

Supplemental legends

Supplemental file 1: Microarray expression values of individual miRNAs in indicated samples. Samples include biological replicates (designated “A” and “B”) of mock, WNV infected, and interferon-treated HEK293 and SK-N-MC cells. Expression values are followed by p-value indicating confidence level of expression. Mature sequence of individual miRNAs and reference for the sequence are given in columns Z and AA, respectively.

Supplemental file 2: Mean expression values for indicated miRNAs, and fold change in WNV-infected and IFN-treated cells, compared to controls. miRNAs are ranked in descending order based on fold change in WNV-infected HEK293 cells compared to uninfected controls.

Fig S1 Hs_154 seed sequence matches in the CTCF 3' UTR. 3' UTR of CTCF showing matches with the seed sequence (nt 2-8) of HS_154 (boxed). Seed matches are designated by the number appearing to the left of the box. Analysis of potential interactions of the 3' UTR with the Hs_154 sequence using RNA hybrid (<http://bibiserv.techfak.uni-bielefeld.de/rmahybrid/>, (45)) revealed the potential structures shown for sites 1 and 2. mfe: minimum free energy.

Fig S2 Hs_154 seed sequence matches in the ECOP 3' UTR. 3' UTR of ECOP showing matches with the seed sequence (nt 2-8) of Hs_154 (boxed). Seed matches are designated by the number appearing to the left of the box. Analysis of potential interactions of the 3' UTR with the Hs_154 sequence using RNA hybrid (<http://bibiserv.techfak.uni-bielefeld.de/rmahybrid/>, (45)) revealed the potential structures shown for site 1. mfe: minimum free energy.

