

Figure S1. Read coverage of heterozygous SNVs in the eCLIP-Seq data of SRSF1 in K562 cells. Two replicates are shown.

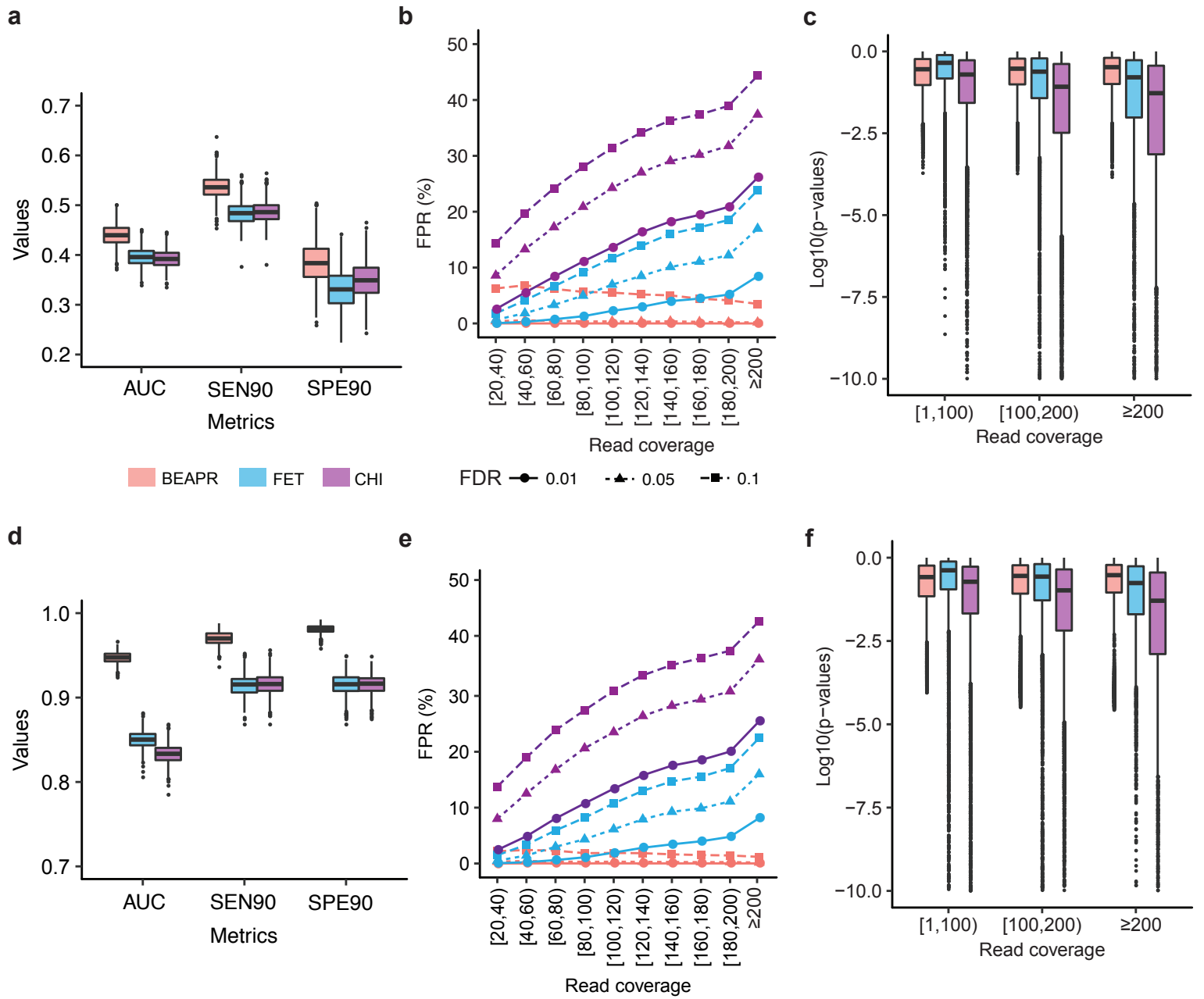
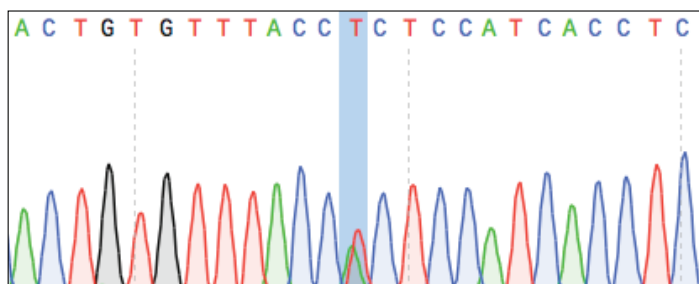


