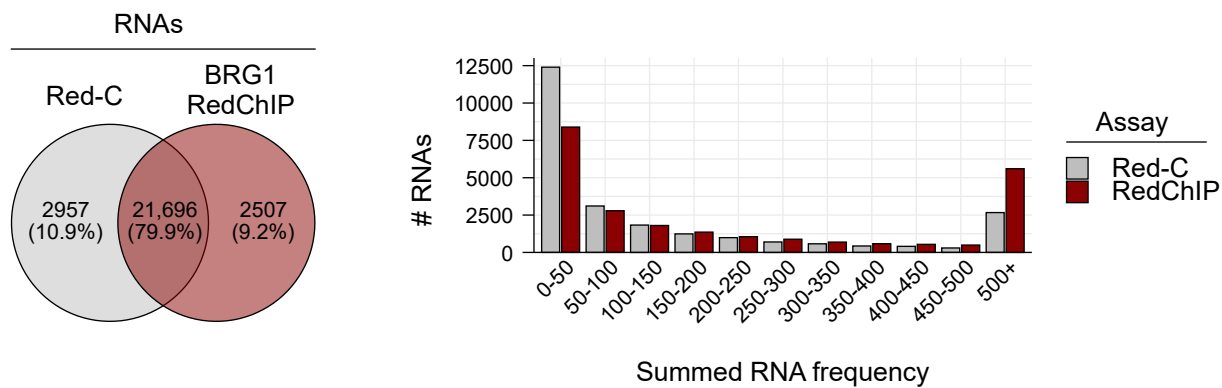
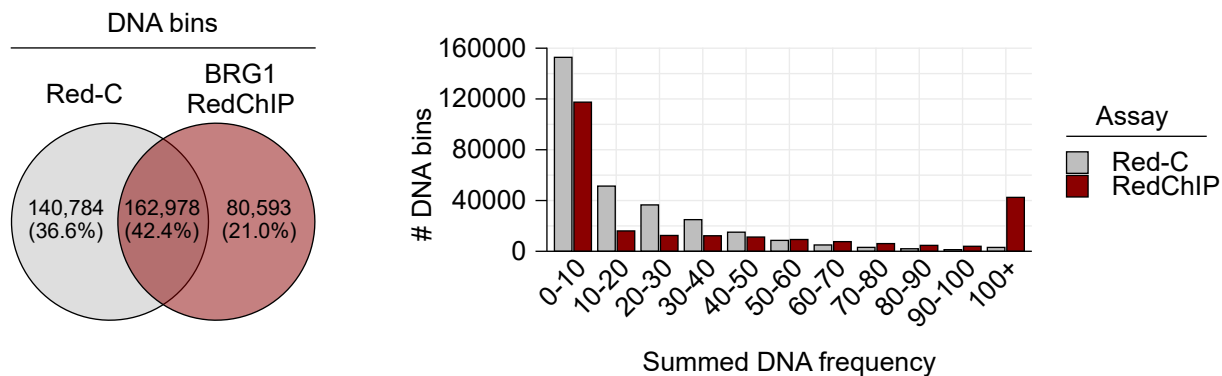
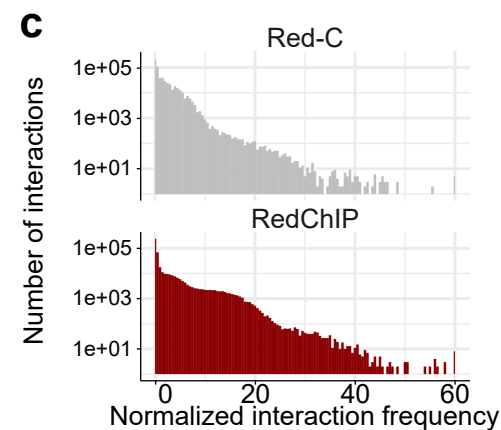
