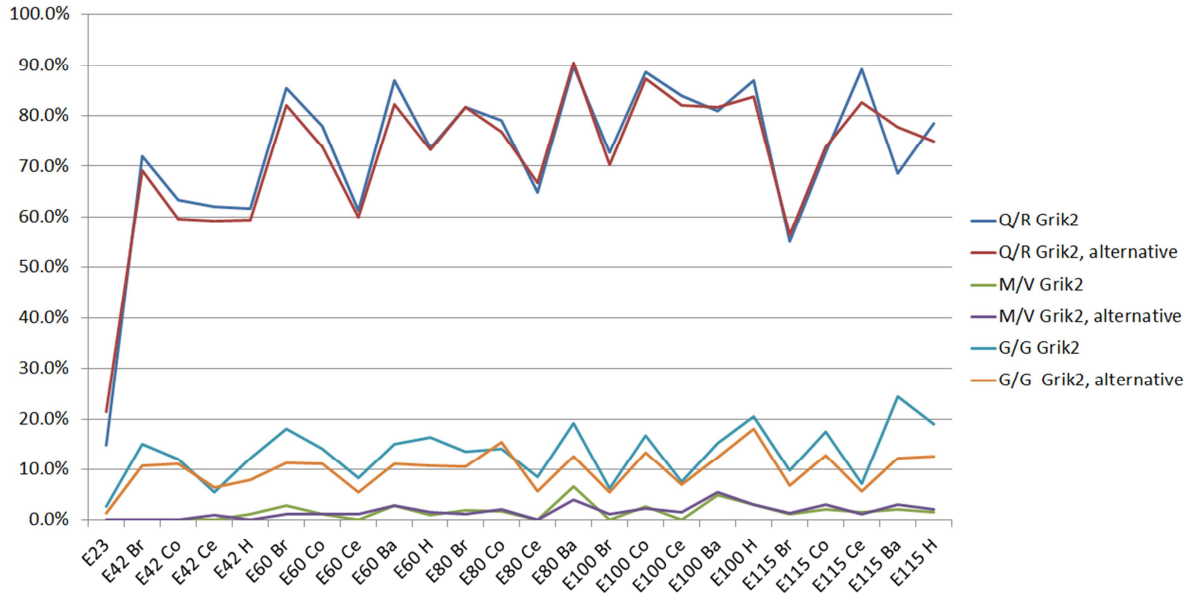
Supplemental Material to: Morten Venø, Jesper Bramsen, Christian Bendixen, Frank Panitz, Ida Holm, Marie Öhman, et al. Spatio-temporal regulation of ADAR editing during development in porcine neural tissues. RNA Biology 2012; 9(8); DOI: 10.4161/rna.21082;
http://www.landesbioscience.com/journals/rnabiology/article/21082/

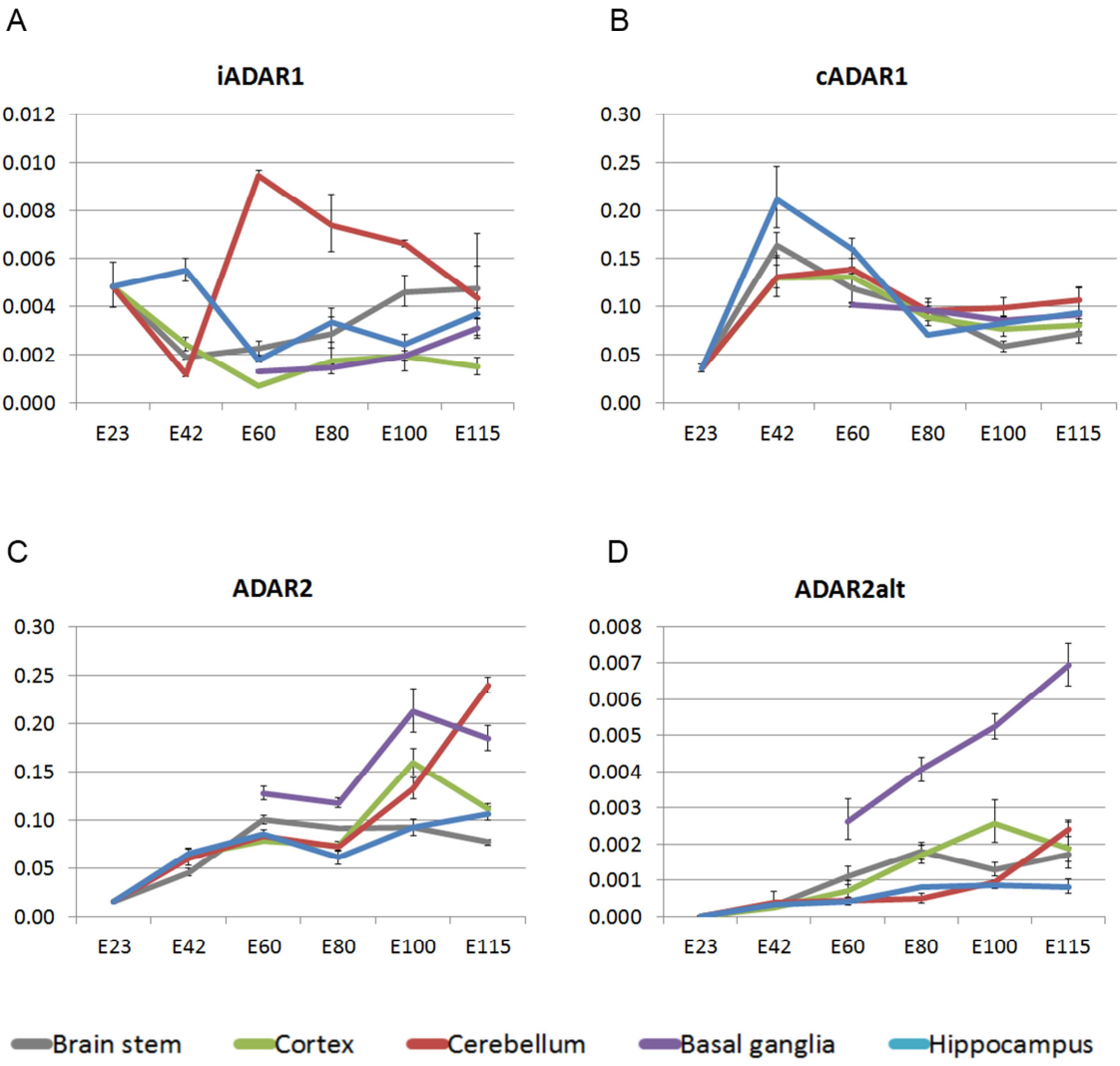


Supplementary Figure S1

Q/R site, M/V site and G/G site editing percentages of the Grik2 amplicon used for analysis and an alternative Grik2 amplicon produced using a different set of primers. The two amplicons were sequenced in the same multiplexed 454 sequencing experiment. The I/V and Y/C sites of Grik2 were not contained in the region of the Grik2 mRNA amplified by the alternative primer set, therefore those sites are not included in this graph.

The editing percentages of the two separate Grik2 amplicons displayed here correlate well, attesting to the reliability of the technique used.

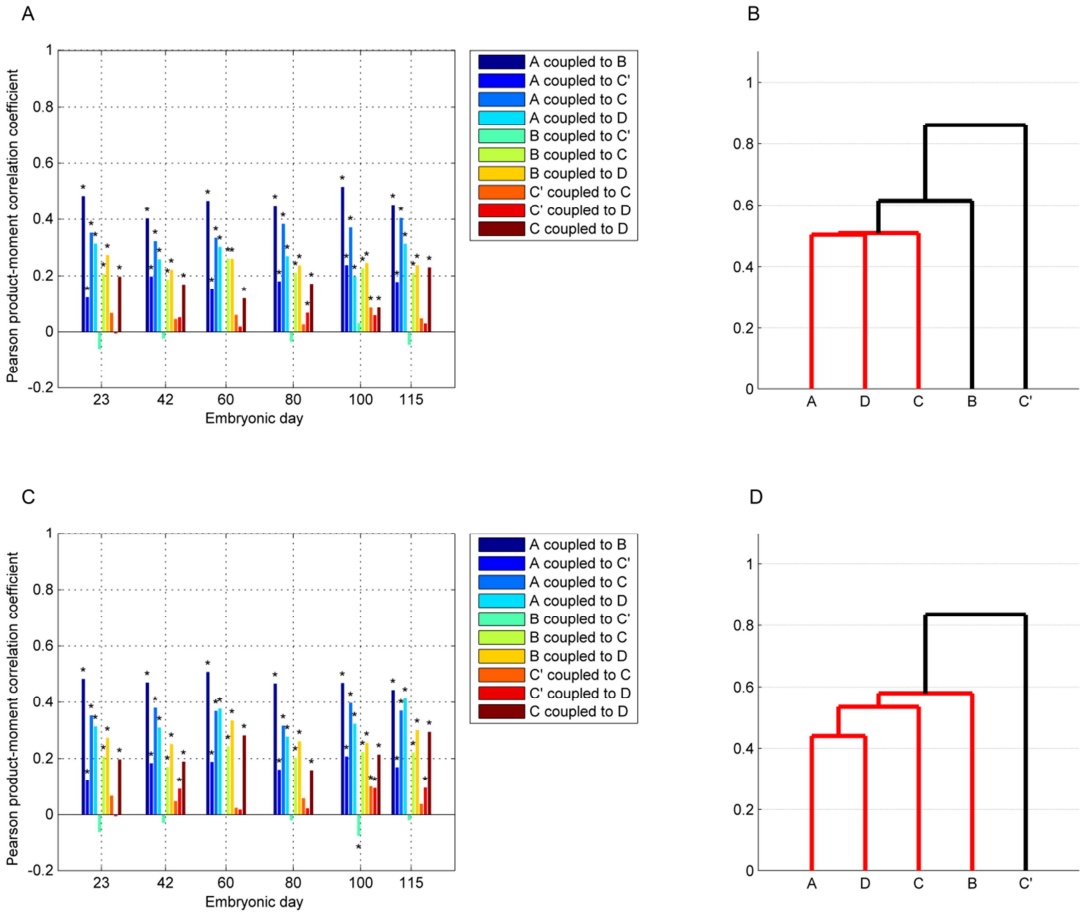
E23 = Forebrain, embryonic day 23. Br = Brain stem. Co = Cortex. Ce= Cerebellum. H = Hippocampus. Ba = Basal ganglia.



