SUPPLEMENTARY METHODS

Multiplex Immunohistochemistry

For Fig. S8G, the staining procedure was performed on a VENTANA Discovery Ultra instrument. The tissues were deparaffinised and rehydrated using EZ prep solution (Ventana Medical Systems, Tucson, USA) in 3 cycles of 8 min each for a total of 24 min at 69 °C. Antigens were retrieved using CC1 buffer (Ventana Medical Systems, Tucson, USA) for 32 min at 95 °C. Then, the primary antibody was diluted in antibody diluent/block (Akoya Biosciences, Marlborough, USA), added manually to the slides and incubated for 32 min at 36 °C or RT. The matching OmniMap horse radish peroxidase secondary antibody (Ventana Medical Systems, Tucson, USA) was automatically applied for 12 min. Subsequently, the Opal TSA fluorophore (Akoya Biosciences, Marlborough, USA) was diluted in amplification diluent (Akoya Biosciences, Marlborough, USA), added to the sections manually and incubated for 8 min. A denaturation step was performed at 100 °C for 24 min in CC2 buffer (Ventana Medical Systems, Tucson, USA) to remove primary and secondary antibodies. All steps, from primary antibody to stripping, were repeated for each marker until a 3-plex staining was achieved. The sections were then counterstained with DAPI (Merck, Darmstadt, Germany), washed and mounted using Fluoromount-G mounting medium (SouthernBiotech, Birmingham, USA). Primary antibodies used: Axl (AF854, R&D Systems, 1:100), Iba1 (NBP2-19019, NovusBiologicals, 1:100) and GFP (ab6673, abcam, 1:350). Detection was carried out using TSA fluorophores Opal 570 (1:250), Opal 520 (1:100), Opal 570 (1:100) and Opal 650 (1:100), respectively. Multispectral images were obtained using the Vectra 3.0 Automated Imaging System (Akoya Biosciences, Marlborough, USA). Spectral unmixing was performed in inForm (Akoya Biosciences, Marlborough, USA), using a previously built library consisting of single stained tissue slides for each TSA fluorophore.

Generation of *Gas6***-deficient NSG Mice by CRISPR-editing of NSG Zygotes**

Immune-compromised *Gas6*-deficient mice were generated by inactivation of the *Gas6* gene using CRISPR-Cas9 editing in *NOD.Cg-Prkdc^{scid} IL2rgtmWjl/Sz* (NSG) zygotes, as indicated in Supplementary Fig. S3C, using a workflow that was previously described by our group (1). Briefly, gRNA targeting exon 2 of the *Gas6* gene, Cas9 mRNA (5meC, Psi) (Tebu-Bio# L- 6125-100) and a single strand DNA donor template were microinjected in NSG zygotes. The ssDNA template was designed to introduce an in-frame stop codon, an EcoRI restriction site and a mutation in the PAM sequence. The EcoRI site was used to screen edited mice by RFLP (Restriction Fragment Length Polymorphism) assay. All primers used are described in the key resources table. Mutation of the PAM site was used to prevent secondary editing of any productively edited allele. Insertion of the stop codon in an early translated exon expectedly halted translation thereby inducing non-sense mediated mRNA decay (NMD) leading to absence of Gas6 protein, as demonstrated by ELISA, in all four newly generated Gas6 homozygous edited mouse lines (line 697-21, 27, 29 and 31; Supplementary Fig. S3D). Experiments were carried out using NSG *Gas6^{-/-}* lines #29 and #31 with indistinguishable results (Figure 1N and Supplementary Figure S3E). Editing at predicted off-target sites was excluded by amplicon sequencing as described previously (1). Genome editing of NSG zygotes using CRISPR/Cas9 was approved by the Regierungspräsidium Karlsruhe under animal protocol number G50/15.

