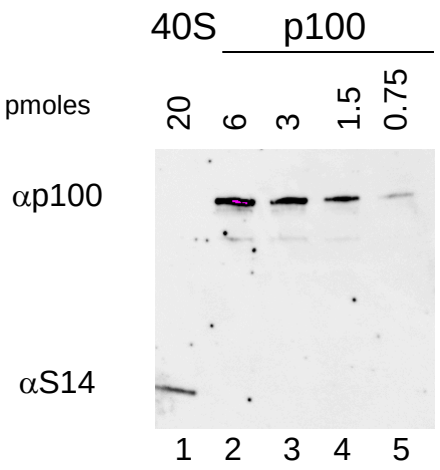
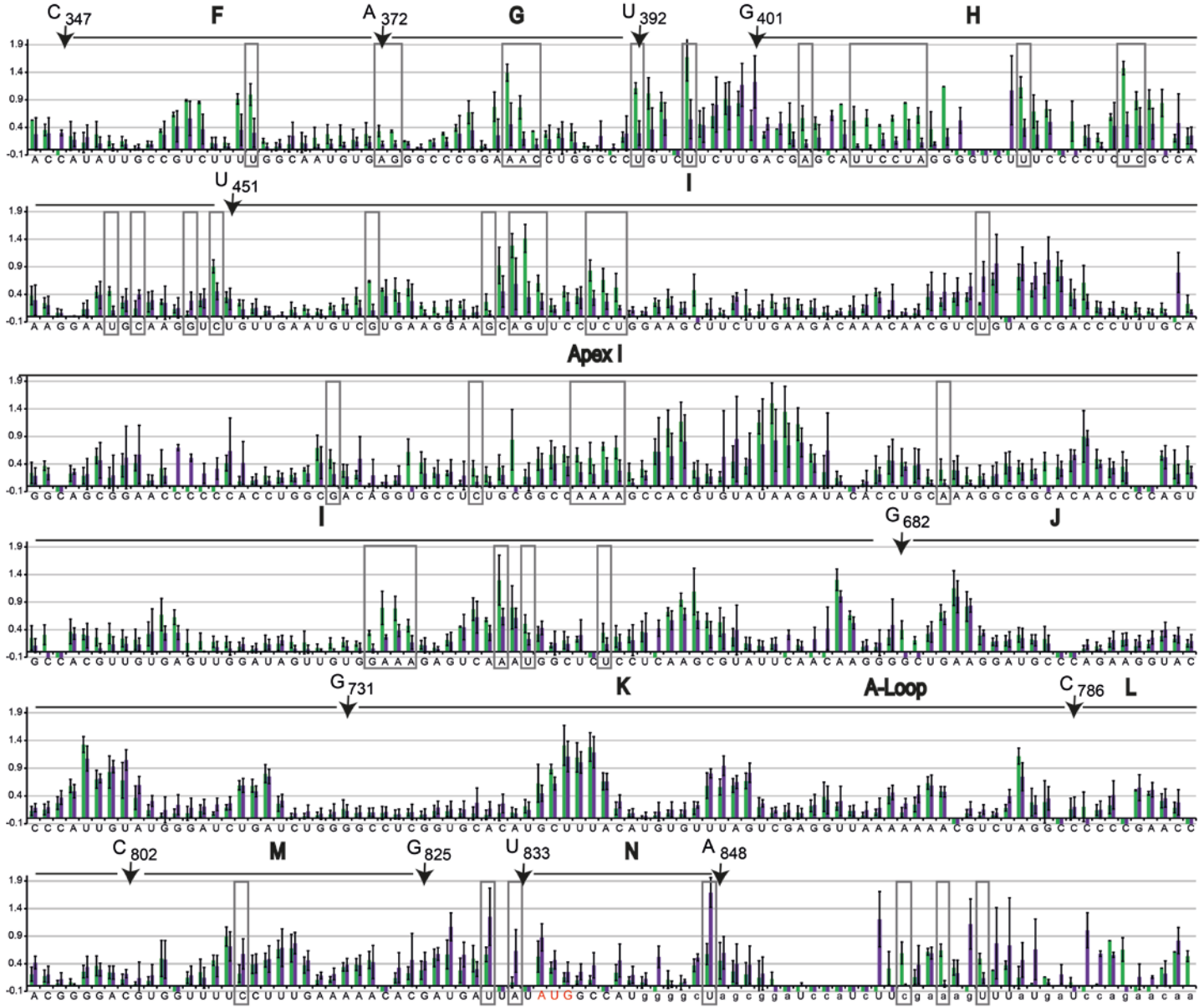
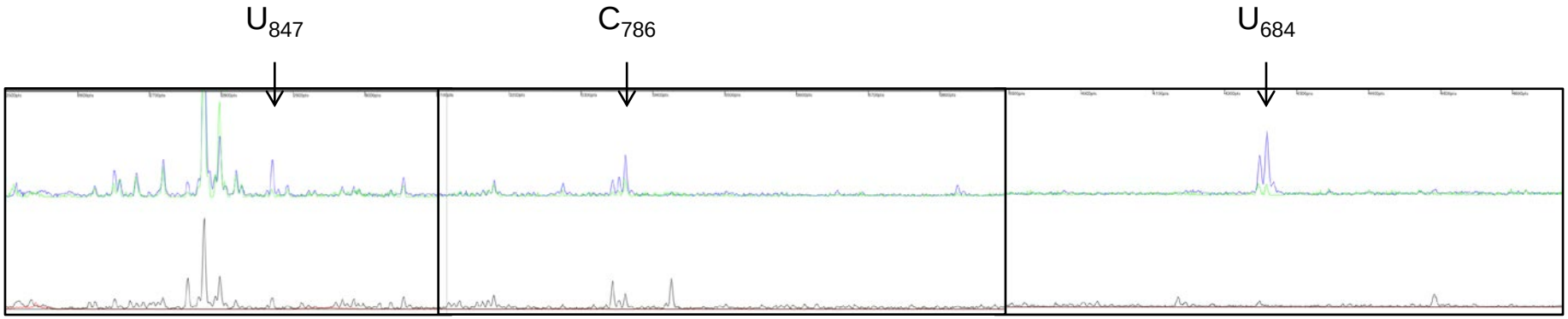


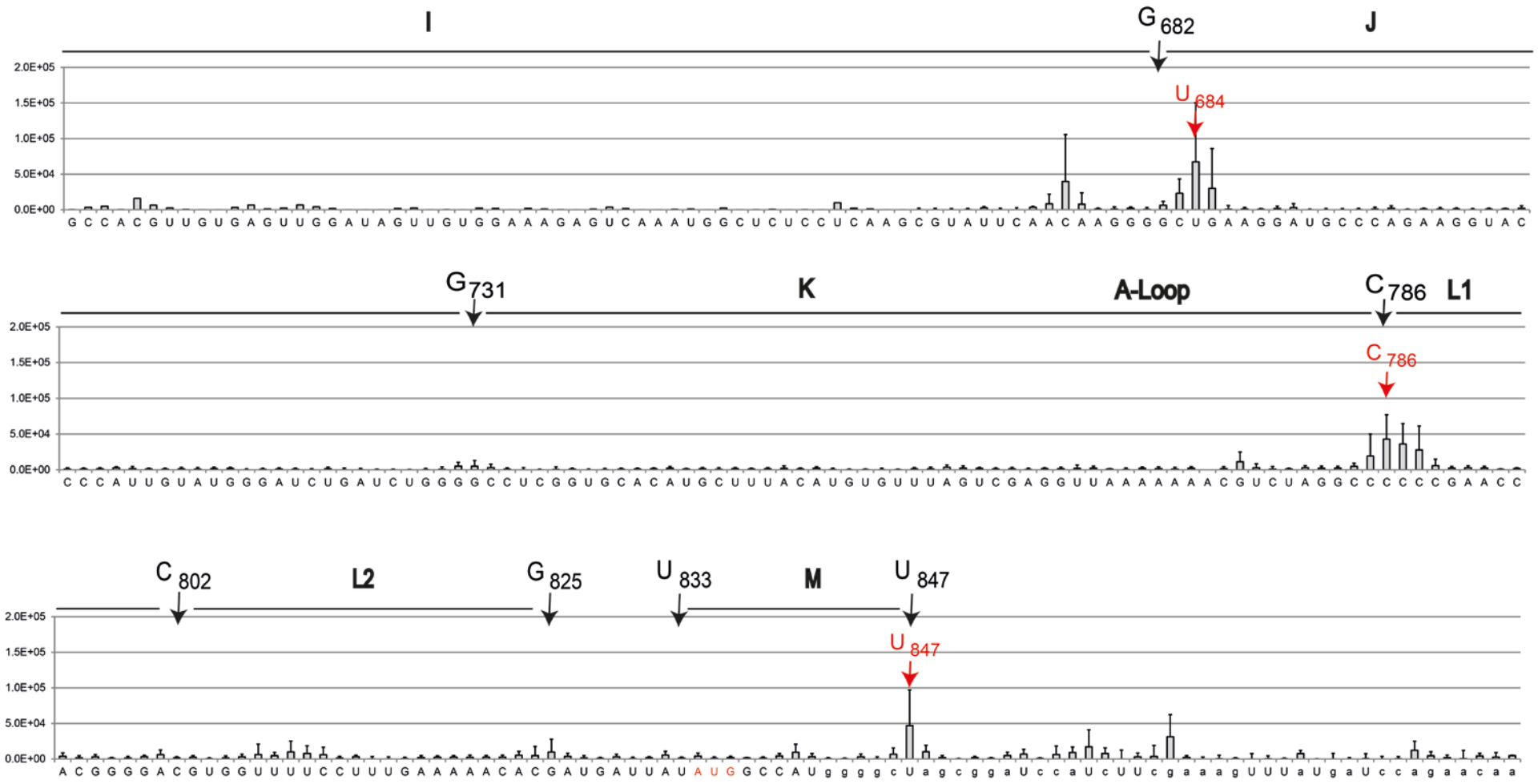
Supplemental Figure 1: Absence of eIF4G contamination (less than 5 %) was ascertained by semi-quantitative Western blot by using 20 pmoles of purified ribosomal 40S subunits (lane 1) and decreasing amounts of purified eIF4G (p100 fragment, lanes 2-5). Initiation factor specificity of the primary antibody is indicated on the left.



