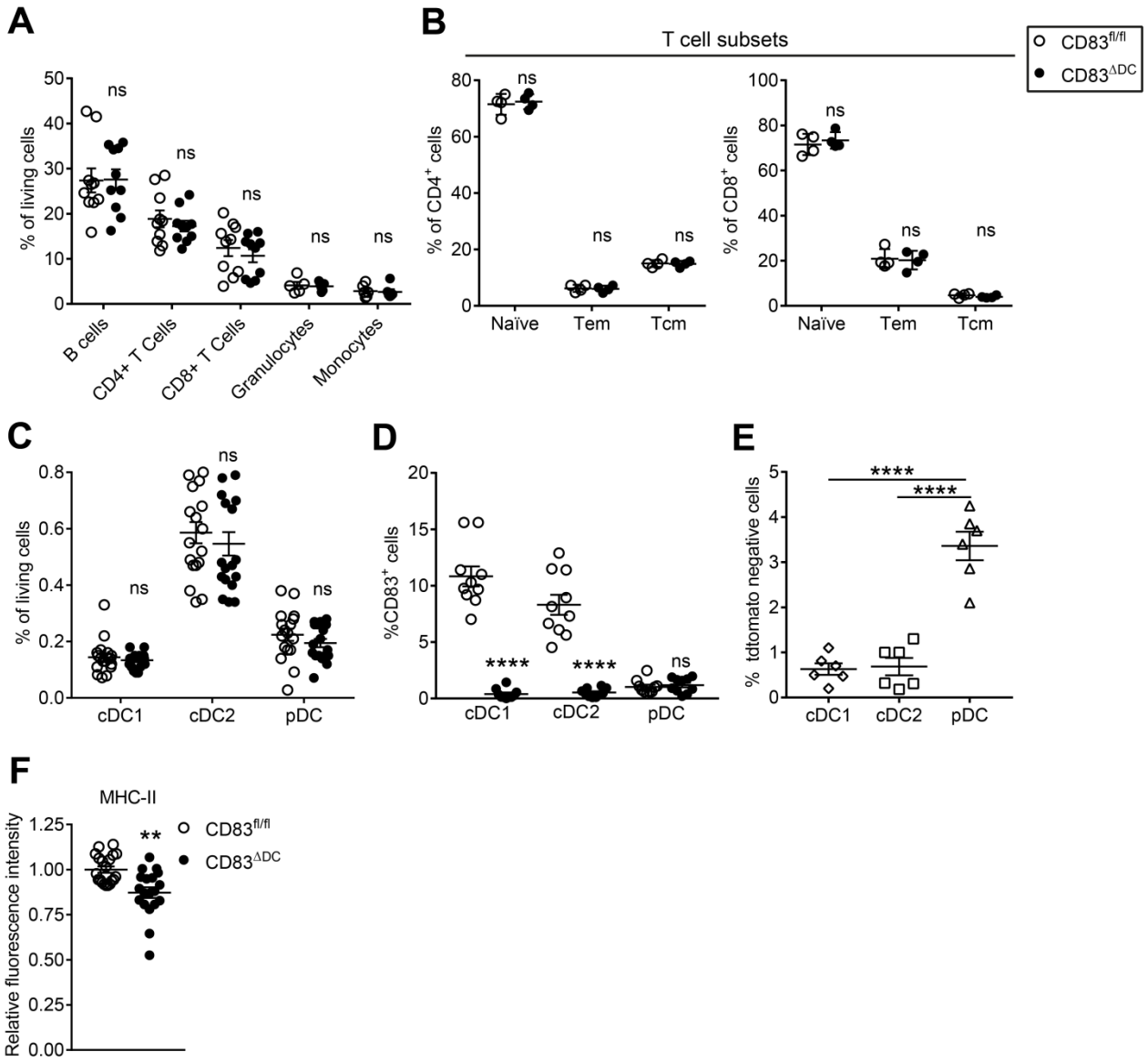
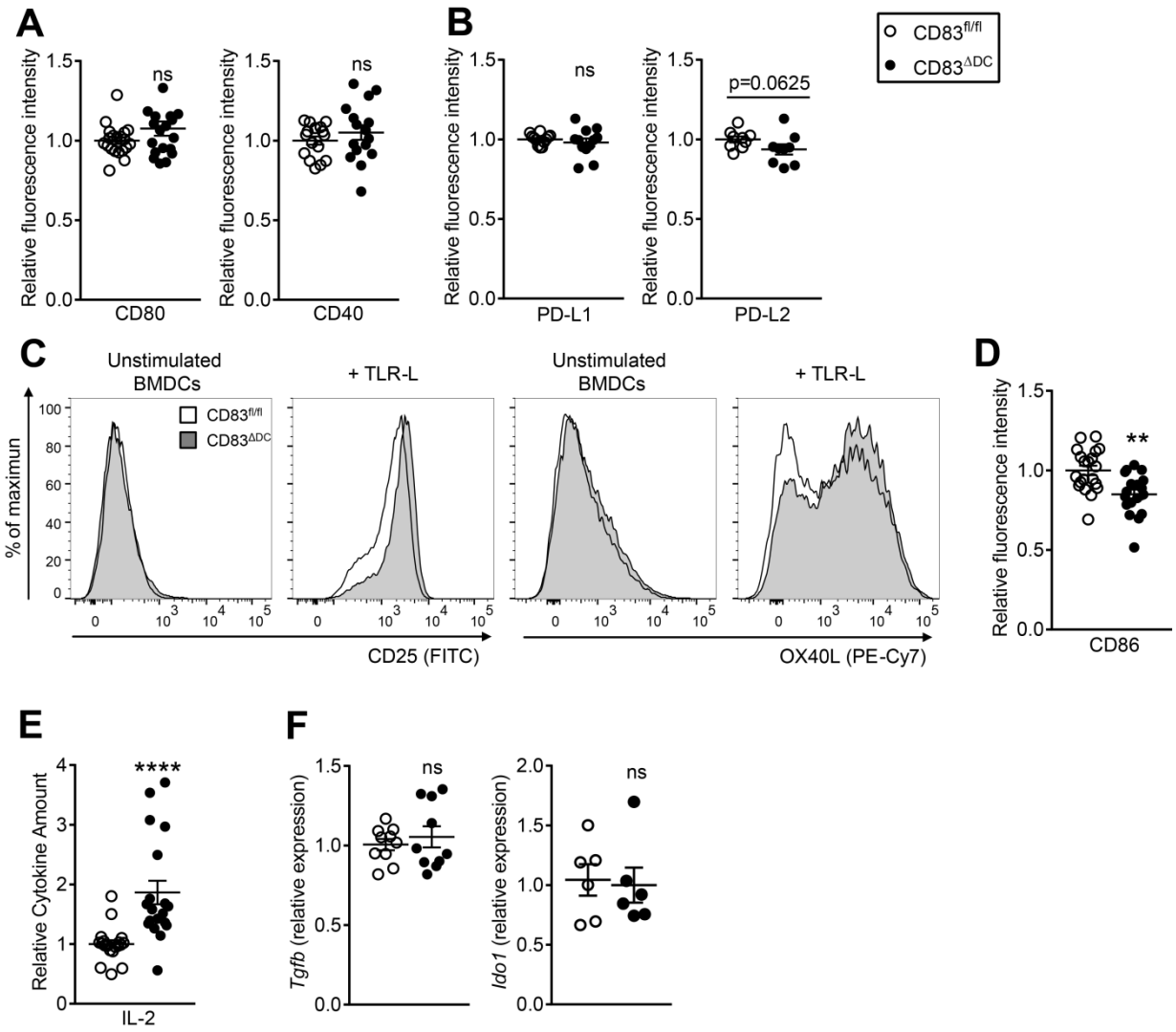
Supplementary Figure S1. Comparison of splenic cell subsets



