Fig.S1

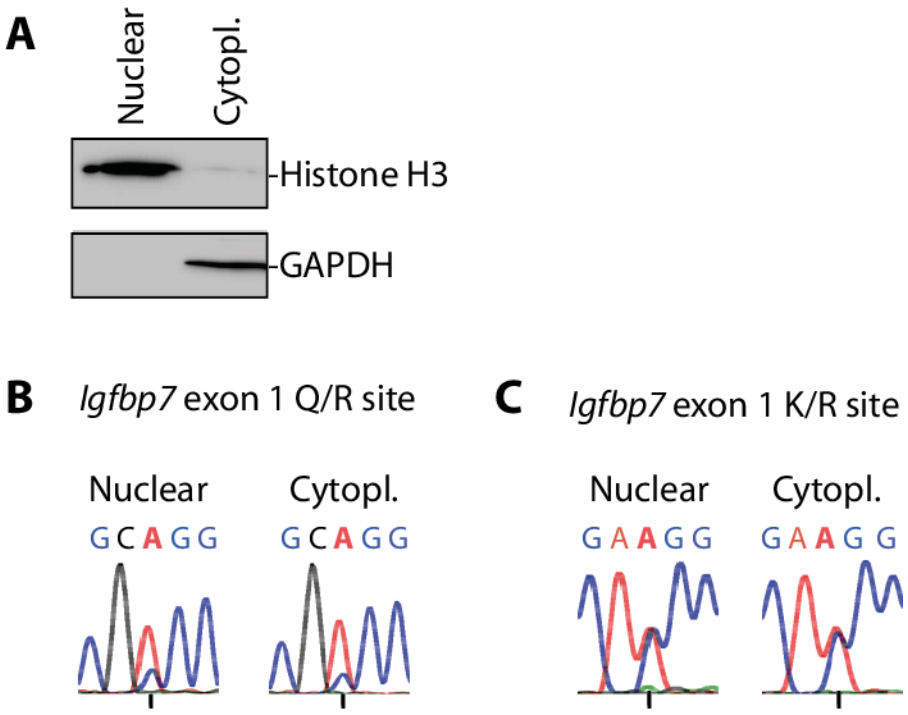

Fig.S1. Nuclear versus cytoplasmic separation of *Igfbp7* mRNA shows that the edited transcript is not selectively retained in the nucleus. A) Western blot confirming efficient nuclear vs. cytoplasmic separation of HEK293 cells co-transfected with ADAR2 and the *Igfbp7* construct exhibiting the largest differences between pre-mRNA and mRNA editing. Antibodies for histone H3 and GAPDH indicate the nuclear and cytoplasmic fraction, respectively. B,C) Direct Sanger sequencing of PCR-products generated from the nuclear and cytoplasmic fraction of *Igfbp7* mRNA exhibit no differences in editing levels for the Q/R-site (B) or K/R-site (C). The edited adenosine is marked by a vertical line.

Fig.S2

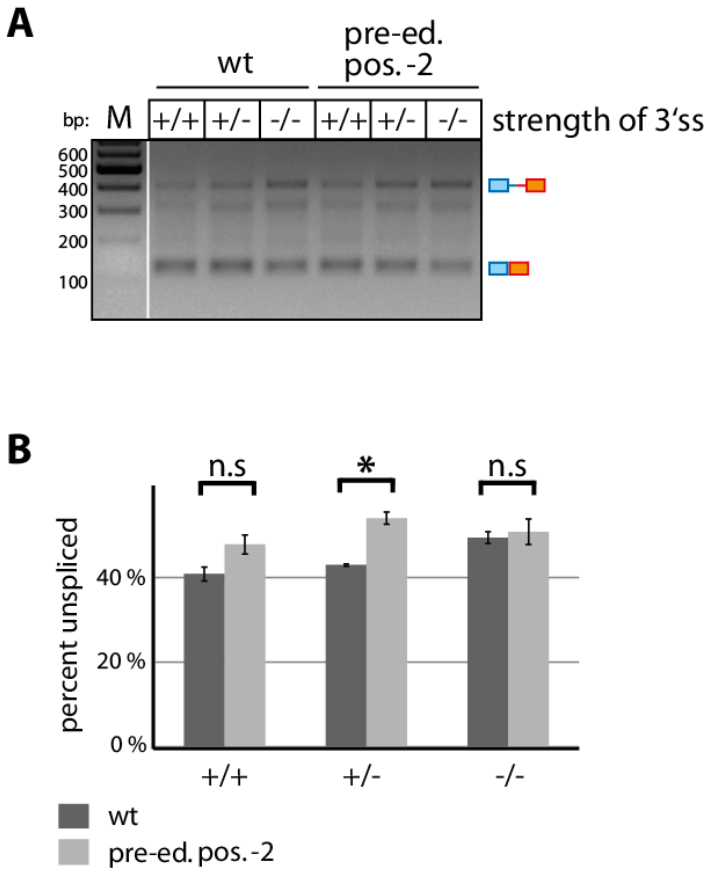

Fig.S2. Editing at position -2 in *Gria2* reduces splicing efficiency only moderately. A) RT-PCR to determine splicing efficiency of *Gria2* transcripts with a strong, intermediate or weak polypyrimidine tract (+/+, +/-, -/-) either as a wildtype or pre-edited version -2. Total RNA was prepared from cells co-transfected with reporter constructs and an ADAR2 expressing construct. Subsequently, the RNA was subjected to reverse transcription and PCR with exon-specific primers. Pre-mRNA and mRNA are indicated at the right side of the panel. M=size standard. bp=basepairs. B) The splicing efficiency – deducted from the gel in panel A - in percent unspliced transcript is given. A significant difference is only seen for the +/- situation with an average polypyrimidine tract. Compare also to Fig. 4 where pre-edited constructs for positions -2 and -3 together have been used. The quantification was done from three independent biological replicates. On top of the panel the significance level is given (* p-value < 0.05; n.s. not significant). Dark grey=wt, light grey=pre-edited position -2.