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(A) Thymocytes (3-week-old mice) generated by crossing OT-II.Aire^{+/-} to RIP-mOVA.Aire^{+/-} mice were analyzed by flow cytometry for expression of CD4, CD8, and V α 2 (representative contour plots, left) and enumerated for SP thymocytes expressing high levels of TCR (CD4+CD8-V α 2⁺ cells, right). (B) Thymocytes (6 weeks postreconstitution) from chimeric mice generated by reconstituting wt.Aire^{+/+}, wt.Aire^{-/-}, RIP-mOVA.Aire^{+/+}, or RIP-mOVA.Aire^{-/-} mice with OT-I BW were analyzed by flow cytometry for expression of CD4, CD8, and V α 2 (representative contour plots, left) and enumerated for SP thymocytes (CD4⁺CD8⁻V α 2⁺ cells, right). Representative contour plots were not all from the same experiment: Aire^{+/+} groups are matched, as are Aire^{-/-} groups. Histograms show the mean ± SEM for each group. n = number of mice pooled from several experiments. Figures 2B and 6 share the same groups lacking expression of the RIP transgene. Significance relative to WT: *** $P \leq .001$; ns indicates not significant.



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(A) Thymocytes (6 weeks postreconstitution) from chimeric mice generated by reconstituting wt.Aire^{+/+}, wt.Aire^{-/-}, RIP-OVA^{hi} Aire^{+/+}, or RIP-OVA^{hi} Aire^{-/-} mice with OT-II BM were analyzed by flow cytometry for expression of CD4, CD8, and V α 2 (representative contour plots, left) and enumerated for SP thymocytes expressing high levels of TCR (CD4⁺CD8⁻V α 2⁺ cells, right). (B) mTECs are not able to present OVA on MHC II. Lethally irradiated 8-week-old B6 or RIP-OVA^{hi} mice were grafted with IAb-deficient OT-II BM. At 6 weeks after reconstitution, thymocytes from the indicated mice were analyzed by flow cytometry for expression of CD4, CD8, and V α 2 (representative contour plots, left) and enumerated for SP thymocytes from the indicated mice were analyzed by flow cytometry for expression of CD4, CD8, and V α 2 (representative contour plots, left) and enumerated for SP thymocytes expressing high levels of TCR (CD4⁺CD8⁻V α 2⁺ cells, right). Contour plots how a representative experiment. Histogram shows the mean ± SEM for each group. n = number of mice pooled from several experiments. Figure 5A and supplemental Figure 3 as well as Figures 5B and 3B share, respectively, the same groups lacking expression of the RIP transgene. Significance relative to WT: ***P ≤ .001; ns indicates not significant.





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7.25-03		un	Ccl25	nkine ligand 25 1 3 1 3	13.06



(c) A the fitted model MA plot representing different genes (4002 down and 4366 up) regulated by Aire (gray dots) according to the fold change and average intensity at a 5% FDR using Illumina beadchip. (B) List of chemokine genes whose expression levels differ significantly between Aire^{+/+} and Aire^{-/-} mTEC according to the Illumina beadchip analysis presented with fold change, average of the intensity, and adjusted *P* value. (C) Relative expression of Ccl1, Ccl3, Ccl6, Ccl7, Ccl8, Ccl9, Ccl11, Ccl17, Cxcl4, Cxcl13, Cxcl13, Cxcl13, Cxcl125 was determined by quantitative real-time PCR on cDNA prepared from thymic CD45⁻MHC Il^{hi} Ly51⁻ cells. Expression values are shown in relative to WT after normalization to Hprt. Data shown are the mean ± SEM of 3 independent experiments. A total of 6-8 individual thymi were pooled per experiment. Significance relative to WT: $*P \le .05$, $**P \le .01$; ns indicates not significant. (D) List of cytokine genes whose expression levels differ significantly between Aire^{+/+} and Aire^{-/-} mTEC according to the Illumina beadchip analysis presented with fold change, average of the intensity, and adjusted *P* value.





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Aire regulates the transfer of antigen from mTECs to dendritic cells for induction of thymic tolerance

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