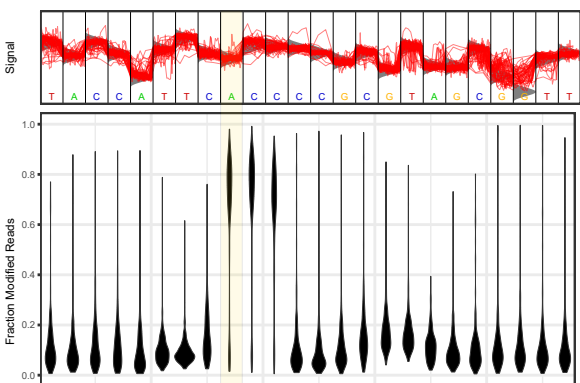
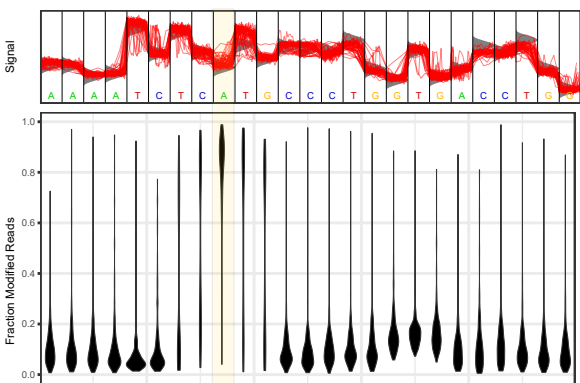


YTCAN⁶GTNG



CYYAN⁷RTGA



ATGCAT

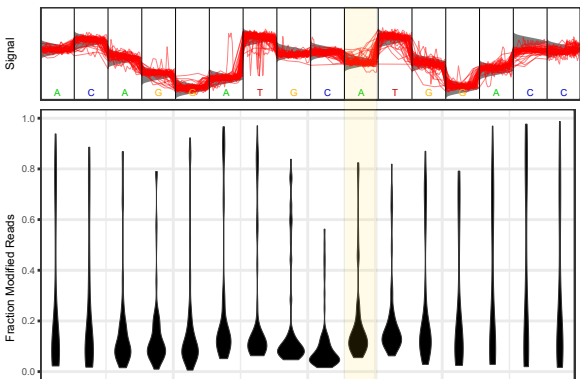


Figure S6. Assessment of m6A modification in *E. coli* DNA motifs.

DNA methylation at YTCAN⁶GTNG, and CYYAN⁷RTGA, and ATGCAT motifs are assessed using ONT LIG sequencing. Top: An example motif is shown, with red lines displaying individual reads mapped to the region. The expected raw signal distribution using a canonical base model (=unmethylated DNA) is shown in grey. The location of known methylation in *E. coli* is highlighted in yellow. Bottom: The fraction of reads supporting a modification event is reported for each position in the motif, and the distribution of proportions are shown. Higher values indicate the motif is more ubiquitously methylated in the *E. coli* genome. Distributions are shown for 242 YTCAN⁶GTNG motifs, 248 CYYAN⁷RTGA motifs, and 66 ATGCAT motifs.