Supplementary Table 1. Sequence similarity between top-ranked off-targets (TMX3 and AAGAB*)* and the target site in ß-actin (ACTB) reveals sequence similarity as the cause of guideRNA-dependent off-target editing.

mRNA	sequence bound by gRNA[a]
ACTB	5’-GGGAGGUGAU**A**GCAUUGCU-3’
TMX3	5’-AGGAGGUGAU**A**GCAUUUUG-3’
AAGAB	5’-CCAGGUUGAU**A**GCAUUGUG-3’

[a] edited adenosines are highlighted in bold and not matching nucleotides in red.

Supplementary Table 2. Comparison SNAP-ADAR and dCas13b-ADAR system (Cox et al. Science 2017)

	SNAP-ADAR (SA) system	**dCas13b-ADAR system**
Targeting System	SNAP-tag – gRNA covalent bond SNAP-tag: human, < 200 aa gRNA: ca. 22 nt, chemically stabilized	guideRNA / dCAS13b RNP assembly[a] Cas13: bacterial >1000 aa gRNA: ~85 nt, genetically encoded
Deaminase tested	4 enzymes fully tested: ADAR1 and ADAR2 each wildtype and E488Q	1 enzyme strongly tested: ADAR2 E488Q (REPAIRv1) 1 enzyme briefly tested: ADRA2 E488Q/T375G (REPAIRv2)
Delivery	SNAP-ADAR: single genomic copy, inducible gRNA: lipofection of chemically stabilized gRNA (22 nt)	dCas-ADAR: massive overexpression via plasmid lipofection guideRNA: massive overexpression via plasmid lipofection
Editing of endogenous targets	ACTB, GAPDH, GUSB, SA, KRAS, STAT1	KRAS and PPIB
Concurrent editing	3 sites or 4 endogenous house keeping transcripts, no loss in efficiency 2 sites or 2 endogenous signaling transcripts (KRAS, STAT1), no loss in efficiency	Nothing shown
Editing range for the best editable codon (UAG) on endogenous targets	wild-type SA: 15 - 90%, (12 sites on 6 targets, ORF & UTRs) SAQ variants: 46 - 90%, (13 sites on 6 targets, ORF & UTRs)	REPAIRv2: 7-25%, (5 sites on 2 targets, only ORF) REPAIRv1: 15-40%, (5 sites on 2 targets, only ORF)
Codon scope	all 16 codons tested on an endogenous target with SA1Q and SA2Q	all 16 codons tested, but on an overexpressed reporter transcript with overexpressed Cas-ADAR. The co-overexpression together with the low editing yields suggest that the shallow codon specificity observed could be an overexpression artefact. Codon scope was only tested for REPAIRv1, not for version 2
Applications in the manuscript	Manipulation of signaling transcripts, KRAS and STAT1, recoding of phosporylation switch Tyr701 in STAT1	Manipulation of the signaling transcript KRAS, but not at a phosphorylation site. The claimed editing of 34 "*release-relevant transcripts*" (Figure 4) is somewhat misleading.[b]
Editing duration	stable over several days	Nothing shown
Off-targets in gRNA/substrate duplex	the guideRNA/mRNA duplex is small (19 bp), chemical modification of guideRNA blocks off-target editing almost entirely even in A-rich codons	General: the guideRNA/mRNA duplex is large (50 bp) REPAIRv1: massive problem, several sites, high yields REPAIRv2: better, but present, too little data is shown yet
Global off-target editing	Wild-type SA: almost absent SAQ variants: moderate (≈1000 sites, might be further decreased by lowering SAQ expression)	REPAIRv2: almost absent (**but** the 125x coverage/deep sequencing analysis (Figure 6D) was done with 15fold less Cas13-ADAR plasmid (10 ng instead of 150 ng) than used in the relevant editing reactions on KRAS and PPIB (Figure 6F & Figure 5). It is unclear if KRAS/PPIB editing would be effective with 15fold less CAS13-ADAR plasmid.[c] REPAIRv1: extremely high (>18 000 sites, even though 15fold less Cas13-ADAR was transfected then in almost all other experiments)
Unique property	1) Chemically stabilized guideRNAs enable perfect specificity inside gRNA/mRNA duplex 2) low expression of editase enables high editing yields with reduced global off-target editing	1) Fashionable there are at least two other RNA editing systems that apply encodable guideRNAs which encounter the same specificity problems as Cas13-ADAR does (local off-target editing in the guideRNA/mRNA duplex, global off-target editing due to

	2) clearly proven, covalent RNA targeting 3) very short guideRNA/mRNA duplex, unlikely to interfere with endogenous ADARs or translation 4) simple co-transfection of guideRNAs enables concurrent editing	overexpression, in particular with hyperactive ADAR deaminases, low editing yields with wildtype or less active ADAR domains like version2)

a) It remains to be determined to which extent the RNA-targeting via the 35 nt DR-helix in the Cas13-guideRNAs and dCas13b interaction contributes to Cas13-ADAR editing, in particular under overexpression conditions on reporter constructs. From previous control experiments we know that under overexpression conditions editing can be obtained even in absence of any RNA targeting mechanism by self-targeting of the ADAR, in particular for long RNA duplexes (like >30 bp). When carefully reading the Cox et al. paper, the evidence is lacking that the dCAS13/guideRNA RNP assembly is strictly required for editing; the respective important control for this (Figure S8 in the Cox et al. paper) is flawed: it shows that overexpression of the ADAR2 deaminase lacking Cas13 doesn´t give editing, but the guideRNA is missing too. There is also no proof that the ADAR deaminase domain they express is giving stable, catalytically functional protein. On one hand, they claim that the free-floating deaminase is giving rise to off-target editing. On the other hand, their control ADAR deaminase alone (ADAR2DD) gives much less off-targets compared to REPAIRv1 (Figure S8, C) indicating that the truncation is less functional per se. The proper control would have been to mutate the guideRNA (at the DR domain or leave the DR domain away). We tested the Cas13 guideRNAs and found them similarly active (editing yields around 25%) when overexpressing them together with either wildtype ADAR2 or SNAP-ADAR2Q, independent of the DR domain (see Supplementary Figure 11, and further Supplementary Notes 1 and 2 below). This shows that any overexpressed highly active ADAR fusion can edit 50 bp guideRNA/mRNA duplexes independent of a targeting mechanism to similar yields under the conditions reported by Cox et al. (their Figure 2-4).

b) Cox et al. suggest that 34 disease-relevant editings have been achieved (Figure 4E). This is somewhat misleading, in particular the suggestive Figure 4G that pretends that the data from the codon screen can be transferred to thousands of clinical variants. As the 34 disease-relevant transcripts are only small pieces of cDNA (ca. 200 bp) that have been overexpressed within a reporter cassette it is unlikely that one will be able to edit the respective real transcripts with the suggested editing yields in a relevant cell with the current Cas-ADAR versions (in particular version2) and the current delivery methods. It is also unclear if any of the mutations (all selected for simple-to-edit 5´-UAG codons) is really relevant for human disease (incidence, penetrance), and what editing yield might be required for therapy. Anyway, only hyperactive, off-target-prone REPAIRv1 has been used, the more precise REPAIRv2, which has a lower editing activity (similar or lower than wildtype ADAR2, see Supplementary Fig. 10), has not been characterized in this respect. Similar experiments with disease-relevant, and overexpressed cDNAs like CFTR, and PINK1 have anyway already been described before by others, however, additionally including a relevant phenotypic change.

c) Cox et al. use very high amounts of plasmids (150 ng/96 well Cas-ADAR, 300 ng/96 well guideRNA plasmid) for the editings. However, for the deep sequencing analysis they transfect only 10 ng/96 well Cas-ADAR plasmid (if understood correctly from their manuscript). One can expect that 15fold less plasmid will strongly reduce the transfection efficiency, thus the background of many untransfected cells will clearly reduce global off-target editing, while editing on a co-transfected reporter transcript (Cluc) is less affected by lowering Cas-ADAR (Cox et al. Fig S15). Nevertheless, one can expect that editing of an endogenous target (like KRAS, PPIB) will strongly suffer if less cells are transfected. If we understand the paper correctly, the editing on endogenous targets was not shown with low plasmid transfection. For the SNAP-ADAR system, however, we can much better and more homogenously control the enzyme expression levels (by doxycycline induction) and we did show to what extent the reduction of SNAP-ADAR does change the editing at endogenous targets and at selected off-targets (see our Supplementary Figure 9).

Supplementary Table 3. Comparison SNAP-ADAR and 4λN-DD / BoxB system (Vallecillo-Viejo et al. RNA Biol 2018 & Sinnamon et al. PNAS 2017)$^{a)}$

	SNAP-ADAR (SA) system	**4λN-DD / BoxB system**
Targeting System	SNAP-tag – gRNA covalent bond SNAP-tag: human, < 200 aa gRNA: ca. 22 nt, chemically stabilized	λN / BoxB RNA peptide interaction λN (typically 4 copies): bacteriophage, ca. 100 aa optional 3x NLS: ca. 30 aa gRNA: ~84 nt, genetically encoded
Deaminase tested	4 enzymes fully tested: ADAR1 and ADAR2 each wildtype and E488Q	several versions, all based on ADAR2 deaminase domain, either wt or E488Q in combination with 1-4 copies λN peptide, with and without NLS 4 copies λN increase efficiency; 3xNLS can reduce off-target editing by ca. 50%
Delivery	SNAP-ADAR: single genomic copy, inducible gRNA: lipofection of chemically stabilized gRNA (22 nt)	Enzyme: currently massive overexpression via plasmid lipofection (or AAV) guideRNA: massive overexpression via plasmid lipofection (or AAV)
Editing of endogenous targets	ACTB, GAPDH, GUSB, SA, KRAS, STAT1	This system has mainly been characterized with reporter constructs, in particular GFP and CFTR; to my knowledge only a single example of an endogenous target has been described (MeCP2); the targeting of endogenous transcripts has not yet been tested systematically
Concurrent editing	3 sites or 4 endogenous housekeeping transcripts, no loss in efficiency 2 sites or 2 endogenous signaling transcripts (KRAS, STAT1), no loss in efficiency	Not shown; it is unclear if several different guideRNAs can ever be co-expressed as very high amounts of U6-guideRNA plasmids are currently used already for a single target (like 4-15fold more than the editase plasmid)
Editing range for the best editable codon (UAG) on endogenous targets	wild-type SA: 15 - 90%, (12 sites on 6 targets, ORF & UTRs) SAQ variants: 46 - 90%, (13 sites on 6 targets, ORF & UTRs)	With the E488Q variant editing levels of 70-80% have been observed on reporter transcripts GFP and CFTR; with the wildtype enzyme editing levels typically stay below (more like 40-60%); so far only a few preferred codons have been targeted, mostly UAG and mostly in reporter transcripts
Codon scope	all 16 codons tested on an endogenous target with SA1Q and SA2Q	There is no systematic test on the full codon scope published
Applications in the manuscript	Manipulation of signaling transcripts, KRAS and STAT1, recoding of phosporylation switch Tyr701 in STAT1	The system has been explored for the repair of CFTR (cDNA) and endogenous MeCP2
Editing duration	stable over several days	Nothing shown yet
Off-targets in gRNA/substrate duplex	the guideRNA/mRNA duplex is small (19 bp), chemical modification of guideRNA blocks off-target editing almost entirely even in A-rich codons	General: the guideRNA/mRNA duplex is large (50 bp, twice interrupted by the two 17 nt BoxB hairpins) The system suffers from major off-target editing inside the gRNA/mRNA duplex (e.g. PNAS 2017), even though endogenous MeCP2 was repaired in primary cells to ca. 75% yield, this came along with 5 off-target editings in the duplex (10-50% yield). The system also elicits strong guideRNA dependent off-target editing in the target transcript but outside the gRNA/mRNA duplex due to a proximity effect; e.g. RNA Biol 2018, depending on the enzyme 5-14 off-target editings (10-55%) have been found along the CFTR transcript

Global off-target editing	Wild-type SA: almost absent SAQ variants: moderate (≈1000 sites, decreased by lowering SAQ expression)	The E488Q version of Vallecillo-Viejo et al. was also tested by Cox et al. (Supporting Figure S9 in their paper) and showed massive global off-editing at rates very similar to Cas13-ADAR repairV1. We performed a re-analysis of Vallecillo-Viejo et al.'s NGS analysis with our pipeline (see Supplementary Figure 8). The wildtype enzymes elicit several hundred-fold more off-target edits compared to the wt SA. The wt Vallecillo-Viejo et al. enzymes are even more off-target-prone than our hyperactive SA1Q/SA2Q mutants. The hyperactive Vallecillo-Viejo et al. enzymes seem extremely off-target-prone.
Unique property	1) Chemically stabilized guideRNAs enable proper specificity inside gRNA/mRNA duplex 2) low expression of editase enables high editing yields with reduced global off-target editing 2) clearly proven, covalent RNA targeting 3) very short guideRNA/mRNA duplex, unlikely to interfere with endogenous ADARs or translation 4) simple co-transfection of guideRNAs enables concurrent editing	1) the system is fully genetically encoded 2) the entire system (editase + 6 copies guideRNA) has been delivered as a single AAV

a) This system has already undergone several rounds of refinement. We focused on the results reported in the two most recent papers.

Supplementary Table 4. Sequences of gRNAs applied in this study. BG-conjugated gRNAs were synthesized and PAGE-purified from commercially acquired oligonucleotides containing a 5’-amino-C6 linker (BioSpring, Germany) as described by Hanswillemenke et al. (*J. Am. Chem. Soc.* **2015**, *137*, 15875-15881). Nucleotides highlighted in bold are unmodified and are placed opposite the triplet with the target adenosine in the middle. Nucleotides highlighted in italic are modified with 2’-O-methylation, those highlighted in red are 2’-fluorinated nucleotides. The backbone contains terminal phosphorothioate linkages as indicated by “s”. The first three nucleotides at the 5’-end are not complementary to the mRNA substrate, but serve as linker sequence between gRNA and SNAP-tag.

target	gRNA sequence	applied gRNA amount[a]
editing of various endogenous transcripts		
5’-UTR SNAP-ADAR	5’-*UsCsAUUAAACG* **CCA** *GAGUCsCsGsGsA*-3’	5 pmol
5’-UTR GAPDH isoform 2	5’-*UsCsUGAAUAAU* **CCA** *GGAAAsAsGsCsA*-3’	5 pmol
ORF #1 GAPDH	5’-*UsAsUAGGGGUG* **CCA** *AGCAGsUsUsGsG*-3’	5 pmol
ORF #2 GAPDH[b]	5’-*UsAsUGGUUUUU* **CCA** *GACGGsCsAsGsG*-3’	5 pmol
ORF #1 GUSB	5’-*GsGsUGCAGAUU* **CCA** *GGUGGsGsAsCsG*-3’	5 pmol
ORF #2 GUSB	5’-*AsCsAGACUUGG* **CCA** *CUGAGsUsGsGsG*-3’	5 pmol
3’-UTR SNAP-ADAR	5’-*UsAsUGUGUCGG* **CCA** *CGGAAsCsAsGsG*-3’	5 pmol
3’-UTR GAPDH[c]	5’-*AsAsUAAGGGGU* **CCA** *CAUGGsCsAsAsC*-3’	5 pmol
3’-UTR ACTB	5’-*UsCsGAGCAAUG* **CCA** *UCACCsUsCsCsC*-3’	5 pmol
3’-UTR GUSB	5’-*UsAsUUUCCCUG* **CCA** *GAAUAsGsAsUsG*-3’	5 pmol
KRAS target A/1	5’-*GsAsUGCUCCAA* **CCA** *CCACAsAsGsUsU*-3’	SA1: 40 pmol , SA1Q: 10 pmol
KRAS target 2	5’-*CsGsUCUCUUGC* **CCA** *CGCCAsCsCsAsG*-3’	20 pmol
STAT1 Y701	5’-*GsUsCUCUUGAU* **ACA** *UCCAGsUsUsCsC*-3’	20 pmol
editing of all 16 adenosine-containing triplets in GAPDH isoform 1		
5’-GAA	5’-*CsAsCAUGGGAU* **UCC** *CAUUGsAsUsGsA*-3’	5 pmol
5’-GAU	5’-*UsAsUCGACCAA* **ACC** *CGUUGsAsCsUsC*-3’	5 pmol
5’-GAC	5’-*CsAsCGUCAUGA* **GCC** *CUUCCsAsCsGsA*-3’	5 pmol
5’-GAG	5’-*AsAsCGAGGGAU* **CCC** *GCUCCsUsGsGsA*-3’	5 pmol
5’-CAA	5’-*GsAsAGAGGCUG* **UCG** *UCAUAsCsUsUsC*-3’	5 pmol
5’-CAU	5’-*CsAsAGAGGUCA* **ACG** *AAGGGsGsUsCsA*-3’	5 pmol
5’-CAC	5’-*AsAsCGCCAGGG* **GCG** *CUAAGsCsAsGsU*-3’	5 pmol
5’-CAG	5’-*UsAsCGCAUGGA* **CCG** *UGGUCsAsUsGsA*-3’	5 pmol
5’-AAA	5’-*UsAsCAUGACCC* **UCU** *UGGCUsCsCsCsC*-3’	5 pmol
5’-AAU	5’-*GsAsCUAGCCAA* **ACU** *CGUUGsUsCsAsU*-3’	5 pmol
5’-AAC	5’-*AsGsUCGCCACA* **GCU** *UCCCGsGsAsGsG*-3’	5 pmol
5’-AAG	5’-*UsGsUAUAUCCA* **CCU** *UACCAsGsAsGsU*-3’	5 pmol
5’-UAA	5’-*AsGsGAGGGGUC* **UCA** *CUCCUsUsGsGsA*-3’	5 pmol
5’-UAU	5’-*CsUsAGGCAACA* **ACA** *UCCACsUsUsUsA*-3’	5 pmol
5’-UAC	5’-*CsCsGAGCGCCA* **GCA** *GAGGCsAsGsGsG*-3’	5 pmol
5’-UAG	5’-*UsAsUGGUUUUU* **CCA** *GACGGsCsAsGsG*-3’	5 pmol
avoiding off-target editing of neighboring adenosine		
5’-CAA methoxy	5’-*GsAsAGAGGCUGU* **CG** *UCAUAsCsUsUsC*-3’	5 pmol
5’-CAA fluoro	5’-*GsAsAGAGGCUG*U **CG** *UCAUAsCsUsUsC*-3’	5 pmol
5’-AAA methoxy	5’-*UsAsCAUGACCCU* **CU** *UGGCUsCsCsCsC*-3’	5 pmol
5’-AAA fluoro	5’-*UsAsCAUGACCC*U **CU** *UGGCUsCsCsCsC*-3’	5 pmol
5’-AAC methoxy	5’-*AsGsUCGCCACA* **GC** *UUCCCGsGsAsGsG*-3’	5 pmol
5’-AAC fluoro	5’-*AsGsUCGCCACA* **GC** U*UCCCGsGsAsGsG*-3’	5 pmol
5’-UAA methoxy	*5’-AsGsGAGGGGUCU* **CA** *CUCCUsUsGsGsA*-3’	5 pmol
5’-UAA fluoro	*5’-AsGsGAGGGGUC*U **CA** *CUCCUsUsGsGsA*-3’	5 pmol

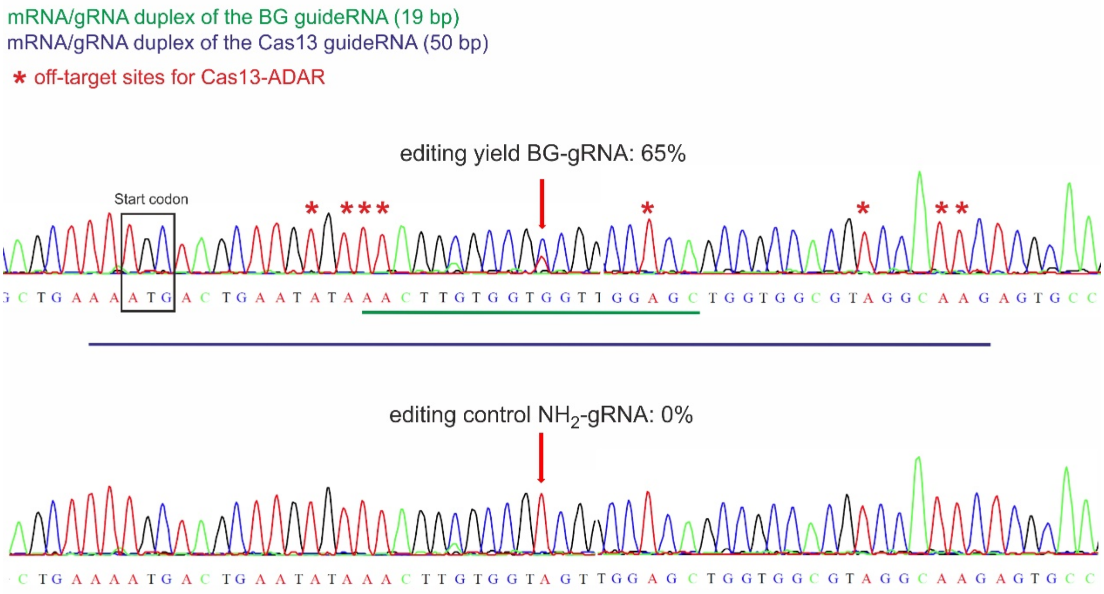
a) The indicated gRNA amounts were used for single and concurrent editings.

