

Supplementary Data

Legends to Supplementary Figures

Fig. S1: Gating strategy for the quantification of macrophages, B cells, and T cells. Total macrophages were evaluated using CD11b, Gr1, and F4/80 staining. Immunostimulatory macrophages were identified based on MHC II staining. B cells were evaluated using CD19 staining. T cells were evaluated using CD3, CD4, and CD8 staining. Effector T cells were evaluated using CD44 and CD62 staining.

Fig. S2: Immune composition of early-stage and late-stage MYCN amplified murine neuroblastoma tumors. FACS plots showing intratumoral CD11b+ myeloid cells, CD11b+Gr1- monocytes and CD11b+Gr1+ granulocytes, CD3+ T cells, CD4+ T cells, and CD8+ T cells in early-stage and late-stage murine NB9464 tumors.

Fig. S3: Macrophages foster NB progression: **A.** NB9464 cells were subcutaneously implanted in C57BL/6 WT mice (n = 5 mice/ gp) and treated with 50mg/kg anti-CSF1R antibody (administered intraperitoneally, every alternate day, until tumors were harvested) or ULTRA-LEAF™ purified mAb (SA271G2) (250µg, administered once on day 10). Fig. shows the tumor volume of NB9464 tumors treated with anti-CSF1R ab or B cell depleting mAb (SA271G2). **B.** FACS quantification of CD11b+ F4/80 + macrophages in NB9464 tumors treated with anti-CSF1R mAb. **C.** FACS quantification of CD19+ B cells in NB9464 tumors treated with anti-CD20 mAb.

Fig. S4: Syk inhibition has no effect on the viability of NB cell lines: Cell viability assay showing no effect of Syk inhibitor R788 on the proliferation of SKNBE2 (A), IMR32 (B), and NB9464 (C) cells.

Fig. S5: Syk inhibition has no impact on T cell proliferation *ex vivo*: **A-B.** T cell proliferation *ex vivo* in CD90+T cells isolated from Syk^{MC-WT} and Syk^{MC-KO} mice or C57BL/6 WT mice and treated *ex vivo* with 500 nM R788.

Fig. S6. Gating strategy for the quantification of PDL1 + TAMs and tumor cells.

Table S1: List of differentially expressed genes in Syk^{MC-WT} and Syk^{MC-KO} TAMs, BMDMs stimulated with TCM media and treated with 500 nM R788, Vehicle NB9464 tumors, R788+ anti-PDL1-treated tumors and Radiation + R788 + anti-PDL1-treated NB9464 tumors.

Table S2: Patient characteristics for the samples used for immunohistochemistry studies.

References:

1. Dobin, A., et al., *STAR: ultrafast universal RNA-seq aligner*. *Bioinformatics*, 2013. **29**(1): p. 15-21.
2. Heinz, S., et al., Simple combinations of lineage-determining transcription factors prime cis-regulatory elements required for macrophage and B cell identities. *Mol Cell*, 2010. **38**(4): p. 576-89.
3. Dean, C.B. and J.D. Nielsen, Generalized linear mixed models: a review and some extensions. *Lifetime Data Anal*, 2007. **13**(4): p. 497-512.
4. Ritchie, M.E., et al., limma powers differential expression analyses for RNA-sequencing and microarray studies. *Nucleic Acids Res*, 2015. **43**(7): p. e47.
5. Kolde, R., et al., Host genetic variation and its microbiome interactions within the Human Microbiome Project. *Genome Med*, 2018. **10**(1): p. 6.

