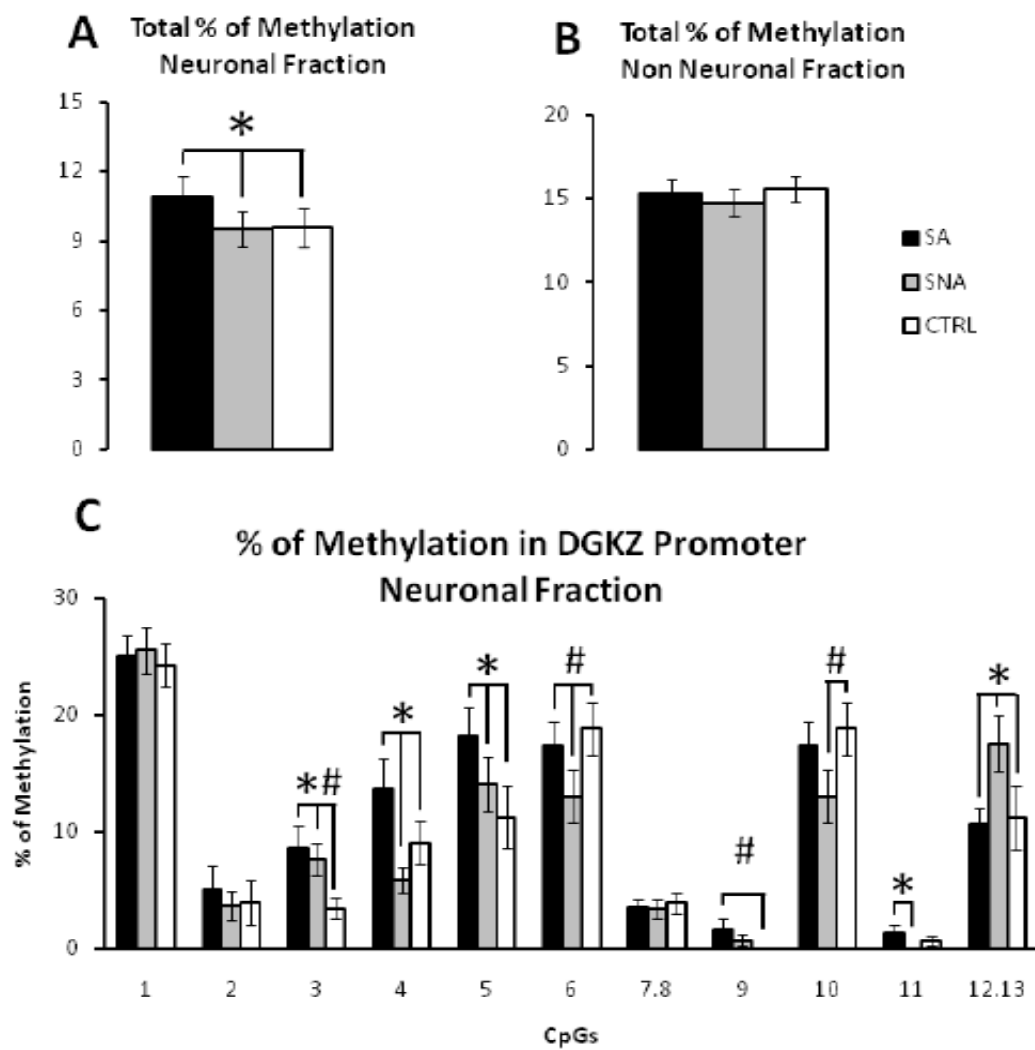


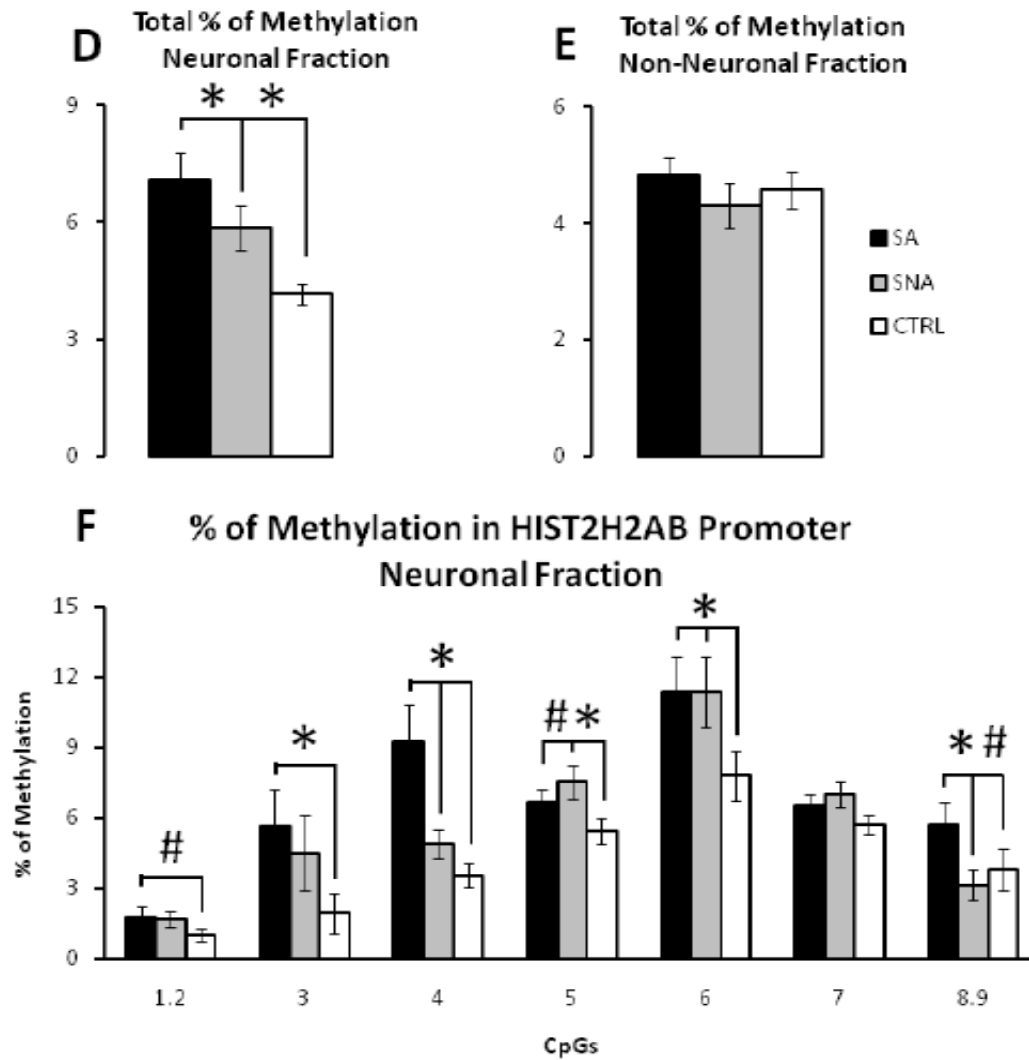
## Supplementary Online Content

Labonte B, Suderman M, Maussion G, Navaro L, Yerko V, Maha I, Bureau A, Mechawar N, Szyf M, Meaney MJ, Turecki G. Genome-wide epigenetic regulation by early-life trauma. *Arch Psychiatry*. 2012. doi:10.1001/archgenpsychiatry.2011.2287.

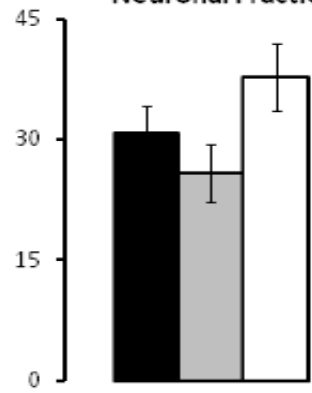
**eFigure.** Methylation levels in gene promoters selected for validation in abused suicide completers

This supplementary material has been provided by the authors to give readers additional information about their work.

