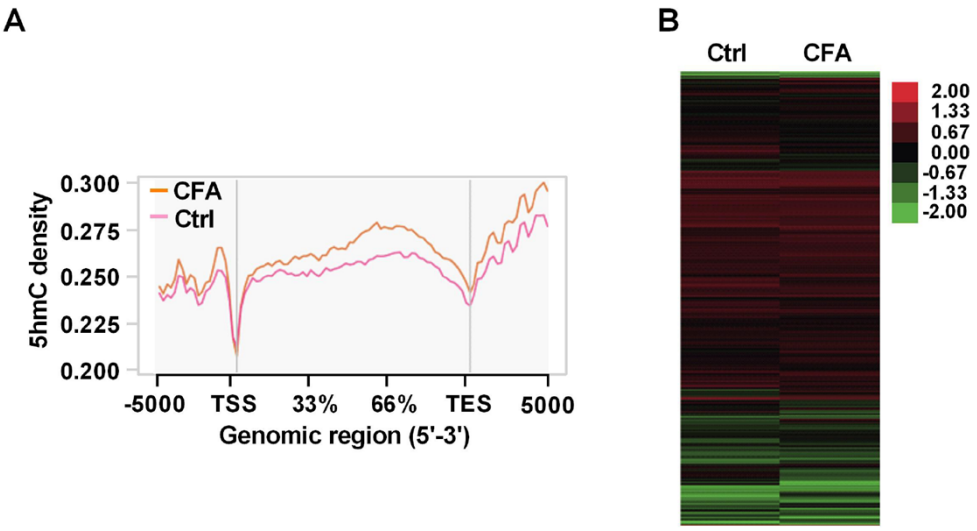

Figure S1. Genomic mapping and features of 5-hmC in spinal cord of control and CFA-treated mice. (*A*) Normalized densities of 5hmC reads across the genome-wide transcript unit of all reference genes from transcription start sites (TSS) to transcription ending sites (TES), as well as up- and downstream regions, in spinal cord from control and CFA mice. The coverage of up- and downstream interpolated 5000 bp sequence is also shown. 5-hmC densities were normalized to the total number of aligned reads from each sample (in millions). (*B*) Heatmap of 5-hmC levels of RefSeq genes. Two distinct clusters of genes were identified based on the dynamic changes of their 5-hmC levels in spinal cord. The heatmap represents the normalized 5-hmC density of each gene.

