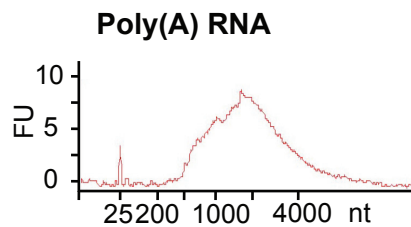
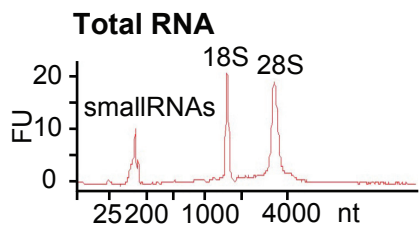
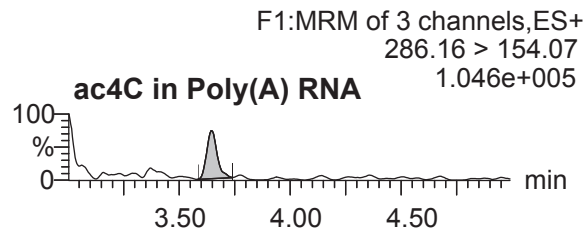
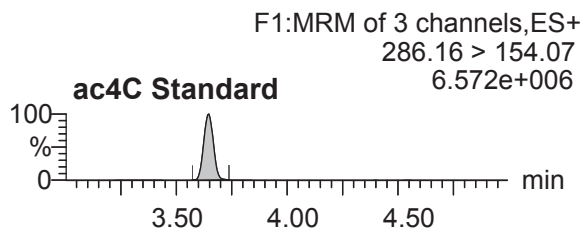
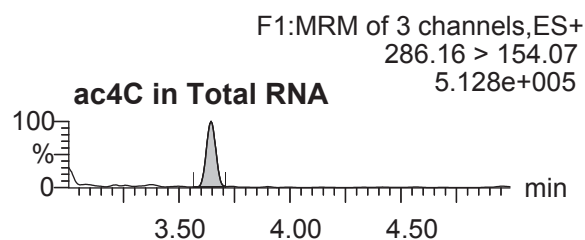
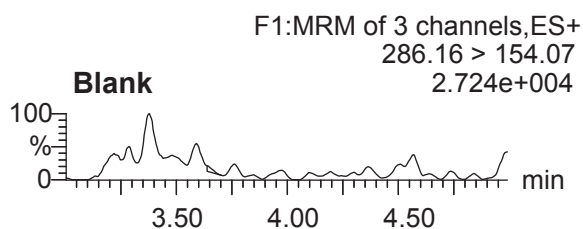


