

Supplementary Figure 1. *Ncor1* **expression profiles in different tissues and thymocyte subsets.** (a) Quantitative RT-PCR analysis of *Ncor1* mRNA expression in various tissues(n=3) and (b) in the indicated thymocyte subsets (n=3, repeat 2 times) sorted using flow cytometry. DN, CD4⁻CD8⁻ double-negative thymocytes; DP, CD4⁺CD8⁺ double-positive thymocytes; CD4 SP, CD4⁺ single-positive thymocytes.



Supplementary Figure 2. Thymocyte profiles in *Ncor1*^{flox/flox}, *Lck-Cre* and *Ncor1*^{flox/flox}*Lck-Cre* mice. (a) Surface expression of CD4 versus CD8 (up) and CD69 versus TCR β (down) on total thymocytes (n=4 for each group) detected by flow cytometry. (b) Quantification of different thymocyte subsets in (a). (c) Flow cytometry analysis of 5 sub-populations (left) by MHCI and CD69 expression on total thymocytes (n=4 for each group, respectively). The right panel shows CD4 and CD8 expression on gated population #3. (d) The proportion of CD4^{*dull*}CD8^{*dull*} subsets in population #3. Statistical significance was analysed using the two-tailed Student's t test (NS, not significant; ** P<0.01; *** P<0.001).



Supplementary Figure 3. Thymocyte profiles in *Ncor1^{flox/flox}CD4-Cre* **mice.** (a) Surface expression of CD4 and CD8 on thymocytes from *Ncor1^{flox/flox}CD4-Cre* (4KO) mice and *Ncor1^{flox/flox}* (WT) mice (n=3 to 5). (b) Quantification of different thymocyte subsets in (a). DP, CD4⁺CD8⁺ double-positive thymocytes; CD4 SP, CD4⁺ single-positive thymocytes; CD8 SP, CD8⁺ single-positive thymocytes. Data are representative of three independent experiments. Statistical significance was analysed using the two-tailed Student's t test (*** P<0.001).



Supplementary Figure 4. CD5 and CD69 expression in NCoR1-deficient thymocytes. (a) Flow cytometry analysis of CD5 expression (left) on total thymocytes from NCoR1-deficient (cKO) and wild type (WT) mice (n=3 to 5) and quantification of the CD5-positive sub-population (right). (b) Mean fluorescence intensity of CD5 on CD69^{lo} and CD69^{hi} DP (CD4⁺CD8⁺ double-positive) thymocytes from cKO (n=4) and WT (n=4) mice. (c) The histogram plot (left) and the mean fluorescence intensity (right) of CD69 expression on total thymocytes from cKO and WT OT-II TCR-transgenic mice (n=3) detected by flow cytometry. Data are representative of two independent experiments. Statistical significance was analysed using the two-tailed Student's t test (NS, not significant, ** P<0.01).



Supplementary Figure 5. Development of both Treg cells and iNKT cells is defective in the thymus of NCoR1-deficient mice. (a) Foxp3 expression in total thymocytes from NCoR1-deficient (cKO) (n=7) and wild type (WT) (n=6) mice by intracellular staining (left) and quantification of Foxp3⁺ cells (right). (b) Quantification of Foxp3⁺ cells in CD4⁺ single-positive (CD4 SP) WT and cKO thymocytes in (a). (c) CD1d Tetramer and TCR β expression in total thymocytes from WT (n=6) or cKO (n=7) mice (left) by flow cytometry and quantification of CD1d Tetramer⁺TCR β ⁺ cells (right). Statistical significance was analysed using the two-tailed Student's t test (NS, not significant; ** P<0.01; *** P<0.001).



Supplementary Figure 6. TCR signaling in NCoR1-deficient thymocytes. Immunoblot analysis of phosphorylated (p)-PLC- γ 1, p-Erk1/2, p-p38 and total protein of PLC- γ 1, Erk and p38 in lysates from wild type (WT) and NCoR1-deficient (cKO) thymocytes without or with stimulation *in vitro* for the indicated amounts of time. β -actin served as a loading control. Data are representative of there independent experiments.