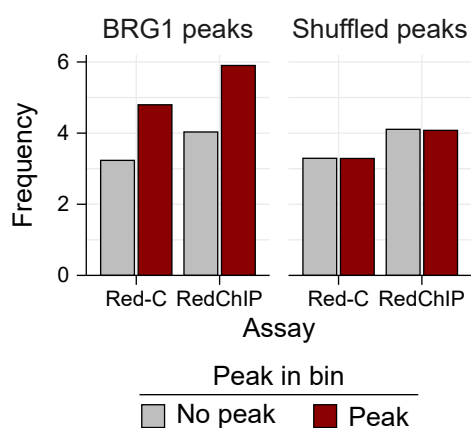
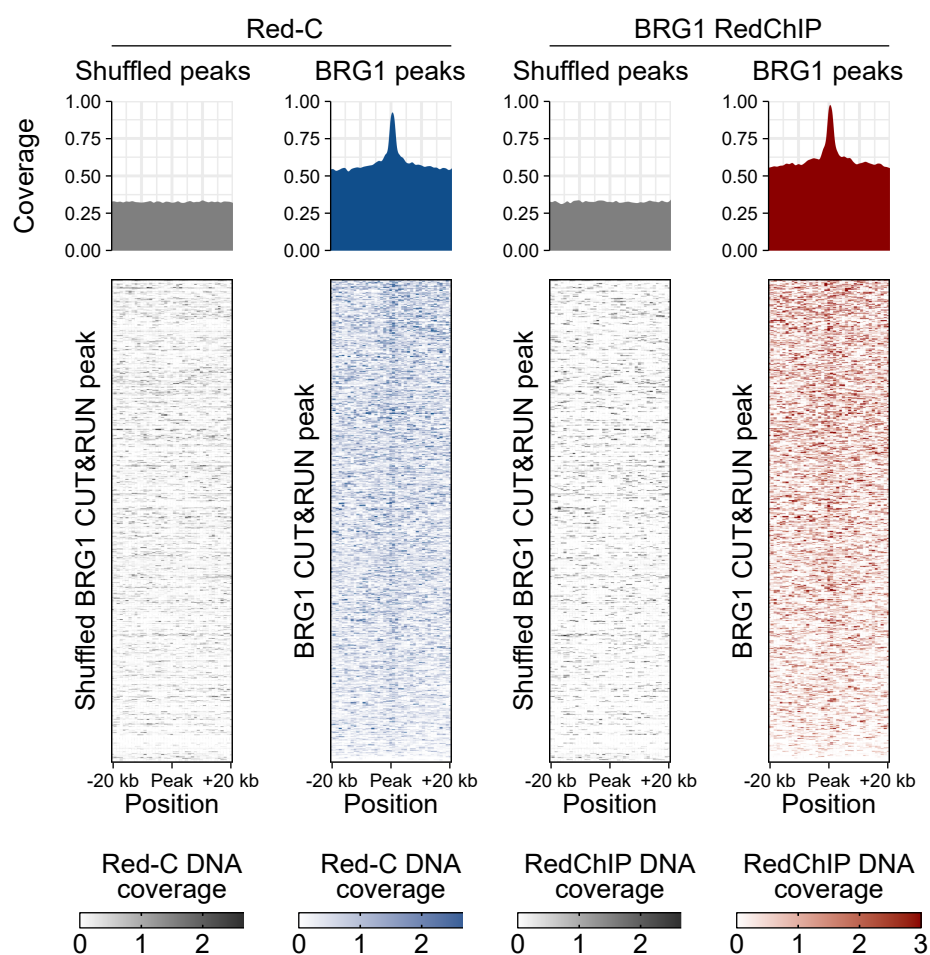