Figure S2. Similar as Fig. 1d, e and f, for simulated allelic ratio of 0.7 (a-c) and 0.9 (d-f) respectively.

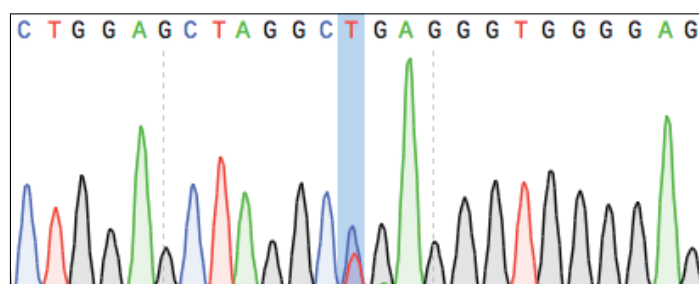
a

HepG2

chr7:155573476 A>T



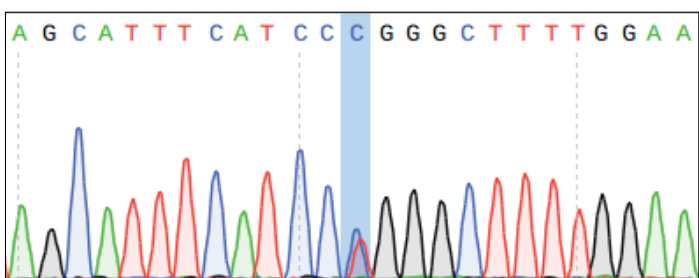
chr17:37896856 C>T



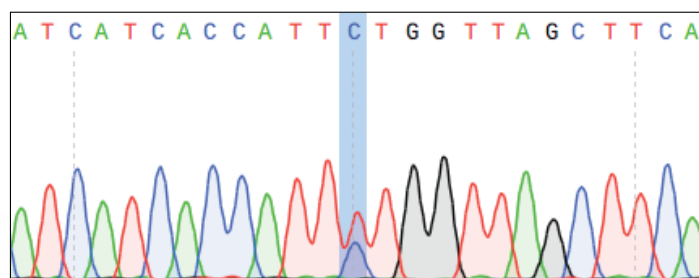
b

K562

chr6 122734545 C>T rs12527592



chr7 139054325 C>T rs6949963



chr7 157027809 T>C rs28367460

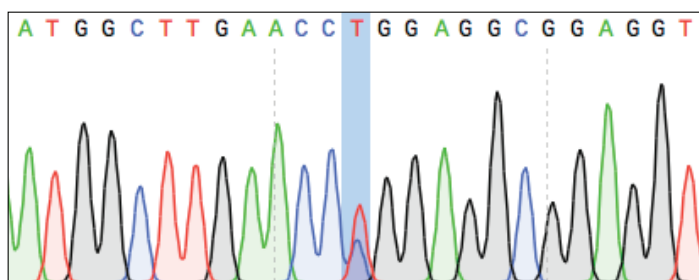


Figure S3. Sanger sequencing of DNA to confirm BEAPR-predicted heterozygous SNPs. (a) HepG2, (b) K562