Arango et al., Figure S2, related to Figure 2

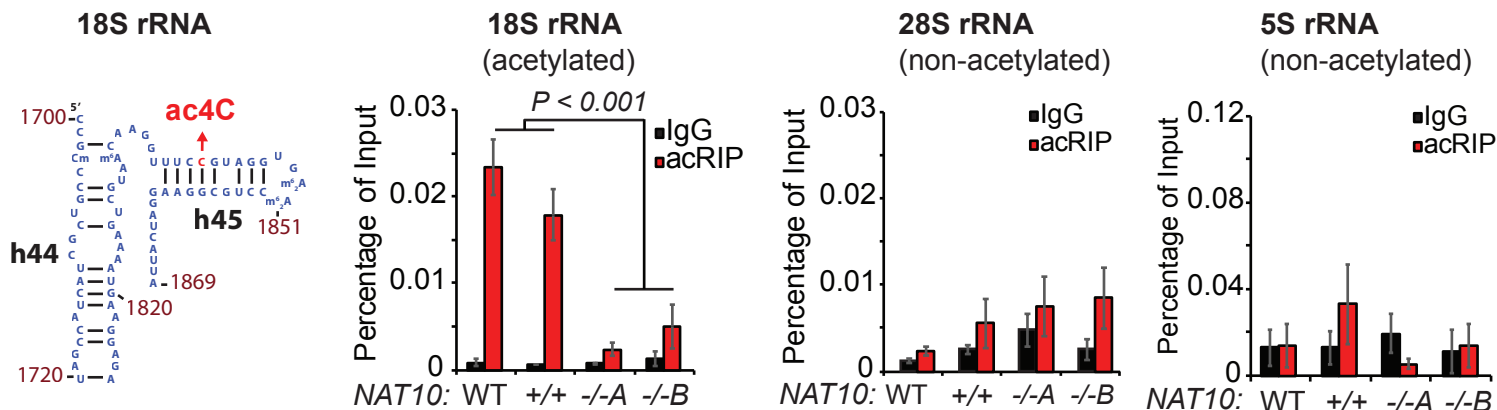
A Bioanalyzer Profiles



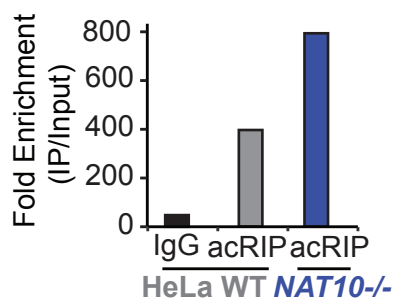
B LC-MS/MS Chromatograms



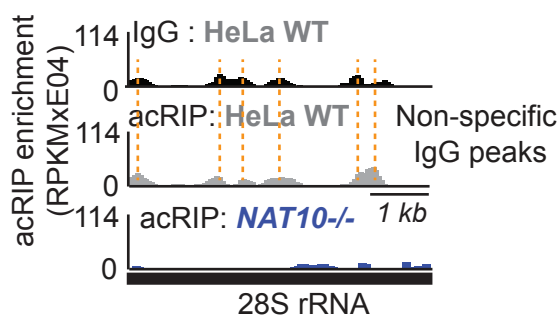
A acRIP RT-qPCR



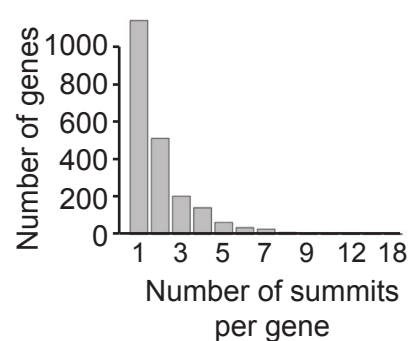
B Acetylated Spike-in Recovery in acRIP-seq



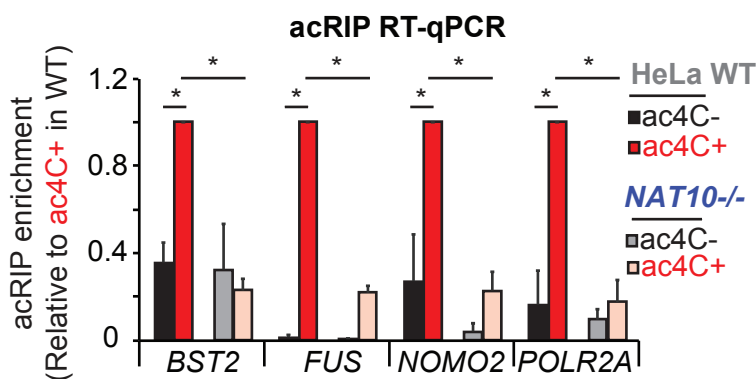
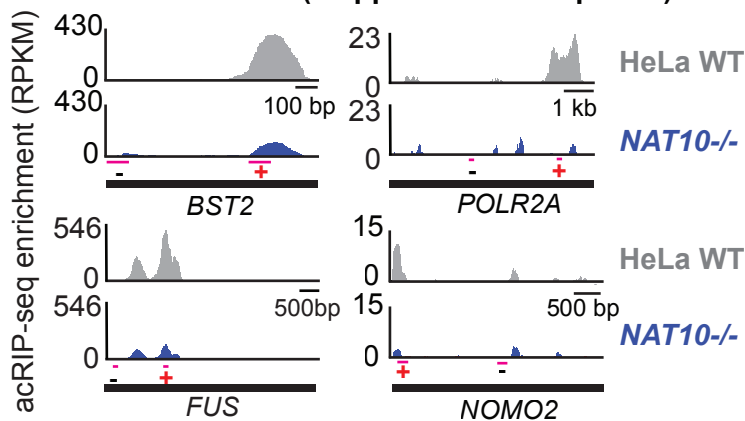
C acRIP-seq Browser Shots of 28S rRNA



