

## Description of Additional Supplementary Files

### **Title:** Supplementary Data 1

**Description:** (Related to Fig. 2b). A list of MyD88 induced genes in mTECs<sup>high</sup>. RNA-sequencing data from mTECs<sup>high</sup> derived from MyD88<sup>fl/fl</sup> and MyD88<sup>ΔTECs</sup> mice. Data represents the analysis of n=5 samples for each condition. Statistical analysis was performed by Wald test, Fold-change cutoff of log<sub>2</sub>=+/-1,0 and p-value 0.05. Differentially expressed genes of interest are depicted in red.

### **Title:** Supplementary Data 2

**Description:** (Related to Fig. 2b). A list of MyD88 repressed genes in mTECs<sup>high</sup>. RNA-sequencing data from mTECs<sup>high</sup> derived from MyD88<sup>fl/fl</sup> and MyD88<sup>ΔTECs</sup> mice. Data represents the analysis of n=5 samples for each condition. Statistical analysis was performed by Wald test, Fold-change cutoff of log<sub>2</sub>=+/-1,0 and p-value 0.05.

### **Title:** Supplementary Data 3

**Description:** (Related to Fig. 2d, e). A list of CpG ODN upregulated genes in mTECs<sup>high</sup>. RNA-sequencing data from CpG ODN or PBS *in vitro* stimulated mTECs<sup>high</sup> (sorted as in Supplementary Fig. 1a) from MyD88<sup>+/+</sup> and MyD88<sup>-/-</sup> mice (n=4 samples for each condition). Statistical analysis was performed by Wald test, Fold-change cutoff of log<sub>2</sub>=+/-1,0 and p-value 0.05. Differentially expressed genes of interest are depicted in red.

### **Title:** Supplementary Data 4

**Description:** (Related to Fig. 2d, e). A list of CpG ODN downregulated genes in mTECs<sup>high</sup>. RNA-sequencing data from CpG ODN or PBS *in vitro* stimulated mTECs<sup>high</sup> (sorted as in Supplementary Fig. 1a) from MyD88<sup>+/+</sup> and MyD88<sup>-/-</sup> mice (n=4 samples for each condition). Statistical analysis was performed by Wald test, Fold-change cutoff of log<sub>2</sub>=+/-1,0 and p-value 0.05.

### **Title:** Supplementary Data 5

**Description:** (Related to Fig. 5a, b, c). Differentially expressed genes determining DC-clusters. ddSEQ single-cell RNA-sequencing from FACS sorted Gr-1<sup>-</sup>CD11c<sup>+</sup>TdTOM<sup>+</sup> DCs from the thymus of Foxn1<sup>Cre</sup>ROSA26<sup>TdTOMATO</sup> mice. Statistical analysis was performed by Wald test, Fold-change cutoff of log<sub>2</sub>=+/-1,0 and p-value 0.05.

### **Title:** Supplementary Data 6

**Description:** (Related to Methods section). A full list of antibodies and primers used throughout the study.