

## Supplementary material for

### **SZT2 maintains hematopoietic stem cell homeostasis via nutrient-mediated mTORC1 regulation**

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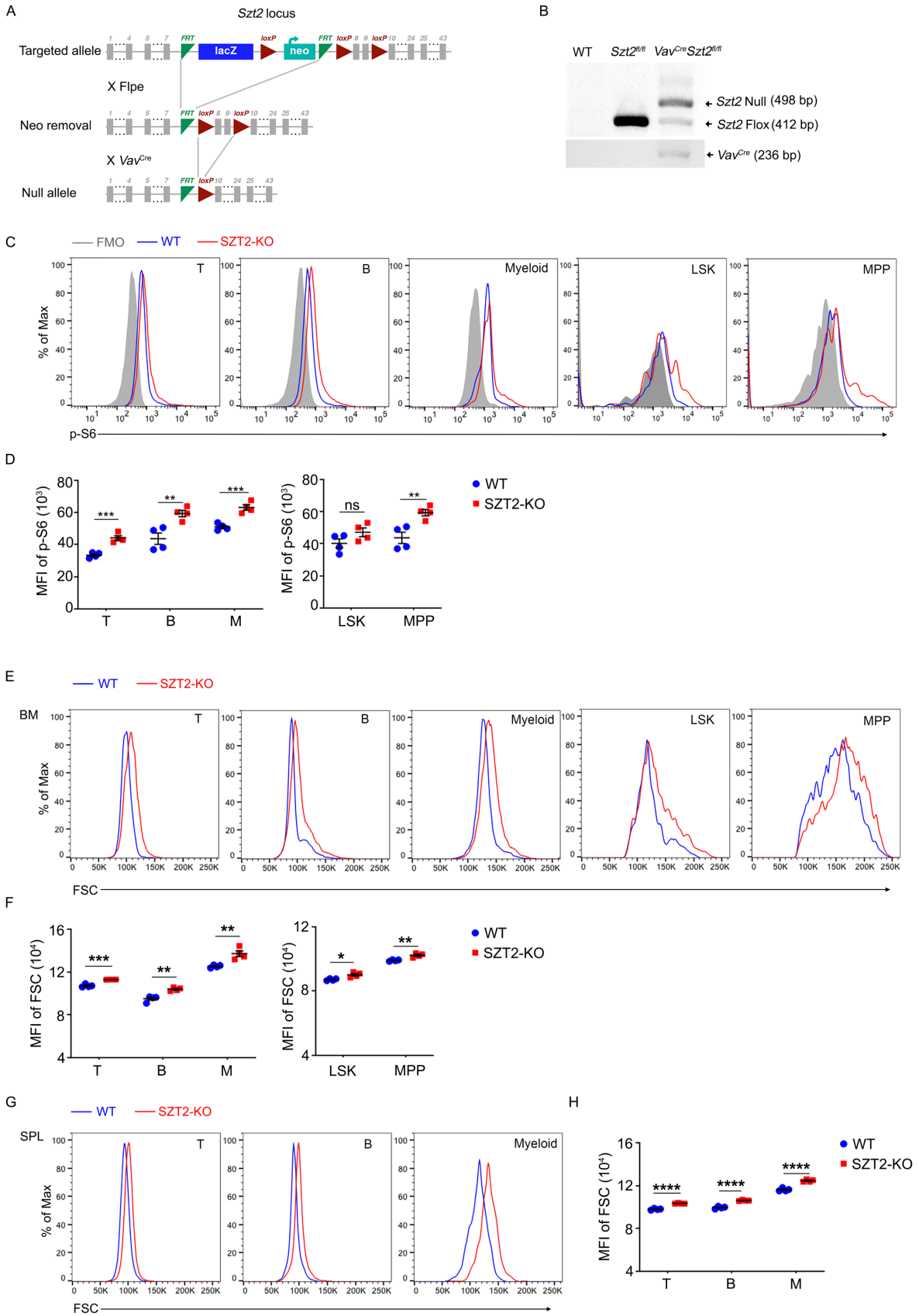
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Authorship Note: N. Yin and G. Jin contributed equally to this study