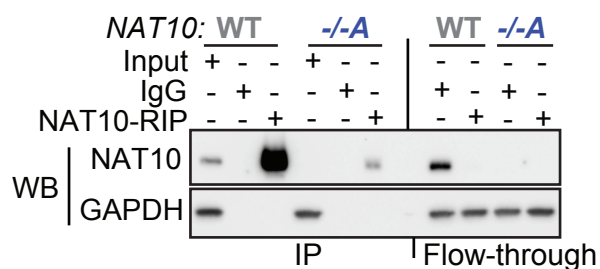
D ac4C Summits per Gene



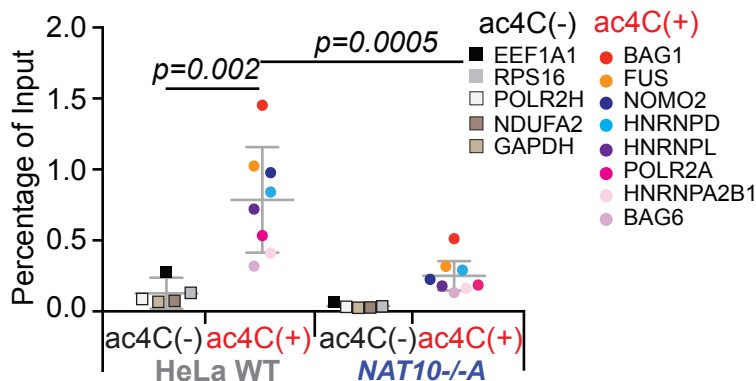
E RT-qPCR Validation of acRIP-seq Browser shots (mapped to transcriptome)