Supplementary Figure S2

Transcript levels of various ADAR species were examined by RT-qPCR. Expression relative to GAPDH, is shown. The interferon inducible variant of ADAR1 (*A*) is expressed significantly less than the constitutively expressed ADAR1 (*B*). Increasing expression is clear for ADAR2 (*C*) and the alternatively spliced (non-functional) ADAR2 transcript (*D*). However, the alternatively spliced ADAR2 is expressed at a much lower level than the functional ADAR2.

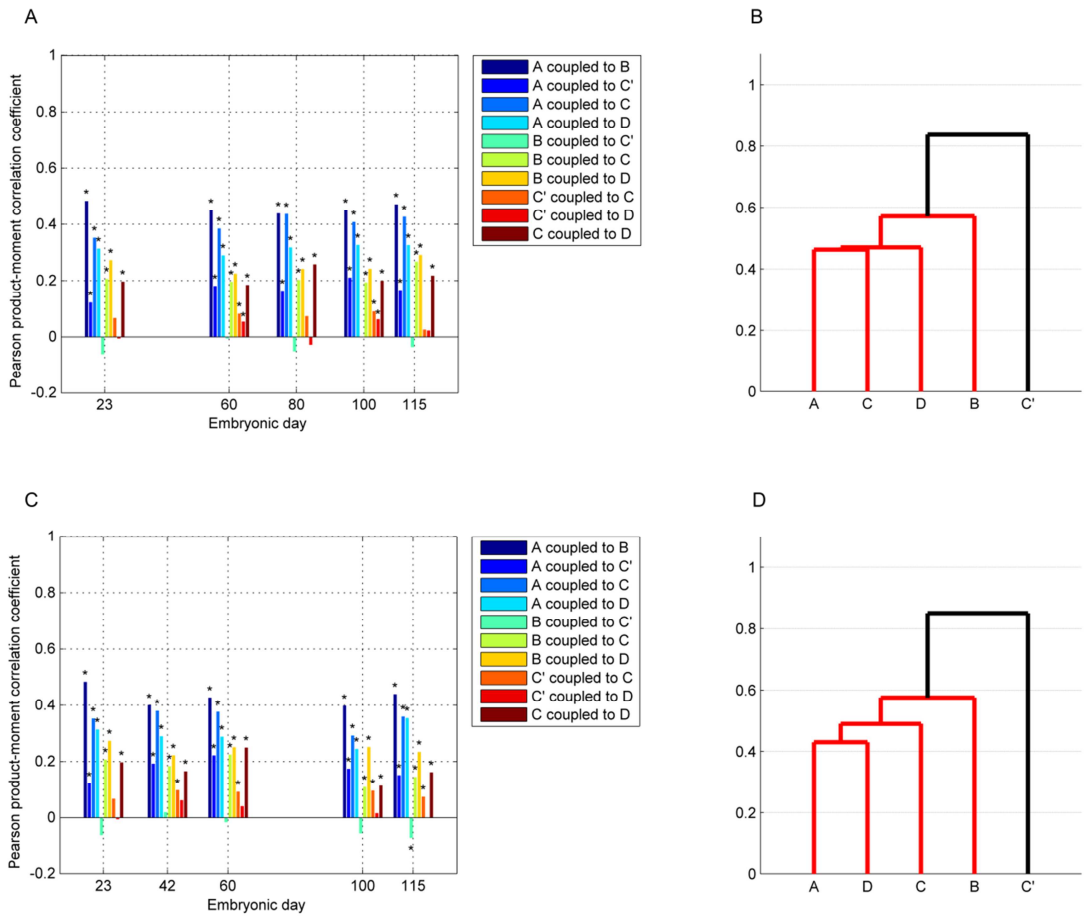
Performed in triplicates, error bars represent standard deviation.



Supplementary Figure S3

Pearson correlation coefficients for coupling between the editing sites on the Htr2c amplicon in Brain stem (*A*) and Cerebellum (*C*). See legend for color codes. Black asterisks denote significance compared to bonferroni corrected critical p-values. Group analysis of E115 Htr2c editing sites in Brain stem (*B*) and Cerebellum (*D*).

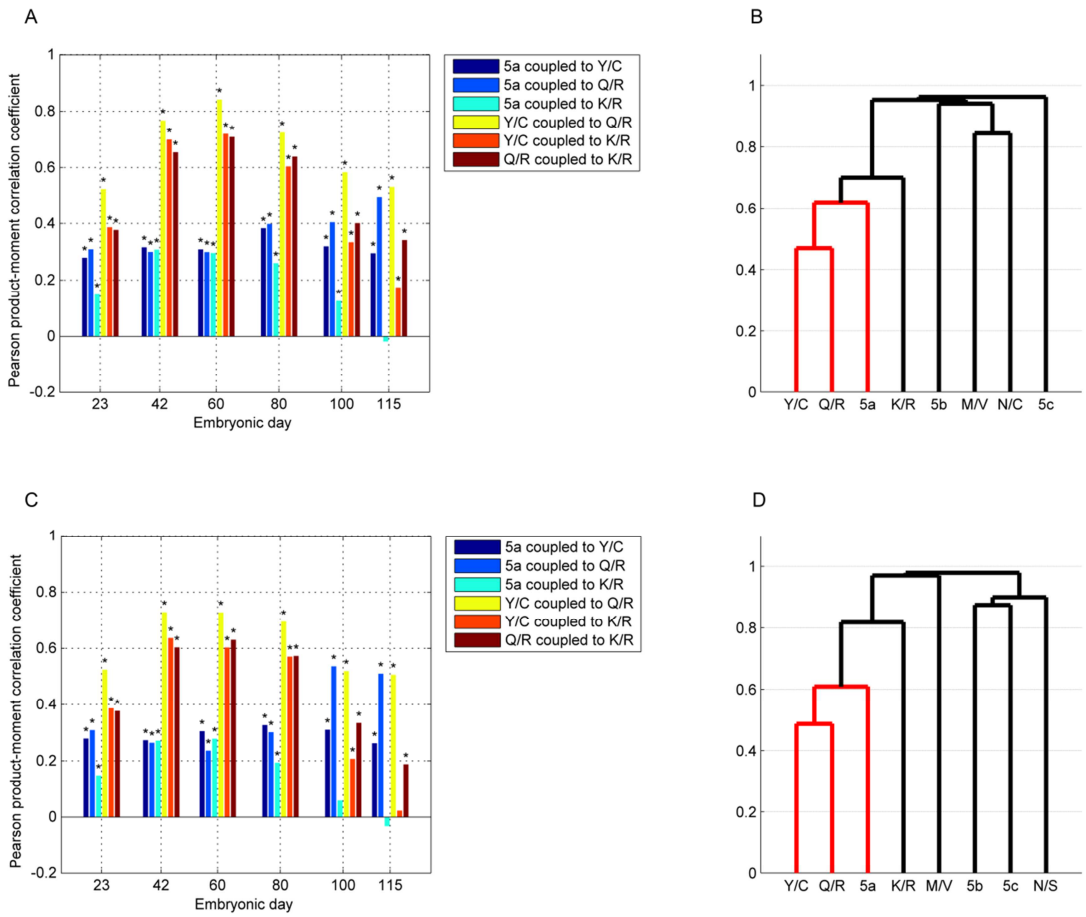
Note that only one tissue, whole forebrain, was dissected from E23.



Supplementary Figure S4

Pearson correlation coefficients for coupling between the editing sites on the Htr2c amplicon in Basal ganglia (*A*) and Hippocampus (*C*). See legend for color codes. Black asterisks denote significance compared to bonferroni corrected critical p-values. Group analysis of E115 Htr2c editing sites in Basal ganglia (*B*) and Hippocampus (*D*).

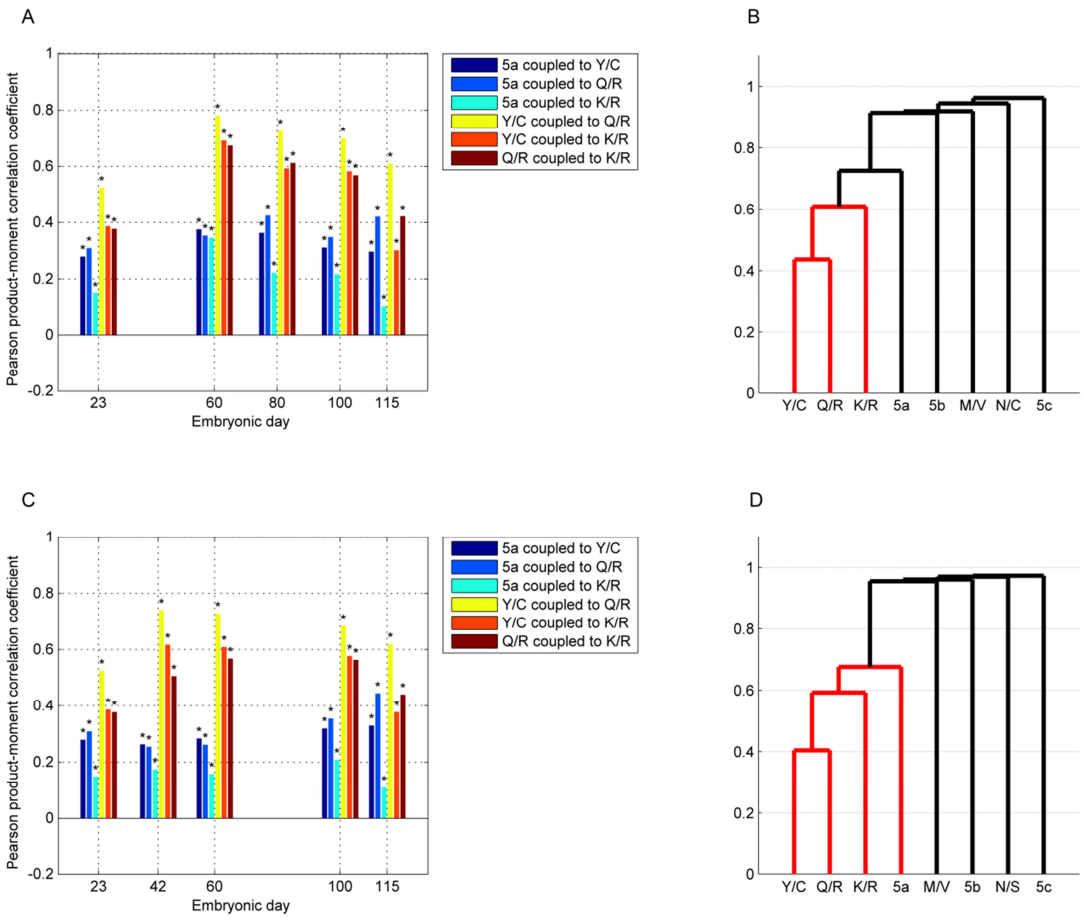
Note that only one tissue, whole forebrain, was dissected from E23.



