Supplementary Information

Oxytocin receptor DNA methylation and alterations of brain volumes in maltreated children

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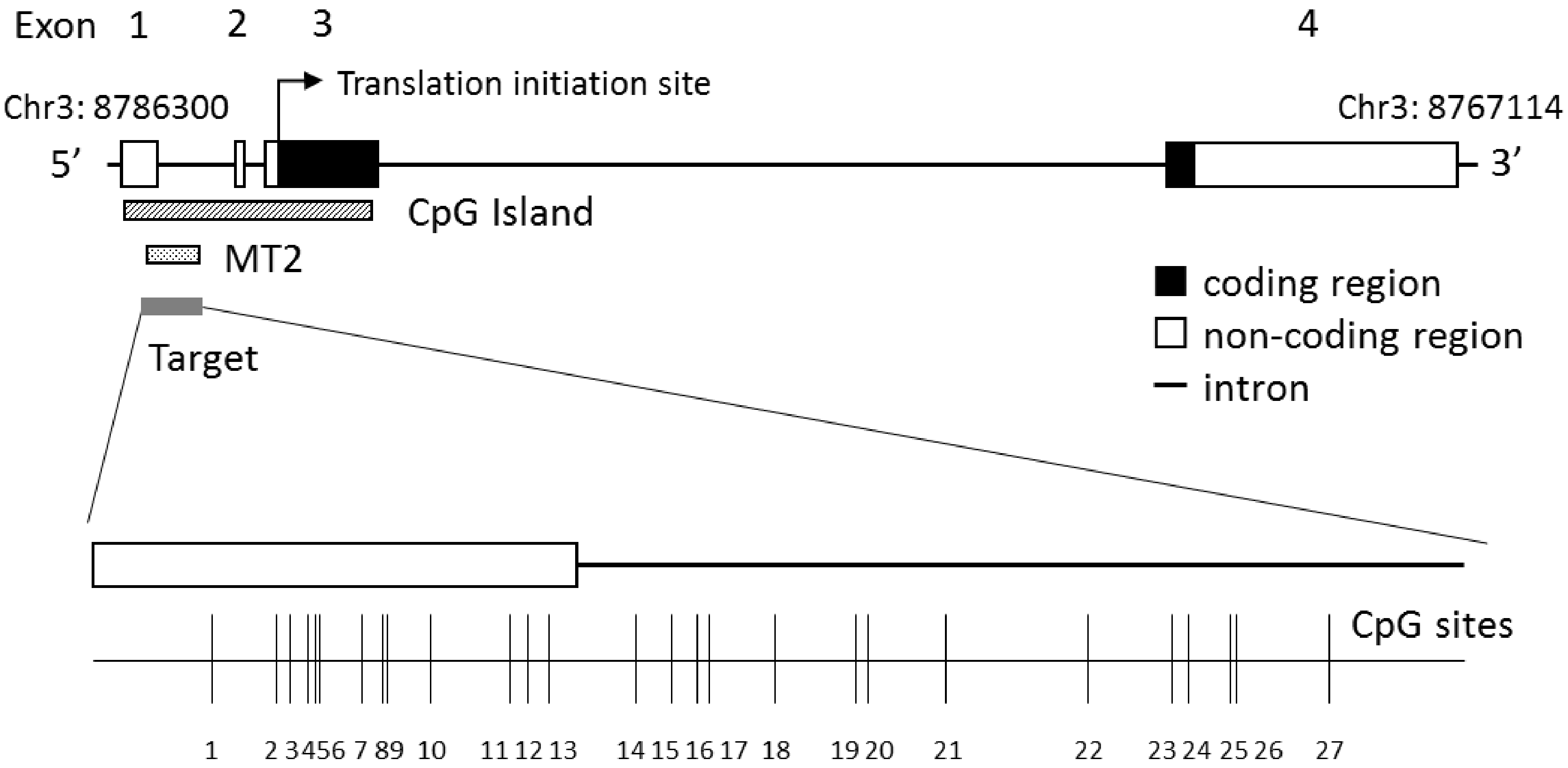

Fig S1. Gene structure of *OXTR* (chr3: 8,792,095-8,811,300; GRCh37/hg19 build). Methylation of the MT2 region suppresses transcription in a human hepatoblastoma cell line[56]. The location of 27 CpG sites in this study are indicated.