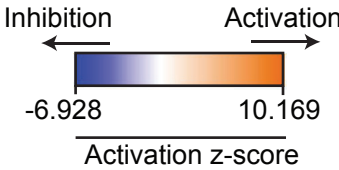
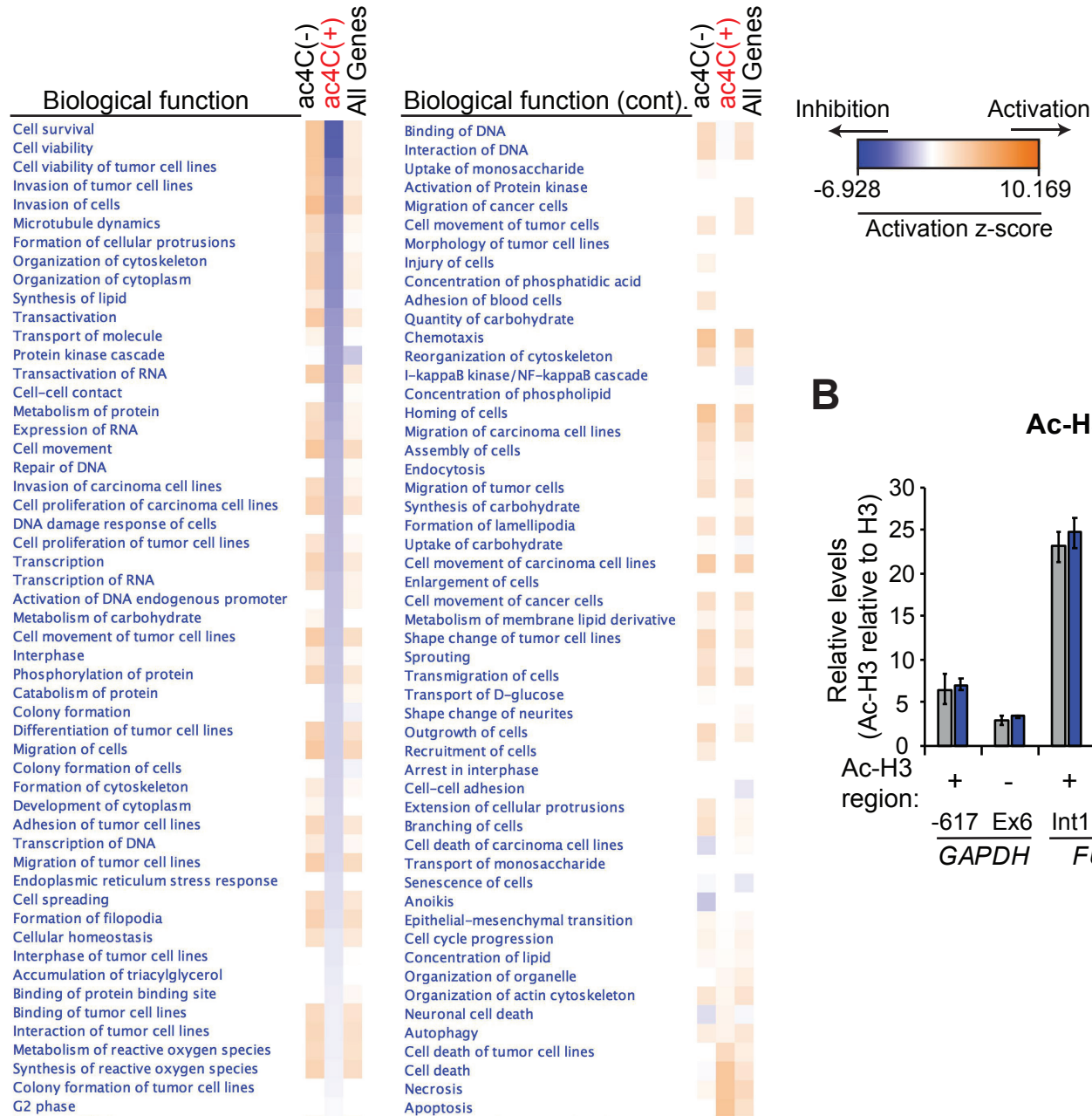
F NAT10 RIP and RT-qPCR NAT10-RIP Western blot



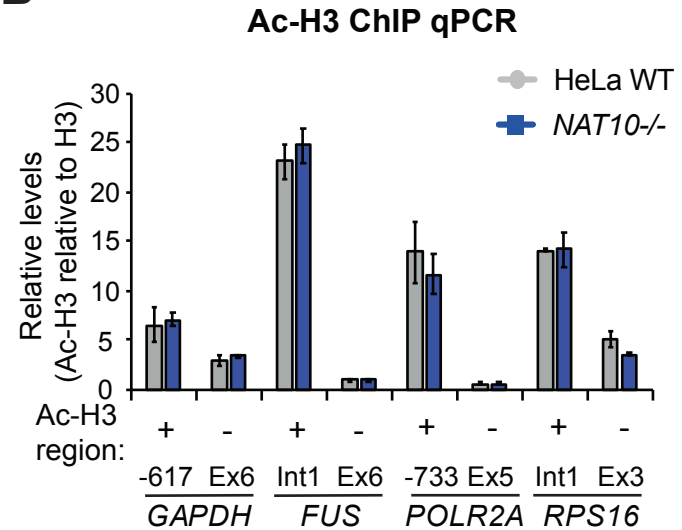
NAT10-RIP RT-qPCR



A Functional category analysis on the basis of differential gene expression in ac4C(-), ac4C(+) mRNAs and all dysregulated transcripts

