Supplemental Material

A high resolution A-to-I editing map in the mouse identifies editing events controlled by pre-mRNA splicing

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Supplemental Figure S6. Validation of bioinformatically predicted editing-complementary sequences (ECS). The genomic DNA encoding for edited transcripts and the corresponding predicted editing complementary sequence was cloned (+ ECS). Subsequently, the editing complementary region has been removed (the predicted secondary structure and the removed ECS (- ECS) regions is displayed in Supplemental Dataset S1). Following co-transfection with a plasmid coding for Flag-rADAR2 into HEK293 cells, RNA was isolated, reverse transcribed, amplified with target-specific primers, and submitted to Sanger sequencing. Genome coordinates: mm10.
Supplemental Figure S7. The persistence of the ECS increases editing levels. (A-C) Boxplots showing binned editing sites according to their \( \log_{10} \) ES/ECS coverage (red: \( \log_{10} \) ES/ECS coverage<0 \( \rightarrow \) ES saturated with ECS; blue: \( \log_{10} \) ES/ECS coverage>0 \( \rightarrow \) ES deprived of ECS) and the respective editing level (left side). The analysis was done separately for (A) exonic editing sites with an intronic ECS (exonic-intronic), for (B) non-repeat associated sites, and for (C) repeat associated sites.
Supplemental Figure S8. Editing sites split according to their repeat status (compare to main figure 4). The editing sites were split according to their repeat status (upper panels: non-repeat, lower panels: repeat). Only sites with a minimum read coverage of 10 are shown. Boxplots showing the log₂ fold change (log₂FC) for editing levels in untreated (DMSO) and treated (MEA) primary cells (left panels: bone marrow, right panels: primary neurons) separated into different genic locations as indicated below the panels (exonic, intronic, UTR, n.a.: not annotated/intergenic). Dots represent editing levels for individual sites that are changed significantly (red; p-value<0.05) or not significantly (grey; p-value>=0.05).
Supplemental Figure S9. Meayamycin treatment leads to increased editing levels in bone marrow and neuronal cells. Two primary cell types were treated with the splicing inhibitor meayamycin (MEA) or vehicle control (DMSO). RNA was isolated after treatment and poly(A)-selected RNA was subjected to RNA-seq. Boxplots showing the log₂ fold change (log₂FC) for editing levels in untreated (DMSO) and treated (MEA) primary cells (top panel: bone marrow, lower panel: primary neurons) separated into different genic locations as indicated on top of the panel (exonic, intronic, UTR, not-annotated i.e. intergenic). The location of the editing complementary site (ECS) is given below the panel (undefined: could not be identified; n.a.: not annotated/intergenic). Dots represent editing levels for individual sites that are changed significantly (red; p-value<0.05) or not significantly (grey; p-value>=0.05).
Supplemental Figure S10. Validation of changes in editing levels upon meayamycin treatment (compare to main figure 4). Sanger sequencing traces of all editing sites used for validation are shown (MEA=meayamycin; DMSO=DMSO vehicle control). The RNA-seq result is depicted below the chromatograms (RNA-seq + or - indicates an increase or decrease seen by RNA-seq). The result of the validation is shown as validated ‘yes’ or ‘no’.
**Supplemental Figure S11.** Deletion of NOVA1 or NOVA2 proteins does not perturb overall splicing efficiency. Re-analysis of publicly available RNA-seq data from cortices of 6 wildtype and 3 Nova1−/− and 3 Nova2−/− mice (please compare to main figure 5). The reads have been mapped to the mouse genome (mm10). The relative intron coverage for editing sites in wildtype, Nova1−/−, and Nova2−/− mice is given. Error bars=s.e.m.
Supplemental Tables S1-S8

**Supplemental Table S1.** Primer sequences (5’ – 3’) used for validation of the Nascent-seq (Nasc.) editing sites and the editing sites with significantly changed editing levels upon meayamycin (Mea) treatment.