(A) Distribution of immune cells in spleens of CD83$^{\Delta DC}$ and control mice. Subsets were analyzed via flow cytometry and percentages were calculated from total living leukocytes (n=6-10 from three to four experiments). (B) Analysis of T cell subsets in the spleen. Flow cytometric assessment of the percentages of naïve (CD62L^{+}CD44^{-}), effector memory (Tem, CD62L^{-}CD44^{+}) and central memory (Tcm, CD62L^{+}CD44^{+}) cells among the CD4^{+} and CD8^{+} compartment (n=4). (C) Assessment of splenic DC populations via flow cytometry. Single cell suspensions of spleens were analyzed for cellular composition regarding cDC1 (CD11c^{+}CD8^{+}), cCD2 (CD11c^{+}CD11b^{+}) and pDCs (B220^{+}SiglecH^{+}). Population percentages are related to all living cells being analyzed (n=18, pooled from five independent experiments). (D) CD83 expression on splenic DC subsets. Splenic DC subsets were analyzed via flow cytometry for their

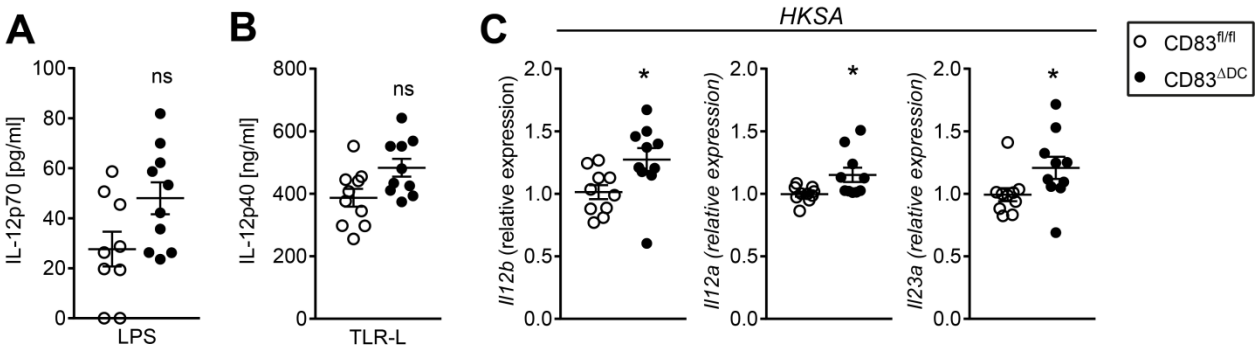
expression of CD83 (n=10, from three independent experiments). (E) Evaluation of recombination efficiency. $CD83^{\Delta DC}$ mice were crossed to a tdtomato-reporter strain and Cre-activity was assessed in splenic DC subsets via flow cytometry. Tdtomato-negative cells were regarded as cells with insufficient Cre-activity (n=6). (F) Flow cytometry analysis of MHC-II on BMDCs BMDCs were stimulated with TLR-L for 16 hours and expression of MHC-II was assessed via flow cytometry. Data are pooled from six experiments and normalized for each single experiment (n=20). Statistical analysis was performed using one-way ANOVA (D) and Mann-Whitney U-test. *p<0.05; **p<0.01;***p<0.001; ns = not significant

Supplementary Figure S2. BMDC phenotype



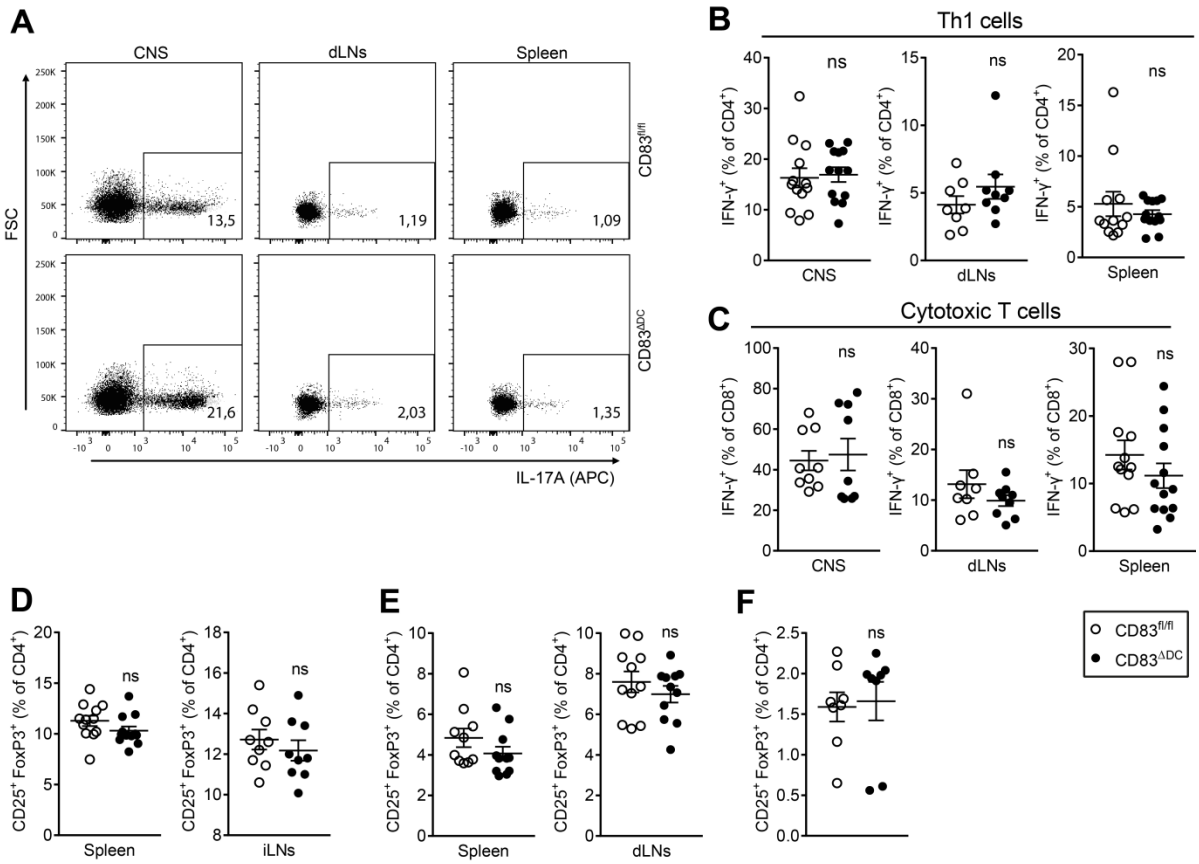
Assessment of co-stimulatory (A) and co-inhibitory (B) markers on BMDCs. BMDCs from CD83$^{\Delta DC}$ or control mice were stimulated with TLR-L for 16 hours and expression of CD40, CD80, PD-L1 and PD-L2 was assessed on CD11c^{+}MHC-II^{hi} mature DCs via flow cytometry. Data are pooled from up to six experiments and normalized for each single experiment (n=12-20). (C) Representative histograms for expression of CD25 and OX40L of unstimulated or TLR-L treated BMDCs. (D) Analysis of CD86 surface expression on TLR-L stimulated BMDCs. Data are pooled from up six experiments (n=18-20). (E) Relative IL-2 amount in supernatants of TLR-L stimulated BMDCs. Data from Figure 2E are presented as cytokine amount relative to control DCs (n=19, pooled from 8 different experiments). (F) Quantitative PCR analysis of *Tgfb* and *Ido1* mRNA expression after stimulation with TLR-L or 100 ng/ml LPS, respectively. Statistical analysis was performed using Mann-Whitney U-test. **p<0.01;****p<0.0001 ns = not significant

