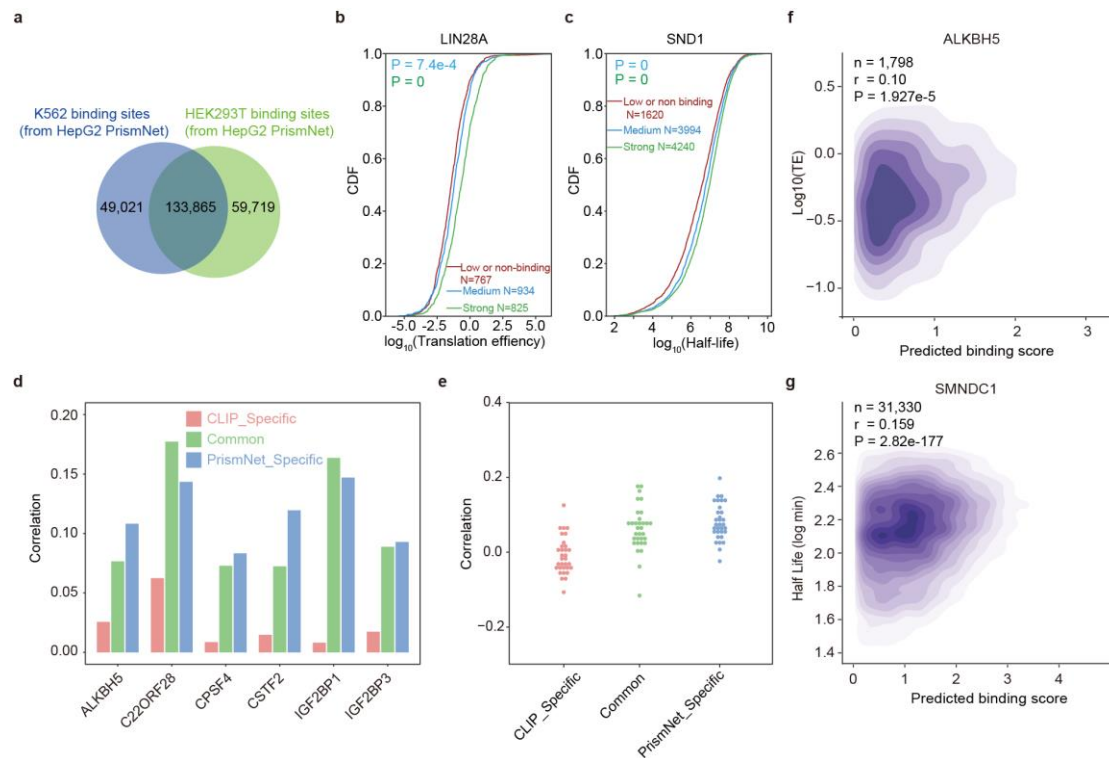




Supplementary information, Fig. S4: PrismNet-predicted differential RBP binding, and correlation of predicted quantitative RBP binding with target translation and degradation.

(a) Venn diagram of SRSF1 binding sites in HEK293T and K562 cells, predicted by the PrismNet model trained on the HepG2 SRSF1 eCLIP dataset.

(b) Cumulative distribution plots of transcript translation efficiency versus different levels of binding probability for RBP LIN28A: Strong binding (predicted binding probability ≥ 0.8), Medium binding ($0.5 \leq$ predicted binding probability < 0.8), and Low or non-binding (predicted binding probability < 0.5).

(c) Cumulative distribution plots of transcript half-life versus different level of binding probability of RBP SND1: Strong binding (predicted binding probability ≥ 0.8), Medium binding ($0.5 \leq$ predicted binding probability < 0.8), and Low or non-binding (predicted binding probability < 0.5).

(d) Bar plot of Pearson correlation coefficients between PrismNet-predicted binding score and RNA half-life values for PrismNet-specific predictions (blue), common bindings (green), and between CLIP binding score and RNA half-life values for CLIP-specific results (red). The pre-calculated RNA half-life data in HEK293 cells were downloaded from a previous

study².

(e) Scatter plot of Pearson correlation coefficients between binding score of each RBP and RNA half-life values for PrismNet-specific predictions (blue), common bindings (green), and CLIP-specific results (red). Each dot represents an RBP.

(f) Density plot of the PrismNet-predicted ALKBH5 binding scores versus translation efficiency of the target transcripts.

(g) Density plot of the PrismNet-predicted SMNDC1 binding scores versus half-lives of the target transcripts.

Reference:

- 2 Schueler, M. *et al.* Differential protein occupancy profiling of the mRNA transcriptome. *Genome Biol* **15**, R15 (2014).