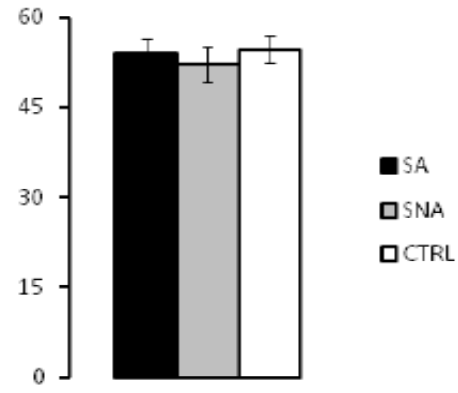


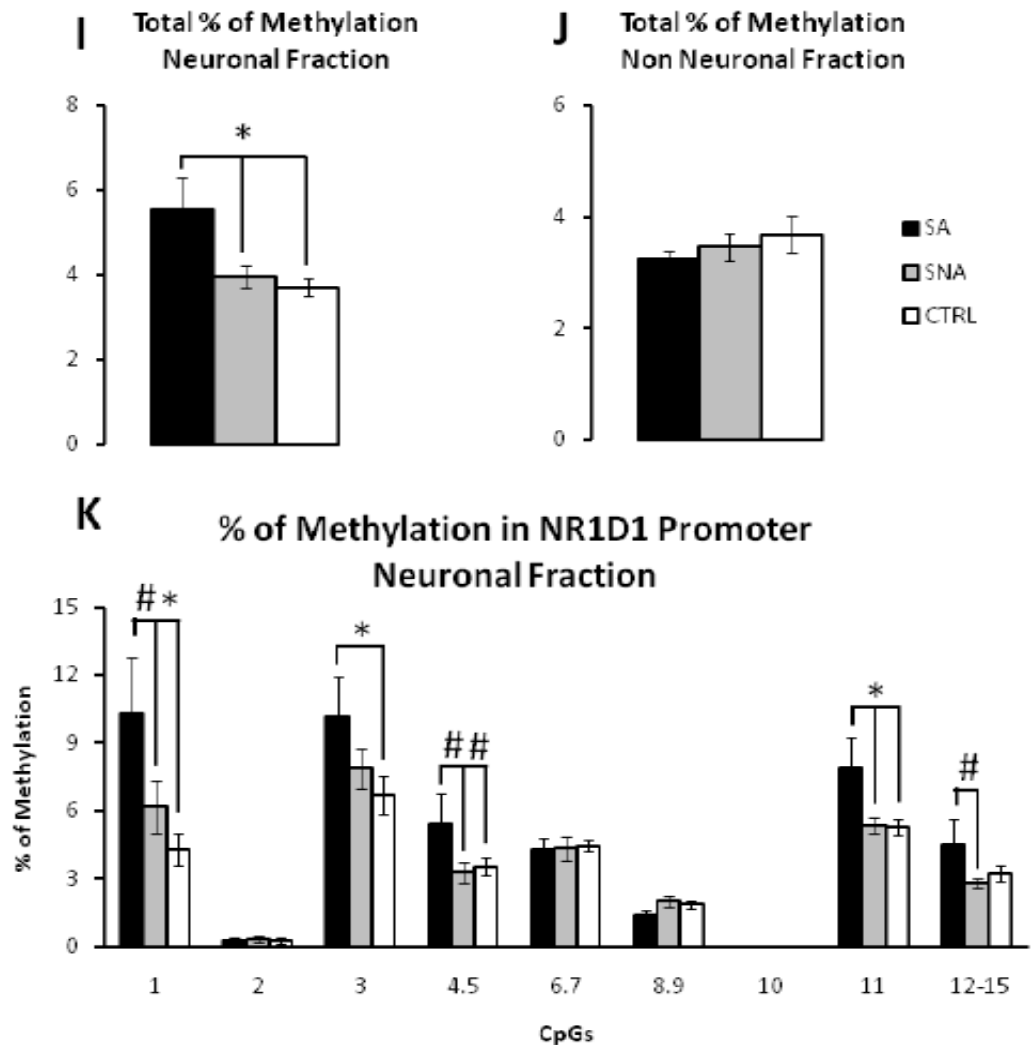


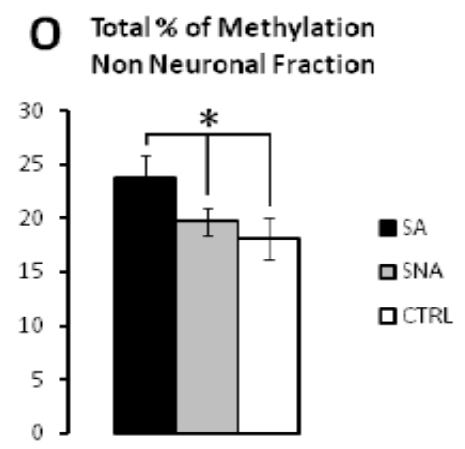
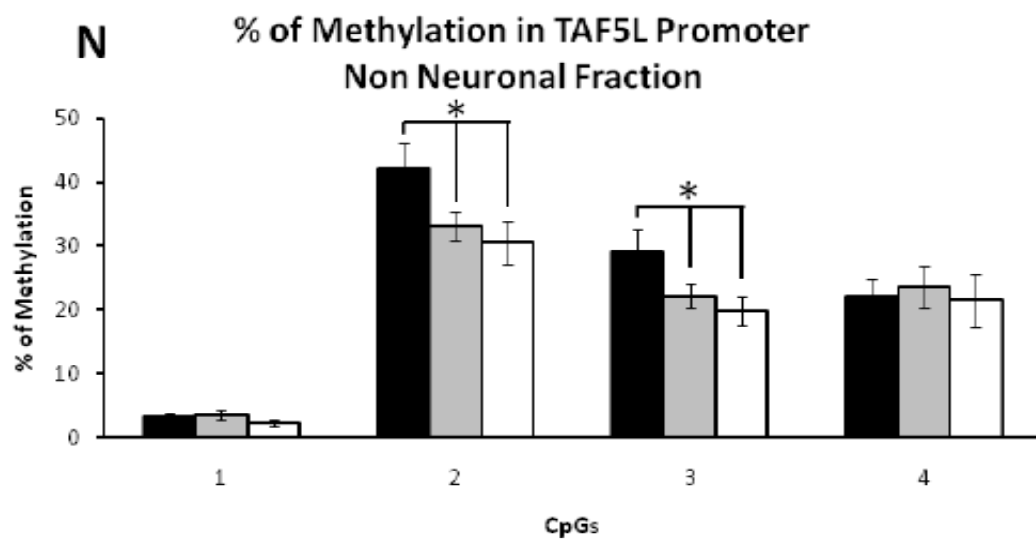
