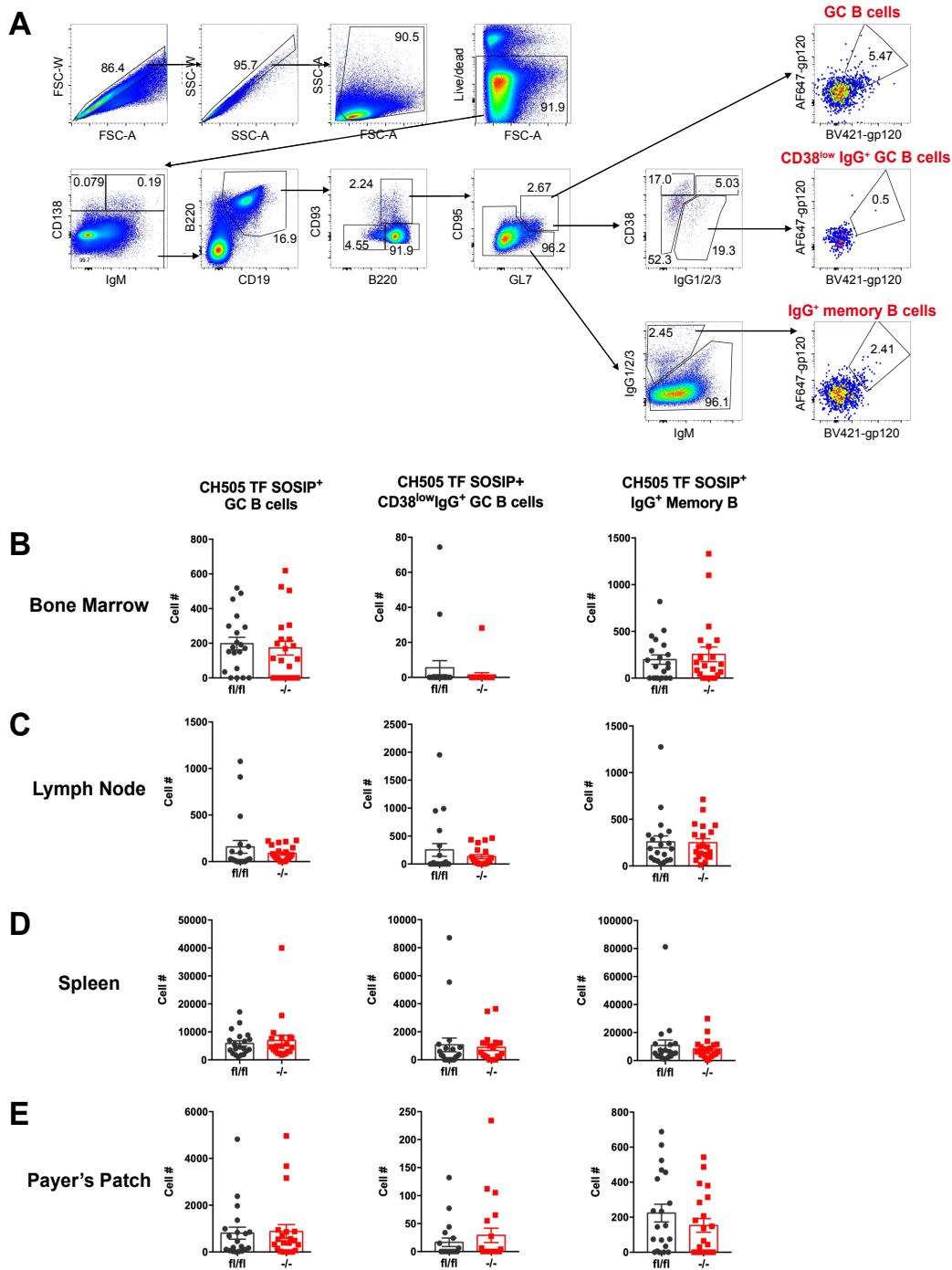
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4 **Figure S1. Generation of constitutive *RAB11FIP5* knockout (*RAB11FIP5^{-/-}*) mice.**
5 *RAB11FIP5^{-/-}* mice were generated by breeding *RAB11FIP5* floxed mice (*RAB11FIP5^{fl/fl}*) with CMV-Cre mice. In
6 the *RAB11FIP5^{fl/fl}* conditional mutant mouse, exon 2 of the *RAB11FIP5* gene is flanked by loxP sites. Mice
7 homozygous for this allele are viable, fertile and produce normal levels of Rab11Fip5 protein. When crossed with a
8 Cre-expressing strain, the floxed exon 2 is excised and therefore the expression of functional *RAB11FIP5* mRNA is
9 abolished. In our study, as the CMV-Cre transgene is X-chromosome linked, F1 female *RAB11FIP5^{fl/fl}* mice were
10 crossed with male CMV-Cre mice. F2 female littermates were kept and bred with *RAB11FIP5^{fl/fl}* mice. In F3
11 approximately half of the female littermates still had the *RAB11FIP5* gene due to X-chromosome inactivation in the
12 CMV-Cre positive allele, while males and the remaining females had *RAB11FIP5* deletion. By inbreeding F3
13 *RAB11FIP5^{-/-}* male and females, we eventually generated constitutive *RAB11FIP5^{-/-}* mice independent of Cre. All
14 experiments in this study were conducted with mice after F5.
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17 **Figure S2. No major perturbations in lymphocyte subsets in *RAB11FIP5*^{-/-} mice.**
18 **(A)** Pictures of spleens of representative *RAB11FIP5*^{-/-} and control *RAB11FIP5*^{fl/fl} mice.
19 **(B)** Body and spleen weights of *RAB11FIP5*^{-/-} (*n*=11) and control *RAB11FIP5*^{fl/fl} mice (*n*=10).
20 **(C-D)** Phenotypic analysis of B cells in *RAB11FIP5*^{-/-} (*n*=3) and control *RAB11FIP5*^{fl/fl} (*n*=3) mice. (C) Gating
21 strategy for B cell subsets. (D) Cells from lymph nodes, spleen, and bone marrow were analyzed and the bar graphs
22 show the absolute number of total cells, IgM⁺ plasma cells (PC; CD138⁺), IgM⁻ PC, total B cells (CD19⁺B220⁺), pro
23 B cells (CD⁺B220⁺), pre-B cells (IgM⁺IgD⁻), immature (Imm) B cells (B220⁺CD93⁺IgM⁺IgD⁻), transitional (Trans) B
24 cells (B220⁺CD93⁺IgM⁺IgD^{+/low}), germinal center (GC) B cells (B220⁺CD93⁻GL7⁺CD95⁺CD38^{low}), marginal zone
25 (MZ) B cells (B220⁺CD93⁻GL7⁻CD95⁻IgG⁻CD21^{high}CD23^{low/+}), follicular (Fo) B cells (B220⁺CD93⁻GL7⁻CD95⁻IgG⁻
26 CD21^{int}CD23^{high}), myeloid cells (IgM⁻CD19⁻B220⁻CD11b⁺CD5⁺), and T cells (IgM⁻CD19⁻B220⁻CD11b⁻CD5⁺).
27 **(E-F)** Phenotypic analysis of T cells and NK cells in *RAB11FIP5*^{-/-} and fl/fl mice. (E) Gating strategy for T cell and
