Supplemental Table 1. Gene expression array analysis for *Gria4* in FeJ, HeJ and backcross mice.

Supplemental Table 1. Microarray results ^a								p-value						
Probe set			Fold change				F-test				False discovery rate adjusted			
Gene	Location	ID	N2-FeJ CX	HeJ-FeJ CX	N2-FeJ H	B HeJ-FeJ H	BN2-FeJ C	X HeJ-FeJ	CX N2-FeJ H	B HeJ-FeJ H	B N2-FeJ (CX HeJ-FeJ (CX N2-FeJ HI	8 HeJ-FeJ HB
Gria4	intron 13	1460097_at	1.9	1.9	1.9	2.0	0	0	0	0	0.0000	0.0000	0.0000	0.0000
Gria4	3' utr	1435722_at	-1.3	-1.2	-1.6	-1.5	0.0001	0.0012	0.0000	0.0000	0.0351	0.0084	0.0012	0.0001
Gria4	intron 2	1443285_at	-1.2	1.0	-1.0	-1.0	0.0417	0.7210	0.6993	0.6912	0.3188	0.4588	0.7507	0.3924
Gria4	intron 8	1440891_at	1.1	-1.2	1.1	-1.1	0.1041	0.0700	0.3964	0.2120	0.4225	5 0.1281	0.6638	0.1961
Gria4	intron 6	1458230_at	1.1	-1.0	1.0	1.1	0.3744	0.9764	0.6065	0.2264	0.5810	0.5316	0.7270	0.2041
Gria4	intron 8	1436772_at	1.0	-1.1	1.1	1.2	0.6692	0.0666	0.3552	0.0415	0.6769	0.1243	0.6511	0.0704
Gria4	last 5 exons	1421351_at	1.0	-1.1	1.1	-1.0	0.9765	0.2127	0.1473	0.8923	0.7466	6 0.2423	0.5485	0.4518

	Probe set		Mean fluorescence intensity (sample replicate-1, -2, -3)								
Gene	Location	ID	FeJ CX-1	FeJ CX-2	FeJ CX-3	N2 CX-1	N2 CX-2	N2 CX-3	HeJ CX-1	HeJ CX-2	HeJ CX-3
Gria4	intron 13	1460097_at	8.00	8.13	8.01	8.89	9.12	9.02	9.18	8.90	8.94
Gria4	3' utr	1435722_at	9.84	9.75	9.73	9.30	9.51	9.38	9.51	9.45	9.46
Gria4	intron 2	1443285_at	6.82	6.66	6.76	6.34	6.64	6.54	6.87	6.93	6.57
Gria4	intron 8	1440891_at	8.19	8.70	8.36	8.42	8.69	8.73	8.26	8.17	8.21
Gria4	intron 6	1458230_at	8.12	7.93	8.06	8.13	8.07	8.16	8.14	7.97	8.02
Gria4	intron 8	1436772_at	8.50	9.05	8.74	8.83	8.75	8.85	8.60	8.69	8.46
Gria4	last 5 exons	1421351_at	7.50	7.14	7.19	7.30	7.19	7.37	7.07	7.23	7.15
Gene	Location	ID	FeJ HB-1	FeJ HB-2	FeJ HB-3	N2 HB-1	N2 HB-2	N2 HB-3	HeJ HB-1	HeJ HB-2	HeJ HB-3
Gria4	intron 13	1460097_at	5.25	5.26	5.32	5.41	5.30	5.40	5.33	5.27	5.29
Gria4	3' utr	1435722_at	10.19	9.91	10.31	9.46	9.42	9.50	9.53	9.70	9.54
Gria4	intron 2	1443285_at	7.06	6.78	6.76	6.78	6.74	6.96	6.55	7.04	6.87
Gria4	intron 8	1440891_at	8.88	8.50	8.89	8.76	8.88	8.92	8.53	8.63	8.68
Gria4	intron 6	1458230_at	7.98	7.85	8.03	7.94	8.00	8.05	7.84	8.28	8.06

Gria4	intron 8	1436772_at	8.96	8.73	8.94	8.97	9.02	8.92	9.06	9.12	9.08
Gria4 las	st 5 exons	1421351_at	7.41	7.13	7.38	7.36	7.37	7.65	7.10	7.38	7.39