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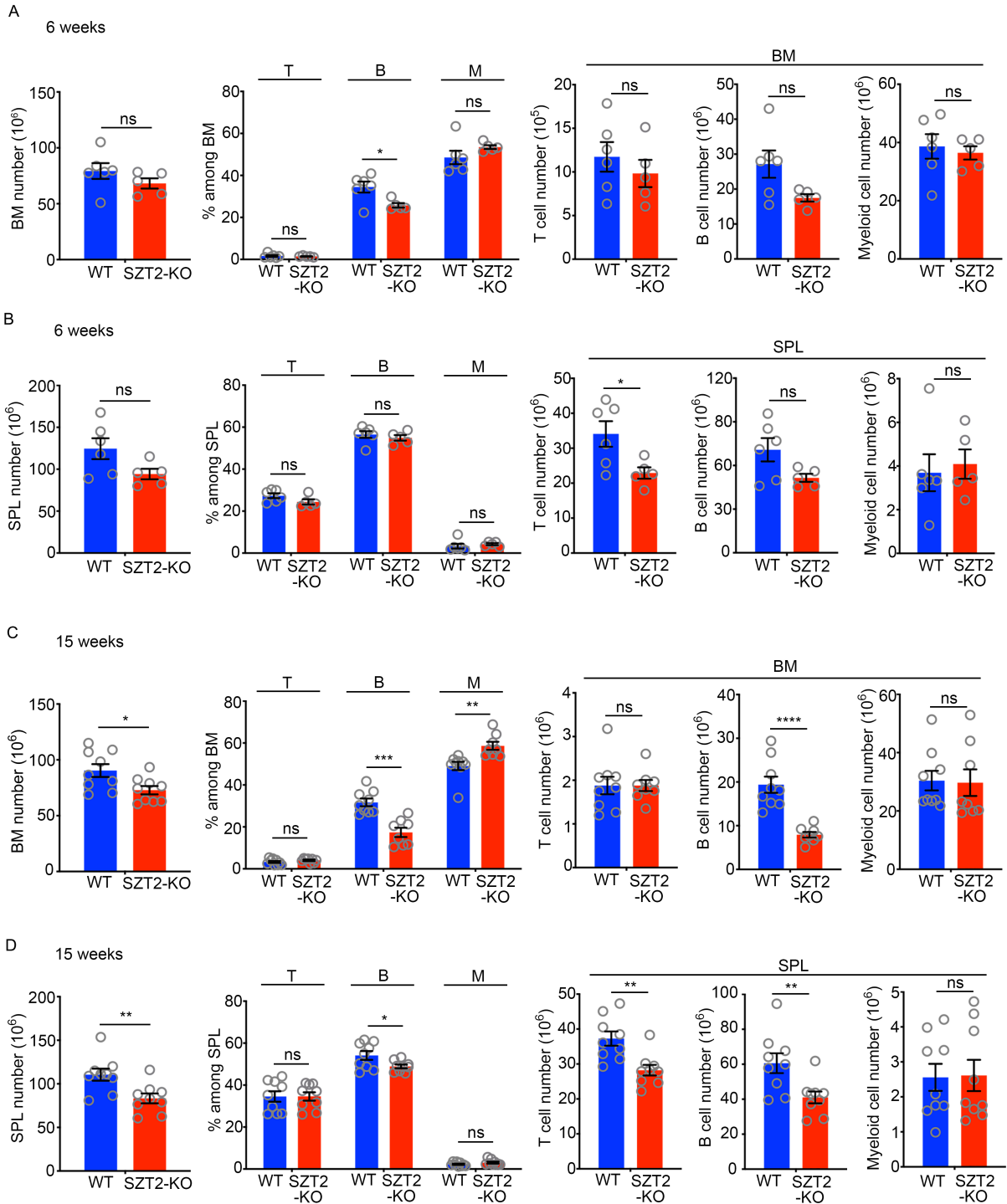
Supplemental Figures 1 to 6

