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## Legends for Table and Figures

Table 1 Sequences of primers and fluorescent hybridization probes used for quantitative polymerase chain reaction.

Figure 1 TetHeLaG2m cell line.

(A) Schematic figure of the GluR2 minigene with pTRE-Tight Vector.

(B) Editing efficiencies at the Q/R site of GluR2 minigene pre-mRNA in conventional HeLa and TetHeLaG2m cell lines cultured in a dish for 48 h. Each symbol represents the extent of Q/R site-editing of GluR2 minigene pre-mRNA isolated from a single culture dish. Each large symbol represents the results of five culture dishes. For each cell line, the mean  $\pm$ SEM (n=15-30) is also indicated.

(C) Culture time-dependent changes of editing efficiency at the Q/R site of GluR2 minigene pre-mRNA and expression levels of ADAR2 mRNA and GluR2 pre-mRNA, and relative abundance of ADAR2 mRNA to GluR2 pre-mRNA in the TetHeLaG2m cell line. TetHeLaG2m cells were plated at a low concentration ( $5 \times 10^5$  cells/well in 6-well plate). The relative abundance of ADAR2 mRNA to GluR2 pre-mRNA increases in parallel with the editing efficiency at the GluR2 Q/R site in a time-dependent manner. For each culture time, the mean  $\pm$  SEM (n=6) is also indicated.

Figure 2 Method of detecting editing efficiency at the Q/R site of GluR2.

(A) Scheme for detecting editing efficiency at the Q/R site of GluR2. Open bars represent nested PCR products. Intrinsic *BbvI* recognition sites are indicated by vertical solid arrowheads. The sizes of the DNA fragments generated by restriction digestion are indicated.

(B) Example of the quantification of editing efficiency using a 2100 Bioanalyzer. The molarity of the 129-bp (derived from edited GluR2 pre-mRNA) and 71-bp (derived from both edited and unedited GluR2 pre-mRNA) bands was quantified after restriction digestion with *BbvI* for 12 h, and the editing efficiency was calculated as the ratio of the former to the latter. The lower figure indicates gel-like image produced by the 2100 Bioanalyzer.

GluR, glutamate receptor; Q, glutamine; R, arginine; PCR, polymerase chain reaction

#### Figure 3 Editing extent of GluR2 Q/R site

Editing efficiency in TetHeLaG2m cells after treatment with antidepressants (0-10  $\mu$ M) for 24 h is expressed as mean  $\pm$  SEM (n = 5 to 8). Statistical analysis was performed by the one-way ANOVA test followed by Dunnett's multiple comparison test (\*P<0.05, \*\*P<0.01 and \*\*\*P<0.001).

GluR, glutamate receptor; Q, glutamine; R, arginine; ANOVA, analysis of variance

#### Figure 4 Expression levels of ADAR2 mRNA, GluR2 mRNA and GluR2 pre-mRNA

Amounts of RNA that were upregulated by seven out of eight antidepressants that upregulated by GluR2 Q/R site-editing (A, B, C, D, E, F, and G) were quantitatively analyzed. The amounts of ADAR2 mRNA, GluR2 mRNA, and GluR2 pre-mRNA are expressed as values relative to that of  $\beta$ -actin mRNA. The amount of ADAR2 mRNA is also expressed as a value relative to that of GluR2 mRNA. Mean  $\pm$  SEM of at least 5-8 wells are displayed. Statistical analysis was performed with Steel's multiple comparison test (\*P<0.05, \*\*P<0.01, \*\*\*P<0.001).

GluR, glutamate receptor; ADAR, adenosine deaminase acting on RNA; Q, glutamine; R, arginine

Table 1

	Oligonucleotide sequence
<b>GluR2</b>	
Forward primer	5'-ATGCGATATTTCGCCAAGA-3'
Reverse primer	5'-CAGTCAGGAAGGCAGCTAAGTT-3'
Universal Probe Library probe #63	5'-CTCCTCCT-3'
<b>pre-GluR2</b>	
Forward primer	5'-GATGGTGTCTCCCATCGAAA-3'
Reverse primer	5'-TCCATAAGCAATTTCTGTTTGCT-3'
Universal Probe Library probe #73	5'-GCTGAGGA-3'
<b>ADAR2</b>	
Forward primer	5'-GTGTAAGCACGCGTTGACTG-3'
Reverse primer	5'-CGTAGTAAGTGGGAGGGAACC-3'
Universal Probe Library probe #42	5'-GCTGGATG-3'
<b><math>\beta</math>-actin</b>	
Forward primer	5'-CCAACCGCGAGAAGATGA-3'
Reverse primer	5'-CCAGAGCGGTACAGGGATAG-3'
Universal Probe Library probe #64	5'-CCAGGCTG-3'