b) This gRNA was additionally applied to test the dose dependency of RNA editing (Fig. 1c)

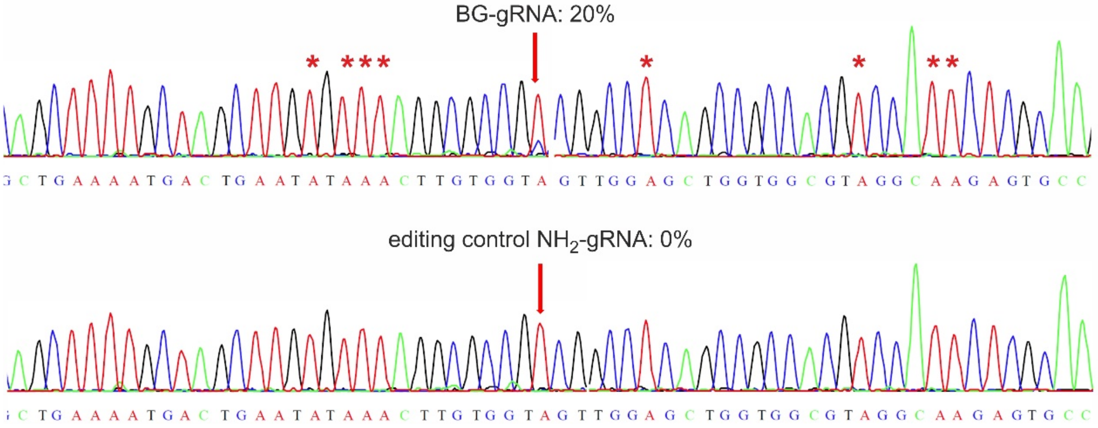
c) This gRNA was additionally applied to test the time dependency of RNA editing (Fig. 1b)

Editing of two sites in endogenous KRAS as previously reported by Cox et al. with Cas13b-ADAR

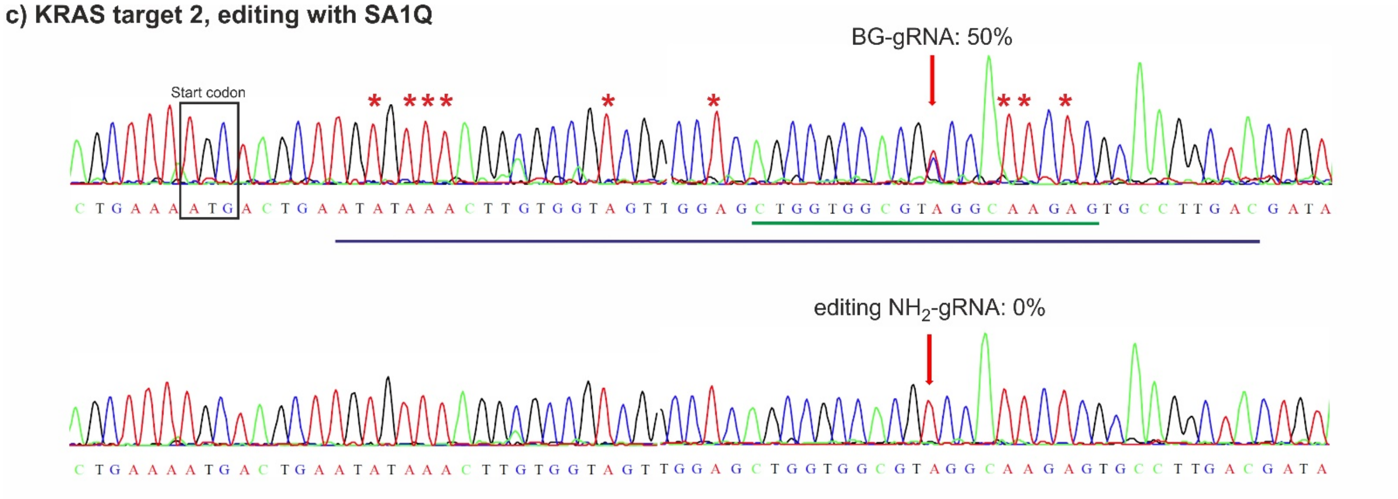
a) KRAS Target 1/A, editing with SA1Q



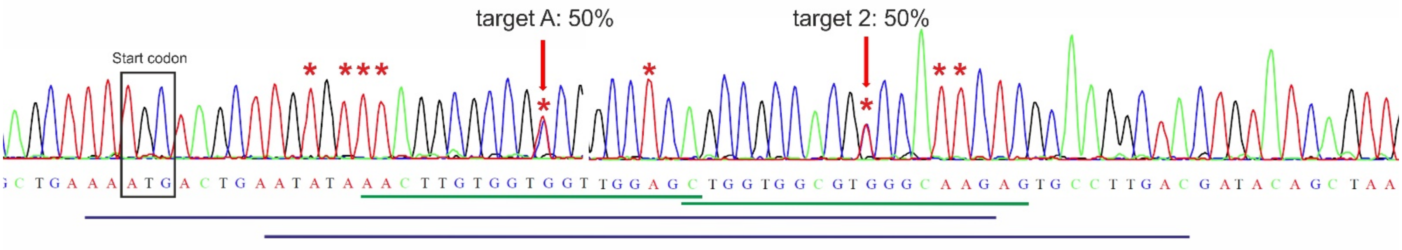
b) KRAS Target 1/A, editing with wt SA1



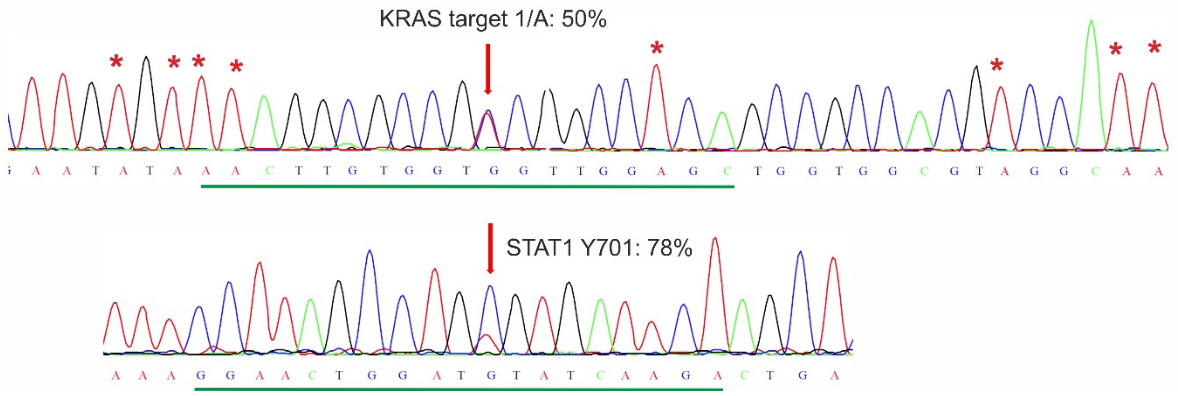
c) KRAS target 2, editing with SA1Q



d) KRAS concurrent editing target1/A and target 2 with SA1Q / BG-guideRNAS



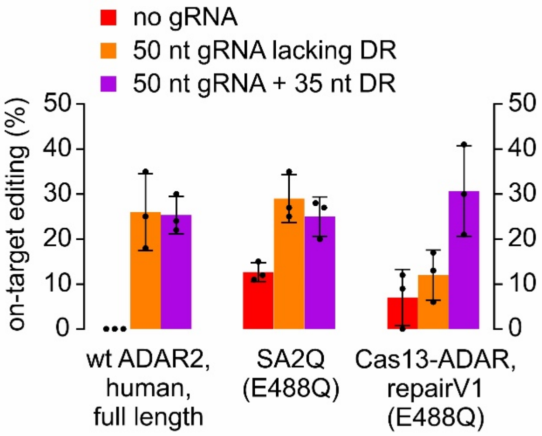
e) Concurrent editing KRAS target 1/A and STAT1 Tyr701 with SA1Q



Supplementary Note 1. Editing of KRAS target #1, #2, and STAT1 with SNAP-ADARs. Editing of KRAS target #1/A gives very high yields with SA1Q and absolutely no off-target editing at the sites reported for Cas13b-ADAR (*). Note also the large mRNA/gRNA duplexes applied for Cas13b-ADAR guideRNAs (50 bp, blue lines) versus the short ones applied for SNAP-ADAR (green lines). For target #1/A, the long Cas13 guideRNA even overlaps with the translation start site (boxed ATG) of the KRAS transcript (translation inhibition?). Also note the strong dependency of the SNAP-ADAR on the targeting mechanism. The same guideRNA lacking the BG modification (NH_2-guideRNA) cannot form the covalent bond with the deaminase and is incapable of editing the target at all (a-c). Panel a), the editing yield is significantly larger (50-65%) compared to off-target prone Cas13b-ADAR version 1 (ca. 25%). The precise wildtype SA1 edits target #1/A better than the precise Cas13-ADAR version 2 (20% versus ca. 12%). Target #2 (panel c) is also better edited by SA1Q than Cas13b version 1 (50% compared to 32%). Finally, we show efficient concurrent editing of KRAS site #1 + site #2, with yields of 50% both (d). And we show concurrent editing of KRAS site #1 with the most important phosphorylation site of STAT1 (Y701) with very good yields (50% and 78%, panel e). a-e) N=3 independent experiments were performed with similar results.

Editing of overexpressed GFP reporter W58X with co-overexpressed Cas13-guideRNAs and co-overexpressed, different ADAR fusions (SA2Q, human full length ADAR2, and Cas13-ADAR version1) following exactly the protocol given by Cox et al.

a) Overview of n=3 experiments

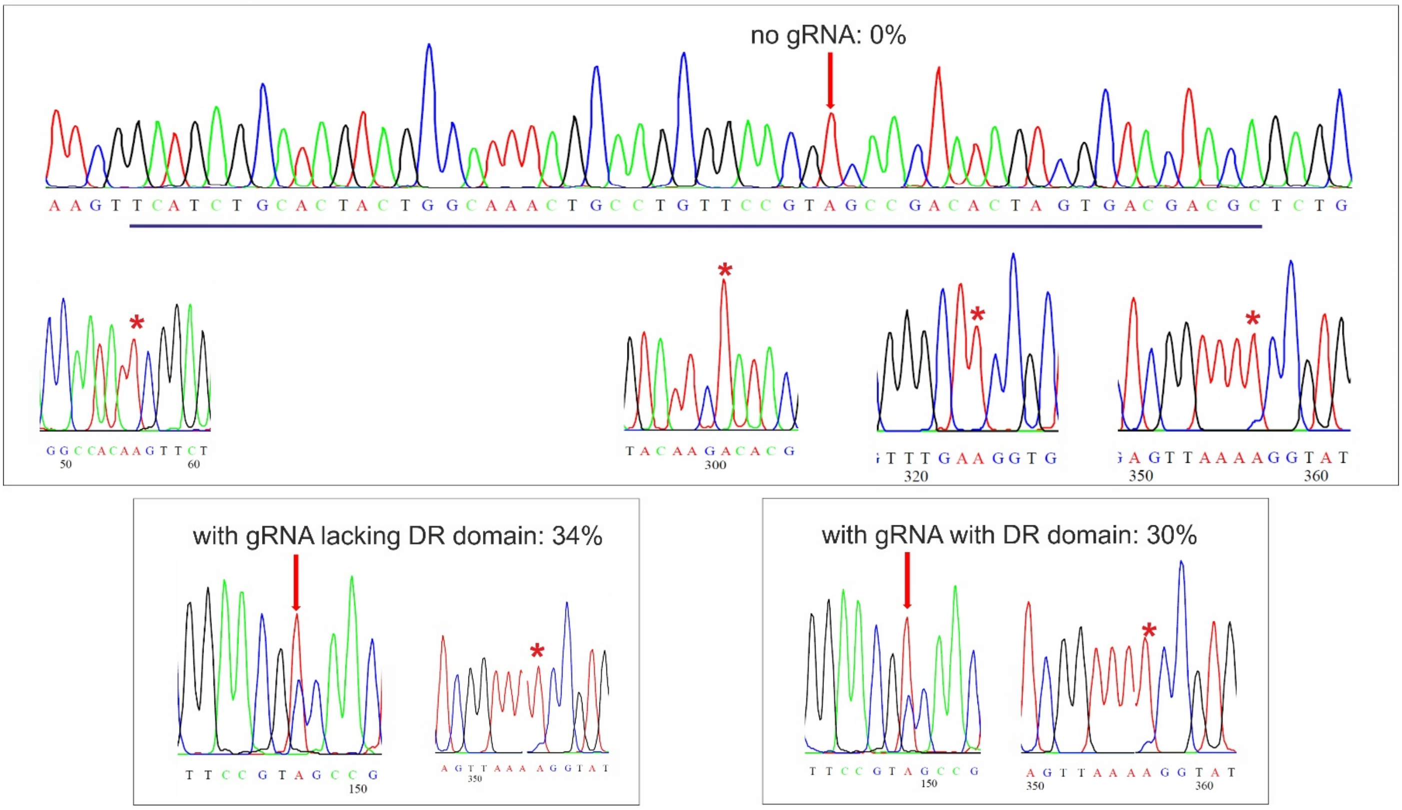


Selected Sanger sequencing traces (selected was always the trace with the highest on-target yield out of 3 experiments)

↓ = on-target editing

* = off-target editing

b) full length wildtype human ADAR2

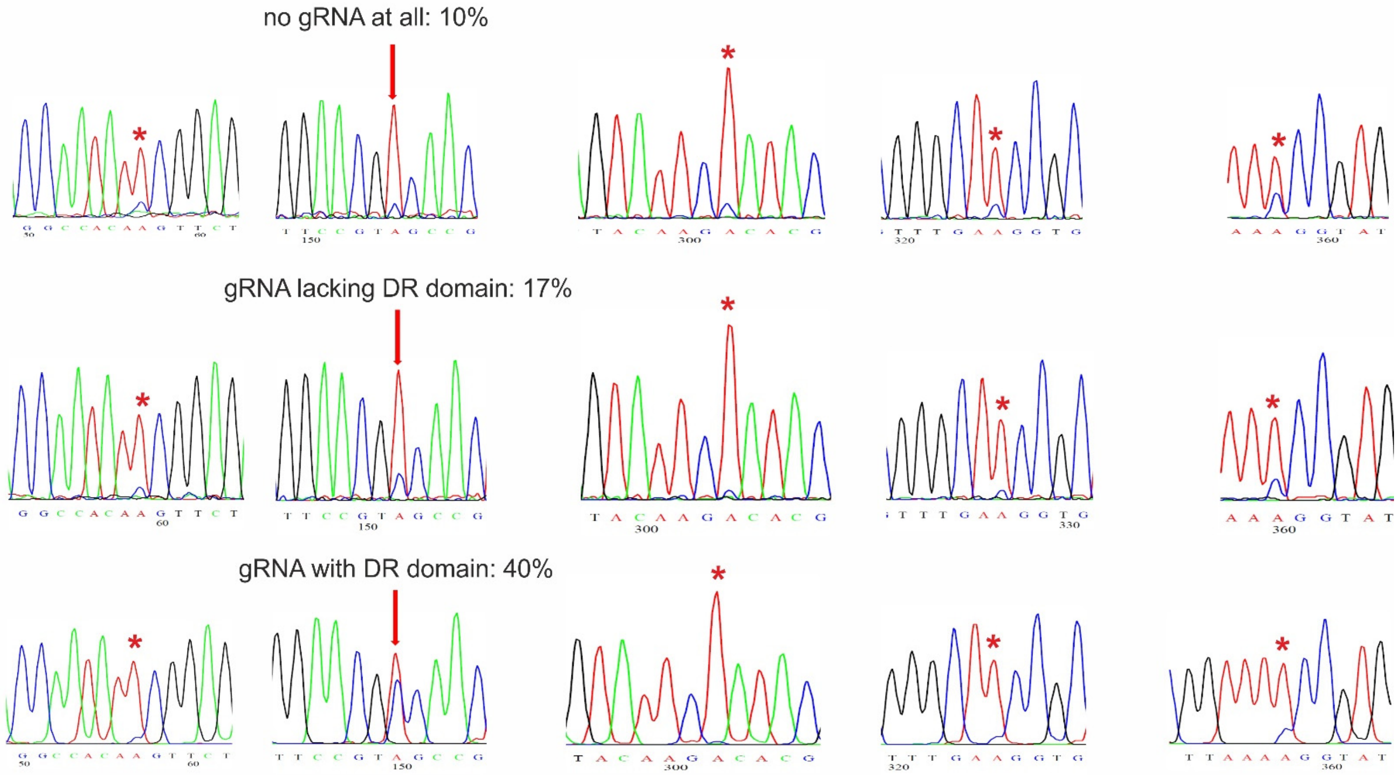

no gRNA: 0%

with gRNA lacking DR domain: 34%

with gRNA with DR domain: 30%

c) SNAP-ADAR2Q

d) Cas-ADAR13, repairV1



Supplementary Note 2. Lacking specificity of overexpressed Cas13-guideRNAs. Cox et al. repeatedly claim a unique Cas-dependent targeting mechanism which is the reason for the claimed higher effectiveness of "repair" compared to other editing systems, the reason for the lacking codon preference they find, and the reason for the lack of a PFS dependency. However, all those claims are built on co-overexpression experiments of Cas-ADAR together with a guideRNA and reporter constructs. Here, we show that the Cas13-guideRNAs, they apply, are able to elicit editing with ADAR2 but also with SNAP-ADAR2Q in yields comparable to Cas-ADAR repair1, demonstrating that the applied guideRNAs under the applied conditions are not specific for Cas-ADAR and that many of the findings, in particular under overexpression / reporter conditions could be partly flawed by self-targeting of the deaminase (domain) itself. Unfortunately, Cox et al.

did not properly address this question in their paper (e.g. control experiments with guideRNAs lacking the DR domain are completely missing).