a**b****c****d****e****Supplementary Fig. 1 | BRG1 RedChIP and CUT&RUN**

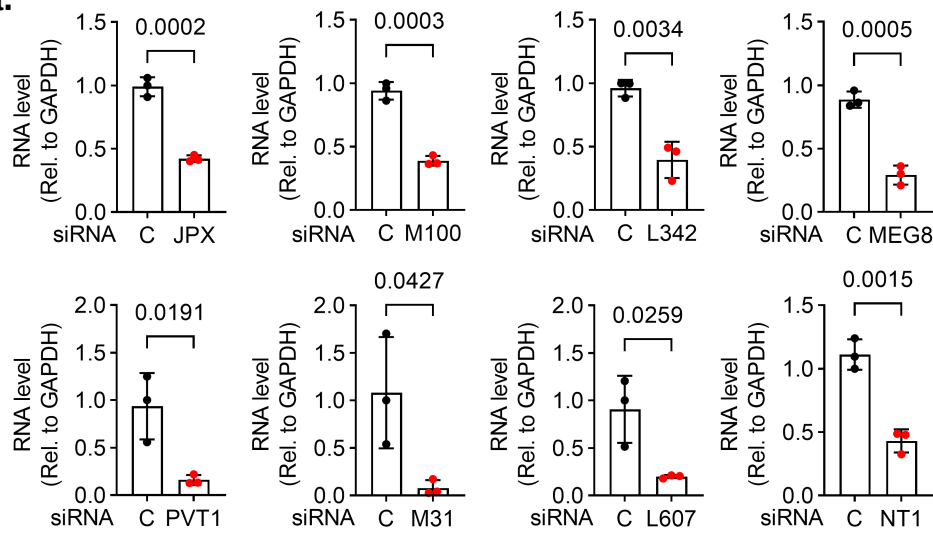
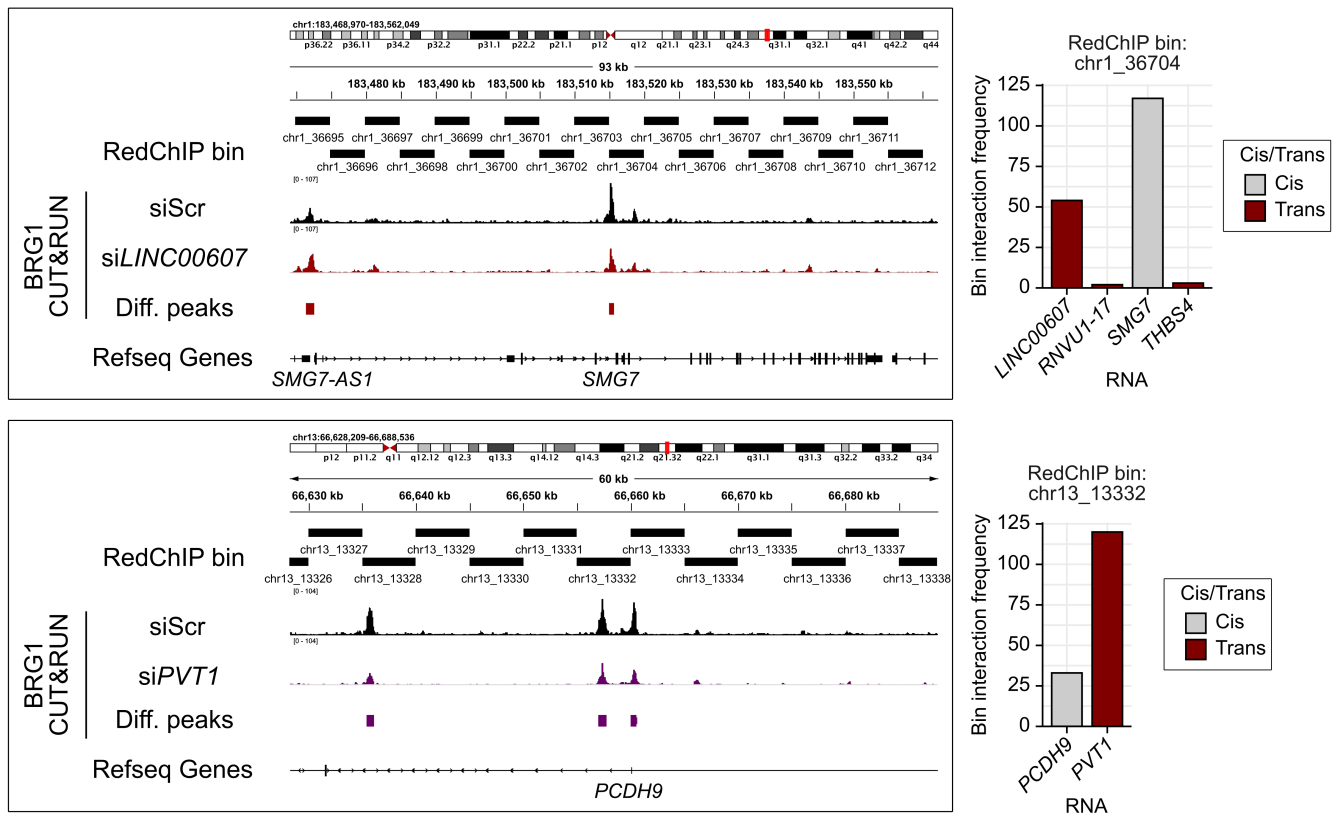
(a) Overlap of RNAs between Red-C and BRG1 RedChIP and plotted individually across summed RNA frequencies.