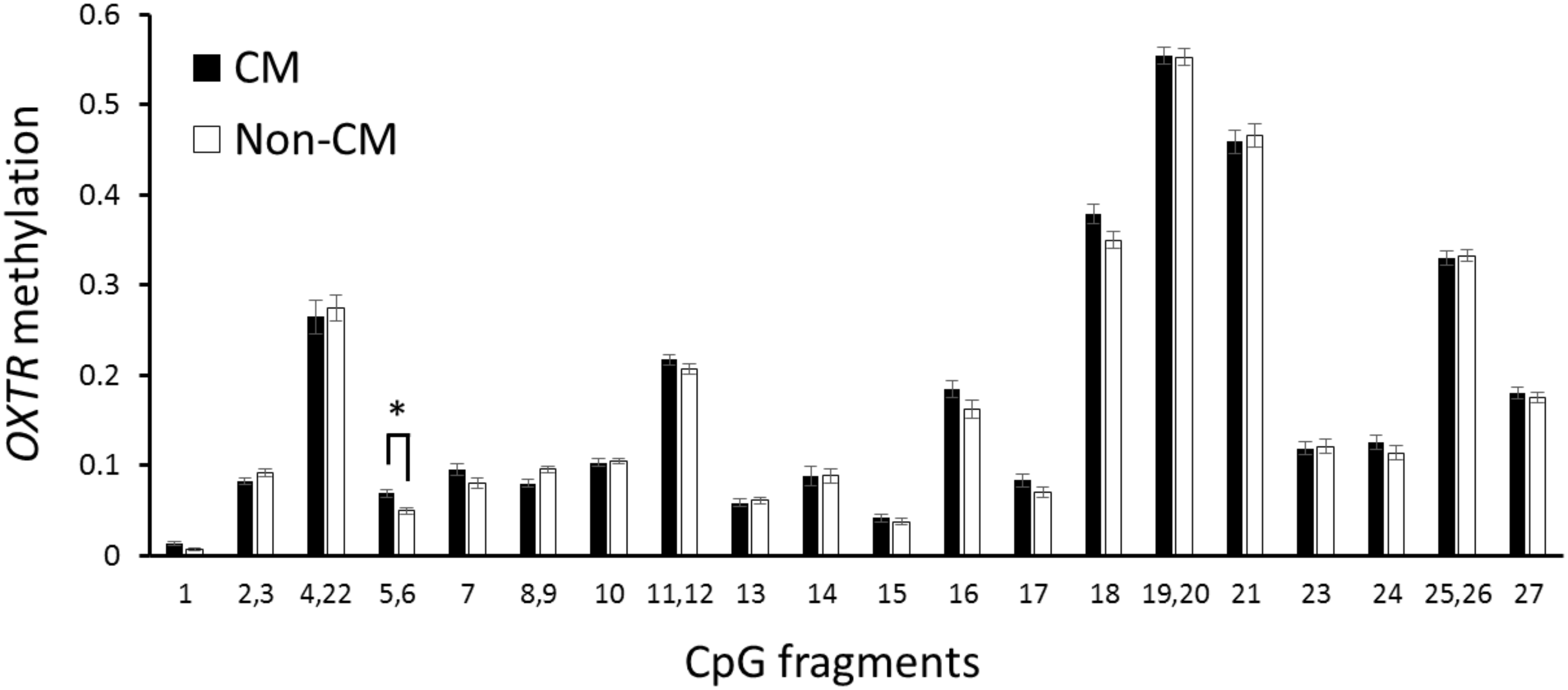

Fig. S2 Group comparison of *OXTR* methylation. The CM and Non-CM groups were compared using *t*-test ($\alpha = 0.05 / 20$, Bonferroni correction). *: $P_{corr} < 0.05$. Error bars indicate SE.

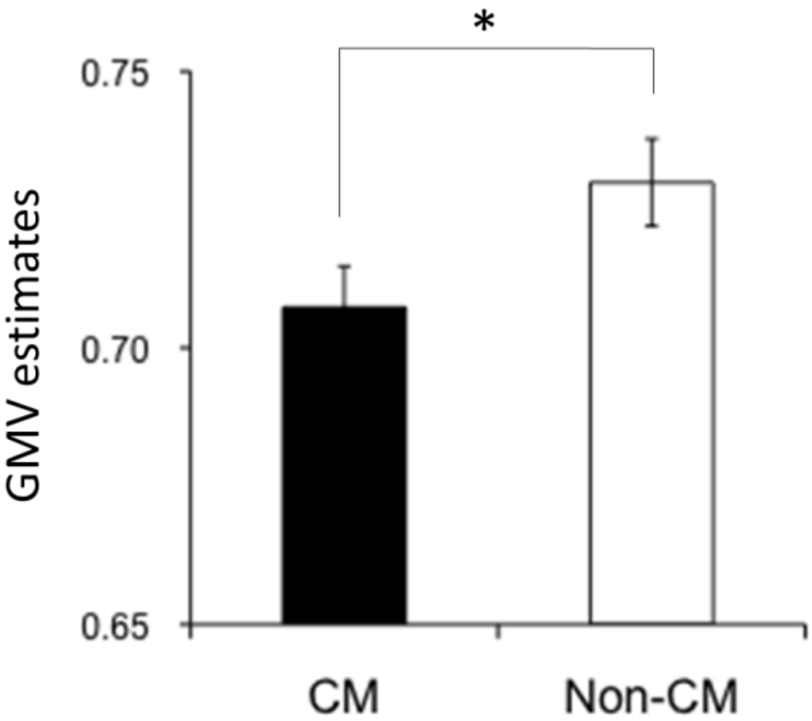

Fig. S3 Structural differences in GMV in the left orbitofrontal cortex (x, y, z = -27, 54, -12 [BA 11]) between the CM and Non-CM groups.