Supplementary Figure S5

Pearson correlation coefficients for coupling between the main editing sites on the Blcap amplicon in Brain stem (*A*) and Cerebellum (*C*). See legend for color codes. Black asterisks denote significance compared to bonferroni corrected critical p-values. Group analysis of all E115 Blcap editing sites in Brain stem (*B*) and Cerebellum (*D*).

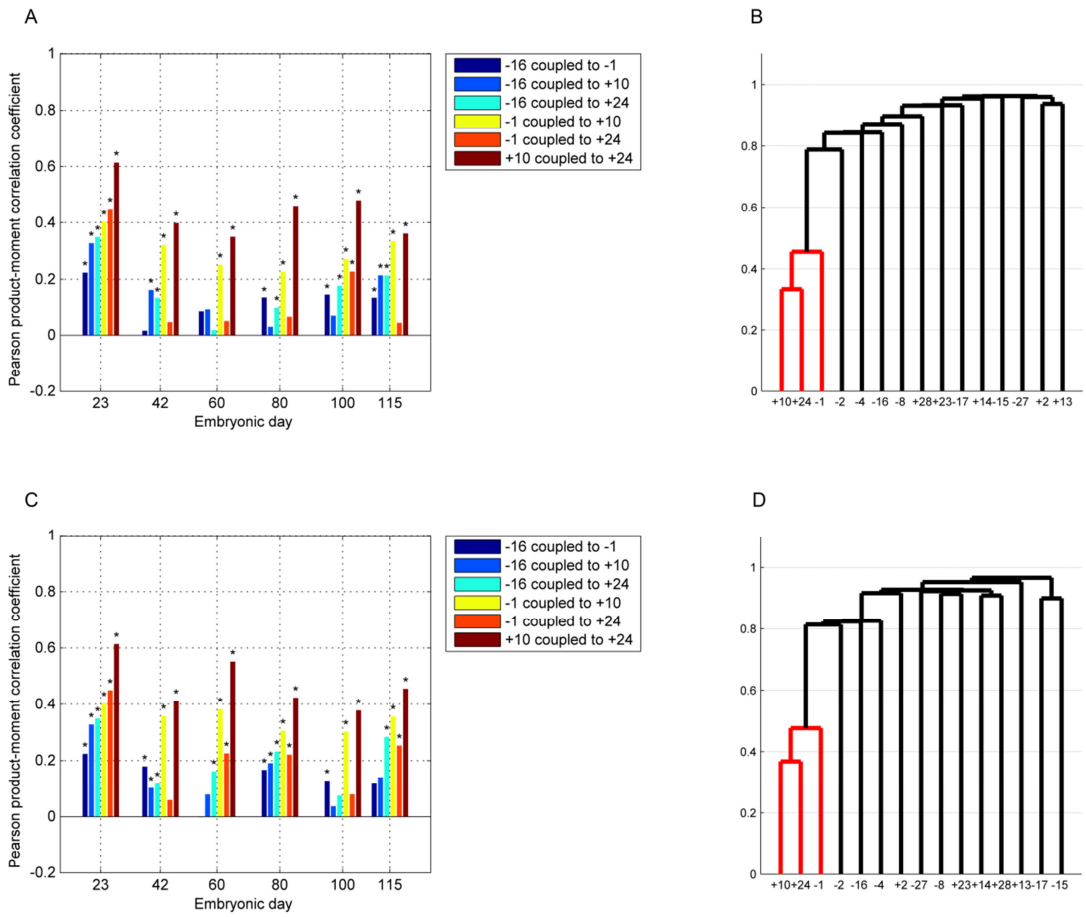
Note that only one tissue, whole forebrain, was dissected from E23.



Supplementary Figure S6

Pearson correlation coefficients for coupling between the main editing sites on the Blcap amplicon in Basal ganglia (*A*) and Hippocampus (*C*). See legend for color codes. Black asterisks denote significance compared to bonferroni corrected critical p-values. Group analysis of all E115 Blcap editing sites in Basal ganglia (*B*) and Hippocampus (*D*).

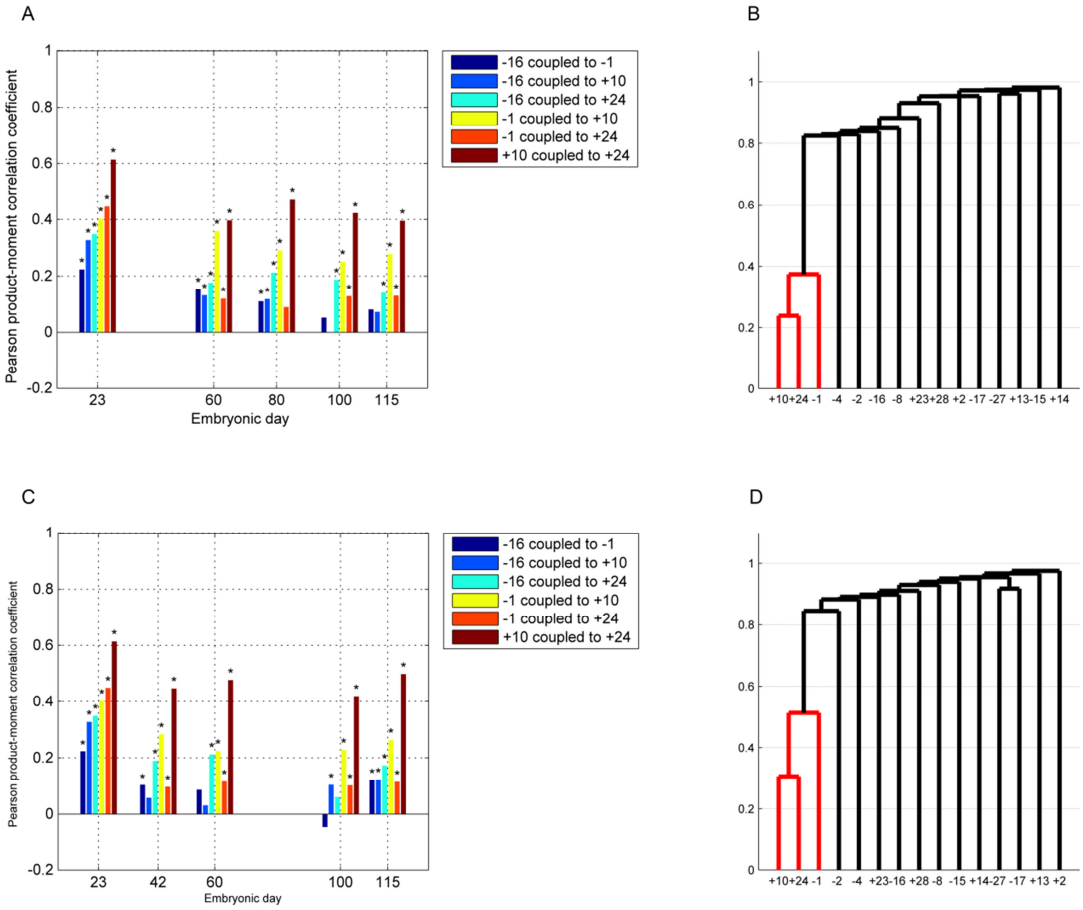
Note that only one tissue, whole forebrain, was dissected from E23.



Supplementary Figure S7

Pearson correlation coefficients for coupling between the predominant self-editing sites on the ADAR2 amplicon in Brain stem (*A*) and Cerebellum (*C*). See legend for color codes. Black asterisks denote significance compared to bonferroni corrected critical p-values. Group analysis of all E115 ADAR2 self-editing sites in Brain stem (*B*) and Cerebellum (*D*).

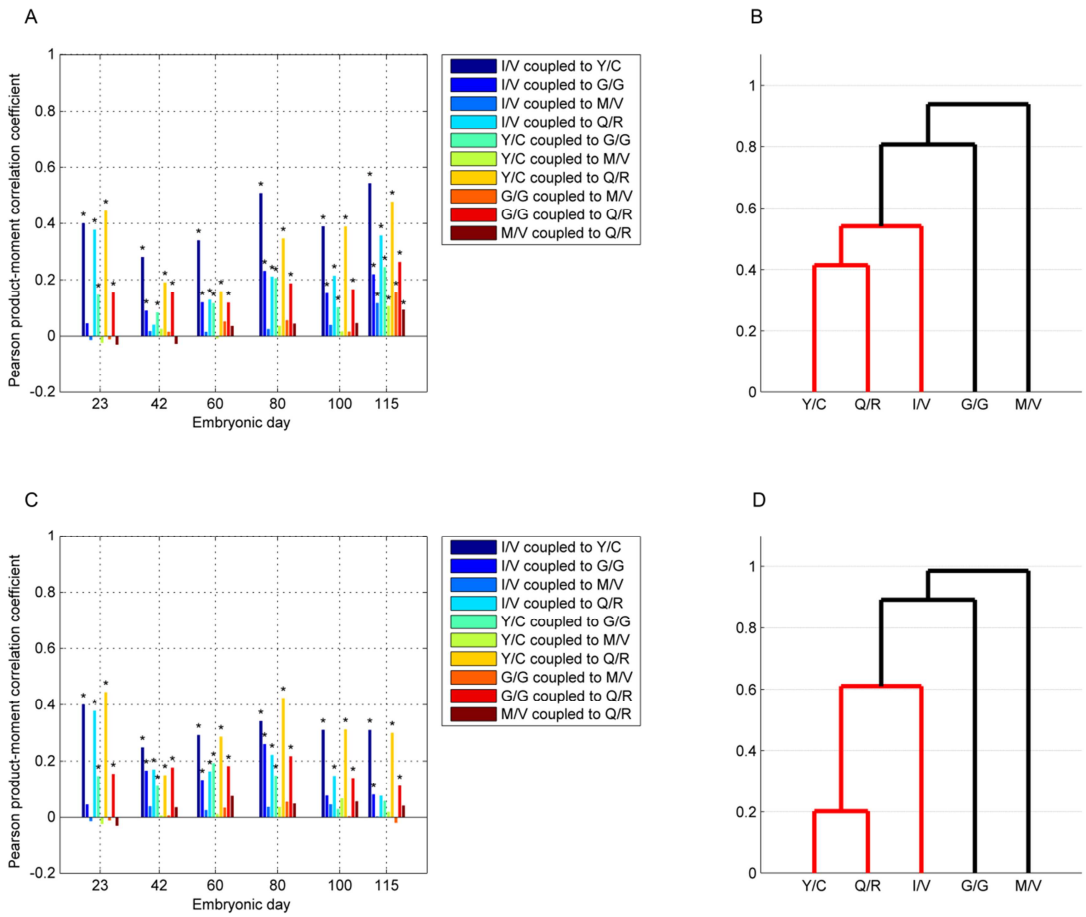
Note that only one tissue, whole forebrain, was dissected from E23.