Legends for Supplemental Figures 1 to 6



Supplemental Figure 1. SZT2 represses mTORC1 signaling in hematopoietic cells

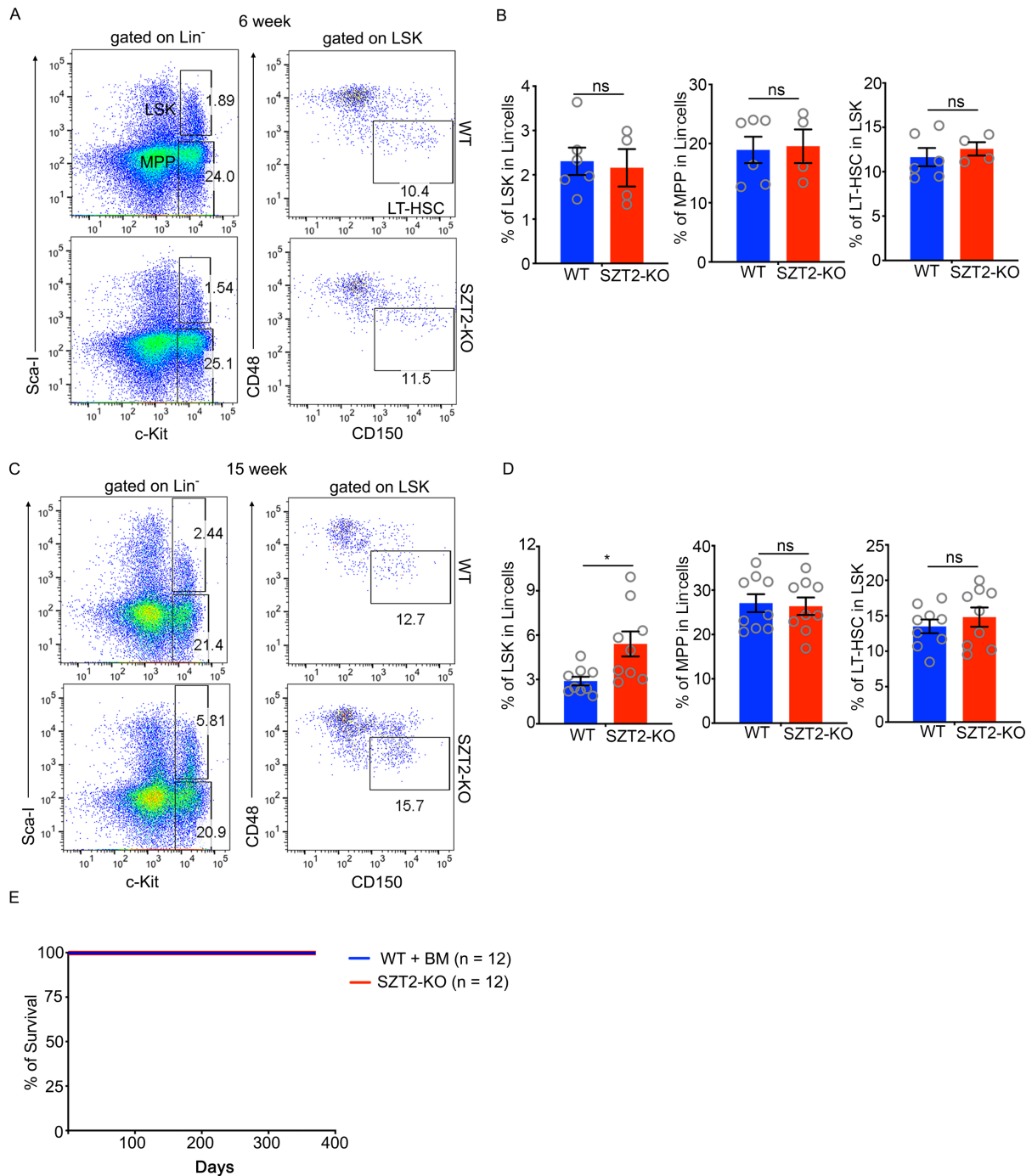
(A) Targeting strategy of *Szt2* floxed mice. (B) PCR detection of floxed and null allele of *Szt2* in total BM cells. (C and D) Flow cytometry analysis of ribosomal S6 protein phosphorylation (pS6) of indicated populations in BM from WT and SZT2-KO mice at 14-week-old age. T cells (CD3<sup>+</sup>), B cells (B220<sup>+</sup>), myeloid cells (CD11b<sup>+</sup>), LSK (Lin<sup>-</sup>Sca1<sup>+</sup>c-Kit<sup>+</sup>) and MPP (Lin<sup>-</sup>Sca1<sup>-</sup>c-Kit<sup>+</sup>). Representative plots (C) and statistics (D) are shown, n = 4 mice per genotype. Data shown are representative of 2 independent experiments. (E and F) Flow cytometry analysis of cell size of indicated populations in BM from 14-week-old WT and SZT2-KO mice. Representative plots (E) and statistics (F) are shown, n = 4 mice per group. Data shown are representative of 4 independent experiments. (G and H) Flow cytometry analysis of cell size of indicated populations in spleen (SPL) from 14-week-old WT and SZT2-KO mice. Representative plots (G) and statistics (H) are shown, n = 4 mice per genotype. Data shown are representative of 4 independent experiments. All error bars represent SEM, unpaired t-test, \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001, \*\*\*\*p < 0.0001, ns, not significant.



