Transcript	Sense Primer	Antisense Primer	1° amplicon (bp)
Blcap	ATTAACCCTCACTAAAGGGAGCCCGGCAGAGATCATGT	TAATACGACTCACTATAGGGGTTCCAGGAGGAAGCTGAGC	172
Cadps	ATTAACCCTCACTAAAGGGATTCTCAGGATGTCCTTCGTGATA	TAATACGACTCACTATAGGGTCAGCCACGTGCAGATGATG	144
Cyfip2	ATTAACCCTCACTAAAGGGAGACATGCAGATAGAGCTGGCC	TAATACGACTCACTATAGGGTGCTCACAGATGTTGTACTGGG	156
Flna	ATTAACCCTCACTAAAGGGACGCCGCCTTACTGTTTCTAG	TAATACGACTCACTATAGGGCTGTGACATAGCACTCCTCCAG	188
Gabra3	ATTAACCCTCACTAAAGGGACGGCCATGGACTGGTTCAT	TAATACGACTCACTATAGGGCTTTGTTGGAGCTGCTGGTG	204
Gria2 (Q/R)	ATTAACCCTCACTAAAGGGAATAGTCTCTGGTTTTCCTTGGG	TAATACGACTCACTATAGGGATGATGAGGGTAAAGAACCACC	152
Gria2 (R/G)	ATTAACCCTCACTAAAGGGACCACACCTAAAGGATCCTCATTA	TAATACGACTCACTATAGGGCTGAGGGCACTGGTCTTTTC	200
Gria4	ATTAACCCTCACTAAAGGGACGACGCCCAAGGGTTCC	TAATACGACTCACTATAGGGCTCAAGGCACTCGTCTTGTCC	200
Grik1	ATTAACCCTCACTAAAGGGATTCTGGTTTGGCGTTGGAG	TAATACGACTCACTATAGGGGATGATTAGGGTGAAAAACCAC	148
Grik2	ATTAACCCTCACTAAAGGGATTCTGGTTTGGAGTTGGAGCT	TAATACGACTCACTATAGGGGATGATAAGTGTGAAAAACCACCA	148
Htr2c	ATTAACCCTCACTAAAGGGAGCTGGACCGGTATGTAGCA	TAATACGACTCACTATAGGGGGATACGAACTGAAACTCCTATTG	196
Igfbp7	ATTAACCCTCACTAAAGGGAGTGAAGAGCCGCAAGAGG	TAATACGACTCACTATAGGGCGCAGCTGGCAGCCG	180
Kcna1	ATTAACCCTCACTAAAGGGATGTGTGCCATCGCTGGTG	TAATACGACTCACTATAGGGGAGGTCACTGTCAGAGGCTAAGT	192
	T3 promoter	T7 promoter	

Supplementary Table 1. Substrate-specific oligonucleotide primers for RT-PCR amplification of ADAR targets. The sequence of sense and antisense oligonucleotide primers for target-specific RT-PCR amplification of the edited region in ADAR substrates is presented with the expected sizes (base pairs, bp) of the corresponding PCR amplicons; all primers are presented in the 5'-to-3' orientation. The positions of the adapter sequences corresponding to the T3 and T7 RNA polymerase promoters are indicated for sense and antisense primers, respectively.

AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**AACCAT**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**AACGTC**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**AACTCA**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**AAGACT**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**ACTATT**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**AGATAC**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**AGGCGG**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**ATATGA**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**CAATAT**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**CCTCGG**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**CGCTTC**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**CGTCTT**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**CTGCAT**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**GCAGAA**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**GCGATG**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**GCGTCC**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**GGAGTC**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**GGTAGG**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**GTTAAT**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**GTTGCC**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**TACCGG**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**TCAGCC**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**TTCGGC**ATTAACCCTCACTAAAGGGA
AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT**TTGACC**ATTAACCCTCACTAAAGGGA

Adapter A — T3 promoter

CAAGCAGAAGACGGCATACGAGCTCTTCCGATCTTAATACGACTCACTATAGGG

Adapter B — T7 promoter

Supplementary Table 2. Universal primers for multiplex high-throughput sequencing of ADAR substrates. The sequences of universal oligonucleotide primers for PCR amplification of T3 and T7 RNA polymerase promoter-tagged RT-PCR products (*see Supplemental Table 1*) are shown in the 5'-to-3' orientation. The positions of the adapter sequences necessary for single-end sequencing on the Illumina platform and the regions corresponding to the T3 and T7 RNA polymerase promoters are shown, as well as unique 6 nt barcodes (*shaded region*) allowing multiplex analysis of editing profiles.