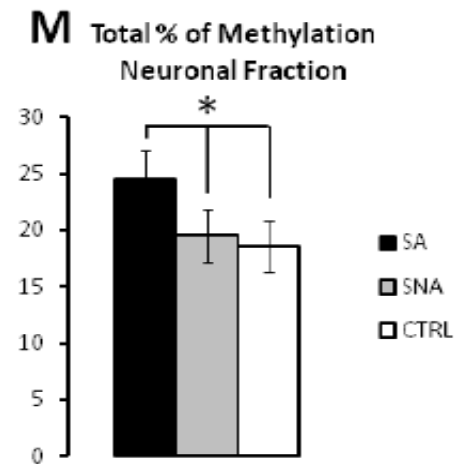
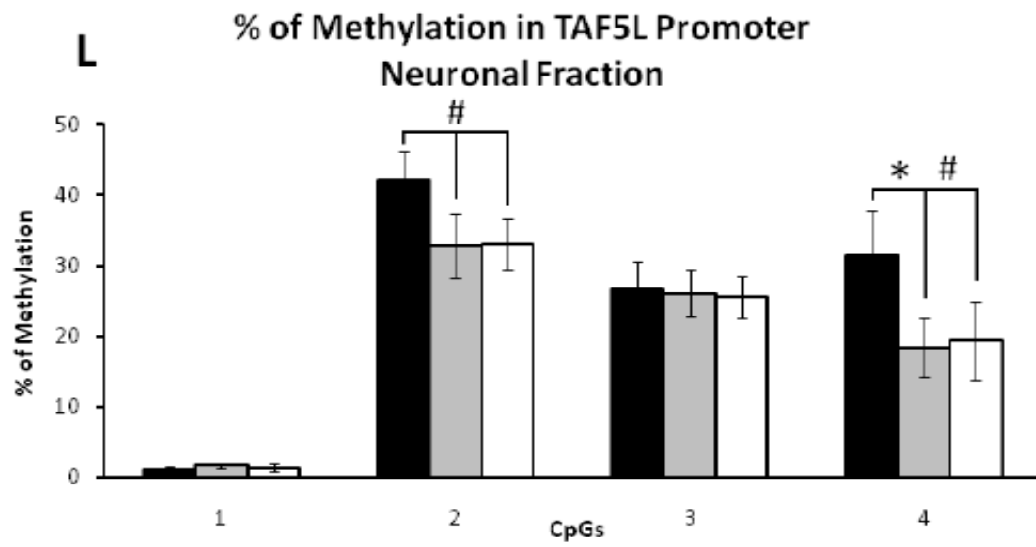
**G** Total % of Methylation  
Neuronal Fraction