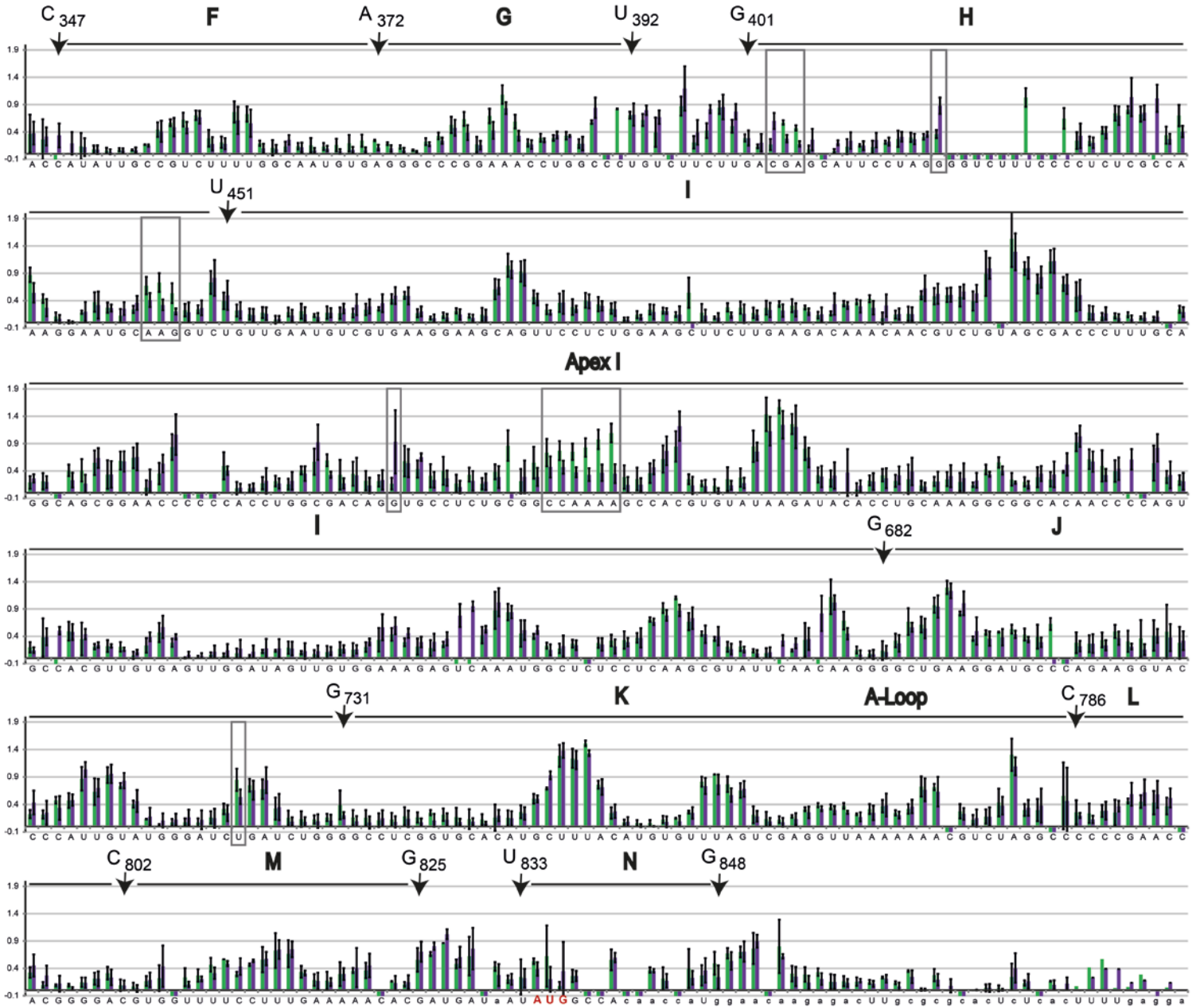
Supplemental Figure 2: SHAPE probing of EMCV-Rluc in the presence of ribosomal 40S. The 1M7 reactivity obtained in the absence (green) or presence (purple) of ribosomal 40S. Domains are indicated in the Figure as well as relevant nucleotide positions. Boxed regions highlight significant differences as measured by a bilateral Student test with an acceptance value of 0.05. Error bars are the s.e.m. of at least four independent experiments.