Fig. S1

A

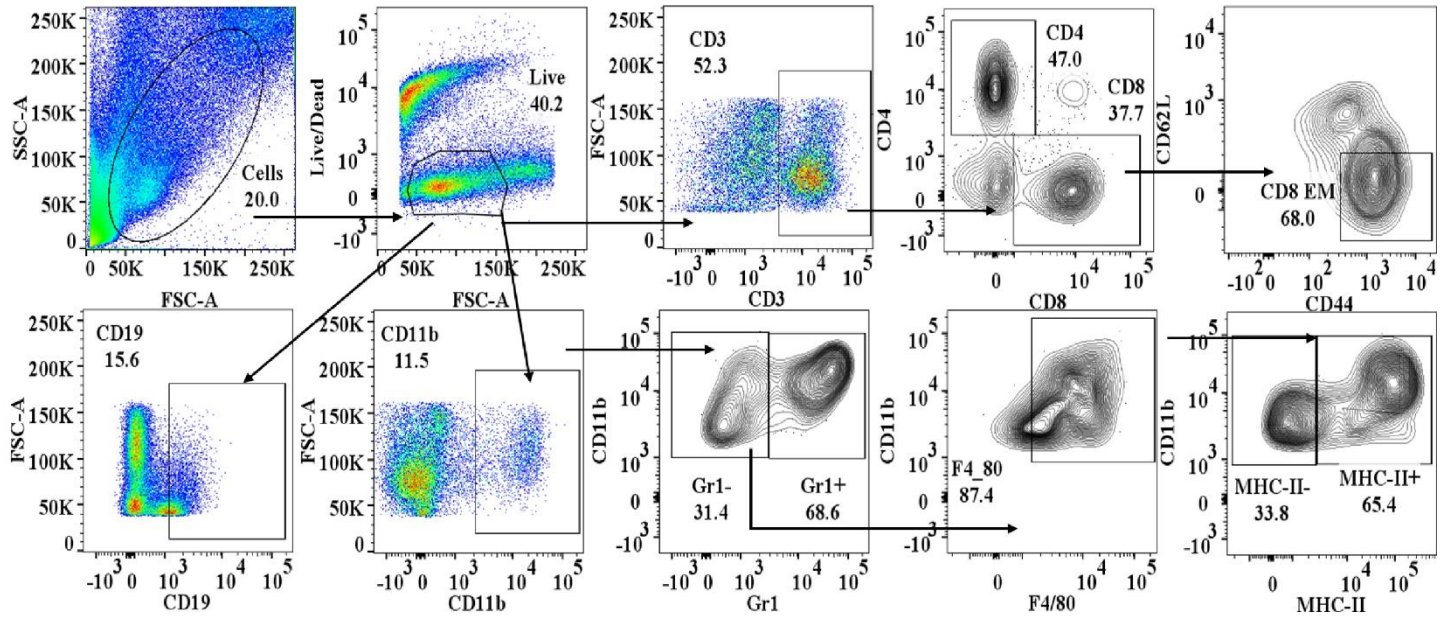


Fig. S2

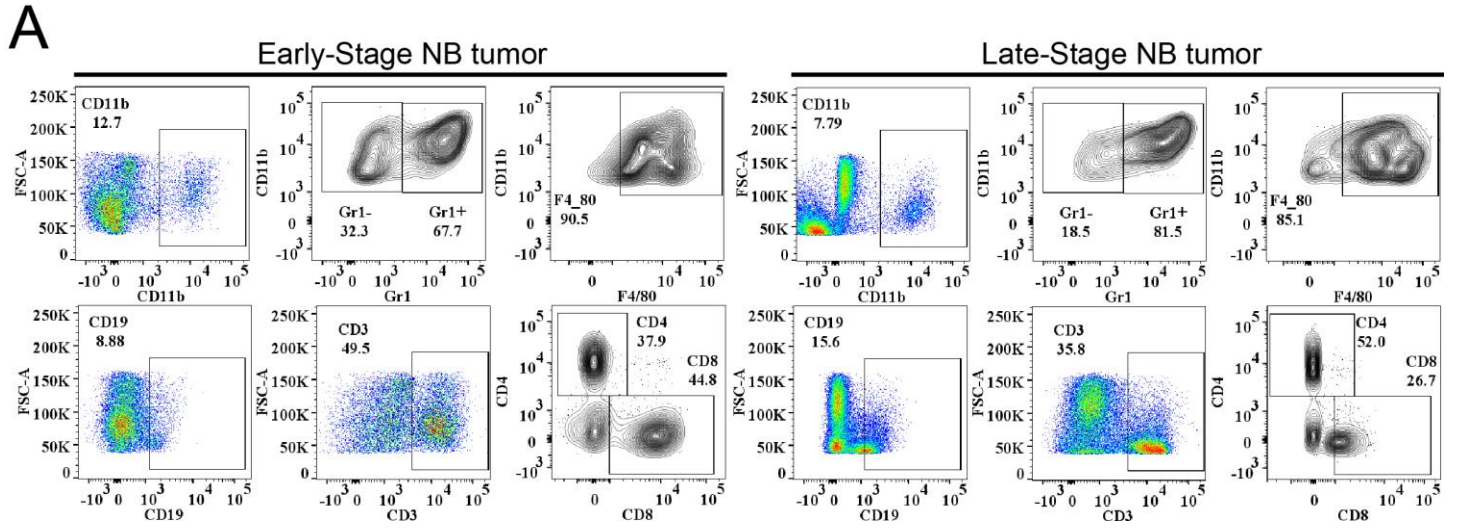