Supplementary Figure S3. IL-12 expression in CD83-deficient DCs



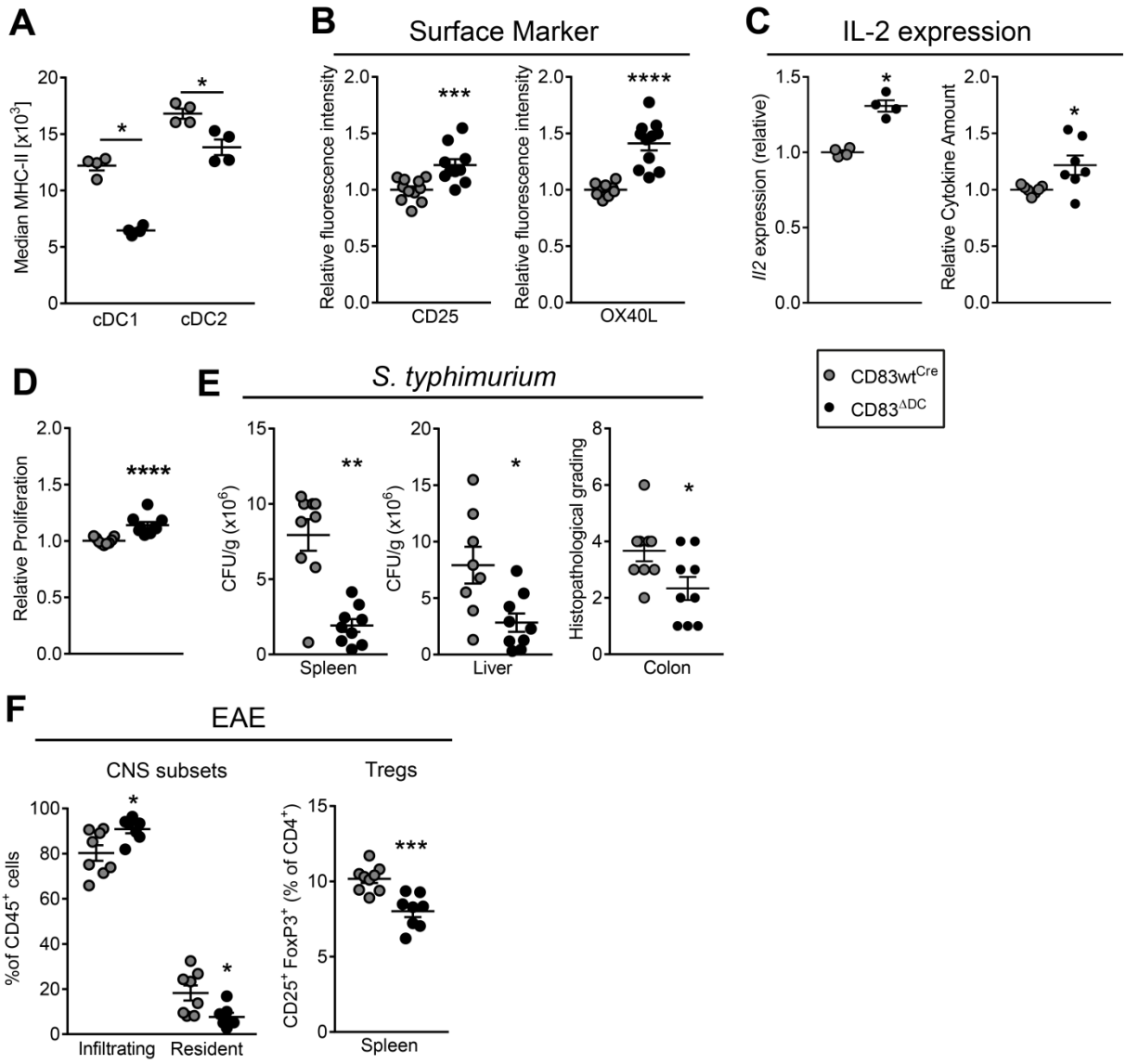
(A) Assessment of IL12 production by DCs. BMDCs were stimulated with 1 µg/ml LPS for 16 hours and supernatants were analyzed via cytometric bead array (n=10 out of three independent experiments). (B) Analysis of IL-12p40 secretion by DCs after different stimulations. BMDCs were treated with either TLR-L for 16 hours and supernatants were analyzed via IL-12p40 ELISA (n=10 from four experiments). (C) Assessment of IL-12 gene expression after stimulation with heat-killed *Staphylococcus aureus* (HKSA). BMDCs were treated with HKSA at a ratio of 10 bacteria per DC for 6 h and mRNA expression analyses of *Il12a*, *Il12b* and *Il23a* were performed by qPCR (n=12 from 3 experiments; expression is normalized to controls). Statistical analysis was performed using Mann-Whitney U-test. *p<0.05; ns = not significant