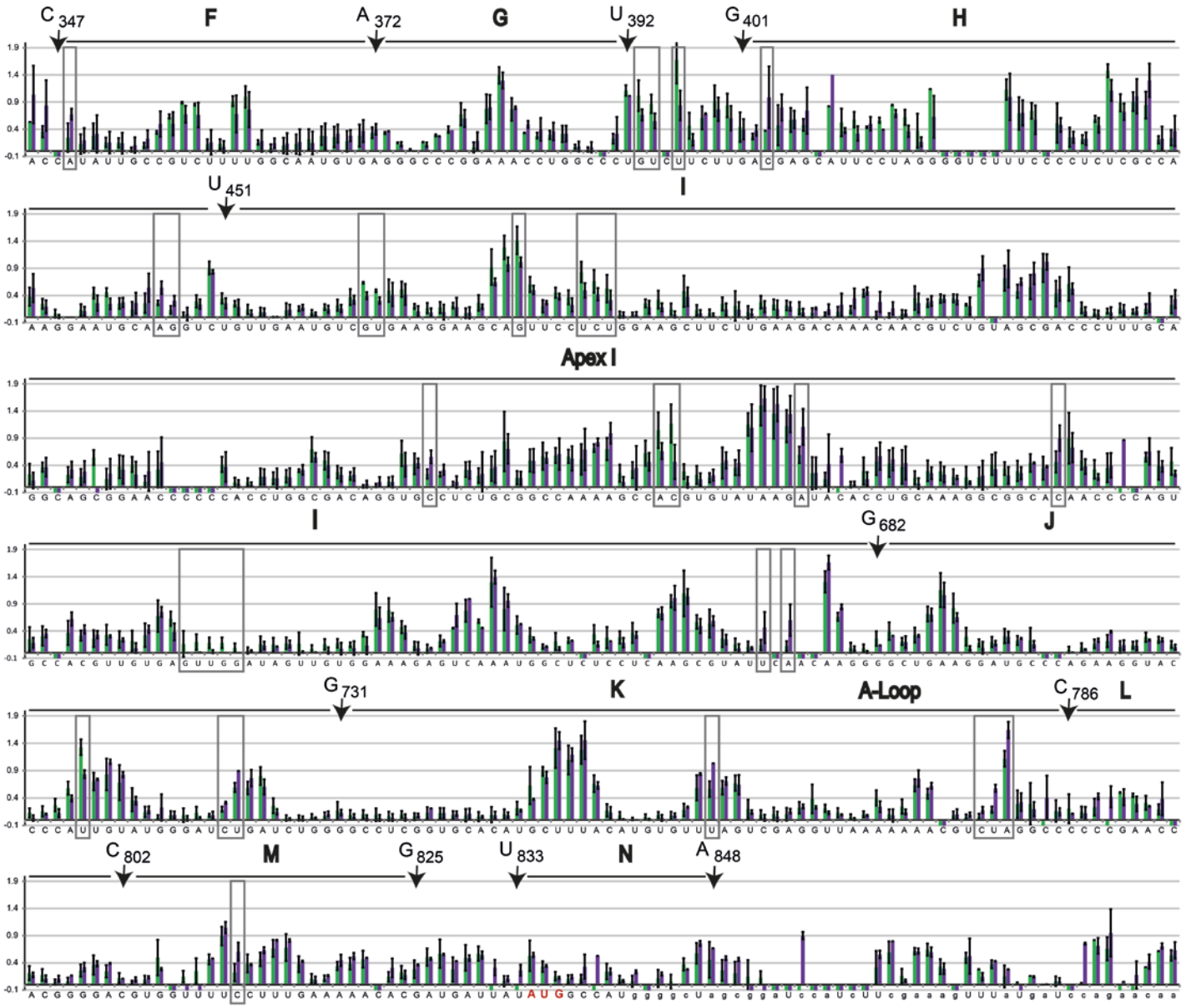
Supplemental Figure 3: Toe- print of EMCV-Rluc in the presence of ribosomal 40S. Capillary electrophoresis electrophoregram exported from a CEQ8000 and analyzed using the software “Shapefinder” (http:bioinfo.unc.edu). Blue, the profile obtained in the presence of 40S, green, the profile obtained in the absence of 40S, red and black the sequencing reactions. The position of the specific reverse transcriptase stops are indicated.