a HepG2

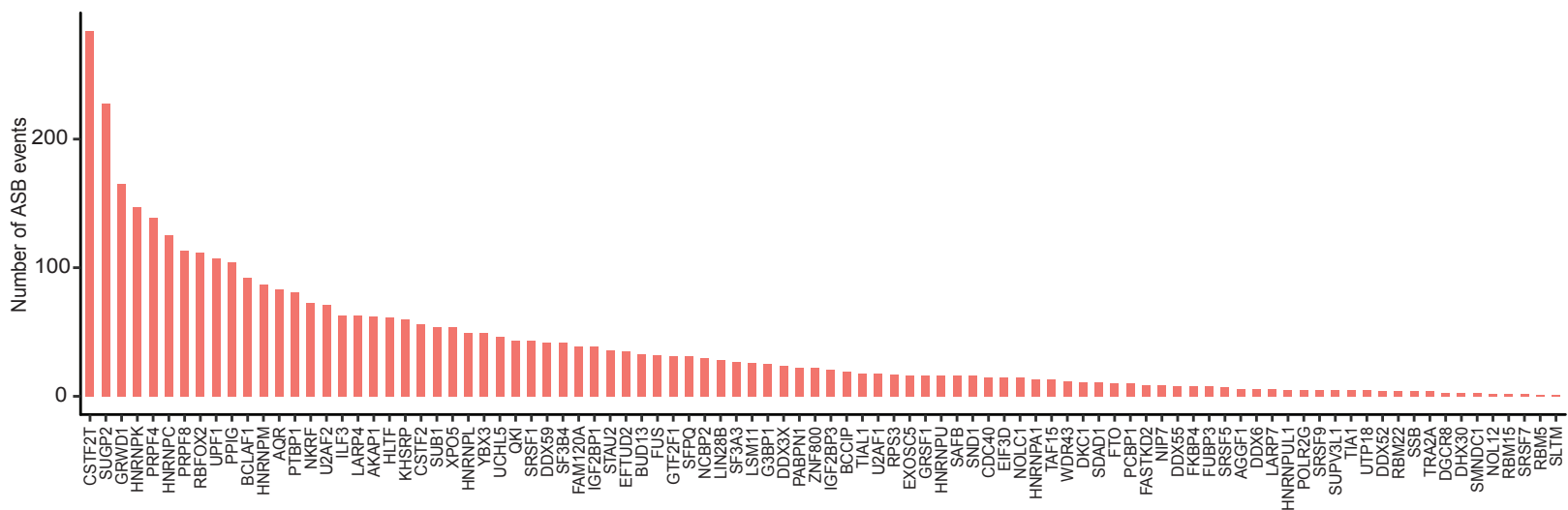
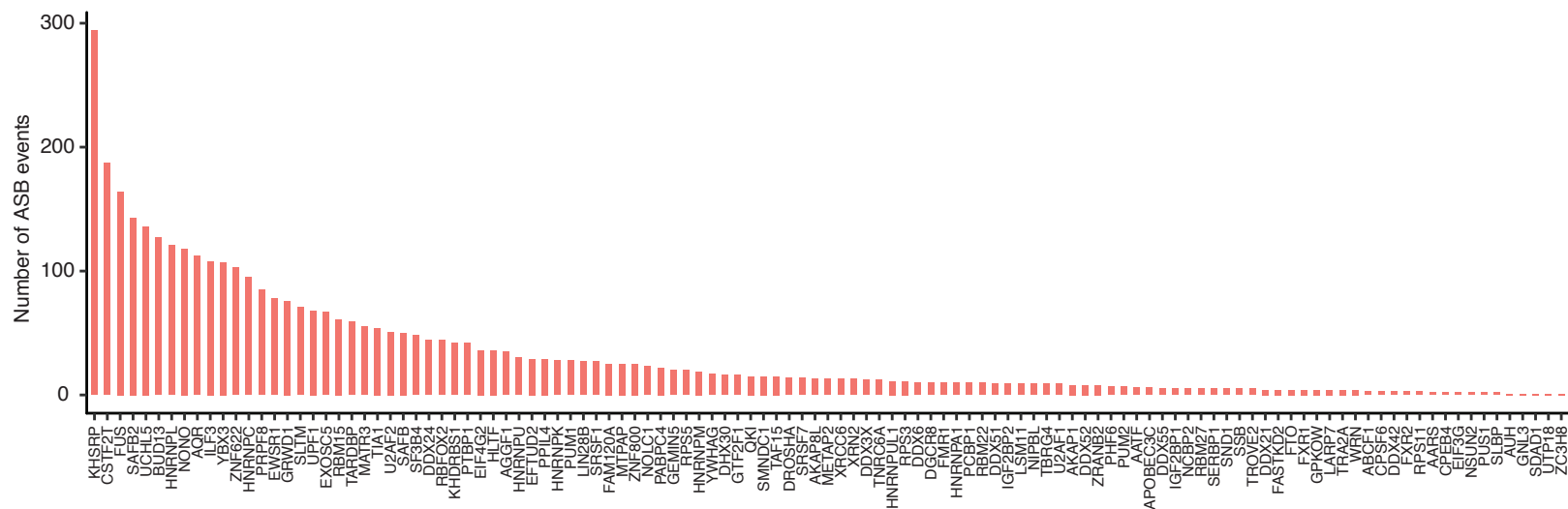
**b K562**