| Target  | For  | For forward | reverse  |
|---------|------|-------------|----------|
| Camk2a  | Nasc.| CAACCATGGTCCCACATCCA | CCCTGCTGAAACTCTGGACTG |
| Rims1   | Nasc.| TCTGTTCACTAAACCCAGGA | GCTGTCCCCTCCTCCTGTCA |
| Asic2   | Nasc.| TGGAAGCAGAGGGTAAAGG | GAGCTGATGCAGAAGCAATG |
| Asic2   | Nasc.| CAGGACCGGAACCTCAACACAT | TGTGGCCTGGGAAATAAAA |
| Fam193a | Nasc.| CATCTGTCCACCCTCTGGGT | TGGCTGTCATATTGAGTCGTG |
| Kctd8   | Nasc.| TGTCATACTAGAGGCTTCCAT | AATCTTGTTCCTCAGTCTGT |
| Cadps2  | Nasc.| ATGGAGCGACAGCACCAGTC | CTCGAGCCTTTCACGGATGA |
| Mical   | Nasc.| AGTGCAGCTGTCCCTCTTTA | CGGTCTCAGATCCTCCTGG |
| Usp3    | Nasc.| ATGACCGCCGACTGCTGGA | CAGCCTACAGCTCCTCCTT |
| Ftx     | Nasc.| CATTTCATTTAGCAGGCAGA | TGGGCTGAACTGCAGTGCTA |
| Blcap   | Mea. | TGTGGTCATTCTTTTCTCTTCA | CCAATGTCAGAAGGGAGCTG |
| Lamp2   | Mea. | TGGGGAGGACAGATTAAATGCC | CAGTCCTCAGGGTCCAGA |
| Trim12c | Mea. | AGGTTAGAGCATCCAGCTAATTAT | GGGTACCTTATTCATTTGG |
| Klc1    | Mea. | GTGGTGCTTCACTGGCAGCTG | ACACGACTGGCTACTGAAG |
| Mrs2    | Mea. | AACTAAGGGCTGTGCTGTG | TCTGCTGTCAGAGAACCT |
| Pmsd6   | Mea. | TGCTATCTTTGTTTGGGCTT | AGCAGTCAGGAGCTGGG |
| Pcnp    | Mea. | ACACATAAACAGAGGCTTTGCT | CAGACAGCTGTGAGATGCCA |
| Esrra   | Mea. | GCTGCCCTGTGTATCACCA | GCAGACAGCAGAGGCTTG |
| H13     | Mea. | AGCAGCCTCAGGGATTTCACCA | AGCTAGTCAGGGAGCTGGG |
| Sh2d5   | Mea. | GGCGTCCAGGGAGAGATTTGCC | TGGGTTCAGGGGAATTTG |
| 2900026A02Rik | Mea. | GCAGGAGCAGAGGGGAGCTAGCAG | TCAAGCAGGTCAGGAGGAG |
| Uch11   | Mea. | CTGGGTATGGGTGCATCAGCCTTG | GTCTGTGTCAGGGGTTTGGC |
| Cttm    | Mea. | TTGTCTAACTGGGCTCTTGA | CGAATCCAAAACGGCAGTGGC |
| Zfp1    | Mea. | ACTCAAGGGGGTTAATTTGGGT | AGGTGGTGTTGCGACTCTCCTT |
| Elav11  | Mea. | AGGTAGAGGCAAGGAGGCA | GGAAGGGCAGTGATCTTCA |

**Supplemental Table S2.** Comparison between A-to-I editing levels detected by Nascent-seq and Sanger sequencing, respectively. Genome coordinates: mm10.

| Gene    | Chromosome | Position | Percent A-to-I editing by nascent-seq | Percent A-to-I editing by Sanger-seq | Validated |
|---------|------------|----------|--------------------------------------|-------------------------------------|-----------|
| Asic2   | Chr11      | 81850116 | 24%                                  | 43%                                 | Yes       |
| Asic2   | Chr11      | 81855010 | 38%                                  | 29%                                 | Yes       |
| Asic2   | Chr11      | 81855013 | 16%                                  | 16%                                 | Yes       |
| Asic2   | Chr11      | 81855050 | 39%                                  | 30%                                 | Yes       |
| Asic2   | Chr11      | 81855086 | 14%                                  | 12%                                 | Yes       |
| Asic2   | Chr11      | 81855102 | 47%                                  | 45%                                 | Yes       |
### Supplemental Table S3. Editing sites identified by Nascent-seq. Available as separate xlsx-file.

