**Figure S5.** Secondary structure predictions of the pre-mRNA sequence in the vicinity of the selectively edited sites listed in Table 1. (a) GluA2 at the Q/R site. (b) Gabra3 at the I/M site. (c) GluA3 at the R/G site. (d) FLNB at the Q/R site. (e) Htrc2 at the I/V site. (f) GluK2 at the Q/R site. (g) ADAR2 at the +24 site. (h) Cyfip2 at the K/E site. (i) GluA2 at the R/G site. (j) GluK1 at the Q/R site. (k) IGFBP7 at the K/E site. (l) FLNA at the Q/R site. (m) Nova1 at the S/G site. (n) KCNA1 at the I/V site. (o) PLCH2 at the R/G site. (p) TMEM63B at the Q/R site. (q) CCNI at the R/G site. (r) Azin1 at the S/G site. (s) Copa at the I/V site. (t) GPATCH8 at the K/R site. (u) NCSTN at the S/G site. (v) OSGEP at the I/M site. (x) BLCAP at the Y/C site.
dG = -186.38 [Initially -197.20] Gria Q/R
dG = -201.60 [Initially -212.40] Gabra3
\[dG = -180.56 \text{ [Initially -195.40] gria3}\]
dG = -124.35 [Initially -139.60] htr2c
dG = -555.71 [Initially -630.00] Grik2 full length
dG = -99.96 [Initially -106.70] ADARB1
dG = -161.90 [Initially -162.30] Cyfip2
[Diagram with RNA secondary structure and annotations]

Exon/intron junction

Conserved sequence

Conserved sequences

$\Delta G = -141.53$ [Initially -162.80] Gria2 R/G
dG = -123.83 [Initially -142.60] 17Aug30-04-53-16
dG = -210.71 [Initially -218.40] IGFBP7
dG = -202.88 [Initially -206.80] FLNA
\[ dG = -128.40 \text{ [Initially -136.00]} \text{ nova1} \]
\[ dG = -232.08 \text{ [Initially -257.10]} \text{ } \text{kcna1} \]
dG = -151.85 [Initially -165.10] PLCH2
\[ dG = -124.04 \text{ [Initially -127.60]} \] TMEM63B
\[ dG = -52.63 \text{ [Initially -59.40]} \text{ CCNI} \]
dG = -94.92 [Initially -104.30] Azin1
\[ dG = -50.72 \text{ [Initially -53.30]} \text{ copa} \]
dG = -125.96 [Initially -142.20] GPATCH8
\[ \text{dG} = -61.78 \text{ [Initially -62.30]} \text{ NCSTN} \]
\[ \text{dG} = -297.87 \ [\text{Initially -304.50}] \text{ Blcap} \]