Figure S4. Number of ASB events for each RBP in (a) HepG2; (b) K562.

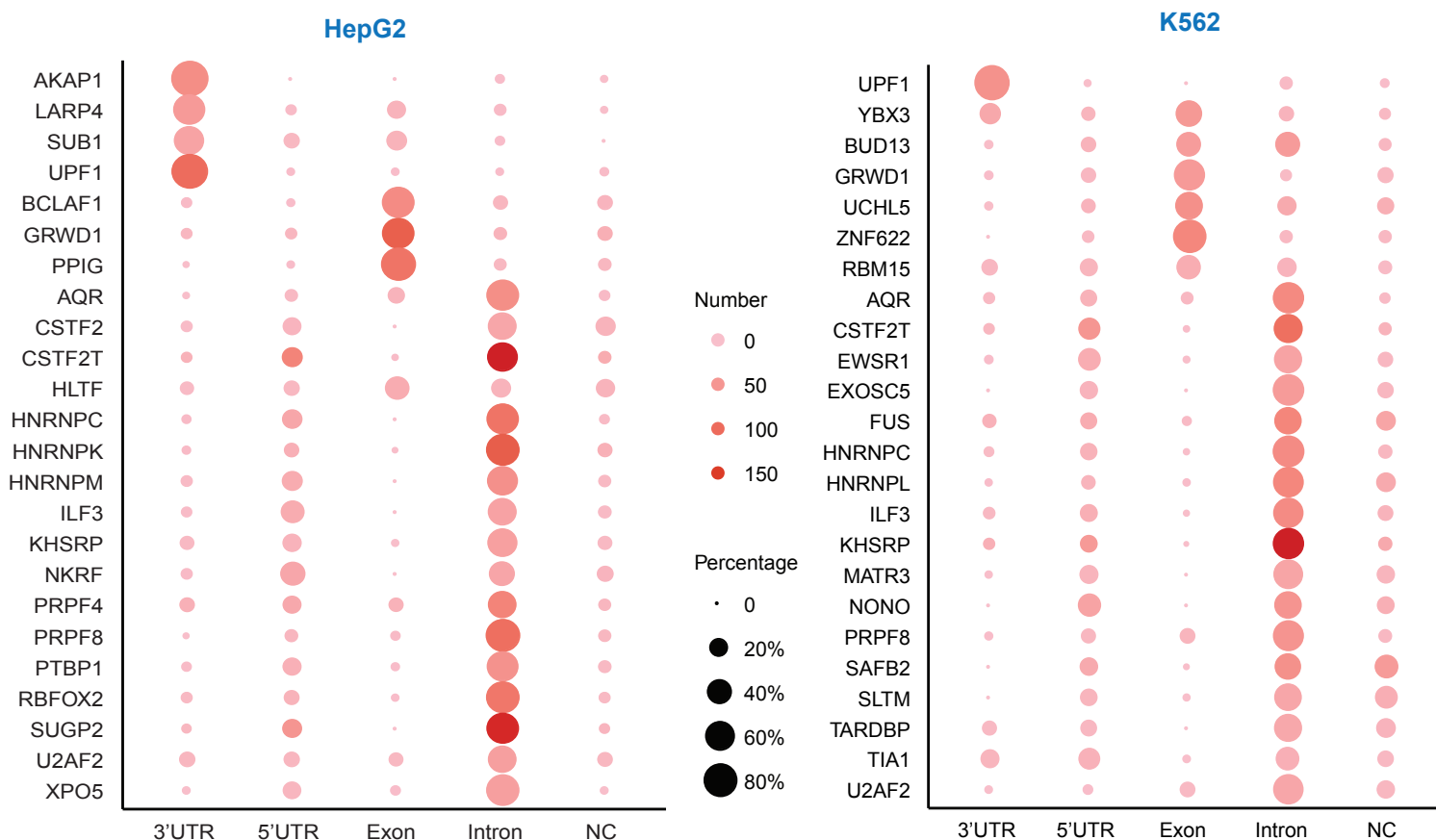


Figure S5. Distribution of ASB SNVs in different types of genomic regions. Only RBPs with ≥ 50 ASB events are shown. NC: non-coding transcripts. The color of the dots denotes number of events. The size of the dots corresponds to the percentage of SNVs in each region for each RBP.

