



Supplementary information, Figure S4 (related to Figure 3) (A) Distribution of mRNA binding regions based on PAR-CLIP sequence clusters for WTAP and METTL3 without normalization of the overall length of the different transcript regions.(B) Other enriched sequence motif of PAR-CLIP binding clusters. WTAP binding motif (Upper panel, $p=1e-12$); METTL3 binding motif (Middle panel, $p=1e-12$); Binding motif when only including genes found in both WTAP and METTL3 binding clusters (Lower panel, $p=1e-10$). Binding Motifs were generated by the HOMER program. (C-D) Representative profiles showing the overlapped distribution of WTAP/METTL3 clusters and m6A sites in the CEP85 (C) and

SLC6AP (D) genes. Arrows show WTAP/METTLL3 binding cluster location. Green triangles represents m6A site.