

Supplementary Figure 1. Generation of a hypomorphic Bcl11b mutant allele. (a) Schematic of the strategy to generate mutant Bcl11b alleles by gene targeting and structures of mutant Bcl11b alleles generated. Filled and open boxes represent coding and 3' untranslated region (3'UTR) in the exon 4 of the murine Bcl11b gene. Triangle and asterisk represent loxP sequences and the single nucleotide deletion, respectively. (b) Sequence of the targeting vector (TV) and the genome fragment (WT) obtained from a phage library indicated that the single nucleotide deletion, which was marked as * in (a), was incorporated into the targeting vector during sequential ligation steps. (c) Predicted structure of mutant Bcl11b protein from the $Bcl11b^m$ allele. The C2H2 zinc finger motifs are shown as open boxes with their corresponding amino acid numbers. Aberrant amino acid sequences in mutant Bcl11^{HM} protein are shown in red font (bottom). (d) Genotypes of offspring obtained from the $Bcl11b^{+/m}$ intercrossing at day 0 (P0), day 2 (P2) and day3 (P3) after birth. (e) Absolute numbers of total thymocytes in control (\bullet) and $Bcl11b^{m/m}$ (\bigcirc) neonates. Means \pm S.D. * P < 0.05 (unpaired t test). (f) Dot plots showing CD4/CD8 expression in total thymocytes from newborn $Bcl11b^{+/+}$ and $Bcl11b^{m/m}$ mice. In contrast to Bcl11b-deficient mice, thymocyte development was not arrested at the DN2 stage in the $Bcl11b^{m/m}$ mice. Data are representative of at least five mice. (g) Development of type-2 innate lymphoid cells (ILC2) from Bcl11b^{+/+} and Bcl11b^{m/m} progenitors in $II2rg^{--}:RagI^{--}$ host mice. ILC2s were defined as CD25⁺IL1RL1⁺ cells in the Lin⁻KLRG1⁺Sca-1⁺ population from the mesentery. Representative result of two host mice.



Supplementary Figure 2. Expression of Thpok-gfp from the *Thpok*^{gfp:ΔTEPE} and *Thpok*^{gfp:ΔTESPE} allele in lymph node cells. (a) Schematic structure of *Thpok*^{gfp} allele and positions of three regulatory elements, *thymic enhancer* (TE), *Thpok silencer* (S) and *proximal enhancer* (PE). Histograms showing Thpok-GFP expression in indicated lymph node (LN) cells from the *Thpok*^{gfp}, *Thpok*^{gfp:ΔTEPE} and *Thpok*^{gfp:ΔTESPE} allele. Dotted line is Thpok-GFP expression from *Thpok*^{+/+} cells. Numbers in dot plots indicate percentage of Thpok-GFP expressing cells. One representative of at least three independent mice. (b) Quantitative RT-PCR for distal P1 (\blacksquare) and proximal P2 (\Box) promoter-derived *Thpok-gfp* mRNA amount in CD4⁺ T and B220⁺ B cells from *Thpok*^{gfp} allele. Levels of P1- and P2-promoter-specific transcripts relative to those in CD4⁺ T cells from the *Thpok*^{gfp} allele is shown. One representative of two independent experiments.



Supplementary Figure 3. Gene expression profiling by RNA-seq. (a) RNA-seq analyses comparing gene expression profiles derived from at least three independent samples of $CD24^{hi}TCR\beta^{lo}$ pre-selection $Bcl11b^{++}$ (WT) and $Bcl11b^{m/m}$ (HM) thymocytes. (b) Principle component analyses showing relationship of WT, $Bcl11b^{m/m}$ (HM) and $Bcl11b^{fl/f}$: *Cd4-Cre* (cKO) pre-selection DP thymocytes.

а	Runx3 -39 Kb region	chr4:134,635,400-134,637,000 500 base	1
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		gRNA 134636458 -134636477 GCGTT <u>TCCGGAGGCAGGCTCGAAGC</u> TGGG - Δ-39 m7 GCGTTTC	gRNA 134636663 -134636682 AGGCTGGGGCCACCGCAGGCTGGC
	gRNA 13465715 -134635737 CCACTCCCCGAACAGACAGTGGTTCCAG Δ-39LD m12 CCACTCCCCGAA		gRNA 134636663 -134636682 AGGCTGGGGCCACCGCAGGCTGGC
b	Runx3 -21 Kb region	chr4:134,653,700-134,655,600 500 base⊢	
	mammalian conservation	างรูสึงขา นไ ปเวลาระไหน่าระไปส่วนสามหาระบาทเป็นไปเป็นเป็นหาระบาทได้เป็นไปไปเป็นเป็นไปได้เป็นได้ได้เป็นได้ได้ได้ได้ได้ได้ได้ได้ได้ได้ได้ได้ได้ไ	<mark>a an an a</mark> n a an
	[gRNA 134654560 -134654582 GG <mark>CCCAGAGTCGTACTCGCTGGGGT</mark> TC ──── ∆-21 m6 GG <mark>CCCA</mark> G	gRNA 134655494 -134655516 ——— TA <u>GCGAGCCCAGTGAAACCCGC<mark>AGG</mark>TCCGA</u>
	∆39∆21 m7 AGGGGCC	89 bp deletionTTGT(GTGC AGGTCCGA

Supplementary Figure 4. Removal of putative enhancers from the *Runx3-tdTomato* locus by CRISPR/Cas9-mediated genome editing. (a and b) Top bar showing homology around -39 kb (a) and -21 kb (b) regions upstream of the distal *P1-Runx3* promoter in mammals. Regions deleted in mutant mouse strains are indicated as dotted lines. Underlined and red font indicate protospacer and PAM sequence, respectively. In the $\Delta 39\Delta 21$ m7 line, TTGTGTGC sequences were inserted.



