Supporting Information

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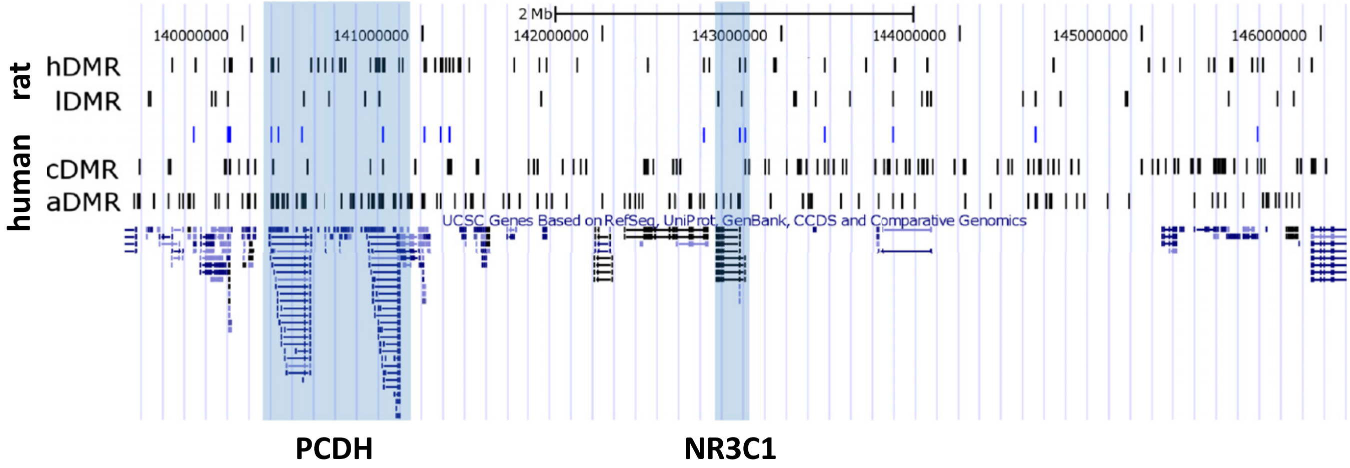

Fig. S1. Rat differentially methylated regions (DMRs) associated with maternal care mapped onto human DNA. The top tracks shown in the University of California, Santa Cruz (UCSC) genome browser image identifies the locations on the human genome to which rat DMRs had similar sequence composition as determined by Blat. The middle track shows those locations that are within 1,000 bp of a human DMR. The bottom two tracks show the locations of the human DMRs.

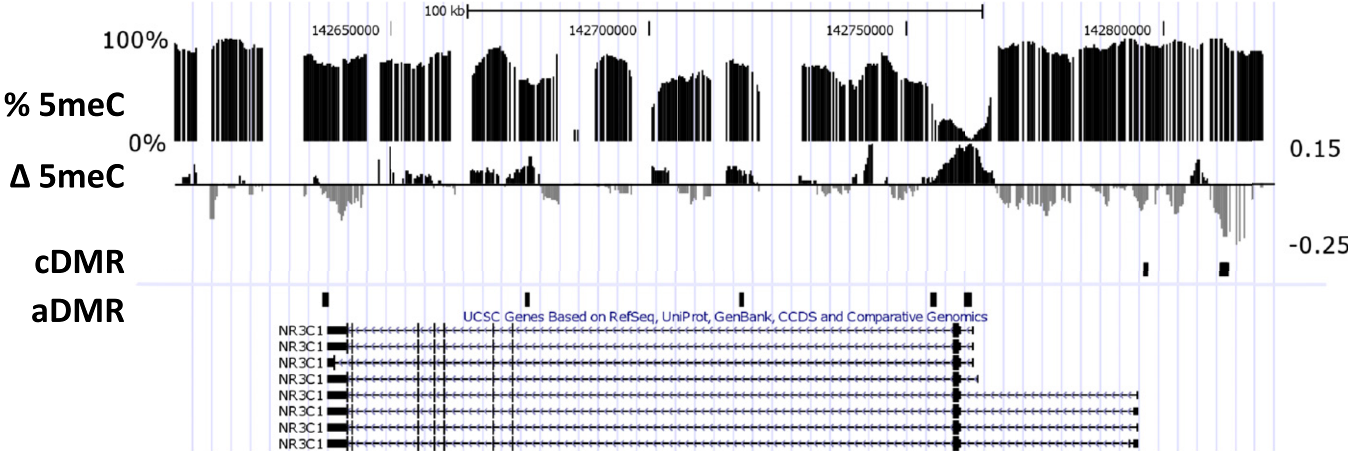

Fig. S2. Association of human DNA methylation with early life abuse across *NR3C1*. Tracks are shown in the UCSC genome browser that display average methylation levels (% 5meC) across all samples estimated from microarray probe intensities, mean $\log_2$ fold differences (Δ 5meC) between abuse and control samples (where positive values are shown in black and indicate higher methylation in abuse samples, and gray values indicate higher methylation in control samples), the locations of cDMRs (significantly higher methylation in control samples), and the locations of aDMRs (significantly higher methylation in abuse samples). The bottom track shows the coordinates of the *NR3C1* gene.

