

**Supplementary Figure 1. Generation of the Pycard conditional knockout allele.** (a) The Pycard gene is localized on chromosome 7 and contains three coding exons. For generation of the conditional knockout allele, the entire open reading frame including all three exons was targeted for conditional deletion. After generation of the targeting vector (using Pcr4.0 backbone), C57BL/6 embryonic stem cells were injected for gene targeting. Southern hybridization was used to identify progeny bearing the recombinant allele. (b) CD4+ T Cells were sorted from  $Asc^{f/+}Lck$ -Cre and  $Asc^{f/-}Lck$ -Cre mice by flow cytometry, and mRNA expression of three different exons of ASC was measured by Real-time PCR analysis. Unpaired t test was used to analyze the data. Data are representative of three independent experiments (b). n=3 mice per group in each experiment. Error bars represent s.e.m. \*P < 0.05.

a

□ ASC <sup>f/+</sup>Lck-Cre □ ASC <sup>f/+</sup>Lck-Cre ASC <sup>f/-</sup>Lck-Cre ■ ASC <sup>f/-</sup>Lck-Cre 30-**25**<sub>1</sub> Cells (<sup>×</sup>10<sup>6</sup>) Cells (<sup>x</sup>10<sup>6</sup>) 20 20-15 10 10 5 CD<sup>A</sup>CD<sup>8</sup>CD<sup>9</sup> 322<sup>9</sup> CDÁ CD<sup>Á</sup> CD<sup>Á</sup> CD<sup>Á</sup> cDô

b

**Supplementary Figure 2. The number of T cells and B cells were similar in the lymph nodes, spleens and thymus between** *Asc<sup>f/+</sup>Lck*-Cre and *Asc<sup>f/-</sup>Lck*-Cre mice . (a) The total cell number of CD4+, CD8+ and B220+CD19+ cells were counted from lymph nodes and spleen of *Asc<sup>f/+</sup>Lck*-Cre and *Asc<sup>f/-</sup>Lck*-Cre mice. (b) Total cell number of CD4-CD8-, CD4+CD8-, CD4+ CD8+ were counted from thymus of *Asc<sup>f/+</sup>Lck*-Cre and *Asc<sup>f/-</sup>Lck*-Cre mice. Data are representative of two independent experiments (**a-b**). n=5 mice per group in each experiment. Error bars represent s.e.m.



Supplementary Figure 3. The EAE phenotype of adoptive-transfer of sorted CD4+ T cell from  $Asc^{f/+}Lck$ -Cre and  $Asc^{f/-}Lck$ -Cre mice. (a) Absolute numbers of CD4+ IL-17A+ cells (left panel) and concentrations of IL-17A in the supernatant of cells (right panel) from the draining lymph nodes and spleens of  $Asc^{f/+}Lck$ -Cre and  $Asc^{f/-}Lck$ -Cre mice immunized with MOG<sub>35-55</sub> and harvested 10 days after immunization, followed by *ex vivo* restimulation in the presence of MOG<sub>35-55</sub> and IL-23. (b-d) Cells from lymph nodes of  $Asc^{f/+}Lck$ -Cre and  $Asc^{f/-}Lck$ -Cre mice 10 days after immunization with MOG<sub>35-55</sub> were re-stimulated with MOG <sub>35-55</sub> in vitro in the presence of recombinant IL-23 for 5 days, sorted for CD4+ T cells by flow cytometry, and then transferred into CD45.1 congenic mice. (b) Graph represents the average clinical score after T cell transfer. (c) Absolute numbers of CNS-infiltrating CD45.2+ CD4+ cells were determined at the peak of disease. Brains and spinal cords were harvested together and CD45.2+CD4+ cells were determined at the peak of disease. Brains and spinal cords were harvested together and Sof CNS-infiltrating cells were determined at the peak of disease. Brains and spinal cords were harvested together and mononuclear infiltrating cells were stained with anti-CD45.2 and anti-CD4 antibodies, followed by flow cytometric analysis. (d) Absolute numbers of CNS-infiltrating cells were determined at the peak of disease. Brains and spinal cords were harvested together and mononuclear infiltrating cells were stained with anti-CD4, anti-CD8, anti-F4/80, anti-Ly6C, anti-CD19 and anti-Ly6G antibodies, followed by flow cytometric analysis. Two-way ANOVA (b) and Unpaired t test (**a**, **c and d**) were used to analyzed the data. Data are representative of three independent experiments (**a-d**). n=5 mice per group in each experiment. Error bars represent s.e.m. \*P < 0.05 (**a**, **c and d**). Error bars represent s.d. \*P < 0.05 (**b**).



**Supplementary Figure 4. The comparison of T cell and macrophages secreted IL-1** $\beta$ . Macrophages and T<sub>H</sub>17 cells were left untreated or treated with LPS for 4 hours (1ug/ul for macrophages) or LPS+ATP (5mM, 30 mins) or ATP alone (5mM, 8 hours). Cell pellet and supernatant were collected and subjected to western blotting for IL-1 $\beta$  and Actin. Data are representative of two independent experiments.



Supplementary Figure 5. Model for T cell intrinsic ASC function during CNS inflammation.



**Supplementary Figure 6. The EAE phenotype of** *Cd3e<sup>-/-</sup>II1b<sup>-/-</sup>***chimera mice.** (a) Lethal irradiated WT mice were reconstituted with WT+*Cd3e<sup>-/-</sup>* bone marrow or *II1b<sup>-/-</sup>+Cd3e<sup>-/-</sup>* bone marrow. 6 weeks after reconstitution, mice were immunized with  $MOG_{35-55}$  peptide and 200 ng pertussis toxin on days 1 and 4. Graph represents the average clinical score after active immunization. (b) Inflammatory gene expression in the lumbar spinal cord was assessed at the peak of disease. (c) Absolute numbers of CNS-infiltrating cells were determined at the peak of disease. Brains and spinal cords were harvested together and mononuclear infiltrating cells were stained with anti-CD45, anti-CD4, anti-CD8, anti-F4/80, anti-Ly6C and anti-Ly6G antibodies, followed by flow cytometric analysis. Two-way ANOVA (a) and Unpaired t test (b and c) were used to analyzed the data. Data are representative of three independent experiments (a-c). n=5 mice per group in each experiment. Error bars represent s.e.m. \*P < 0.05.