

SUPPLEMENTARY INFORMATION

Loss of MAPK-activated protein kinase 2 enables potent dendritic cell-driven anti-tumour T cell response

Klara Soukup^{1,4*}, Angela Halfmann¹, Barbara Dillinger¹, Fiona Poyer¹, Katharina Martin¹, Bernadette Blauensteiner¹, Maximilian Kauer², Mario Kuttke³, Gernot Schabbauer³ and Alexander M. Dohnal^{1,5*}

¹Tumour Immunology, St. Anna Kinderkrebsforschung, Children's Cancer Research Institute, Vienna, Austria

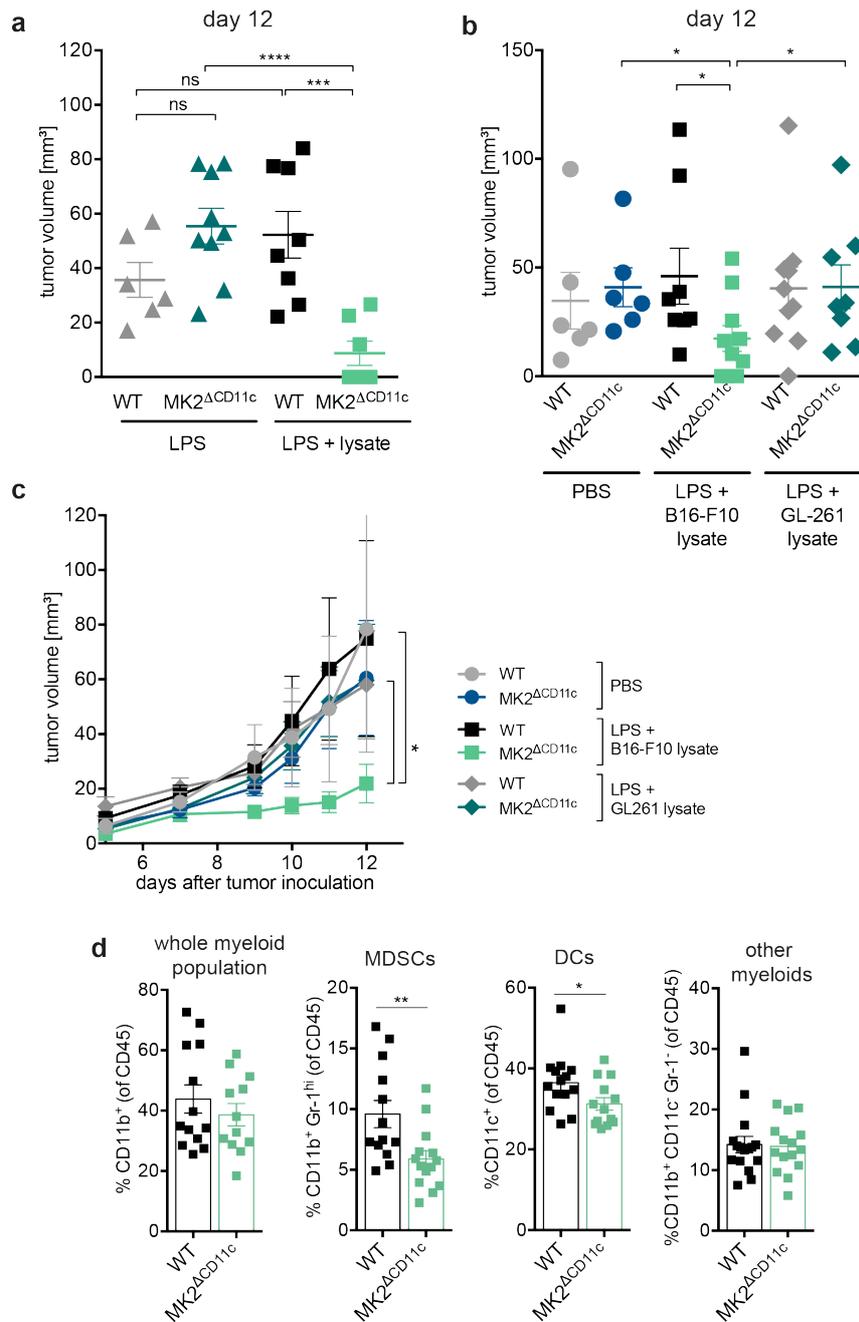
²Bioinformatics, St. Anna Kinderkrebsforschung, Children's Cancer Research Institute, Vienna, Austria