Fig. S3

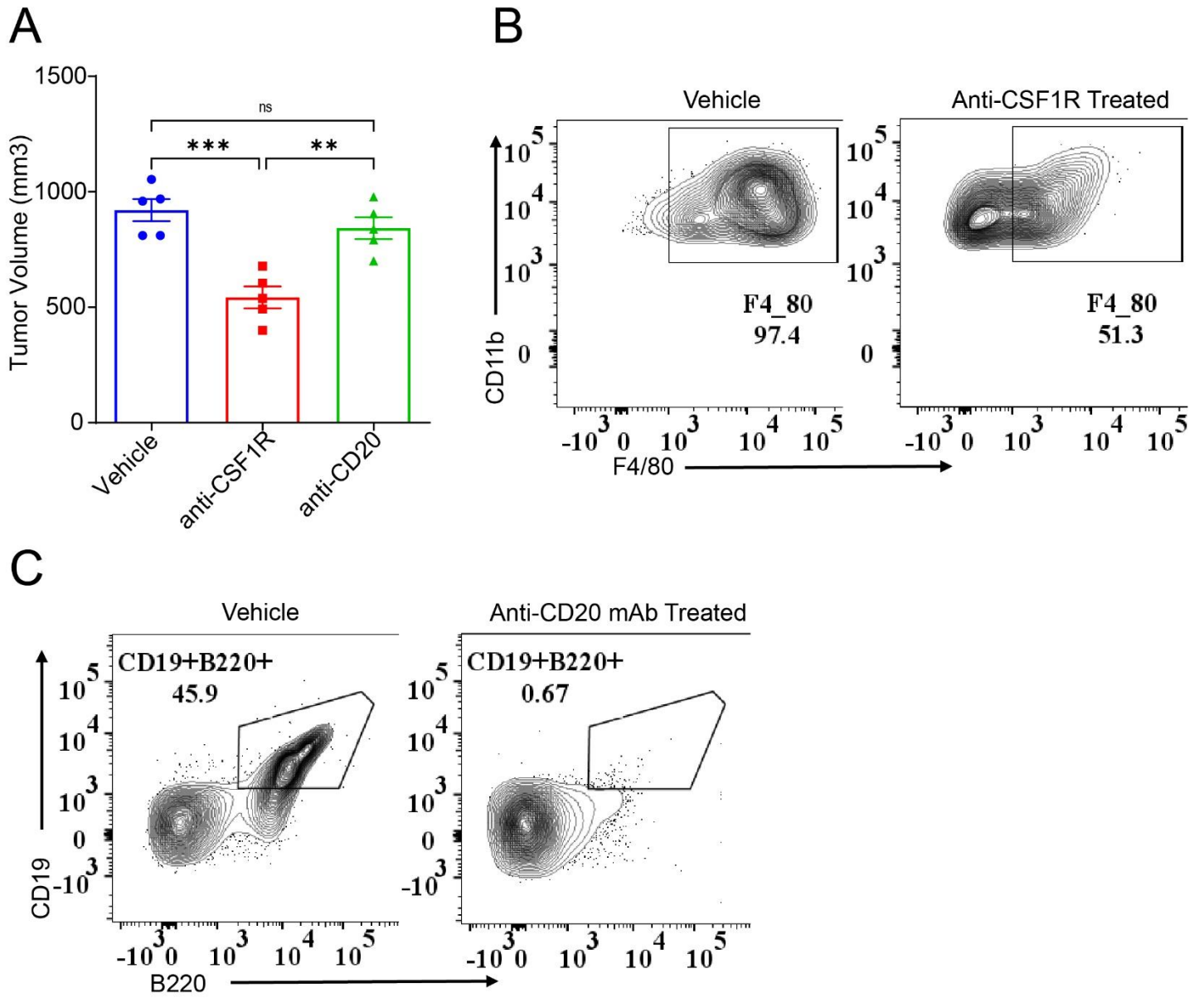


Fig. S4

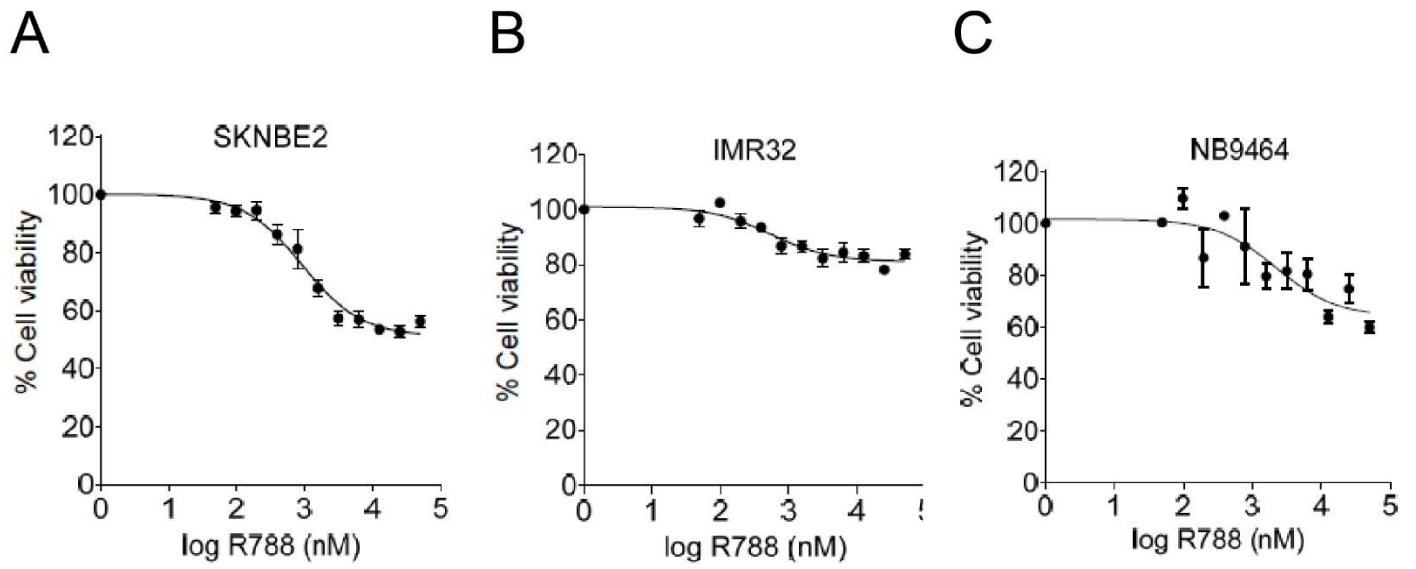