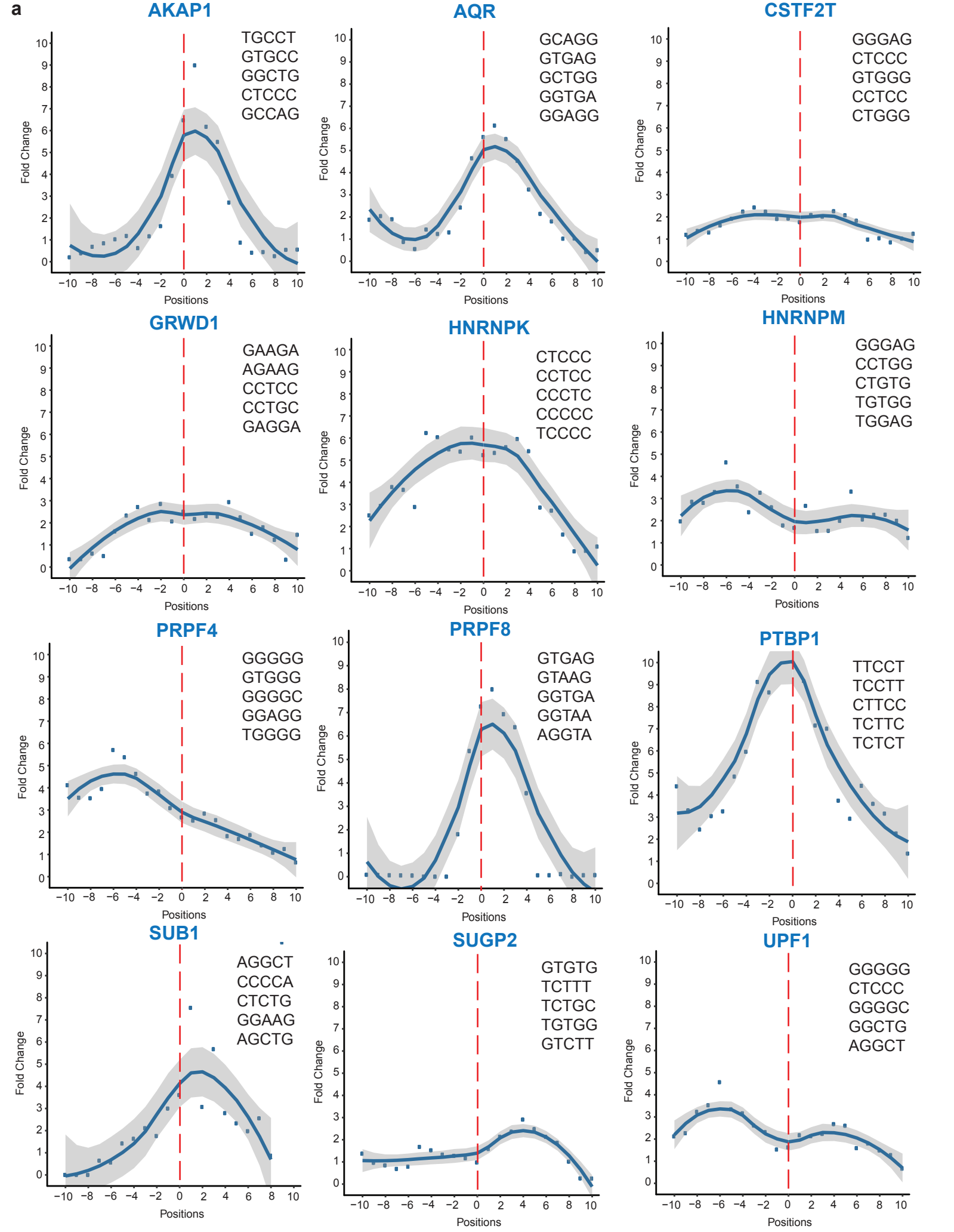


Figure S6a. Positional enrichment of pentamers around ASB SNV sites ($x = 0$) in HepG2 cells. The top 5 pentamers that are most enriched in regions of ASB were identified, and listed in each panel.