Figure 1

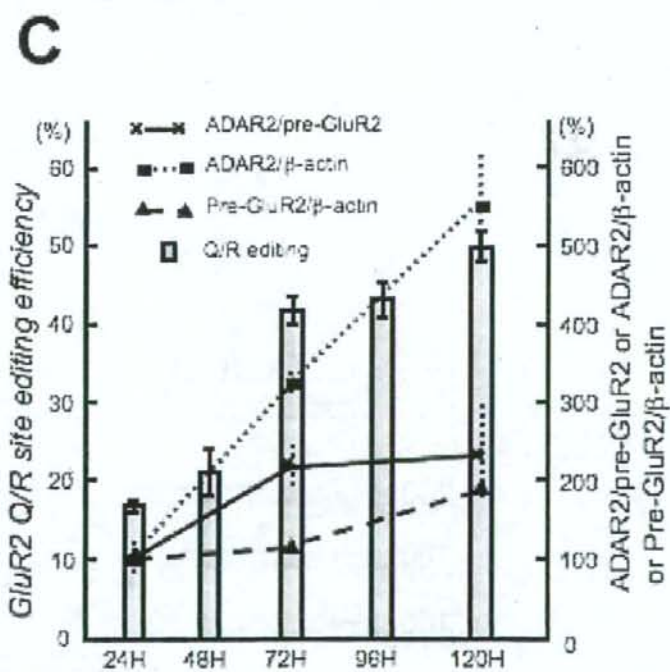
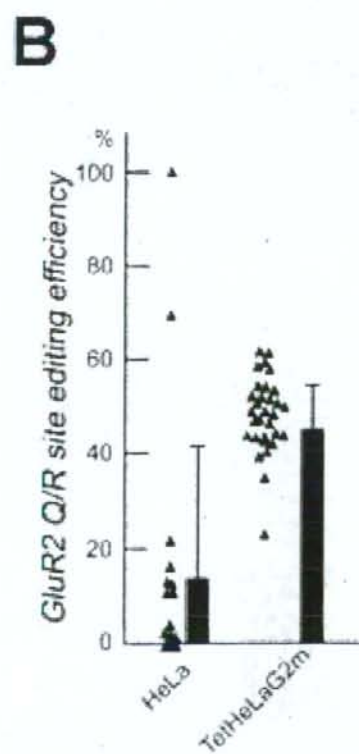
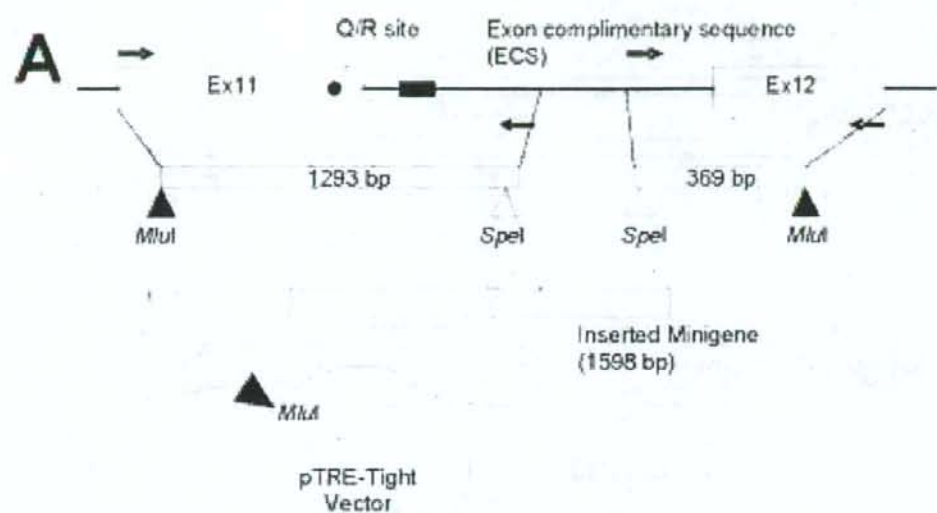