### Supplemental Figure 2. Steady-state hematopoiesis is preserved in SZT2-KO mice

(A and B) Cell number and percentage of T cells ( $CD3^+$ ), B cells ( $B220^+$ ) and myeloid cells ( $CD11b^+$ ) in bone marrow (BM) (A) and spleen (SPL) (B) from 6-week-old WT and SZT2-KO mice,  $n = 5 - 6$  mice per genotype. Data shown are representative of 3 independent experiments. (C and D) Cell number and percentage of T cells, B cells and myeloid cells in

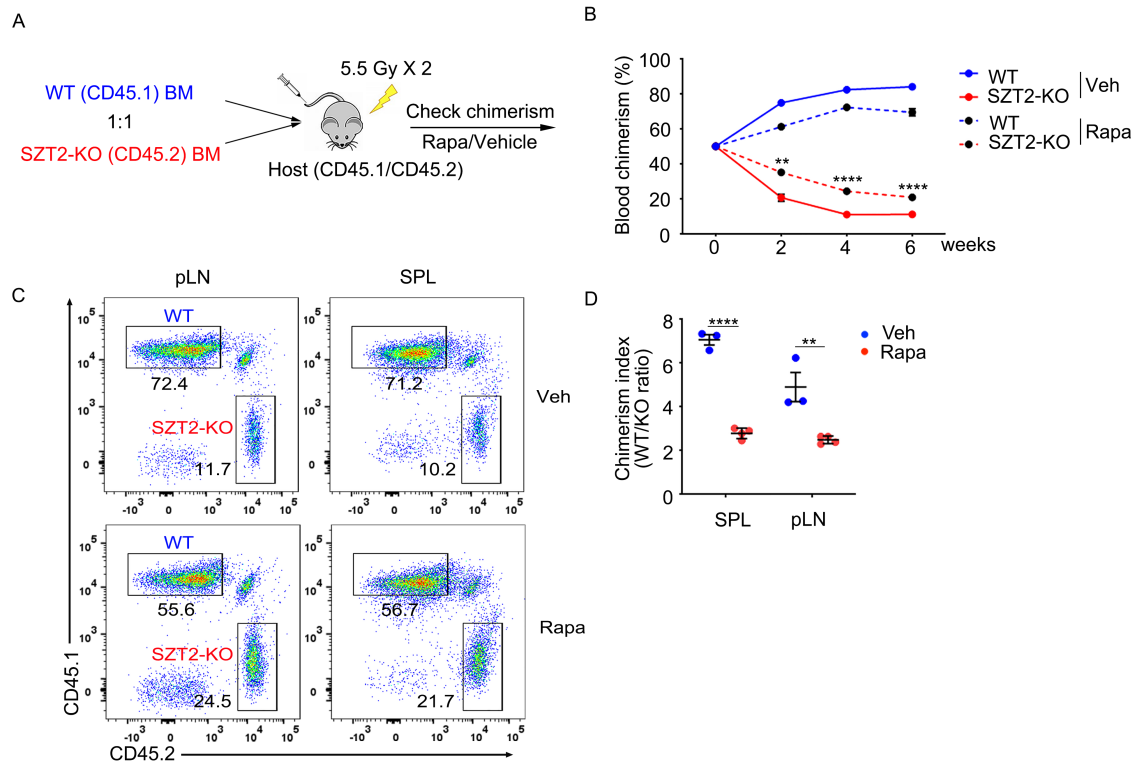
bone marrow (BM) (C) and spleen (SPL) (D) from 15-week-old WT and SZT2-KO mice, n = 8 - 9 mice per genotype. Data shown are representative of 2 independent experiments. All error bars represent SEM, unpaired t-test, \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001, \*\*\*\*p < 0.0001, ns, not significant.



