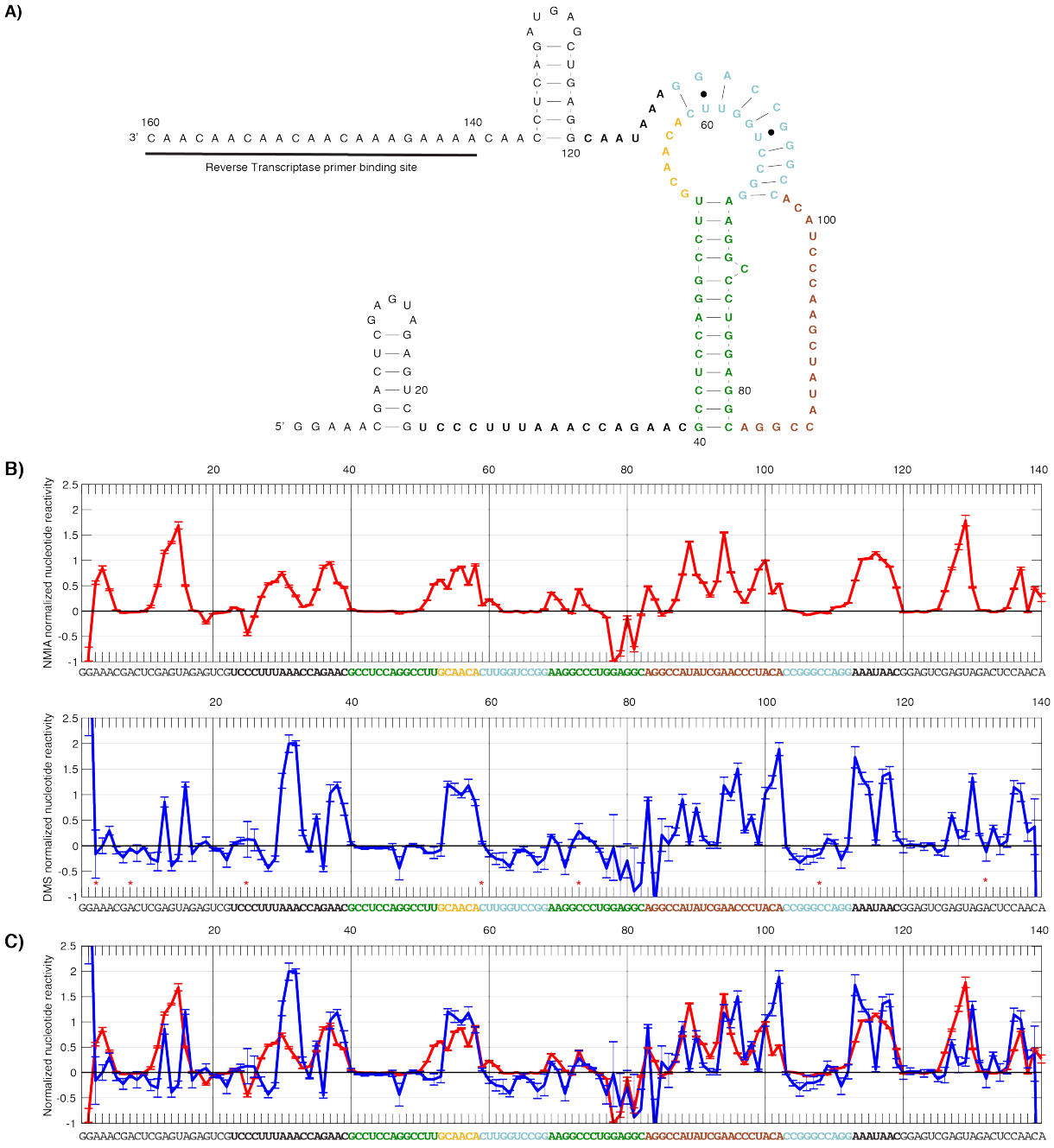
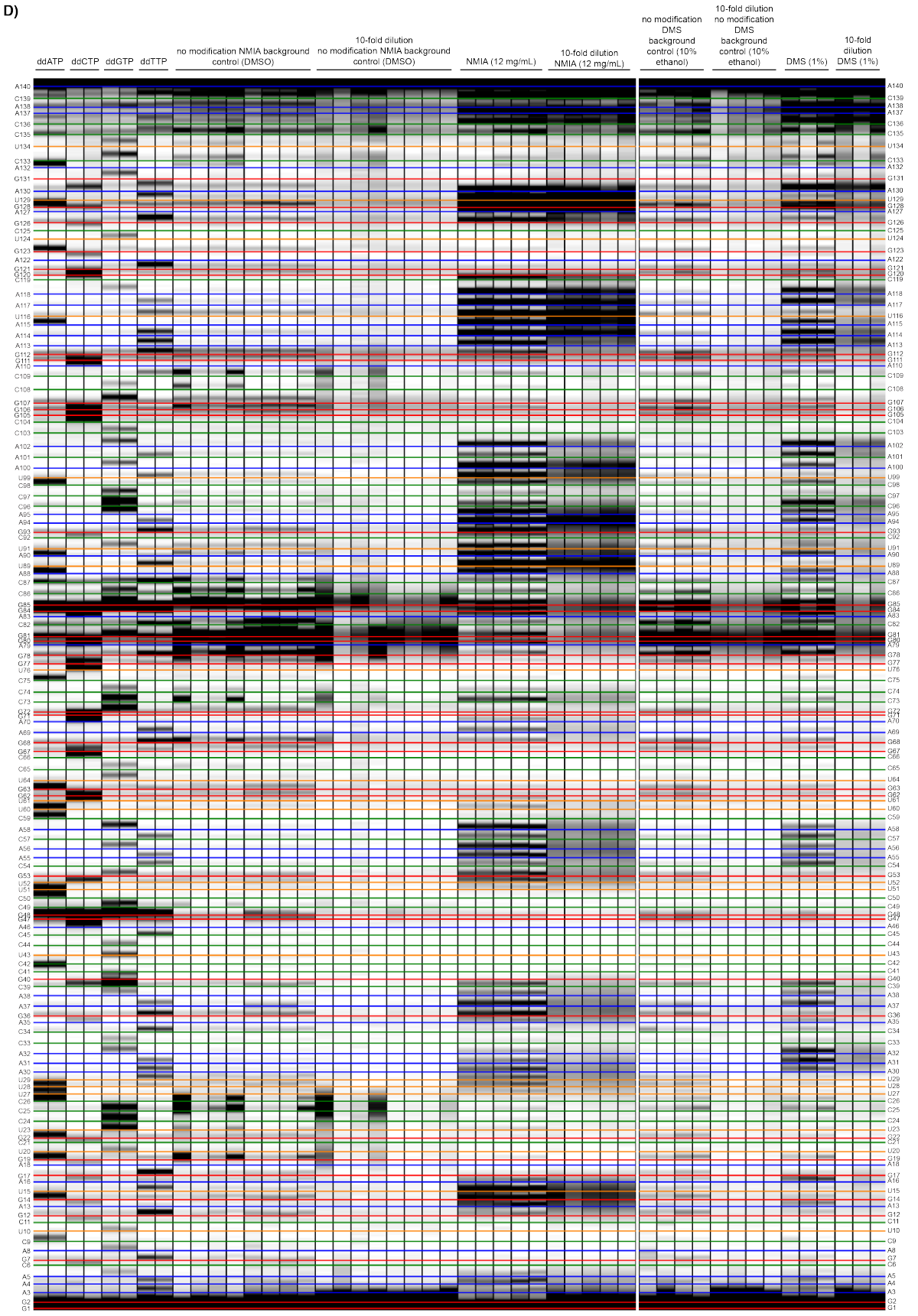

