

## Supplementary Materials for

### **DNA methylation regulates neuronal glutamatergic synaptic scaling**

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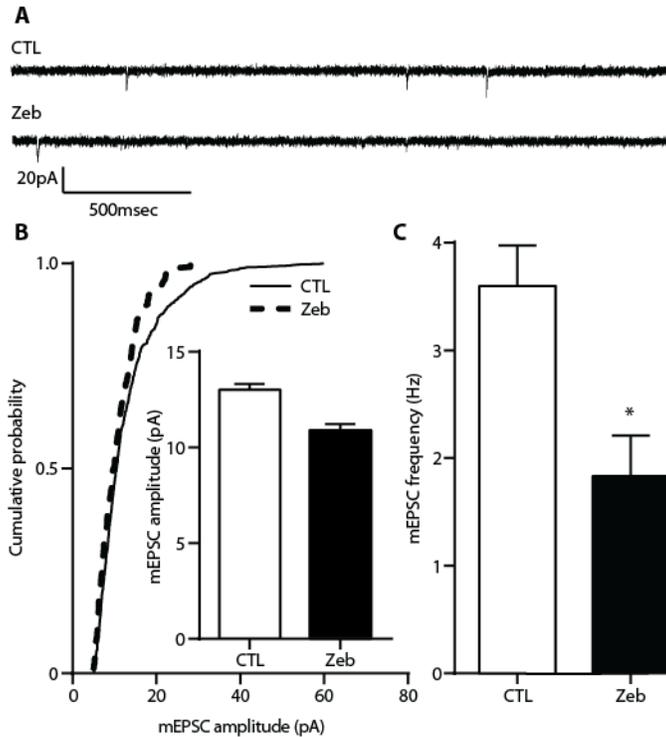
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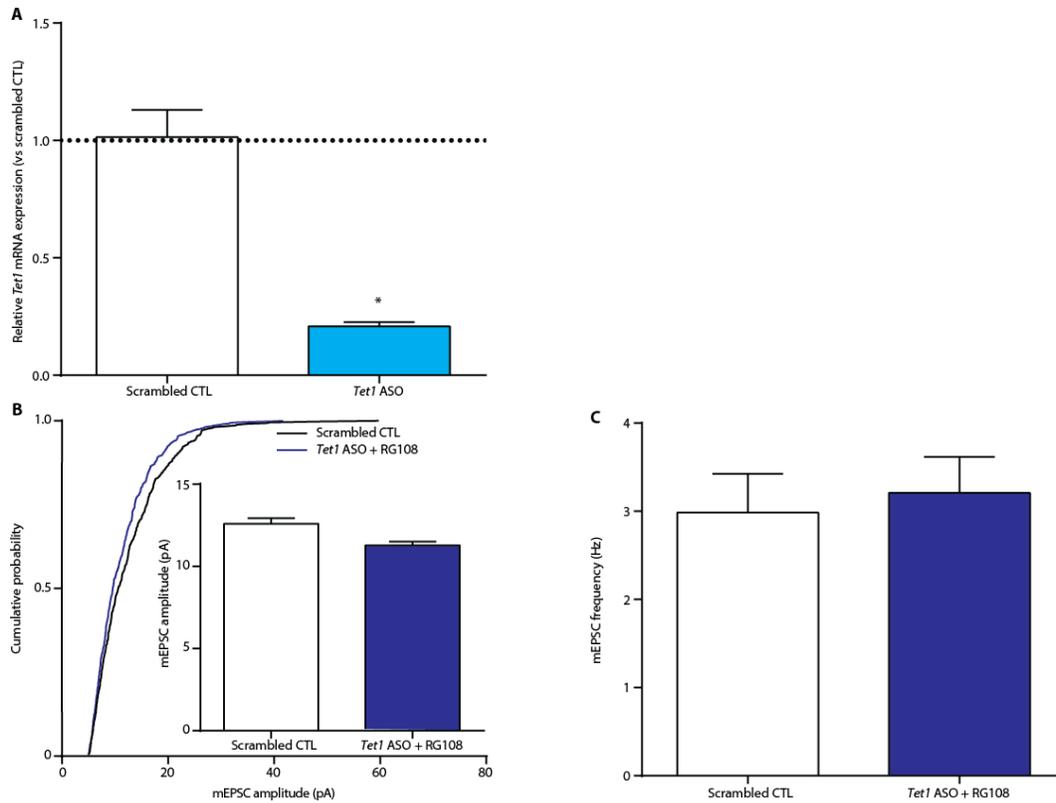
Fig. S1. Indirect DNMT inhibition with the nucleoside analog zebularine decreases mEPSC frequency with no effect on amplitude.

