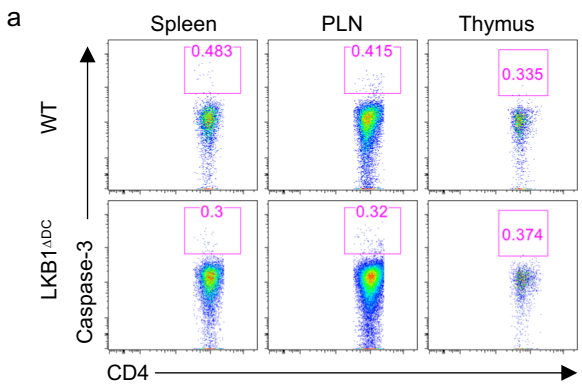
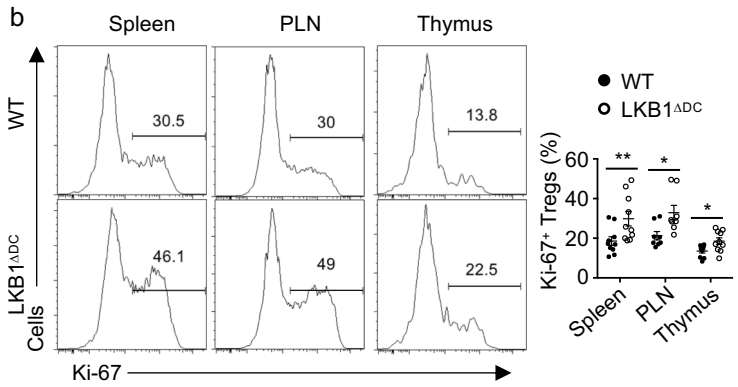
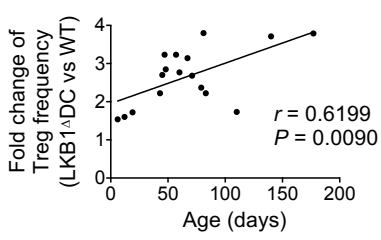
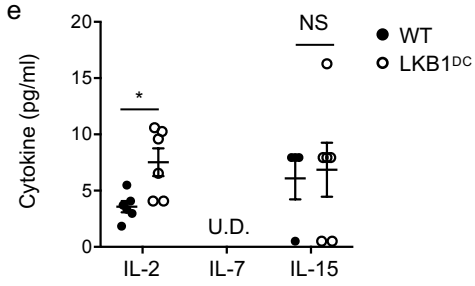