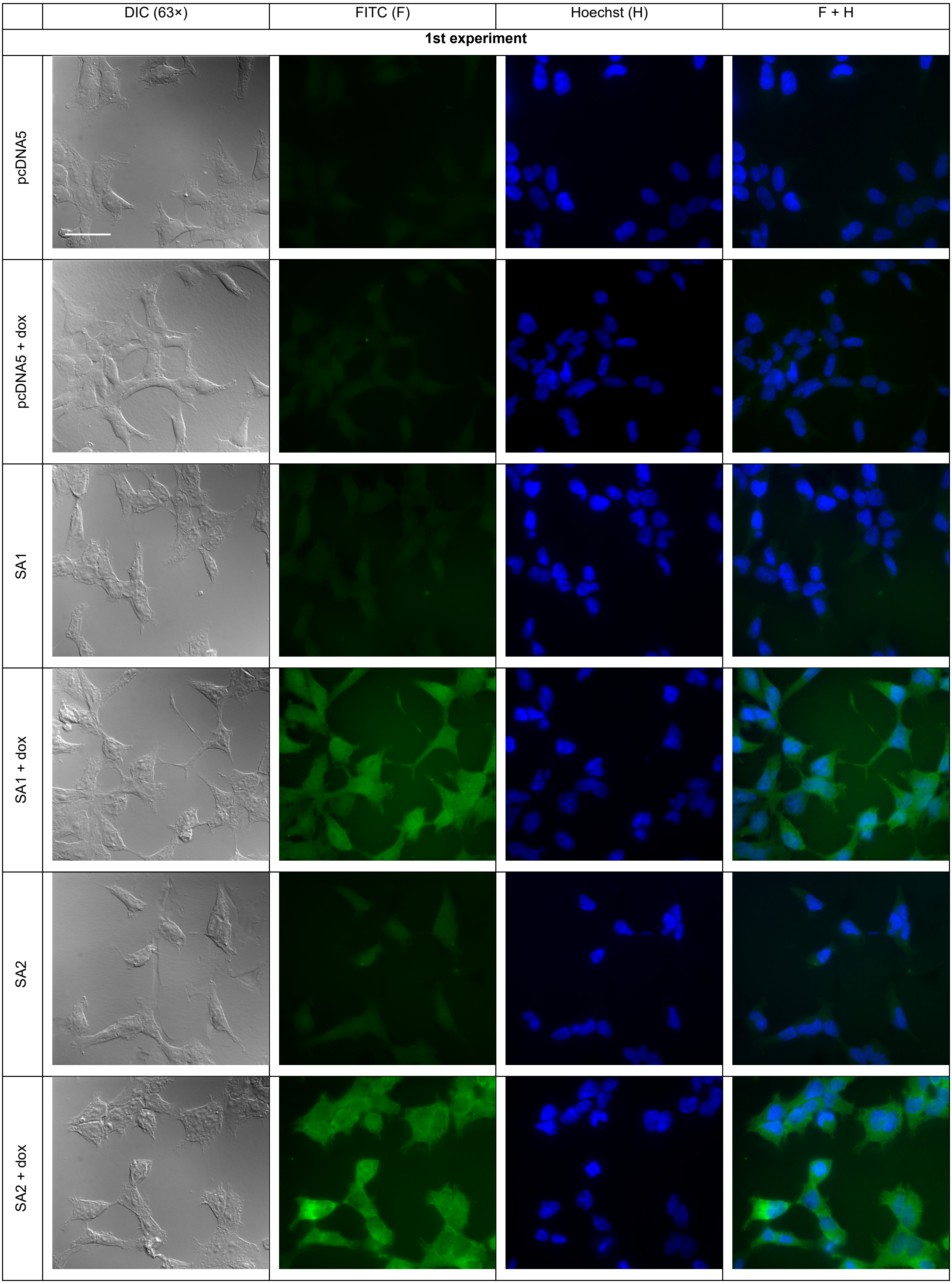
For this, we designed a Cas13 guideRNA according to Cox et al. containing a 50 nt part antisense to our GFP reporter (W58amber), putting the targeted A into mismatch with C. Mismatch position was 34. We constructed guideRNAs with the 3´-terminal DR hairpin for Cas-targeting but also lacking the DR motif (the DR motif is a 34 nt hairpin that has the function to recruit Cas13). The guideRNAs were expressed from a U6 promotor (pSilencer plasmid), as applied by Cox et al. Co-transfection was carried out as described by Cox et al.: 150 ng editing enzyme, 300 ng guideRNA vector, 40 ng GFP reporter plasmid in a coated 96 well into 293T cells. As enzymes, we co-transfected either full length human ADAR2 (wildtype), or the respective hyperactive SNAP-ADAR2Q, or Cas13-ADAR repairV1 (containing the same mutated deaminase domain of ADAR2 E488Q as SA2Q). guideRNA (antisense part: capital letters; DR domain: small letters):GCGTCACTAGTGTCGGCCACGGAACAGGCAGTTTGCCAGTAGTGCAGATGAgttgtggaaggtccagtt ttgaggggctattacaac. In panel b), the position and length of the gRNA is indicated as a blue line under the sequence, the on-target site is marked by a red arrow, main off-target sites are marked by red asterisks.

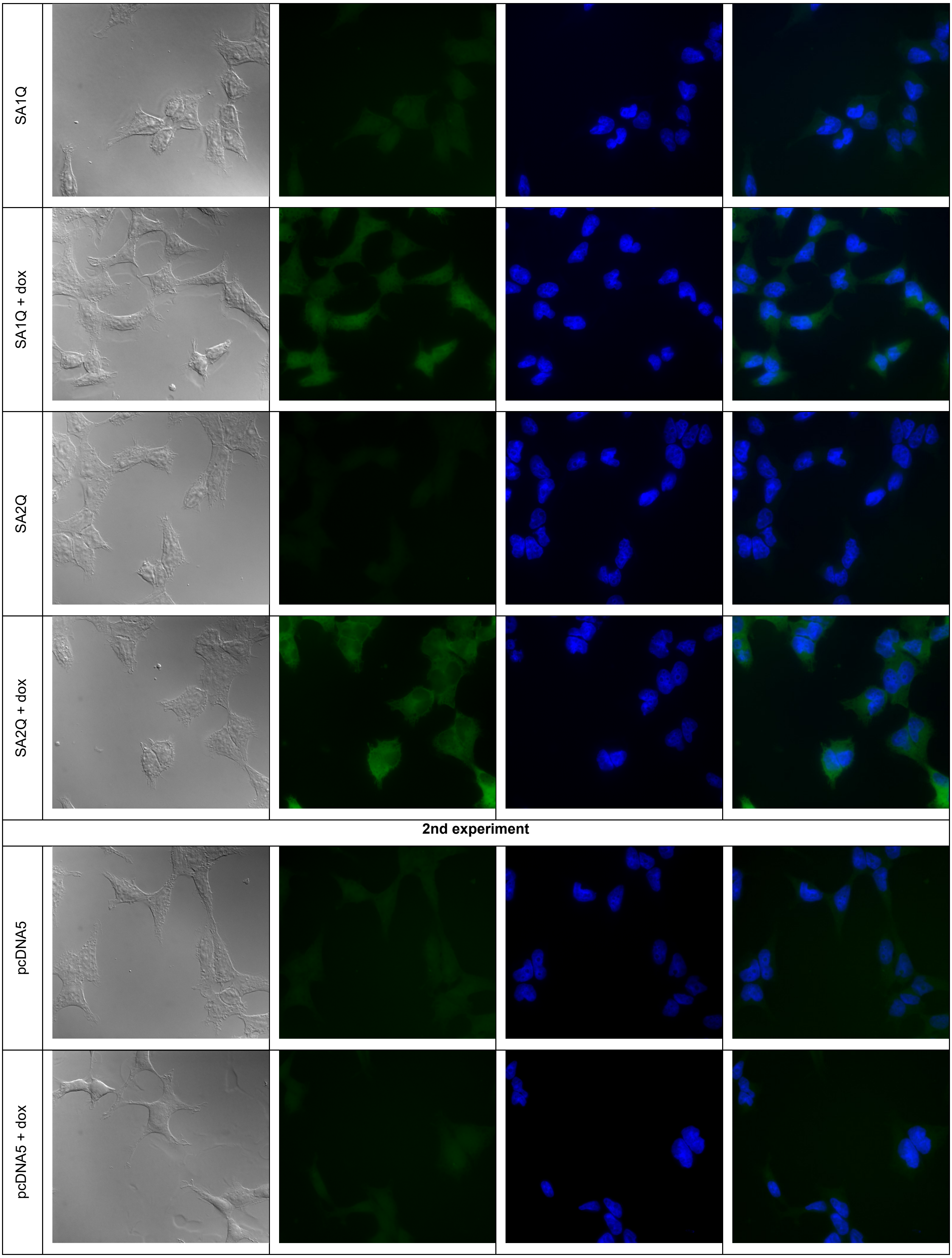
a) shows that the Cas13-guideRNA can also recruit human ADAR2 or SNAP-ADAR2Q to elicit editing yields similar to Cas13-ADAR. The average editing levels (25-30%) are very similar to those described by Cox et al. for various similar overexpression / reporter experiments in their Figures 2-4 (15-30%). As expected the recruitment of ADAR2 and SNAP-ADAR2Q is independent of the DR motif. In contrast, we have shown in the past that short chemically stabilized (BG)-guideRNAs (as we apply) are unable to recruit ADAR2 (see NAR 2016, gkw911, Figure S9A); and as we have shown repeatedly in our manuscript that SNAP-ADARs are only recruited by short chemically stabilized guideRNAs when the BG moiety is present, clearly demonstrating the SNAP-tag-dependent targeting mechanism. The editing control with Cas13-ADAR shows several interesting things. First, editing is to some extent depending on the DR motif, but second, editing also occurs without a guideRNA and also with a guideRNA lacking the DR motif, even though with reduced editing yields; this indicates that the editing yields reported by Cox et al. are composed of an unknown Cas-dependent and an unknown Cas-independent (self-targeting) part, probably differing for each respective target and condition; third, the editing yield with Cas13-ADAR with the ideal guideRNA (30%) was not notably better than that with other deaminases (25-30%); d) the off-target editing of Cas13-ADAR was higher than that of ADAR2 but lower than that of SA2Q. Finally, we want to mention that editing yields are strongly varying under co-overexpression conditions as seen in the error bars of N=3 independent experiments (Data are shown with the mean±SD, black dots represent individual data points). This is in agreement with our earlier experience.

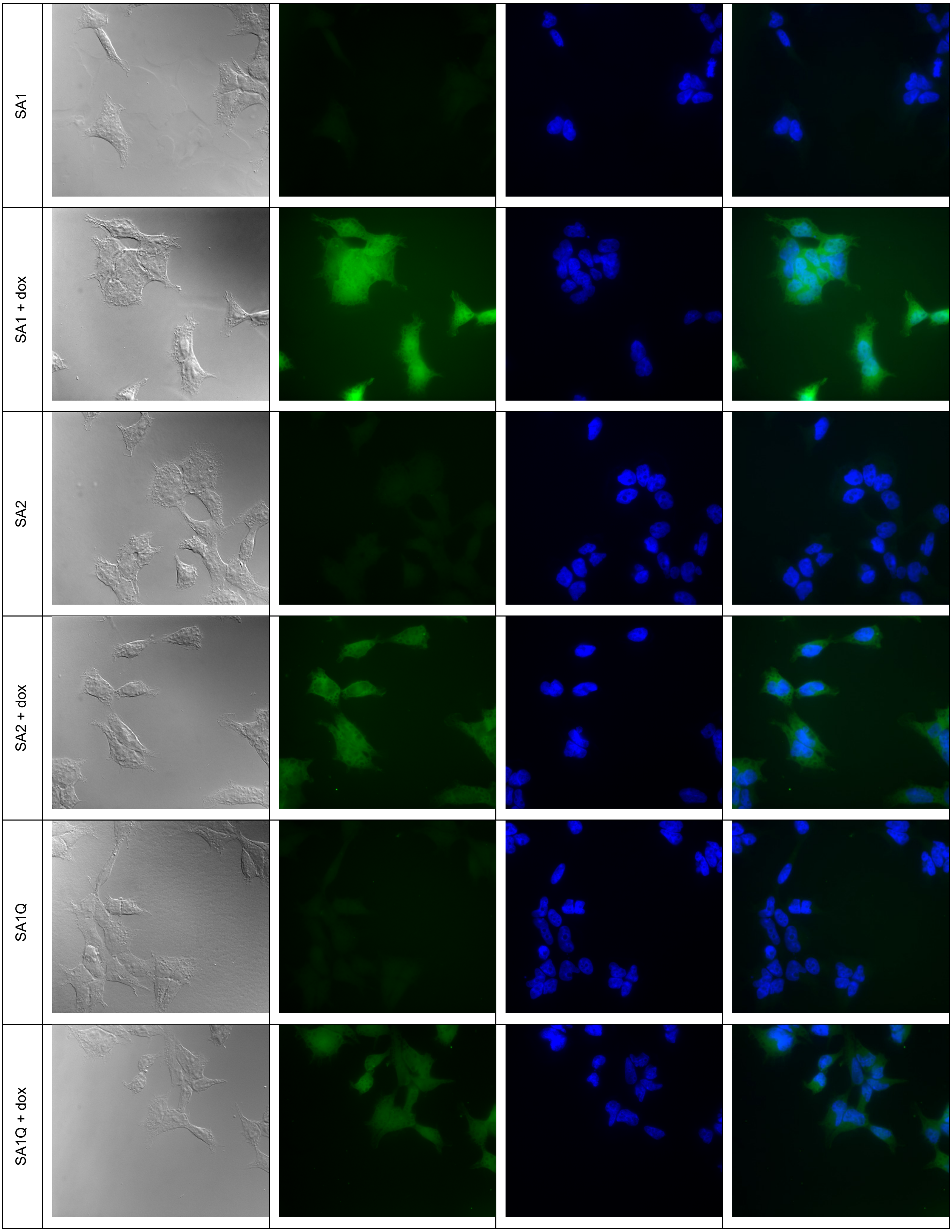
b-d) show selected Sanger sequencing traces (always the trace with the highest on-target editing yield was chosen) to give an idea of off-target editing. While ADAR2 (**b**) gives decent on-target editing (25%) there was only very little off-target editing seen and on-target editing was fully dependent on the presence of the guideRNA, even though not on the DR motif in the guideRNA. The respective single off-target editing site was described before by us (NAR 2017). Co-transfection with hyperactive SA2Q (**c**) largely shows the misery of overexpressing hyperactive deaminases (like Cas13-ADAR repairV1 too): even in absence of the guideRNA, there is massive off-target editing all over the transcript (only few sites are picked here). On-target editing was achieved with 10% yield if though no gRNA was transfected. With the Cas13-guideRNA, on-target editing increased to 25%, independent of the DR-motif. With respect to off-target editing, the experiment with Cas13-ADAR overexpression (**d**) shows results similar to the overexpression of SA2Q, which contains the same ADAR deaminase mutant (E488Q). Off-target editing is found all over the transcript, on-target editing is already found prior to the expression of the guideRNA. However, such off-target yields are roughly half that strong as found for SA1Q, which might be due to lower expression levels. After adding the guideRNA, editing levels increase and there is a targeting effect, however, there is also a notable increase in editing yield with the guideRNA lacking the DR domain. N=3 independent experiments were performed with similar results.

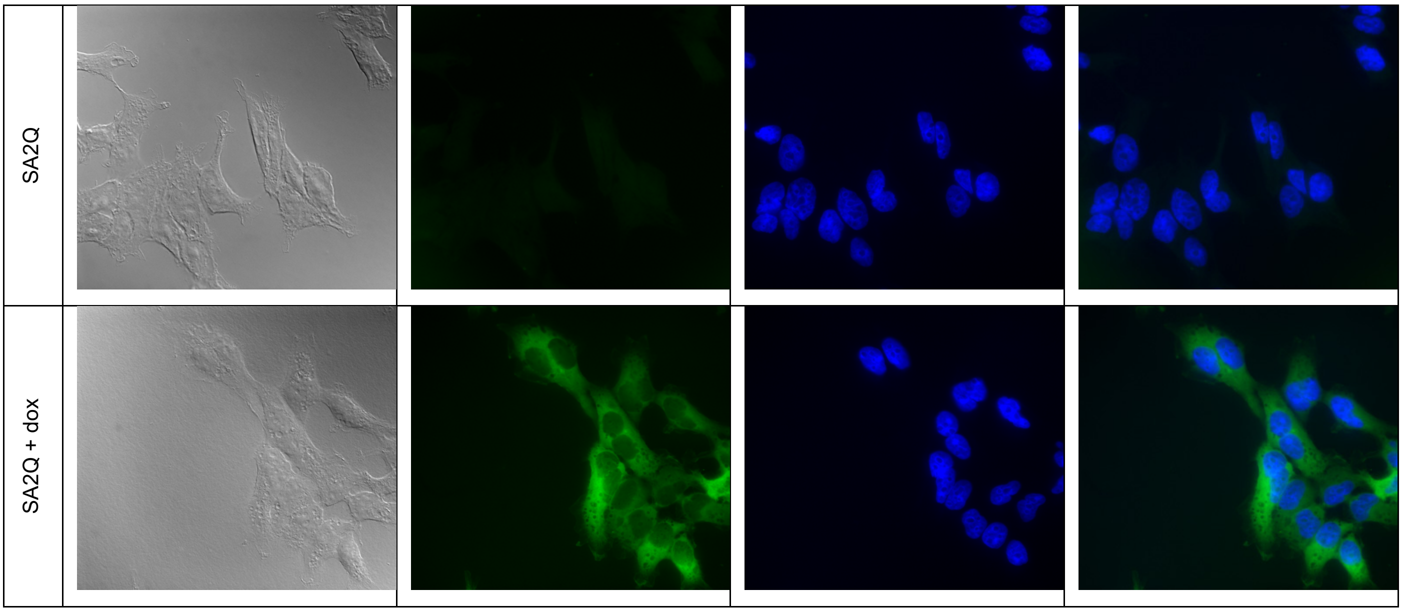
Together, panels **a-d)** suggest that the conditions (overexpression & reporters) under which Cas13-ADAR has mostly been characterized today are not sufficient to support the general claims made by Cox et al.

Determination of intracellular SNAP-ADAR localization by fluorescence microscopy




SA1Q
SA1Q + dox
SA2Q
SA2Q + dox
2nd experiment
pcDNA5
pcDNA5 + dox

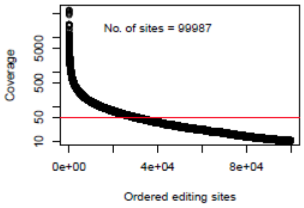
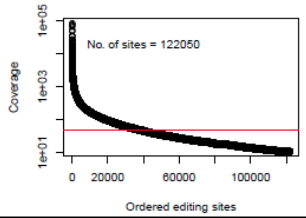
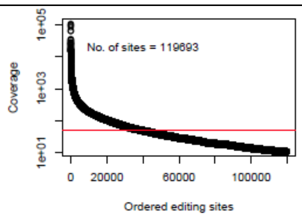
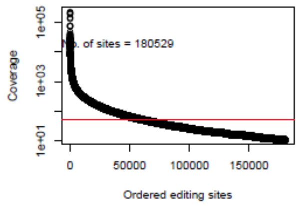
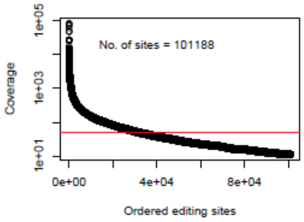
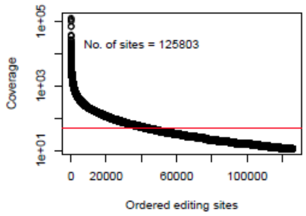
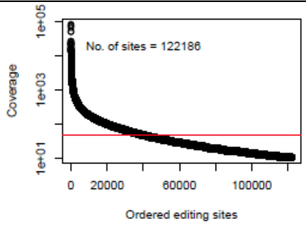
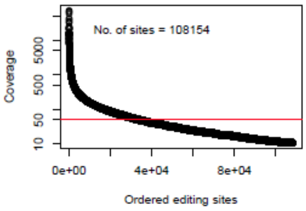
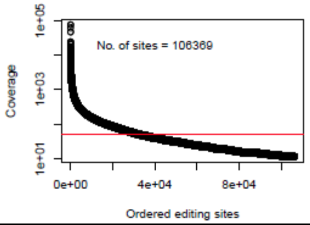
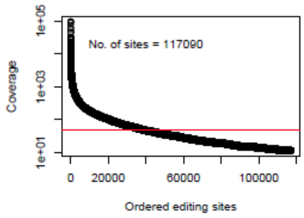
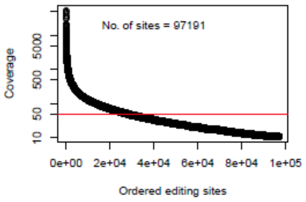
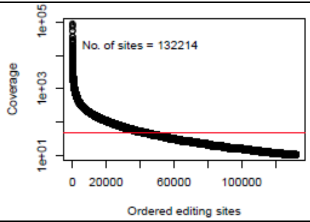
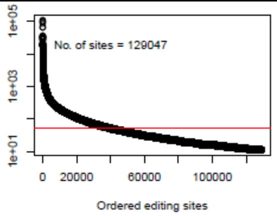
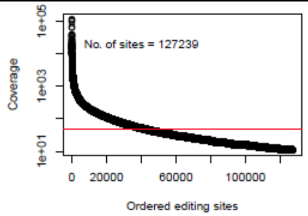

SA1
SA1 + dox
SA2
SA2 + dox
SA1Q
SA1Q + dox



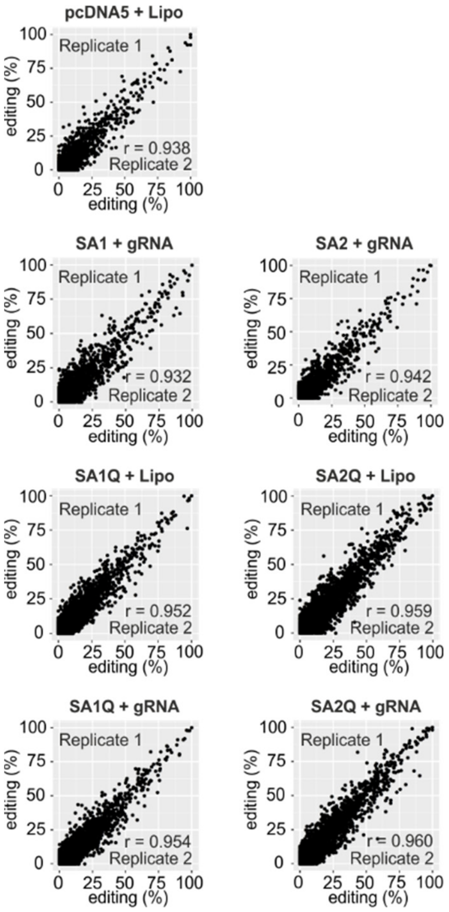
Supplementary Note 3. Protein expression was induced by doxycycline (dox) for 24 h. Cells were incubated with BG-FITC to stain SNAP-ADARs (green) and with Hoechst 33342 to stain nuclei (blue). Microscopy was performed with a Zeiss CellObserverZ1 under 630x total magnification. The scale bar represents 40 µm. FITC-BG/SNAP-tag labeling was done as described before (Vogel et al., ACS Synth. Biol. 2017, doi: 10.1021/acssynbio.7b00113). N=3 independent experiments were performed with similar results.