(b) Overlap of DNA bins between Red-C and BRG1 RedChIP and plotted individually across ranges of summed DNA frequencies.

(c) Red-C and BRG1 RedChIP coverage. Number of RNA-DNA interactions across the normalized interaction frequencies.

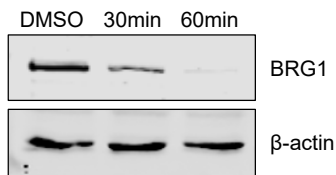
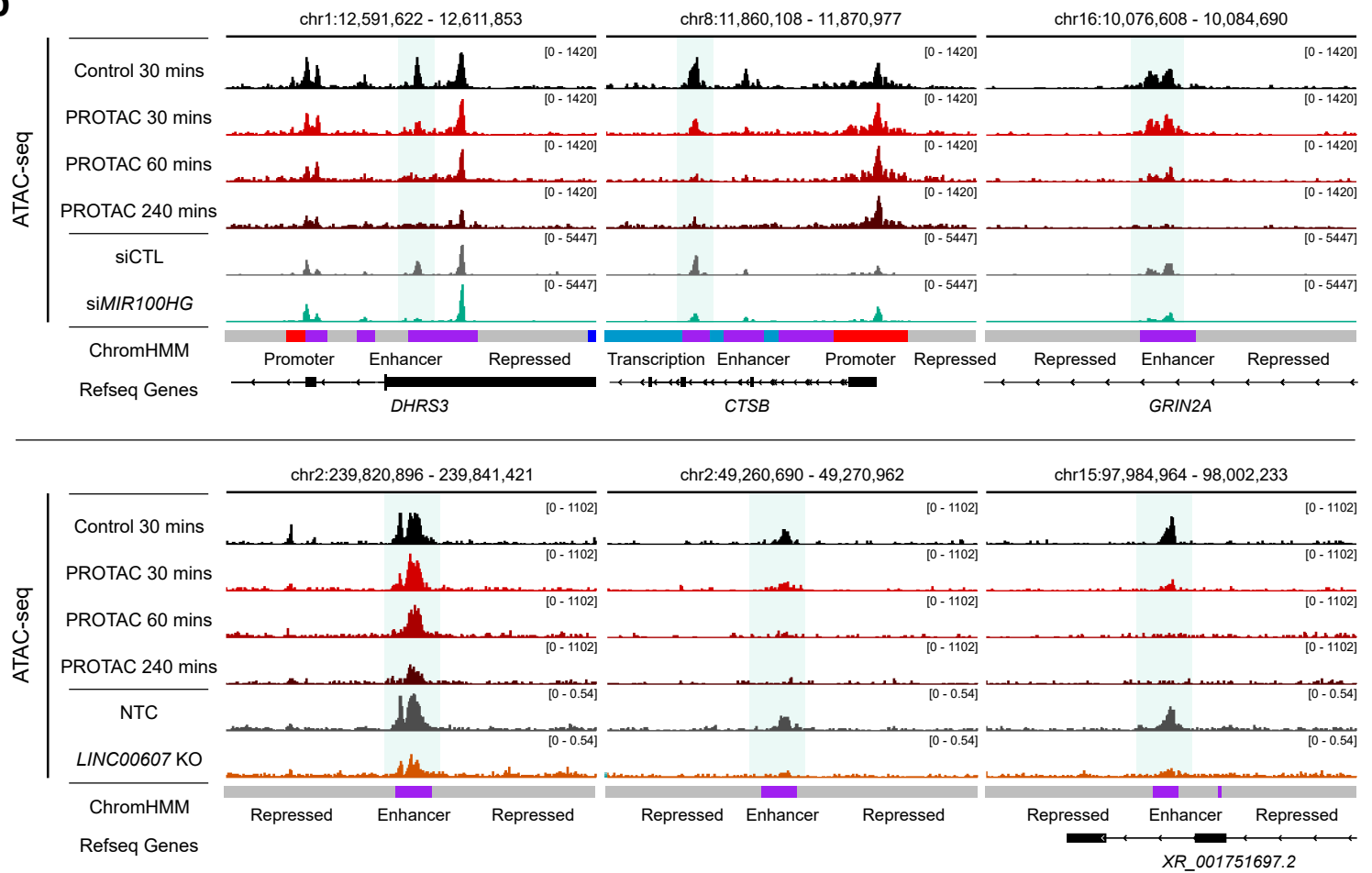
(d) Mean DNA bin interaction frequency in Red-C and BRG1 RedChIP data at BRG1 CUT&RUN peaks versus a size-matched set of shuffled peaks.