³Institute for Physiology, Centre for Physiology and Pharmacology, Medical University of Vienna, Vienna, Austria

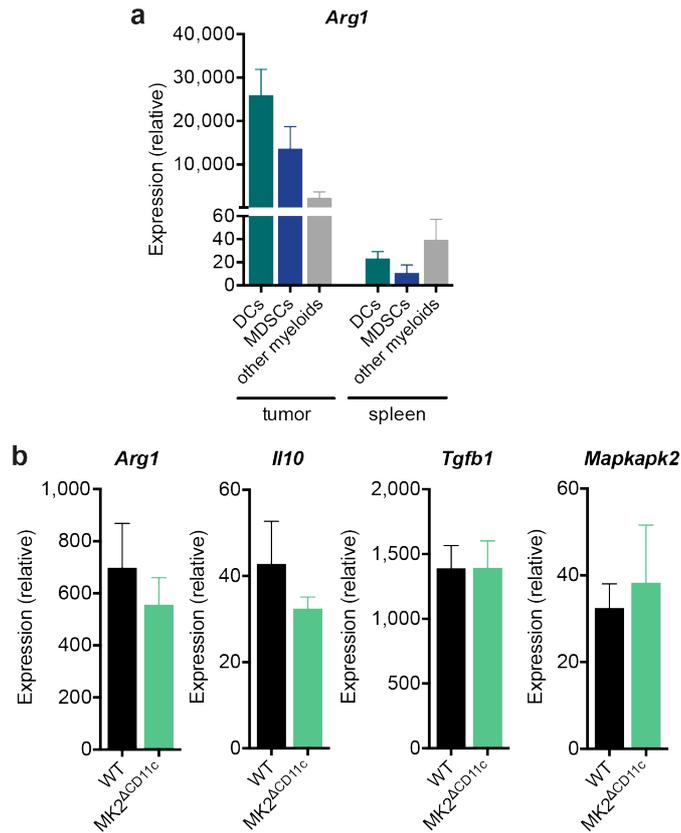
⁴Current address: Department of Fundamental Oncology, Ludwig Institute for Cancer Research, University of Lausanne, Lausanne, Switzerland

⁵Current address: APEIRON Biologics AG, Vienna, Austria

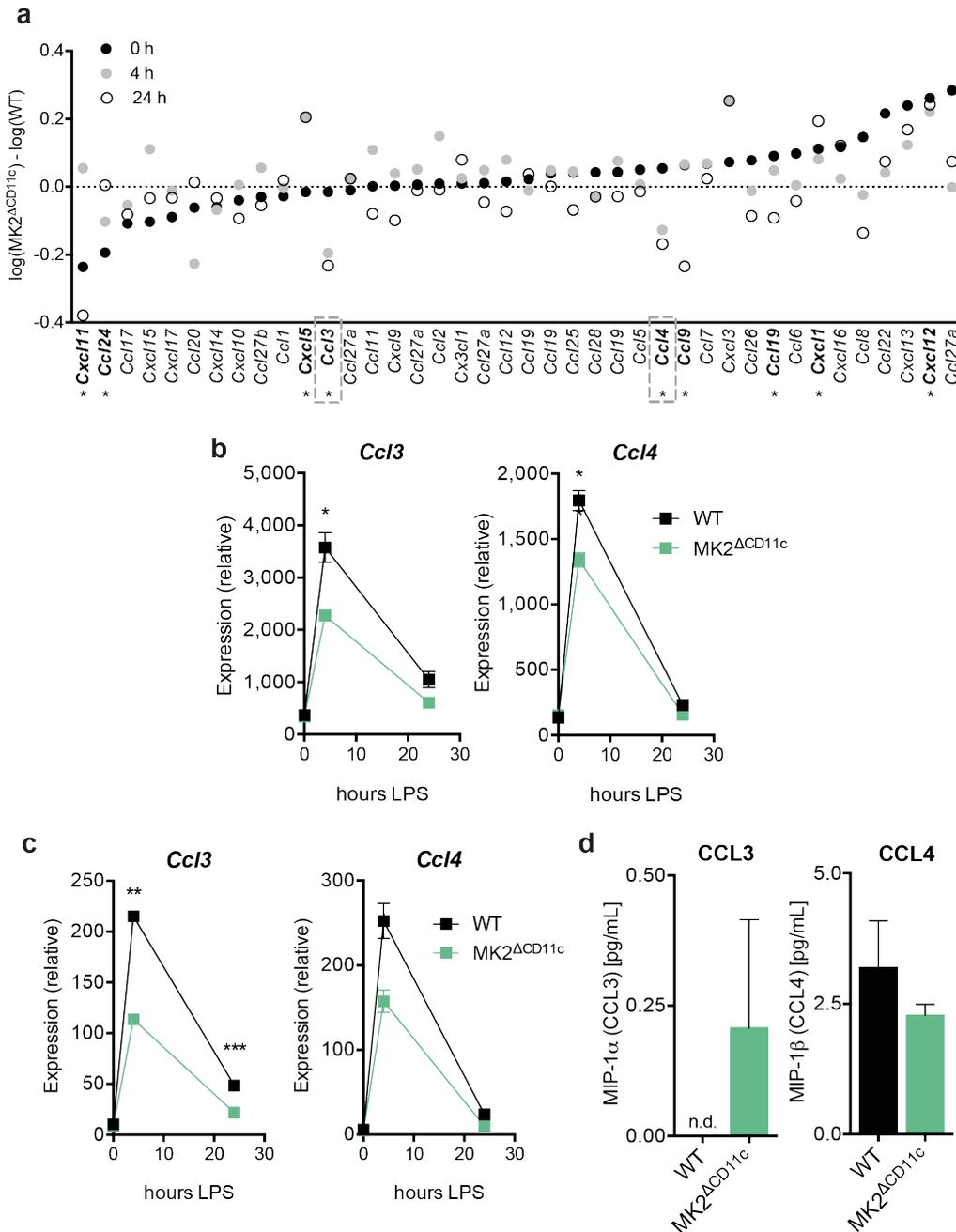
*Correspondence and requests for materials should be addressed to K.S. (email: klara.soukup@unil.ch) or A.M.D. (email: alexander.dohnal@apeiron-biologics.com)



