Supporting Information

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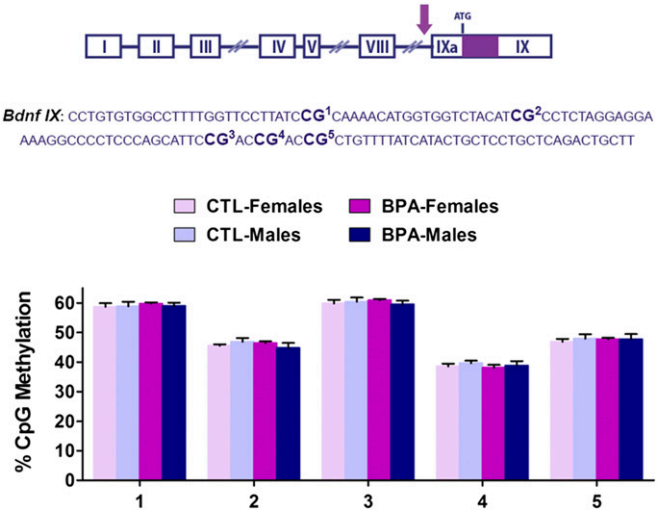

Fig. S1. CpG methylation of *Bdnf* IX in the P28 hippocampus after prenatal BPA exposure. Schematic representation of the *Bdnf* gene and the sequence of *Bdnf* promoter IX including five CpG sites that were examined using the bisulfite pyrosequencing method.

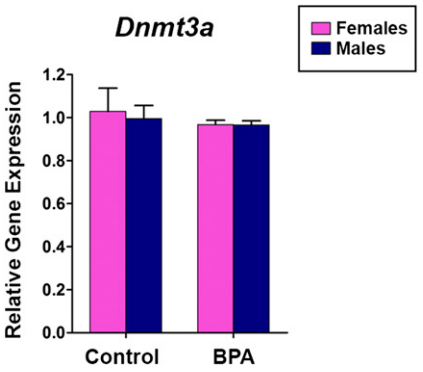

Fig. S2. Gene expression analysis of *Dnmt3a* in the P60 hippocampus of males and females prenatally exposed to BPA (200 μg/kg per day) or vehicle (CTL).

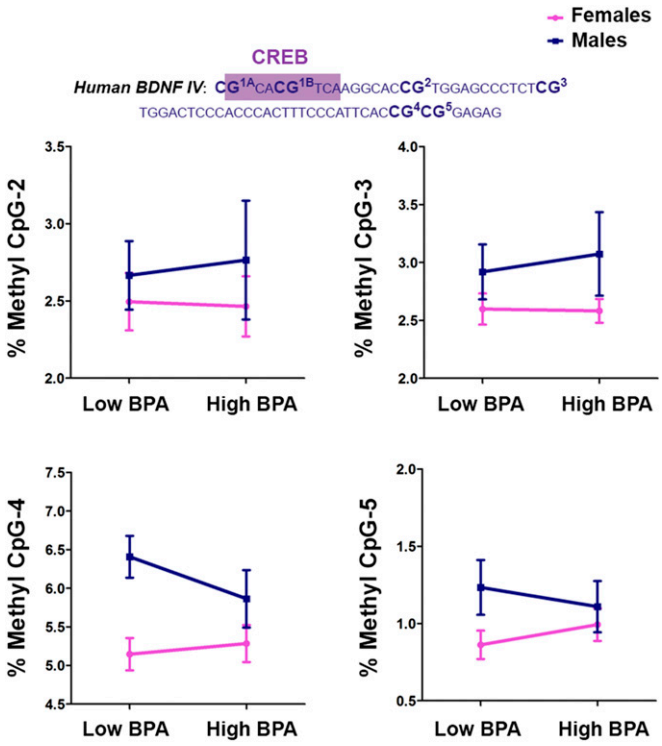

Fig. S3. The sequence of the human *BDNF* promoter IV and four CpG sites (CpG2 to -5) that did not show any associations with maternal BPA levels in humans.

Table S1. Primers used for gene expression analysis

Gene	Forward primer	Reverse primer
Bdnf	CATAAGGACGCGGACTTGTACA	AGACATGTTTGCGGCATCCA
Grin2b	TGAAGATGGCTACCAGATGC	GCAGGGACTTGTCTTTCCAT
Gadd45b	AGACATTGGGCACAACCGAA	ACCCATTGGTTATTGCCTCTGC
Dnmt1	GCCATGTGAACAGGAAGATGAC	GTCCAAGTGAGTTTCCGGTCTT
Dnmt3a	TCTTGAGTCTAACCCCGTGATG	CCTCACTTTGCTGAACTTGGCT
CypA	GAGCTGTTTGCAGACAAAGTTC	CCCTGGCACATGAATCCTGG

RNA samples were treated with DNase I, and primers were designed to cross an intron/exon boundary or to span a long intron to exclude any possibility of genomic DNA contamination.

Table S2. PCR and pyrosequencing primers used for DNA methylation analysis

Genomic region	Primer sequence
Mouse *Bdfn IV*; CpG sites 1–4; chr2:109,532,399–109,532,715*	
PCR primer forward	TAGGATTGGAAGTGAAAATATTTATAAAGT
PCR primer reverse-biotinylated	/5Biosg/CCTTCAACCAAAAACTCCATTTAATCT
Pyrosequencing primer	AGAGGAGGTATTATATGATAG
Mouse *Bdnf IX*; CpG sites 1–5; chr2:109,562,918–109,563,064*	
PCR primer forward	GGTGTTTGGTGTTTTAAGTAGTT
PCR primer reverse-biotinylated	/5Biosg/ACAAATCCTATATAACCTTTTAATTCC
Pyrosequencing primer	TGAGTAGGAGTAGTATGATAA
Mouse *Grin2b*; CpG sites 1–5; chr6:136,123,503–136,123,781*	
PCR primer forward	AGGTTTAGGAGGAGAAATTTAAGAG
PCR primer reverse-biotinylated	/5Biosg/TAACCACTATTTCCCCTCTCCCTTA
Pyrosequencing primer F1 (CpG 1–3)	TTGGTTGAGGTTGTT
Pyrosequencing primer F2 (CpG 4–5)	TTTTTGGTAGTAAGAAGGA
Human *BDNF IV*; CpG sites 1–6; chr11:27,723,070–27,723,280†	
PCR primer forward	GATTTTGGTAATTAGTGTATTAGAGTGTT
PCR primer reverse-biotinylated	/5Biosg/ATCAACCAAAAACTCCATTTAATCTC
Pyrosequencing primer	GGTAGAGGAGGTATTATATGATAG

*Genomic coordinates show genomic regions amplified by PCR and are based on the University of California, Santa Cruz (UCSC) Genome Browser Mouse July 2007 (NCBI37/mm9) Assembly.

†Genomic coordinates show genomic region amplified by PCR and are based on the UCSC Genome Browser Human February 2009 (GRCh37/hg19) Assembly.