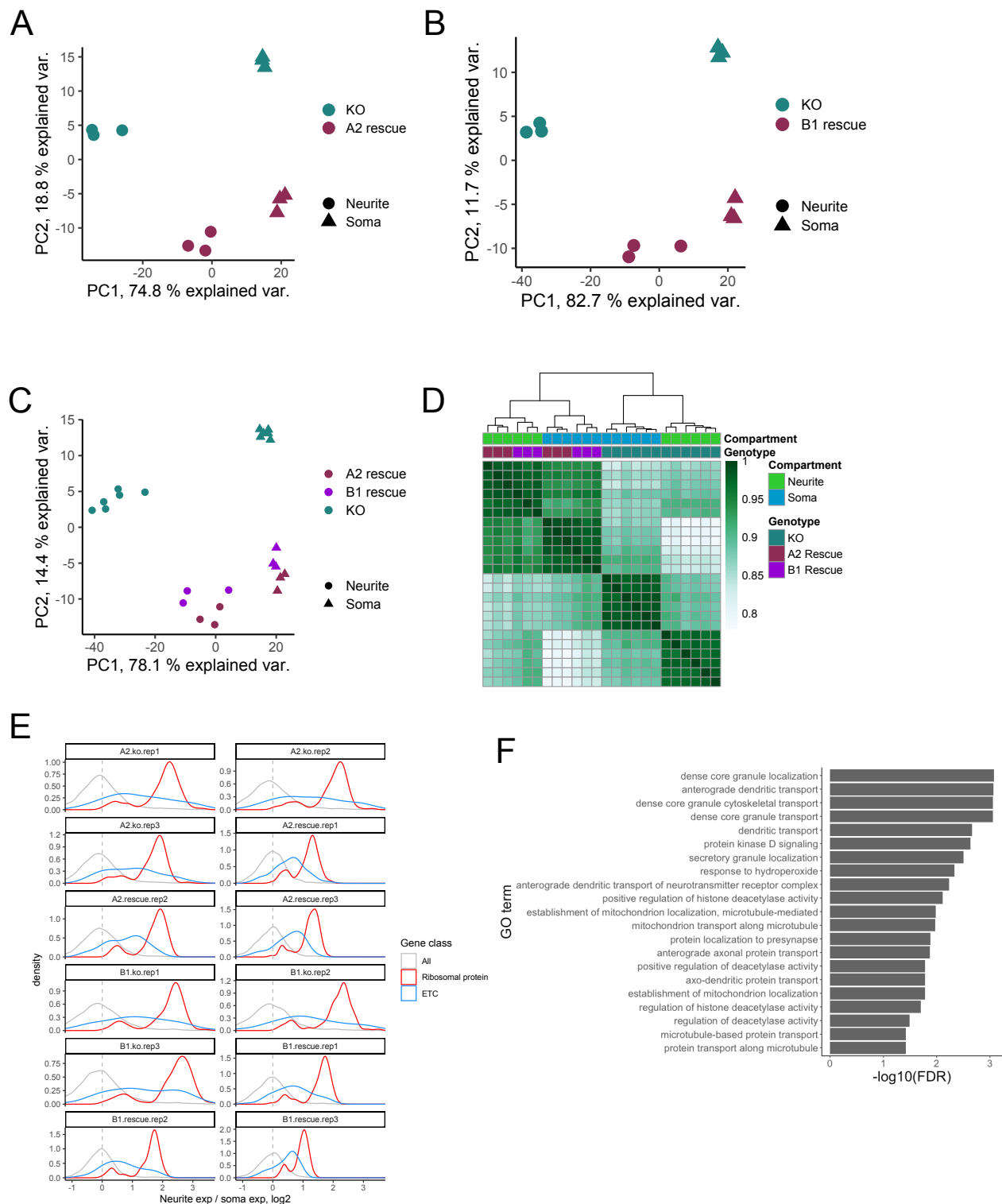
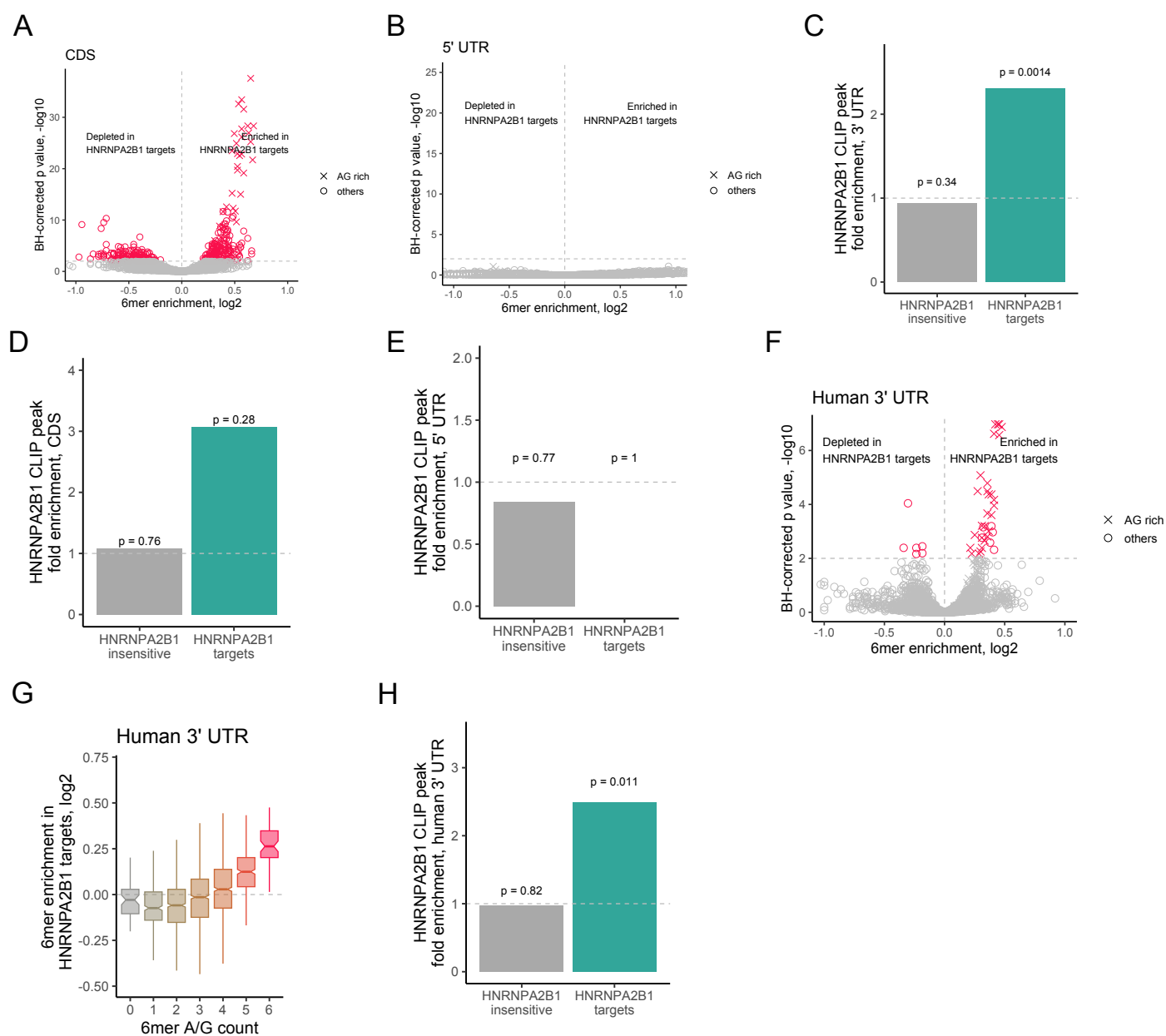