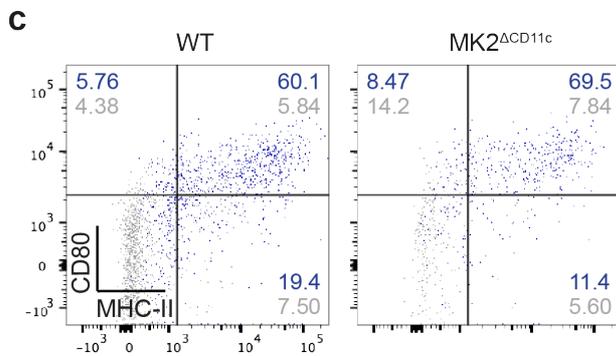
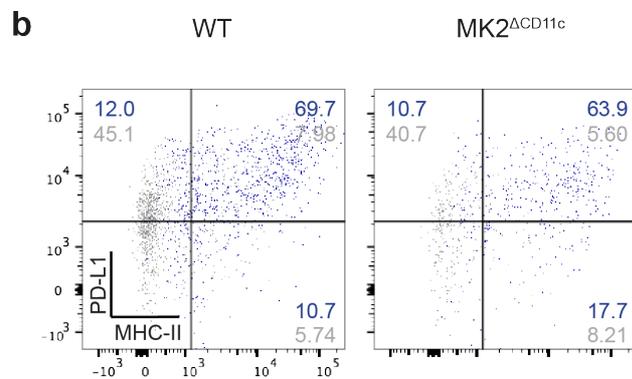
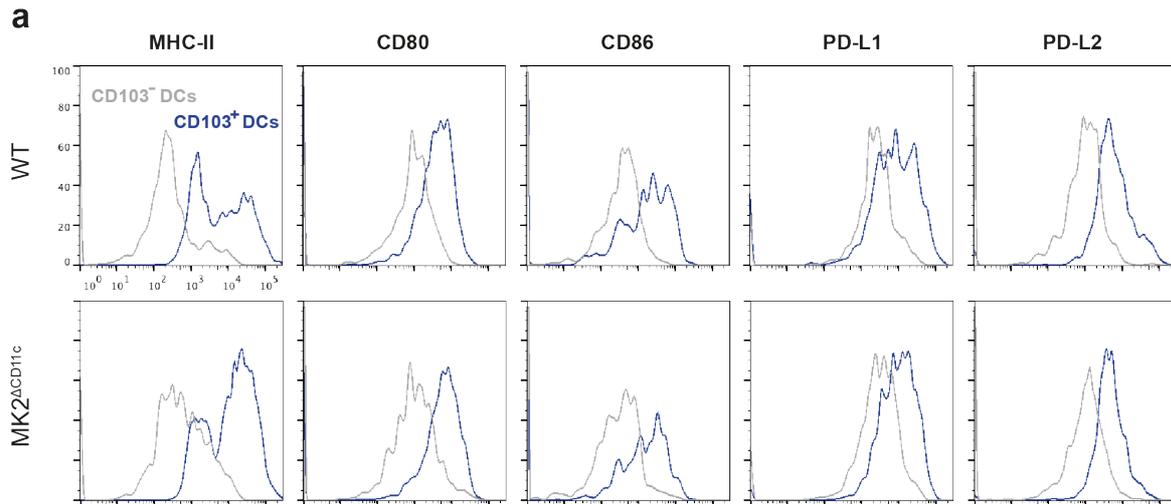
Supplementary Figure 1. Tumours of immunized MK2^{ΔCD11c} mice are infiltrated by fewer dendritic and immature myeloid cells. (a-b) B16-F10 tumour volumes at day 12 post-tumour cell injection in MK2^{ΔCD11c} and WT control mice immunized with (a) LPS alone or in combination with B16-F10 whole cell lysate or (b) PBS, LPS + B16-F10 lysate or LPS + GL-261 lysate (n = 5-8 per group, one representative of three independent experiments). (c) B16-F10 tumour growth in MK2^{ΔCD11c} and WT mice immunized with PBS, LPS + B16-F10 or LPS + GL-261 lysate on days 5 and 9 post-tumour cell injection (n = 5-8 mice per group). (d) Mean frequencies of overall myeloid cells (CD11b⁺), DCs (CD11c⁺ MHC-II⁺), MDSCs (CD11b⁺ Gr-1⁺) and other myeloid populations (CD11b⁺ Gr-1⁻ CD11c⁻) within tumour-infiltrating CD45⁺ leukocytes measured by flow cytometry. Each symbol represents one individual animal (n = 15-18 per group, pooled from three independent experiments). Data are presented as mean ± SEM. ns, not significant. *P<0.05, **P<0.01, ***P<0.001, ****P<0.0001. P-values were determined using (a-b, d) Student's *t*-test and (c) repeated-measures two-way ANOVA with Bonferroni correction for multiple comparisons.



