

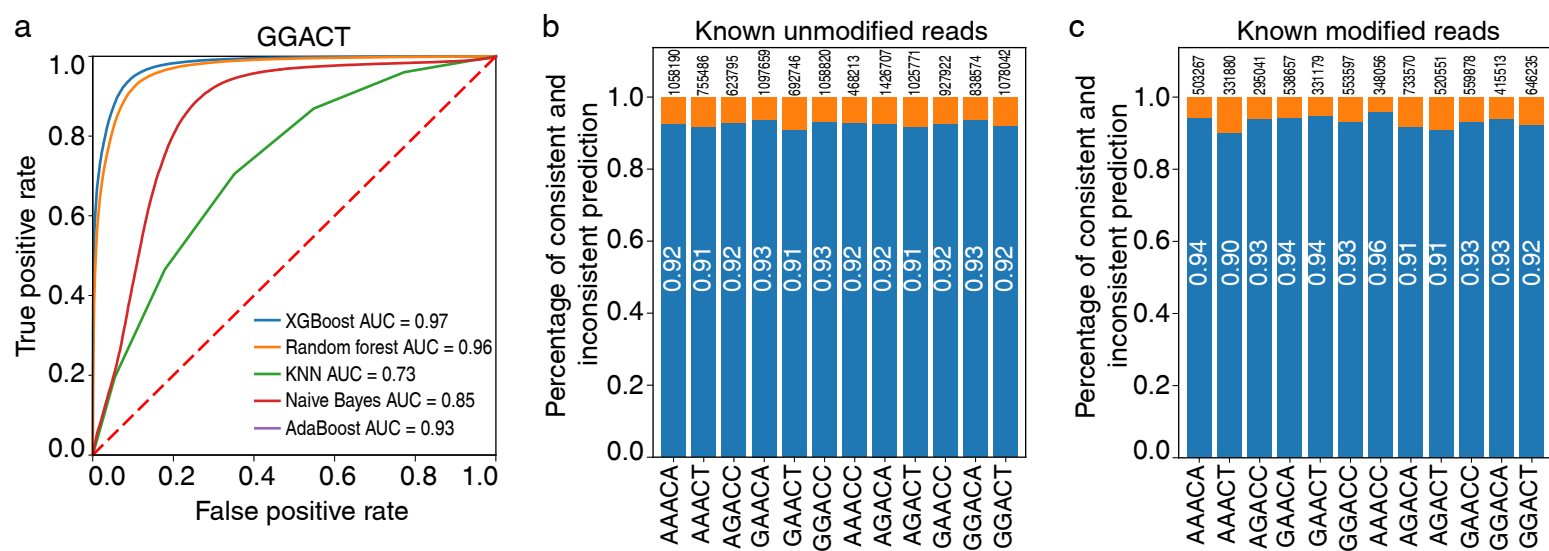


Figure S1: (a) ROC curve from several models (using one of the k-mer GGACT as an example). (b) Bar plot of predicted accuracy for all unmodified RRACH k-mers. (c) Bar plot of predicted accuracy for all modified RRACH k-mers.