Supplementary Figure S8

Pearson correlation coefficients for coupling between the predominant self-editing sites on the ADAR2 amplicon in Basal ganglia (*A*) and Hippocampus (*C*). See legend for color codes. Black asterisks denote significance compared to bonferroni corrected critical p-values. Group analysis of all E115 ADAR2 self-editing sites in Basal ganglia (*B*) and Hippocampus (*D*).

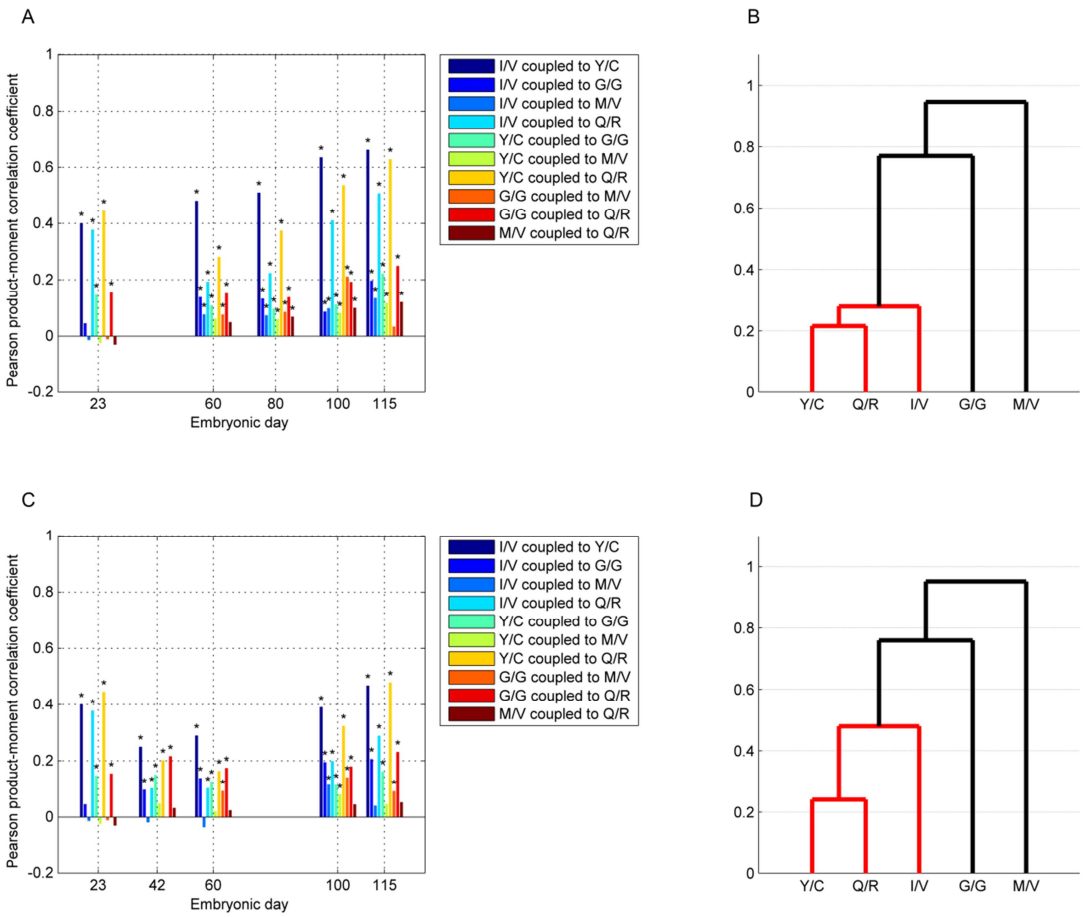
Note that only one tissue, whole forebrain, was dissected from E23.



Supplementary Figure S9

Pearson correlation coefficients for coupling between the editing sites on the Grik2 amplicon in Brain stem (*A*) and Cerebellum (*C*). See legend for color codes. Black asterisks denote significance compared to bonferroni corrected critical p-values. Group analysis of E115 Grik2 editing sites in Brain stem (*B*) and Cerebellum (*D*).

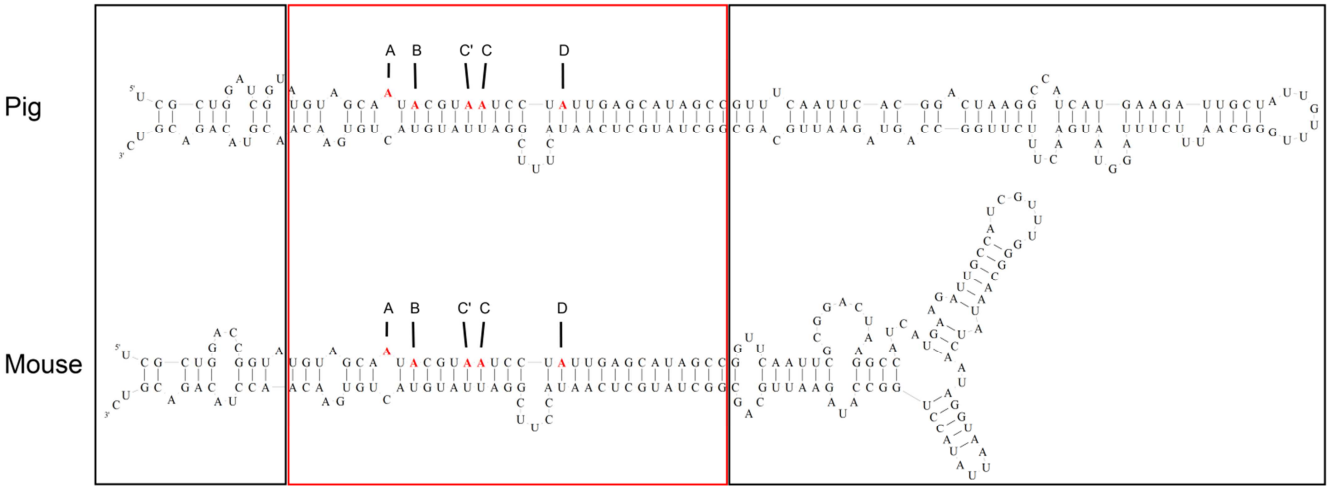
Note that only one tissue, whole forebrain, was dissected from E23.



Supplementary Figure S10

Pearson correlation coefficients for coupling between the editing sites on the Grik2 amplicon in Basal ganglia (*A*) and Hippocampus (*C*). See legend for color codes. Black asterisks denote significance compared to bonferroni corrected critical p-values. Group analysis of E115 Grik2 editing sites in Basal ganglia (*B*) and Hippocampus (*D*).

Note that only one tissue, whole forebrain, was dissected from E23.



Supplementary Figure S11

Secondary structure prediction of the edited region of the Htr2c pre-mRNA and the downstream sequence including the intronic editing complementary sequence from pig, genome Sscrofa9.2 (top) and mouse, genome mm9 (bottom). Editing sites (A, B, C', C, D) are indicated. Sequence and secondary structure are identical between pig and mouse in the region immediately surrounding the editing sites (red box), whereas differences are observed further away from the editing sites (black boxes). It could be speculated that the longer stem of the porcine Htr2c pre-mRNA could increase the binding affinity for ADAR enzymes, resulting in maximal RNA editing at developmental time points where low levels of ADAR enzymes are present such as embryonic day 23.

Secondary structure prediction was done using the UNAFold algorithm[1] implemented in the program "The RNA Folder", http://www.ncrnalab.dk/rnafolder/.

