

Figure S1

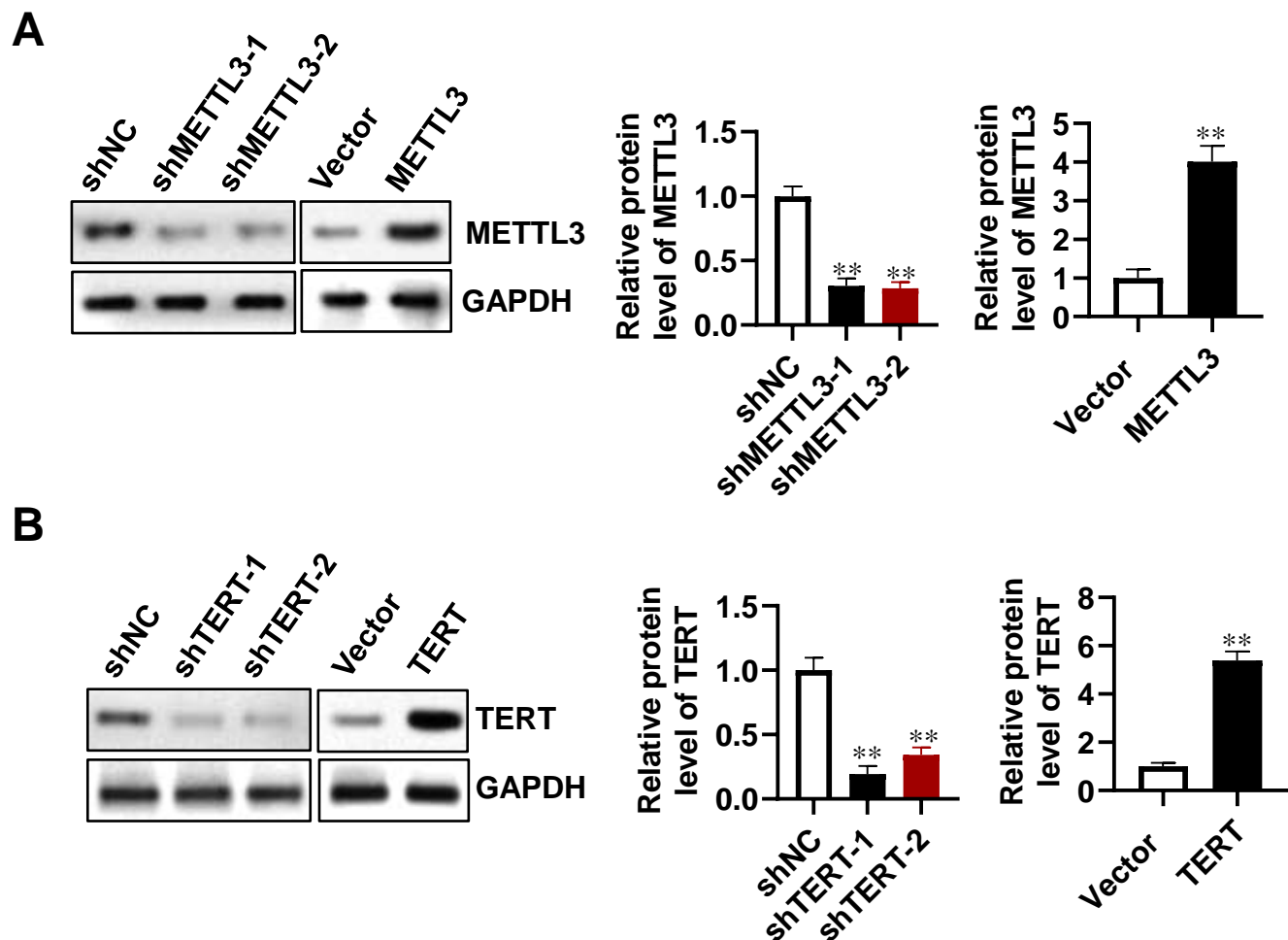


Figure S1. A. Western blotting was employed to assess METTL3 expression following knockdown and overexpression via lentivirus transfection. B. Western blotting was used to evaluate TERT expression after knockdown and overexpression through lentivirus transfection. Error bars represent the mean \pm SD of triplicate experiments. All experiments were performed in biological triplicate. ns indicates no significance. ** $P < 0.01$