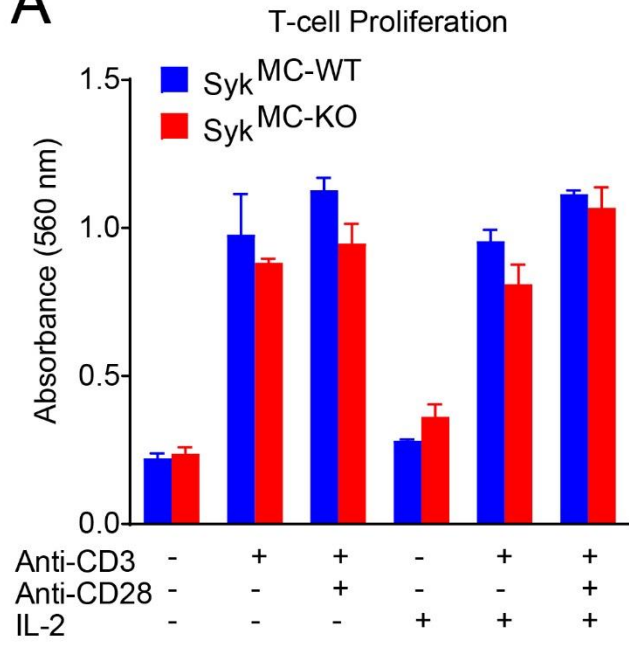


Fig. S5

A



B

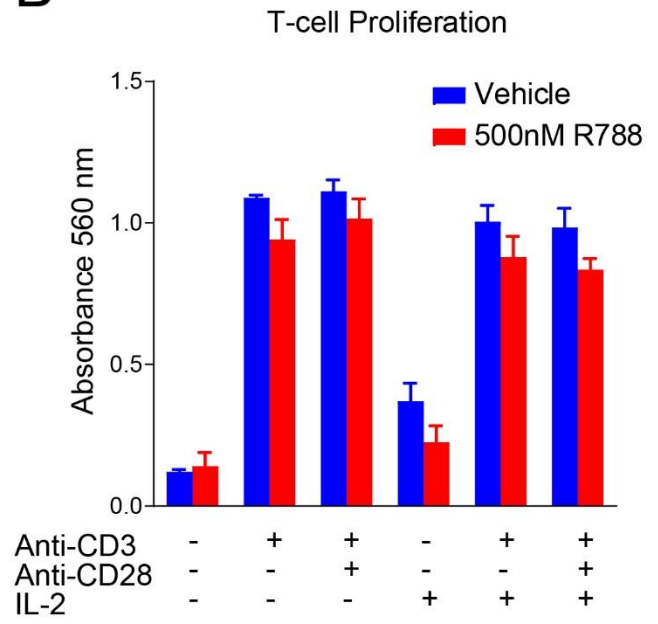


Fig. S6

A

