| RBP | Known sequence preference | Recovered in this study  (6-mers/SSMART/both/novel) |
| --- | --- | --- |
| CPSF1 | UGU (1) | both |
| CSTF2 | GU-rich (2) | both |
| CSTF2T | UGU (1) | both |
| ELAVL1 | AU-rich, U stretches (3, 4) | both |
| ELAVL2 | AU-rich (5) | both |
| ELAVL3 | AU-rich (6) | both |
| ELAVL4 | AU-rich (7) | both |
| EWSR1 | stem-loop (8) | *weak specificity/U-rich* |
| FUS | GGUG (9); stem-loop (8) | *weak specificity/U-rich* |
| FXR1 | AUGAC 23846655 | *weak specificity/U-rich* |
| IGF2BP1 | CAU (10) | both |
| L1RE1 | GAUC (11) | both |
| LIN28B | RGGSWG (12) | *weak specificity/U-rich* |
| MBNL1 | YGCU, GCUU (13) | both |
| ORF1 | GAUC (11) | both |
| PUM2 | UGUAHAUA (14) | both |
| QKI | ACUAAY (10) | both |
| RBM20 | UCUU (15) | SSMART |
| RBPMS | CAC (16) | both |
| TAF15 | stem-loop (8) | *weak specificity/U-rich* |
| TARDBP | UG-rich  (17) | both |
| UPF1 | - | *A-rich/U-rich* |
| XPO5 | - | *GUGCAAU/AAUG* |
| ZFP36 | AU-rich (18) | both |

**Supplemental Table 2**

Many motifs checked with AtTRACT ([https://attract.cnic.es](https://attract.cnic.es/)) and RBPmap (rbpmap.technion.ac.il). Where possible, reference to an X-ray/NMR structure is given rather then to the same CLIP dataset. Nevertheless, despite differences in data analysis strategies between labs, we recover the identified motif in the same data across most published PAR-CLIP datasets, emphasizing the robustness of our pipeline. Novel motifs or motifs not corresponding to reported are highlighted in italics.

For RBM20, the 6-mers are enriched for AAGA which is reverse complement to UCUU, and SSMART detected that UCUU is paired, so it is very likely to bind a hairpin.

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