Figure S2

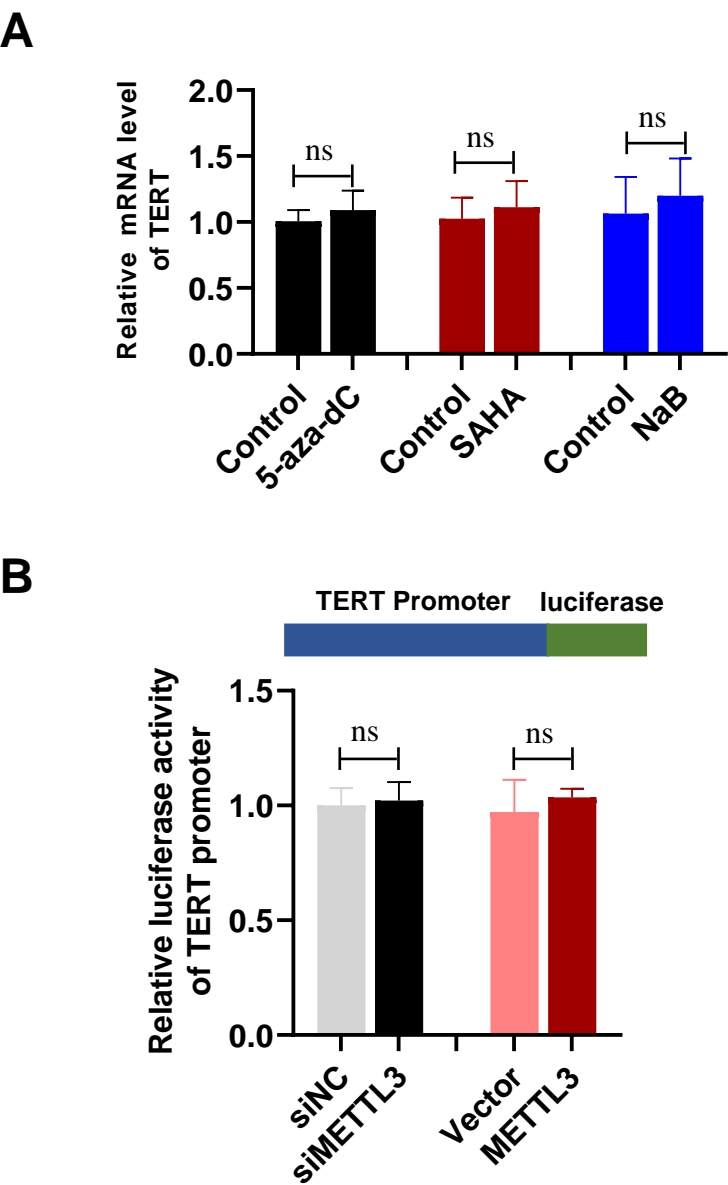


Figure S2. m6A modification contributes to the upregulation of TERT in HESCs. A. RT-qPCR analysis of TERT expression HESCs cells with or without treatment of 5-aza-dC, SAHA, or NaB. B. The luciferase activity of TERT promoter in the indicated group. Error bars represent the mean \pm SD of triplicate experiments. All experiments were performed in biological triplicate. ns indicates no significance.

Figure S3

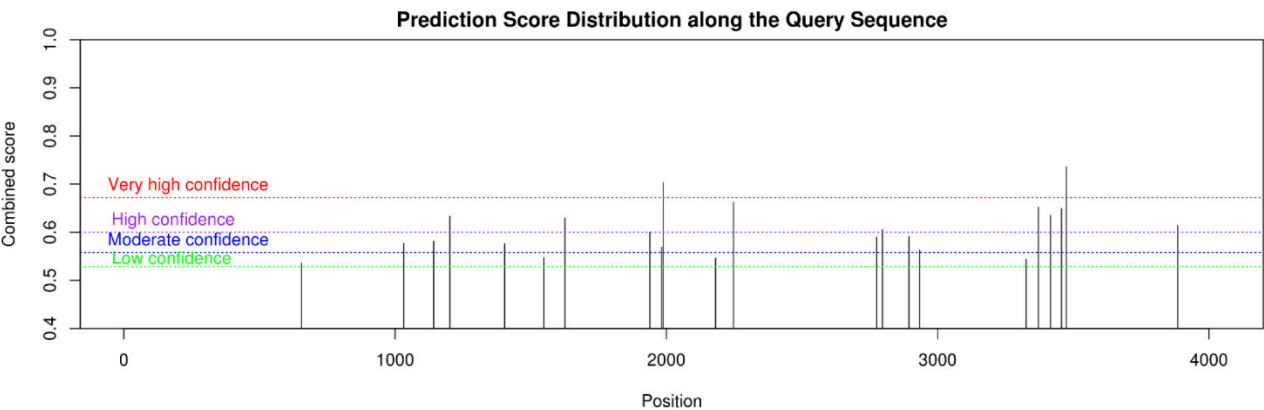


Figure S3. Prediction score of m6A distribution according to the sequence-based RNA adenosine methylation site predictor (SRAMP) algorithm. Y axis presents the combined score at different levels of high (H), moderate (M), and low (L) probability. Vertical bars show the score for predictive m6A sites. X axis shows TERT genome in base pair resolution.