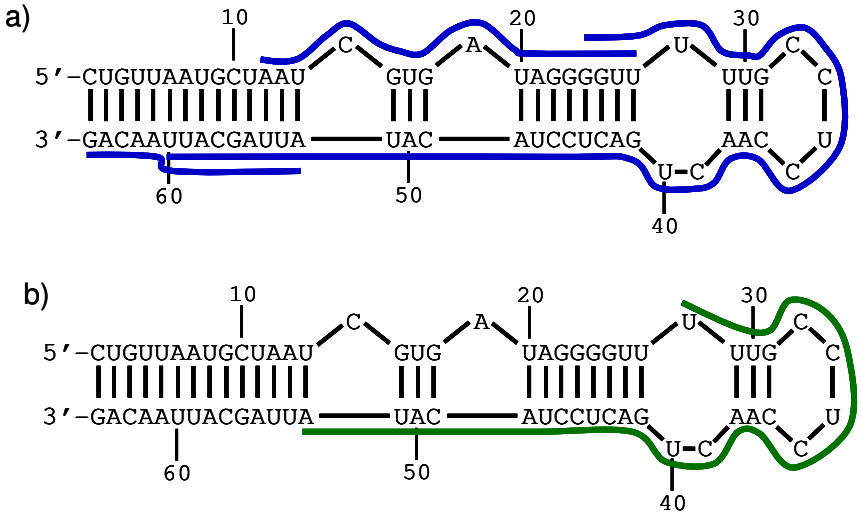
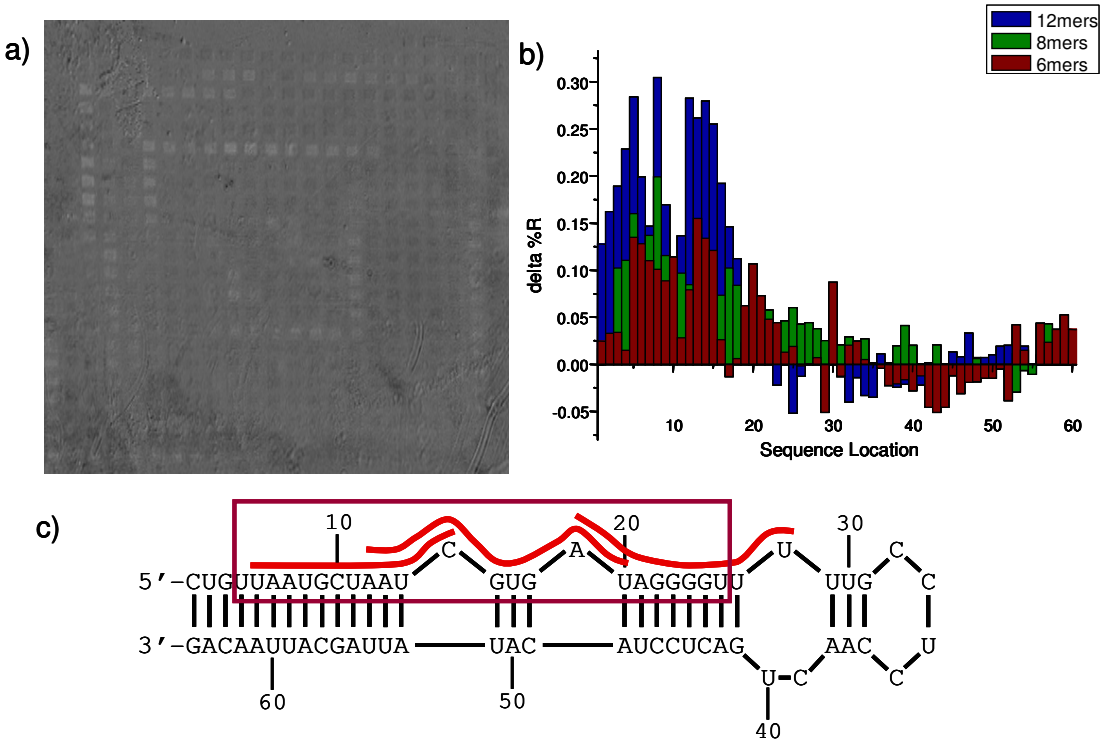
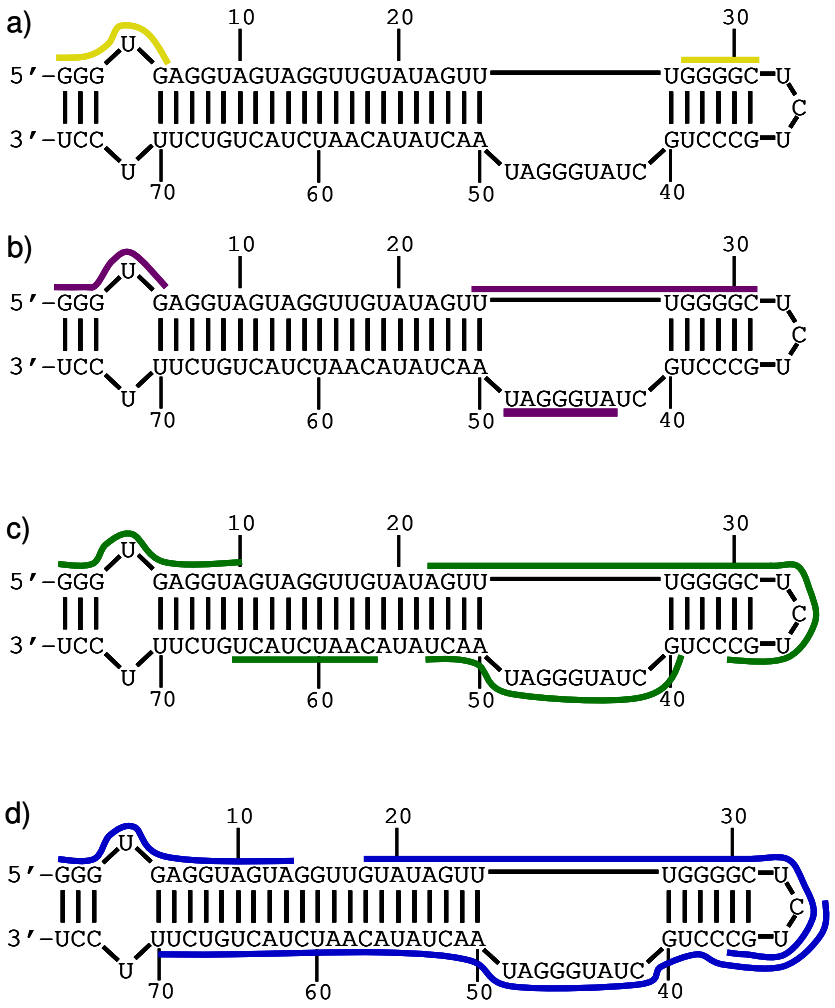
Supplementary Figures:



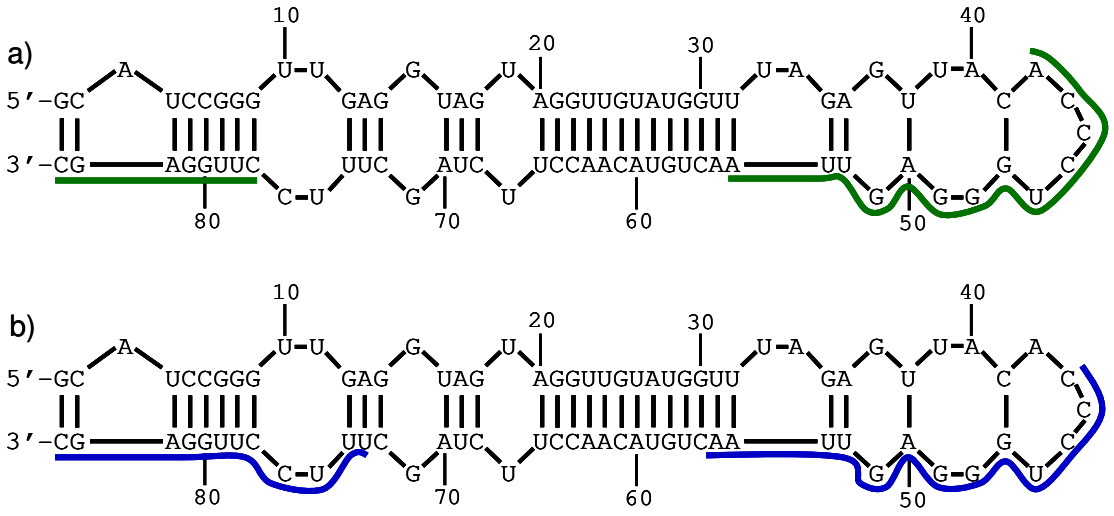
Supplementary Figure 1: Accessible site maps for pre-miR-155. a) Map based on hybridization to 8mer perfect complement probes. b) Map based on hybridization to 12mer perfect complement probes.



Supplementary Figure 2: Hybridization of miR-155 RNA to the pre-miR-155 array. a) SPRi difference image indicating hybridization of target RNA (bright features). b) Average SPR signal change after application of RNA. The y-axis corresponds to the average change in % reflectivity, while the x-axis corresponds to the location of the surface probe along the RNA sequence (Location 1 corresponds to nts 1-6 for 6mers, 1-8 for 8mers, etc.). The red histogram represents 6mer probes, green is 8mer probes, and blue corresponds to 12mer probes. The binding region is the same no matter which probes are used, but expanded and higher signal change occurs with longer probes. c) The lowest energy predicted structure by mfold of pre-miR-155 RNA with the 23mer miR-155 RNA outlined in purple box. The experimentally determined 6mer probe accessible sites are indicated by the red line. Red is chosen here to correspond to the red 6mer features shown in Figure 1 panel a) and plotted in panel b) of this figure. The 23mer RNA target has no predicted structure.



Supplementary Figure 3: Accessible site maps for pre-let-7a3. a) Map based on hybridization to 4mer perfect complement probes. b) Map based on 5mer perfect complement probes. c) Map based on hybridization to 8mer perfect complement probes. b) Map based on hybridization to 12mer perfect complement probes.



Supplementary Figure 4: Accessible site maps for pre-let-7c. a) Map based on hybridization to 8mer perfect complement probes. b) Map based on hybridization to 12mer perfect complement probes.