Fig. S2. *Tet1* knockdown blocks RG108-induced upscaling of excitatory synaptic strength.

Table S1. Primers used in this study.



**Figure S1. Indirect DNMT inhibition with the nucleoside analog zebularine decreases mEPSC frequency with no effect on amplitude.** (A) Sample mEPSCs traces from cortical pyramidal neurons after 24 hour control (CTL) or zebularine (Zeb) treatment. (B and C) Cumulative probability distributions and mean mEPSC amplitudes (B) and mean mEPSC frequencies (C) from cortical pyramidal neurons exposed to Zeb. Bar graphs are means  $\pm$  SEM, cumulative of cells pooled from four experiments (CTL,  $n = 7$  cells; Zeb,  $n = 6$  cells); (B)  $P = 0.0352$ , Kolmogorov-Smirnov (K - S) test; Inset,  $P = 0.0352$ , Mann-Whitney (M - W) test; (C)  $*P < 0.05$ , Student's unpaired  $t$  test.



**Figure S2. *Tet1* knockdown blocks RG108-induced upscaling of excitatory synaptic strength.** An ASO was utilized that selectively targets positions 6059-6078 of the transcript for the TET1 dioxygenase, a known regulator of activity-dependent active de-methylation in neurons. As described in the Materials and Methods, the *Tet1*-targeted ASO nucleotide was a 5'-10-5 2'-OMe gapmer. (A) Bar graphs show relative expression of *Tet1* mRNA in cultured cortical neurons after *Tet1* ASO (light blue) treatment. Bar graphs are means  $\pm$  SEM from 3 biological replicates from one experiment, each performed in technical triplicate;  $*P < 0.05$  compared to scrambled CTL, Student's unpaired *t* test. (B and C) Cumulative probability distributions and mean mEPSC amplitudes (B) and mean mEPSC frequencies (C) from cortical pyramidal cells after *Tet1* ASO + RG108 treatment (dark blue). Bar graphs are means  $\pm$  SEM. Data are cumulative of cells pooled from two independent experiments (scrambled CTL,  $n = 4$  cells; *Tet1* ASO + RG108,  $n = 7$  cells); (B)  $P = 0.0182$  compared to scrambled CTL, K - S test; Inset,  $P = 0.0041$ , M - W test; (C)  $P = 0.7142$ , Student's unpaired *t* test.

**Table S1:** Primers used in this study.

<b>Gene</b>	<b>Sense primer (5'-&gt; 3')</b>	<b>Antisense primer (5'-&gt; 3')</b>
<i>Gapdh</i>	ACCTTTGATGCTGGGGCTGGC	GGGCTGAGTTGGGATGGGGACT
<i>Bdnf IX</i>	GAGAAGAGTGATGACCATCCT	TCACGTGCTCAAAGTGTCTCAG
<i>Smug1</i>	TCGCTACTGCCAAGGCCCA	AGGGGACAGCACAGAGCCCC
<i>Arc/Arg3.1</i>	GCTGAAGCAGCAGACCTGA	TTCCTGGTATGAATCACTGCTG
<i>Apobec1</i>	GCACGGCTTTATCACCACGCA	CCCACAGATGGGGGTACCTTGG
<i>Mecp2</i>	TTGCCTGAAGGTTGGACGCGA	GGGTCCAAGGAGGTGTCTCCCA
<i>Dnmt1</i>	GTGTGCGGGAATGTGCTCGCT	CAGTGGTGGTGGCACAGCGT
<i>Dnmt3a</i>	AGCAAAGTGAGGACCATTACCACCA	TGTGTAGTGGACAGGGAAGCCA
<i>Dnmt3a1</i>	TGCCAAGACTCACCTTCCAG	GGCTTTCCTCCACAGCATTC
<i>Dnmt3a2</i>	CTGTACTGCAGAGGGGCTG	CTGGCTTTCCTCCACAGCAT
<i>Dnmt3b</i>	TGGCAAGGATGACGTTCTGTGGT	CTGGCACACTCCAGGACCTTCC
<i>Tet1</i>	GCCAACCAGGAAGAGGCGACTG	GAGGAAGCCTGCAGGGGACAG
<i>Tet3</i>	GGAGTTGGCTGGAGTCACCACT	CCGAGTAGCTCTCCACCACAGCA