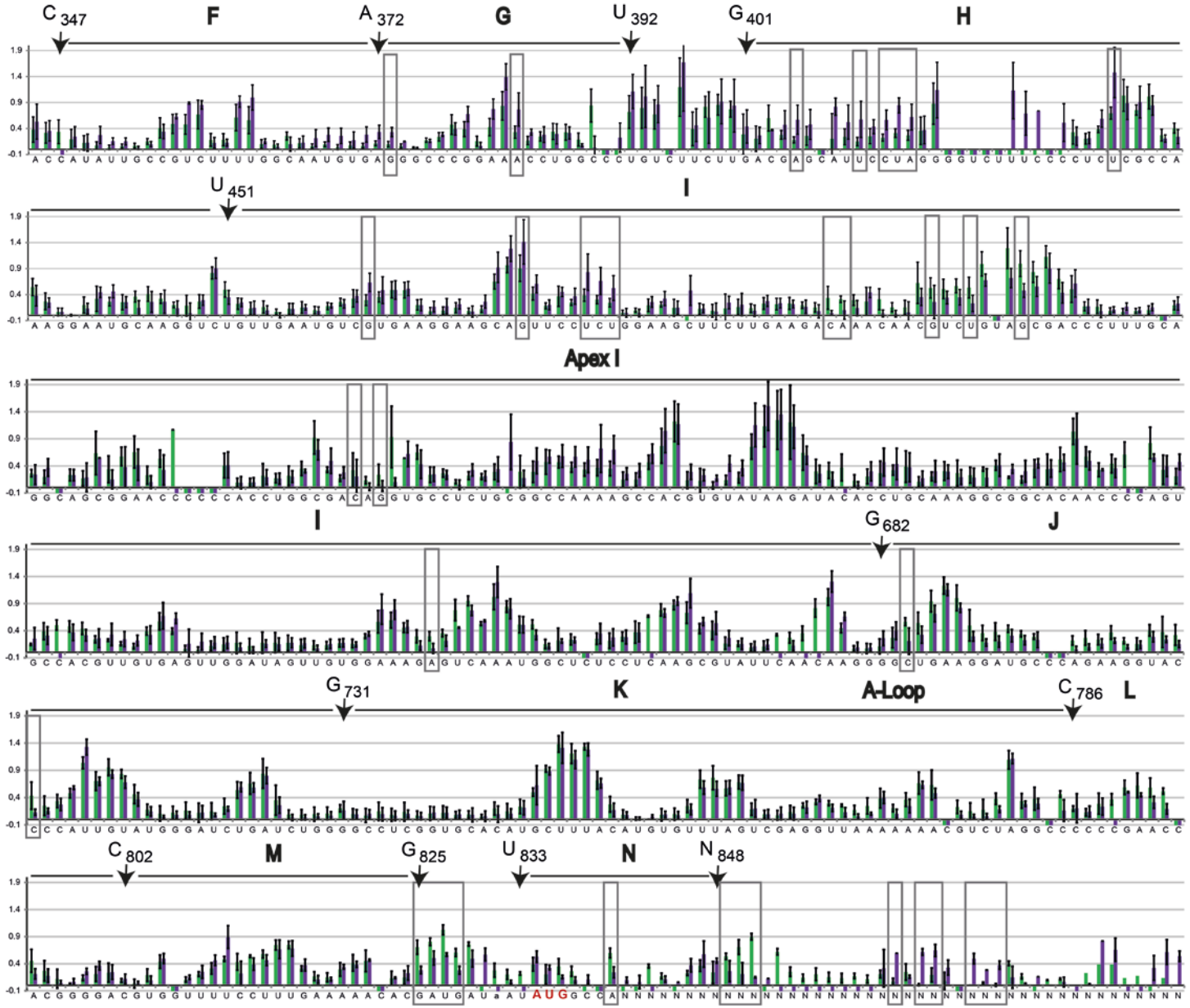
Supplemental Figure 4: Toe-print analysis of EMCV-RLuc in the presence of ribosomal 40S. Toe print was performed by capillary electrophoresis as described in [19]. Histograms represent the differential peak intensity (with–without 40S) for each position. Domains are indicated in the Figure as well as relevant nucleotide positions. Error bars are the s.e.m. for at least three independent experiments.