### Supplemental Table S4. Primers used to clone randomly selected editing sites and editing complementary sites into pcDNA3.1(1). Fw primer 1 and rev primer 1 (fw 1, rev 1) denote the primer pair used to clone the original sequence. Fw primer 2 in combination with rev primer 1 (fw 2, rev 1) and vice versa was used to amplify the DNA without ECS. No 1 and No 2: restriction enzymes used.

| Gene      | Primers | Sequences                          | No 1   | No 2   |
|-----------|---------|------------------------------------|--------|--------|
| Armc9     | fw 1    | ATATTCTAGACCTGGGCTTCTTGCTGAGAA     | XbaI   | KpnI   |
|           | rev 1   | ATATGGTACCAGATGGAGAGGTTGCGCT      |         |        |
|           | fw 2    | TCCCCAAGTAGCAGATTTAAGTACAAACAGGATGTGTCAGC   |         |        |
|           | rev 2   | GTGCCCTACATCCTGTTTCTTACTTTAAATGTCACTTTGGGAA |         |        |
| Cep112    | fw 1    | ATATAGAATTCACCTCAGATGAAACAGTACCTT | EcoRI  | KpnI   |
|           | rev 1   | ATATGGTACCCTGGAACACAGGATACAGAGGCC |         |        |
|           | fw 2    | GGAAGTTTTACAAACAGCAGTTGAGTTTTACTGGGACAGTTGTAC |         |        |
|           | rev 2   | GTCAACACTCTTCCAGTTAAATACACTGCTGTGTTTGAATAACTTCC |         |        |
| Cep89     | fw 1    | ATATGAATTTCCACCTGTTCCATCTTGTAACCT | EcoRI  | KpnI   |
|           | rev 1   | ATATGGTACCCCAAAAGGATTGGCTGATGTTT |         |        |
|           | fw 2    | AATCTGGGTCGGGTGAGCGACCTTTTGGAGGTGAGT |         |        |
|           | rev 2   | CACTCCAGAAGGGGCGTCAACAGCCGACCCAGAGT |         |        |
| Chrm2     | fw 1    | ATATGAATTTCTTCTTGTAAGTTATAGACAATAATGTGTTG | EcoRI  | KpnI   |
|           | rev 1   | ATATGGTACCCCAAAAGGATTGGCTGATGTTT |         |        |
|           | fw 2    | GAAGGGGTGTCTTGAGTAAATGCGACAGAAGAAATGTGATCCTG |         |        |
|           | rev 2   | CAGATCAGAAATTCTTTCCTTGAGCTAGAAAAATATGGATTAGA |         |        |
| Chst7     | fw 1    | ATATCTAGATGCTAAGTGGATTGTTCTTTTAAA | XbaI   | KpnI   |
|           | rev 1   | ATATGGTACCCGATTCCACTACACCTTTAATGAGA |         |        |
|           | fw 2    | TTCAGAACACACACAAAGGAGGCGACCCACCTTCTCACCA |         |        |
Supplemental Table S5. Oligonucleotides used to amplify and sequence the editing sites in the test constructs used to validate the accuracy of the ECS prediction. Please note that some primers match to the vector sequence and are common to several targets. Fw/rev primer=oligonucleotides used to amplify the sequence. Sanger=primer used for Sanger sequencing.

| Gene   | fw primer             | rev primer                     | Sanger             |
|--------|-----------------------|--------------------------------|--------------------|
| Kcnh1  | ATCCCAACAGGAGCGCTAGT  | GCTGATCGCGGTTAAAACCTT          | GGTTGATAGAAAGTCAACTCC |
| Armc9  | CAGGTCAAGGGCAAGAGAC   | GCTGATCGCGGTTAAAACCTT          | TCTGGAAGGCTATCATTTTGT   |
| Cep112 | ACCAGGGCTCAACACATGG   | GCTGATCGCGGTTAAAACCTT          | TCTGGAAGGCTATTAAATTGT   |
| Eri3   | CGGCGTGCTGACACTGGAGAG| GCTGATCGCGGTTAAAACCTT          | GCCACCTTCTAGCTGTCTTCT  |
| Chst7  | GGAGACCCAAAGCTGCTAGCT| GTGTGACCGGAAGGACTCCAAGGTAAGTGCTGAAGAGAAAGTCAACTCC |
| Snx19  | GGAGACCAAGGAGGCTGCTAG| GTGTGACCGGAAGGACTCCAAGGTAAGTGCTGAAGAGAAAGTCAACTCC |
| Cep89  | GGAGACCAAGGAGGCTGCTAG| GTGTGACCGGAAGGACTCCAAGGTAAGTGCTGAAGAGAAAGTCAACTCC |
| Rappgef4| GGAGACCAAGGAGGCTGCTAG| GTGTGACCGGAAGGACTCCAAGGTAAGTGCTGAAGAGAAAGTCAACTCC |
| Raf1   | AGCAGACAGAAGGTGCTAGCT| AAAGTGAGGAGGAGGACTCCAAGGTAAGTGCTGAAGAGAAAGTCAACTCC |
| Chrm2  | AGTGTGCTGCTGCTGCTGCTAG| GTGTGACCGGAAGGACTCCAAGGTAAGTGCTGAAGAGAAAGTCAACTCC |

