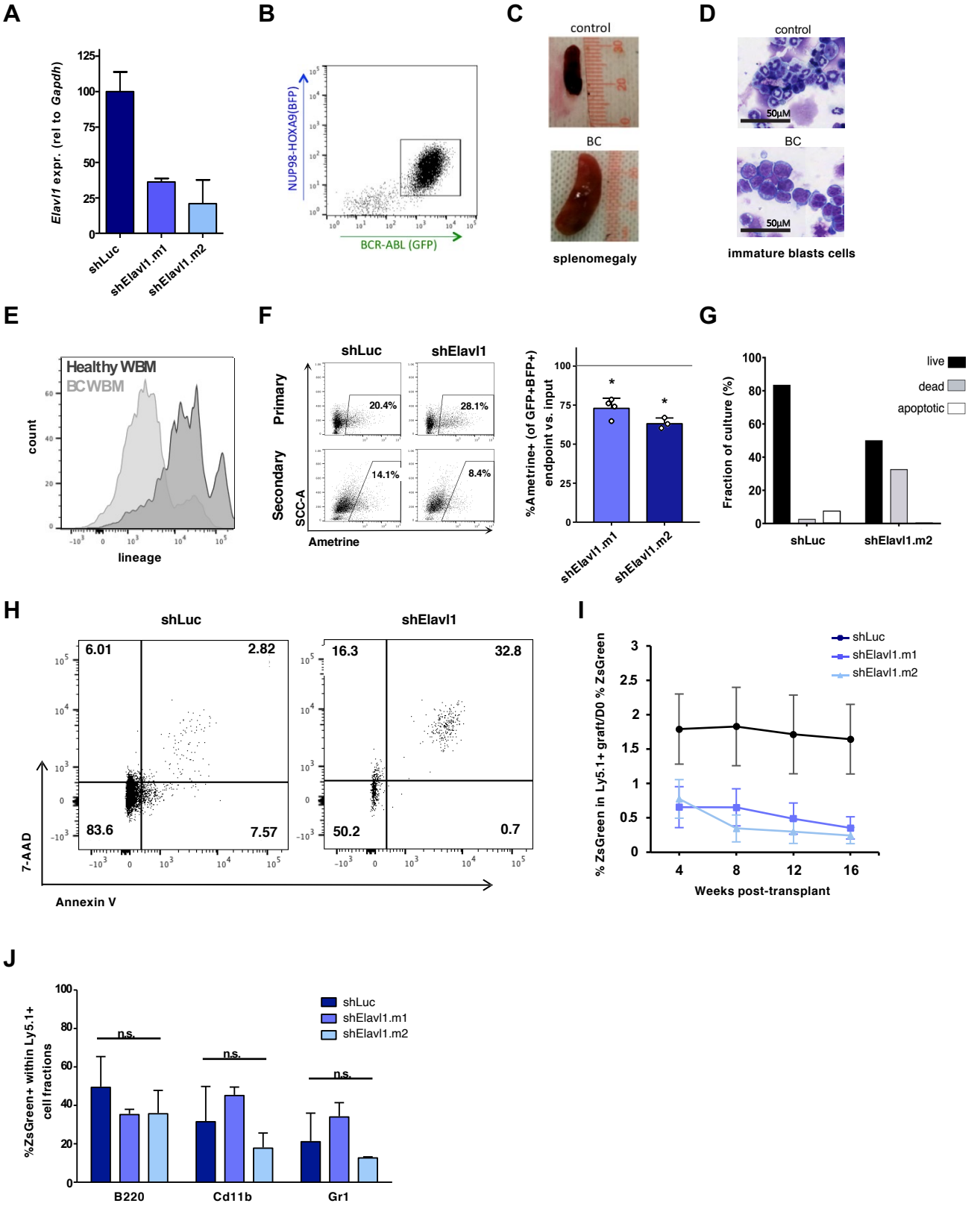
Supplemental Figure S3



Supplemental Figure S3. Generation of mouse myeloid leukemia models and analysis of Elavl1 knockdown in murine healthy versus malignant hematopoietic cells. (A) qPCR knockdown validation of shElavl1.6 and shElavl1.7 Ametrine+ cells in primary mouse BM. Data is normalized to *Gapdh*. (B) B6.SJL LSK cells were retrovirally infected with NUP98-HOXA9-BFP and BCR- ABL-GFP. $BFP^{+}GFP^{+}$ cells isolated 48h post-infection were transplanted into C57Blk/6 recipients. Flow cytometric evaluation of endpoint blast- crisis BM grafts (10 days post- transplantation) is shown. (C, D) Splenomegaly (C) and infiltration of BM with immature blast cells (Wright-Giemsa staining of peripheral blood sampled from primary engrafted recipient mouse) (D) indicate advanced stages of disease (blast-crisis) 10 days PT. Scale bars of 50μM are shown. (E) Flow cytometric evaluation of recipient mice whole BM (WBM) at blast-crisis shows a drastic decrease in lineage positive cells as compared to WBM from healthy mice (control). *$p < 0.05$ as determined by a two-sided Student's t test. (F) Output vs. input analysis of the Ametrine+ fraction of shElavl1 transduced BC CML BM. $GFP^{+}BFP^{+}$ BM was analyzed at the endpoint of secondary transplantation; data is normalized to shLuciferase (dotted line). Representative flow plots are shown at left. (G) Fraction of apoptotic cells was measured in shLuciferase- and shElavl1- transduced BC CML cultures, 3 days post-infection. Flow plots are shown in (H). (I) Percentage of ZsGreen+ cells within Ly5.1+ fractions in peripheral blood (PB) samples at 4-week intervals post-transplant relative to the percent of $ZsGreen^{+}$ cells at day 0 (D0). (J) Quantification of lineage marker expression in 18-week endpoint BM grafts initiated by shLuciferase, shElavl1.6- or shElavl1.7-transduced cells.