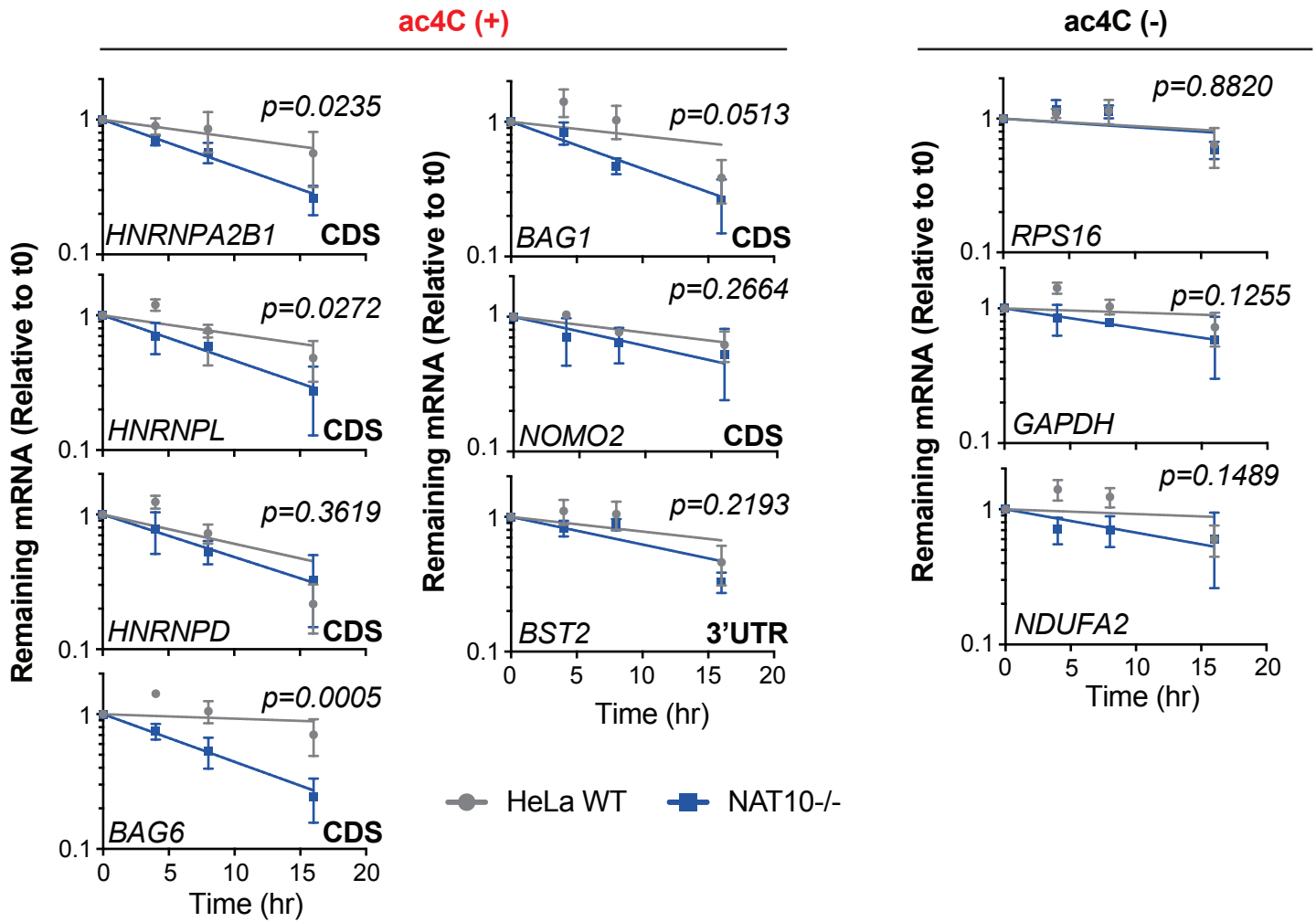


B



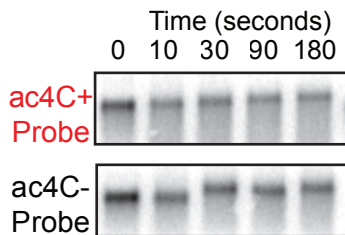
A

BRIC RT-qPCR in Parental and *NAT10*^{-/-} HeLa Cells



B

XRN-1 Digestion of *in vitro* Transcribed Probes



Arango et al., Figure S6, related to Figure 6