A)
Reverse Transcriptase primer binding site
B)
NMIA normalized nucleotide reactivity
DMS normalized nucleotide reactivity
C)
Normalized nucleotide reactivity

D)


ddATP
ddCTP
ddGTP
ddTTP
no modification NMIA background control (DMSO)
10-fold dilution no modification NMIA background control (DMSO)
NMIA (12 mg/mL)
10-fold dilution NMIA (12 mg/mL)
no modification DMS background control (10% ethanol)
10-fold dilution no modification DMS background control (10% ethanol)
DMS (1%)
10-fold dilution DMS (1%)

Supplemental Figure S2. Chemical probing of the HTLV-1 WT *pro-pol* frameshift site RNA. A) The RNA cassette used in chemical modification experiments is shown. Nucleotides 2235-2331 from the HTLV-1 consensus sequence (NC_001436.1) are shown in bold. Pseudoknot elements stem 1, loop 1, stem 2, and loop 2 are highlighted with green, orange, cyan, and copper font, respectively. B) Normalized and averaged nucleotide reactivities are shown in red (NMIA) and blue (DMS) for cassette nucleotides 1-140. Points with more scatter than expected were deemed to be outliers and are indicated by red asterisks. Error estimates were calculated using a minimum of three replicates and are shown with horizontal lines. Pseudoknot elements are highlighted in the RNA sequence as shown in (A). C) An overlay of the data in (B). D) The aligned and assigned CE traces from the HTLV-1 WT *pro-pol* frameshift site chemical probing experiments. Assignments are shown on the left and right side of the traces with numbering consistent with (A). Colored horizontal lines are positioned just below the corresponding band assignments.