Supplementary Figure 7. NCoR1-deficient thymocytes are prone to apoptosis. (a) The surface marker CD69 and intracellular staining of the active caspase-3 (Act.Casp.3) detected by flow cytometry in total NCoR1-deficient (cKO) (n=3) and wild type (WT) (n=3) thymocytes stimulated or not with TCR β and CD28 for 6 hr. (b) The mean fluorescence intensity of CD69 expression in Act.Casp3⁺ and Act.Casp3⁺ thymocytes in (a). (c) Flow cytometric staining of Annexin V and propidium iodide (PI) on WT and cKO thymocytes stimulated *in vitro* for 6 hr (n=3 to 5). (d) Quantification of the apoptotic thymocytes shown in (c). Data are representative of two independent experiments. Statistical significance was analysed using the two-tailed Student's t test (** P<0.01; *** P<0.001).



Supplementary Figure 8. Bim expression in TCR signalling stimulated thymocytes *in vitro* and in sorted non-activated and activated thymocytes *in vivo*. (a) Bim protein levels in NCoR1-deficient (cKO) and wild type (WT) thymocytes stimulated with different concentrations of anti-TCR β . (b) Non-activated thymocytes (population 1 + 2, p1+2) and activated thymocytes (population 4 + 5, p4+5) were sorted by the surface expression of CD69 and TCR β on total WT (n=7) and cKO (n=7) thymocytes according to the gating in Fig. 2a. *Bim* mRNA levels in these sorted thymocytes were analysed by quantitative RT-PCR. Statistical significance was analysed using the two-tailed Student's t test (NS, not significant, ** P<0.01; *** P<0.001).







Supplementary Figure 10. Proportions of mature (CD62L^{hi}CD69^{lo} or CD62L^{hi}CD24^{lo}) and immature (CD62L^{lo}CD69^{hi} or CD62L^{lo}CD24^{hi}) subsets in WT (n=4), cKO (n=4), *Bim* KO (n=4) and dKO (n=5) thymocytes. Flow cytometry analysis and gating of mature or immature subsets were performed as shown in Fig. 6c. WT, wild type; cKO, NCoR1-deficient; dKO, *Ncor1* and *Bim* double knockout.Statistical significance was analysed using the two-tailed Student's t test (NS, not significant).



Supplementary Figure 11. Loss of NCoR1 reduces peripheral CD4 and CD8 T cells in the spleen but increases the proportion of Tregs. (a) The surface expression of CD4 and CD8 on NCoR1-deficient (cKO) (n=4) and wild type (WT) (n=4) splenocytes detected by flow cytometry. (b) The percentages (left) or numbers (right) of CD4 and CD8 T cells gated in (a). Data were generated from three independent experiments. (c) Intracellular expression of Foxp3 in CD4⁺ TCR β^+ cKO (n=6) and WT (n=6) splenocytes detected by flow cytometry. (d) Quantification of the Foxp3⁺CD4⁺ T cells in (c). Data are representative of three independent experiments with more than three mice per group. Statistical significance was analysed using the two-tailed Student's t test (** P<0.01; *** P<0.001).



Supplementary Figure 12. Gating strategies for flow cytometry analyses. Representive FACS plots showing: (a) Gating strategy for CD4, CD8, CD69, TCR β , CD5, and V α 2 (for OTII background) expression. (b) Gating strategy for intracellular Act.Casp.3 in CD69^{hi}MHCI⁻CD4^{dull}CD8^{dull} thymocytes. (c) Gating strategy to detect apoptosis of thymocytes stimulated *in vitro*.(d) Gating strategy to analyze thymocytes profiling in bone marrow chimeras. (e) Gating strategy to analyze T regulatory cells and invariant natural killer T cells in thymus.

Fig. 5d	Suppl. Fig. 6		Suppl. Fig. 8a
anti-NCoR1	anti-p-PLCγ1	anti-Erk	anti-NCoR1
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4 4:4:4	anti-PLCγ1	anti-p-p38	anti-Bim
anti-Bim			
		anti-p38	
	anti-p-Erk1/2		anti-tubulin
anti-tubulin		anti-β-actin	
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Supplementary Figure 13. The uncropped scans of western blots from Figure 5, Supplemenary Figure 6 and 8a.

