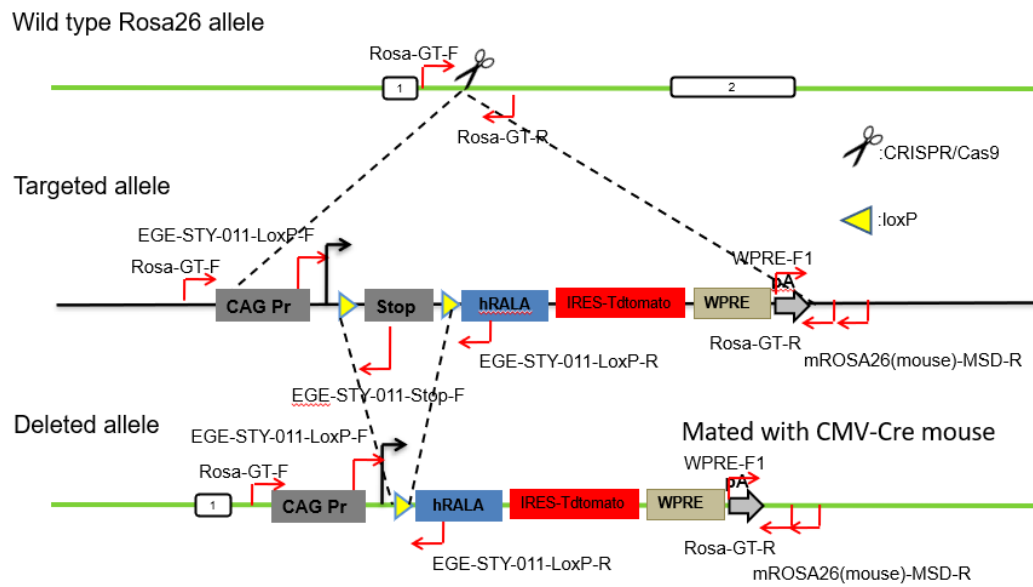


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2 **Supplementary information**

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4 **A**5 **B**

Primer	Sequence	T _m (°C)	Product size(bp)
Rosa-GT-F	AGTCGCTCTGAGTTGTTATCAG	56	WT:469
Rosa-GT-R	TGAGCATGTCTTTAATCTACCTCGATG	58	Mut:7265
WPRE-F1	GCATCGATACCGTCGACCTC	58	Mut: 792
mROSA26(mouse)-MSD-R	TTTGATAAGGCTGCAGAAGGAGCGG	62	
EGE-STY-011-LoxP-F	CAACGTGCTGGTTATTGTGCTG	61	Mut: 212
EGE-STY-011-LoxP-R	<u>GCCCACCATGATGACTTTGTG</u>	59	WT: 1649
<u>EGE-STY-011-Loxp-F</u>	CAACGTGCTGGTTATTGTGCTG	63	Mut: 304
<u>EGE-STY-011-Stop-R</u>	<u>GCAACAACCGTCGTGGTGGT</u>	64	
Cre-F4	GCGATCGCTGCCAGGATATACG	61	Mut:385
Cre-R4	CCAGAGTCATCCTTAGCGCCGT	62	

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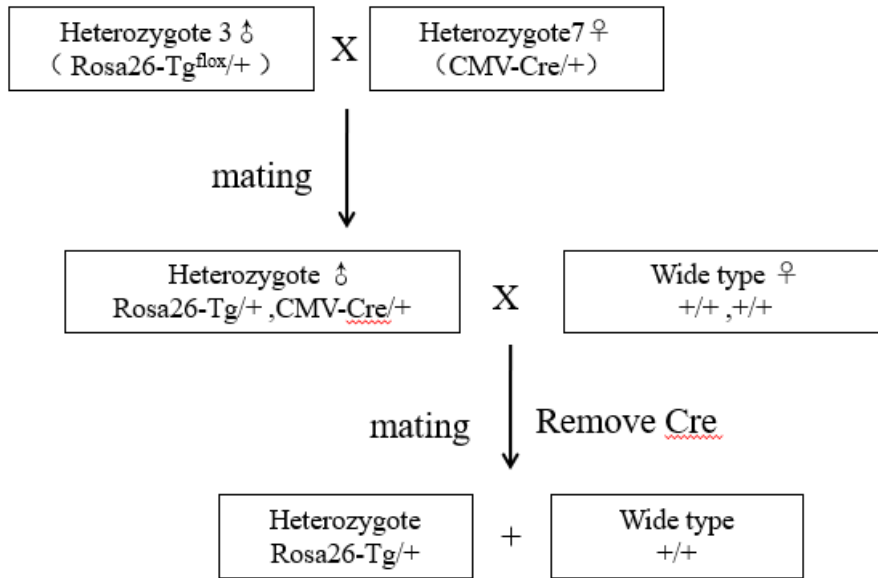
7 **Supplementary Figure S1. Gene editing, identifying strategy and Primer**
8 **information for genotyping**