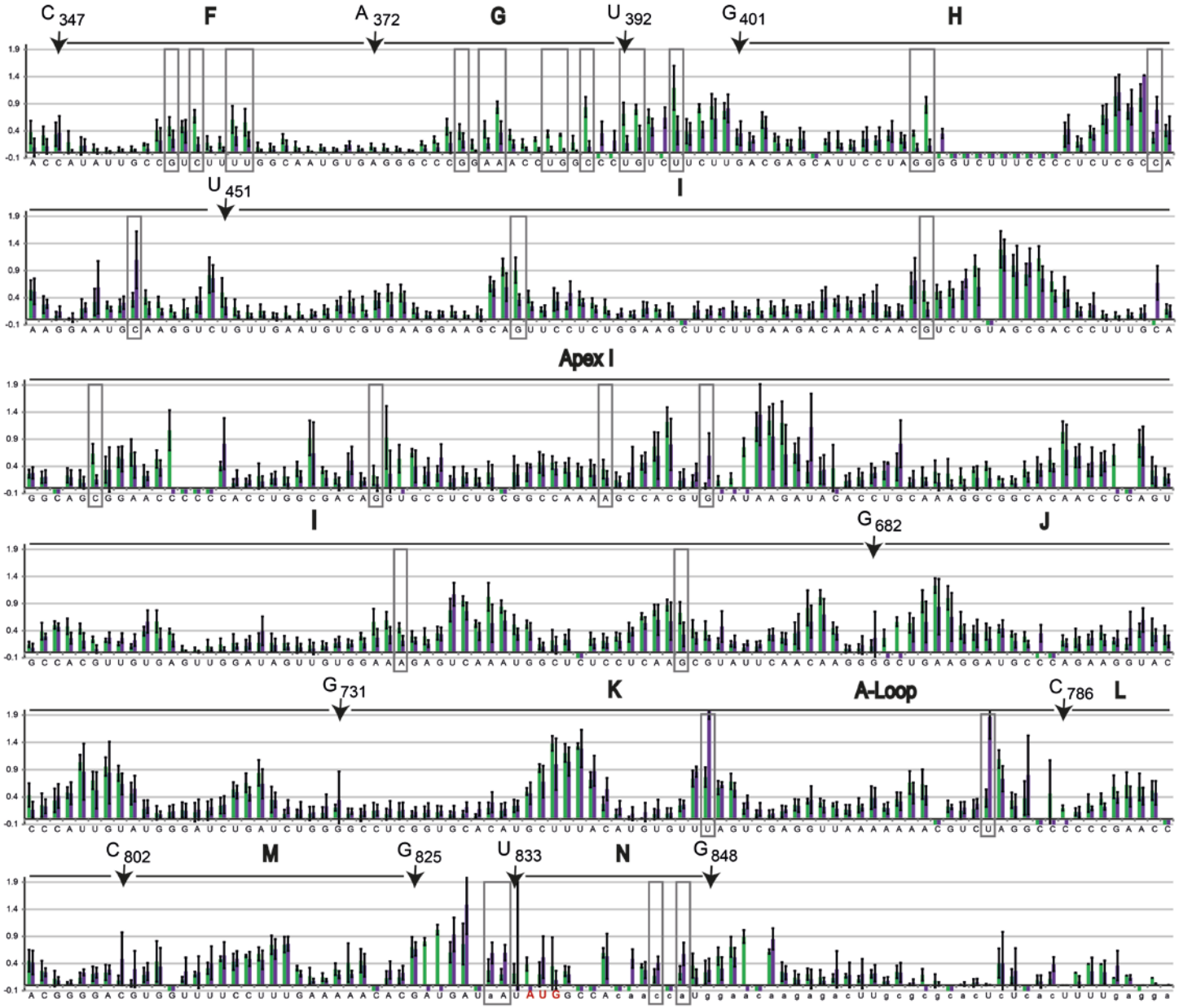
Supplemental Figure 5: SHAPE probing of EMCV-L. The 1M7 reactivity obtained in the absence (green) or presence (purple) of magnesium. Domains are indicated in the Figure as well as relevant nucleotide positions. Boxed regions highlight significant differences as measured by a bilateral Student test with an acceptation value of 0.05. Error bars are the s.e.m. of at least four independent experiments.



