Supplementary Information

An approach for systematic profiling of drug-induced remodeling of RNA-RBP (RNA-binding protein) interactions

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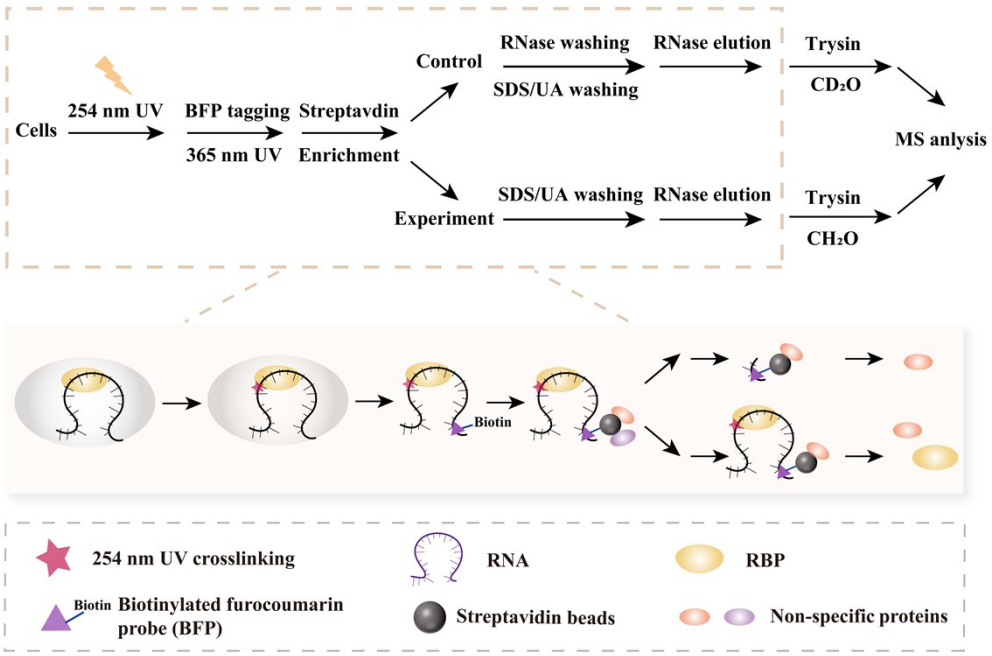

Figure S1. Schematic diagram of the experimental design for quantitative differential proteomic comparison between the experimental group and the control group (RNase washing).

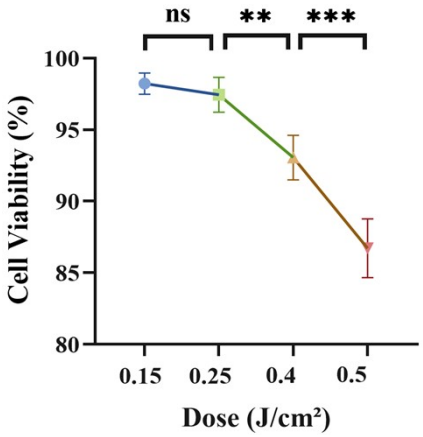

Figure S2. UV dose-response analysis of cell viability. Data are presented as mean ± SD (n = 4). ns, not significant; **P < 0.01; ***P < 0.001.

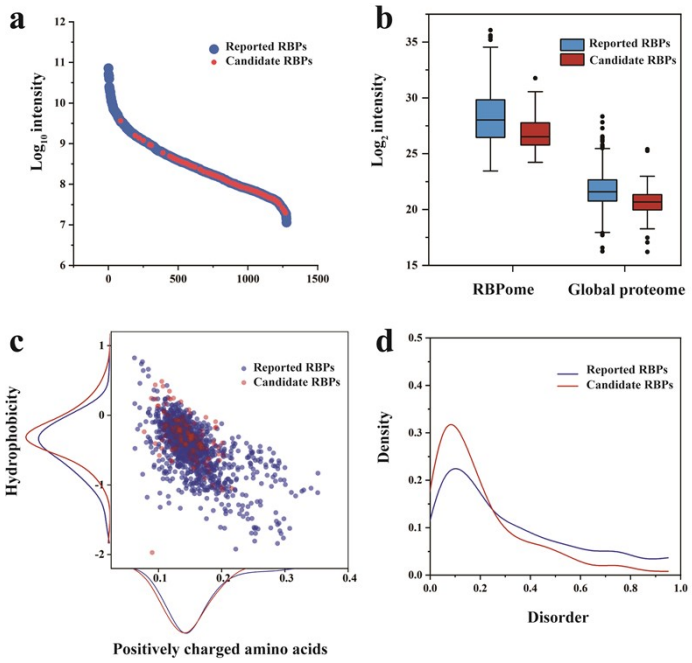

Figure S3. Comparison of the candidate RBPs with the overlapping RBPs identified in previously reported human RBPome datasets. (a) Scatter plot of abundance ranking of the overlapping RBPs and candidate RBPs. (b) Box plot of abundance of the overlapping RBPs and candidate RBPs in the RBPome and global proteome. (c) Scatter plot showing hydrophobicity and percentage of positively charged amino acids of the overlapping RBPs and candidate RBPs, with density distribution of each feature outside the coordinate axis. (d) Density distribution pattern of disorder for the overlapping RBPs and candidate RBPs.

Table S3 Technical comparison of BFP-based method with established RBP enrichment methods

Method	Cellular perturbation	Specificity	Identified RBPs	Time of enrichment procedure	Throughput	Reference
ChIRP-MS	Without	Low	81	27-28 h	Low	[53]
RAP-MS	Without	High	10	18-19 h	Low	[54]
CARIC	With	High	597	19-20 h	Medium	[55]
OOPS	Without	High	1838	15-16 h	Medium	[56]

BFP-based method	Without	High	1369	5-6 h	High	Present work