^aN2, homozygous $Gria4^{spwk1}$ from the (HeJ x FeJ)F1 x HeJ backross,

FeJ, C3HeB/FeJ

HeJ, C3H/HeJ

CX, cerebral cortex

HB, midbrain & hindbrain

Gria4 ^{spkw1/spkw1} (n=4)	Frequency (Hz)	Amplitude (pA)	10-90 % Rise (ms)	Half width (ms)	90-10% Decay (ms)
Control	30.5 ± 11.5	28.5 ± 3.5	0.24 ± 0.04	0.40 ± 0.04	0.76 ± 0.11
TTX	30.4 ± 11.5	26.7 ± 3.8	0.25 ± 0.05	0.40 ± 0.05	0.75 ± 0.11
TTX % of control	97 ± 4 % N.S.	93 ± 2 % N.S.	103 ± 5 % N.S.	99 ± 6 % N.S.	99 ± 8 % N.S.

Supplemental Table 2. Effect of TTX on spontaneous EPSCs in nRT

Supplemental Figure 1. Examples of EEG recordings from various genotypes displaying spike-wave discharges. Shown in each are six differential traces from the four electrodes, over the right front (RF), left front (LF), right back (RB), left back (LB) surfaces of the cerebral cortex. Two sets of traces are shown for each genotype, illustrating the range of form in each. (also see uploaded high resolution file)



Supplemental Figure 2. Genomic sequence of IAP insertion in Gria4 locus of HeJ

mice, including junctions.