Supplementary Figure 5. Expression of mutant Bcl11b proteins from retroviral vectors. (a) Schematic structures of wild-type and mutant Bcl11b proteins lacking C-terminal end sequences. C2H2 zinc finger motifs are shown as open boxes. The C-terminal end amino acid sequences of each Bcl11b mutant proteins are indicated with that of hypomorphic (HM) Bcl11b mutant protein. Sequences corresponding to the last zing-finger domain (844 - 867 a.a.) are underlined. Aberrant amino acid sequences in mutant Bcl11b^{HM} protein are shown in red font. (b) Western blot using an antibody that reacts with anti-N-terminal Bcl11b sequences showing expression of each mutant Bcl11b protein in the packaging cell line, Plat-E.



Supplementary Figure 6. Evolutionary conservation of zinc-finger motifs in the Bcl11 family. (a) Schematic structures of Bcl11related proteins and Bcl11 orthologues in several species. In mouse, only Zfp296 possesses the zinc-finger motifs similar to Bcl11a and Bcl11b. Ascidian (*C. intestinalis*) and worm (*C. elegans*), have a Bcl11-related protein that lacks the middle two zinc-finger motifs. (b and c) Alignment of amino acid sequences around the middle two zinc-finger motifs (b) and the C-terminal triplet zinc-finger motifs (c) of Bcl11 orthologues from several species. Each zinc-finger is indicated as a dashed box.



Supplementary Figure 7. Gating strategies for cell analyses and sorting. Representative FACS plots showing: Gating strategy for analysis and sorting of the thymocytes (a) and peripheral lymphoid population (spleen and lymph node) (b). (c) Gating scheme for analysis of mesenteric ILC2.



Supplementary Figure 8. Full size images of Immunoblot analyses in Figure 1a and 1b.



Supplementary Figure 9. Full size images of Immunoblot analyses in Figure 2a and Supplementary Figure 4b.

Supplementary Table 1. Primers for ChIP-qPCR

Target	Forward primer (5'-3')	Reverse primer (5'-3')	
Pok-silencer	GGGTAGCACTATTTATAACTGC	AGATCCCAGCGGCGATTAGC	
Thpok-PE	CTCCGCCATCTTTATCTTGTTCC	GGTTAAGCTCCCACCAAGTCC	
Thpok-intron 1	TGCTGGCCCAGTAAGTTCTG	ATGGCATTGGTGTTGGTACC	
URE Sfpi-1	ACTGACCCCTGACACCAAAG	GCCCATCGTGACCTAGAAGA	
Foxp3 CNS2	ATCTGGCCAAGTTCAGGTTGTGAC	GGGCGTTCCTGTTTGACTGTTTCT	
Foxp3 CNS3	CAGGAAGTGGTTTATGGGTC	ATGAGGATTGGGAGGGGTG	
Runx3 -39E	GAAGCTTTTCTCCTGCTCCTC	TATTCACACCCACAGGGAAG	
<i>Runx3 -21E</i>	ACAGAGGAAGCAGCATTTGG	TAGCTGTGGGGGAACACAAAC	
Neg. cont. region	Mouse Negative control primer set 1 (ACTIVE MOTIF: 71011)		

Supplementary Table 2. Primers and probes for qRT-PCR

Target	Forward primer (5'-3')	Reverse primer (5'-3')	Probe
P1-Thpok	AACGAGCAGCGAGCCACT	CTGCTGTGGGTCTGGGAATG	FAM-CTGTGCCTCTGCAGCT
	GAC		CCAGCGA-TAMRA
P2-Thpok	TTGCCGGCAAGGCCCCTC	GAAGTAGTGGCTACAGGCA	FAM-ACCACAGCAGCGAGC
	AGCGTTC	GCC	TCCTGAGC-TAMRA
P1-Runx3	GTCAGCGTGCGACATGGC	AGCACGTCCACCATCGAGC	FAM-TGAAGCGGCGGCTGG
	TTCCAACAG	GCACTTCGG	TGCTC-TAMRA
Socs1	GTGGTTGTGGAGGGTGAG	CCTGAGAGGTGGGATGAGG	UPL #20
	AT		
Socs3	ATTTCGCTTCGGGACTAG	AACTTGCTGTGGGTGACCA	UPL #83
	С	Т	
Hprt	TCCTCCTCAGACCGCTTTT	CCTGGTTCATCATCGCTAAT	UPL #95
		С	