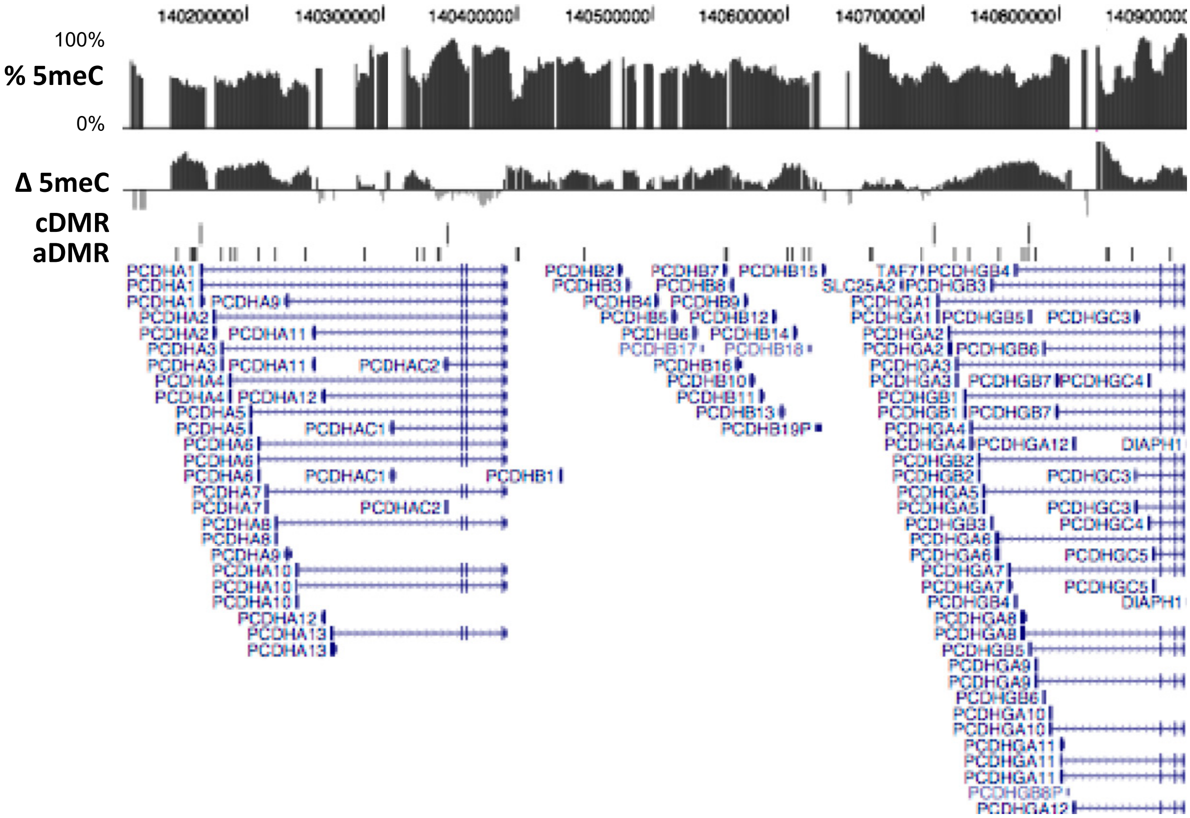

Fig. S3. Association of human DNA methylation with early life abuse across the *Pcdh* gene clusters. Tracks are shown in the UCSC genome browser as in Fig. S2, this time spanning the *Pcdh* gene clusters.