LOCUS EU5297 BASE COUNT 15	42. 5567 вн 23 а 121	.7 C 12	56 G 1!	569 т	2 OTHER
ORIGIN -					
1 TTTATTAT	ΑΤ GAAATTTAAC	TTATAAAAAG	TCTCTCTCAC	ACACATATTC	ATATATATAT
61 ATGAAGGA	TG TAAACAAAAA	TGAAAGTTTG	TGTGGGAAGC	CGCCCCCACA	TTCGCCGTCA
121 CAAGATGG	CG CTGACATCCT	GIGITCIAAG	'I'I'GG'I'AAACA	AATAATCTGC	GCATGAGCCA
181 AGGGTATT	TA CGACCACTTC	GCCCCCCCTGTTT	TTCCCCGTGAA	CGTCAGCTCG	GCCATGGGCT
241 GCAGCCAA 301 ጥጥጥሮሮጥጥጥ			TCATIGGTIGI	TUTUTITAAA	MIAGAAGGGGG TCCTTCTTCC
361 TOTOTOT			CCTCTCTTGC	TICCCICICI	
421 TTGCTCTC	TT TTCCTGAAGA	TGTAAGAATA	AAGCTTTTGTC	GCAGAAGATT	СТССТССТСТС
481 GTGTTCTT	CC TGGCCGGTCC	TGAGAACGCG	TCGAATAACA	ATTGGTGCCG	AATTCCGGGA
541 CGAGAAAA	TC CGGGACGAGA	AAAAACTCCG	GACTGGCGCA	GGAGGGATAC	CTCATTCCAG
601 AACCAGAA	CT GCGAATCAAG	GTTATAAGGT	TCCCGTAACA	CAGACTGTTG	AGAAGGATTC
661 AACTGCCG	AA TTCAGAACTO	ATCAGCTGGG	GAACGACGGT	GATAAAGGTT	CCCGTAAAGC
721 AGACTGTT	AA GAAGGATTCA	A ACTGTATGAA	TTCAGAACTT	TTCAGCTGGG	GAACGAGGTA
781 AGTCTGAT	CT TGAACTTTCI	AAGGAAATTC	AAGACAGTCT	ATCAGAAGTA	AAGTGGAAAA
841 TGGCTTTA	CA AGTTATGTTI	GGCCTTAAAT	TTTTTTCTAGT	GTTAGAAGCC	CTTTTGTTCC
901 TTTTCACA	IG TTATATAGTO	G CTTAAGATAG	GGC'I'GAAAA'I'	TCTAGAGGAA	A'I''I'CAGGACA
961 GTCTATCA		GGAGAGAGAGAG	1 AGGAGCAAG	GAGAAACGGT	AAGTATACAG
1021 GCCIIICC 1091 ACATTACA	AA GGGICIIGAA	CCCGAGGAAA	AGIIAAGGIC	AGGIAGGAAI	CACCTGGGGGAG
11/1 CC2C22CC	AG COTOTOTO	CAACAAAGAAA	AGAAAAAAGA	AAAACCGCCT	CATTATCAAA
1201 GAAAAGGA	TA CCAGCCGCCZ	AGTAAAGTGC	TAACTAGTCA	TTCAAGAAAA	AAGCCAAAAG
1261 CGGCTGGC	GA AGGCCAGTTI	GCTAATTGGC	CTCAGGGCAA	TCGGCTACCA	GGTGCACTCC
1321 CGCCCTAT	GC GGAGTCCCCC	CCCTGCGTAG	TGCGTCAGCC	CGTAGTGCGT	CAGCAATGCG
1381 CAGAGAGG	CA GTGCGCAGAG	AGGCAGTGCG	CAGACTCATT	CATTCCCCGA	GAGGAACAAA
1441 GGAAAATA	GA ACAGGCATTI	CCAGTCTTTA	AAGGAGCCGA	GGGTGGGCGT	GTCCACGCTC
1501 CGGTAGAA	TA CGTACAGATI	AAGGAAATTG	CCGAGTCGGT	TCGTAAATAC	GGAACCAATG
1561 CTAATTTT	AC CTTGGCGCAG	G TTAGACAGGC	TCGCTGGCGT	GGCACTGACT	CCTGCCGACT
1621 GGCAAATG	AT TGCAAAAGTC	GCTCTCCCTA	GTATGGCCAA	ATATGTGGAA	TGGCGAGCTC
1681 TGTGGCAG	GA GGCGGCACAG	GCGCAGGCCC	GAGCAAACGC	TGCTGCTTTA	ACTCCAGAGC
1/41 AGAGAGA'I	I'G GAC'I"I"I"IGAC	TTGTTAACGG	GTCAGAGAGC	TTATTCTGCT	GAACCTGATA
1801 AGAGGTAT	CA ATGGAAGATC		GAATGTCCAA	TAGTCCTATA	ATGTGCCAGC
1001 IIIAIAIA 1021 TTTAIAIA		CTGCCAGIGA	ACACCETTAC	CATCCTACAA	ATTTIGCICC
1981 CTTTACAIG	OT TAAAACTUUIC	AGTCAGTGGG	GTCTACAGAT	AGCCACAGAA	AAGGCAIAIC
2041 TTTCTGAT	AC AGGACAATTO	TTGGGCTCTG	TGGTGTCCCC	AGATAAGATT	GTGCCCCAAA
2101 AGGTAGAG	AT AAGAAGAGAT	CACCTCCATA	CCTTAAATGA	TTTTCAAAAG	CTGTTGGGAG
2161 ATATTAAT	TG GCTCAGACCO	TTTTTAAAGA	TTCCTTCTGC	TGAGTTAAGG	CCTTTGTTTA
2221 GTATTTTA	GA AGGAGATCCT	CATATCTCCT	CCCCTAGGAC	TCTTACTCTA	GCTGCTAACC
2281 AGGCCTTA	CA AAAGGTAGAA	AAGGCCTTAC	AGAATGCACA	ATTACAACGT	ATTGAGGATT
2341 CGCAGCCT	TT CAGTTTGTGT	GTCTTTAAGA	CAGCACAATT	GCCAACTGCA	GTTTTGTGGC
2401 AGAATGGG	CC ATTGTTGTGC	G ATCCATCCAA	ACGTATCCCC	AGCTAAAATA	ATAGATTGGT
2461 ATCCTGAT	GC AATTGCACAG	G CITIGCCCTTA	AAGGCCTAAA	AGCAGCAATC	ACCCACTTTG
2521 GGCAAAGT 2581 CCCCATCT		ATTGTACCTT	CCTCCTTCC	ACAGGIICAA	CATAACCAT
2641 ATCCAAAG	CA TOAIIGGGCA	CAGTTTAGITA		TGTTGTTGTTT	CCACAAATAA
2701 CAGTAAGA	AA CCCACTTAAA	AATGGGATTG	TGGTATATAC	TGATGGATCA	AAAACTGGCA
2761 TAGGTGCC	TA TGTGGCTAAT	GGTAAAGTGG	TATCCAAACA	GTATAATGAA	AATTCACCTC
2821 AAGTGGTA	GA ATGTTTAGTO	GTCTTAGAAG	TTTTAAAAAC	CTTTTTAAAA	CCCCTTAATA
2881 TTGTGTCA	GA TTCCTGTTAT	GTGGTAAATG	CAGTAAATCT	TTTAGAAGTG	GCTGGAGTGA
2941 TTAAGCCT	TC CAGTAGAGTI	GCCAATATTT	TTCAGCAGAT	ACAATTAGTT	TTGTTATCTA
3001 GAAGATCT	CC TGTTTATATI	ACTCATGTTA	GAGCCCATTC	AGGCCTACCT	GGCCCCATGG
3061 CTCTGGGA	AA TGATTTGGCI	GATAAGGCCA	CTAAAGTGGT	GGCTGCTGCC	CTATCATCCC
3121 CGGTAGAG	GC 'I'GCAAGAAA'I	' TTTCATAACA	ATTTTCATGT	GACGGC'I'GAA	ACA'I'I'ACGCA
3181 GTCGT"I"IC 3241 GTCGT"I"IC			GIGACATIGT	CCCMAMMCCA	CARAGCTGCT
3301 TOTOCON	AT CCAGIICU			ΔΟΨΨΟΔΔΨΔΨ	
3361 CCATTGAC	AC ATGTTCTCC	ATCATGTTCT	СТТСТССССТ	AACTGGAGAA	AAAGCCTCAC
3421 ATGTGATT	CA ACATTGTCTT	GAGGCATGGA	GTGCTTGGGG	GAAACCCAGA	CTCCTTAAGA
3481 CTGATAAT	GG ACCAGCTTAT	ACGTCCCAAA	AATTTCAGCA	GTTCTGCCGT	CAGATGGACG
3541 TAACCCAC	CT GACTGGACTI	CCATACAACC	CTCAAGGACA	GGGTATTGTT	GAGCGTGCGC
3601 ATCGCACC	CT CAAAGCCTAT	CTTATAAAAC	AGAAGAGGGG	AACTTTTGAG	GAGACTGTAC
3661 CCCGAGCA	CC AAGAGTGTCC	GTGTCTTTGG	CACTCTTTAC	ACTCAATTTT	TTAAATATTG
3721 ATGCTCAT	GG CCATACTGCO	GCTGAACGTC	ATTGTTCAGA	GCCAGATAGG	CCCAATGAGA