Appendix (NGS quality data, SNAP-ADAR gene sequences, target sites on endogenous transcripts)

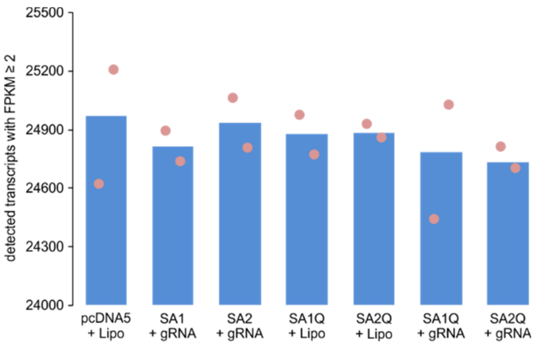
Additional NGS quality data

	Replicate 1	Replicate 2
pcDNA5 + Lipo		
SA1 + gRNA		
SA2 + gRNA		
SA1Q + Lipo		
SA2Q + Lipo		
SA1Q + gRNA		
SA2Q + gRNA		

Detected editing sites ranked by coverage for each experiment. For testing significant editing differences, a coverage cut-off of 50 (red line) for the sum of each experiment with its replicate was applied. This typically yielded around 50.000 sites / experiment to be analyzed.



Scatter plots of editing levels of all called editing sites of replicate 1 against replicate 2 for the indicated editing experiments show good replicability with correlation ranging from 0.932-0.960.



Number of transcript covered in RNA sequencing was performed with two replicates of each sample. Shown are number of detected transcripts with a FPKM value ≥ 2 for both replicates combined (light blue bars) or separated (pink dots).

Sequences of editing enzymes and editing targets

```
                  10        20        30        40        50        60
1         ATGGGGAAGGTGAAGGTCGGAGTCAACGGATTTGGTCGTATTGGGCGCCTGGTCACCAGG
1          M  G  K  V  K  V  G  V  N  G  F  G  R  I  G  R  L  V  T  R
                  70        80        90       100       110       120
61        GCTGCTTTTAACTCTGGTAAAGTGGATATTGTTGCCATCAATGACCCCTTCATTGACCTC
21         A  A  F  N  S  G  K  V  D  I  V  A  I  N  D  P  F  I  D  L
                 130       140       150       160       170       180
121       AACTACATGGTTTACATGTTCCAATATGATTCCACCCATGGCAAATTCCATGGCACCGTC
41         N  Y  M  V  Y  M  F  Q  Y  D  S  T  H  G  K  F  H  G  T  V
                 190       200       210       220       230       240
181       AAGGCTGAGAACGGGAAGCTTGTCATCAATGGAAATCCCATCACCATCTTCCAGGAGCGA
61         K  A  E  N  G  K  L  V  I  N  G  N  P  I  T  I  F  Q  E  R
                 250       260       270       280       290       300
241       GATCCCTCCAAAATCAAGTGGGGCGATGCTGGCGCTGAGTACGTCGTGGAGTCCACTGGC
81         D  P  S  K  I  K  W  G  D  A  G  A  E  Y  V  V  E  S  T  G
                 310       320       330       340       350       360
301       GTCTTCACCACCATGGAGAAGGCTGGGGCTCATTTGCAGGGGGGAGCCAAAAGGGTCATC
101        V  F  T  T  M  E  K  A  G  A  H  L  Q  G  G  A  K  R  V  I
                 370       380       390       400       410       420
361       ATCTCTGCCCCCTCTGCTGATGCCCCCATGTTCGTCATGGGTGTGAACCATGAGAAGTAT
121        I  S  A  P  S  A  D  A  P  M  F  V  M  G  V  N  H  E  K  Y
                 430       440       450       460       470       480
421       GACAACAGCCTCAAGATCATCAGCAATGCCTCCTGCACCACCAACTGCTTAGCACCCCTG
141        D  N  S  L  K  I  I  S  N  A  S  C  T  T  N  C  L  A  P  L
                 490       500       510       520       530       540
481       GCCAAGGTCATCCATGACAACTTTGGTATCGTGGAAGGACTCATGACCACAGTCCATGCC
161        A  K  V  I  H  D  N  F  G  I  V  E  G  L  M  T  T  V  H  A
                 550       560       570       580       590       600
541       ATCACTGCCACCCAGAAGACTGTGGATGGCCCCTCCGGGAAACTGTGGCGTGATGGCCGC
181        I  T  A  T  Q  K  T  V  D  G  P  S  G  K  L  W  R  D  G  R
                 610       620       630       640       650       660
601       GGGGCTCTCCAGAACATCATCCCTGCCTCTACTGGCGCTGCCAAGGCTGTGGGCAAGGTC
201        G  A  L  Q  N  I  I  P  A  S  T  G  A  A  K  A  V  G  K  V
                 670       680       690       700       710       720
661       ATCCCTGAGCTGAACGGGAAGCTCACTGGCATGGCCTTCCGTGTCCCCACTGCCAACGTG
221        I  P  E  L  N  G  K  L  T  G  M  A  F  R  V  P  T  A  N  V
                 730       740       750       760       770       780
721       TCAGTGGTGGACCTGACCTGCCGTCTAGAAAAACCTGCCAAATATGATGACATCAAGAAG
241        S  V  V  D  L  T  C  R  L  E  K  P  A  K  Y  D  D  I  K  K
                 790       800       810       820       830       840
781       GTGGTGAAGCAGGCGTCGGAGGGCCCCCTCAAGGGCATCCTGGGCTACACTGAGCACCAG
261        V  V  K  Q  A  S  E  G  P  L  K  G  I  L  G  Y  T  E  H  Q
                 850       860       870       880       890       900
841       GTGGTCTCCTCTGACTTCAACAGCGACACCCACTCCTCCACCTTTGACGCTGGGGCTGGC
281        V  V  S  S  D  F  N  S  D  T  H  S  S  T  F  D  A  G  A  G
                 910       920       930       940       950       960
901       ATTGCCCTCAACGACCACTTTGTCAAGCTCATTTCCTGGTATGACAACGAATTTGGCTAC
301        I  A  L  N  D  H  F  V  K  L  I  S  W  Y  D  N  E  F  G  Y
                 970       980       990      1000
961       AGCAACAGGGTGGTGGACCTCATGGCCCACATGGCCTCCAAGGAGTAA
321        S  N  R  V  V  D  L  M  A  H  M  A  S  K  E  *
```

Open reading frame of GAPDH transcript isoform 1 (NM_002046.5). All 16 adenosine-containing triplets (yellow and cyan) were tested for editing. Most of the triplets (yellow), sites could be chosen with no resulting amino acid change. Only for 4 triplets (cyan), editing of the corresponding site lead to amino acid change. However, these changes happen in the variable region of the protein and thus, are supposed not to disturb protein activity.

```
               10        20        30        40        50        60
1         GGAGACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCC
1
                  70        80        90       100       110       120
61        GGACTCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTCGGATCCACCATGGACAAAGACT
20                                                        M  D  K  D
                 130       140       150       160       170       180
121       GCGAAATGAAGCGCACCACCCTGGATAGCCCTCTGGGCAAGCTGGAACTGTCTGGGTGCG
40        C  E  M  K  R  T  T  L  D  S  P  L  G  K  L  E  L  S  G  C
                 190       200       210       220       230       240
181       AACAGGGCCTGCACCGTATCATCTTCCTGGGCAAAGGAACATCTGCCGCCGACGCCGTGG
60        E  Q  G  L  H  R  I  I  F  L  G  K  G  T  S  A  A  D  A  V
                 250       260       270       280       290       300
241       AAGTGCCTGCCCCAGCCGCCGTGCTGGGCGGACCAGAGCCACTGATGCAGGCCACCGCCT
80        E  V  P  A  P  A  A  V  L  G  G  P  E  P  L  M  Q  A  T  A
                 310       320       330       340       350       360
301       GGCTCAACGCCTACTTTCACCAGCCTGAGGCCATCGAGGAGTTCCCTGTGCCAGCCCTGC
100       W  L  N  A  Y  F  H  Q  P  E  A  I  E  E  F  P  V  P  A  L
                 370       380       390       400       410       420
361       ACCACCCAGTGTTCCAGCAGGAGAGCTTTACCCGCCAGGTGCTGTGGAAACTGCTGAAAG
120       H  H  P  V  F  Q  Q  E  S  F  T  R  Q  V  L  W  K  L  L  K
                 430       440       450       460       470       480
421       TGGTGAAGTTCGGAGAGGTCATCAGCTACAGCCACCTGGCCGCCCTGGCCGGCAATCCCG
140       V  V  K  F  G  E  V  I  S  Y  S  H  L  A  A  L  A  G  N  P
                 490       500       510       520       530       540
481       CCGCCACCGCCGCCGTGAAAACCGCCCTGAGCGGAAATCCCGTGCCCATTCTGATCCCCT
160       A  A  T  A  A  V  K  T  A  L  S  G  N  P  V  P  I  L  I  P
                 550       560       570       580       590       600
541       GCCACCGGGTGGTGCAGGGCGACCTGGACGTGGGGGGCTACGAGGGCGGGCTCGCCGTGA
180       C  H  R  V  V  Q  G  D  L  D  V  G  G  Y  E  G  G  L  A  V
                 610       620       630       640       650       660
601       AAGAGTGGCTGCTGGCCCACGAGGGCCACAGACTGGGCAAGCCTGGGCTGGGTCCTGCAG
200       K  E  W  L  L  A  H  E  G  H  R  L  G  K  P  G  L  G  P  A
                 670       680       690       700       710       720
661       GCGGAGGCGCGCCAGGGTCTGGCGGCGGCAGTAAGGCAGAACGCATGGGTTTCACAGAGG
220       G  G  G  A  P  G  S  G  G  G  S  K  A  E  R  M  G  F  T  E
                 730       740       750       760       770       780
721       TAACCCCAGTGACAGGGGCCAGTCTCAGAAGAACTATGCTCCTCCTCTCAAGGTCCCCAG
240       V  T  P  V  T  G  A  S  L  R  R  T  M  L  L  L  S  R  S  P
                 790       800       810       820       830       840
781       AAGCACAGCCAAAGACACTCCCTCTCACTGGCAGCACCTTCCATGACCAGATAGCCATGC
260       E  A  Q  P  K  T  L  P  L  T  G  S  T  F  H  D  Q  I  A  M
                 850       860       870       880       890       900
841       TGAGCCACCGGTGCTTCAACACTCTGACTAACAGCTTCCAGCCCTCCTTGCTCGGCCGCA
280       L  S  H  R  C  F  N  T  L  T  N  S  F  Q  P  S  L  L  G  R
                 910       920       930       940       950       960
901       AGATTCTGGCCGCCATCATTATGAAAAAAGACTCTGAGGACATGGGTGTCGTCGTCAGCT
300       K  I  L  A  A  I  I  M  K  K  D  S  E  D  M  G  V  V  V  S
                 970       980       990      1000      1010      1020
961       TGGGAACAGGGAATCGCTGTGTAAAAGGAGATTCTCTCAGCCTAAAAGGAGAAACTGTCA
320       L  G  T  G  N  R  C  V  K  G  D  S  L  S  L  K  G  E  T  V
                1030      1040      1050      1060      1070      1080
1021      ATGACTGCCATGCAGAAATAATCTCCCGGAGAGGCTTCATCAGGTTTCTCTACAGTGAGT
340       N  D  C  H  A  E  I  I  S  R  R  G  F  I  R  F  L  Y  S  E
                1090      1100      1110      1120      1130      1140
1081      TAATGAAATACAACTCCCAGACTGCGAAGGATAGTATATTTGAACCTGCTAAGGGAGGAG
360       L  M  K  Y  N  S  Q  T  A  K  D  S  I  F  E  P  A  K  G  G
                1150      1160      1170      1180      1190      1200
1141      AAAAGCTCCAAATAAAAAAGACTGTGTCATTCCATCTGTATATCAGCACTGCTCCGTGTG
380       E  K  L  Q  I  K  K  T  V  S  F  H  L  Y  I  S  T  A  P  C
                1210      1220      1230      1240      1250      1260
1201      GAGATGGCGCCCTCTTTGACAAGTCCTGCAGCGACCGTGCTATGGAAAGCACAGAATCCC
400       G  D  G  A  L  F  D  K  S  C  S  D  R  A  M  E  S  T  E  S
                1270      1280      1290      1300      1310      1320
1261      GCCACTACCCTGTCTTCGAGAATCCCAAACAAGGAAAGCTCCGCACCAAGGTGGAGAACG
420       R  H  Y  P  V  F  E  N  P  K  Q  G  K  L  R  T  K  V  E  N
                1330      1340      1350      1360      1370      1380
1321      GAGAAGGCACAATCCCTGTGGAATCCAGTGACATTGTGCCTACGTGGGATGGCATTCGGC
440       G  E  G  T  I  P  V  E  S  S  D  I  V  P  T  W  D  G  I  R
                1390      1400      1410      1420      1430      1440
1381      TCGGGGAGAGACTCCGTACCATGTCCTGTAGTGACAAAATCCTACGCTGGAACGTGCTGG
460       L  G  E  R  L  R  T  M  S  C  S  D  K  I  L  R  W  N  V  L
                1450      1460      1470      1480      1490      1500
1441      GCCTGCAAGGGGCACTGTTGACCCACTTCCTGCAGCCCATTTATCTCAAATCTGTCACAT
480       G  L  Q  G  A  L  L  T  H  F  L  Q  P  I  Y  L  K  S  V  T
                1510      1520      1530      1540      1550      1560
1501      TGGGTTACCTTTTCAGCCAAGGGCATCTGACCCGTGCTATTTGCTGTCGTGTGACAAGAG
500       L  G  Y  L  F  S  Q  G  H  L  T  R  A  I  C  C  R  V  T  R
                1570      1580      1590      1600      1610      1620
1561      ATGGGAGTGCATTTGAGGATGGACTACGACATCCCTTTATTGTCAACCACCCCAAGGTTG
520       D  G  S  A  F  E  D  G  L  R  H  P  F  I  V  N  H  P  K  V
                1630      1640      1650      1660      1670      1680
```

```
1621       GCAGAGTCAGCATATATGATTCCAAAAGGCAATCCGGGAAGACTAAGGAGACAAGCGTCA
540        G  R  V  S  I  Y  D  S  K  R  Q  S  G  K  T  K  E  T  S  V
                 1690      1700      1710      1720      1730      1740
1681       ACTGGTGTCTGGCTGATGGCTATGACCTGGAGATCCTGGACGGTACCAGAGGCACTGTGG
560        N  W  C  L  A  D  G  Y  D  L  E  I  L  D  G  T  R  G  T  V
                 1750      1760      1770      1780      1790      1800
1741       ATGGGCCACGGAATGAATTGTCCCGGGTCTCCAAAAAGAACATTTTTCTTCTATTTAAGA
580        D  G  P  R  N  E  L  S  R  V  S  K  K  N  I  F  L  L  F  K
                 1810      1820      1830      1840      1850      1860
1801       AGCTCTGCTCCTTCCGTTACCGCAGGGATCTACTGAGACTCTCCTATGGTGAGGCCAAGA
600        K  L  C  S  F  R  Y  R  R  D  L  L  R  L  S  Y  G  E  A  K
                 1870      1880      1890      1900      1910      1920
1861       AAGCTGCCCGTGACTACGAGACGGCCAAGAACTACTTCAAAAAAGGCCTGAAGGATATGG
620        K  A  A  R  D  Y  E  T  A  K  N  Y  F  K  K  G  L  K  D  M
                 1930      1940      1950      1960      1970      1980
1921       GCTATGGGAACTGGATTAGCAAACCCCAGGAGGAAAAGAACTTTTATCTCTGCCCAGTAT
640        G  Y  G  N  W  I  S  K  P  Q  E  E  K  N  F  Y  L  C  P  V
                 1990      2000      2010      2020      2030      2040
1981       CTAGATGACTGCCTGTTCCGTAGCCGACACGGGCCCGTTTAAACCCGCTGATCAGCCTCG
660        S  R  *
                 2050      2060      2070      2080      2090      2100
2041       ACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACC
680
```