Table S1. Gene promoters containing DNA methylation levels associated with early life abuse in humans

Symbol	Ensembl ID	More methylated in	Ensembl ID (rat)	More methylated in (rat)
AC116353.2-2	ENSG00000113141	Abuse	ENSRNOG00000017251	
ARHGAP26	ENSG00000145819	Abuse	ENSRNOG00000013920	
C5orf16	ENSG00000164620	Abuse	ENSRNOG00000019575	
DND1	ENSG00000183403	Abuse	ENSRNOG00000016894	High
HBEGF	ENSG00000113070	Abuse	ENSRNOG00000018646	Low
HDAC3	ENSG00000171720	Abuse	ENSRNOG00000019618	
KIAA0141	ENSG00000081791	Abuse	ENSRNOG00000019276	
PCDHA13	ENSG00000081842	Abuse	ENSRNOG00000020119	
PCDHA3	ENSG00000204968	Abuse	ENSRNOG00000020234	Low
PCDHA5	ENSG00000204965	Abuse		
PCDHA6	ENSG00000204964	Abuse		
PCDHA7	ENSG00000204963	Abuse		
PCDHB15	ENSG00000113248	Abuse	ENSRNOG00000020028	
PCDHGA12	ENSG00000081853	Abuse		Low
PCDHGA2	ENSG00000204955	Abuse	ENSRNOG00000034126	
PCDHGA6	ENSG00000214580	Abuse	ENSRNOG00000027296	
PCDHGB7	ENSG00000214570	Abuse	ENSRNOG00000039454	
PFDN1	ENSG00000113068	Abuse	ENSRNOG00000018653	
PLAC8L1	ENSG00000173261	Abuse	ENSRNOG00000018820	
POU4F3	ENSG00000091010	Abuse	ENSRNOG00000018842	
RBM27	ENSG00000091009	Abuse	ENSRNOG00000027250	
SPRY4	ENSG00000187678	Abuse	ENSRNOG00000013851	
TCERG1	ENSG00000113649	Abuse	ENSRNOG00000018849	
WDR55	ENSG00000120314	Abuse		
YIPF5	ENSG00000145817	Abuse	ENSRNOG00000014564	Low
APBB3	ENSG00000113108	Control	ENSRNOG00000017849	
NR3C1	ENSG00000113580	Control	ENSRNOG00000014096	
PCDHA4	ENSG00000204967	Control		

Genes are listed whose promoters contain DMRs. The last two columns indicate the orthologous rat gene identifier and whether the orthologous gene promoter contains a DMR in the rat data set. Promoters are defined as the region from 2,000 bp upstream to 200 downstream of the gene transcription start site.

Table S2. Regions spanning >100 Kb containing no significant DNA methylation associations with early life abuse in humans

Chr	Start	End	Genes
5	139727792	139842017	ANKHD1, U4
5	140449572	140553729	AC074130.3, PCDHB10, PCDHB16, PCDHB2, PCDHB3, PCDHB4, PCDHB5, PCDHB6, PCDHB7, PCDHB8
5	141339508	141446791	GNPDA1
5	141992319	142128928	FGF1
5	143840561	143962140	7SK, AC008716.7-1
5	144019854	144161558	
5	144675916	144810451	
5	144811452	144924824	

The first three columns provide the coordinates of the region spanned, and the final column (Genes) lists the genes within the region. Chr, chromosome.

Table S3. Primers for quantitative real-time PCR of immunoprecipitated samples

Gene	ID	Forward	Reverse	Chr	Start	End	TSS distance
HBEGF	h28	CCAGGCTTCTGAGATTGGAG	AAAAGCACATGGGTTGGAAG	5	139707017	139707197	−748
KIAA0141	h33.3	CATAACTTTTGCCACGTCTGAA	CGGTCCAGCTTTATCTCACTGT	5	141282899	141283091	−598
PCDHA3	h3	TGAGGAGTGACCGAAGGATATT	GCACGCTGTTATTTCTTTTGTG	5	140160659	140160825	−225
PCDHA5	h53.2	TGGAACCTAAACATTTTGTGAAA	TTTGGTAAATCGTCTTTGCACT	5	140180487	140180669	−967
PCDHA6	h56	TGAATGATGGCGGACGCAGAAGAA	GAGGAGCAGACATTGCTTTCCCAA	5	140187753	140187908	−31
PCDHA7	h38	AAGCACATGGTTCCCATAAGAG	TCCTGGTGTATTGCAGTAGCTT	5	140192773	140193022	−1256
PCDHB3	h21.2	GCAATGGCTTCCTTTTGTTC	GTGTGAAGGCCCTGAGAGAG	5	140459169	140459342	−1163
PCDHGC5	h51	AATGTCTCCACGGAAATGCT	GCTAGCCGTTCTGCAAGTCT	5	140835253	140835458	−398
POU4F3	h35	CAGCAGAAATGCACTGAAGG	CACGCTTGCCTTTCTTTCTT	5	145697899	145698054	−804
RMB27	h16.4	TGCCAATCAACATGAGTGTGTA	GTTCCTTCCTCTCGTTTTTCT	5	145562859	145563016	−448
TCERG1	h24.2	AGTTCTGCTTACCGCGAGAG	ATGCGGTTGGTCAAACTTTC	5	145806817	145807004	−156

Chr, chromosome.