Figure 2

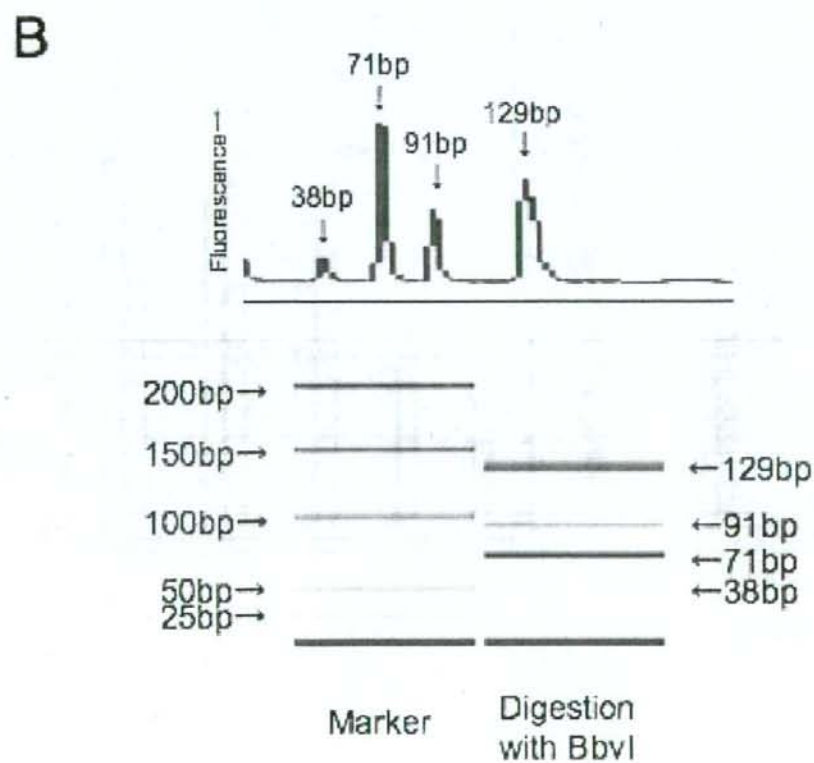
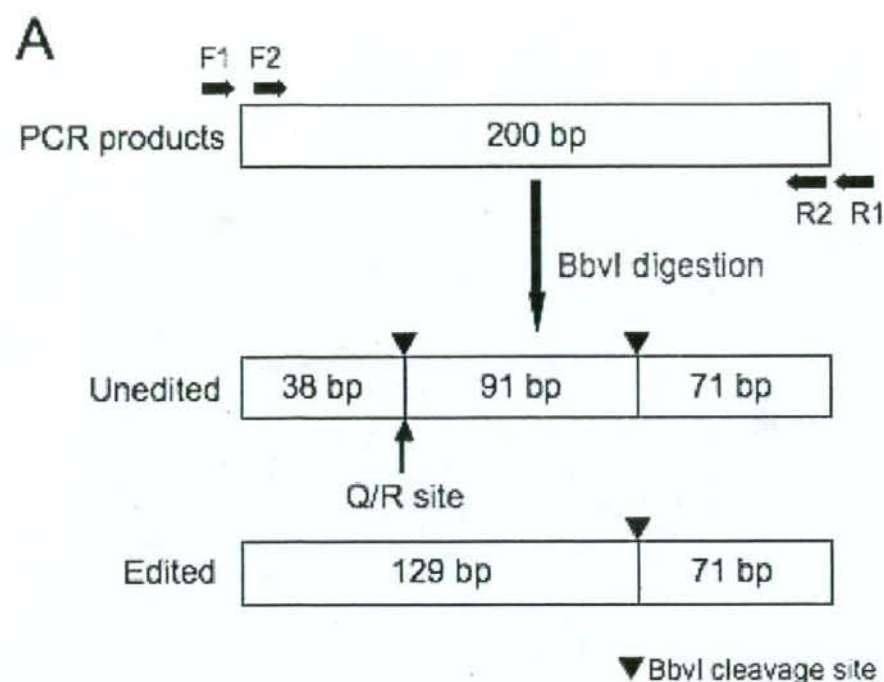