Sequence of SNAP-ADAR1 as expressed from the 293 genome with chosen editing sites (yellow).

```
                    10        20        30        40        50        60
1           GGAGACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCC
1
                    70        80        90       100       110       120
61          GGACTCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTCGGATCCACCATGGACAAAGACT
20                                                          M  D  K  D
                   130       140       150       160       170       180
121         GCGAAATGAAGCGCACCACCCTGGATAGCCCTCTGGGCAAGCTGGAACTGTCTGGGTGCG
40          C  E  M  K  R  T  T  L  D  S  P  L  G  K  L  E  L  S  G  C
                   190       200       210       220       230       240
181         AACAGGGCCTGCACCGTATCATCTTCCTGGGCAAAGGAACATCTGCCGCCGACGCCGTGG
60          E  Q  G  L  H  R  I  I  F  L  G  K  G  T  S  A  A  D  A  V
                   250       260       270       280       290       300
241         AAGTGCCTGCCCCAGCCGCCGTGCTGGGCGGACCAGAGCCACTGATGCAGGCCACCGCCT
80          E  V  P  A  P  A  A  V  L  G  G  P  E  P  L  M  Q  A  T  A
                   310       320       330       340       350       360
301         GGCTCAACGCCTACTTTCACCAGCCTGAGGCCATCGAGGAGTTCCCTGTGCCAGCCCTGC
100         W  L  N  A  Y  F  H  Q  P  E  A  I  E  E  F  P  V  P  A  L
                   370       380       390       400       410       420
361         ACCACCCAGTGTTCCAGCAGGAGAGCTTTACCCGCCAGGTGCTGTGGAAACTGCTGAAAG
120         H  H  P  V  F  Q  Q  E  S  F  T  R  Q  V  L  W  K  L  L  K
                   430       440       450       460       470       480
421         TGGTGAAGTTCGGAGAGGTCATCAGCTACAGCCACCTGGCCGCCCTGGCCGGCAATCCCG
140         V  V  K  F  G  E  V  I  S  Y  S  H  L  A  A  L  A  G  N  P
                   490       500       510       520       530       540
481         CCGCCACCGCCGCCGTGAAAACCGCCCTGAGCGGAAATCCCGTGCCCATTCTGATCCCCT
160         A  A  T  A  A  V  K  T  A  L  S  G  N  P  V  P  I  L  I  P
                   550       560       570       580       590       600
541         GCCACCGGGTGGTGCAGGGCGACCTGGACGTGGGGGGCTACGAGGGCGGGCTCGCCGTGA
180         C  H  R  V  V  Q  G  D  L  D  V  G  G  Y  E  G  G  L  A  V
                   610       620       630       640       650       660
601         AAGAGTGGCTGCTGGCCCACGAGGGCCACAGACTGGGCAAGCCTGGGCTGGGTCCTGCAG
200         K  E  W  L  L  A  H  E  G  H  R  L  G  K  P  G  L  G  P  A
                   670       680       690       700       710       720
661         GCGGAGGCGCGCCAGGGTCTGGCGGCGGCAGTAAGAAGCTTGCCAAGGCCCGGGCTGCGC
220         G  G  G  A  P  G  S  G  G  G  S  K  K  L  A  K  A  R  A  A
                   730       740       750       760       770       780
721         AGTCTGCCCTGGCCGCCATTTTTAACTTGCACTTGGATCAGACGCCATCTCGCCAGCCTA
240         Q  S  A  L  A  A  I  F  N  L  H  L  D  Q  T  P  S  R  Q  P
                   790       800       810       820       830       840
781         TTCCCAGTGAGGGTCTTCAGCTGCATTTACCGCAGGTTTTAGCTGACGCTGTCTCACGCC
260         I  P  S  E  G  L  Q  L  H  L  P  Q  V  L  A  D  A  V  S  R
                   850       860       870       880       890       900
841         TGGTCCTGGGTAAGTTTGGTGACCTGACCGACAACTTCTCCTCCCCTCACGCTCGCAGAA
280         L  V  L  G  K  F  G  D  L  T  D  N  F  S  S  P  H  A  R  R
                   910       920       930       940       950       960
901         AAGTGCTGGCTGGAGTCGTCATGACAACAGGCACAGATGTTAAAGATGCCAAGGTGATAA
300         K  V  L  A  G  V  V  M  T  T  G  T  D  V  K  D  A  K  V  I
                   970       980       990      1000      1010      1020
961         GTGTTTCTACAGGAACAAAATGTATTAATGGTGAATACATGAGTGATCGTGGCCTTGCAT
320         S  V  S  T  G  T  K  C  I  N  G  E  Y  M  S  D  R  G  L  A
                  1030      1040      1050      1060      1070      1080
1021        TAAATGACTGCCATGCAGAAATAATATCTCGGAGATCCTTGCTCAGATTTCTTTATACAC
340         L  N  D  C  H  A  E  I  I  S  R  R  S  L  L  R  F  L  Y  T
                  1090      1100      1110      1120      1130      1140
1081        AACTTGAGCTTTACTTAAATAACAAAGATGATCAAAAAAGATCCATCTTTCAGAAATCAG
360         Q  L  E  L  Y  L  N  N  K  D  D  Q  K  R  S  I  F  Q  K  S
                  1150      1160      1170      1180      1190      1200
1141        AGCGAGGGGGGTTTAGGCTGAAGGAGAATGTCCAGTTTCATCTGTACATCAGCACCTCTC
380         E  R  G  G  F  R  L  K  E  N  V  Q  F  H  L  Y  I  S  T  S
                  1210      1220      1230      1240      1250      1260
1201        CCTGTGGAGATGCCAGAATCTTCTCACCACATGAGCCAATCCTGGAAGAACCAGCAGATA
400         P  C  G  D  A  R  I  F  S  P  H  E  P  I  L  E  E  P  A  D
                  1270      1280      1290      1300      1310      1320
1261        GACACCCAAATCGTAAAGCAAGAGGACAGCTACGGACCAAAATAGAGTCTGGTGAGGGGA
420         R  H  P  N  R  K  A  R  G  Q  L  R  T  K  I  E  S  G  E  G
                  1330      1340      1350      1360      1370      1380
1321        CGATTCCAGTGCGCTCCAATGCGAGCATCCAAACGTGGGACGGGGTGCTGCAAGGGGAGC
440         T  I  P  V  R  S  N  A  S  I  Q  T  W  D  G  V  L  Q  G  E
                  1390      1400      1410      1420      1430      1440
1381        GGCTGCTCACCATGTCCTGCAGTGACAAGATTGCACGCTGGAACGTGGTGGGCATCCAGG
460         R  L  L  T  M  S  C  S  D  K  I  A  R  W  N  V  V  G  I  Q
                  1450      1460      1470      1480      1490      1500
1441        GATCCCTGCTCAGCATTTTCGTGGAGCCCATTTACTTCTCGAGCATCATCCTGGGCAGCC
480         G  S  L  L  S  I  F  V  E  P  I  Y  F  S  S  I  I  L  G  S
                  1510      1520      1530      1540      1550      1560
1501        TTTACCACGGGGACCACCTTTCCAGGGCCATGTACCAGCGGATCTCCAACATAGAGGACC
500         L  Y  H  G  D  H  L  S  R  A  M  Y  Q  R  I  S  N  I  E  D
                  1570      1580      1590      1600      1610      1620
1561        TGCCACCTCTCTACACCCTCAACAAGCCTTTGCTCAGTGGCATCAGCAATGCAGAAGCAC
520         L  P  P  L  Y  T  L  N  K  P  L  L  S  G  I  S  N  A  E  A
                  1630      1640      1650      1660      1670      1680
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1621      GGCAGCCAGGGAAGGCCCCCAACTTCAGTGTCAACTGGACGGTAGGCGACTCCGCTATTG
540       R  Q  P  G  K  A  P  N  F  S  V  N  W  T  V  G  D  S  A  I
                1690      1700      1710      1720      1730      1740
1681      AGGTCATCAACGCCACGACTGGGAAGGATGAGCTGGGCCGCGCGTCCCGCCTGTGTAAGC
560       E  V  I  N  A  T  T  G  K  D  E  L  G  R  A  S  R  L  C  K
                1750      1760      1770      1780      1790      1800
1741      ACGCGTTGTACTGTCGCTGGATGCGTGTGCACGGCAAGGTTCCCTCCCACTTACTACGCT
580       H  A  L  Y  C  R  W  M  R  V  H  G  K  V  P  S  H  L  L  R
                1810      1820      1830      1840      1850      1860
1801      CCAAGATTACCAAGCCCAACGTGTACCATGAGTCCAAGCTGGCGGCAAAGGAGTACCAGG
600       S  K  I  T  K  P  N  V  Y  H  E  S  K  L  A  A  K  E  Y  Q
                1870      1880      1890      1900      1910      1920
1861      CCGCCAAGGCGCGTCTGTTCACAGCCTTCATCAAGGCGGGGCTGGGGGCCTGGGTGGAGA
620       A  A  K  A  R  L  F  T  A  F  I  K  A  G  L  G  A  W  V  E
                1930      1940      1950      1960      1970      1980
1921      AGCCCACCGAGCAGGACCAGTTCTCACTCACGCCCTCTAGATGACTGCCTGTTCCGTAGC
640       K  P  T  E  Q  D  Q  F  S  L  T  P  S  R  *
                1990      2000      2010      2020      2030      2040
1981      CGACACGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCA
660
```

Sequence of SNAP-ADAR2 as expressed from the 293 genome with chosen editing sites (yellow).

```
                  10        20        30        40        50        60
1         GGAGACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCC
1
                  70        80        90       100       110       120
61        GGACTCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTCGGATCCACCATGGACAAAGACT
20                                                        M  D  K  D
                 130       140       150       160       170       180
121       GCGAAATGAAGCGCACCACCCTGGATAGCCCTCTGGGCAAGCTGGAACTGTCTGGGTGCG
40        C  E  M  K  R  T  T  L  D  S  P  L  G  K  L  E  L  S  G  C
                 190       200       210       220       230       240
181       AACAGGGCCTGCACCGTATCATCTTCCTGGGCAAAGGAACATCTGCCGCCGACGCCGTGG
60        E  Q  G  L  H  R  I  I  F  L  G  K  G  T  S  A  A  D  A  V
                 250       260       270       280       290       300
241       AAGTGCCTGCCCCAGCCGCCGTGCTGGGCGGACCAGAGCCACTGATGCAGGCCACCGCCT
80        E  V  P  A  P  A  A  V  L  G  G  P  E  P  L  M  Q  A  T  A
                 310       320       330       340       350       360
301       GGCTCAACGCCTACTTTCACCAGCCTGAGGCCATCGAGGAGTTCCCTGTGCCAGCCCTGC
100       W  L  N  A  Y  F  H  Q  P  E  A  I  E  E  F  P  V  P  A  L
                 370       380       390       400       410       420
361       ACCACCCAGTGTTCCAGCAGGAGAGCTTTACCCGCCAGGTGCTGTGGAAACTGCTGAAAG
120       H  H  P  V  F  Q  Q  E  S  F  T  R  Q  V  L  W  K  L  L  K
                 430       440       450       460       470       480
421       TGGTGAAGTTCGGAGAGGTCATCAGCTACAGCCACCTGGCCGCCCTGGCCGGCAATCCCG
140       V  V  K  F  G  E  V  I  S  Y  S  H  L  A  A  L  A  G  N  P
                 490       500       510       520       530       540
481       CCGCCACCGCCGCCGTGAAAACCGCCCTGAGCGGAAATCCCGTGCCCATTCTGATCCCCT
160       A  A  T  A  A  V  K  T  A  L  S  G  N  P  V  P  I  L  I  P
                 550       560       570       580       590       600
541       GCCACCGGGTGGTGCAGGGCGACCTGGACGTGGGGGGCTACGAGGGCGGGCTCGCCGTGA
180       C  H  R  V  V  Q  G  D  L  D  V  G  G  Y  E  G  G  L  A  V
                 610       620       630       640       650       660
601       AAGAGTGGCTGCTGGCCCACGAGGGCCACAGACTGGGCAAGCCTGGGCTGGGTCCTGCAG
200       K  E  W  L  L  A  H  E  G  H  R  L  G  K  P  G  L  G  P  A
                 670       680       690       700       710       720
661       GCGGAGGCGCGCCAGGGTCTGGCGGCGGCAGTAAGGCAGAACGCATGGGTTTCACAGAGG
220       G  G  G  A  P  G  S  G  G  G  S  K  A  E  R  M  G  F  T  E
                 730       740       750       760       770       780
721       TAACCCCAGTGACAGGGGCCAGTCTCAGAAGAACTATGCTCCTCCTCTCAAGGTCCCCAG
240       V  T  P  V  T  G  A  S  L  R  R  T  M  L  L  L  S  R  S  P
                 790       800       810       820       830       840
781       AAGCACAGCCAAAGACACTCCCTCTCACTGGCAGCACCTTCCATGACCAGATAGCCATGC
260       E  A  Q  P  K  T  L  P  L  T  G  S  T  F  H  D  Q  I  A  M
                 850       860       870       880       890       900
841       TGAGCCACCGGTGCTTCAACACTCTGACTAACAGCTTCCAGCCCTCCTTGCTCGGCCGCA
280       L  S  H  R  C  F  N  T  L  T  N  S  F  Q  P  S  L  L  G  R
                 910       920       930       940       950       960
901       AGATTCTGGCCGCCATCATTATGAAAAAAGACTCTGAGGACATGGGTGTCGTCGTCAGCT
300       K  I  L  A  A  I  I  M  K  K  D  S  E  D  M  G  V  V  V  S
                 970       980       990      1000      1010      1020
961       TGGGAACAGGGAATCGCTGTGTAAAAGGAGATTCTCTCAGCCTAAAAGGAGAAACTGTCA
320       L  G  T  G  N  R  C  V  K  G  D  S  L  S  L  K  G  E  T  V
                1030      1040      1050      1060      1070      1080
1021      ATGACTGCCATGCAGAAATAATCTCCCGGAGAGGCTTCATCAGGTTTCTCTACAGTGAGT
340       N  D  C  H  A  E  I  I  S  R  R  G  F  I  R  F  L  Y  S  E
                1090      1100      1110      1120      1130      1140
1081      TAATGAAATACAACTCCCAGACTGCGAAGGATAGTATATTTGAACCTGCTAAGGGAGGAG
360       L  M  K  Y  N  S  Q  T  A  K  D  S  I  F  E  P  A  K  G  G
                1150      1160      1170      1180      1190      1200
1141      AAAAGCTCCAAATAAAAAAGACTGTGTCATTCCATCTGTATATCAGCACTGCTCCGTGTG
380       E  K  L  Q  I  K  K  T  V  S  F  H  L  Y  I  S  T  A  P  C
                1210      1220      1230      1240      1250      1260
1201      GAGATGGCGCCCTCTTTGACAAGTCCTGCAGCGACCGTGCTATGGAAAGCACAGAATCCC
400       G  D  G  A  L  F  D  K  S  C  S  D  R  A  M  E  S  T  E  S
                1270      1280      1290      1300      1310      1320
1261      GCCACTACCCTGTCTTCGAGAATCCCAAACAAGGAAAGCTCCGCACCAAGGTGGAGAACG
420       R  H  Y  P  V  F  E  N  P  K  Q  G  K  L  R  T  K  V  E  N
                1330      1340      1350      1360      1370      1380
1321      GACAAGGCACAATCCCTGTGGAATCCAGTGACATTGTGCCTACGTGGGATGGCATTCGGC
440       G  Q  G  T  I  P  V  E  S  S  D  I  V  P  T  W  D  G  I  R
                1390      1400      1410      1420      1430      1440
1381      TCGGGGAGAGACTCCGTACCATGTCCTGTAGTGACAAAATCCTACGCTGGAACGTGCTGG
460       L  G  E  R  L  R  T  M  S  C  S  D  K  I  L  R  W  N  V  L
                1450      1460      1470      1480      1490      1500
1441      GCCTGCAAGGGGCACTGTTGACCCACTTCCTGCAGCCCATTTATCTCAAATCTGTCACAT
480       G  L  Q  G  A  L  L  T  H  F  L  Q  P  I  Y  L  K  S  V  T
                1510      1520      1530      1540      1550      1560
1501      TGGGTTACCTTTTCAGCCAAGGGCATCTGACCCGTGCTATTTGCTGTCGTGTGACAAGAG
500       L  G  Y  L  F  S  Q  G  H  L  T  R  A  I  C  C  R  V  T  R
                1570      1580      1590      1600      1610      1620
1561      ATGGGAGTGCATTTGAGGATGGACTACGACATCCCTTTATTGTCAACCACCCCAAGGTTG
520       D  G  S  A  F  E  D  G  L  R  H  P  F  I  V  N  H  P  K  V
                1630      1640      1650      1660      1670      1680
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1621      GCAGAGTCAGCATATATGATTCCAAAAGGCAATCCGGGAAGACTAAGGAGACAAGCGTCA
540       G  R  V  S  I  Y  D  S  K  R  Q  S  G  K  T  K  E  T  S  V
                1690      1700      1710      1720      1730      1740
1681      ACTGGTGTCTGGCTGATGGCTATGACCTGGAGATCCTGGACGGTACCAGAGGCACTGTGG
560       N  W  C  L  A  D  G  Y  D  L  E  I  L  D  G  T  R  G  T  V
                1750      1760      1770      1780      1790      1800
1741      ATGGGCCACGGAATGAATTGTCCCGGGTCTCCAAAAAGAACATTTTTCTTCTATTTAAGA
580       D  G  P  R  N  E  L  S  R  V  S  K  K  N  I  F  L  L  F  K
                1810      1820      1830      1840      1850      1860
1801      AGCTCTGCTCCTTCCGTTACCGCAGGGATCTACTGAGACTCTCCTATGGTGAGGCCAAGA
600       K  L  C  S  F  R  Y  R  R  D  L  L  R  L  S  Y  G  E  A  K
                1870      1880      1890      1900      1910      1920
1861      AAGCTGCCCGTGACTACGAGACGGCCAAGAACTACTTCAAAAAAGGCCTGAAGGATATGG
620       K  A  A  R  D  Y  E  T  A  K  N  Y  F  K  K  G  L  K  D  M
                1930      1940      1950      1960      1970      1980
1921      GCTATGGGAACTGGATTAGCAAACCCCAGGAGGAAAAGAACTTTTATCTCTGCCCAGTAT
640       G  Y  G  N  W  I  S  K  P  Q  E  E  K  N  F  Y  L  C  P  V
                1990      2000      2010      2020      2030      2040
1981      CTAGATGACTGCCTGTTCCGTAGCCGACACGGGCCCGTTTAAACCCGCTGATCAGCCTCG
660       S  R  *
                2050      2060      2070      2080      2090      2100
2041      ACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGTGCCTTCCTTGACC
680
```