(e) Genome-wide density plots for RNA-DNA interactions for both Red-C and RedChIP DNA coverage at BRG1 CUT&RUN peaks versus a size-matched set of shuffled peaks.

a.**b.**

Supplementary Fig. 2 | RT-qPCR validation of knockdowns and knockdowns on *cis/trans* RNA binding sites

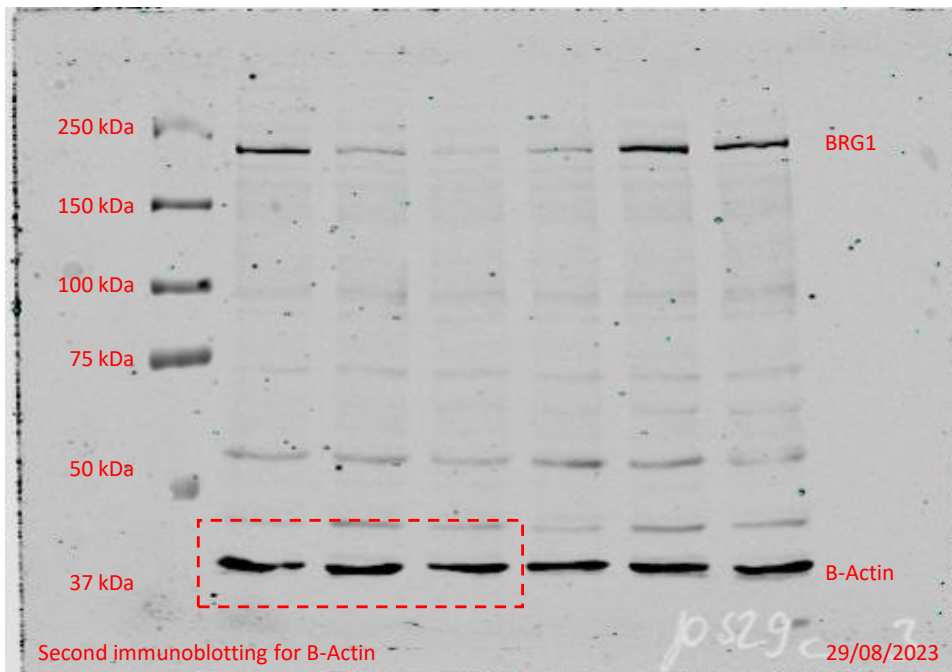
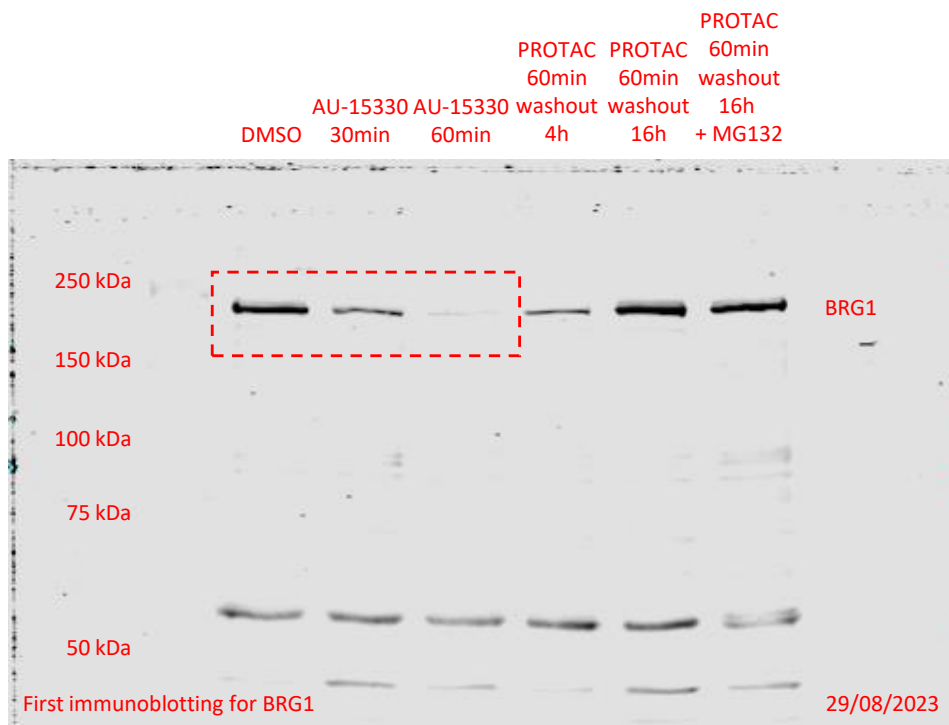
- (a) siRNA against *JPX*, *MIR100HG* (M100), *LINC00342* (L342), *MEG8*, *PVT1*, *MIR31HG* (M31), *LINC00607* (L607) and *NEAT1* (NT1) followed by RT-qPCR. RNA level relative to GAPDH RNA displayed as mean $\pm$ SD, n=3, unpaired t-test. P-values are indicated above each bar plot.
- (b) Browser traces demonstrating BRG1 CUT&RUN peaks at mixed *cis/trans* RNA binding sites. Depletion of the trans RNA e.g. *LINC00607* (top panel) and *PVT1* (bottom panel) reduces BRG1 binding at the genomic locus of the *cis* RNA (*SMG7* and *PCDH9* respectively). Graphs on the right demonstrate the degree of binding for each RNA at the respective mixed *cis/trans* binding site.

a**b**

Supplementary Fig. 3 | PROTAC AU-15330 on BRG1 levels and ATAC-seq

(a) Western blot of HUVEC treated with 1 μ M AU-15330 PROTAC (30 and 60 min) or DMSO (60 min). Antibodies against BRG1 and β -actin. Blot representative of 3 biological replicates with each giving similar results.

(b) ATAC-seq following treatment of HUVEC with 1 μ M AU-15330 PROTAC (30, 60 or 240 min) or DMSO (30 min), with control or *MIR100HG* siRNAs (top), and non-targeting control (NTC) or *LINC00607* CRISPR-Cas9 (bottom).



Uncropped blots for Supplementary Fig. 3a.