Figure 3

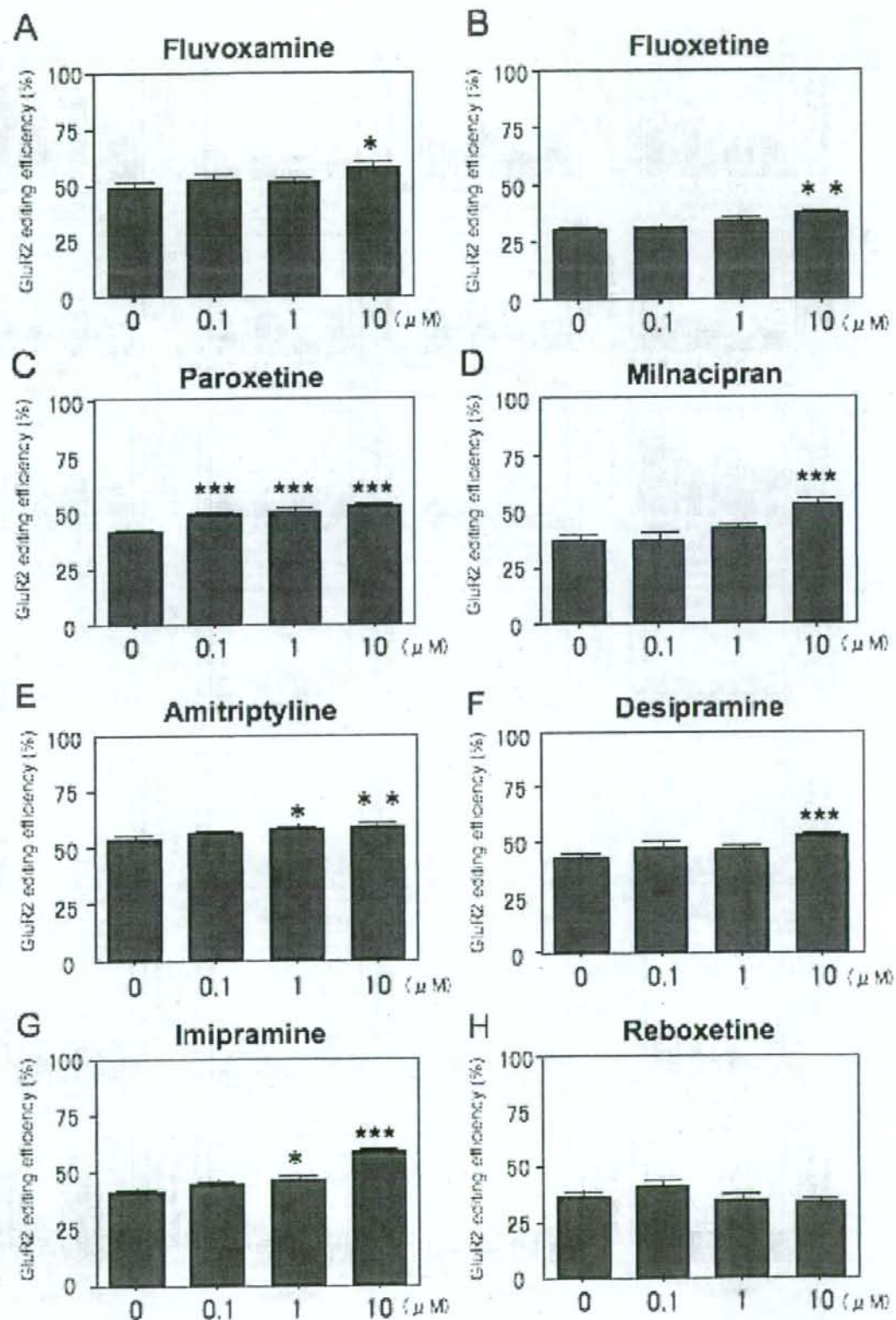


Figure 4

