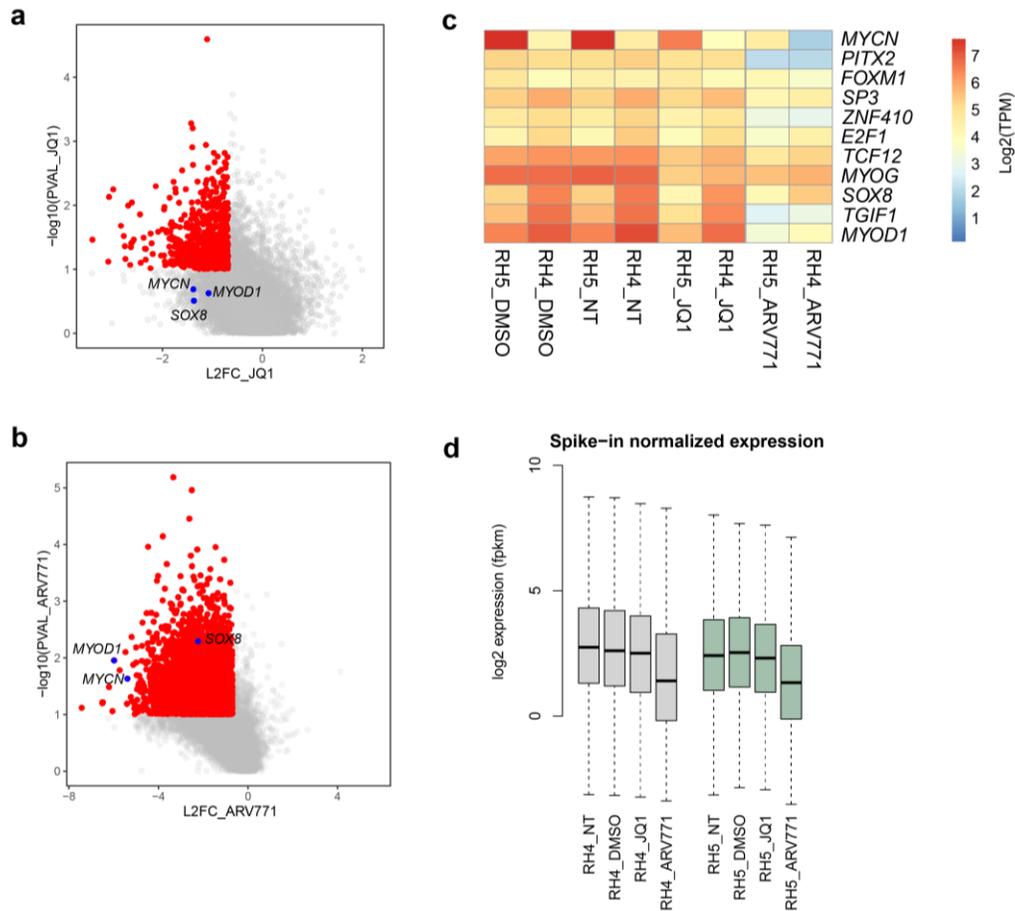


Supplemental figures for

BET bromodomain degradation disrupts function but not 3D formation of RNA Pol2 clusters

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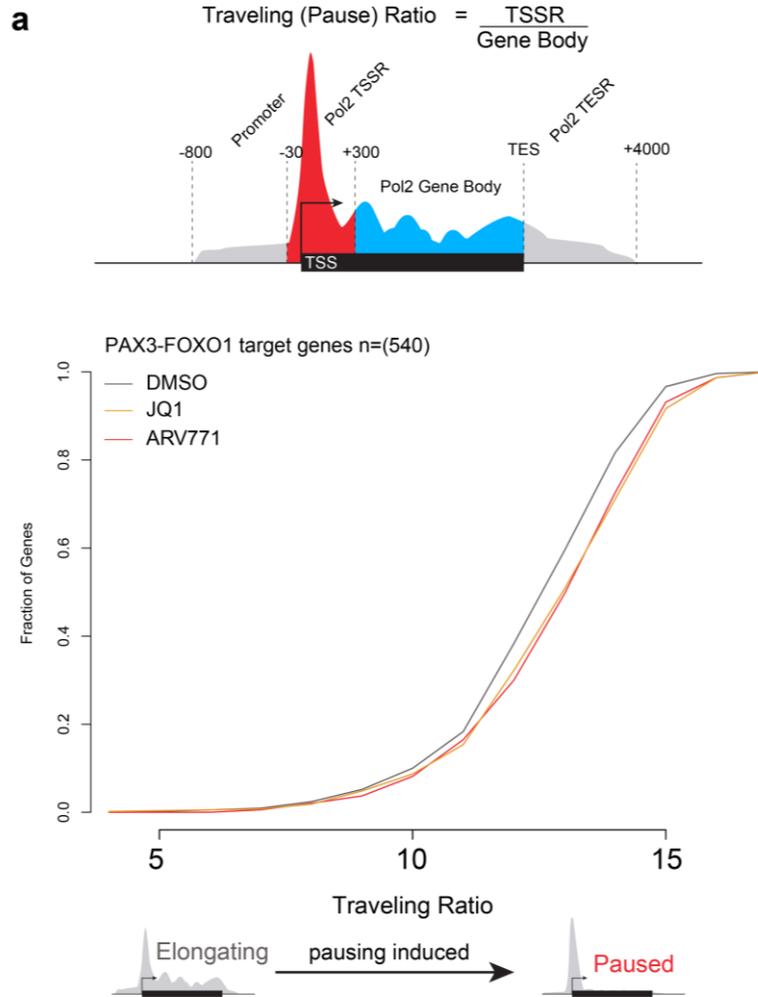


