Fig. S1



Figure S1. The effect of rapamycin on GM-CSF-driven DC development. Rapamycin (10 ng/ml) was added on day 0 to GM-CSF-supplemented cultures of wildtype BM. Shown are staining profiles on day 8, and the histograms of MHC cl. II expression in the gated CD11c⁺ cDC (representative of 3 independent cultures). No reduction in the total cell output of rapamycin-treated cultures was noted (not shown).



Figure S2. DC development from Pten-deficient bone marrow.

Pten deletion was induced by tamoxifen administration to *Pten*^{fl/fl} *Gt(ROSA)26Sor*-CreER⁺ animals (*Pten*^{Δ}) or littermate controls (Ctrl) as in Fig. 2.

(A) GM-CSF-driven DC development. Shown are staining profiles of GM-CSFsupplemented control and *Pten*[△] BM cultures on days 5 and 8. No difference in the total cell output of the cultures was noted (not shown).

(B) The effect of rapamycin on Flt3L-driven DC development. Control and *Pten*^{Δ} BM cells were cultured with Flt3L in the presence or absence of 10 ng/ml rapamycin, and analyzed on days 5 and 8. Shown are staining profiles (representative of two independent experiments) with live CD11c⁺ DC highlighted.

Fig. S3



Figure S3. Characterization of DC-specific Pten deletion.

Pten^{fl/fl} *Itgax*-Cre⁺ animals (DC-*Pten*^{Δ}) and control *Itgax*-Cre⁻ littermates were analyzed.

(A) The specificity of Cre recombination in DC-*Pten*^{Δ} animals crossed with the Creinducible *Gt(ROSA)26Sor*-StopFlox-EYFP allele (Srinivas et al., 2001). Shown are histograms of EYFP fluorescence in the CD11c^{hi} MHC cl. II⁺ cDC subsets, T or B lymphocytes from *Gt(ROSA)26Sor*-StopFlox-EYFP⁺ Cre-negative (Ctrl), *Itgax*-Cre⁺ *Pten* heterozygous (*Pten*^{fl/wt}, Het) or *Itgax*-Cre⁺ *Pten*^{fl/fl} (DC-*Pten*^{Δ}) animals.

(B) Age-dependent development of T cell lymphomas in DC-*Pten*^{Δ} mice. Shown is Kaplan-Meyer survival plot of the DC-*Pten*^{Δ} and littermate control mice. On necropsy all DC-*Pten*^{Δ} mice showed a large thymic mass in the mediastinum, splenomegaly and lymphadenopathy. Flow cytometry plots represent the analysis of a moribund *Gt*(*ROSA*)*26Sor*-StopFlox-EYFP⁺ DC-*Pten*^{Δ} mouse, showing a recombined EYFP⁺ double-positive T cell lymphoma.

(C) The expression of *Pten* mRNA in monocytes or macrophages (M, side scatter^{lo} $CD11c^{-}CD11b^{+}$), cDC (CD11c^{hi} MHC cl. II⁺ CD8⁺ or CD8⁻) or PDC (CD11c^{lo} Bst2⁺) from DC-*Pten*^A or control (Ctrl) mice. Shown are normalized quantitative RT-PCR results relative to the expression value in control monocytes (mean \pm S.D. of triplicate reactions). RT-PCR was performed using SYBR Green method with primers specific for Pten exon deleted after Cre recombination: 5'-TGGATTCAAAGCATAAAACCATTAC-3' and 5'- CAAAAGGATACTGTGCAACTCTGC-3'.

(**D**) Western blot analysis of PI3K signaling in BM-derived cDC. GM-CSF-supplemented BM cultures from control and DC-*Pten*^{Δ} mice were left untreated (0) or stimulated with 1 μ g/ml LPS for 15 or 30 min., and analyzed using antibodies against phosphorylated Akt

Ser473 and GSK3 β Ser9 (Cell Signaling Technology). Note the constitutive Akt and GSK3 β phosphorylation in untreated DC-*Pten*^{Δ} DC.

(E) Donor contribution to different cell types of chimeric mice. Irradiated CD45.1⁺ recipients were reconstituted with CD45.2⁺ DC-*Pten*^{Δ} or control donor BM and CD45.1⁺ competitor BM. Shown are representative CD45.1 expression profiles in the indicated splenic cell types, with the fraction of CD45.1⁻ donor-derived cells indicated. Note the substantial (~30-45%) donor contribution in lymphocytes, poor (15-20% contribution in myeloid cells and an overwhelming (>80%) contribution of DC-*Pten*^{Δ} but not control donor cells to CD8⁺ cDC.

(F) Splenic pre-DC after DC-specific Pten deletion. Control or DC-*Pten*^A mice carrying the *Cx3cr1*-EGFP knock-in reporter allele were analyzed. Shown is the CD8⁺ cDC population among total splenocytes (left), and the Cx3cr1^{hi} CD11c^{lo} pre-cDC population among the gated lineage-negative (MHC II⁻ CD11b⁻ Gr-1⁻ CD8⁻) cells. Percentages out of total splenocytes are indicated. Additional staining for pre-DC markers Flt3 and CD115 confirmed equal fraction of pre-DC in control and DC-*Pten*^A spleens (not shown).

Fig. S4



Figure S4. DC populations in mice with DC-specific deletion of Tsc1

Tsc1 conditional strain (Kwiatkowski et al., 2002) obtained from Jackson Labs was used for DC-specific targeting in *Tsc1*^{fl/fl} *Itgax*-Cre⁺ (DC-*Tsc1*^{Δ}) animals. Shown are staining profiles of splenic DC in the DC-*Tsc1*^{Δ} and Cre-negative littermate control mice (representative of three animals per genotype). Note the lack of CD8⁺ cDC expansion in DC-*Tsc1*^{Δ} mice.





Figure S5. T cell response to LM-OVA in DC-*Pten*[∆] mice.

(A) Clustering of OVA-specific T cells in the early phase of LM-OVA infection. Splenic $CD8^+$ T cells were isolated from OVA-specific OT-I TCR transgenic mice or from wild-type C57BL/6 mice and labeled with Cell Tracker (Invitrogen) Blue and Orange dyes, respectively. Labeled T cells were transferred (2x10⁶/animal i.v.) into DC-*Pten*^A or control animals six hours prior to infection with 10⁵ LM-OVA. After 24 hr spleens were imaged by multiphoton microscopy as described (Aoshi et al., 2008). Shown are representative still images of OVA-specific (blue) and non-specific polyclonal (red) CD8⁺

T cells from uninfected control, infected control or two infected DC-*Pten*^{Δ} animals. Note the prominent clustering of OVA-specific T cells in all infected animals.

(B) Expansion of OVA-specific T cells following LM-OVA infection. Splenic CD8⁺ T cells from OVA-specific OT-I TCR transgenic mice were transferred to DC-*Pten*^{Δ} or control animals (10⁶/animal i.v.) 24 hours prior to infection with 2x10⁴ LM-OVA. Six days later, spleen and lymph nodes were analyzed for the presence of OT-I TCR-expressing T cells by flow cytometry. Shown are staining profiles from two control and DC-*Pten*^{Δ} animals. Similarly, no difference in the endogenous OVA-specific CD8⁺ T cell expansion was observed between control and DC-*Pten*^{Δ} animals (not shown).

Supplemental References

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