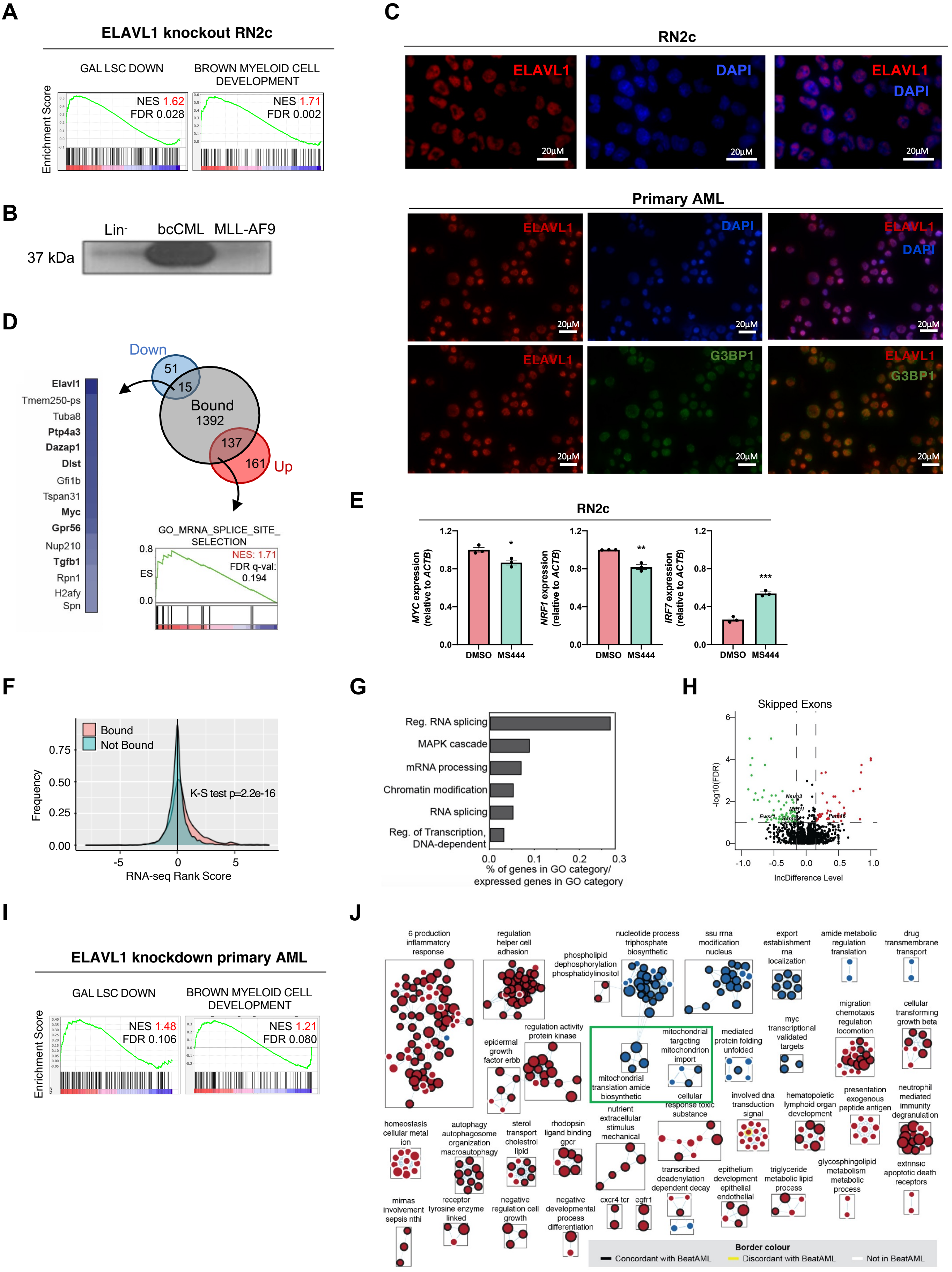
Supplemental Figure S6



Supplemental Figure S6: Characterization of ELAVL1 targets and global influence on the transcriptional landscape. (A) GSEA plots showing LSC and myeloid signature enrichments in the Elavl1-knockout RN2c transcriptome. (B) Western blot of Elavl1 in murine Lin^{-}, bcCML and MLL-AF9 cells. (C) Immunofluorescent microscopy of ELAVL1, nuclear marker (DAPI) and cytoplasmic marker (G3BP1). Scale bars of 20µM are shown. (D) Summary of intersection of transcripts bound (grey) and differentially expressed (up=red, down=blue, p. adj <0.05) upon Elavl1-deletion. (E) qPCR of ELAVL1 targets in RN2c 24-72h post-treatment with 2.2uM MS-444 or vehicle control (DMSO). (F) Expression distribution of bound and not bound transcripts in Elavl1-knockout RN2c cells. (G) GO term enrichment analysis for transcripts both bound and differentially expressed (p adj <0.05) upon Elavl1-deletion. (H) Volcano plot of differential exon skipping in ELAVL1 knockout RN2c cells, >15% inclusion and exclusion at FDR<0.1 indicated in red and green respectively. (I) GSEA plots of LSC and myeloid signature enrichments in AML. (J) Enrichment map of pathways significantly (FDR<0.1) changed in human AML following ELAVL1 knockdown with borders demarcating concordance/discordance with enrichments from below-median expressors of ELAVL1 from the BeatAML data set.