

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: List of editing sites (included in Figure 6c), their respective gene expression levels and miRNA target information. Each editing site was required to be “edited” (editing level >0.3) in at least 3 individuals and “non-edited” (editing level = 0) in at least 3 individuals. Additionally, the closest predicted miRNA target site was required to be located within 100nt from the editing site. The relative accessibility at the miRNA target site was calculated as log₂ ratio of accessibility of the “G”-containing versus “A”-containing structures, predicted using RNAplfold.

File Name: Supplementary Software 1

Description: A python script to identify the nucleotide in the opposing position of a given editing site in the RNA secondary structure predicted by RNAFold.

File Name: Supplementary Software 2

Description: A python script to calculate the relative accessibility in the RNA secondary structures containing an edited “G” nucleotide vs. a reference “A” nucleotide. This script takes the output file from Supplementary Software 1 as an input file.