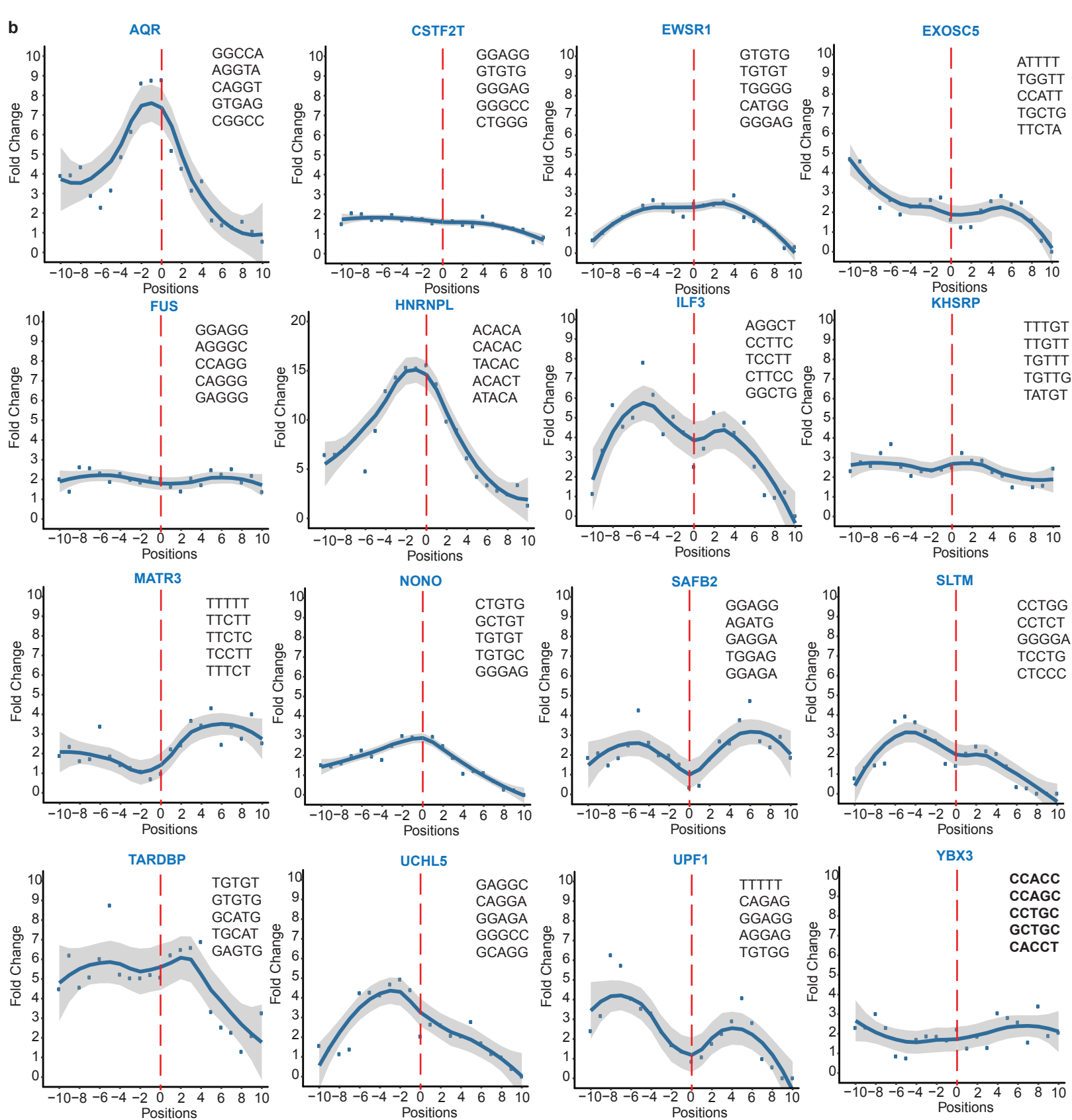


Figure S6b. Positional enrichment of pentamers around ASB SNV sites (x = 0) in K562 cells, similar as S6a.