9 A. Gene editing, identifying strategy. B. Primer information for genotyping

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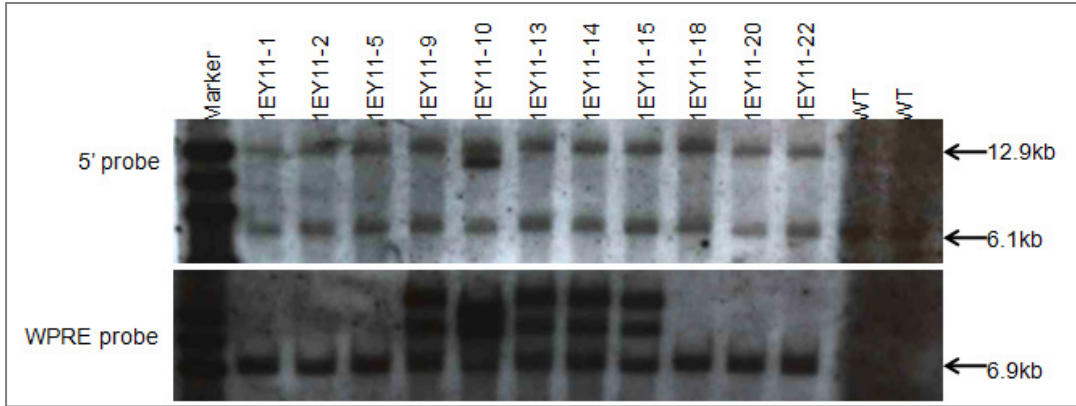
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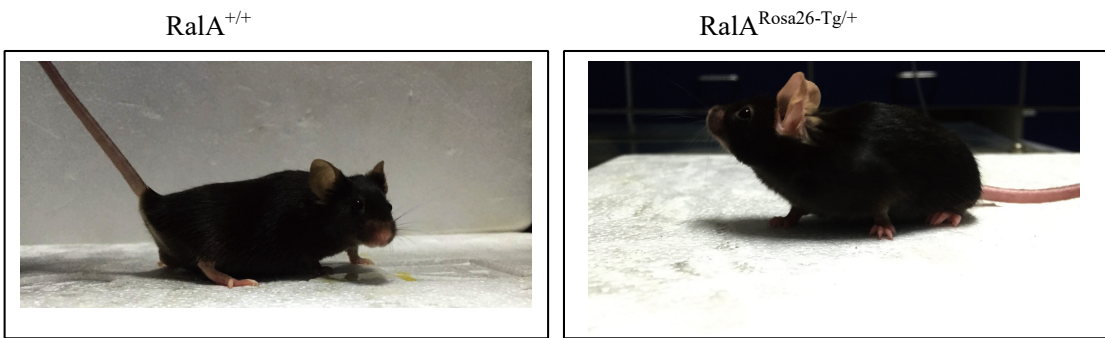
15 **Supplementary Figure S2. Mating scheme to get the mice for CML mouse model**