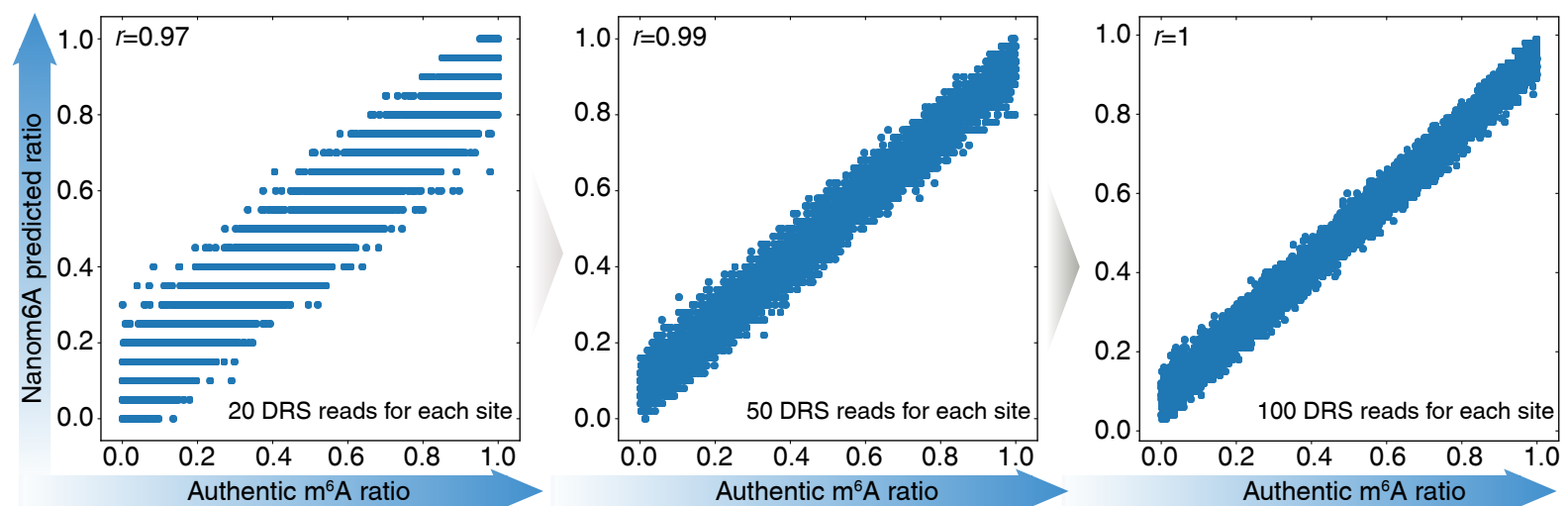


Figure S2: Scatter plot shows the correlation between authentic m⁶A ratio and Nanom6A prediction. The x-axis represents known m⁶A ratio (authentic m⁶A-modified reads/authentic unmodified reads) based on random sub-sample of synthetic DRS transcripts. The y-axis represents the predicted m⁶A ratio based on Nanom6A. The number of random rounds is 1000. Three panels from left to right represent 20, 50, and 100 DRS reads for each m⁶A ratio, respectively.

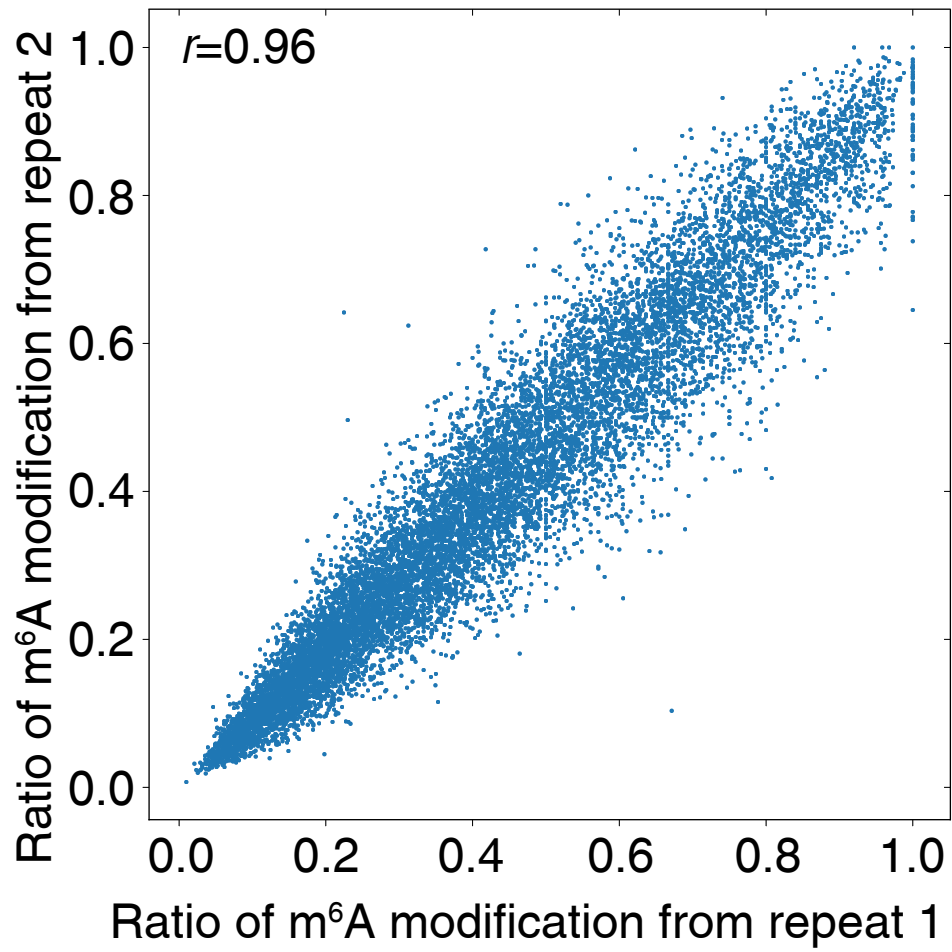


Figure S3: The correlation between two biological repeats.