# Supplemental Table 1. Genes expressed differentially in thymocytes by RNA-seq

Gene	cKO/WT (ex vivo)				
	log2(fold_change)				
Gm7125	infinite				
Gm6594	infinite				
AC163653.5	infinite				
Gh	infinite				
AC158672.3	infinite				
Sfn	1.41297				
Spsb1	1.2823				
St3gal6	1.25667				
Wnt8b	1.24523				
Gm8186	1.10604				
Dusp4	1.08605				
lfngr1	1.05791				
Tbl1xr1	0.954922				
Cdk5r1	0.926474				
Bcl6	0.918982				
Mbnl1	0.853401				
Dusp5	0.831608				
Slc9a9	0.798935				
Scd2	0.785073				
Cd74	0.72575				
Pik3r1	0.725251				
Pik3cg	0.720207				
Gimap6	0.692412				
Ctsl	0.683771				
Lig4	0.680034				
Tespa1	0.670143				
Tubb2b	0.627266				
Abcg1	0.595489				
Esyt1	-0.632325				
Ltb	-0.645846				
Gpr56	-0.670893				
Rpl23a	-0.674669				
Nrp1	-0.728366				
Ntn1	-0.742279				
Smoc1	-0.791651				

In	steady	state	thymocytes	
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Gene	cKO/WT (ex vivo)			
	log2(fold_change)			
Adcy7	-0.801285			
ltgb7	-0.82898			
Cxxc5	-0.833748			
Als2cl	-0.847795			
MIIt6	-0.866141			
Cnn2	-0.918308			
Pdcd1	-0.949894			
Cd53	-0.964088			
St3gal1	-1.00801			
Slc6a19	-1.0084			
Shisa5	-1.01297			
Sema7a	-1.0856			
AB124611	-1.08824			
H2-K1	-1.10853			
Fgf13	-1.16045			
Padi4	-1.1741			
AC165246.1	-1.21028			
Ccr7	-1.26486			
Slfn1	-1.30495			
H2-Q7	-1.31484			
Ephx1	-1.32313			
Ctsw	-1.32528			
Nkg7	-1.32796			
Xrra1	-1.36339			
Jup	-1.40723			
Phlda1	-1.42058			
Paqr7	-1.57394			
Ccnd2	-1.59108			
Lfng	-1.67108			
Cd7	-1.67425			
Gm10499	-1.73999			
Sdc4	-1.93547			
n-R5-8s1	-2.25768			
Cd200	-3.59722			
Gm11223	-4.56491			

### In activated thymocytes

	KO/WT (3h			
Gene	activation)			
	log2(fold_change)			
Gm7125	infinite			
Gm6594	infinite			
lghv1-49	infinite			
AC160982.1	2.03594			
Sfn	1.3304			
Acoxl	1.14459			
Tbl1xr1	1.06335			
Scd2	1.06322			
ll12rb1	0.956431			
Dusp4	0.913305			
ERDR1	0.896455			
Gimap9	0.89101			
Bcl6	0.852289			
Abcg1	0.841595			
Ptger4	0.739682			
Ldlr	0.732622			
Gimap8	0.719569			
Gramd3	0.707089			
Bcl2l11	0.673482			
Mr1	0.651132			
Mbnl1	0.638582			
Ccnd3	0.630751			
Ctsl	0.612296			
Ccr4	0.592412			
Irf4	-0.655463			
Cd53	-0.671309			
Ntn1	-0.739517			
lcos	-0.75102			
Gpr56	-0.800305			

	KO/WT (3h			
Gene	activation)			
	log2(fold change)			
B4gaInt1	-0.800943			
Мус	-0.803976			
Gm14085	-0.814945			
Slc6a19	-0.820457			
Ccr7	-0.823115			
H2-K1	-0.839568			
Fam134b	-0.856552			
Adora2a	-0.886581			
Tnf	-0.955403			
Cxxc5	-0.955899			
Evl	-1.04317			
Pdcd1	-1.07871			
H2-Q7	-1.11737			
Cd83	-1.25182			
lfi27l2a	-1.3544			
Cited4	-1.38267			
Lad1	-1.43564			
Tagap	-1.43739			
Egr3	-1.63327			
Xcl1	-1.71541			
Lfng	-1.89111			
Tnfrsf9	-2.02836			
Rgs16	-2.09375			
Ccnd2	-2.23925			
n-R5-8s1	-2.32324			
Sh3gl3	-2.4747			
Apbb2	-3.47654			
Gm11223	-3.80225			