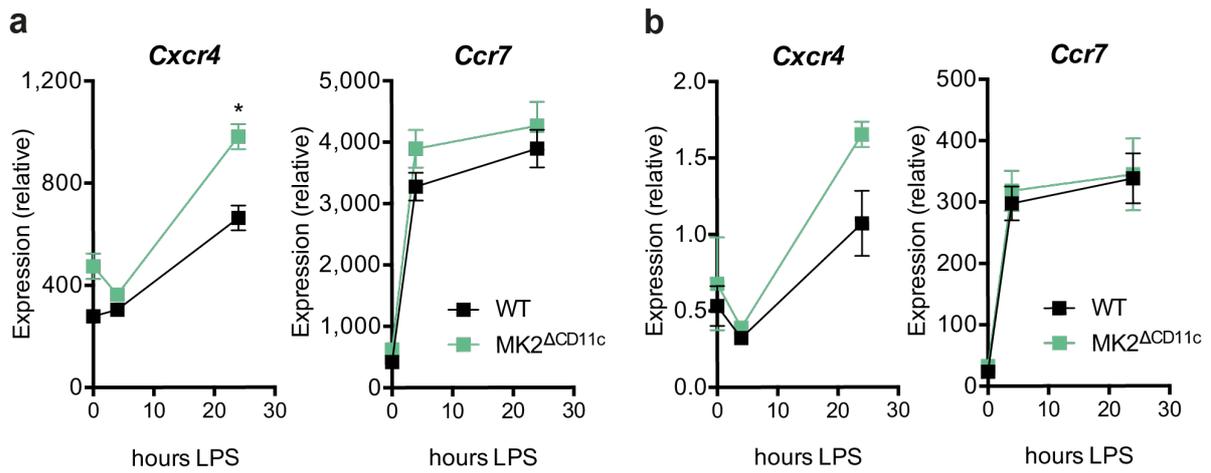
Supplementary Figure 2. Expression of immune suppressive genes in MDSCs is not affected by CD11c-targeted MK2 deletion. (a) Relative expression of *Arg1* in myeloid populations sorted from tumours and spleens of melanoma-bearing C57BL/6 WT mice determined by RT-qPCR and normalized to *Ubc* (n = 3). (b) Relative expression of *Arg1*, *Il10*, *Tgfb1* and *Mapkapk2* in MDSCs sorted from tumours of MK2^{ΔCD11c} and WT mice determined by RT-qPCR and normalized to *Ubc* (n = 4). Data are presented as mean ± SEM. *P*-values were determined using Mann-Whitney U test (not significant).