Supplemental Figure S1: Gene expression following loss of BET bromodomain proteins shows global decrease with degradation, but not inhibition.

a-b. Genes are plotted based on log₂ fold change (L2FC) and the negative log₁₀ of the p-value comparing TPM with JQ1 (a) or ARV-771 (b) treatment to TPM with DMSO treatment. Each gene is represented by one dot. Genes with L2FC less than -1 (fold-change < 0.5) and -log₁₀(p-value) greater than 1 (p-val < 0.1) are shown in red. CRTFs MYOD1, MYCN, and SOX8 are highlighted.

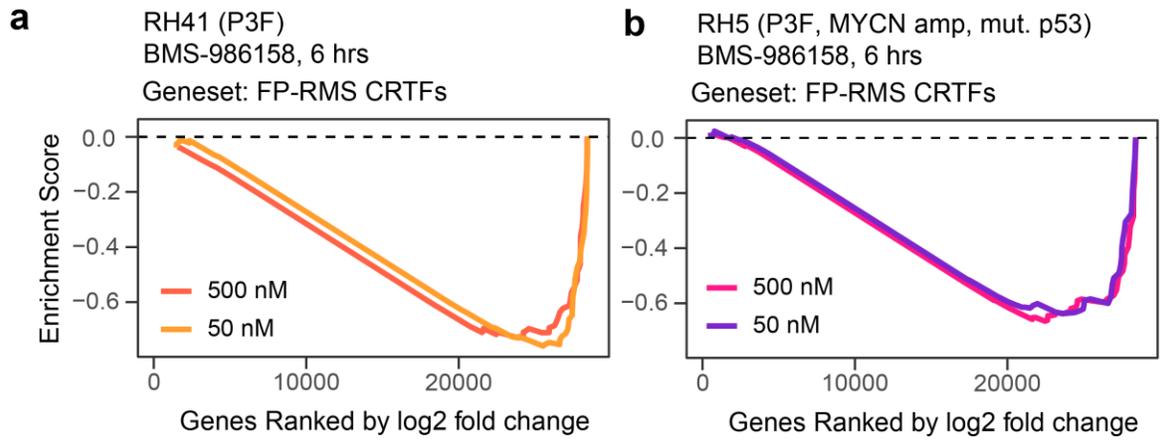
c. Heatmap with log₂ of total TPM for key genes in RH4 and RH5 treated with DMSO, JQ1, or ARV771. Red represents more transcripts, blue represents fewer. RH5 harbors amplified MYCN.

d. Boxplot with log₂ of total FPKM for RH4 (gray) and RH5 (green) treated with DMSO, JQ1, or ARV771.



Supplemental Figure S2: Pol2 distribution within P3F targets upon the loss of BET bromodomain proteins.

a. Diagram of RNA Pol2 distribution as measured by the traveling ratio in a set of P3F target genes for RH4 cells treated with DMSO, JQ1, or ARV771. The traveling ratio is calculated by the ratio of reads at the transcriptional start site region (-30 to +300bp from the TSS) and the gene body (+300 from TSS to TES).



Supplemental Figure S3: BMS-986158 gene expression response in FP-RMS.

(a) Gene set enrichment analysis (GSEA) of RH41 and (b) RH5 cells treated shows strong downregulation of FP-RMS CRTFs following BMS-986158 treatment.