1. Markham NR, Zuker M. UNAFold: software for nucleic acid folding and hybridization. Methods Mol Biol 2008; 453:3-31.

		Distance to	Forebrain	Hippocampus				Cortex					Cerebellum					Brain stem					Basal ganglia			
Gene	Editing site	principal site	E23	E42	E60	E100	E115	E42	E60	E80	E100	E115	E42	E60	E80	E100	E115	E42	E60	E80	E100	E115	E60	E80	E100	E115
Grik2	I/V	-163 (and 32kb intron)	3.7%	7.8%	13.3%	39.0%	38.2%	10.2%	17.7%	29.4%	41.0%	42.1%	9.3%	13.2%	14.2%	25.7%	31.6%	12.5%	21.6%	25.9%	29.5%	22.4%	35.0%	53.4%	62.7%	49.9%
	Y/C	-150 (and 32kb intron)	10.3%	25.5%	42.5%	75.6%	71.1%	31.7%	48.7%	62.0%	78.4%	69.2%	32.5%	45.3%	51.0%	74.3%	81.6%	37.8%	57.7%	55.4%	68.1%	47.5%	65.9%	79.1%	78.7%	67.0%
	G/G	-17	1.4%	8.0%	10.8%	18.0%	12.6%	11.1%	11.1%	15.5%	13.3%	12.8%	6.4%	5.6%	5.8%	7.1%	5.7%	10.8%	11.3%	10.6%	5.5%	6.9%	11.1%	12.6%	12.4%	12.3%
	M/V	-4			1.6%	3.0%	2.2%		1.2%	2.1%	2.4%	3.1%	1.1%	1.2%		1.7%	1.2%		1.3%	1.1%	1.3%	1.4%	2.8%	4.0%	5.5%	3.1%
	Q/R	0	14.9%	61.6%	73.7%	86.9%	78.6%	63.3%	77.9%	79.1%	88.7%	72.8%	62.0%	61.2%	64.9%	83.9%	89.2%	71.9%	85.5%	81.6%	72.7%	55.1%	87.0%	89.8%	80.9%	68.5%
Gria2	-86	-86			2.6%	11.8%	3.3%	7.1%				2.9%	7.1%		2.5%			1.9%		4.2%	6.6%	3.7%	3.5%	6.0%			
	-84	-84	14.3%		2.2%		4.6%				3.4%					1.4%						2.1%		2.0%		1.8%
	Q/R	0	53.8%	97.6%	98.9%	96.3%	99.2%	93.7%	94.7%	95.7%	100.0%	100.0%	100.0%	97.2%	98.0%	100.0%	100.0%	98.6%	100.0%	98.3%	98.2%	99.1%	93.8%	96.5%	100.0%	98.9%
	+4	4	7.1%	3.4%	6.8%	16.7%	5.9%	3.8%	6.1%		15.0%	7.0%	2.9%	1.7%		11.2%	5.6%	5.0%	20.8%	5.8%	8.7%	8.3%	5.9%	6.8%	8.2%	12.3%
	+45	45				3.7%	1.4%								2.8%	2.8%				1.5%	1.6%					1.5%
	Hotspot (+60)	60	17.1%	52.1%	49.4%	60.0%	54.6%	56.0%	49.2%	60.0%	65.5%	70.3%	39.1%	52.3%	61.6%	73.0%	64.5%	56.0%	50.0%	62.8%	71.0%	67.6%	70.4%	51.4%	81.2%	73.6%
Gria3	-37	-37	1.1%	1.4%		1.1%							1.2%	1.1%			1.1%						1.1%			1.1%
	-1	-1	3.2%	3.1%	1.3%	1.8%	2.6%	3.3%	2.1%		2.4%	3.3%	1.9%	2.4%	2.6%	2.9%	3.7%	2.4%	2.5%	2.4%	2.0%	2.3%	2.0%	3.2%	2.1%	2.8%
	R/G	0	35.7%	32.8%	25.2%	36.2%	44.2%	35.6%	26.2%	42.3%	36.5%	45.6%	31.7%	35.2%	41.4%	37.9%	36.4%	33.3%	45.0%	33.2%	36.8%	28.3%	26.9%	36.4%	35.2%	34.2%
	+11	11	1.8%	1.7%														1.0%		1.1%			1.6%	1.3%	1.1%	
	+19	19	2.3%	1.6%		1.8%	1.8%	1.8%	1.3%		2.0%	2.0%	2.0%	1.3%	1.4%	1.7%	2.6%	1.7%		1.4%	2.3%	2.7%	2.4%	1.5%	2.3%	1.5%
Kcna1	I/V	0	8.3%	7.1%	2.4%	9.5%	8.2%	5.2%	4.8%	6.2%	7.7%	11.7%	9.1%	3.4%	10.1%	10.0%	13.4%	10.5%	8.0%	9.1%	28.9%	22.5%	7.0%	10.1%	19.4%	20.0%
Htr2c	A	-12	41.2%	38.9%	42.1%	50.1%	51.8%	42.0%	42.1%	42.9%	49.7%	47.0%	45.4%	39.9%	40.5%	41.9%	46.9%	43.1%	48.7%	42.2%	51.5%	44.1%	39.5%	43.1%	44.2%	48.2%
	B	-10	8.6%	7.3%	6.4%	11.8%	13.1%	9.8%	7.2%	8.6%	10.6%	11.6%	9.3%	9.4%	8.4%	8.3%	11.3%	7.4%	7.3%	7.6%	12.0%	8.8%	8.8%	9.2%	7.7%	8.2%
	C'	-6	8.6%	8.4%	8.6%	9.2%	10.3%	8.0%	9.1%	9.0%	10.4%	10.9%	8.3%	8.0%	9.1%	8.6%	10.6%	9.6%	8.0%	9.0%	9.9%	8.4%	7.0%	7.5%	9.7%	10.8%
	C	-5	30.0%	28.3%	31.3%	33.8%	36.7%	28.3%	29.1%	29.0%	35.8%	36.0%	34.4%	28.6%	30.2%	29.4%	27.1%	31.5%	33.8%	31.5%	38.1%	32.2%	27.2%	33.1%	33.6%	34.4%
	D	0	60.2%	59.2%	57.9%	67.8%	67.9%	59.5%	60.5%	57.3%	65.2%	72.5%	62.5%	57.7%	60.4%	59.6%	61.1%	59.6%	66.5%	61.8%	74.4%	63.9%	60.4%	62.4%	59.5%	64.6%
Gabra3	I/M	0																								
Adar2	-27	-50					1.3%		1.2%		2.2%					1.9%	2.4%				3.0%	1.3%	1.3%	2.1%	2.5%	1.4%
	-17	-40		2.7%	3.6%	3.9%	1.5%	3.3%	4.6%	2.6%	3.2%	2.5%	4.8%			1.0%	1.8%	4.5%	3.5%	3.4%	1.2%	3.5%	2.2%	2.2%	2.3%	2.0%
	-16	-39	7.2%	7.1%	5.3%	8.3%	8.0%	7.6%	5.2%	11.6%	11.6%	11.5%	9.1%	3.2%	3.7%	4.1%	11.6%	5.3%	6.7%	6.8%	9.6%	12.4%	10.6%	9.5%	11.9%	14.4%
	-15	-38	3.2%	1.3%		1.2%	2.8%			1.5%	2.1%							2.2%		1.5%		1.6%	2.2%			
	-8	-31	1.2%	1.9%		6.6%	5.3%	2.1%	1.8%	4.5%	4.8%	6.4%	2.6%	2.3%	1.9%	2.5%	5.4%	1.8%	2.1%	3.9%	3.7%	9.1%	5.1%	6.8%	9.0%	12.5%
	-4	-27	2.0%	5.9%	5.6%	12.8%	7.9%	4.4%	6.7%	10.8%	10.9%	10.1%	5.8%	3.3%	2.1%	3.2%	9.8%	6.5%	7.4%	7.5%	8.2%	9.1%	8.5%	10.0%	12.0%	12.3%
	-2	-25	4.9%	5.2%	4.3%	6.3%	7.9%	2.3%	4.0%	7.1%	11.7%	7.3%	5.0%	2.8%	4.9%	2.9%	6.3%	4.7%	5.5%	5.7%	8.2%	8.2%	6.1%	9.0%	9.0%	8.8%
	-1	-24	19.2%	19.3%	19.5%	37.8%	44.0%	19.0%	20.5%	39.4%	44.7%	48.2%	21.4%	16.5%	27.9%	33.6%	41.8%	25.5%	33.7%	31.8%	46.9%	48.4%	44.1%	48.3%	52.1%	58.8%
	+2	-22			1.1%	1.2%	1.6%					1.0%		1.1%			2.4%	1.1%	1.8%	1.2%	1.2%			1.2%	1.5%	
	+10	-14	31.7%	39.8%	38.0%	62.6%	68.3%	43.7%	43.5%	58.7%	71.6%	70.7%	48.5%	32.4%	40.8%	52.5%	63.6%	49.4%	57.3%	58.3%	67.1%	69.5%	69.7%	72.3%	78.8%	79.5%
	+13	-11	1.2%				1.2%	2.0%				1.1%					1.1%					1.3%		1.6%	1.6%	
	+14	-10		1.4%		1.4%	1.5%				1.3%	2.2%		2.8%	1.0%			1.1%	1.6%	1.2%	1.5%	1.1%	1.1%		2.5%	1.1%
	+23	-1	1.0%	1.3%		1.9%	3.4%	1.4%	1.2%	2.5%	2.2%	3.9%	1.4%			1.2%	4.4%	1.6%	5.3%	2.3%	2.8%	3.6%	2.7%	4.8%	4.0%	5.9%
	+24	0	28.4%	47.1%	41.6%	62.8%	60.6%	47.8%	46.2%	55.0%	73.7%	66.6%	47.9%	27.2%	27.8%	34.2%	54.6%	56.5%	54.9%	59.3%	58.5%	67.4%	62.5%	64.0%	70.1%	75.1%
	+28	4	5.2%	1.5%	2.1%	4.8%	4.2%	2.8%	1.3%	2.1%	2.7%	3.7%	1.4%	1.3%		1.5%	2.2%	1.2%	2.1%	2.4%	5.0%	4.6%	2.9%	4.8%	5.9%	4.4%
Flna	Q/R	0	3.9%	7.7%	5.6%	19.9%	14.1%	4.7%	7.4%	6.6%	14.9%	15.7%	8.0%	5.0%	4.9%	12.2%	15.2%	5.0%	12.6%	8.5%	14.1%	19.6%	21.1%	9.8%	8.8%	18.3%
	K/R	15					2.8%			1.4%		1.9%	2.1%			1.2%	5.1%				1.3%	2.6%		2.2%		2.8%
Blcap	5a	-25	7.7%	9.3%	8.6%	10.5%	12.2%	7.1%	10.9%	10.1%	12.0%	10.3%	6.9%	8.1%	9.9%	14.6%	14.1%	7.8%	8.5%	10.4%	13.4%	14.7%	10.4%	10.6%	8.7%	9.3%
	5b	-11	1.0%	1.6%	2.2%	2.8%	1.4%	1.3%	2.5%	2.1%	1.5%	1.8%	2.0%	1.4%		1.2%		1.9%	2.4%	1.8%	1.1%		2.7%	2.5%	2.1%	2.7%
	5c	-9		2.2%	1.1%			2.0%	1.4%	1.8%	1.0%	1.0%	1.0%	2.0%	1.3%			1.9%	1.1%	1.6%	1.2%		1.5%	1.4%		
	M/V	-4	1.1%	3.3%	4.2%	3.0%	1.6%	4.1%	3.9%	1.7%	3.4%	3.2%	2.4%	5.2%	2.0%			2.5%	3.5%	2.2%	1.2%		2.9%	1.0%	2.1%	2.3%
	Y/C	0	42.4%	45.0%	48.5%	48.9%	53.8%	50.7%	53.3%	48.6%	55.5%	51.2%	43.7%	46.4%	47.1%	63.2%	65.6%	42.9%	47.6%	43.6%	53.7%	64.3%	40.8%	46.1%	38.6%	51.0%
	Q/R	9	21.5%	34.2%	35.8%	33.3%	33.2%	36.8%	38.5%	34.7%	34.9%	33.6%	32.1%	33.5%	31.2%	33.2%	34.0%	32.7%	39.4%	29.7%	32.2%	34.5%	31.9%	33.6%	26.7%	29.3%
	K/R	39	18.5%	32.7%	32.6%	30.5%	22.1%	28.8%	34.1%	29.0%	27.5%	27.6%	25.6%	27.6%	25.6%	17.6%	12.0%	30.1%	37.6%	24.3%	19.1%	16.6%	30.5%	29.1%	24.7%	20.4%
	N/S	48				1.9%					1.2%	1.1%								1.1%			1.5%	1.2%	2.2%	1.4%
Igfbp7		-19			1.3%	2.1%	1.6%				1.7%	1.2%	1.0%			1.1%	1.6%		2.4%	1.3%			1.1%	1.5%	1.3%	1.6%
	B (K/R)	0	33.5%	53.7%	54.9%	68.7%	63.8%	52.0%	67.0%	55.1%	64.8%	67.1%	59.4%	51.7%	48.4%	61.4%	68.8%	58.6%	60.4%	62.4%	65.9%	58.2%	70.1%	71.2%	63.8%	66.6%
	C (K/R)	6	3.2%	4.6%	6.5%	8.2%	6.2%	4.8%	6.9%	4.8%	9.7%	8.0%	6.1%	4.2%	5.3%	6.0%	9.3%	5.3%	6.6%	8.1%	7.0%	6.2%	11.7%	12.0%	11.0%	10.1%
Ednrb	Q/R	0																								
Cyfip2		-27		1.0%						1.1%	1.0%		1.5%	1.5%	1.3%				1.1%	1.3%				1.4%	1.1%	
		-23			1.1%					1.8%			1.0%	1.1%			1.2%			1.5%	1.2%		1.2%	1.7%		
		-22						1.4%	1.5%		1.2%		2.5%			1.0%			1.3%			1.1%		1.4%		
		-21		1.5%	1.3%					1.4%			1.3%		1.0%		2.3%	1.0%	1.3%		1.1%	1.1%	1.1%			
		-16					1.0%			1.3%			2.1%	1.2%	1.3%	1.1%		1.5%		1.2%	1.0%		1.3%			
		-10		1.2%						1.1%					1.0%		1.1%	1.8%	1.0%					1.2%		
		-7	1.7%						1.4%		1.8%		1.2%				1.1%	1.8%		1.2%	1.6%	1.4%				
	K/E	0																								
		1						2.4%		1.1%				1.1%	1.2%		1.4%	1.1%		1.4%	1.4%			1.2%		
		3						1.4%	1.2%	2.2%			1.9%		1.1%	1.4%	1.7%	1.2%	1.1%							1.5%
		23							1.5%					2.0%	1.5%		1.3%		1.2%	1.6%	1.4%	1.0%	1.2%	1.2%		
		45			1.4%	1.2%		1.0%			1.1%			1.2%	1.2%			1.4%		1.1%		1.4%		1.6%	1.1%	
		57		1.2%		1.2%			1.3%		1.1%		1.7%				1.0%									1.2%
		60			1.3%					1.6%							1.1%						1.2%	1.5%		1.4%
		72	1.1%					1.2%	1.7%										1.0%	1.1%	1.0%					

