**Supplementary Figure 1:** DC differentiation KI and WT.

The proportions of DCs and macrophages in β2-integrin KI and WT mouse bone marrow cultures were analysed on day 9 by flow cytometry. Gating strategy for representative KI and WT samples **a)** and corresponding bar graphs **b)** are shown. Cell proportions are shown either in the parent population **a)** or in total leukocytes **b)**. Data in **b)** are shown as mean ± SEM with each symbol representing an individual mouse. GM refers to GM-CSF used in the cell culture, GM-Macs = macrophages, GM-DNs = CD115 CD135 double negative cells, GM-DCs = dendritic cells.

**Supplementary Figure 2:** KI DCs compared toLPS stimulated WT DCs.

**a)** Overlap of flow charts for CD40, CD80, CD86 of KI NT, WT NT and WT LPS of representative examples. **b)** Concentration of IL-12 of WT NT and WT LPS DCs **c)** Average3D migration speeds in the presence of CCL19, of non-treated and LPS-treated WT DCs over the time course of 4h. N=4. **d)** Average CTCF of H3K4me3 and H3K27me3 in non-treated and LPS-treated WT DCs. N=3

**Supplementary Figure 3:** Analysis of pooled tumour-draining lymph nodes from tumour rejection experiments

**a)** Number of CD4+ T cells relative to tumour volume. **b)** Percentage of CD4+ T-cells in the tumour-draining lymph node. **c)** Percentage of CD4+ T-cells in the bloodstream. Depicted is the fold change from baseline level before DC injection to 4 days after injection. p-value shown as <0.05 \*

**Supplementary Figure 4:** Analysis of Lamin KO DC phenotype

**a)** Expression of CD40, CD86, CD80 in lamin Ctrl and KO DCs. N=3 **b)** IL-12 production of lamin A/C knockout and control DCs was measured by ELISA. N=4 **c)** 3D migration speeds in collagen towards CCl19 of lamin A/C knockout and control DCs N=4.

**Supplementary Figure 5:** ATAC-Seq read profile.

**a)** Histogram depicting ATAC-seq insert size distribution histogram in WT and **b)** KI. ATAC-Seq peak annotations in **c)** WT and **d)** KI. **e)** Aggregated footprint signal plots for Ikaros. These plots are centered on the predicted binding sites for Ikaros between KI and WT conditions. The total possible binding sites for Ikaros (n = 3338) are separated into bound and unbound sites, and here only bound sites are shown. The dashed lines represent the edges of the Ikaros motif.

**Supplementary Figure 6:** Transcription Factor Networks.

TF-TF interaction networks produced by TOBIAS centering around IKZF1.

**Supplementary Figure 7:** Treg numbers in B16.OVA WT TCP+suspension tumour experiments.

**a)** number of total CD4+ T cells in tumours from MOCK, KI, WT NT and WT TCP+suspension DCs injected groups **b)** Tregs shown in the CD4+ T cell population