Supplementary Figure S4. T cell response during autoimmune inflammation



(A) Representative dot plots of flow cytometry in Figure 5E. Single cell suspension of CNS, draining lymph nodes (dLNs) and spleen were restimulated for 5 h with PMA/ionomycin in the presence of golgi transport inhibitors and IL-17 production was analyzed by intracellular flow cytometry. (B, C) Assessment of IFN-γ producing cells during EAE. Single cell suspensions of CNS, dLNs and spleens of animals on day 15 after EAE induction were restimulated with PMA and ionomycin and stained intracellularly for analysis of IFN-γ production. (B) Percentage of Th1 T cells (IFN-γ producing $CD4^+$ T cells). (C) Proportion of cytotoxic CD8+ T cells. Data are pooled from two to three experiments (n=8-13). (D) Treg numbers at EAE onset. Single cell suspensions of draining lymph nodes (dLN) and spleens of animals on day 8 after EAE were analyzed for Treg numbers via flow cytometry. Tregs were gated as $CD4^+CD25^+FoxP3^+$ cells (n=11, pooled from three independent experiments). (E) Treg numbers in naïve mice. Spleens and inguinal lymph nodes (iLN) from $CD83^{\Delta DC}$ and control mice were analyzed for presence of Tregs via flow cytometry (n=12 (spleens), n=9 (iLNs), pooled from three to four experiments). (F) Assessment of Treg induction in BMDC – T cell co-cultures. TLR-L and MOG_{35-55} pulsed BMDCs were cultivated with $CD4^+$ T cells from 2D2 mice for 4 days. Proportion of Tregs in co-culture was assessed via flow cytometry (n=8, four different experiments). Statistical analysis was performed using Mann-Whitney U-test. *p<0.05; **p<0.01;***p<0.001; ns = not significant

977 ***Supplementary Figure S5. Comparison of CD83$^{\Delta DC}$ with Cre-control mice***