Supplementary Table S1: Editing in percentage for each individual site. The identity of the sites is denoted to the left. The distance to the assumed primary editing site is indicated in column 2. Only sites displaying > 1 % editing in at least five samples are included in the figure.

Igfbp7			
		B (K/R)	C (K/R)
	% single	**31.8**	**0.4**
	% total	33.5	3.2
E23	% multiple	1.7	2.8
	% single	**51.7**	**0.1**
	% total	58.6	5.3
E42 Br	% multiple	6.9	5.1
	% single	**51.7**	**0.3**
	% total	59.4	6.1
E42 Ce	% multiple	7.7	5.8
	% single	**46.2**	**0.5**
	% total	52.0	4.8
E42 Co	% multiple	5.8	4.4
	% single	**46.6**	**0.3**
	% total	53.7	4.6
E42 H	% multiple	7.1	4.3
	% single	**58.7**	**0.2**
	% total	70.1	11.7
E60 Ba	% multiple	11.4	11.5
	% single	**53.7**	**1.0**
	% total	60.4	6.6
E60 Br	% multiple	6.7	5.6
	% single	**47.3**	**0.3**
	% total	51.7	4.2
E60 Ce	% multiple	4.4	3.9
	% single	**58.7**	**0.4**
	% total	67.0	6.9
E60 Co	% multiple	8.3	6.5
	% single	**47.4**	**0.4**
	% total	54.9	6.5
E60 H	% multiple	7.5	6.1
	% single	**58.2**	**0.1**
	% total	71.2	12.0
E80 Ba	% multiple	13.0	11.9
	% single	**53.7**	**0.3**
	% total	62.4	8.1
E80 Br	% multiple	8.7	7.8
	% single	**43.8**	**0.3**
	% total	48.4	5.3
E80 Ce	% multiple	4.6	5.1
	% single	**50.6**	**0.2**
	% total	55.1	4.8
E80 Co	% multiple	4.5	4.5
	% single	**51.9**	**0.3**
	% total	63.8	11.0
E100 Ba	% multiple	11.9	10.7
	% single	**57.6**	**0.2**
	% total	65.9	7.0
E100 Br	% multiple	8.3	6.8
	% single	**54.0**	**0.2**
	% total	61.4	6.0
E100 Ce	% multiple	7.4	5.8
	% single	**53.5**	**0.5**
	% total	64.8	9.7
E100 Co	% multiple	11.3	9.2
	% single	**59.0**	**0.4**
	% total	68.7	8.2
E100 H	% multiple	9.7	7.8
	% single	**54.7**	**0.6**
	% total	66.6	10.1
E115 Ba	% multiple	11.9	9.5
	% single	**51.3**	**0.1**
	% total	58.2	6.2
E115 Br	% multiple	6.9	6.1
	% single	**57.1**	**0.3**
	% total	68.8	9.3
E115 Ce	% multiple	11.7	9.0
	% single	**57.4**	**0.2**
	% total	67.1	8.0
E115 Co	% multiple	9.7	7.8
	% single	**56.2**	**0.3**
	% total	63.8	6.2
E115 H	% multiple	7.6	5.9

Grik2					
		I/V	Y/C	Q/R	
	% single	**0.4**	**3.6**	**8.1**	
	% total	3.7	10.3	14.9	
E23	% multiple	3.3	6.7	6.8	
	% single	**0.8**	**4.2**	**38.8**	
	% total	12.5	37.8	71.9	
E42 Br	% multiple	11.7	33.6	33.1	
	% single	**0.6**	**8.0**	**37.3**	
	% total	9.3	32.5	62.0	
E42 Ce	% multiple	8.7	24.5	24.7	
	% single	**1.0**	**5.2**	**36.8**	
	% total	10.2	31.7	63.3	
E42 Co	% multiple	9.2	26.5	26.5	
	% single	**0.7**	**4.3**	**39.7**	
	% total	7.8	25.5	61.6	
E42 H	% multiple	7.1	21.2	21.9	
	% single	**0.1**	**2.7**	**24.6**	
	% total	35.0	65.9	87.0	
E60 Ba	% multiple	34.9	63.2	62.4	
	% single	**0.2**	**4.5**	**31.6**	
	% total	21.6	57.7	85.5	
E60 Br	% multiple	21.4	53.2	53.9	
	% single	**0.8**	**8.6**	**25.8**	
	% total	13.2	45.3	61.2	
E60 Ce	% multiple	12.4	36.7	35.4	
	% single	**0.5**	**4.6**	**32.8**	
	% total	17.7	48.7	77.9	
E60 Co	% multiple	17.2	44.1	45.1	
	% single	**0.6**	**6.2**	**37.2**	
	% total	13.3	42.5	73.7	
E60 H	% multiple	12.7	36.3	36.5	
	% single	**0.1**	**1.5**	**13.7**	
	% total	53.4	79.1	89.8	
E80 Ba	% multiple	53.3	77.6	76.1	
	% single	**0.0**	**2.3**	**29.6**	
	% total	25.9	55.4	81.6	
E80 Br	% multiple	25.9	53.1	52.0	
	% single	**0.1**	**6.4**	**21.3**	
	% total	14.2	51.0	64.9	
E80 Ce	% multiple	14.1	44.6	43.6	
	% single	**0.2**	**3.2**	**21.0**	
	% total	29.4	62.0	79.1	
E80 Co	% multiple	29.2	58.8	58.1	
	% single	**0.2**	**2.3**	**8.2**	
	% total	62.7	78.7	80.9	
E100 Ba	% multiple	62.5	76.4	72.7	
	% single	**0.4**	**7.0**	**14.7**	
	% total	29.5	68.1	72.7	
E100 Br	% multiple	29.1	61.1	58.0	
	% single	**0.1**	**5.0**	**16.5**	
	% total	25.7	74.3	83.9	
E100 Ce	% multiple	25.6	69.3	67.4	
	% single	**0.2**	**2.6**	**14.1**	
	% total	41.0	78.4	88.7	
E100 Co	% multiple	40.8	75.8	74.6	
	% single	**0.4**	**3.8**	**15.6**	
	% total	39.0	75.6	86.9	
E100 H	% multiple	38.6	71.8	71.3	
	% single	**0.3**	**3.8**	**8.1**	
	% total	49.9	67.0	68.5	
E115 Ba	% multiple	49.6	63.2	60.4	
	% single	**0.2**	**6.8**	**17.0**	
	% total	22.4	47.5	55.1	
E115 Br	% multiple	22.2	40.7	38.1	
	% single	**0.3**	**3.4**	**12.9**	
	% total	31.6	81.6	89.2	
E115 Ce	% multiple	31.3	78.2	76.3	
	% single	**0.4**	**4.5**	**11.7**	
	% total	42.1	69.2	72.8	
E115 Co	% multiple	41.7	64.7	61.1	
	% single	**0.2**	**3.8**	**13.8**	
	% total	38.2	71.1	78.6	
E115 H	% multiple	38.0	67.3	64.8	