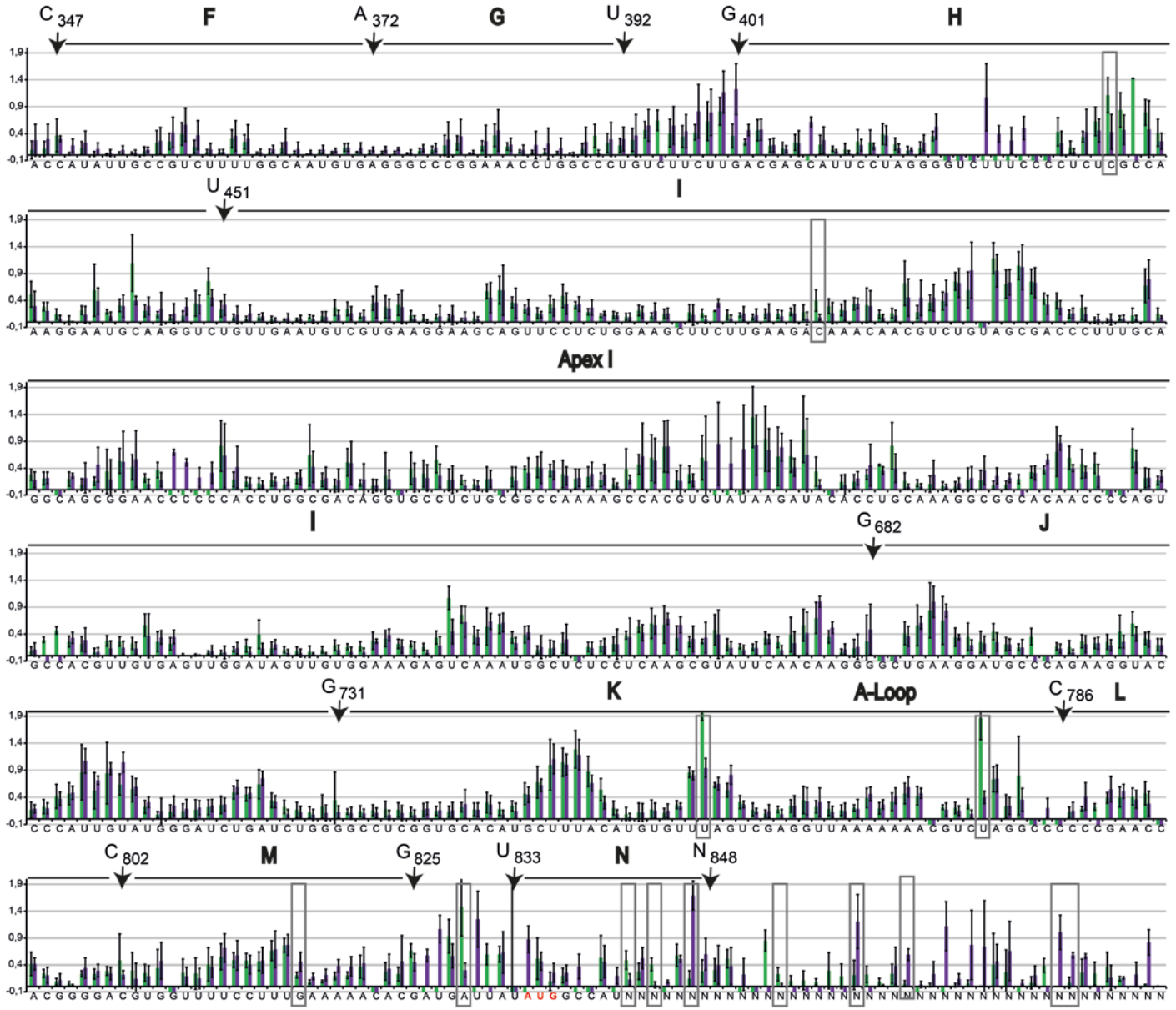
Supplemental Figure 6: SHAPE probing of EMCV-RLuc. The 1M7 reactivity obtained in the absence (green) or presence (purple) of magnesium. Domains are indicated in the Figure as well as relevant nucleotide positions. Boxed regions highlight significant differences as measured by a bilateral Student test with an acceptation value of 0.05. Error bars are the s.e.m. of at least four independent experiments.



