



Figure S5: Secondary structures of the six RNA sites that are tested experimentally. The structures were determined using the minimum free energy method of the RNAfold webserver with the default parameters.<sup>36</sup> The arrows here indicate the Adenine base that is being edited by the various ABEs. The bases are colored by their base-pairing probabilities. For unpaired regions the color denotes the probability of being unpaired. All sites, except site 6, predict the target adenine to occur as unpaired hairpin loop regions.