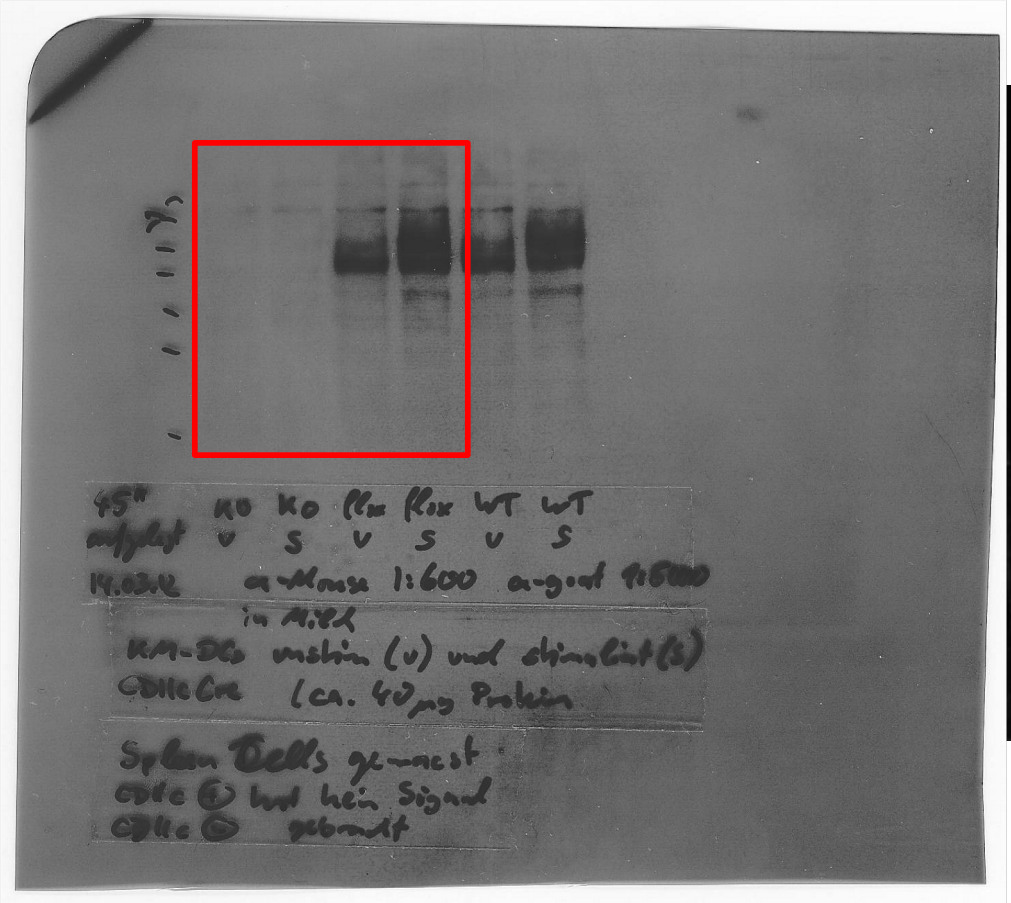


978

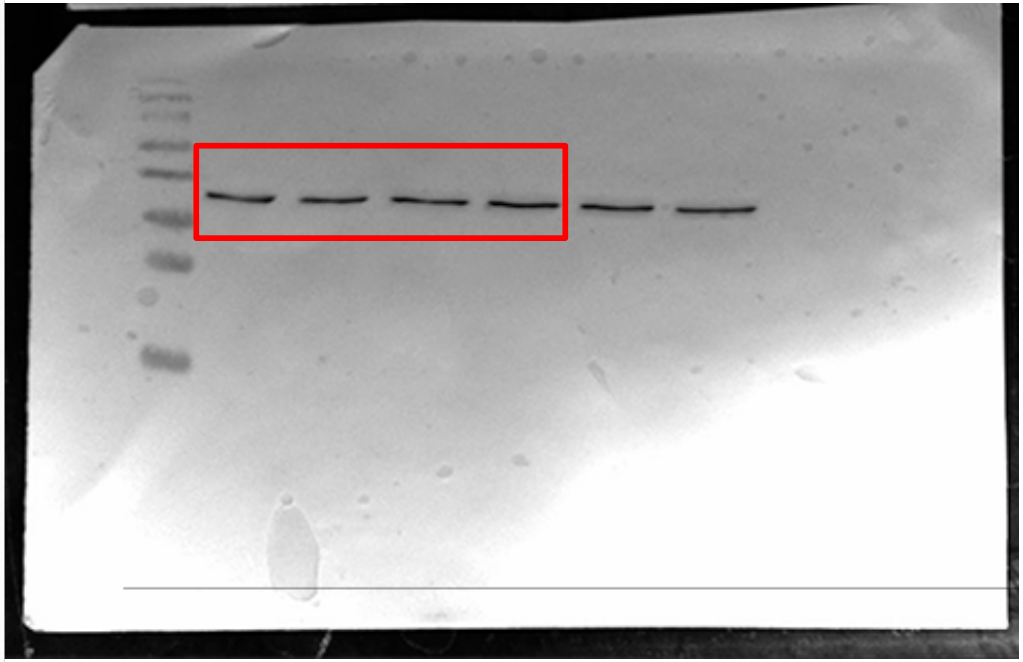
979 (A) Expression level of MHC-II on splenic DC subsets. Flow cytometric assessment
980 of MHC-II expression levels on cDC1 and cDC2 subsets of spleens derived from
981 CD83$^{\Delta DC}$ and control mice (n=4, compare to Figure 1E). (B) Assessment of BMDC
982 surface markers. BMDCs were stimulated with TLR-L for 16 h and surface
983 expression of CD25 and OX40L was examined via flow cytometry (n=11, from four
984 experiments; compare to Figure 2A). (C) Expression of IL-2. BMDCs were stimulated
985 with TLR-L for either 6 h or 16 h and IL-2 expression was assessed via qPCR or
986 ELISA, respectively. (n=4-7, from two to three experiments; compare to Figure
987 2D+E). (D) Proliferative response of 2D2 T cells after co-culture with TLR-L activated
988 and MOG_{35-55} pulsed BMDCs (n=9, pooled from four independent experiments;
989 compare to Figure 3B). (E) Analysis of S. *typhimurium* infected mice. Four days after
990 infection, organs were harvested and analyzed with regard to bacterial load
991 (spleen/liver) and tissue damage (colon) (n=9, pooled from two experiments;