Sequence of SNAP-ADAR1Q as expressed from the 293 genome with chosen editing sites (yellow). E/Q site is highlighted in cyan.

```
                  10        20        30        40        50        60
1         GGAGACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCC
1
                  70        80        90       100       110       120
61        GGACTCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTCGGATCCACCATGGACAAAGACT
20                                                        M  D  K  D
                 130       140       150       160       170       180
121       GCGAAATGAAGCGCACCACCCTGGATAGCCCTCTGGGCAAGCTGGAACTGTCTGGGTGCG
40        C  E  M  K  R  T  T  L  D  S  P  L  G  K  L  E  L  S  G  C
                 190       200       210       220       230       240
181       AACAGGGCCTGCACCGTATCATCTTCCTGGGCAAAGGAACATCTGCCGCCGACGCCGTGG
60        E  Q  G  L  H  R  I  I  F  L  G  K  G  T  S  A  A  D  A  V
                 250       260       270       280       290       300
241       AAGTGCCTGCCCCAGCCGCCGTGCTGGGCGGACCAGAGCCACTGATGCAGGCCACCGCCT
80        E  V  P  A  P  A  A  V  L  G  G  P  E  P  L  M  Q  A  T  A
                 310       320       330       340       350       360
301       GGCTCAACGCCTACTTTCACCAGCCTGAGGCCATCGAGGAGTTCCCTGTGCCAGCCCTGC
100       W  L  N  A  Y  F  H  Q  P  E  A  I  E  E  F  P  V  P  A  L
                 370       380       390       400       410       420
361       ACCACCCAGTGTTCCAGCAGGAGAGCTTTACCCGCCAGGTGCTGTGGAAACTGCTGAAAG
120       H  H  P  V  F  Q  Q  E  S  F  T  R  Q  V  L  W  K  L  L  K
                 430       440       450       460       470       480
421       TGGTGAAGTTCGGAGAGGTCATCAGCTACAGCCACCTGGCCGCCCTGGCCGGCAATCCCG
140       V  V  K  F  G  E  V  I  S  Y  S  H  L  A  A  L  A  G  N  P
                 490       500       510       520       530       540
481       CCGCCACCGCCGCCGTGAAAACCGCCCTGAGCGGAAATCCCGTGCCCATTCTGATCCCCT
160       A  A  T  A  A  V  K  T  A  L  S  G  N  P  V  P  I  L  I  P
                 550       560       570       580       590       600
541       GCCACCGGGTGGTGCAGGGCGACCTGGACGTGGGGGGCTACGAGGGCGGGCTCGCCGTGA
180       C  H  R  V  V  Q  G  D  L  D  V  G  G  Y  E  G  G  L  A  V
                 610       620       630       640       650       660
601       AAGAGTGGCTGCTGGCCCACGAGGGCCACAGACTGGGCAAGCCTGGGCTGGGTCCTGCAG
200       K  E  W  L  L  A  H  E  G  H  R  L  G  K  P  G  L  G  P  A
                 670       680       690       700       710       720
661       GCGGAGGCGCGCCAGGGTCTGGCGGCGGCAGTAAGAAGCTTGCCAAGGCCCGGGCTGCGC
220       G  G  G  A  P  G  S  G  G  G  S  K  K  L  A  K  A  R  A  A
                 730       740       750       760       770       780
721       AGTCTGCCCTGGCCGCCATTTTTAACTTGCACTTGGATCAGACGCCATCTCGCCAGCCTA
240       Q  S  A  L  A  A  I  F  N  L  H  L  D  Q  T  P  S  R  Q  P
                 790       800       810       820       830       840
781       TTCCCAGTGAGGGTCTTCAGCTGCATTTACCGCAGGTTTTAGCTGACGCTGTCTCACGCC
260       I  P  S  E  G  L  Q  L  H  L  P  Q  V  L  A  D  A  V  S  R
                 850       860       870       880       890       900
841       TGGTCCTGGGTAAGTTTGGTGACCTGACCGACAACTTCTCCTCCCCTCACGCTCGCAGAA
280       L  V  L  G  K  F  G  D  L  T  D  N  F  S  S  P  H  A  R  R
                 910       920       930       940       950       960
901       AAGTGCTGGCTGGAGTCGTCATGACAACAGGCACAGATGTTAAAGATGCCAAGGTGATAA
300       K  V  L  A  G  V  V  M  T  T  G  T  D  V  K  D  A  K  V  I
                 970       980       990      1000      1010      1020
961       GTGTTTCTACAGGAACAAAATGTATTAATGGTGAATACATGAGTGATCGTGGCCTTGCAT
320       S  V  S  T  G  T  K  C  I  N  G  E  Y  M  S  D  R  G  L  A
                1030      1040      1050      1060      1070      1080
1021      TAAATGACTGCCATGCAGAAATAATATCTCGGAGATCCTTGCTCAGATTTCTTTATACAC
340       L  N  D  C  H  A  E  I  I  S  R  R  S  L  L  R  F  L  Y  T
                1090      1100      1110      1120      1130      1140
1081      AACTTGAGCTTTACTTAAATAACAAAGATGATCAAAAAAGATCCATCTTTCAGAAATCAG
360       Q  L  E  L  Y  L  N  N  K  D  D  Q  K  R  S  I  F  Q  K  S
                1150      1160      1170      1180      1190      1200
1141      AGCGAGGGGGGTTTAGGCTGAAGGAGAATGTCCAGTTTCATCTGTACATCAGCACCTCTC
380       E  R  G  G  F  R  L  K  E  N  V  Q  F  H  L  Y  I  S  T  S
                1210      1220      1230      1240      1250      1260
1201      CCTGTGGAGATGCCAGAATCTTCTCACCACATGAGCCAATCCTGGAAGAACCAGCAGATA
400       P  C  G  D  A  R  I  F  S  P  H  E  P  I  L  E  E  P  A  D
                1270      1280      1290      1300      1310      1320
1261      GACACCCAAATCGTAAAGCAAGAGGACAGCTACGGACCAAAATAGAGTCTGGTCAGGGGA
420       R  H  P  N  R  K  A  R  G  Q  L  R  T  K  I  E  S  G  Q  G
                1330      1340      1350      1360      1370      1380
1321      CGATTCCAGTGCGCTCCAATGCGAGCATCCAAACGTGGGACGGGGTGCTGCAAGGGGAGC
440       T  I  P  V  R  S  N  A  S  I  Q  T  W  D  G  V  L  Q  G  E
                1390      1400      1410      1420      1430      1440
1381      GGCTGCTCACCATGTCCTGCAGTGACAAGATTGCACGCTGGAACGTGGTGGGCATCCAGG
460       R  L  L  T  M  S  C  S  D  K  I  A  R  W  N  V  V  G  I  Q
                1450      1460      1470      1480      1490      1500
1441      GATCCCTGCTCAGCATTTTCGTGGAGCCCATTTACTTCTCGAGCATCATCCTGGGCAGCC
480       G  S  L  L  S  I  F  V  E  P  I  Y  F  S  S  I  I  L  G  S
                1510      1520      1530      1540      1550      1560
1501      TTTACCACGGGGACCACCTTTCCAGGGCCATGTACCAGCGGATCTCCAACATAGAGGACC
500       L  Y  H  G  D  H  L  S  R  A  M  Y  Q  R  I  S  N  I  E  D
                1570      1580      1590      1600      1610      1620
1561      TGCCACCTCTCTACACCCTCAACAAGCCTTTGCTCAGTGGCATCAGCAATGCAGAAGCAC
520       L  P  P  L  Y  T  L  N  K  P  L  L  S  G  I  S  N  A  E  A
                1630      1640      1650      1660      1670      1680
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1621      GGCAGCCAGGGAAGGCCCCCAACTTCAGTGTCAACTGGACGGTAGGCGACTCCGCTATTG
540       R  Q  P  G  K  A  P  N  F  S  V  N  W  T  V  G  D  S  A  I
                1690      1700      1710      1720      1730      1740
1681      AGGTCATCAACGCCACGACTGGGAAGGATGAGCTGGGCCGCGCGTCCCGCCTGTGTAAGC
560       E  V  I  N  A  T  T  G  K  D  E  L  G  R  A  S  R  L  C  K
                1750      1760      1770      1780      1790      1800
1741      ACGCGTTGTACTGTCGCTGGATGCGTGTGCACGGCAAGGTTCCCTCCCACTTACTACGCT
580       H  A  L  Y  C  R  W  M  R  V  H  G  K  V  P  S  H  L  L  R
                1810      1820      1830      1840      1850      1860
1801      CCAAGATTACCAAGCCCAACGTGTACCATGAGTCCAAGCTGGCGGCAAAGGAGTACCAGG
600       S  K  I  T  K  P  N  V  Y  H  E  S  K  L  A  A  K  E  Y  Q
                1870      1880      1890      1900      1910      1920
1861      CCGCCAAGGCGCGTCTGTTCACAGCCTTCATCAAGGCGGGGCTGGGGGCCTGGGTGGAGA
620       A  A  K  A  R  L  F  T  A  F  I  K  A  G  L  G  A  W  V  E
                1930      1940      1950      1960      1970      1980
1921      AGCCCACCGAGCAGGACCAGTTCTCACTCACGCCCTCTAGATGACTGCCTGTTCCGTAGC
640       K  P  T  E  Q  D  Q  F  S  L  T  P  S  R  *
                1990      2000      2010      2020      2030      2040
1981      CGACACGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCA
660
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Sequence of SNAP-ADAR2Q as expressed from the 293 genome with chosen editing sites (yellow). E/Q site is highlighted in cyan.

```
                10        20        30        40        50        60
1         GGAGACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCC
1
                  70        80        90       100       110       120
61        GGACTCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTCGGATCCACCATGGACAAAGACT
20                                                        M  D  K  D
                 130       140       150       160       170       180
121       GCGAAATGAAGCGCACCACCCTGGATAGCCCTCTGGGCAAGCTGGAACTGTCTGGGTGCG
40        C  E  M  K  R  T  T  L  D  S  P  L  G  K  L  E  L  S  G  C
                 190       200       210       220       230       240
181       AACAGGGCCTGCACCGTATCATCTTCCTGGGCAAAGGAACATCTGCCGCCGACGCCGTGG
60        E  Q  G  L  H  R  I  I  F  L  G  K  G  T  S  A  A  D  A  V
                 250       260       270       280       290       300
241       AAGTGCCTGCCCCAGCCGCCGTGCTGGGCGGACCAGAGCCACTGATGCAGGCCACCGCCT
80        E  V  P  A  P  A  A  V  L  G  G  P  E  P  L  M  Q  A  T  A
                 310       320       330       340       350       360
301       GGCTCAACGCCTACTTTCACCAGCCTGAGGCCATCGAGGAGTTCCCTGTGCCAGCCCTGC
100       W  L  N  A  Y  F  H  Q  P  E  A  I  E  E  F  P  V  P  A  L
                 370       380       390       400       410       420
361       ACCACCCAGTGTTCCAGCAGGAGAGCTTTACCCGCCAGGTGCTGTGGAAACTGCTGAAAG
120       H  H  P  V  F  Q  Q  E  S  F  T  R  Q  V  L  W  K  L  L  K
                 430       440       450       460       470       480
421       TGGTGAAGTTCGGAGAGGTCATCAGCTACAGCCACCTGGCCGCCCTGGCCGGCAATCCCG
140       V  V  K  F  G  E  V  I  S  Y  S  H  L  A  A  L  A  G  N  P
                 490       500       510       520       530       540
481       CCGCCACCGCCGCCGTGAAAACCGCCCTGAGCGGAAATCCCGTGCCCATTCTGATCCCCT
160       A  A  T  A  A  V  K  T  A  L  S  G  N  P  V  P  I  L  I  P
                 550       560       570       580       590       600
541       GCCACCGGGTGGTGCAGGGCGACCTGGACGTGGGGGGCTACGAGGGCGGGCTCGCCGTGA
180       C  H  R  V  V  Q  G  D  L  D  V  G  G  Y  E  G  G  L  A  V
                 610       620       630       640       650       660
601       AAGAGTGGCTGCTGGCCCACGAGGGCCACAGACTGGGCAAGCCTGGGCTGGGTCCTGCAG
200       K  E  W  L  L  A  H  E  G  H  R  L  G  K  P  G  L  G  P  A
                 670       680       690       700       710       720
661       GCGGAGGCGCGCCAGGGTCTGGCGGCGGCAGTAAGAAGCTTGCCAAGGCCCGGGCTGCGC
220       G  G  G  A  P  G  S  G  G  G  S  K  K  L  A  K  A  R  A  A
                 730       740       750       760       770       780
721       AGTCTGCCCTGGCCGCCATTTTTAACTTGCACTTGGATCAGACGCCATCTCGCCAGCCTA
240       Q  S  A  L  A  A  I  F  N  L  H  L  D  Q  T  P  S  R  Q  P
                 790       800       810       820       830       840
781       TTCCCAGTGAGGGTCTTCAGCTGCATTTACCGCAGGTTTTAGCTGACGCTGTCTCACGCC
260       I  P  S  E  G  L  Q  L  H  L  P  Q  V  L  A  D  A  V  S  R
                 850       860       870       880       890       900
841       TGGTCCTGGGTAAGTTTGGTGACCTGACCGACAACTTCTCCTCCCCTCACGCTCGCAGAA
280       L  V  L  G  K  F  G  D  L  T  D  N  F  S  S  P  H  A  R  R
                 910       920       930       940       950       960
901       AAGTGCTGGCTGGAGTCGTCATGACAACAGGCACAGATGTTAAAGATGCCAAGGTGATAA
300       K  V  L  A  G  V  V  M  T  T  G  T  D  V  K  D  A  K  V  I
                 970       980       990      1000      1010      1020
961       GTGTTTCTACAGGAGGAAAATGTATTAATGGTGAATACATGAGTGATCGTGGCCTTGCAT
320       S  V  S  T  G  G  K  C  I  N  G  E  Y  M  S  D  R  G  L  A
                1030      1040      1050      1060      1070      1080
1021      TAAATGACTGCCATGCAGAAATAATATCTCGGAGATCCTTGCTCAGATTTCTTTATACAC
340       L  N  D  C  H  A  E  I  I  S  R  R  S  L  L  R  F  L  Y  T
                1090      1100      1110      1120      1130      1140
1081      AACTTGAGCTTTACTTAAATAACAAAGATGATCAAAAAAGATCCATCTTTCAGAAATCAG
360       Q  L  E  L  Y  L  N  N  K  D  D  Q  K  R  S  I  F  Q  K  S
                1150      1160      1170      1180      1190      1200
1141      AGCGAGGGGGGTTTAGGCTGAAGGAGAATGTCCAGTTTCATCTGTACATCAGCACCTCTC
380       E  R  G  G  F  R  L  K  E  N  V  Q  F  H  L  Y  I  S  T  S
                1210      1220      1230      1240      1250      1260
1201      CCTGTGGAGATGCCAGAATCTTCTCACCACATGAGCCAATCCTGGAAGAACCAGCAGATA
400       P  C  G  D  A  R  I  F  S  P  H  E  P  I  L  E  E  P  A  D
                1270      1280      1290      1300      1310      1320
1261      GACACCCAAATCGTAAAGCAAGAGGACAGCTACGGACCAAAATAGAGTCTGGTCAGGGGA
420       R  H  P  N  R  K  A  R  G  Q  L  R  T  K  I  E  S  G  Q  G
                1330      1340      1350      1360      1370      1380
1321      CGATTCCAGTGCGCTCCAATGCGAGCATCCAAACGTGGGACGGGGTGCTGCAAGGGGAGC
440       T  I  P  V  R  S  N  A  S  I  Q  T  W  D  G  V  L  Q  G  E
                1390      1400      1410      1420      1430      1440
1381      GGCTGCTCACCATGTCCTGCAGTGACAAGATTGCACGCTGGAACGTGGTGGGCATCCAGG
460       R  L  L  T  M  S  C  S  D  K  I  A  R  W  N  V  V  G  I  Q
                1450      1460      1470      1480      1490      1500
1441      GATCCCTGCTCAGCATTTTCGTGGAGCCCATTTACTTCTCGAGCATCATCCTGGGCAGCC
480       G  S  L  L  S  I  F  V  E  P  I  Y  F  S  S  I  I  L  G  S
                1510      1520      1530      1540      1550      1560
1501      TTTACCACGGGGACCACCTTTCCAGGGCCATGTACCAGCGGATCTCCAACATAGAGGACC
500       L  Y  H  G  D  H  L  S  R  A  M  Y  Q  R  I  S  N  I  E  D
                1570      1580      1590      1600      1610      1620
1561      TGCCACCTCTCTACACCCTCAACAAGCCTTTGCTCAGTGGCATCAGCAATGCAGAAGCAC
520       L  P  P  L  Y  T  L  N  K  P  L  L  S  G  I  S  N  A  E  A
                1630      1640      1650      1660      1670      1680
```

```
1621      GGCAGCCAGGGAAGGCCCCCAACTTCAGTGTCAACTGGACGGTAGGCGACTCCGCTATTG
540       R  Q  P  G  K  A  P  N  F  S  V  N  W  T  V  G  D  S  A  I
                1690      1700      1710      1720      1730      1740
1681      AGGTCATCAACGCCACGACTGGGAAGGATGAGCTGGGCCGCGCGTCCCGCCTGTGTAAGC
560       E  V  I  N  A  T  T  G  K  D  E  L  G  R  A  S  R  L  C  K
                1750      1760      1770      1780      1790      1800
1741      ACGCGTTGTACTGTCGCTGGATGCGTGTGCACGGCAAGGTTCCCTCCCACTTACTACGCT
580       H  A  L  Y  C  R  W  M  R  V  H  G  K  V  P  S  H  L  L  R
                1810      1820      1830      1840      1850      1860
1801      CCAAGATTACCAAGCCCAACGTGTACCATGAGTCCAAGCTGGCGGCAAAGGAGTACCAGG
600       S  K  I  T  K  P  N  V  Y  H  E  S  K  L  A  A  K  E  Y  Q
                1870      1880      1890      1900      1910      1920
1861      CCGCCAAGGCGCGTCTGTTCACAGCCTTCATCAAGGCGGGGCTGGGGGCCTGGGTGGAGA
620       A  A  K  A  R  L  F  T  A  F  I  K  A  G  L  G  A  W  V  E
                1930      1940      1950      1960      1970      1980
1921      AGCCCACCGAGCAGGACCAGTTCTCACTCACGCCCTCTAGATGACTGCCTGTTCCGTAGC
640       K  P  T  E  Q  D  Q  F  S  L  T  P  S  R  *
                1990      2000      2010      2020      2030      2040
1981      CGACACGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCA
660
```

Sequence of SNAP-ADAR2QG as expressed from the 293 genome with chosen editing sites (yellow). E/Q and T/G sites are highlighted in cyan.

```
                  10        20        30        40        50        60
1         GGCACCGCAGGCCCCGGGATGCTAGTGCGCAGCGGGTGCATCCCTGTCCGGATGCTGCGC

                  70        80        90       100       110       120
61        CTGCGGTAGAGCGGCCGCCATGTTGCAACCGGGAAGGAAATGAATGGGCAGCCGTTAGGA

                 130       140       150       160       170       180
121       AAGCCTGCCGGTGACTAACCCTGCGCTCCTGCCTCGATGGGTGGAGTCGCGTGTGGCGGG

                 190       200       210       220       230       240
181       GAAGTCAGGTGGAGCGAGGCTAGCTGGCCCGATTTCTCCTCCGGGTGATGCTTTTCCTAG

                 250       260       270       280       290       300
241       ATTATTCTCTGATTTGGTCGTATTGGGCGCCTGGTCACCAGGGCTGCTTTTAACTCTGGT

                 310       320       330       340       350       360
301       AAAGTGGATATTGTTGCCATCAATGACCCCTTCATTGACCTCAACTACATGGTTTACATG
                                                           M  V  Y  M
                 370       380       390       400       410       420
361       TTCCAATATGATTCCACCCATGGCAAATTCCATGGCACCGTCAAGGCTGAGAACGGGAAG
121        F  Q  Y  D  S  T  H  G  K  F  H  G  T  V  K  A  E  N  G  K
                 430       440       450       460       470       480
421       CTTGTCATCAATGGAAATCCCATCACCATCTTCCAGGAGCGAGATCCCTCCAAAATCAAG
141        L  V  I  N  G  N  P  I  T  I  F  Q  E  R  D  P  S  K  I  K
                 490       500       510       520       530       540
481       TGGGGCGATGCTGGCGCTGAGTACGTCGTGGAGTCCACTGGCGTCTTCACCACCATGGAG
161        W  G  D  A  G  A  E  Y  V  V  E  S  T  G  V  F  T  T  M  E
                 550       560       570       580       590       600
541       AAGGCTGGGGCTCATTTGCAGGGGGGAGCCAAAAGGGTCATCATCTCTGCCCCCTCTGCT
181        K  A  G  A  H  L  Q  G  G  A  K  R  V  I  I  S  A  P  S  A
                 610       620       630       640       650       660
601       GATGCCCCCATGTTCGTCATGGGTGTGAACCATGAGAAGTATGACAACAGCCTCAAGATC
201        D  A  P  M  F  V  M  G  V  N  H  E  K  Y  D  N  S  L  K  I
                 670       680       690    #1 700       710       720
661       ATCAGCAATGCCTCCTGCACCACCAACTGCTTAGCACCCCTGGCCAAGGTCATCCATGAC
221        I  S  N  A  S  C  T  T  N  C  L  A  P  L  A  K  V  I  H  D
                 730       740       750       760       770       780
721       AACTTTGGTATCGTGGAAGGACTCATGACCACAGTCCATGCCATCACTGCCACCCAGAAG
241        N  F  G  I  V  E  G  L  M  T  T  V  H  A  I  T  A  T  Q  K
                 790       800       810       820       830       840
781       ACTGTGGATGGCCCCTCCGGGAAACTGTGGCGTGATGGCCGCGGGGCTCTCCAGAACATC
261        T  V  D  G  P  S  G  K  L  W  R  D  G  R  G  A  L  Q  N  I
                 850       860       870       880       890       900
841       ATCCCTGCCTCTACTGGCGCTGCCAAGGCTGTGGGCAAGGTCATCCCTGAGCTGAACGGG
281        I  P  A  S  T  G  A  A  K  A  V  G  K  V  I  P  E  L  N  G
                 910       920       930       940       950       960
901       AAGCTCACTGGCATGGCCTTCCGTGTCCCCACTGCCAACGTGTCAGTGGTGGACCTGACC
301        K  L  T  G  M  A  F  R  V  P  T  A  N  V  S  V  V  D  L  T
                  #2       980       990      1000      1010      1020
961       TGCCGTCTAGAAAAACCTGCCAAATATGATGACATCAAGAAGGTGGTGAAGCAGGCGTCG
321        C  R  L  E  K  P  A  K  Y  D  D  I  K  K  V  V  K  Q  A  S
                1030      1040      1050      1060      1070      1080
1021      GAGGGCCCCCTCAAGGGCATCCTGGGCTACACTGAGCACCAGGTGGTCTCCTCTGACTTC
341        E  G  P  L  K  G  I  L  G  Y  T  E  H  Q  V  V  S  S  D  F
                1090      1100      1110      1120      1130      1140
1081      AACAGCGACACCCACTCCTCCACCTTTGACGCTGGGGCTGGCATTGCCCTCAACGACCAC
361        N  S  D  T  H  S  S  T  F  D  A  G  A  G  I  A  L  N  D  H
                1150      1160      1170      1180      1190      1200
1141      TTTGTCAAGCTCATTTCCTGGTATGACAACGAATTTGGCTACAGCAACAGGGTGGTGGAC
381        F  V  K  L  I  S  W  Y  D  N  E  F  G  Y  S  N  R  V  V  D
                1210      1220      1230      1240      1250      1260
1201      CTCATGGCCCACATGGCCTCCAAGGAGTAAGACCCCTGGACCACCAGCCCCAGCAAGAGC
401        L  M  A  H  M  A  S  K  E  *
                1270      1280      1290      1300      1310      1320
1261      ACAAGAGGAAGAGAGAGACCCTCACTGCTGGGGAGTCCCTGCCACACTCAGTCCCCCACC
421

                1330      1340      1350      1360      1370      1380
1321      ACACTGAATCTCCCCTCCTCACAGTTGCCATGTAGACCCCTTGAAGAGGGGAGGGGCCTA
441

                1390      1400      1410      1420      1430      1440
1381      GGGAGCCGCACCTTGTCATGTACCATCAATAAAGTACCCTGTGCTCAACCAGTTAAAAAA
461

                1450
1441      AAAAAAAAAAAAAAA
481
```

Sequence of GAPDH mRNA isoform 2 (NM_001256799.2) with chosen editing sites (yellow).