### Supplemental Figure 3. HSC are preserved in SZT2-KO mice under steady-state

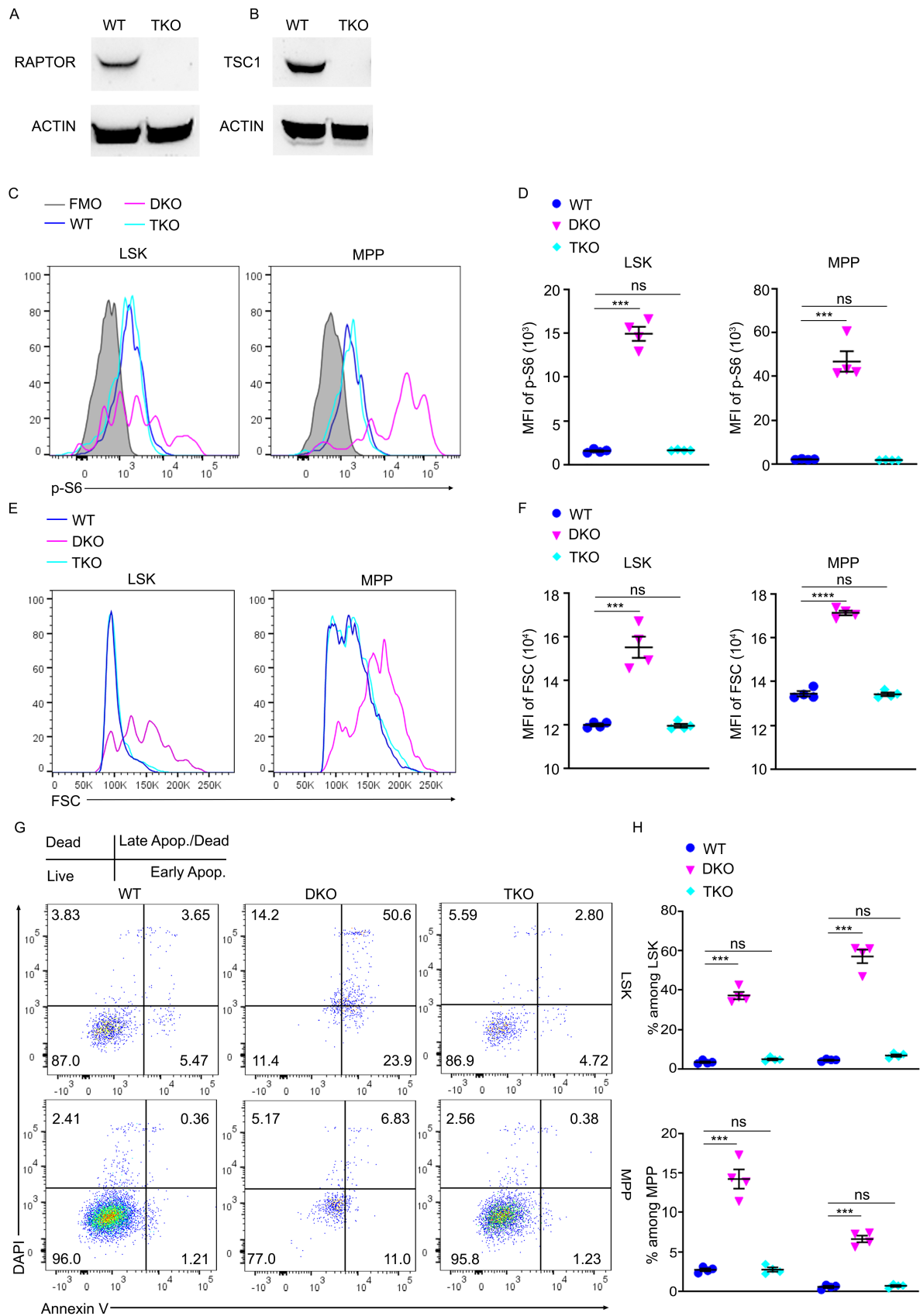
Flow cytometry analysis of LSK, MPP and LT-HSC populations in WT and SZT2-KO mice at different ages. **(A and B)** Representative plots **(A)** and statistics **(B)** from 6-week-old mice are shown,  $n = 4 - 6$  mice per genotype. Data shown are representative of 3 independent experiments. **(C and D)** Representative plots **(C)** and statistics **(D)** from 15-week-old mice are shown,  $n = 9$  mice per genotype. Data shown are representative of 2 independent experiments.