		# reads					
		Cortex		Hippocampus		Cerebellum	
Transcript	Editing site	PBS	reovirus	PBS	reovirus	PBS	reovirus
Blcap	Y/C, Q/R, K/R	417139 ± 32047	233664 ± 43956	630866 ± 65297	331906 ± 56514	784195 ± 34691	486031 ± 20920
Cadps	E/G	71999 ± 39765	668524 ± 58414	812813 ± 62407	741918 ± 8672	674482 ± 16528	627556 ± 42837
Cyfip2	K/E	296973 ± 10857	340403 ± 18242	401207 ± 28692	338967 ± 15362	356857 ± 6325	369017 ± 22793
Flna	Q/R	253895 ± 6262	593520 ± 66178	547222 ± 61181	473303 ± 25432	484645 ± 51800	511340 ± 45452
Gabra3	I/M	171768 ± 14151	220496 ± 18752	108851 ± 9936	91993 ± 8176	63069 ± 6101	40662 ± 3831
Gria2	Q/R	418136 ± 17146	457867 ± 50084	578149 ± 32982	403210 ± 9314	521658 ± 16549	475000 ± 39488
Gria2 (flip)	R/G	111561 ± 4161	112579 ± 17357	122476 ± 10217	101648 ± 7441	33362 ± 2439	21188 ± 2573
Gria2 (flop)	R/G	49530 ± 1760	45955 ± 7544	94121 ± 7929	75386 ± 5596	112448 ± 5192	69827 ± 9948
Gria4 (flip)	R/G	55609 ± 3294	78590 ± 15363	123129 ± 12164	75709 ± 10431	728331 ± 16624	326049 ± 33328
Gria4 (flop)	R/G	96908 ± 5051	102122 ± 20607	264250 ± 26793	158433 ± 18555	349008 ± 10433	219839 ± 36725
Grik1	Q/R	62826 ± 3687	58386 ± 10100	80753 ± 13298	69865 ± 8429	167811 ± 15162	102858 ± 11980
Grik2	Q/R	49269 ± 2368	37936 ± 6509	68833 ± 10204	56935 ± 6614	185029 ± 5514	158169 ± 20817
Htr2c	A, B, E, C, D	368679 ± 31704	432487 ± 95001	999864 ± 114964	510826 ± 18697	519467 ± 64137	189939 ± 29457
Igfbp7	R/G	229014 ± 30471	159127 ± 7682	301641 ± 16071	376504 ± 15691	352346 ± 11765	297454 ± 21709
Kcna1	I/V	178874 ± 9443	251983 ± 42414	208942 ± 30373	244569 ± 23553	374929 ± 46206	573854 ± 47129

Supplementary Table 3. Deep-sequencing reads. For quantitative analysis of RNA editing patterns (Table 1), the total number of multiplexed sequence-specific reads (Means ± SEM; n = 4 animals/treatment group) in dissected brain regions is shown for control and reovirus-infected mice.

Transcript	Editing Site	Bar-code	T3 primer	Reference sequence
Blcap	Y/C; Q/R	NNNNNN	ATTAACCCTCACTAAAGGGA	GCCCGGCAGAGATCATGTRTTGCCTCCRGTGGCTGCTGCCCGTCCT
	K/R	CCTCATCCCCARGCCCCTCAACCCCGCTCTGTGGTTCAGCCACTCCATGTTCATGGGCTTCTACCTGCTCAG		
Cadps	E/G	NNNNNN	ATTAACCCTCACTAAAGGGA	TTCTCAGGATGTCCTTCGTGATAAGGTCAATGRGGAGATGTATATA
Cyfip2	K/E	NNNNNN	ATTAACCCTCACTAAAGGGA	GACATGCAGATAGAGCTGGCCAGATACATTRAGACCAGTGCTCACT
Flna	Q/R	NNNNNN	ATTAACCCTCACTAAAGGGA	CGCCGCCTTACTGTTTCTAGTCTTCRGGAGTCAGGGTTAAAGGTCA
Gabra3	I/M	NNNNNN	ATTAACCCTCACTAAAGGGA	CGGCCATGGACTGGTTCATRGCCGTCTGTTATGCCTTTGTATTTTC
Gria2	Q/R; Q/Q	NNNNNN	ATTAACCCTCACTAAAGGGA	ATAGTCTCTGGTTTTCCTTGGGTGCCTTTATGCRGCARGGATGCGA
Gria2 (flip)	R/G	NNNNNN	ATTAACCCTCACTAAAGGGA	CCACACCTAAAGGATCCTCATTARGAACCCCAGTAAATCTTGCAGT
Gria2 (flop)	R/G	NNNNNN	ATTAACCCTCACTAAAGGGA	CCACACCTAAAGGATCCTCATTARGAAATGCGGTTAACCTCGCAGT
Gria4 (flip)	R/G	NNNNNN	ATTAACCCTCACTAAAGGGA	CCACACCTAAAGGATCCTCATTARGAAATGCTGTTAACCTCGCAGT
Gria4 (flop)	R/G	NNNNNN	ATTAACCCTCACTAAAGGGA	CCACACCTAAAGGATCCTCATTARGAAATGCTGTTAACCTCGCAGT
Grik1	Q/R	NNNNNN	ATTAACCCTCACTAAAGGGA	TTCTGGTTTGGCGTTGGAGCTCTCATGCRGCAAGGATCGGAGCTGA
Grik2	Q/R	NNNNNN	ATTAACCCTCACTAAAGGGA	TTCTGGTTTGGAGTTGGAGCTCTCATGCRGCAAGGTTCTGAGCTCA
Htr2c	A; B; E; C; D	NNNNNN	ATTAACCCTCACTAAAGGGA	GCTGGACCGGTATGTAGCARTRCGTRRTCCTRTTGAGCATAGCCGG
Igfbp7	R/G	NNNNNN	ATTAACCCTCACTAAAGGGA	GTGAAGAGCCGCAAGAGGCGGARGGGTAAAGCCGGGGCAGCAGCCG
Kcna1	I/V	NNNNNN	ATTAACCCTCACTAAAGGGA	TGTGTGCCATCGCTGGTGTGCTGACARTTGCCCTGCCCGTACCTGT

Supplementary Table 4. Reference sequences for analysis of high-throughput sequencing data. The expected DNA sequence for RT-PCR amplicons subjected to high-throughput sequence analysis is shown along with the relative position of the 6-nucleotide barcode (NNNNN) and the T3 RNA polymerase promoter. Editing sites are named according to the amino acid encoded by non-edited and edited transcripts, respectively, and their positions are indicated by an **R** (purine), corresponding to adenosine or guanosine moieties in cDNAs derived from non-edited and edited RNAs.