Blcap						
		5a	Y/C	Q/R	K/R	
	% single	**0.6**	**15.9**	**0.7**	**2.0**	
	% total	7.7	42.4	21.5	18.5	
E23	% multiple	7.1	26.5	20.8	16.5	
	% single	**0.3**	**5.6**	**0.7**	**1.2**	
	% total	7.8	42.9	32.7	30.1	
E42 Br	% multiple	7.5	37.3	32.0	28.9	
	% single	**0.4**	**7.1**	**0.9**	**0.9**	
	% total	6.9	43.7	32.1	25.6	
E42 Ce	% multiple	6.4	36.6	31.2	24.7	
	% single	**0.2**	**8.3**	**0.4**	**1.2**	
	% total	7.1	50.7	36.8	28.8	
E42 Co	% multiple	6.9	42.4	36.4	27.6	
	% single	**1.1**	**4.4**	**0.7**	**2.9**	
	% total	9.3	45.0	34.2	32.7	
E42 H	% multiple	8.2	40.6	33.5	29.8	
	% single	**0.7**	**4.9**	**0.7**	**2.1**	
	% total	10.4	40.8	31.9	30.5	
E60 Ba	% multiple	9.7	35.9	31.2	28.4	
	% single	**0.4**	**4.1**	**0.0**	**1.6**	
	% total	8.5	47.6	39.4	37.6	
E60 Br	% multiple	8.1	43.5	39.4	36.0	
	% single	**0.4**	**9.2**	**0.3**	**0.8**	
	% total	8.1	46.4	33.5	27.6	
E60 Ce	% multiple	7.7	37.2	33.2	26.8	
	% single	**0.5**	**9.2**	**0.3**	**1.9**	
	% total	10.9	53.3	38.5	34.1	
E60 Co	% multiple	10.4	44.1	38.2	32.2	
	% single	**0.7**	**6.6**	**0.7**	**2.2**	
	% total	8.6	48.5	35.8	32.6	
E60 H	% multiple	8.0	41.9	35.1	30.4	
	% single	**0.2**	**9.2**	**0.7**	**2.0**	
	% total	10.6	46.1	33.6	29.1	
E80 Ba	% multiple	10.4	36.9	32.9	27.1	
	% single	**0.1**	**9.1**	**0.3**	**1.3**	
	% total	10.4	43.6	29.7	24.3	
E80 Br	% multiple	10.3	34.5	29.4	23.0	
	% single	**0.5**	**10.3**	**0.6**	**1.1**	
	% total	9.9	47.1	31.2	25.6	
E80 Ce	% multiple	9.3	36.8	30.6	24.5	
	% single	**0.3**	**9.8**	**0.5**	**1.1**	
	% total	10.1	48.6	34.7	29.0	
E80 Co	% multiple	9.8	38.8	34.2	27.9	
	% single	**1.2**	**7.9**	**0.9**	**2.3**	
	% total	8.7	38.6	26.7	24.7	
E100 Ba	% multiple	7.5	30.7	25.8	22.4	
	% single	**0.9**	**18.2**	**1.3**	**2.3**	
	% total	13.4	53.7	32.2	19.1	
E100 Br	% multiple	12.5	35.5	30.9	16.8	
	% single	**0.2**	**26.6**	**0.3**	**2.5**	
	% total	14.6	63.2	33.2	17.6	
E100 Ce	% multiple	14.4	36.6	32.9	15.1	
	% single	**0.4**	**15.4**	**0.6**	**2.4**	
	% total	12.0	55.5	34.9	27.5	
E100 Co	% multiple	11.6	40.1	34.3	25.1	
	% single	**0.4**	**10.0**	**0.4**	**2.3**	
	% total	10.5	48.9	33.3	30.5	
E100 H	% multiple	10.1	38.9	32.9	28.2	
	% single	**0.3**	**18.8**	**0.4**	**4.2**	
	% total	9.3	51.0	29.3	20.4	
E115 Ba	% multiple	9.0	32.2	28.9	16.2	
	% single	**0.4**	**27.4**	**0.1**	**2.8**	
	% total	14.7	64.3	34.5	16.6	
E115 Br	% multiple	14.3	36.9	34.4	13.8	
	% single	**0.6**	**30.2**	**0.2**	**3.8**	
	% total	14.1	65.6	34.0	12.0	
E115 Ce	% multiple	13.5	35.4	33.8	8.2	
	% single	**0.3**	**14.2**	**1.0**	**2.7**	
	% total	10.3	51.2	33.6	27.6	
E115 Co	% multiple	10.0	37.0	32.6	24.9	
	% single	**0.3**	**16.9**	**0.6**	**2.1**	
	% total	12.2	53.8	33.2	22.1	
E115 H	% multiple	11.9	36.9	32.6	20.0	

ADAR2						
		-16	-1	+10	+24	
	% single	**0.4**	**2.7**	**6.3**	**3.1**	
	% total	7.2	19.2	31.7	28.4	
E23	% multiple	6.8	16.5	25.4	25.3	
	% single	**0.2**	**3.8**	**4.5**	**16.0**	
	% total	5.3	25.5	49.4	56.5	
E42 Br	% multiple	5.1	21.7	44.9	40.5	
	% single	**0.8**	**3.4**	**6.1**	**12.0**	
	% total	9.1	21.4	48.5	47.9	
E42 Ce	% multiple	8.4	18.0	42.4	35.9	
	% single	**0.7**	**3.1**	**4.9**	**10.6**	
	% total	7.6	19.0	43.7	47.8	
E42 Co	% multiple	6.9	15.9	38.8	37.2	
	% single	**0.7**	**3.8**	**5.3**	**13.6**	
	% total	7.1	19.3	39.8	47.1	
E42 H	% multiple	6.3	15.5	34.5	33.5	
	% single	**0.1**	**2.9**	**5.7**	**6.9**	
	% total	10.6	44.1	69.7	62.5	
E60 Ba	% multiple	10.5	41.2	64.0	55.6	
	% single	**0.7**	**4.3**	**6.4**	**10.9**	
	% total	6.7	33.7	57.3	54.9	
E60 Br	% multiple	6.1	29.4	50.9	44.0	
	% single	**0.7**	**4.0**	**7.4**	**5.6**	
	% total	3.2	16.5	32.4	27.2	
E60 Ce	% multiple	2.6	12.5	25.0	21.6	
	% single	**0.4**	**3.6**	**7.7**	**12.9**	
	% total	5.2	20.5	43.5	46.2	
E60 Co	% multiple	4.7	16.9	35.8	33.3	
	% single	**0.3**	**5.9**	**6.3**	**9.6**	
	% total	5.3	19.5	38.0	41.6	
E60 H	% multiple	4.9	13.6	31.7	32.0	
	% single	**0.0**	**5.2**	**5.4**	**4.8**	
	% total	9.5	48.3	72.3	64.0	
E80 Ba	% multiple	9.5	43.1	66.9	59.2	
	% single	**0.4**	**4.7**	**5.6**	**9.7**	
	% total	6.8	31.8	58.3	59.3	
E80 Br	% multiple	6.4	27.1	52.7	49.6	
	% single	**0.3**	**9.1**	**12.3**	**5.9**	
	% total	3.7	27.9	40.8	27.8	
E80 Ce	% multiple	3.4	18.8	28.5	21.9	
	% single	**0.5**	**4.0**	**6.9**	**9.3**	
	% total	11.6	39.4	58.7	55.0	
E80 Co	% multiple	11.1	35.4	51.8	45.7	
	% single	**0.1**	**4.2**	**6.1**	**3.0**	
	% total	11.9	52.1	78.8	70.1	
E100 Ba	% multiple	11.8	47.9	72.7	67.1	
	% single	**0.1**	**6.1**	**7.8**	**3.9**	
	% total	9.6	46.9	67.1	58.5	
E100 Br	% multiple	9.5	40.8	59.3	54.6	
	% single	**0.4**	**6.9**	**10.9**	**5.0**	
	% total	4.1	33.6	52.5	34.2	
E100 Ce	% multiple	3.7	26.7	41.6	29.2	
	% single	**0.4**	**4.0**	**4.6**	**7.8**	
	% total	11.6	44.7	71.6	73.7	
E100 Co	% multiple	11.2	40.7	67.0	65.9	
	% single	**0.3**	**5.7**	**5.9**	**9.0**	
	% total	8.3	37.8	62.6	62.8	
E100 H	% multiple	7.9	32.1	56.7	53.8	
	% single	**0.1**	**2.8**	**3.5**	**4.1**	
	% total	14.4	58.8	79.5	75.1	
E115 Ba	% multiple	14.3	56.0	76.0	71.0	
	% single	**0.3**	**3.9**	**3.8**	**9.4**	
	% total	12.4	48.4	69.5	67.4	
E115 Br	% multiple	12.1	44.5	65.7	58.0	
	% single	**0.0**	**4.7**	**8.7**	**5.8**	
	% total	11.6	41.8	63.6	54.6	
E115 Ce	% multiple	11.6	37.1	54.9	48.8	
	% single	**0.2**	**5.0**	**4.7**	**6.8**	
	% total	11.5	48.2	70.7	66.6	
E115 Co	% multiple	11.3	43.2	66.0	59.8	
	% single	**0.2**	**6.1**	**6.5**	**5.6**	
	% total	8.0	44.0	68.3	60.6	
E115 H	% multiple	7.8	37.9	61.8	55.0	

Htr2c						
		A	B	C'	C	D
	% single	**3.1**	**0.6**	**2.0**	**5.6**	**8.9**
	% total	41.2	8.6	8.6	30.0	60.2
E23	% multiple	38.1	8.0	6.6	24.4	51.3
	% single	**4.4**	**0.7**	**0.8**	**5.1**	**12.6**
	% total	43.1	7.4	9.6	31.5	59.6
E42 Br	% multiple	38.7	6.7	8.7	26.4	47.0
	% single	**3.2**	**0.4**	**0.7**	**6.0**	**13.7**
	% total	45.4	9.3	8.3	34.4	62.5
E42 Ce	% multiple	42.2	9.0	7.6	28.4	48.8
	% single	**4.5**	**0.4**	**1.2**	**4.5**	**9.8**
	% total	42.0	9.8	8.0	28.3	59.5
E42 Co	% multiple	37.5	9.4	6.9	23.8	49.7
	% single	**3.4**	**0.9**	**0.9**	**5.6**	**10.3**
	% total	38.9	7.3	8.4	28.3	59.2
E42 H	% multiple	35.5	6.4	7.5	22.7	48.9
	% single	**3.4**	**0.7**	**0.9**	**5.3**	**15.5**
	% total	39.5	8.8	7.0	27.2	60.4
E60 Ba	% multiple	36.1	8.2	6.1	21.9	44.9
	% single	**2.9**	**0.1**	**0.8**	**5.8**	**6.9**
	% total	48.7	7.3	8.0	33.8	66.5
E60 Br	% multiple	45.8	7.2	7.2	28.0	59.6
	% single	**3.0**	**0.2**	**1.4**	**5.1**	**4.5**
	% total	39.9	9.4	8.0	28.6	57.7
E60 Ce	% multiple	36.9	9.2	6.6	23.5	53.2
	% single	**4.2**	**0.4**	**0.8**	**4.5**	**7.0**
	% total	42.1	7.2	9.1	29.1	60.5
E60 Co	% multiple	37.9	6.8	8.3	24.6	53.5
	% single	**4.1**	**0.6**	**0.7**	**5.2**	**9.2**
	% total	42.1	6.4	8.6	31.3	57.9
E60 H	% multiple	38.0	5.8	8.0	26.1	48.7
	% single	**2.8**	**1.1**	**1.2**	**5.2**	**6.9**
	% total	43.1	9.2	7.5	33.1	62.4
E80 Ba	% multiple	40.3	8.1	6.3	27.9	55.5
	% single	**3.5**	**0.4**	**0.8**	**5.5**	**11.6**
	% total	42.2	7.6	9.0	31.5	61.8
E80 Br	% multiple	38.7	7.2	8.1	26.0	50.2
	% single	**3.7**	**0.3**	**1.0**	**5.9**	**9.8**
	% total	40.5	8.4	9.1	30.2	60.4
E80 Ce	% multiple	36.8	8.2	8.1	24.3	50.6
	% single	**3.5**	**0.5**	**1.2**	**6.0**	**13.0**
	% total	42.9	8.6	9.0	29.0	57.3
E80 Co	% multiple	39.4	8.0	7.9	23.0	44.3
	% single	**3.0**	**0.5**	**0.8**	**5.7**	**13.4**
	% total	44.2	7.7	9.7	33.6	59.5
E100 Ba	% multiple	41.2	7.2	8.8	27.9	46.1
	% single	**1.5**	**0.2**	**0.4**	**4.6**	**11.1**
	% total	51.5	12.0	9.9	38.1	74.4
E100 Br	% multiple	50.0	11.8	9.6	33.5	63.3
	% single	**3.6**	**0.5**	**0.7**	**5.8**	**13.0**
	% total	41.9	8.3	8.6	29.4	59.6
E100 Ce	% multiple	38.3	7.8	7.9	23.6	46.6
	% single	**2.1**	**0.5**	**0.5**	**4.8**	**12.8**
	% total	49.7	10.6	10.4	35.8	65.2
E100 Co	% multiple	47.6	10.1	9.9	31.0	52.4
	% single	**3.3**	**0.4**	**0.4**	**4.0**	**11.2**
	% total	50.1	11.8	9.2	33.8	67.8
E100 H	% multiple	46.8	11.4	8.8	29.8	56.6
	% single	**2.8**	**0.5**	**1.3**	**5.4**	**14.2**
	% total	48.2	8.2	10.8	34.4	64.6
E115 Ba	% multiple	45.4	7.6	9.5	29.0	50.4
	% single	**2.8**	**0.5**	**1.1**	**4.9**	**17.7**
	% total	44.1	8.8	8.4	32.2	63.9
E115 Br	% multiple	41.3	8.2	7.3	27.3	46.2
	% single	**4.3**	**1.5**	**1.7**	**4.1**	**5.3**
	% total	46.9	11.3	10.6	27.1	61.1
E115 Ce	% multiple	42.6	9.8	8.9	23.0	55.8
	% single	**2.1**	**0.7**	**0.8**	**4.7**	**17.4**
	% total	47.0	11.6	10.9	36.0	72.5
E115 Co	% multiple	44.9	10.9	10.1	31.3	55.1
	% single	**1.8**	**0.7**	**1.4**	**5.0**	**10.0**
	% total	51.8	13.1	10.3	36.7	67.9
E115 H	% multiple	50.0	12.4	8.9	31.7	57.9