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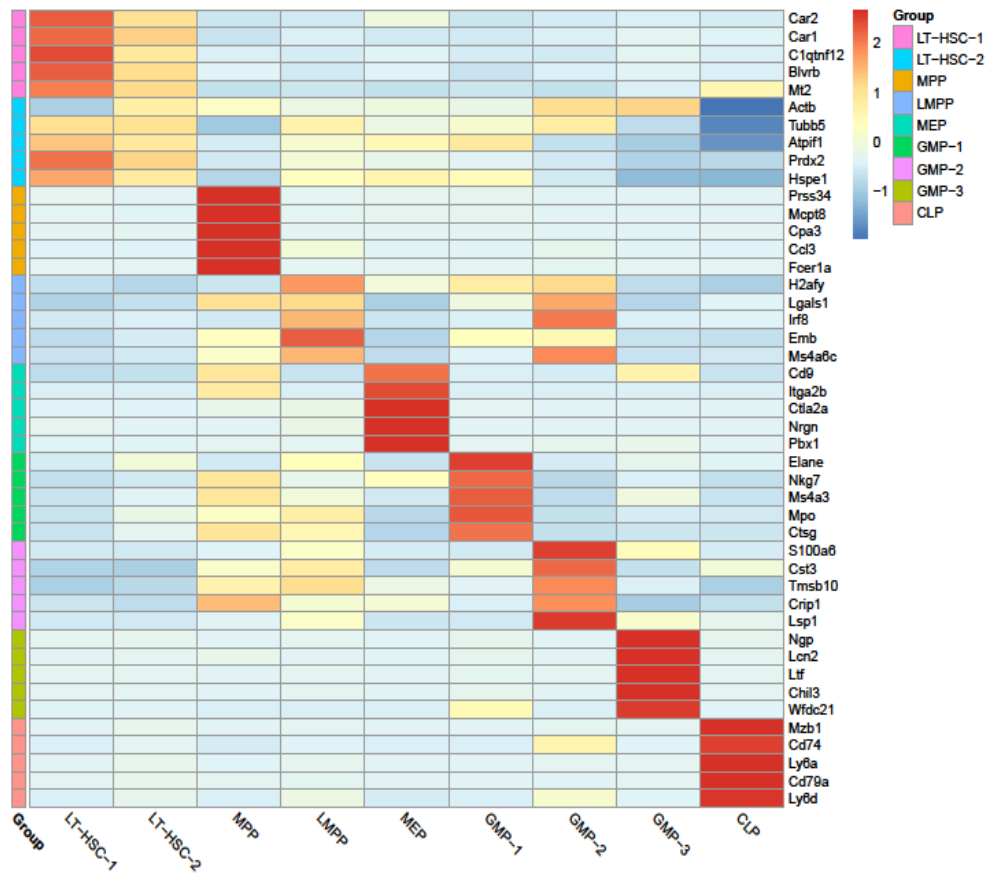
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Supplementary Figure S3. Northern blotting results of F1 generation mice



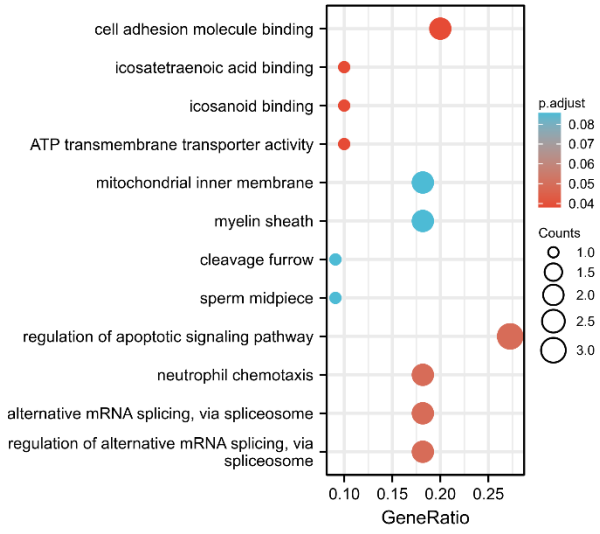
Supplementary Figure S4. The growth status of RalA^{+/+} and RalA^{Rosa26-Tg/+} mice



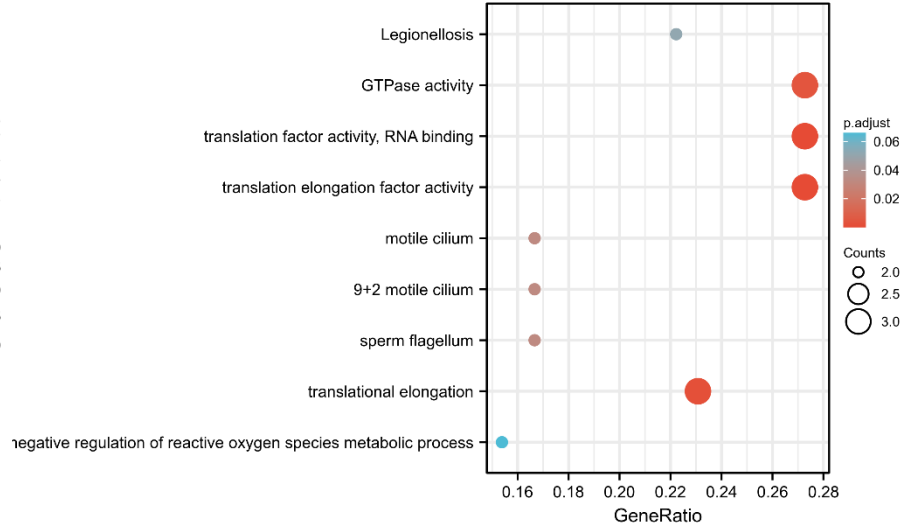
55 **Supplementary Figure S5. Heatmap showing the expression of top 5 enriched**
 56 **genes in each cluster. Expression values are scaled (z-scored) for visualization**

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A



B



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Supplementary Figure S6. Pathway enrichment analysis of the top 10 up-/down-regulated genes from GMP2 (A) and GMP3 (B), respectively.