3781	TGGTTAAATG	GAAAAATGTC	CTTGATAATA	AATGGTATGG	CCCGGATCCT	ATCTTGATAA
3841	GATCCAGGGG	AGCTATCTGT	GTTTTCCCAC	AGAATGAAGA	CAACCCATTT	TGGGTACCAG
3901	AAAGACTCAC	CCGAAAAATC	CAGACTGACC	AAGGGAATAC	TAATGTCCCT	CGTCTTGGTG
3961	ATGTCCAGGG	CGTCAATAAT	AAAGAGAGAG	CAGCGTTGGG	GGATAATGTC	GACATTTCCA
4021	CTCCCAATGA	CGGTGATGTA	TAATGCTCAA	GTATTCTCCT	GCTTTTTTAC	CACTAACTAG
4081	GAACTGGGTT	TGGCCTTAAT	TCAGACAGCC	TTGGCTCTGT	CTGGACAGGT	CCAGATGACT
4141	GACAACATTA	ACACTTTGTC	AGCCTCAGTG	ACTACAGTCA	TAGATGAACA	GGCCTCAGCT
4201	AATGTCAAGA	TACAGAGAGG	TCTCATGCTG	GTTAATCAAC	TCATAGATCT	TGTCCAGAAA
4261	CAACTGGATG	TATTATGACA	AATAACTCAG	CAGGGATGTG	AACAAAAGTT	TCCGGGATTG
4321	TGTGTTATTT	CCATTCAGTA	TGTTAAATTT	ACTAGGACAG	CTAATTTGTC	AAAAAGTCTT
4381	TTTCAGTATA	TGTTACAGAA	TTGGATGGCT	GAATTTGAAT	AGATCCTTCG	AGAATTGAGA
4441	CTTCAGGTCA	ACTCCACGCG	CTTGGACCTG	TCGCTGACCA	AAAGATTACC	CAATTGGATC
4501	TCCTCAGCAT	TTTCTTTCTT	TAAAAATTG	GGTGGGATTA	ATATTATTTG	GAGATACACT
4561	TTGCTGTGGA	TTAGTGTTGC	TTCTTTGATT	GGTCTGTAAG	CTTAAGGCCC	AAACTAAGAG
4621	AGACAAGGTG	GTTATTGCCC	AGGCGCTTGC	AGGACTAGAA	CATGGAGCTT	CCCCTGATAT
4681	ATCTATGCTT	AGGCAATAGG	TCGCTGGCCA	CTCAGCTCTT	ATATCTCACG	AGGCTAGACT
4741	CATTGCACGA	GATAGAGTGA	GTGTGCTTCA	GCAGCCCGAG	AGAGTTGCAA	GGCTAAGCAC
4801	TGCAGTAGAA	GGGCTCTGCG	GCACATATGA	GCCTATTCTA	GGGAGACATG	TCATCTTTCA
4861	TGAAGGTTCA	GTGTCCTAGT	TCCCTTCCCC	CAGGCAAAAC	GACACGGGAG	CAGGTCAGGG
4921	TTGCTCTGGG	TAAAAGCCTG	TAAGCCTAAG	AGCTAATCCT	GTACATGGCT	CCTTTACCTA
4981	CACACTGGGG	ATTTGACCTC	TATCTCCACT	CTCATTAATA	TGGGTGGCCT	ATTTGCTCTT
5041	ATTAAAAGAA	AAAGGGGGAA	CTGTGGGAAG	CCGCCCCAC	ATTCGCCGTC	ACAAGATGGC
5101	GCTGACATCC	TGTGTTCTAA	GTTGGTAAAC	AAATAATCTG	CGCATGAGCC	AAGGGTATTT
5161	ACGACCACTT	GTACTCTGTT	TTTCCCGTGA	ACGTCAGCTC	GGCCATGGGC	TGCAGCCAAT
5221	CAGGGAGTGA	TGCGCCCTAG	GCAATGGTTG	TTCTCTTTAA	AATAGAAGGG	GTTTCGTTTT
5281	TCTCTCTCTC	TTGCTTCTTG	CTCTCTCTTG	CTTCCCTCTC	TTGCTTCTTG	CTCTCTCTTG
5341	CTTCTTGCTC	TCTCTTGCTT	CCCTCTCTTG	CTTCTTGCTC	TCTCTTGCTT	CTTGCTCTCT
5401	TTTCCTGAAG	ATGTAAGAAT	AAAGCTTTGT	CGCANAANAT	TCTGGTCTGT	GGTGTTCTTC
5461	CTGGCCGGTC	GTGAGAACGC	GTCGAATAAC	AAGTTTGCAG	TGAGGTACTA	TACATTTTTT
5521	TCCATTTTGT	CCCCCTTTTA	CATAAACCAT	GTCACCCACA	CTTATAC	

