

Table S1 Primer sequences used in this paper

<i>Dnmt1</i>	forward	CAGAGGAGAGAGACCAGGATAA
	reverse	GCTGTTACCTCTTCCAGTTTCT
<i>Tet1</i>	forward	ACGCTGGAACAAGTGGTAGCCATA
	reverse	TGAACGTTTGGGTCTTGGAGGTCT
<i>Tet2</i>	forward	TCCATACAATGGGAGTGTGCCAGT
	reverse	TTGGTGAGATGGTCCTGGTTTGGGA
<i>Tet3</i>	forward	AACCAGGGCGCCAAGGTCAGTAGT
	reverse	TTGATCTTCTCTGGCGTGCTCAGT
<i>Bdnf I</i>	forward	AGTTGCTTTGTCTTCTGTAGTCGC
<i>Bdnf II</i>	forward	GAGCAGAGTCCATTACAGCACCTTG
<i>Bdnf III</i>	forward	GAGAGTTCCGGGTGCTGGCTTGGGA
<i>Bdnf IV</i>	forward	GAGTACATATCGGCCACCAAAGAC
<i>Bdnf V</i>	forward	CCGCTGGCTGGCTGTCTGCACGGTTC
<i>Bdnf VI</i>	forward	TCTGCGGAACTCCAGGACAGCCTC
<i>Bdnf IX</i>	forward	GCAGCTGGAGTGGATCAGTAA
	reverse-C	CATTCACGCTCTCCACAGTCCC
<i>Bdnf exon I</i>	forward	CATCCGCCTTTCAAGAGATTATTT
	reverse	TTGAGAACTGAAGCCGCAAGCT
<i>Bdnf exon II</i>	forward	AGCTTGCGGCTTCAGTTCTCAA
	reverse	ATGAGAGTTAACAGCCTCTGTG
<i>Bdnf exon III</i>	forward	AAGGCGAAGGGTTTCTTACCT
	reverse	TACGCAAACGCCCTCATTCT
<i>Bdnf exon IV</i>	forward	AGGTCCTTTCTAGATCGAAGAGC
	reverse	GCTTATCTCCAATCCCTCCATC
<i>Bdnf exon V</i>	forward	GATGGAGGGATTGGAGATAAGC
	reverse	CAAAGCTCCTGGCCTGAACAAA
<i>Bdnf exon VI</i>	forward	CCACACAAAGGGAGCGTAG
	reverse	CACGCTTGGAATTGCATCAG
<i>Bdnf exon IX</i>	forward	CGGGCTTGGAGAAGGAAAC
	reverse	TACCTCAGGGTCCACACAAA
<i>Hdac1</i>	forward	CCGCATGACTCACAATTTGCTGCT
	reverse	TCTGGGCGAATAGAACGAAGGAAT
<i>Hdac 2</i>	forward	TGCCAAGAAGTCAGAAGCATCAGG
	reverse	ACGGTCATCACGCGATCTGTTGTA
<i>Hdac 3</i>	forward	TCTCTGCAAGGAGCAACACAGCTA
	reverse	ATAGCAGAAGCCAGAGGCCTCAAA
<i>Mll</i>	forward	CGAGGAAAGAGATCAGCAGAAG
	reverse	AGTCCGCGTGAAGTTGTAATAG
<i>Lsd1</i>	forward	TCAGTTTGTGCCACCTCTTC
	reverse	GAACACACGGTCAAAGCATAAC
<i>Setd7</i>	forward	CAAGGTAGCAGTTGGACCTAATA
	reverse	GGGAGAGAGTGTTCCCATTTAG
<i>G9a</i>	forward	ACAACGCACGCCACTAAT
	reverse	CATCCTCTTCCTTGCTGTAGAC
<i>Ezh1</i>	forward	CTTGTAGGAGCACTGGGATAAC
	reverse	GAGATGGTTCA TGGGTCAAA
<i>Mecp2</i>	forward	GGTTGTCTCCACTGCTACTTAC
	reverse	GCTAACTGGGTGCTGATCT
<i>β-actin</i>	forward	TGTGATGGTGGAATGGGTCAGAA
	reverse	TGTGGTGCCAGATCTTCTCCATGT
<i>Gad2</i>	forward	CTTTGGAGCTCTTCCTGATTGA
	reverse	TTGTTTGAGGGCTGTCTCTG
<i>Gapdh</i>	forward	ACCAGGGAGGGCTGCAGTCC
	reverse	TCAGTTCGGAGCCCACACGC

