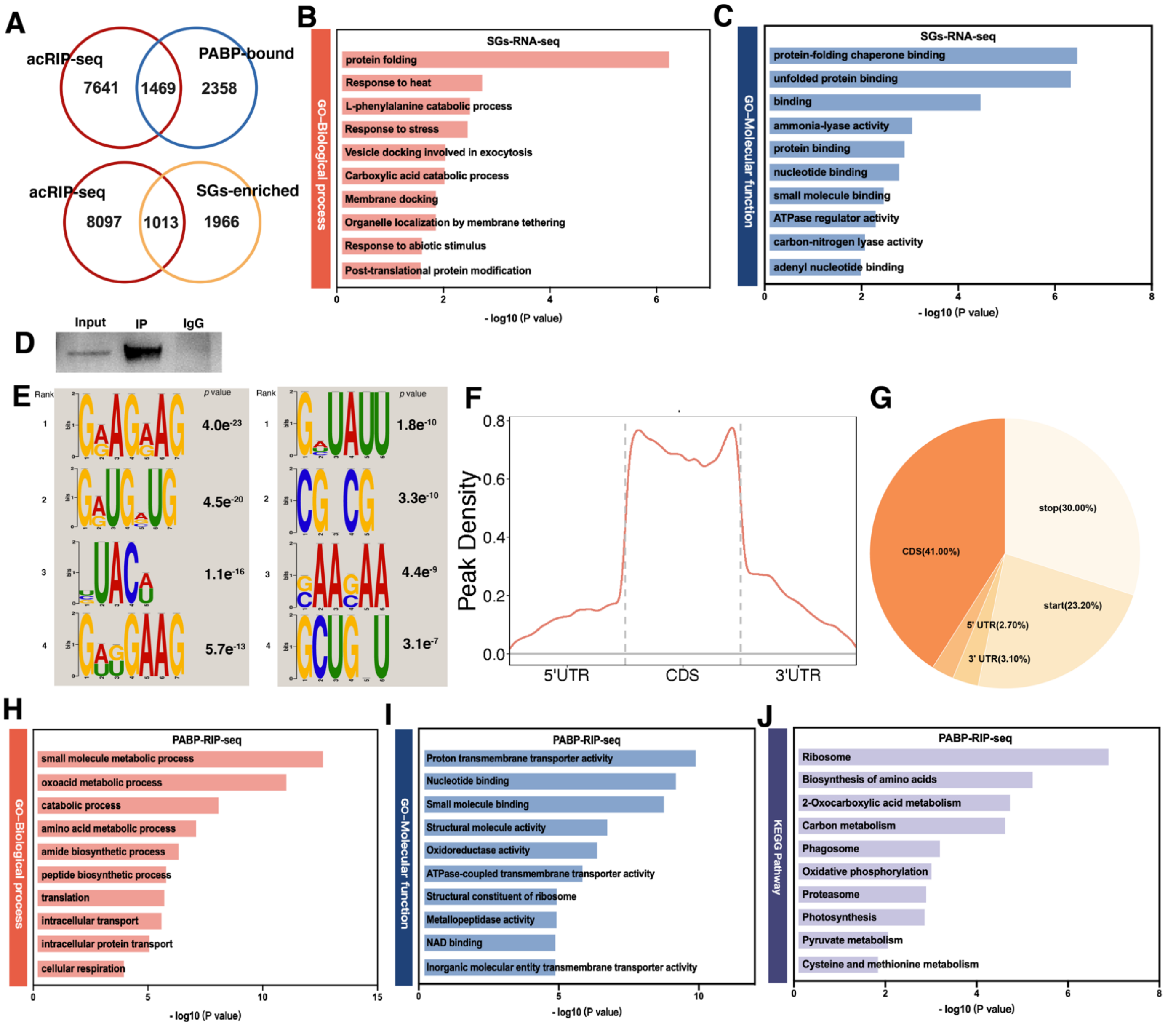

Extended Data Fig. 5 Analysis of SGs-enriched and PABP-bound transcription.

a. Determine of the extent of overlap between ac^{4}C-modified transcripts and PABP-bound or SG-enriched transcripts, respectively.

b. Gene Ontology (GO) enrichment analysis of biological processes (BP) for SG-enriched transcripts.

c. GO enrichment analysis of molecular functions (MF) for SG-enriched transcripts.

d. Immunoprecipitation was performed using GFP antibody-conjugated magnetic beads on protein extracts from *N. benthamiana* overexpressing PABP-GFP, with IgG-conjugated magnetic beads as a negative control. Western blot analysis was used to assess the enrichment of the target protein in the input (Input), immunoprecipitated (IP), and control (IgG) samples.

e. Top 8 motifs identified from transcripts bound by PABP in RIP-seq.

f. The metaplot is presented of the distribution of PABP-bound transcripts. The relative position of UTRs and CDS is shown at the bottom.

g. Proportional distribution of PABP-bound transcripts across different functional regions of genes.

h. GO enrichment analysis of biological processes (BP) for PABP-bound transcripts.

i. GO enrichment analysis of molecular functions (MF) for PABP-bound transcripts.

j. KEGG pathway analysis of PABP-bound transcripts.