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Supplemental Figure 3. Structure of the *Gria4*^{tm1Dgen} allele. a) Graphic depiction of the first four exons of the wild-type (wt) allele of *Gria4*, and below it a depiction of the targeting construct made by Deltagen, intended to replace exon 3 with a truncated exon 3-lacZ-neopgk cassette. At the bottom is a genomic map of the eventual targeted allele, showing that the left (L) arm of the construct inserted 3' to exon 3 and did not effect the replacement of exon 3, resulting in a mostly deleted lacZ-neopgk cassette and a partial duplication of intron 3 just downstream of exon 3, as determined by long-PCR (data not shown) and genomic DNA sequencing. Presumably at least some of the right (R) arm of the targeting construct underwent homologous recombination with endogenous intron 3. b) Genomic sequence of deletion junction of lacZ-neo targeting cassette in the *Gria4* locus of *Gria4*^{tm1Dgen}.

A.



B.

Supplemental Figure 4. GluR3 protein levels are not affected by *Gria4* genotype. Representative (of two trials each) western blot analysis of GluR3 expression in cerebellar preps from B6, *Gria4*^{tm1Dgen}, and *Gria4*^{spwk1} intra-C3H backcross adult mice. Below, the calbindin level is shown as the loading control for this blot. Overall GluR3 protein levels appear not to be affected by mutant genotypes at the *Gria4* locus.