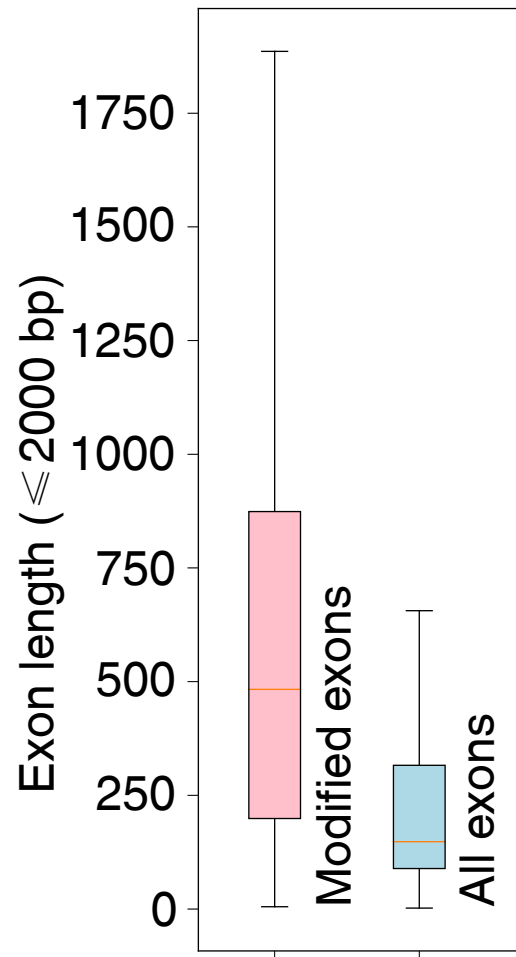


Figure S4: The length of exons with or without m⁶A modification.

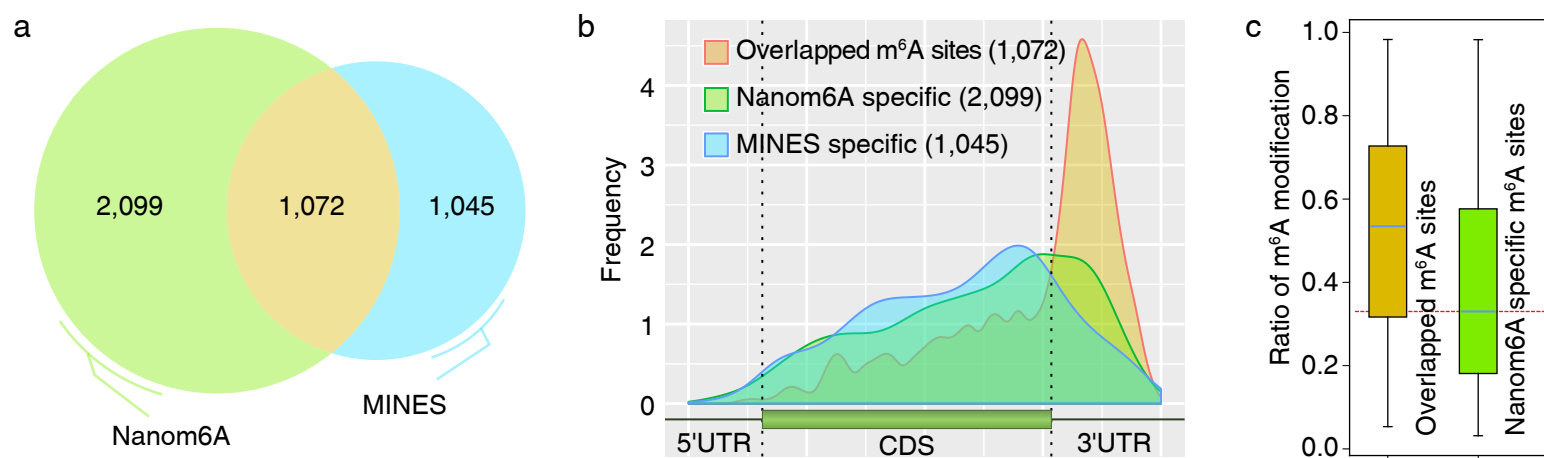


Figure S5: (a) Comparison of m⁶A sites from AGACT, GGACA, GGACC, and GGACT sites between Nanom6A and MINES. (b) The distribution of m⁶A site for overlapped sites, Nanom6A specific sites and MINES specific sites. (c) The m⁶A ratio for overlapped sites and Nanom6A specific sites.