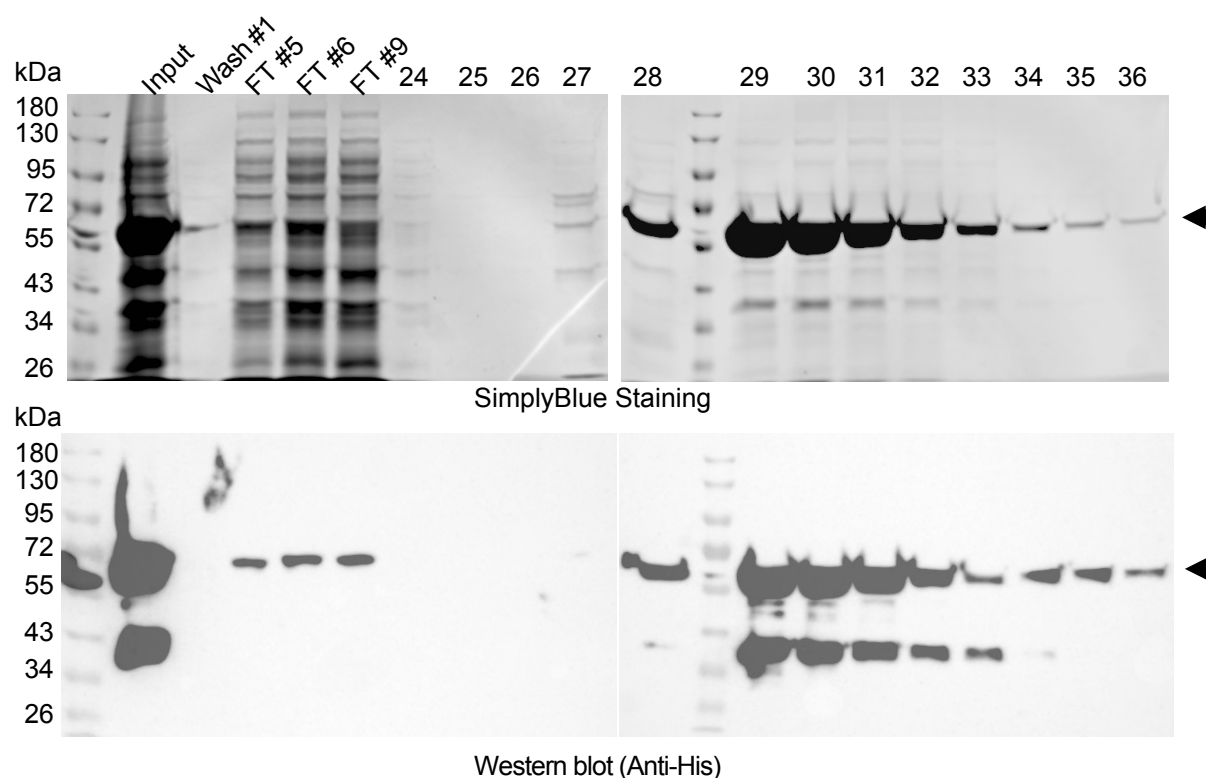


Figure S7. Recombinant PTBP1 bacterial overexpression and electrophoretic mobility shift assay (EMSA). Bacterial overexpression of human PTBP1. PTBP1-pET28a plasmid was obtained from Dr. Doug Black's lab and PTBP1 recombinant proteins were purified from BL21 Star (DE3) using the HisTrap purification column. Detailed purification conditions are described in Methods. Fractions from each purification step were loaded onto 8% SDS-PAGE. (FT: flow through, elution 24-36). Purified PTBP1 proteins were confirmed by SimplyBlue Safe staining (top) and western blot (bottom). Extra bands of smaller protein sizes are likely due to degradation. 