(E) Survival curves of WT and SZT2-KO mice. All error bars represent SEM, unpaired t-test, \*p < 0.05, ns, not significant.



#### Supplemental Figure 4. Rapamycin treatment partially rescues the repopulating capacity of SZT2-KO HSC

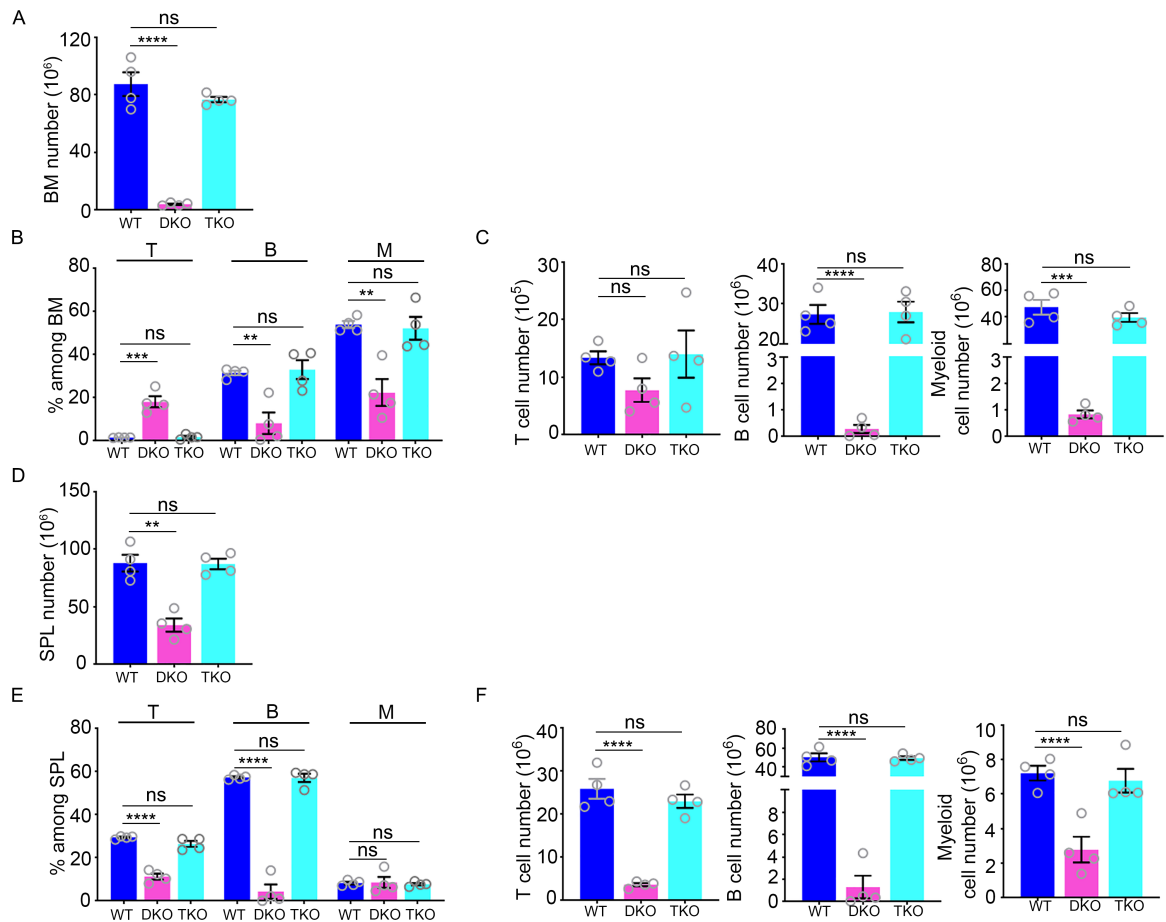
(A) A diagram of BM chimera experiment. WT (CD45.1) and SZT2-KO (CD45.2) BM cells were mixed at 1:1 ratio and injected into lethally irradiated CD45.1/CD45.2 recipient mice, followed by intraperitoneal injection of rapamycin (Rapa) or vehicle (Veh) every 2 days for 6 weeks. Chimerism was monitored. (B) Blood chimerism of recipient mice at indicated time points. (C and D) Chimerism of peripheral lymph node (pLN) and spleen (SPL) at 6 weeks post-transplantation. Representative plots (C) and statistics data (D) are shown,  $n = 3 - 4$  mice per genotype. Data shown are representative of 2 independent experiments. All error bars represent SEM, unpaired t-test,  $**p < 0.01$ ,  $****p < 0.0001$ .