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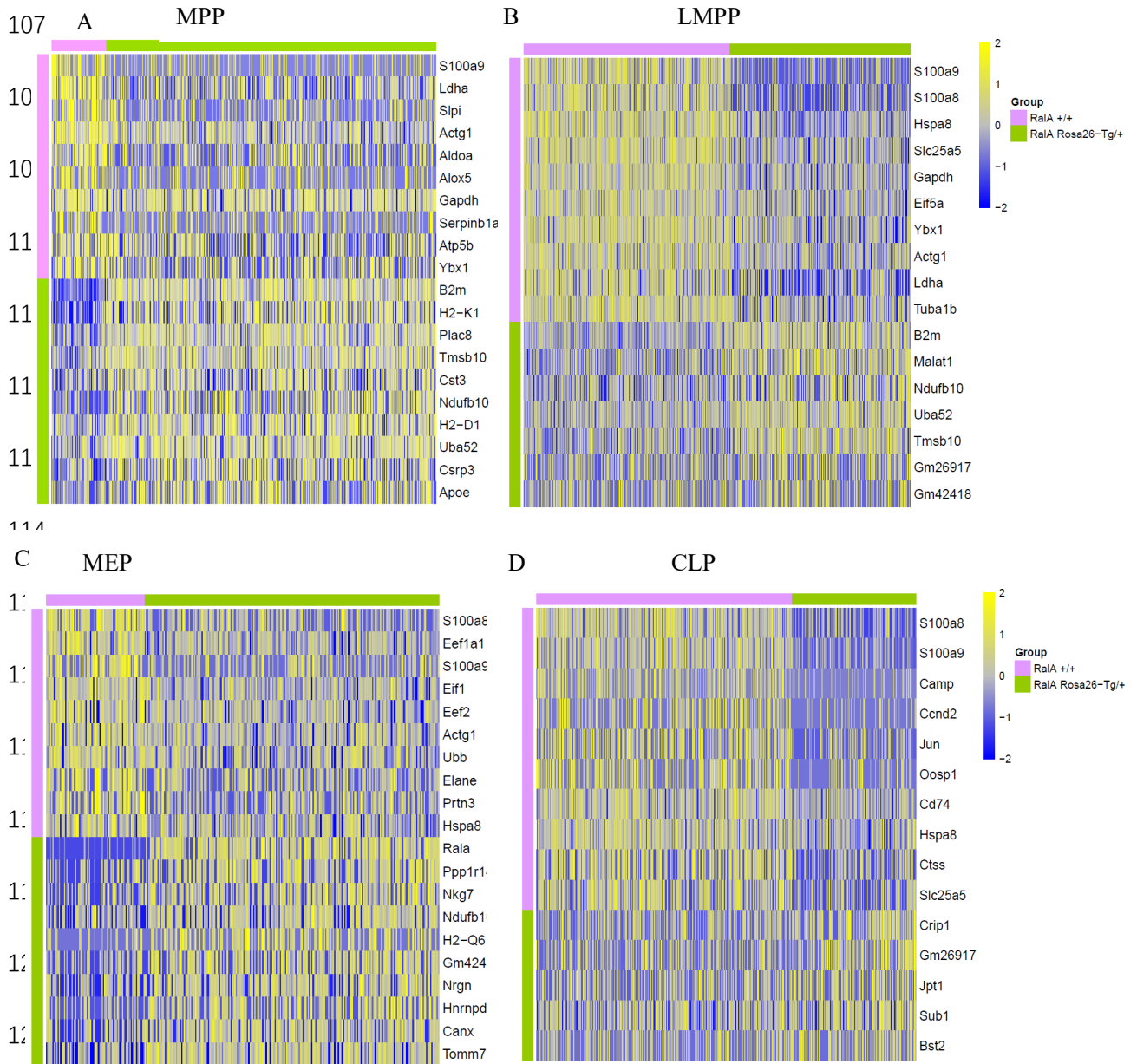
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124 **Supplementary Figure S7. The top 10 up or down-regulated genes enriched in**
 125 **MPP (A, left), LMPP (B, right), MEP (C, left) and CLP (D, right) clusters are**
 126 **displayed in the heat map.**