28 to 33 fractions were used, followed by 20K dialysis. (bottom). Extra bands of smaller protein sizes are likely due to degradation.

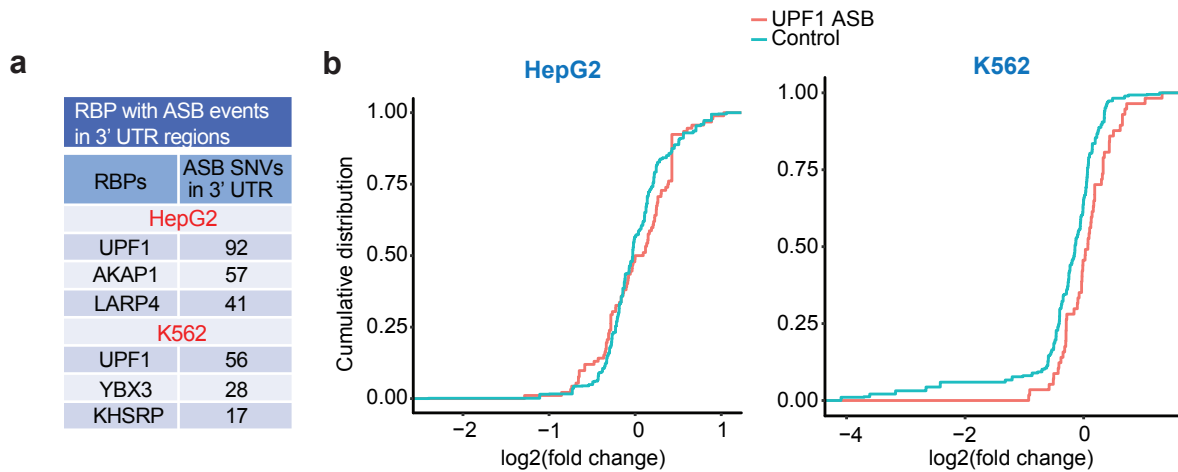


Figure S8. ASB events in 3' UTRs. (a) The top 3 RBPs in each cell line with the highest number of ASB SNVs in 3' UTRs. (b) Expression fold change (UPF1 knockdown/control cells) of genes with ASB SNVs of UPF1 in their 3' UTRs. "Control" curves were generated using genes that match the RPKM of UPF1 target genes (within +/-30%) and have no UPF1 eCLIP peak. A total of 20 sets of controls were generated, with their results collated in the plot.