Antibodies for Flow	v cytometry anal	ysi	S	
Antibody	Clone		Dilution	Company
CD4	GK15		1:200	eBioscience
CD8a	53-6.7		1:200	eBioscience
CD69	H1.2F3		1:200	eBioscience
TCRβ	H57-597		1:200	eBioscience
MHCI	AF6-88.5.5.3		1:200	eBioscience
CD5	53-7.3		1:200	eBioscience
CD24	M1/69		1:200	eBioscience
CD62L	MEL-14		1:200	eBioscience
CD45.1	A20		1:200	BD Bioscience
CD45.2	104		1:200	BD Bioscience
Foxp3	FJK-16s		1:200	eBioscience
Vα2	20.1		1:200	eBioscience
Antibodies for Imm	unoblot analysis	\$		
Antibody	Code		Dilution	Company
anti-rabbit-NCoR1	5948S		1:1000	Cell Signaling Technology
anti-rabbit-Bim	2933S		1:1000	Cell Signaling Technology
anti-rabbit-p-PLCγ1	2821S		1:1000	Cell Signaling Technology
anti-mouse-PLCγ1	ab76155		1:1000	Abcam
anti-mouse-p- Erk1/2	sc-7383		1:500	Santa Cruz Biotechnology
anti-rabbit-Erk	sc-93		1:2000	Santa Cruz Biotechnology
anti-rabbit-p-p38	9211S		1:1000	Cell Signaling Technology
anti-rabbit-p38	sc-728		1:2000	Santa Cruz Biotechnology
anti-rabbit-β-actin	4970S		1:2000	Cell Signaling Technology
anti-rabbit-tublin	CP06		1:2000	EMD Millipore
Goat anti-rabbit-	111_035_003		1.3000	Jackson Immuno&Research
lgG(H+L)	111-035-005		1.5000	Jackson minunoartesearch
Donkey anti-	715-035-150		1.3000	Jackson Immuno&Research
mouse-IgG(H+L)	110 000 100		1.0000	
Antibodies for CHIP analysis				
Antibody	Code	Di	lution	Company
anti-NCoR1	5948S	1	g per IP	Cell Signaling Technology
anti-H3ac	06-599	1	g per IP	Millipore
anti-H4ac	06-598	1	g per IP	Millipore
anti-H3K27ac	ab4729	1	g per IP	Abcam
anti-H3K4me1	ab8580	1	g per IP	Abcam
anti-H3K4me3	ab6002	1	g per IP	Abcam

1 g per IP

Cell Signaling Technology

## Supplemental Table 2. Antibodies Information Antibodies for Flow cytometry analysis

3900S

lgG

Ncor1	Forward	5'-TGCGTCAGCTTTCTGTGA TTCCACC-3'
	Reverse	5'-TGA TTTCTGCCTCTGCGTTTTCCA-3'
Bim	Forward	5'-CGACAGTCTCAGGAGGAACC-3'
	Reverse	5'-CCTTCTCCATACCAGACGGA-3'
Fasl	Forward	5'-TGAATTACCCATGTCCCCAG-3'
	Reverse	5'-AAACTGACCCTGGAGGAGCC-3'
Tnf	Forward	5'-CATCTTCTCAAAATTCGAGTGACAA-3'
	Reverse	5'-TGGGAGTAGACAAGGTACAACCC-3'
Trail	Forward	5'-ATGATGGTGATTTGCATAGTGCT-3'
	Reverse	5'-AGCTGCTTCATCTCGTTGGTG-3'
Bak	Forward	5'-AATGGCATCCGGACAAGGAC-3'
	Reverse	5'-TGTTCCTGCTGGTGGAGGTA-3'
Actb	Forward	5'-GGCTGTATTCCCCTCCATCG-3'
	Reverse	5'-CCAGTTGGTAACAATGCCATGT-3'

# Supplemental Table 3. Primer for Quantitative RT-PCR analysis