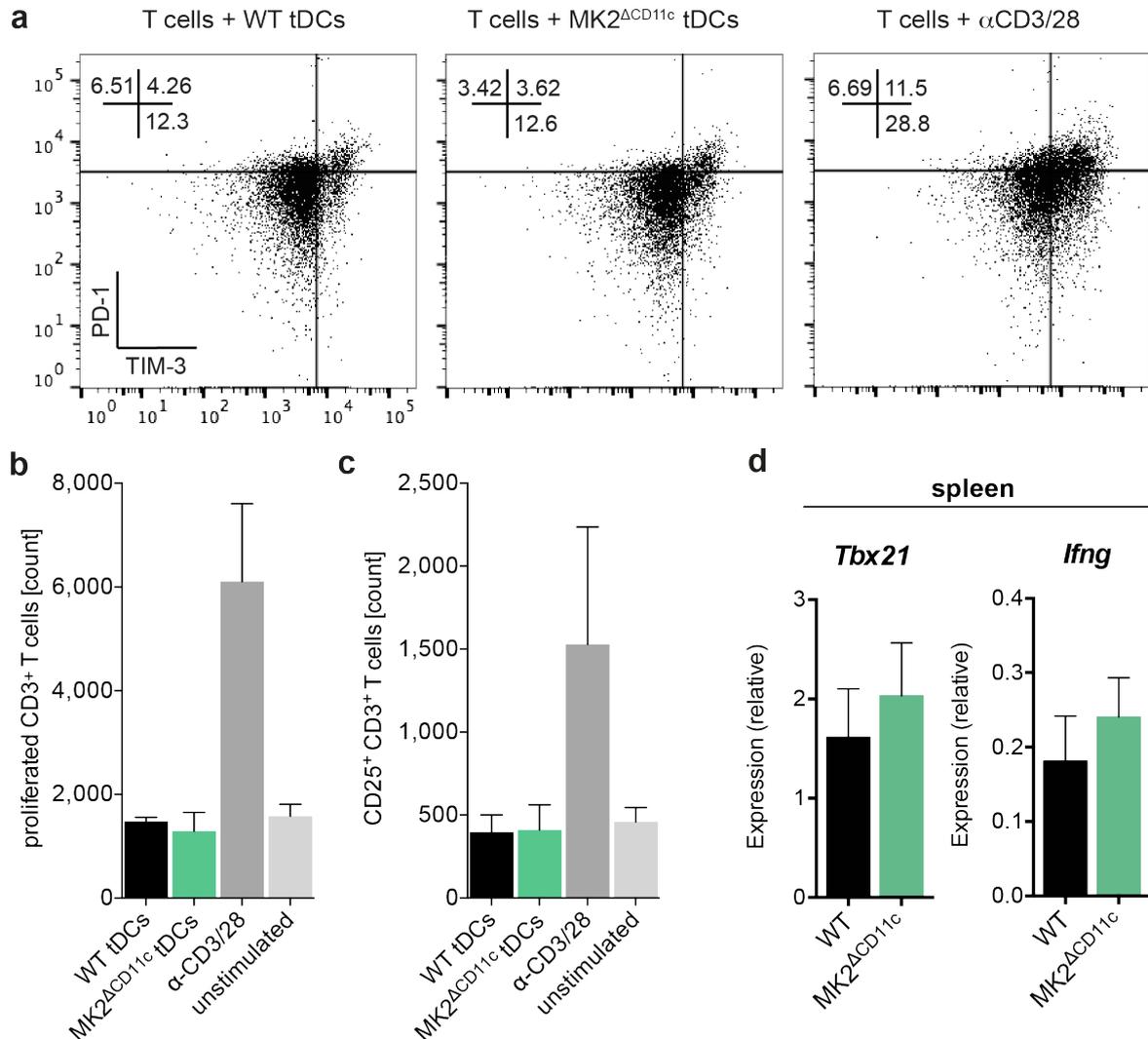
Supplementary Figure 3. Expression of various chemokines is differentially regulated in MK2-deficient DCs. (a) Expression of chemokines in splenic CD11c⁺ DCs of MK2^{ΔCD11c} and WT control mice stimulated over 24 hours with LPS by gene expression array. Differential normalized log₂ gene expression between genotypes at 0 (black circles), 4 (grey circles) and 24 hours (white circles) post-LPS stimulation is shown (n = 2). Genes printed in bold show significantly different expression levels between genotypes. (b-c) Kinetics of *Ccl3* and *Ccl4* expression in splenic CD11c⁺ DCs over 24 hours of LPS stimulation by (b) gene expression array and (c) RT-qPCR normalized to *Ubc* (n = 2). (d) Serum levels of CCL3 and CCL4 in melanoma-bearing MK2^{ΔCD11c} and WT mice measured by ProcartaPlex™ Multiplex Immunoassay (n = 5). Data are presented as mean ± SEM. n.d., not detectable. **P*<0.05, ***P*<0.01, ****P*<0.001. *P*-values were determined using (a-b, d) Student's *t*-test and (c) Mann-Whitney U test.