28 NK cell subsets. (F) Cells from lymph node, spleen and bone marrow were analyzed and the bar graphs show the
29 absolute number of total cells, erythroid cells (TER119⁺B220⁻), B cells (TER119⁻B220⁺), total NK cells (CD3⁻
30 NK1.1⁺), Thy1.2⁻CD62L⁺ NK cells, Thy1.2⁺CD62L⁺ NK cells, Thy1.2⁺CD62L⁻ NK cells, Thy1.2⁻CD62L⁻ NK cells,
31 total T cells (CD3⁺), CD8⁺ T cells, naive CD8⁺ T cells (CD8⁺CD44⁻CD62L⁺), central memory (CM) CD8⁺ T cells
32 (CD8⁺CD44⁺CD62L⁺), effector CD8⁺ T cells (CD8⁺CD44⁺CD62L⁻), effector memory (EM) CD8⁺ T cells
33 (CD8⁺CD44⁺CD62L⁻), CD4⁺ T cells, non-Treg (CD4⁺CD127^{high}CD25^{low}), Tfh (CD4⁺CD127^{high}CD25^{low}CXCR5⁺PD-
34 1⁺), Thy1.2⁻ Tfh, Thy1.2⁺ Tfh, Treg (CD4⁺CD127^{low}CD25^{high}), Tfr (CD4⁺CD127^{low}CD25^{high}CXCR5⁺PD-1⁺), naive
35 CD4⁺ T cells (CD4⁺CD44⁻CD62L⁺), central memory (CM) CD4⁺ T cells (CD4⁺CD44⁺CD62L⁺), effector CD4⁺ T
36 cells (CD4⁺CD44⁺CD62L⁻), and effector memory (EM) CD4⁺ T cells (CD4⁺CD44⁺CD62L⁻).
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Figure S3. *RAB11FIP5* deficiency has no effect on expression of other RAB11 family genes and RAB11 family interacting protein (Fip) genes. FPKMs of *RAB11A*, *RAB11B*, and *RAB11FIPs* genes in B cells, Tfh cells, Tfr cells, CD8⁺ T cells and NK cells are shown as dots; each dot indicates data from one animal. While the deletion of exon 2 in *RAB11FIP5* alleles results in the absence of a complete and functional *RAB11FIP5* mRNA, incomplete/partial *RAB11FIP5* transcripts may still exist at various levels in different cell types as indicated by decreased FPKM in the *RAB11FIP5^{-/-}* mice.



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Figure S4. Analysis of antigen-specific B cell responses in immunized mice.

(A) Gating strategy to identify HIV-Env binding cells (double-positive for binding to CH505 gp120 tetramers labeled with two different fluorochromes) in germinal center (GC) B cells, CD38^{low} IgG⁺ GC B cells, and IgG⁺ memory B cells.

(B-E) HIV-1 CH505 TF SOSIP-specific GC B cells, CD38^{low} IgG⁺ GC B cells, and memory B cells were compared between *RAB11FIP5*^{-/-} mice (*n*=21) and control *RAB11FIP5*^{fl/fl} mice (*n*=20) in different tissues. Cells from bone marrow (B), spleen (C), lymph node (D), and Peyer's patch (E) were analyzed and absolute numbers of SOSIP-binding cells are shown in each tissue. Bars represent mean ± SD and each dot indicates one animal. Combined data from three independent immunization studies are shown. The statistical significance of differences between groups was determined by Mann-Whitney U test, and no significant differences were found.