Bowtie2 (v2.2.6), hisat2-align-s (v2.0.5) were used to do the alignment for Input-seq and MeRIP-seq data. Then, Picard (v2.16.0) and SAMtools (v0.1.09) were used for removal the ribosomal RNA, tRNA and PCR duplicates. FeatureCounts was used to count fragment reads that mapped to genes or peaks.

MACS2 (2.1.1) was used to identify m(6)A and METTL3 peaks.

Bedtools toolset (v2.26.0) was used for manipulating about peaks.

Alternative splicing events were detected by rMATS (3.2.5).

The corrplot package in R was used to calculate and visualize pearson coefficients between samples. The package Guitar was conducted to plot the distribution of m(6)As on mRNA and lincRNA. The TSS information was taken from the ChIPseeker R package. The clusterProfiler package in R was used to calculate the over-representation of biological process categories of genes.

findMotifsGenome.pl, annotatePeaks.pl and makeTagDirectory scripts from Homer software suite were used to search m6a motif, annotate peak and generate tag directory.

The igvtools was used to determine the m(6)A profile.

The genomic coordinates of enhancers, eQTL SNPs and ChIP-seq peaks were transformed to hg38 coordinate by ucsc liftOver.

The profile plot of RPKM normalized reads of METTL3 ChIP-seq in those regions was calculated by deepTools2.

Data processing, hypothesis test and data visualization were conducted by custom codes which write in Python and R and were available upon request.