**Supplemental Figure 5. Hyperactivation of mTOCR1 and increased ROS production in**

## **HSC from DKO mice are reversed to wild-type level by RAPTOR-deficiency in TKO mice**

(A and B) Immunoblot analysis of RAPTOR and TSC1 expression in bone marrow cells from WT and TKO mice. Data shown are representative of 2 independent experiments. (C and D) Phosphorylation of ribosomal S6 protein (pS6) in LSK and MPP population from WT, DKO or TKO mice at 4-week-old age was measured by flow cytometry. Representative plots (C) and statistics of mean fluorescence intensity (MFI) (D) are shown, n = 4 mice per genotype. Data shown are representative of 2 independent experiments. (E and F) Flow cytometry analysis of cell size of indicated populations in BM from 4-week-old mice. Representative plots (E) and statistics (F) are shown, n = 4 mice per genotype. Data shown are representative of 2 independent experiments. (G and H) Flow cytometry analysis of apoptosis of LSK and MPP population from mice with indicated genotypes at 4-week-old age. Representative plots (G) and statistics (H) are shown, n = 4 mice per genotype. Data shown are representative of 2 independent experiments. All error bars represent SEM, one-way ANOVA followed by Dunnett's test, \*p < 0.05, \*\*\* p < 0.001, ns, not significant.



**Supplemental Figure 6. Hematopoiesis defect of DKO mice is reversed to wild-type level by RAPTOR-deficiency in TKO mice**

(A, B and C) Percentage and absolute number of T cells (CD3<sup>+</sup>), B cells (B220<sup>+</sup>) and myeloid cells (CD11b<sup>+</sup>) in BM from 4-week-old WT, DKO or TKO mice, n = 4 mice per genotype. (D, E and F) Percentage and absolute number of T cells, B cells and myeloid cells in spleen (SPL) from mice with indicated genotypes, n = 4 mice per genotype. Data shown are representative of 2 independent experiments. All error bars represent SEM, one-way ANOVA followed by Dunnett's test, \*\*p < 0.01, \*\*\*p < 0.001, \*\*\*\*p < 0.0001, ns, not significant.