```
                 10        20        30        40        50        60
1         GCCTCAAGACCTTGGGCTGGGACTGGCTGAGCCTGGCGGGAGGCGGGGTCCGAGTCACCG
1
                  70        80        90       100       110       120
61        CCTGCCGCCGCGCCCCCGGTTTCTATAAATTGAGCCCGCAGCCTCCCGCTTCGCTCTCTG
20
                 130       140       150       160       170       180
121       CTCCTCCTGTTCGACAGTCAGCCGCATCTTCTTTTGCGTCGCCAGCCGAGCCACATCGCT
40
                 190       200       210       220       230       240
181       CAGACACCATGGGGAAGGTGAAGGTCGGAGTCAACGGATTTGGTCGTATTGGGCGCCTGG
60                 M  G  K  V  K  V  G  V  N  G  F  G  R  I  G  R  L
                 250       260       270       280       290       300
241       TCACCAGGGCTGCTTTTAACTCTGGTAAAGTGGATATTGTTGCCATCAATGACCCCTTCA
80        V  T  R  A  A  F  N  S  G  K  V  D  I  V  A  I  N  D  P  F
                 310       320       330       340       350       360
301       TTGACCTCAACTACATGGTTTACATGTTCCAATATGATTCCACCCATGGCAAATTCCATG
100       I  D  L  N  Y  M  V  Y  M  F  Q  Y  D  S  T  H  G  K  F  H
                 370       380       390       400       410       420
361       GCACCGTCAAGGCTGAGAACGGGAAGCTTGTCATCAATGGAAATCCCATCACCATCTTCC
120       G  T  V  K  A  E  N  G  K  L  V  I  N  G  N  P  I  T  I  F
                 430       440       450       460       470       480
421       AGGAGCGAGATCCCTCCAAAATCAAGTGGGGCGATGCTGGCGCTGAGTACGTCGTGGAGT
140       Q  E  R  D  P  S  K  I  K  W  G  D  A  G  A  E  Y  V  V  E
                 490       500       510       520       530       540
481       CCACTGGCGTCTTCACCACCATGGAGAAGGCTGGGGCTCATTTGCAGGGGGGAGCCAAAA
160       S  T  G  V  F  T  T  M  E  K  A  G  A  H  L  Q  G  G  A  K
                 550       560       570       580       590       600
541       GGGTCATCATCTCTGCCCCCTCTGCTGATGCCCCCATGTTCGTCATGGGTGTGAACCATG
180       R  V  I  I  S  A  P  S  A  D  A  P  M  F  V  M  G  V  N  H
                 610       620       630       640       650        #1
601       AGAAGTATGACAACAGCCTCAAGATCATCAGCAATGCCTCCTGCACCACCAACTGCTTAG
200       E  K  Y  D  N  S  L  K  I  I  S  N  A  S  C  T  T  N  C  L
                 670       680       690       700       710       720
661       CACCCCTGGCCAAGGTCATCCATGACAACTTTGGTATCGTGGAAGGACTCATGACCACAG
220       A  P  L  A  K  V  I  H  D  N  F  G  I  V  E  G  L  M  T  T
                 730       740       750       760       770       780
721       TCCATGCCATCACTGCCACCCAGAAGACTGTGGATGGCCCCTCCGGGAAACTGTGGCGTG
240       V  H  A  I  T  A  T  Q  K  T  V  D  G  P  S  G  K  L  W  R
                 790       800       810       820       830       840
781       ATGGCCGCGGGGCTCTCCAGAACATCATCCCTGCCTCTACTGGCGCTGCCAAGGCTGTGG
260       D  G  R  G  A  L  Q  N  I  I  P  A  S  T  G  A  A  K  A  V
                 850       860       870       880       890       900
841       GCAAGGTCATCCCTGAGCTGAACGGGAAGCTCACTGGCATGGCCTTCCGTGTCCCCACTG
280       G  K  V  I  P  E  L  N  G  K  L  T  G  M  A  F  R  V  P  T
                 910       920       930   #2  940       950       960
901       CCAACGTGTCAGTGGTGGACCTGACCTGCCGTCTAGAAAAACCTGCCAAATATGATGACA
300       A  N  V  S  V  V  D  L  T  C  R  L  E  K  P  A  K  Y  D  D
                 970       980       990      1000      1010      1020
961       TCAAGAAGGTGGTGAAGCAGGCGTCGGAGGGCCCCCTCAAGGGCATCCTGGGCTACACTG
320       I  K  K  V  V  K  Q  A  S  E  G  P  L  K  G  I  L  G  Y  T
                1030      1040      1050      1060      1070      1080
1021      AGCACCAGGTGGTCTCCTCTGACTTCAACAGCGACACCCACTCCTCCACCTTTGACGCTG
340       E  H  Q  V  V  S  S  D  F  N  S  D  T  H  S  S  T  F  D  A
                1090      1100      1110      1120      1130      1140
1081      GGGCTGGCATTGCCCTCAACGACCACTTTGTCAAGCTCATTTCCTGGTATGACAACGAAT
360       G  A  G  I  A  L  N  D  H  F  V  K  L  I  S  W  Y  D  N  E
                1150      1160      1170      1180      1190      1200
1141      TTGGCTACAGCAACAGGGTGGTGGACCTCATGGCCCACATGGCCTCCAAGGAGTAAGACC
380       F  G  Y  S  N  R  V  V  D  L  M  A  H  M  A  S  K  E  *
                1210      1220      1230      1240      1250      1260
1201      CCTGGACCACCAGCCCCAGCAAGAGCACAAGAGGAAGAGAGAGACCCTCACTGCTGGGGA
400
                1270      1280      1290      1300      1310      1320
1261      GTCCCTGCCACACTCAGTCCCCCACCACACTGAATCTCCCCTCCTCACAGTTGCCATGTA
420
                1330      1340      1350      1360      1370      1380
1321      GACCCCTTGAAGAGGGGAGGGGCCTAGGGAGCCGCACCTTGTCATGTACCATCAATAAAG
440
                1390      1400      1410      1420
1381      TACCCTGTGCTCAACCAGTTAAAAAAAAAAAAAAAAAAAAA
460
```

Sequence of GAPDH mRNA isoform 1 (NM_002046.5) with chosen editing sites (yellow).

```
                10        20        30        40        50        60
1         ACCGCCGAGACCGCGTCCGCCCCGCGAGCACAGAGCCTCGCCTTTGCCGATCCGCCGCCC
1          T  A  E  T  A  S  A  P  R  A  Q  S  L  A  F  A  D  P  P  P
                70        80        90       100       110       120
61        GTCCACACCCGCCGCCAGCTCACCATGGATGATGATATCGCCGCGCTCGTCGTCGACAAC
21         V  H  T  R  R  Q  L  T  M  D  D  D  I  A  A  L  V  V  D  N
               130       140       150       160       170       180
121       GGCTCCGGCATGTGCAAGGCCGGCTTCGCGGGCGACGATGCCCCCCGGGCCGTCTTCCCC
41         G  S  G  M  C  K  A  G  F  A  G  D  D  A  P  R  A  V  F  P
               190       200       210       220       230       240
181       TCCATCGTGGGGCGCCCCAGGCACCAGGGCGTGATGGTGGGCATGGGTCAGAAGGATTCC
61         S  I  V  G  R  P  R  H  Q  G  V  M  V  G  M  G  Q  K  D  S
               250       260       270       280       290       300
241       TATGTGGGCGACGAGGCCCAGAGCAAGAGAGGCATCCTCACCCTGAAGTACCCCATCGAG
81         Y  V  G  D  E  A  Q  S  K  R  G  I  L  T  L  K  Y  P  I  E
               310       320       330       340       350       360
301       CACGGCATCGTCACCAACTGGGACGACATGGAGAAAATCTGGCACCACACCTTCTACAAT
101        H  G  I  V  T  N  W  D  D  M  E  K  I  W  H  H  T  F  Y  N
               370       380       390       400       410       420
361       GAGCTGCGTGTGGCTCCCGAGGAGCACCCCGTGCTGCTGACCGAGGCCCCCCTGAACCCC
121        E  L  R  V  A  P  E  E  H  P  V  L  L  T  E  A  P  L  N  P
               430       440       450       460       470       480
421       AAGGCCAACCGCGAGAAGATGACCCAGATCATGTTTGAGACCTTCAACACCCCAGCCATG
141        K  A  N  R  E  K  M  T  Q  I  M  F  E  T  F  N  T  P  A  M
               490       500       510       520       530       540
481       TACGTTGCTATCCAGGCTGTGCTATCCCTGTACGCCTCTGGCCGTACCACTGGCATCGTG
161        Y  V  A  I  Q  A  V  L  S  L  Y  A  S  G  R  T  T  G  I  V
               550       560       570       580       590       600
541       ATGGACTCCGGTGACGGGGTCACCCACACTGTGCCCATCTACGAGGGGTATGCCCTCCCC
181        M  D  S  G  D  G  V  T  H  T  V  P  I  Y  E  G  Y  A  L  P
               610       620       630       640       650       660
601       CATGCCATCCTGCGTCTGGACCTGGCTGGCCGGGACCTGACTGACTACCTCATGAAGATC
201        H  A  I  L  R  L  D  L  A  G  R  D  L  T  D  Y  L  M  K  I
               670       680       690       700       710       720
661       CTCACCGAGCGCGGCTACAGCTTCACCACCACGGCCGAGCGGGAAATCGTGCGTGACATT
221        L  T  E  R  G  Y  S  F  T  T  T  A  E  R  E  I  V  R  D  I
               730       740       750       760       770       780
721       AAGGAGAAGCTGTGCTACGTCGCCCTGGACTTCGAGCAAGAGATGGCCACGGCTGCTTCC
241        K  E  K  L  C  Y  V  A  L  D  F  E  Q  E  M  A  T  A  A  S
               790       800       810       820       830       840
781       AGCTCCTCCCTGGAGAAGAGCTACGAGCTGCCTGACGGCCAGGTCATCACCATTGGCAAT
261        S  S  S  L  E  K  S  Y  E  L  P  D  G  Q  V  I  T  I  G  N
               850       860       870       880       890       900
841       GAGCGGTTCCGCTGCCCTGAGGCACTCTTCCAGCCTTCCTTCCTGGGCATGGAGTCCTGT
281        E  R  F  R  C  P  E  A  L  F  Q  P  S  F  L  G  M  E  S  C
               910       920       930       940       950       960
901       GGCATCCACGAAACTACCTTCAACTCCATCATGAAGTGTGACGTGGACATCCGCAAAGAC
301        G  I  H  E  T  T  F  N  S  I  M  K  C  D  V  D  I  R  K  D
               970       980       990      1000      1010      1020
961       CTGTACGCCAACACAGTGCTGTCTGGCGGCACCACCATGTACCCTGGCATTGCCGACAGG
321        L  Y  A  N  T  V  L  S  G  G  T  T  M  Y  P  G  I  A  D  R
              1030      1040      1050      1060      1070      1080
1021      ATGCAGAAGGAGATCACTGCCCTGGCACCCAGCACAATGAAGATCAAGATCATTGCTCCT
341        M  Q  K  E  I  T  A  L  A  P  S  T  M  K  I  K  I  I  A  P
              1090      1100      1110      1120      1130      1140
1081      CCTGAGCGCAAGTACTCCGTGTGGATCGGCGGCTCCATCCTGGCCTCGCTGTCCACCTTC
361        P  E  R  K  Y  S  V  W  I  G  G  S  I  L  A  S  L  S  T  F
              1150      1160      1170      1180      1190      1200
1141      CAGCAGATGTGGATCAGCAAGCAGGAGTATGACGAGTCCGGCCCCTCCATCGTCCACCGC
381        Q  Q  M  W  I  S  K  Q  E  Y  D  E  S  G  P  S  I  V  H  R
              1210      1220      1230      1240      1250      1260
1201      AAATGCTTCTAGGCGGACTATGACTTAGTTGCGTTACACCCTTTCTTGACAAAACCTAAC
401        K  C  F  *
              1270      1280      1290      1300      1310      1320
1261      TTGCGCAGAAAACAAGATGAGATTGGCATGGCTTTATTTGTTTTTTTTGTTTTGTTTTGG
421

              1330      1340      1350      1360      1370      1380
1321      TTTTTTTTTTTTTTTTGGCTTGACTCAGGATTTAAAAACTGGAACGGTGAAGGTGACAGC
441

              1390      1400      1410      1420      1430      1440
1381      AGTCGGTTGGAGCGAGCATCCCCCAAAGTTCACAATGTGGCCGAGGACTTTGATTGCACA
461

              1450      1460      1470      1480      1490      1500
1441      TTGTTGTTTTTTTAATAGTCATTCCAAATATGAGATGCGTTGTTACAGGAAGTCCCTTGC
481                                                                  C
              1510      1520      1530      1540      1550      1560
1501      CATCCTAAAAGCCACCCCACTTCTCTCTAAGGAGAATGGCCCAGTCCTCTCCCAAGTCCA
501

              1570      1580      1590      1600      1610      1620
1561      CACAGGGGAGGTGATAGCATTGCTTTCGTGTAAATTATGTAATGCAAAATTTTTTTAATC
521

              1630      1640      1650      1660      1670      1680
```

```
1621      TTCGCCTTAATACTTTTTTATTTTGTTTTATTTTGAATGATGAGCCTTCGTGCCCCCCCT
541                                                                 P
                1690      1700      1710      1720      1730      1740
1681      TCCCCCTTTTTTGTCCCCCAACTTGAGATGTATGAAGGCTTTTGGTCTCCCTGGGAGTGG
561
                1750      1760      1770      1780      1790      1800
1741      GTGGAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCAGTTGAATAAAAGTGCACA
581
                1810      1820      1830      1840      1850
1801      CCTTAAAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
601
```

Sequence of ACTB mRNA (NM_001101.3) with chosen editing site (yellow).

```
                     10        20        30        40        50        60
1            GTCCTCAACCAAGATGGCGCGGATGGCTTCAGGCGCATCACGACACCGGCGCGTCACGCG
1
                     70        80        90       100       110       120
61           ACCCGCCCTACGGGCACCTCCCGCGCTTTTCTTAGCGCCGCAGACGGTGGCCGAGCGGGG
20
                    130       140       150       160       170       180
121          GACCGGGAAGCATGGCCCGGGGGTCGGCGGTTGCCTGGGCGGCGCTCGGGCCGTTGTTGT
40                       M  A  R  G  S  A  V  A  W  A  A  L  G  P  L  L
                    190       200       210       220       230       240
181          GGGGCTGCGCGCTGGGGCTGCAGGGCGGGATGCTGTACCCCCAGGAGAGCCCGTCGCGGG
60           W  G  C  A  L  G  L  Q  G  G  M  L  Y  P  Q  E  S  P  S  R
                    250       260       270       280       290       300
241          AGTGCAAGGAGCTGGACGGCCTCTGGAGCTTCCGCGCCGACTTCTCTGACAACCGACGCC
80           E  C  K  E  L  D  G  L  W  S  F  R  A  D  F  S  D  N  R  R
                    310       320       330       340       350       360
301          GGGGCTTCGAGGAGCAGTGGTACCGGCGGCCGCTGTGGGAGTCAGGCCCCACCGTGGACA
100          R  G  F  E  E  Q  W  Y  R  R  P  L  W  E  S  G  P  T  V  D
                    370       380       390       400       410       420
361          TGCCAGTTCCCTCCAGCTTCAATGACATCAGCCAGGACTGGCGTCTGCGGCATTTTGTCG
120          M  P  V  P  S  S  F  N  D  I  S  Q  D  W  R  L  R  H  F  V
                    430       440       450       460       470       480
421          GCTGGGTGTGGTACGAACGGGAGGTGATCCTGCCGGAGCGATGGACCCAGGACCTGCGCA
140          G  W  V  W  Y  E  R  E  V  I  L  P  E  R  W  T  Q  D  L  R
                    490       500       510       520       530       540
481          CAAGAGTGGTGCTGAGGATTGGCAGTGCCCATTCCTATGCCATCGTGTGGGTGAATGGGG
160          T  R  V  V  L  R  I  G  S  A  H  S  Y  A  I  V  W  V  N  G
                    550       560       570       580       590       600
541          TCGACACGCTAGAGCATGAGGGGGGCTACCTCCCCTTCGAGGCCGACATCAGCAACCTGG
180          V  D  T  L  E  H  E  G  G  Y  L  P  F  E  A  D  I  S  N  L
                    610       620       630       640       650       660
601          TCCAGGTGGGGCCCCTGCCCTCCCGGCTCCGAATCACTATCGCCATCAACAACACACTCA
200          V  Q  V  G  P  L  P  S  R  L  R  I  T  I  A  I  N  N  T  L
                    670       680       690       700       710       720
661          CCCCCACCACCCTGCCACCAGGGACCATCCAATACCTGACTGACACCTCCAAGTATCCCA
220          T  P  T  T  L  P  P  G  T  I  Q  Y  L  T  D  T  S  K  Y  P
                    730       740       750       760       770       780
721          AGGGTTACTTTGTCCAGAACACATATTTTGACTTTTTCAACTACGCTGGACTGCAGCGGT
240          K  G  Y  F  V  Q  N  T  Y  F  D  F  F  N  Y  A  G  L  Q  R
                    790       800       810       820       830       840
781          CTGTACTTCTGTACACGACACCCACCACCTACATCGATGACATCACCGTCACCACCAGCG
260          S  V  L  L  Y  T  T  P  T  T  Y  I  D  D  I  T  V  T  T  S
                    850       860       870       880       890       900
841          TGGAGCAAGACAGTGGGCTGGTGAATTACCAGATCTCTGTCAAGGGCAGTAACCTGTTCA
280          V  E  Q  D  S  G  L  V  N  Y  Q  I  S  V  K  G  S  N  L  F
                    910       920       930       940       950       960
901          AGTTGGAAGTGCGTCTTTTGGATGCAGAAAACAAAGTCGTGGCGAATGGGACTGGGACCC
300          K  L  E  V  R  L  L  D  A  E  N  K  V  V  A  N  G  T  G  T
                    970       980       990      1000      1010      1020
961          AGGGCCAACTTAAGGTGCCAGGTGTCAGCCTCTGGTGGCCGTACCTGATGCACGAACGCC
320          Q  G  Q  L  K  V  P  G  V  S  L  W  W  P  Y  L  M  H  E  R
                   1030      1040      1050      1060      1070      1080
1021         CTGCCTATCTGTATTCATTGGAGGTGCAGCTGACTGCACAGACGTCACTGGGGCCTGTGT
340          P  A  Y  L  Y  S  L  E  V  Q  L  T  A  Q  T  S  L  G  P  V
                   1090      1100      1110      1120      1130      1140
1081         CTGACTTCTACACACTCCCTGTGGGGATCCGCACTGTGGCTGTCACCAAGAGCCAGTTCC
360          S  D  F  Y  T  L  P  V  G  I  R  T  V  A  V  T  K  S  Q  F
                   1150      1160      1170      1180      1190      1200
1141         TCATCAATGGGAAACCTTTCTATTTCCACGGTGTCAACAAGCATGAGGATGCGGACATCC
380          L  I  N  G  K  P  F  Y  F  H  G  V  N  K  H  E  D  A  D  I
                   1210      1220      1230      1240      1250      1260
1201         GAGGGAAGGGCTTCGACTGGCCGCTGCTGGTGAAGGACTTCAACCTGCTTCGCTGGCTTG
400          R  G  K  G  F  D  W  P  L  L  V  K  D  F  N  L  L  R  W  L
                   1270      1280      1290      1300      1310      1320
1261         GTGCCAACGCTTTCCGTACCAGCCACTACCCCTATGCAGAGGAAGTGATGCAGATGTGTG
420          G  A  N  A  F  R  T  S  H  Y  P  Y  A  E  E  V  M  Q  M  C
                   1330      1340      1350      1360      1370      1380
1321         ACCGCTATGGGATTGTGGTCATCGATGAGTGTCCCGGCGTGGGCCTGGCGCTGCCGCAGT
440          D  R  Y  G  I  V  V  I  D  E  C  P  G  V  G  L  A  L  P  Q
                   1390      1400      1410      1420      1430      1440
1381         TCTTCAACAACGTTTCTCTGCATCACCACATGCAGGTGATGGAAGAAGTGGTGCGTAGGG
460          F  F  N  N  V  S  L  H  H  H  M  Q  V  M  E  E  V  V  R  R
                   1450      1460      1470      1480      1490        #1
1441         ACAAGAACCACCCCGCGGTCGTGATGTGGTCTGTGGCCAACGAGCCTGCGTCCCACCTAG
480          D  K  N  H  P  A  V  V  M  W  S  V  A  N  E  P  A  S  H  L
                   1510      1520      1530      1540      1550      1560
1501         AATCTGCTGGCTACTACTTGAAGATGGTGATCGCTCACACCAAATCCTTGGACCCCTCCC
500          E  S  A  G  Y  Y  L  K  M  V  I  A  H  T  K  S  L  D  P  S
                   1570      1580      1590      1600      1610      1620
1561         GGCCTGTGACCTTTGTGAGCAACTCTAACTATGCAGCAGACAAGGGGGCTCCGTATGTGG
520          R  P  V  T  F  V  S  N  S  N  Y  A  A  D  K  G  A  P  Y  V
                   1630      1640      1650      1660      1670      1680
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1621        ATGTGATCTGTTTGAACAGCTACTACTCTTGGTATCACGACTACGGGCACCTGGAGTTGA
540         D  V  I  C  L  N  S  Y  Y  S  W  Y  H  D  Y  G  H  L  E  L
                  1690      1700      1710      1720      1730      1740
1681        TTCAGCTGCAGCTGGCCACCCAGTTTGAGAACTGGTATAAGAAGTATCAGAAGCCCATTA
560         I  Q  L  Q  L  A  T  Q  F  E  N  W  Y  K  K  Y  Q  K  P  I
                  1750      1760      1770      1780      1790      1800
1741        TTCAGAGCGAGTATGGAGCAGAAACGATTGCAGGGTTTCACCAGGATCCACCTCTGATGT
580         I  Q  S  E  Y  G  A  E  T  I  A  G  F  H  Q  D  P  P  L  M
                  1810      1820      1830      1840      1850      1860
1801        TCACTGAAGAGTACCAGAAAAGTCTGCTAGAGCAGTACCATCTGGGTCTGGATCAAAAAC
600         F  T  E  E  Y  Q  K  S  L  L  E  Q  Y  H  L  G  L  D  Q  K
                  1870      1880      1890      1900      1910      1920
1861        GCAGAAAATACGTGGTTGGAGAGCTCATTTGGAATTTTGCCGATTTCATGACTGAACAGT
620         R  R  K  Y  V  V  G  E  L  I  W  N  F  A  D  F  M  T  E  Q
                  1930      1940      1950      1960      1970      1980
1921        CACCGACGAGAGTGCTGGGGAATAAAAAGGGGATCTTCACTCGGCAGAGACAACCAAAAA
640         S  P  T  R  V  L  G  N  K  K  G  I  F  T  R  Q  R  Q  P  K
                  1990      2000      2010      2020      2030      2040
1981        GTGCAGCGTTCCTTTTGCGAGAGAGATACTGGAAGATTGCCAATGAAACCAGGTATCCCC
660         S  A  A  F  L  L  R  E  R  Y  W  K  I  A  N  E  T  R  Y  P
                   #2       2060      2070      2080      2090      2100
2041        ACTCAGTAGCCAAGTCACAATGTTTGGAAAACAGCCTGTTTACTTGAGCAAGACTGATAC
680         H  S  V  A  K  S  Q  C  L  E  N  S  L  F  T  *
                  2110      2120      2130      2140      2150      2160
2101        CACCTGCGTGTCCCTTCCTCCCCGAGTCAGGGCGACTTCCACAGCAGCAGAACAAGTGCC
700
                  2170      2180      2190      2200      2210      2220
2161        TCCTGGACTGTTCACGGCAGACCAGAACGTTTCTGGCCTGGGTTTTGTGGTCATCTATTC
720
                  2230      2240      2250      2260      2270      2280
2221        TAGCAGGGAACACTAAAGGTGGAAATAAAAGATTTTCTATTATGGAAATAAAGAGTTGGC
740
                  2290      2300      2310      2320
2281        ATGAAAGTGGCTACTGAAAAAAAAAAAAAAAAAAAAAAAAAA
760
```

Sequence of GUSB mRNA (NM_000181.3) with chosen editing sites (yellow).

