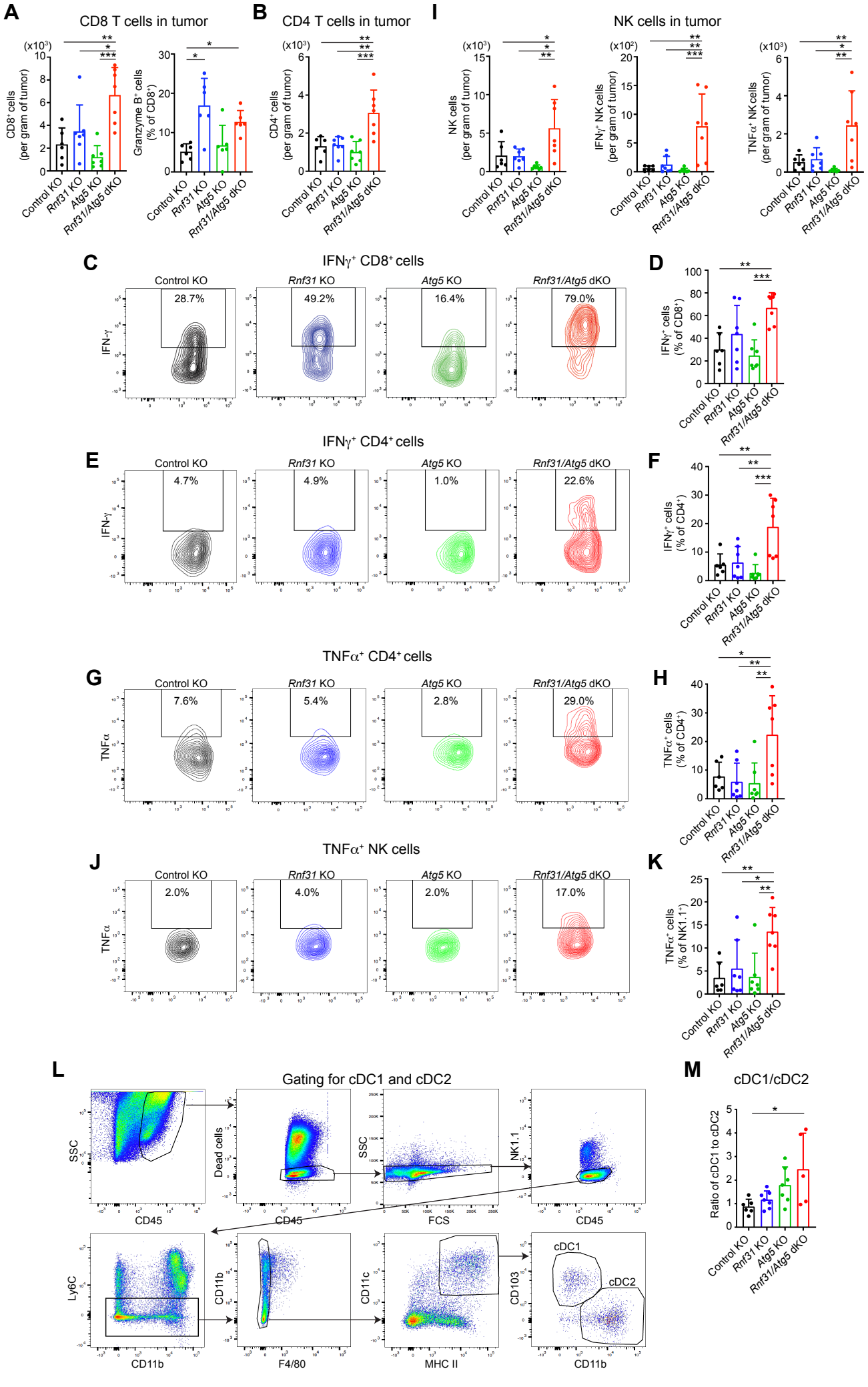
Figure S9


A
CD8 T cells in tumor
CD8⁺ cells (per gram of tumor)
Granzyme B⁺ cells (% of CD8⁺)
B
CD4 T cells in tumor
CD4⁺ cells (per gram of tumor)
I
NK cells in tumor
NK cells (per gram of tumor)
IFNγ⁺ NK cells (per gram of tumor)
TNFα⁺ NK cells (per gram of tumor)
Control KO
Rnf31 KO
Atg5 KO
Rnf31/Atg5 dKO
C
IFNγ⁺ CD8⁺ cells
28.7%
49.2%
16.4%
79.0%
IFN-γ
D
IFNγ⁺ cells (% of CD8⁺)
E
IFNγ⁺ CD4⁺ cells
4.7%
4.9%
1.0%
22.6%
F
IFNγ⁺ cells (% of CD4⁺)
G
TNFα⁺ CD4⁺ cells
7.6%
5.4%
2.8%
29.0%
TNFα
H
TNFα⁺ cells (% of CD4⁺)
J
TNFα⁺ NK cells
2.0%
4.0%
2.0%
17.0%
K
TNFα⁺ cells (% of NK1.1⁺)
L
Gating for cDC1 and cDC2
SSC
CD45
Dead cells
FCS
NK1.1
Ly6C
CD11b
F4/80
CD11c
MHC II
CD103
cDC1
cDC2
M
cDC1/cDC2
Ratio of cDC1 to cDC2

Supplementary Fig. S9. Enhanced IFNγ and TNFα expression by T cells and NK cells in *Rnf31/Atg5*-dKO tumors

B2m+/+ B16 exp-KO tumor cells ($5x10^5$ cells) were injected subcutaneously, and tumor infiltrating immune cells were analyzed on day 14.

(**A**) Absolute number of CD8 T cells per gram of tumor and percentage of granzyme B+ cells among total CD8 T cells.

(**B**) Absolute number of CD4 T cells per gram of tumor.

(**C-D**) Representative flow cytometry plots of IFNγ expression by CD8 T cells (**C**) and summary of percentage of IFNγ+ cells among total CD8 T cells across tumors with the indicated gene edits (**D**).

(**E-H**) Representative flow cytometry plot of IFNγ or TNFα expression by CD4 T cells (**E, G**) and summary of percentage of IFNγ+ or TNFα+ cells among total CD4 T cells across tumors with the indicated gene edits (**F, H**).

(**I**) Absolute numbers of NK cells, IFNγ+ NK cells and TNFα+ NK cells per gram of tumor.

(**J-K**) Representative flow cytometry plot of TNFα expression by NK cells (**J**) and summary of percentage of TNFα+ cells among NK1.1+ cells across tumors with the indicated gene edits (**K**).

(**L**) Gating strategy for quantification of cDC1s and cDC2s.

(**M**) Ratio of cDC1s to cDC2s in tumors with the indicated gene edits.

Data are representative of two experiments and depicted as the mean ± SEM (n = 5-7 mice/group). Statistical significance was assessed by a one-way ANOVA with Tukey's multiple comparison test. ***p <0.001; **p <0.01; *p <0.05; NS, not significant.