Supplemental Table S6. Editing sites identified in bone marrow and primary neurons plus changes in editing levels upon splicing inhibition. Available as separate xlsx-file.

Supplemental Table S7. Editing sites identified in Nova1−/− and Nova2−/− knockout mice plus changes in editing levels as compared to wildtype. Available as separate xlsx-file.
Supplemental Table S8. Best evidence and a reference for the location of editing complementary sites (ECS) for the editing targets used in main figure 6 are listed. The structure prediction has been done using RNAfold and visualized using fonna. All structure predictions are shown in Supplemental Dataset S2. We define the ECS_type as intronic if the editing-competent double-stranded RNA is formed between the edited exon and the downstream or upstream intron. Vice versa we call the ECS_type exonic if the editing-competent stem is formed within the edited exon. Genome coordinates: hg19.

| Gene   | Chr. | Coordinate | ECS_type | Best evidence          | Reference                       |
|--------|------|------------|----------|------------------------|---------------------------------|
| Best1  | Chr11| 61724916   | intronic | structure prediction   | this study                      |
| Flna   | ChrX | 153579950  | intronic | mutational analysis     | (Jain et al. 2018)              |
| Flnb   | Chr3 | 58141801   | intronic | mutational analysis     | Pullirsch et al. (unpublished)  |
| Cog3   | Chr13| 46090371   | intronic | structure prediction   | this study                      |
| Copa   | Chr1 | 160302244  | intronic | structure prediction   | this study                      |
| Gria2  | Chr4 | 158257875  | intronic | mutational analysis     | (Higuchi et al. 1993)           |
| Gria2  | Chr4 | 158257879  | intronic | mutational analysis     | (Higuchi et al. 1993)           |
| Gria2  | Chr4 | 158281294  | intronic | mutational analysis     | (Lomeli et al. 1994)            |
| Gria3  | ChrX | 122598962  | intronic | mutational analysis     | (Lomeli et al. 1994)            |
| Gria4  | Chr11| 105804694  | intronic | mutational analysis     | (Lomeli et al. 1994)            |
| Grik1  | Chr21| 30953750   | intronic | mutational analysis     | (Herb et al. 1996)              |
| Grik2  | Chr6 | 102372572  | intronic | mutational analysis     | (Herb et al. 1996)              |
| Grik2  | Chr6 | 102372589  | intronic | mutational analysis     | (Herb et al. 1996)              |
| Neil1  | Chr15| 75646087   | intronic | mutational analysis     | (Yeo et al. 2010)               |
| Neil1  | Chr15| 75646086   | intronic | mutational analysis     | (Yeo et al. 2010)               |
| Tmem63b| Chr6 | 44120349   | intronic | structure prediction   | this study                      |
| Azin1  | Chr8 | 103841636  | exonic   | structure prediction   | this study                      |
| Blicap | Chr20| 36147563   | exonic   | structure prediction   | this study                      |
| Cacna1d| Chr3 | 53820892   | exonic   | structure prediction   | this study                      |
| Cadps  | Chr3 | 62423807   | exonic   | structure prediction   | this study                      |
| Cdk13  | Chr7 | 39990302   | exonic   | structure prediction   | (Maas et al. 2011); this study  |
| Dcaf16 | Chr4 | 17805279   | exonic   | structure prediction   | this study                      |
| Elfn2  | Chr22| 37770174   | exonic   | structure prediction   | this study                      |
| Gabra3 | ChrX | 151358319  | exonic   | mutational analysis     | (Ohlson et al. 2007)            |
| Gipc1  | Chr19| 14593693   | exonic   | structure prediction   | this study                      |
| Grm4   | Chr4 | 34100903   | exonic   | structure prediction   | this study                      |
| Igfbp7 | Chr4 | 57976234   | exonic   | structure prediction   | (Gommans et al. 2008); this study|
| Igfbp7 | Chr4 | 57976286   | exonic   | structure prediction   | (Gommans et al. 2008); this study|
| Kcna1  | Chr12| 5021742    | exonic   | mutational analysis     | (Bhalla et al. 2004); this study|
| Kcnma1 | Chr10| 79397298   | exonic   | structure prediction   | this study                      |
| Mll4   | Chr19| 36211399   | exonic   | structure prediction   | this study                      |
| Myo19  | Chr17| 34866719   | exonic   | structure prediction   | this study                      |
| Nova1  | Chr14| 26917515   | exonic   | structure prediction   | (Irimia et al. 2012); this study|
| Osgep  | Chr14| 20920211   | exonic   | structure prediction   | this study                      |
| Pdcd7  | Chr15| 65425319   | exonic   | structure prediction   | this study                      |
| Pdcd7  | Chr15| 65425334   | exonic   | structure prediction   | this study                      |
| Gene  | Chr  | Start   | Type   | Method                        | Notes       |
|-------|------|---------|--------|-------------------------------|-------------|
| Pdcd7 | Chr15| 65425992| exonic | structure prediction         | this study  |
| Pdcd7 | Chr15| 65426067| exonic | structure prediction         | this study  |
| Plch2 | Chr1 | 2436080 | exonic | structure prediction         | this study  |
| Sh3bp2| Chr4 | 2835556 | exonic | structure prediction         | this study  |
| Son   | Chr21| 34923319| exonic | structure prediction         | this study  |
| Son   | Chr21| 34924105| exonic | structure prediction         | this study  |
| Son   | Chr21| 34922801| exonic | structure prediction         | this study  |
| Ttll3 | Chr3 | 9876560 | exonic | structure prediction         | this study  |
| Unc80 | Chr2 | 210835613| exonic | structure prediction        | this study  |