```
                  10        20        30        40        50        60
1         TCCTAGGCGGCGGCCGCGGCGGCGGAGGCAGCAGCGGCGGCGGCAGTGGCGGCGGCGAAG
1
                  70        80        90       100       110       120
61        GTGGCGGCGGCTCGGCCAGTACTCCCGGCCCCCGCCATTTCGGACTGGGAGCGAGCGCGG
21
                 130       140       150       160       170       180
121       CGCAGGCACTGAAGGCGGCGGCGGGGCCAGAGGCTCAGCGGCTCCCAGGTGCGGGAGAGA
41
                 190       200       210  target A/1         target 2
181       GGCCTGCTGAAAATGACTGAATATAAACTTGTGGTAGTTGGAGCTGGTGGCGTAGGCAAG
61                     M  T  E  Y  K  L  V  V  V  G  A  G  G  V  G  K
                 250       260       270       280       290       300
241       AGTGCCTTGACGATACAGCTAATTCAGAATCATTTTGTGGACGAATATGATCCAACAATA
81         S  A  L  T  I  Q  L  I  Q  N  H  F  V  D  E  Y  D  P  T  I
                 310       320       330       340       350       360
301       GAGGATTCCTACAGGAAGCAAGTAGTAATTGATGGAGAAACCTGTCTCTTGGATATTCTC
101        E  D  S  Y  R  K  Q  V  V  I  D  G  E  T  C  L  L  D  I  L
                 370       380       390       400       410       420
361       GACACAGCAGGTCAAGAGGAGTACAGTGCAATGAGGGACCAGTACATGAGGACTGGGGAG
121        D  T  A  G  Q  E  E  Y  S  A  M  R  D  Q  Y  M  R  T  G  E
                 430       440       450       460       470       480
421       GGCTTTCTTTGTGTATTTGCCATAAATAATACTAAATCATTTGAAGATATTCACCATTAT
141        G  F  L  C  V  F  A  I  N  N  T  K  S  F  E  D  I  H  H  Y
                 490       500       510       520       530       540
481       AGAGAACAAATTAAAAGAGTTAAGGACTCTGAAGATGTACCTATGGTCCTAGTAGGAAAT
161        R  E  Q  I  K  R  V  K  D  S  E  D  V  P  M  V  L  V  G  N
                 550       560       570       580       590       600
541       AAATGTGATTTGCCTTCTAGAACAGTAGACACAAAACAGGCTCAGGACTTAGCAAGAAGT
181        K  C  D  L  P  S  R  T  V  D  T  K  Q  A  Q  D  L  A  R  S
                 610       620       630       640       650       660
601       TATGGAATTCCTTTTATTGAAACATCAGCAAAGACAAGACAGGGTGTTGATGATGCCTTC
201        Y  G  I  P  F  I  E  T  S  A  K  T  R  Q  G  V  D  D  A  F
                 670       680       690       700       710       720
661       TATACATTAGTTCGAGAAATTCGAAAACATAAAGAAAAGATGAGCAAAGATGGTAAAAAG
221        Y  T  L  V  R  E  I  R  K  H  K  E  K  M  S  K  D  G  K  K
                 730       740       750       760       770       780
721       AAGAAAAAGAAGTCAAAGACAAAGTGTGTAATTATGTAAATACAATTTGTACTTTTTTCT
241        K  K  K  K  S  K  T  K  C  V  I  M  *
                 790       800       810       820       830       840
781       TAAGGCATACTAGTACAAGTGGTAATTTTTGTACATTACACTAAATTATTAGCATTTGTT
261
```

Sequence of KRAS mRNA (NM_004985.4) with chosen editing sites (yellow).

```
                    10        20        30        40        50        60
1           GCTGAGCGCGGAGCCGCCCGGTGATTGGTGGGGGCGGAAGGGGGCCGGGCGCCAGCGCTG
1
                    70        80        90       100       110       120
61          CCTTTTCTCCTGCCGGGTAGTTTCGCTTTCCTGCGCAGAGTCTGCGGAGGGGCTCGGCTG
21
                   130       140       150       160       170       180
121         CACCGGGGGGATCGCGCCTGGCAGACCCCAGACCGAGCAGAGGCGACCCAGCGCGCTCGG
41
                   190       200       210       220       230       240
181         GAGAGGCTGCACCGCCGCGCCCCCGCCTAGCCCTTCCGGATCCTGCGCGCAGAAAAGTTT
61
                   250       260       270       280       290       300
241         CATTTGCTGTATGCCATCCTCGAGAGCTGTCTAGGTTAACGTTCGCACTCTGTGTATATA
81
                   310       320       330       340       350       360
301         ACCTCGACAGTCTTGGCACCTAACGTGCTGTGCGTAGCTGCTCCTTTGGTTGAATCCCCA
101
                   370       380       390       400       410       420
361         GGCCCTTGTTGGGGCACAAGGTGGCAGGATGTCTCAGTGGTACGAACTTCAGCAGCTTGA
121                                      M  S  Q  W  Y  E  L  Q  Q  L  D
                   430       440       450       460       470       480
421         CTCAAAATTCCTGGAGCAGGTTCACCAGCTTTATGATGACAGTTTTCCCATGGAAATCAG
141           S  K  F  L  E  Q  V  H  Q  L  Y  D  D  S  F  P  M  E  I  R
                   490       500       510       520       530       540
481         ACAGTACCTGGCACAGTGGTTAGAAAAGCAAGACTGGGAGCACGCTGCCAATGATGTTTC
161           Q  Y  L  A  Q  W  L  E  K  Q  D  W  E  H  A  A  N  D  V  S
                   550       560       570       580       590       600
541         ATTTGCCACCATCCGTTTTCATGACCTCCTGTCACAGCTGGATGATCAATATAGTCGCTT
181           F  A  T  I  R  F  H  D  L  L  S  Q  L  D  D  Q  Y  S  R  F
                   610       620       630       640       650       660
601         TTCTTTGGAGAATAACTTCTTGCTACAGCATAACATAAGGAAAAGCAAGCGTAATCTTCA
201           S  L  E  N  N  F  L  L  Q  H  N  I  R  K  S  K  R  N  L  Q
                   670       680       690       700       710       720
661         GGATAATTTTCAGGAAGACCCAATCCAGATGTCTATGATCATTTACAGCTGTCTGAAGGA
221           D  N  F  Q  E  D  P  I  Q  M  S  M  I  I  Y  S  C  L  K  E
                   730       740       750       760       770       780
721         AGAAAGGAAAATTCTGGAAAACGCCCAGAGATTTAATCAGGCTCAGTCGGGGAATATTCA
241           E  R  K  I  L  E  N  A  Q  R  F  N  Q  A  Q  S  G  N  I  Q
                   790       800       810       820       830       840
781         GAGCACAGTGATGTTAGACAAACAGAAAGAGCTTGACAGTAAAGTCAGAAATGTGAAGGA
261           S  T  V  M  L  D  K  Q  K  E  L  D  S  K  V  R  N  V  K  D
                   850       860       870       880       890       900
841         CAAGGTTATGTGTATAGAGCATGAAATCAAGAGCCTGGAAGATTTACAAGATGAATATGA
281           K  V  M  C  I  E  H  E  I  K  S  L  E  D  L  Q  D  E  Y  D
                   910       920       930       940       950       960
901         CTTCAAATGCAAAACCTTGCAGAACAGAGAACACGAGACCAATGGTGTGGCAAAGAGTGA
301           F  K  C  K  T  L  Q  N  R  E  H  E  T  N  G  V  A  K  S  D
                   970       980       990      1000      1010      1020
961         TCAGAAACAAGAACAGCTGTTACTCAAGAAGATGTATTTAATGCTTGACAATAAGAGAAA
321           Q  K  Q  E  Q  L  L  L  K  K  M  Y  L  M  L  D  N  K  R  K
                  1030      1040      1050      1060      1070      1080
1021        GGAAGTAGTTCACAAAATAATAGAGTTGCTGAATGTCACTGAACTTACCCAGAATGCCCT
341           E  V  V  H  K  I  I  E  L  L  N  V  T  E  L  T  Q  N  A  L
                  1090      1100      1110      1120      1130      1140
1081        GATTAATGATGAACTAGTGGAGTGGAAGCGGAGACAGCAGAGCGCCTGTATTGGGGGGCC
361           I  N  D  E  L  V  E  W  K  R  R  Q  Q  S  A  C  I  G  G  P
                  1150      1160      1170      1180      1190      1200
1141        GCCCAATGCTTGCTTGGATCAGCTGCAGAACTGGTTCACTATAGTTGCGGAGAGTCTGCA
381           P  N  A  C  L  D  Q  L  Q  N  W  F  T  I  V  A  E  S  L  Q
                  1210      1220      1230      1240      1250      1260
1201        GCAAGTTCGGCAGCAGCTTAAAAAGTTGGAGGAATTGGAACAGAAATACACCTACGAACA
401           Q  V  R  Q  Q  L  K  K  L  E  E  L  E  Q  K  Y  T  Y  E  H
                  1270      1280      1290      1300      1310      1320
1261        TGACCCTATCACAAAAAACAAACAAGTGTTATGGGACCGCACCTTCAGTCTTTTCCAGCA
421           D  P  I  T  K  N  K  Q  V  L  W  D  R  T  F  S  L  F  Q  Q
                  1330      1340      1350      1360      1370      1380
1321        GCTCATTCAGAGCTCGTTTGTGGTGGAAAGACAGCCCTGCATGCCAACGCACCCTCAGAG
441           L  I  Q  S  S  F  V  V  E  R  Q  P  C  M  P  T  H  P  Q  R
                  1390      1400      1410      1420      1430      1440
1381        GCCGCTGGTCTTGAAGACAGGGGTCCAGTTCACTGTGAAGTTGAGACTGTTGGTGAAATT
461           P  L  V  L  K  T  G  V  Q  F  T  V  K  L  R  L  L  V  K  L
                  1450      1460      1470      1480      1490      1500
1441        GCAAGAGCTGAATTATAATTTGAAAGTCAAAGTCTTATTTGATAAAGATGTGAATGAGAG
481           Q  E  L  N  Y  N  L  K  V  K  V  L  F  D  K  D  V  N  E  R
                  1510      1520      1530      1540      1550      1560
1501        AAATACAGTAAAAGGATTTAGGAAGTTCAACATTTTGGGCACGCACACAAAAGTGATGAA
501           N  T  V  K  G  F  R  K  F  N  I  L  G  T  H  T  K  V  M  N
                  1570      1580      1590      1600      1610      1620
1561        CATGGAGGAGTCCACCAATGGCAGTCTGGCGGCTGAATTTCGGCACCTGCAATTGAAAGA
521           M  E  E  S  T  N  G  S  L  A  A  E  F  R  H  L  Q  L  K  E
                  1630      1640      1650      1660      1670      1680
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1621      ACAGAAAAATGCTGGCACCAGAACGAATGAGGGTCCTCTCATCGTTACTGAAGAGCTTCA
541         Q  K  N  A  G  T  R  T  N  E  G  P  L  I  V  T  E  E  L  H
                1690      1700      1710      1720      1730      1740
1681      CTCCCTTAGTTTTGAAACCCAATTGTGCCAGCCTGGTTTGGTAATTGACCTCGAGACGAC
561         S  L  S  F  E  T  Q  L  C  Q  P  G  L  V  I  D  L  E  T  T
                1750      1760      1770      1780      1790      1800
1741      CTCTCTGCCCGTTGTGGTGATCTCCAACGTCAGCCAGCTCCCGAGCGGTTGGGCCTCCAT
581         S  L  P  V  V  V  I  S  N  V  S  Q  L  P  S  G  W  A  S  I
                1810      1820      1830      1840      1850      1860
1801      CCTTTGGTACAACATGCTGGTGGCGGAACCCAGGAATCTGTCCTTCTTCCTGACTCCACC
601         L  W  Y  N  M  L  V  A  E  P  R  N  L  S  F  F  L  T  P  P
                1870      1880      1890      1900      1910      1920
1861      ATGTGCACGATGGGCTCAGCTTTCAGAAGTGCTGAGTTGGCAGTTTTCTTCTGTCACCAA
621         C  A  R  W  A  Q  L  S  E  V  L  S  W  Q  F  S  S  V  T  K
                1930      1940      1950      1960      1970      1980
1921      AAGAGGTCTCAATGTGGACCAGCTGAACATGTTGGGAGAGAAGCTTCTTGGTCCTAACGC
641         R  G  L  N  V  D  Q  L  N  M  L  G  E  K  L  L  G  P  N  A
                1990      2000      2010      2020      2030      2040
1981      CAGCCCCGATGGTCTCATTCCGTGGACGAGGTTTTGTAAGGAAAATATAAATGATAAAAA
661         S  P  D  G  L  I  P  W  T  R  F  C  K  E  N  I  N  D  K  N
                2050      2060      2070      2080      2090      2100
2041      TTTTCCCTTCTGGCTTTGGATTGAAAGCATCCTAGAACTCATTAAAAAACACCTGCTCCC
681         F  P  F  W  L  W  I  E  S  I  L  E  L  I  K  K  H  L  L  P
                2110      2120      2130      2140      2150      2160
2101      TCTCTGGAATGATGGGTGCATCATGGGCTTCATCAGCAAGGAGCGAGAGCGTGCCCTGTT
701         L  W  N  D  G  C  I  M  G  F  I  S  K  E  R  E  R  A  L  L
                2170      2180      2190      2200      2210      2220
2161      GAAGGACCAGCAGCCGGGGACCTTCCTGCTGCGGTTCAGTGAGAGCTCCCGGGAAGGGGC
721         K  D  Q  Q  P  G  T  F  L  L  R  F  S  E  S  S  R  E  G  A
                2230      2240      2250      2260      2270      2280
2221      CATCACATTCACATGGGTGGAGCGGTCCCAGAACGGAGGCGAACCTGACTTCCATGCGGT
741         I  T  F  T  W  V  E  R  S  Q  N  G  G  E  P  D  F  H  A  V
                2290      2300      2310      2320      2330      2340
2281      TGAACCCTACACGAAGAAAGAACTTTCTGCTGTTACTTTCCCTGACATCATTCGCAATTA
761         E  P  Y  T  K  K  E  L  S  A  V  T  F  P  D  I  I  R  N  Y
                2350      2360      2370      2380      2390      2400
2341      CAAAGTCATGGCTGCTGAGAATATTCCTGAGAATCCCCTGAAGTATCTGTATCCAAATAT
781         K  V  M  A  A  E  N  I  P  E  N  P  L  K  Y  L  Y  P  N  I
                2410      2420      2430      2440      2450      2460
2401      TGACAAAGACCATGCCTTTGGAAAGTATTACTCCAGGCCAAAGGAAGCACCAGAGCCAAT
801         D  K  D  H  A  F  G  K  Y  Y  S  R  P  K  E  A  P  E  P  M
                2470      2480      2490      2500      2510      2520
2461      GGAACTTGATGGCCCTAAAGGAACTGGATATATCAAGACTGAGTTGATTTCTGTGTCTGA
821         E  L  D  G  P  K  G  T  G  Y  I  K  T  E  L  I  S  V  S  E
                2530      2540      2550      2560      2570      2580
2521      AGTTCACCCTTCTAGACTTCAGACCACAGACAACCTGCTCCCCATGTCTCCTGAGGAGTT
841         V  H  P  S  R  L  Q  T  T  D  N  L  L  P  M  S  P  E  E  F
                2590      2600      2610      2620      2630      2640
2581      TGACGAGGTGTCTCGGATAGTGGGCTCTGTAGAATTCGACAGTATGATGAACACAGTATA
861         D  E  V  S  R  I  V  G  S  V  E  F  D  S  M  M  N  T  V  *
                2650      2660      2670      2680      2690      2700
2641      GAGCATGAATTTTTTTCATCTTCTCTGGCGACAGTTTTCCTTCTCATCTGTGATTCCCTC
881
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Sequence of STAT1 mRNA (NM_007315.3) with chosen editing site Y701 (yellow).