Supplementary Figure 4. CD103⁺ DCs in melanoma-bearing MK2^{ΔCD11c} mice exhibit a more stimulatory profile. (a) Representative flow cytometry histograms showing surface expression of MHC-II, CD80, CD86, PD-L1 and PD-L2 on tumour-resident CD103⁺ (blue) vs CD103⁻ (grey) DCs. Cells were pre-gated for live, single, CD45⁺, CD11c⁺ CD103⁺ or CD103⁻ cells. (b-c) Representative dot plots depicting frequency of (b) MHC-II- and CD80-expressing DC subpopulations and (c) MHC-II- and PD-L1-expressing DC subsets. Frequency within parental population is indicated (blue, CD103⁺ DCs; grey, CD103⁻ DCs).



Supplementary Figure 5. *Cxcr4* and *Ccr7* expression is enhanced upon MK2 deletion in DCs. (a-b) Kinetics of *Ccr7* and *Cxcr4* expression in splenic CD11c⁺ DCs over 24 hours of LPS stimulation by (a) gene expression array and (b) RT-qPCR normalized to *Ubc* (n = 2). Data are presented as mean \pm SEM. * $P < 0.05$. P -values were determined using (a) Student's t -test and (b) Mann-Whitney U test.



Supplementary Figure 6. CD11c-specific MK2 deletion renders T cells less exhausted and enhances Th1 polarization. (a) Representative dot plots depicting relative frequencies of PD-1- and TIM-3-expressing T cells after 5 days of co-culture with freshly isolated CD11c⁺ DCs from tumours of MK2^{ΔCD11c} and WT control mice. T cells stimulated with αCD3/28 Dynabeads served as activation control. Numbers indicate frequency within parental CD3⁺ population (n = 3). (b) Numbers of proliferated T cells after co-culture as analysed by flow cytometry (n = 3). (c) Numbers of CD25⁺ T cells after co-culture as analysed by flow cytometry (n = 3). (d) *Tbx21* and *Ifng* expression in frozen spleen tissue of tumour-bearing MK2^{ΔCD11c} and WT littermate control mice by RT-qPCR and normalized to *Ubc* (n = 10-15). Data are presented as mean ± SEM. tDC, tumour-infiltrating DC. *P*-values were determined using (b-c) Student's *t*-test and (d) Mann-Whitney U test (not significant).

Rearrangement	Productive Frequency (total)	Present in (samples)	Productive Frequency (MK2ΔCD11c)						Productive Frequency (WT)					
			KO1	KO2	KO3	KO4	KO5	KO6	WT1	WT2	WT3	WT4	WT5	WT6
CTTT...GTAC	1.334	4	0.000	0.000	0.000	0.200	0.094	0.000	0.000	0.993	0.000	0.047	0.000	0.000
TCTA...GTAT	1.295	2	0.000	0.000	0.000	0.798	0.000	0.000	0.000	0.496	0.000	0.000	0.000	0.000
TCAA...CTTC	1.505	2	1.310	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.195	0.000
GAGA...GTAT	12.543	2	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	11.954	0.000	0.588
GACC...CTAT	0.481	2	0.291	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.190	0.000	0.000
CATA...CTAT	1.532	2	0.291	0.000	0.000	0.000	0.000	0.000	0.000	1.241	0.000	0.000	0.000	0.000
CACT...CTAC	1.127	2	0.146	0.000	0.982	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ATTC...GTTC	0.735	2	0.000	0.000	0.000	0.000	0.000	0.000	0.501	0.000	0.234	0.000	0.000	0.000

Supplementary Table 1. Frequency of T cell receptor (TCR) clones occurring in more than one sample.