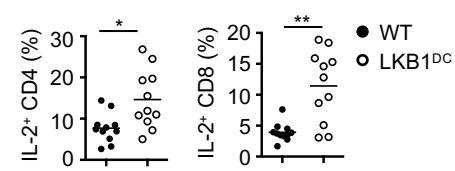



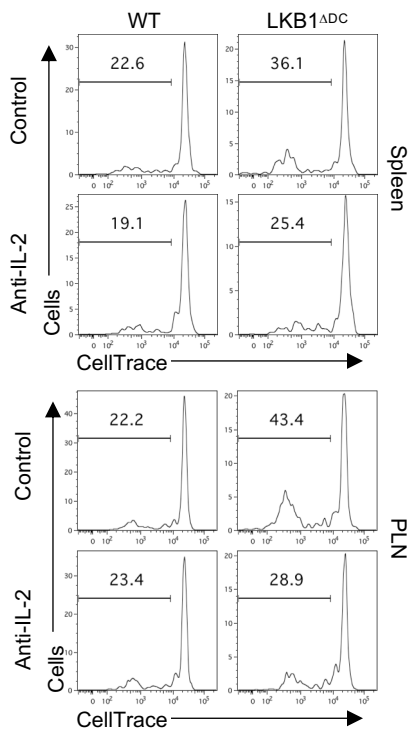



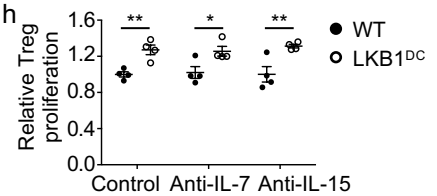

d

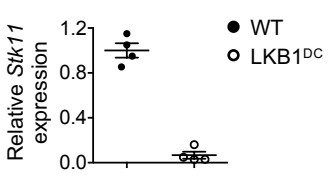
| NAME | SIZE | NES | FDR q-val |
|---|---|---|---|
| HALLMARK_E2F_TARGETS | 194 | 3.4869616 | <0.001 |
| HALLMARK_G2M_CHECKPOINT | 193 | 3.3285758 | <0.001 |
| HALLMARK_MTORC1_SIGNALING | 189 | 2.9780955 | <0.001 |
| HALLMARK_MYC_TARGETS_V1 | 195 | 2.8366065 | <0.001 |
| HALLMARK_OXIDATIVE_PHOSPHORYLATION | 190 | 2.8153539 | <0.001 |
| HALLMARK_IL2_STAT5_SIGNALING | 194 | 2.70177 | <0.001 |
| HALLMARK_DNA_REPAIR | 136 | 2.5621157 | <0.001 |
| HALLMARK_GLYCOLYSIS | 191 | 2.538851 | <0.001 |
| HALLMARK_HEME_METABOLISM | 180 | 2.502701 | <0.001 |
| HALLMARK_COMPLEMENT | 181 | 2.4497638 | <0.001 |
| HALLMARK_IL6_JAK_STAT3_SIGNALING | 85 | 2.4139924 | <0.001 |
| HALLMARK_UV_RESPONSE_UP | 145 | 2.3865178 | <0.001 |
| HALLMARK_INTERFERON_GAMMA_RESPONSE | 183 | 2.3598511 | <0.001 |
| HALLMARK_XENOBIOTIC_METABOLISM | 187 | 2.3489466 | <0.001 |
| HALLMARK_ALLOGRAFT_REJECTION | 182 | 2.3111455 | <0.001 |
| HALLMARK_MITOTIC_SPINDLE | 195 | 2.3106244 | <0.001 |
| HALLMARK_CHOLESTEROL_HOMEOSTASIS | 68 | 2.3004844 | <0.001 |
| HALLMARK_APOPTOSIS | 156 | 2.2915757 | <0.001 |
| HALLMARK_ESTROGEN_RESPONSE_LATE | 191 | 2.2427185 | <0.001 |
| HALLMARK_PEROXISOME | 100 | 2.2407382 | <0.001 |
| HALLMARK_ADIPOGENESIS | 194 | 2.2366297 | <0.001 |
| HALLMARK_MYC_TARGETS_V2 | 57 | 2.232941 | <0.001 |
| HALLMARK_UNFOLDED_PROTEIN_RESPONSE | 111 | 2.2167182 | <0.001 |
| HALLMARK_INTERFERON_ALPHA_RESPONSE | 86 | 2.2079468 | <0.001 |
| HALLMARK_INFLAMMATORY_RESPONSE | 194 | 2.1959453 | <0.001 |
| HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY | 44 | 2.1947317 | <0.001 |
| HALLMARK_FATTY_ACID_METABOLISM | 145 | 2.15793 | <0.001 |
| HALLMARK_P53_PATHWAY | 195 | 2.1560001 | <0.001 |
| HALLMARK_COAGULATION | 130 | 2.0983825 | <0.001 |
| HALLMARK_ANDROGEN_RESPONSE | 94 | 2.01235 | 0.001 |

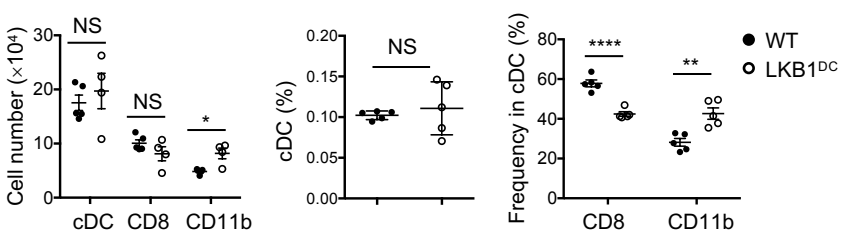


**Supplementary information, Figure S3. Role of LKB1 in splenic and thymic DCs to restrain Tregs. a**, Flow cytometry analysis of active caspase-3 expression in Tregs in the spleen, PLN and thymus of WT and LKB1$^{\Delta DC}$ mice. **b**, Flow cytometry analysis (left) and statistics (right) of Ki-67 expression in Tregs in the spleen, PLN and thymus of WT and LKB1$^{\Delta DC}$ mice. **c**, Correlation between fold change of Treg frequency in the spleen of LKB1$^{\Delta DC}$ vs WT mice and mouse age by linear regression analysis. In the plot, *r* and *P* indicate the Pearson correlation coefficient and the *P* value of significance, respectively. **d**, List of the top 30 upregulated (FDR < 0.02) pathways (out of 41) in splenic Tregs from LKB1$^{\Delta DC}$ mice (compared to WT counterparts) profiled using gene expression, as revealed by gene set enrichment analysis (GSEA). **e**, Cytokine production by WT and LKB1-deficient splenic DCs stimulated with 100 ng/ml LPS for 2 days. U.D., undetermined. **f**, Statistics of IL-2 expression in splenic CD4$^+$ and CD8$^+$ T cells from WT and LKB1$^{\Delta DC}$ mice. **g**, At day 0, CellTrace-labelled CD45.1$^+$ Tregs were transferred into WT and LKB1$^{\Delta DC}$ mice that were treated with anti-IL-2 antibodies at days -1, 2, and 5. CellTrace dilution of transferred Tregs was analyzed seven days later. **h**, Relative thymidine incorporation of WT Tregs cultured with splenic DCs from WT and LKB1$^{\Delta DC}$ mice in the presence of absence of anti-IL-7 or anti-IL-15 blocking antibodies (values cultured with WT thymic DCs without antibody treatment was set as 1). **i**, Real-time PCR analysis of *Stk11* mRNA expression in thymic DCs from WT and LKB1$^{\Delta DC}$ mice. **j**, Statistics of cell frequencies and numbers of thymic DC populations from WT and LKB1$^{\Delta DC}$ mice. Data in plots indicate the means ± s.e.m; each symbol represents an individual mouse. Numbers in gates indicate percentage of cells. NS, not significant; **P* < 0.05, ***P* < 0.01; *****P* < 0.0001; two-tailed Mann-Whitney test (b; f; j, frequency) or two-tailed unpaired Student's *t* test (e; h; j, cell number). Data are from three (a, e), four (b), fourteen (c), five (f), or two (g–j) independent experiments.