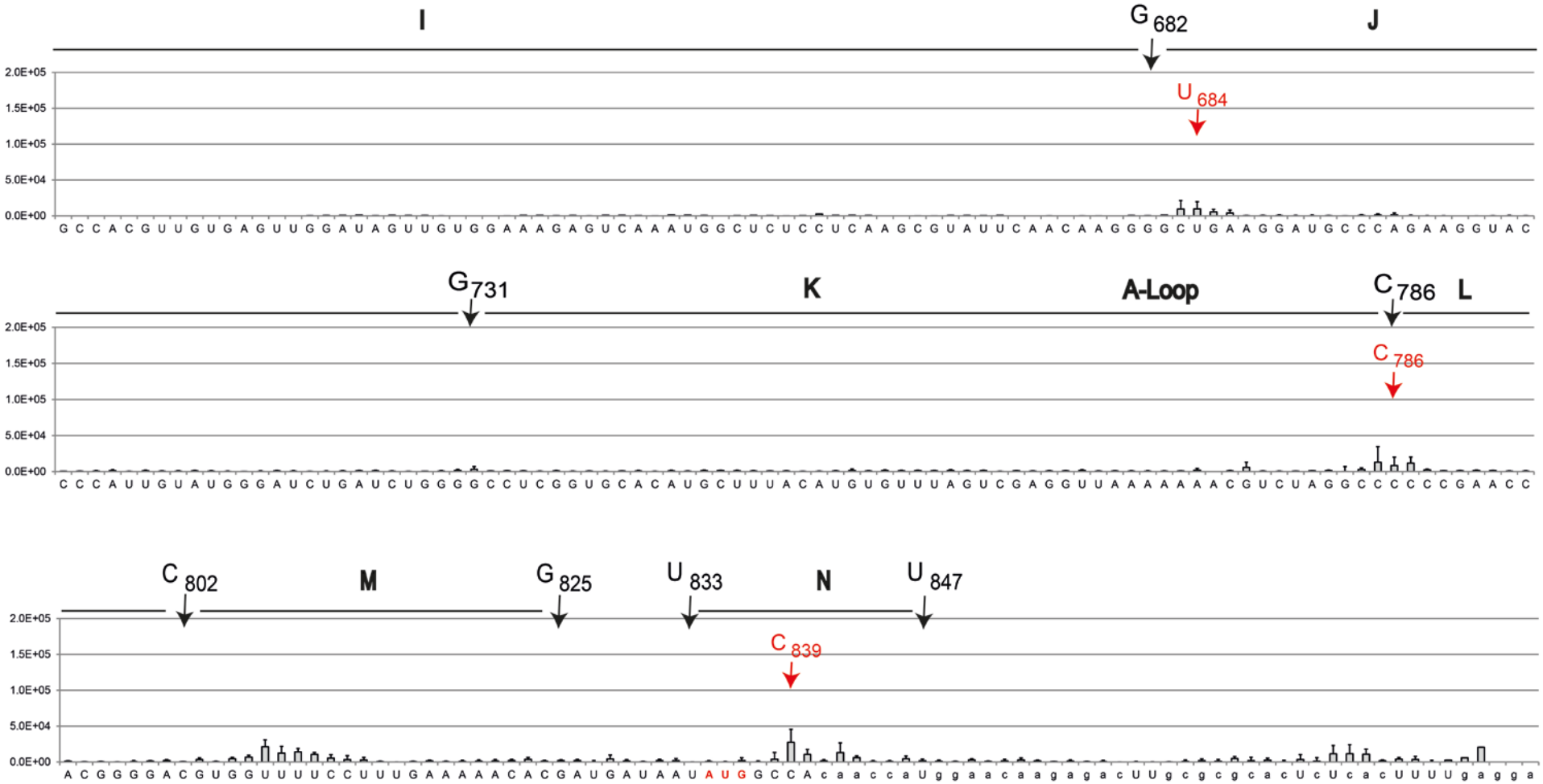
Supplemental Figure 7: Comparison of EMCV-L and EMCV-RLuc. The 1M7 reactivity obtained in the presence of magnesium for EMCV-L (green) or EMCV-RLuc (purple) RNA. Domains are indicated in the Figure as well as relevant nucleotide positions. Boxed r egions highlight significant differences as measured by a bilateral Student test with an acceptation value of 0.05. Error bars are the s.e.m. of at least four independent experiments.



Supplemental Figure 8: SHAPE probing of EMCV-L in the presence of ribosomal 40S. The 1M7 reactivity obtained in the absence (green) or presence (purple) of ribosomal 40S. Domains are indicated in the Figure as well as relevant nucleotide positions. Boxed regions highlight significant differences as measured by a bilateral Student test with an acceptation value of 0.05. Error bars are the s.e.m. of at least four independent experiments.



Supplemental Figure 9: SHAPE probing of EMCV-L (green) and EMCV-RLuc (purple) in the presence of ribosomal 40S. Domains are indicated in the Figure as well as relevant nucleotide positions. Boxed regions highlight significant differences as measured by a bilateral Student test with an acceptation value of 0.05. Error bars are the s.e.m. of at least four independent experiments.



Supplemental Figure 10: Toe-print analysis of EMCV-L in the presence of ribosomal 40S. Toe print was performed by capillary electrophoresis as described in [19]. Histograms represent the differential peak intensity (with–without 40S) for each position. Domains are indicated in the Figure as well as relevant nucleotide positions. Error bars are the s.e.m. of at least three independent experiments.