**H** Total % of Methylation  
Non Neuronal Fraction







**Supplemental Figure 1.** Methylation levels in gene promoters selected for validation in abused suicide completers (SA; black), non abused suicide completers (SNA; grey) and controls (CTRL; white). **A** Total % methylation in all CpGs for DGKZ in the neuronal cell fraction. **B** Total % of methylation in all CpGs in DGKZ promoter in the non-neuronal cell fraction. **C** Individual CpG methylation levels in the promoter of DGKZ in the neuronal cell fraction. Neuronal fraction N= SA, 21; SNA, 19; CTRL, 14; Non Neuronal fraction N= SA, 27; SNA, 20; CTRL, 17. For DGKZ, methylation values for CpGs 7 and 8 and 12, and 13 are pooled together. **D** Total % of methylation in all CpGs in HIST2H2AB in the neuronal cell fraction. **E** Total % of methylation in all CpGs in HIST2H2AB promoter in the non-neuronal cell fraction. **F** Individual CpG methylation levels in the promoter of HIST2H2AB in the neuronal cell fraction. Neuronal fraction N= SA, 24; SNA, 20; CTRL, 16; Non Neuronal fraction N= SA, 27; SNA, 20; CTRL, 17. For HIST2H2AB, methylation values for CpGs 1 and 2 and 8 and 9 are pooled together. **G** Total % methylation in all CpGs in RGS3 in the neuronal cell fraction. **H** Total % methylation in all CpGs for RGS3 promoter in the non-neuronal cell fraction. Neuronal fraction N= SA, 19; SNA, 19; CTRL, 15; Non Neuronal fraction N= SA, 26; SNA, 20; CTRL, 16. **I** Total % of methylation in all CpGs in NR1D1 in the neuronal cell fraction. **J** Total % methylation in all CpGs for NR1D1 promoter in the non-neuronal cell fraction. **K** Individual CpG methylation levels in the promoter of NR1D1 in the neuronal cell fraction. Neuronal fraction N= SA, 22; SNA, 18; CTRL, 15; Non Neuronal fraction N= SA, 27; SNA, 20; CTRL, 17. For NR1D1, methylation values for CpGs 4 and 5, 6 and 7, 8 and 9, and 12 to 15 are pooled together. **L** Individual CpG methylation levels in the promoter of TAF5L in the neuronal cell fraction. **M** Total % methylation in all CpGs in TAF5L promoter in the non-neuronal cell fraction. **N** Individual CpG methylation levels in the promoter of TAF5L in the neuronal cell fraction. **O** Total % methylation in all CpGs in TAF5L in the non-neuronal cell fraction. Neuronal fraction N= SA, 24; SNA, 18; CTRL, 15; Non Neuronal fraction N= SA, 27; SNA, 20; CTRL, 17. Values are given as mean % of methylation  $\pm$  SEM. \*  $p < 0.05$ ; #  $p < 0.01$ .