compare to Figure 4C). (F) Analysis of EAE mice. Mice were sacrificed at the peak of disease and cellular composition of the CNS and the spleen was investigated. For the CNS, the proportion of infiltrating vs. resident cells was examined, while Treg numbers were analyzed in the spleens (n=8-9, two different experiments). Statistical analysis was performed using Mann-Whitney U-test. *p<0.05; **p<0.01;***p<0.001; ****p<0.0001; ns = not significant

Full unedited gel for Figure 1C

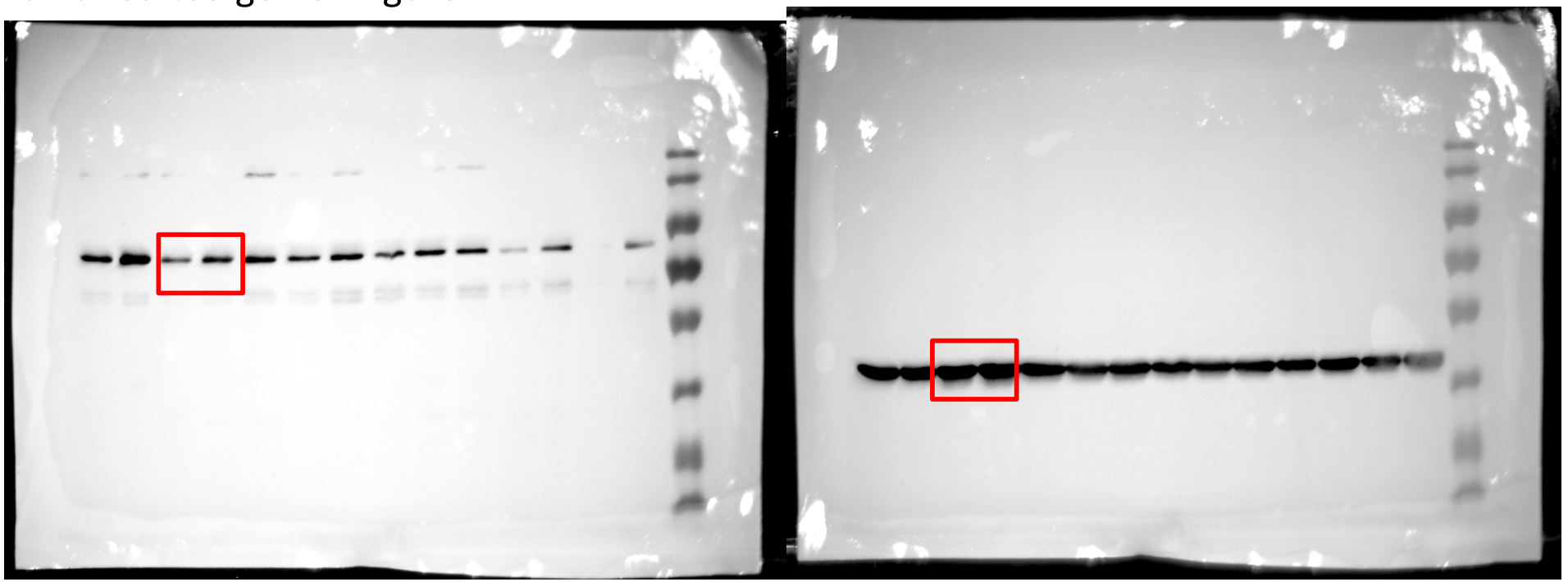


CD83



GapDH

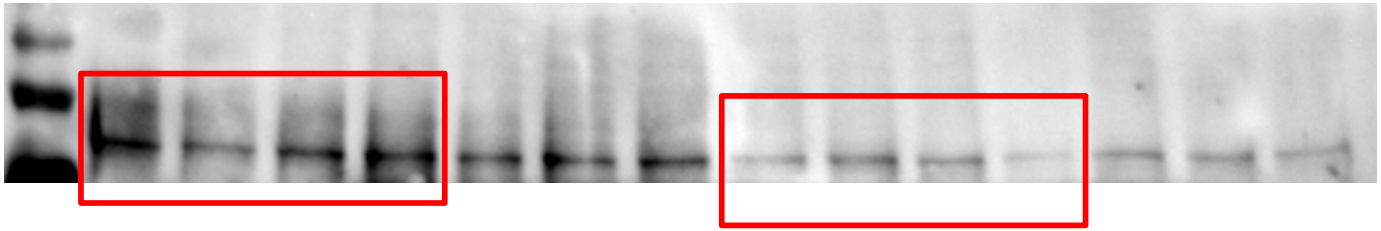
Full unedited gel for Figure 2B



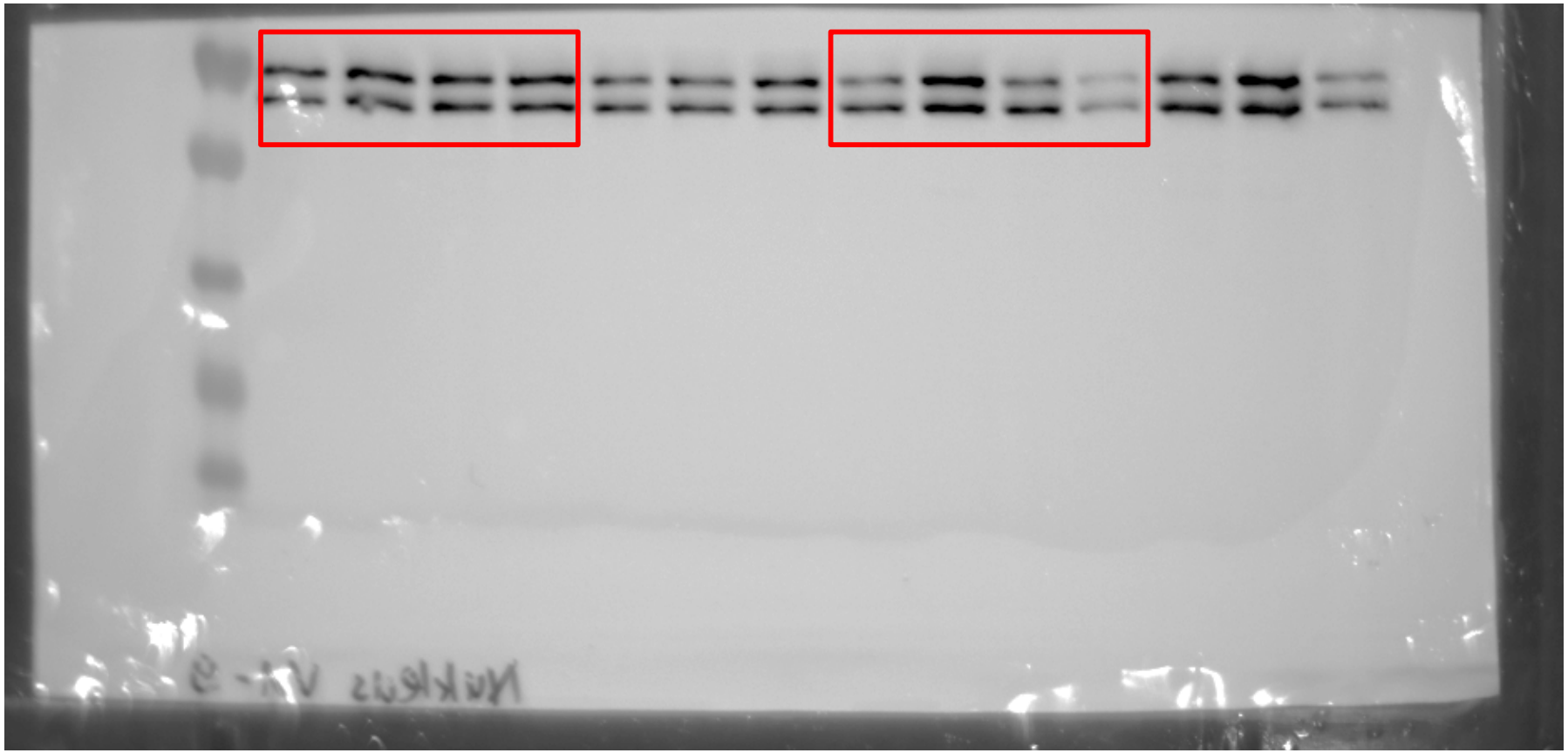
IRAK1

β-Actin

Full unedited gel for Figure 2F



NFATc2



LaminA/C

Remark: The blot was cut in half prior to staining