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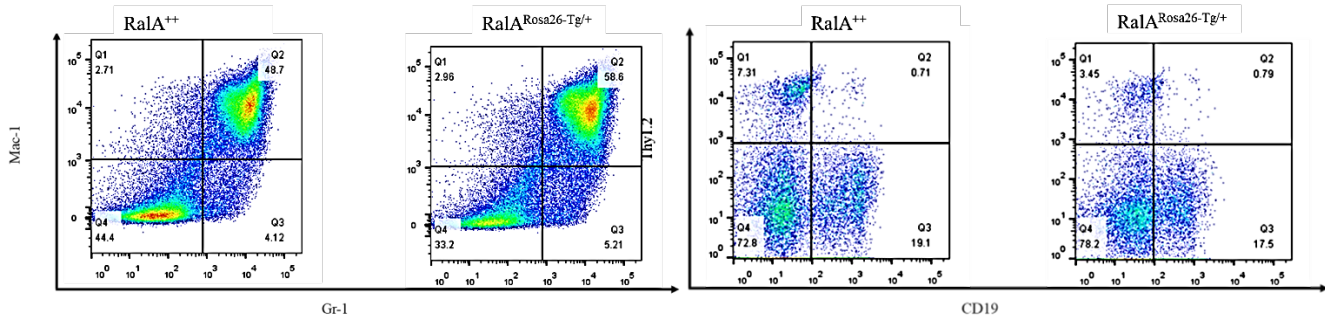
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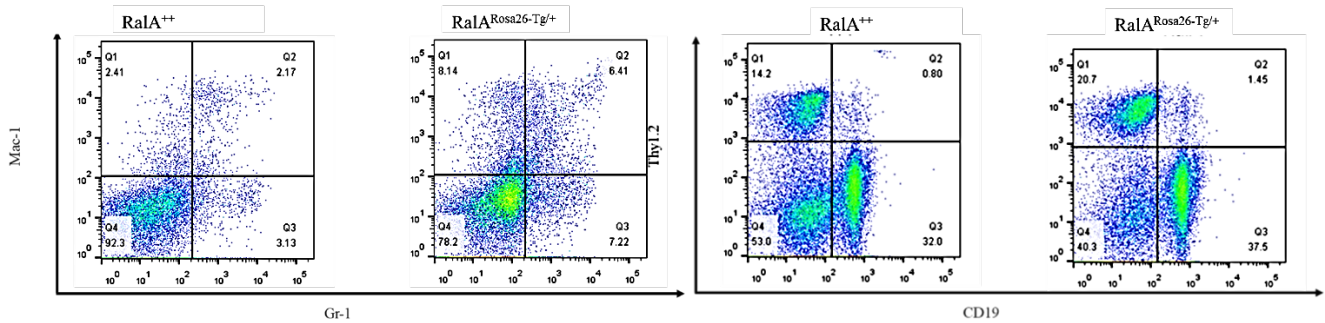
A (Bone marrow)



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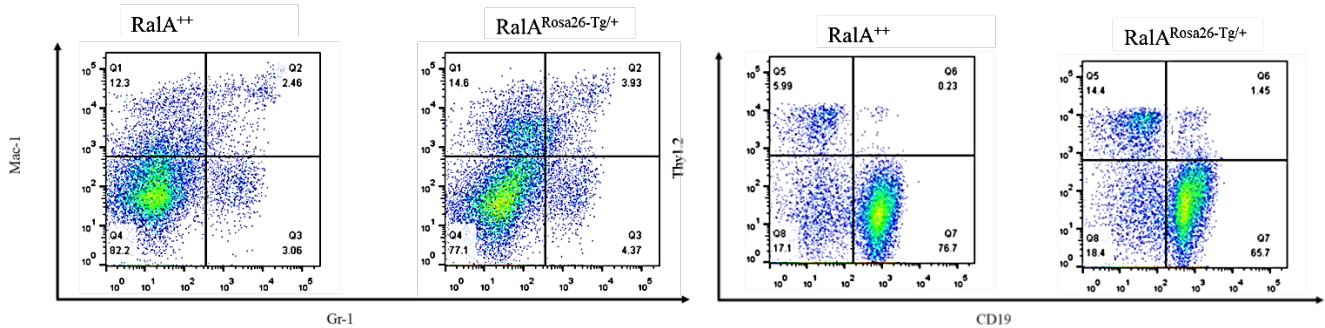
B (Peripheral Blood)



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C (Spleen)



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Supplementary Figure S8. RalA induces cell differentiation in some organs. BM (A), PB (B) and Spleen (C) cells were collected from RalA^{+/+} and RalA^{Rosa26-Tg/+} mice and stained with antibodies against Mac1, Gr1, CD19, or Thy1.2 analyzed by FACS. RalA overexpression promotes the percentage of myeloid cells in bone marrow, peripheral blood, and spleen in RalA^{Rosa26-Tg/+} mice.