### Supplemental Materials and Methods

**Experimental validation of editing complementary site (ECS) predictions**

A DNA sequence encompassing the randomly selected editing site and the predicted ECS was amplified from genomic mouse DNA and cloned into pcDNA3.1 (Supplemental Table S4). To remove the ECS primers fw 1/rev 2 and fw 2/rev 1 were used, respectively. Subsequently, both PCR products were combined and again amplified with primers fw 1 and rev 1. Restriction enzymes were used as indicated (Supplemental Table S4). To test editing, 3x10⁵ Hek293 cells were plated per well using 6-well dishes. 24 h after plating, 0.5 µg of plasmid (plus or minus ECS) was co-transfected with 3.5 µg of a plasmid expressing Flag-rADAR2 using poly-ethyleneimine (Polysciences cat# 23966). 2 days after transfection RNA was isolated using Trifast™ (Peqlab cat# 30-2010) following the manufacturer’s instructions. Subsequently, RNA was DNase I treated (New England Biolabs, cat# M0303). Following reverse transcription with random hexamers (Integrated DNA Technologies) and M-MuLV reverse transcriptase (New England Biolabs, cat# M0253) the editing site was PCR amplified using OneTaq Green PCR mix (New England Biolabs, cat# M0482) and primer pairs as indicated (Supplemental Table S5). Following gel extraction using Monarch® DNA Gel Extraction Kit (New England Biolabs, cat# T1020) the PCR product was submitted to Sanger sequencing (Eurofins Genomics) using the primer as indicated (Supplemental Table S5). If not stated otherwise all custom primers were obtained from Microsynth Austria.
Supplemental Datasets

Supplemental Dataset S1: Structure predictions to validate bioinformatically predicted ECS. The structure has been predicted using RNAfold and visualized using forna (Lorenz et al. 2011; Kerpedjiev et al. 2015). The editing site is shown in red; the editing complementary site is highlighted in blue. Light blue indicates the sequence that has been deleted in the deltaECS constructs.

Transcript: Armc9
Transcript: *Cep89*
Transcript: Chst7
Transcript: *Eri3*
Transcript: \textit{Kcnh1}
Transcript: *Snx19*
**Supplemental Dataset S2.** Structure predictions of all edited transcripts used in Figure 6 were no experimental evidence for the location of the editing complementary site (ECS) is available. The structure has been predicted using RNAfold and visualized using forna. The exonic sequence is highlighted in yellow. The edited adenosine is marked in red. The intronic sequence is not colored.
Transcript: *lgfbp7*

Transcript: *Kcna1*
Transcript: *TII3*

Transcript: *Unc80*
Supplemental References

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