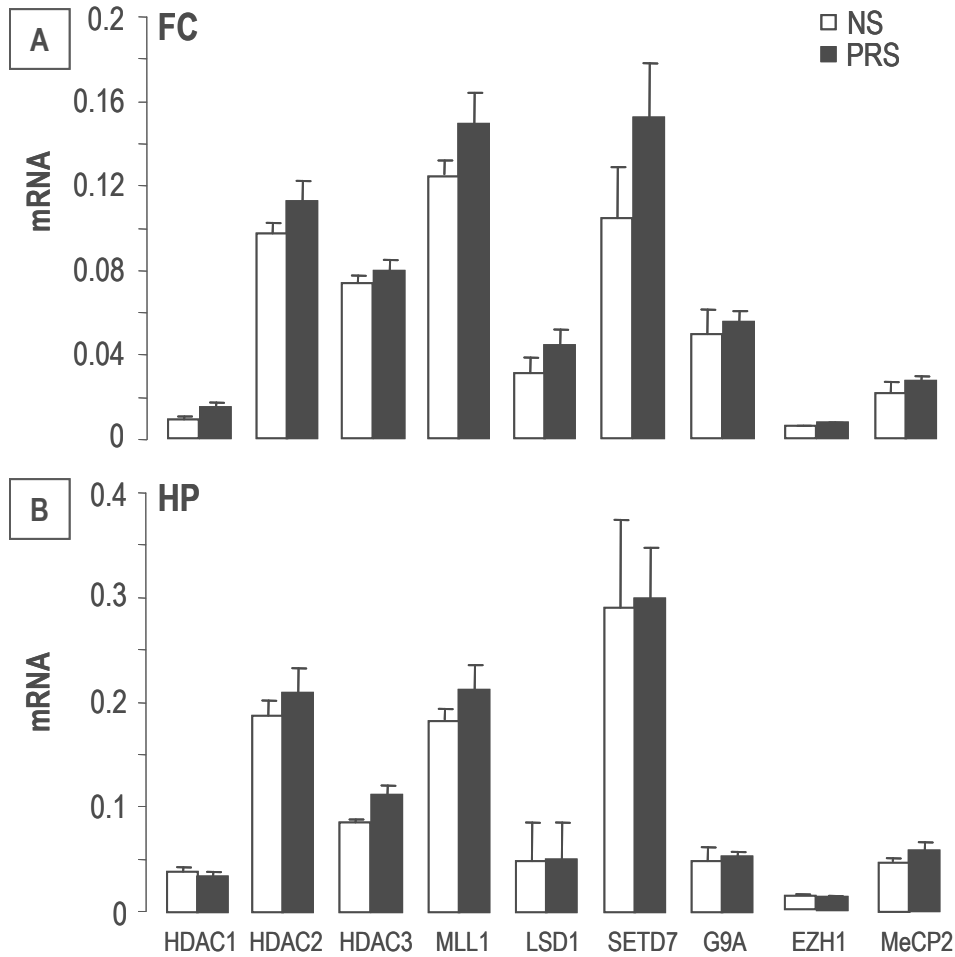


Figure S1. PRS fails to alter the expression of histone acetylating or methylating transcripts and MECP2 both in the FC (A) and HP (B) in adult (PDN 75) offspring. HDAC = histone deacetylase, MLL = Mixed-Lineage, Leukemia; LSD1 = Lysine (K)-specific demethylase 1, SETD7 = SET domain containing (lysine methyltransferase) 7, G9A (EHMT2) = euchromatic histone-lysine N-methyltransferase 2, EZH1 = enhancer of zeste homolog 1, MECP2 = methyl CpG binding protein 2. Data are presented as mean $\pm$ SEM of 10 mice.