Supplementary Table S2: Full list of singular editing for every tissue. E23 = Forebrain, embryonic day 23. Br = Brain stem. Co = Cortex. Ce = Cerebellum. H = Hippocampus. Ba = Basal ganglia.

Tissue	Grik2	Gria2	Gria3	Kcna1	Htr2c	Gabra3	ADAR2	Flna	Blcap	Igfbp7	Ednrb	Cyfip2
E23, Forebrain	3153	141	2266	2204	2533	1812	825	1923	1414	2121	2273	1976
E42, Brain stem	5572	246	3394	2294	3776	2309	1598	2142	2075	2802	2945	3147
E42, Cortex	3687	178	2197	1498	2719	2178	771	2097	1793	2734	2733	2469
E42, Cerebellum	4059	198	4434	2282	4250	2714	1526	2334	1921	2521	3658	2024
E42, Hippocampus	4175	126	3258	1794	2614	1479	2147	1538	1297	1801	1801	1464
E60, Brain stem	5034	83	1166	1414	2045	1128	468	814	739	1945	12	2348
E60, Cortex	3276	176	9610	2009	1907	1697	1456	3060	1828	3033	2633	1732
E60, Cerebellum	4301	196	2890	2294	1565	2279	764	1637	1381	4124	5029	2751
E60, Basal ganglia	5909	306	4767	3923	6467	5762	2790	4015	3724	4801	5161	3277
E60, Hippocampus	3800	338	2165	2155	2761	2156	1338	2846	2350	2538	2396	2171
E80, Brain stem	6241	268	3457	3056	5301	3420	2226	3921	2263	3675	3515	3801
E80, Cortex	3789	90	154	1851	4044	2740	1015	2351	2220	2710	1928	1911
E80, Cerebellum	3783	164	2472	1734	2816	2080	1720	2335	1683	2707	3060	2084
E80, Basal ganglia	7284	337	2788	1906	1956	1475	1050	2089	1416	1828	2613	2216
E100, Brain stem	3714	190	2724	2748	3128	2071	1519	2444	1784	3220	2569	2509
E100, Cortex	5549	291	3618	5258	4891	3934	1900	4300	2602	3979	3596	3033
E100, Cerebellum	3317	256	2517	2647	3778	2035	1170	2256	2627	6505	3750	2062
E100, Basal ganglia	5613	136	2408	3807	4321	2041	1478	2237	1124	3380	2059	2677
E100, Hippocampus	7158	341	4208	3342	3576	2889	1295	3455	1607	5751	6481	2897
E115, Brain stem	6603	190	2779	4215	4933	2502	1147	4452	2570	3995	4967	3692
E115, Cortex	6845	187	4717	4133	8509	4355	4028	3859	4672	6352	4759	4216
E115, Cerebellum	8868	169	1077	1656	2111	1599	392	1999	1886	2384	2670	1645
E115, Basal ganglia	10710	285	3611	6084	4839	3374	1195	2797	1611	2142	4581	2819
E115, Hippocampus	4471	203	3602	2853	3622	3285	1829	2931	2910	3874	3065	2814

Supplementary Table S3: The number sequences analyzed for each of the twelve different amplicons, 5 tissues and 6 time points.

Grik2
AGAGAAGCTTTACCGCAAGCCCAATGGTACAAACCCAGGCGTCTTCTCCTTCCTGAATCCTCTCTCCCCTGATATCTGGATGTATA
TTCTGCTGGCTTACTTGGGTGTCAGTTGTGTGCTCTTTGTCATAGCCAGGTTTAGTCCCTATGAGTGGTATAACCCACACCCTTGC
AATCCTGACTCAGACGTGGTGGAAAACAATTTTACCTTGCTAAATAGTTTCTGGTTTGGAGTTGGAGCTCTCATGCAGCAAGGTT

Gria2
AGGAAAGCTTGGTCAGCAGATTTAGCCCCTACGAGTGGCACACTGAGGAGTTCGAAGATGGAAGAGAAACTCAAAGTAGTGAA
TCAACTAATGAATTTGGGATTTTTAATAGTCTCTGGTTTTCCTTGGGTGCCTTTATGCAGCAAGGATGCGATATTTCGCCAAGGTT
GGTTACTTCCCTGCTTCAGCTTTGTGCATTTTAGGTCTCAAGTGGATATTCATGGTGTTTATGAATTCACTCTGAAGAAATTAGCA
GCCGCCGACTACCTGTCCAAGCAGTACATTAAGGACAGATTTTTACCATCGGCATAAGCCTGTGAAATATTTGAGCAATGTTCTT

Gria3
AGAGAAGCTTAACCATGTGATACGATGAAAGTTGGTGGAAATCTGGATTCCAAAGGCTATGGTGTGGCAACCCCTAAAGGCTC
AGCATTAAGGTGGGTGGAATAATATAACAATATCCGTGTTGTTATAGTATTCCACCTACCCTGACTCGAGTCCT

Kcna1
AGAGAAGCTTACTGTAGGATACGGTGACATGTACCCTGTGACAATTGGAGGCAAGATCGTGGGCTCCTTGTGTGCCATCGCTGG
TGTGCTGACAATTGCCCTGCCCGTACCTGTCATTGTGTCCAATTTCAACTATTTCTACCACCGAGAAACTGAGGGGGAAGAGCAG

Htr2c
AAGGAAGCTTGTCCATCATGCACCTCTGCGCTATTTCGCTGGATCGGTATGTAGCAATACGTAATCCTATTGAGCATAGCCGTTT
CAATTCACGGACTAAGGCCATCATGAAGATTGCTATTGTTTGGGCAACTCGAGTCCT

Gabra3
GAGAAAGCTTATGACGACCCTCAGTATCAGTGCCCGGAACTCTCTGCCCAAAGTGGCTTATGCGACGGCCATGGACTGGTTCAT
AGCCGTGTGCTATGCTTTTGTGTTCTCTGCGCTGATCGAGTTTGCCACAGTCAACTATTTCACCACTCGAGTCCT

ADAR2
AGAGAAGCTTAAGCACACAGCACTTAACCAGTTGCAAAGACAGATGAAGGAATCCATAAATTTTGCATTTACAAGATCCTGCAA
CGAAGGCGTTGTAAGTTACTCTTTCTGGGCACCGCAGGTTGGAGCAGCGCAGAGGTTAAGGAACTCGAGTCTC

Flna
AGGAAAGCTTATCCCTGACAGCCCTTTTGTGGTGCCCGTGGCCTCTCCGTCTGGTGACGCCCGCCGCCTTACTGTTTCTAGTCTTC
AGGAGTCAGGGCTAAAGGTCAACCAGCCAGCCTCTTTTGCAGTCAGCCTGACTCGAGCTCT

Blcap
AGGAAAGCTTATTAGGTCGGTTCCTGCAGCGGTGCCCGGTGGCCTTGGCGAAGGCCCTGTCCGGCAGAGATCATGTATTGCCTC
CAGTGGCTGCTGCCCGTCCTCCTCATCCCCAAGCCCCTCAACCCCGCCCTGTGGTTCAGCCACTCCATGCTCGAGCTCG

Igfbp7
AGAGAAGCTTACTGCGCGCCGGGCATGGAGTGCGTGAAGAGCCGCAAGAGGCGGAAGGGTAAAGCGGGCGCAGCAGCCGGC
GGCCCGGGCGTAAGCGGTGTGTGCGTGTGCAAGAGCCGCTACCCGGTGTCTCGAGTCCT

Ednrb
AGAGAAGCTTTTTCTGCTTGCCACTAGCCATCACTGCATTTTTTTATACCCTGATGACCTGTGAAATGCTGAGAAAGAAGAGTGG
CATGCAAATTGCTTTAAATGATCACTTAAAGCAGAGACGGGAAGTGGCCAAAACCGTATTTTGCCTGGTCCTTGTCTTTGCCCTG

Cyfip2
AGAGAAGCTTAGCAGCCCCAGGTGGTTCCGCTGTTTGGGGACATGCAAATAGAACTGGCAAGATACATCAAGACCAGCGCTCA
CTATGAGGAAAATAAATCTCGGTGGACGTGCACATCCTCTAGCAGCAGCCCACAGTACAACATCTGCGAGCAGATGGTTCAGAT

Supplementary Table S4: The genomic sequence of each RT-PCR amplicon analyzed.