Generation of Syngeneic Leukemia Models

The Asxl1 myeloid leukemia model was established by serially transplanting spleen cells from a mouse that developed disease symptoms 39 weeks after inducible ablation of *Asxl1* selectively in hematopoietic cells. Briefly, aged $MxCre^+ Asx/1^{tf}$ mice (50 weeks) were treated with polyinosinic-polycytidylic acid (pI:pC) (InvivoGen) every other day at a dose of 20 mg/kg of body weight, and followed for signs of disease by monthly bleeding. Over an additional period of 39 weeks, 4 out of 5 mice remained symptoms free with white blood counts within normal range. One mouse (#83501) however developed disease symptoms with prominent expansion of immature blasts with significantly reduced *Asxl1* expression as shown by real time PCR and an aberrant CD11b^{dim}B220^{dim} surface phenotype (Supplementary Fig. S1C). H&E staining of the spleen and liver, as well as myeloperoxidase staining in the liver, demonstrated massive infiltration of both organs by immature myeloblasts as well as limited signs of extramedullary hematopoiesis in the spleen as shown by prominent erythroid cell clusters and detectable megakaryocytes. However, no mature granulocytes were detected (Supplementary Fig. S1D). Most importantly the disease was serially transplantable, using spleen cells from the primary mouse, to non-irradiated recipients with a penetrance that was dependent on the cells dose injected (Supplementary Fig. S1E). Non-irradiated recipient mice displayed massive hepatosplenomegaly (Supplementary Fig. S1F) with massive infiltration of spleen and liver by blast cells (Supplementary Fig. S1G) as well as a high number of circulating blasts as evidenced by Pappenheim's staining of peripheral blood smears (Supplementary Fig. S1H). Bio-banked cells from the spleens of the primary and secondary wild type recipients were used for all experiments described in this study. Secondary and tertiary recipients showed comparable hepatosplenomegaly and high number of circulating myeloblasts in the peripheral blood (Supplementary Fig. S1H)

Primary BCR-ABL1-driven B-cell acute lymphoblastic leukemia (Ph⁺ B-ALL) were generated by isolating untreated bone marrow cells from *Arf-/-* mice (The Jackson Laboratories, line #029676) and subsequently subjecting them to *ex-vivo* spin infection (3000 rpm, 33C, 2h) in IMDM media (Gibco) supplemented with 20 ng/ml recombinant mouse IL7 (Peprotech) and 4.5 µg/ml polybrene (Merck Millipore), using a retrovirus expressing both the human BCR-ABL1^{p190} fusion oncoprotein and the green fluorescent protein (GFP) that serves as a reporter for BCR-ABL1 expression (MSCV-BCR-ABL1-IRES-GFP; gift from Dr. Jacques Ghysdael). After transduction these cells were transferred to lethally irradiated (9 Gy) wild type C57BL/6 host recipients. All mice developed full blow precursor B-ALL within 30-60 days (data not shown). Bone marrow cells from these primary mice exhibited high frequency of GFP⁺B220^{dim} B-ALL blasts. Bone marrow cells from several primary mice were explanted and *in vitro* adapted by culturing on MS5 mesenchymal stromal cells in RPMI containing 15% FBS, 1% penicillin-streptomycin, 1% L-Glutamine and 10mM HEPES. After a short adaptation period on MS5 cells, primary leukemic cells could be expanded and maintained as independent primary GFP⁺ leukemic lines (L1, L2, L3) in a stroma-independent fashion and serially transplanted in non-irradiated mice as depicted by the Kaplan-Meier survival analysis of recipient mice transplanted with a 10³ GFP⁺ B-ALL cells from $n = 3$ independent primary leukemia lines (L1, L2 and L3) in Supplementary Fig. S1J. For all established B-ALL lines, disease penetrance was 100% after transplantation of as little as $10³$ cells to non-irradiated recipients. Latencies were also comparable for all established leukemia, with a median survival between 12 and 20 days (Supplementary Fig. S1J and data not shown).

KEY RESOURCES

Supplementary References

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