## SUPPLEMENTARY FIGURES



**Figure S1.** (A) Principal components analysis of gene expression levels from the soma and neurite of HNRNPA2B1 knockout and HNRNPA2 rescue cells. (B) Principal components analysis of gene expression levels from the soma and neurite of HNRNPA2B1 knockout and HNRNPB1 rescue cells. (C) Combined analysis of HNRNPA2 and HNRNPB1 rescue samples. (D) Hierarchical clustering of gene expression levels from HNRNPA2B1 knockout, HNRNPA2 rescue, and HNRNPB1 rescue soma and neurite samples. (E) Neurite enrichment levels for all RNAs (gray), those encoding ribosomal proteins (red), and those encoding components of the electron transport chain (blue). (F) Gene ontology terms enriched among the HNRNPA2B1-target RNAs, i.e. those that were mislocalized upon loss of HNRNPA2B1.



**Figure S2.** (A) Enrichment of 6mers in the coding sequences of HNRNPA2B1-targets compared to HNRNPA2B1-insensitive RNAs. 6mers comprised solely of adenosine and guanosine are marked with X. (B) As in A, but comparing the 5' UTRs of HNRNPA2B1-targets and HNRNPA2B1-insensitive RNAs. (C) HNRNPA2B1 CLIP peak enrichment in the 3' UTRs of HNRNPA2B1-target and HNRNPA2B1-insensitive RNAs. The dotted gray line represents frequency of HNRNPA2B1 CLIP peaks in the 3' UTRs of all genes, normalized to 1. P values were calculated using a binomial test. (D) As in C, but looking at the coding sequences of the indicated RNAs. (E) As in C, but looking at the 5' UTRs of the indicated RNAs. (F) As in A, but comparing the 3' UTR sequences of the human orthologs of the HNRNPA2B1-target and HNRNPA2B1-insensitive RNAs. (G) Distribution of enrichments of 6mers with varying numbers of A/G residues in the 3' UTRs of the human orthologs of the HNRNPA2B1-target and HNRNPA2B1-insensitive RNAs. (H) As in C, but comparing the 3' UTRs of the human orthologs of the HNRNPA2B1-target and HNRNPA2B1-insensitive RNAs.