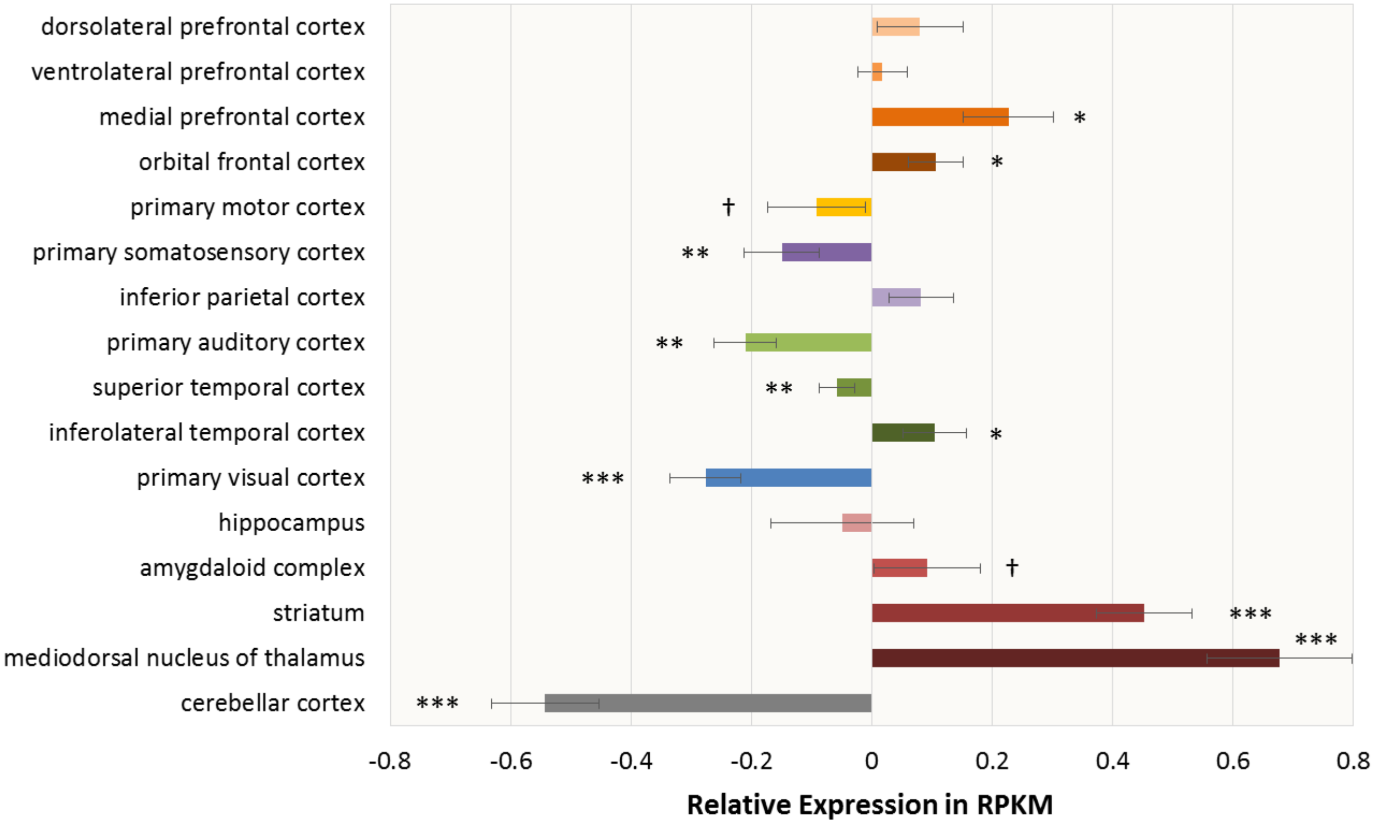

Fig. S4 Relative gene expression of *OXTR* in the human brain. The figure shows the *OXTR* gene expression measured via RNA-seq in BrainSpan (http://www.brainspan.org) datasets (*n* = 16; mean age: 12.3±8.4; age range: 1-30 years). The relative expression level of each brain region was derived by the mean-centering of all brain regions for each individual (mean = 0), and the value of each brain area was tested for the difference from the 0 level. The striatum, thalamus, and cortical regions such as the medial prefrontal, orbital frontal, and inferolateral temporal cortices exhibit significantly higher *OXTR* expression than other brain regions. † $P < 0.10$, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, 2-tailed. Error bars represent standard errors of the mean.