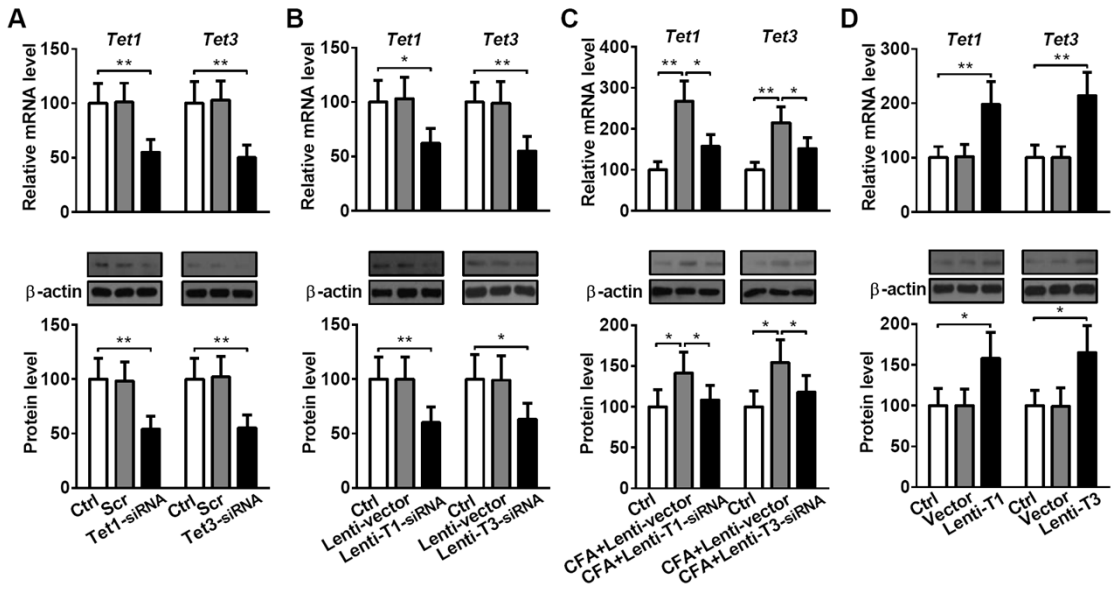

Figure S2. The validation of transfection efficiency of modulation tool *in vivo*. (*A-C*) The expression of *Tet1* and *Tet3* in mRNA and protein after the intrathecal injection of exogenous siRNA in naïve mice (*A*), endogenous siRNA mediated by lentivirus in naïve mice (*B*) or CFA mice *(C)*. n=6/group. The injection of siRNA or Lenti-siRNA in naïve mice: *$p<0.05$; **$P < 0.01$ versus the corresponding control or scramble or Lenti-vector group by two-tailed unpaired Student's *t* test. The injection of Lenti-siRNA in naïve mice: One-way ANOVA (expression *vs.* the treated groups) followed by post *hoc* Tukey test, Tet1 mRNA: $F(2, 15) = 43.3$, Tet3 mRNA: $F(2, 15) = 30.72$; TET1 protein: $F(2, 15) = 13.24$; TET3 protein: $F(2, 15) = 17.85$; *$P < 0.05$, **$P < 0.01$. (*D*) The expression of *Tet1* and *Tet3* mRNA and protein after the intrathecal injection of lentivirus overexpressing TET1 and TET3. The expression of mRNA and protein was measured at 1 day after 2 consecutive days injection of siRNA or at 2 d after 3 consecutive days injection of lentivirus in naive mice or CFA mice. n=6/group, *$p<0.05$; **$p<0.01$ versus the corresponding control or vector group by two-tailed unpaired Student's *t* test.

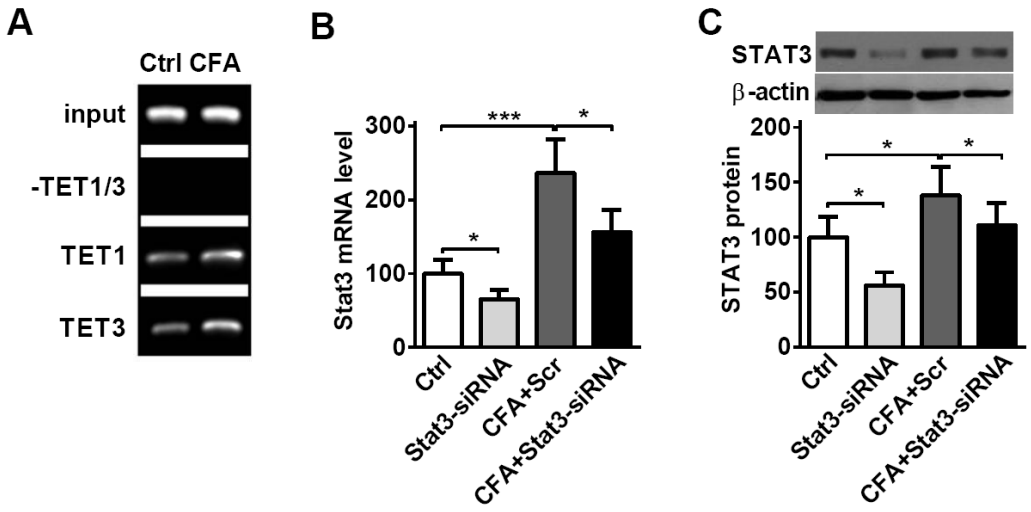

Figure S3. The binding of TET1 and TET3 with Stat3 promoter and the validation of Stat3 knockdown tool. (A) The capacity of TET1 and TET3 could bind to *Stat3* promoter in CFA group versus control by chromatin immuno-precipitation (ChIP-sqPCR) method. In input group, genome DNA was used as PCR template. -TET1/3, without TET1 and TET3 antibody in ChIP experiment. (B-C) The expression of *Stat3* in mRNA and protein after the intrathecal injection of siRNA in naïve mice (B) or CFA mice *(C)*. n=5/group; One-way ANOVA (expression *vs.* the treated groups) followed by post *hoc* Tukey test, mRNA: $F(3, 16) = 37.22$; protein: $F(3, 16) = 18.48$; *$p<0.05$; ***$p<0.001$.