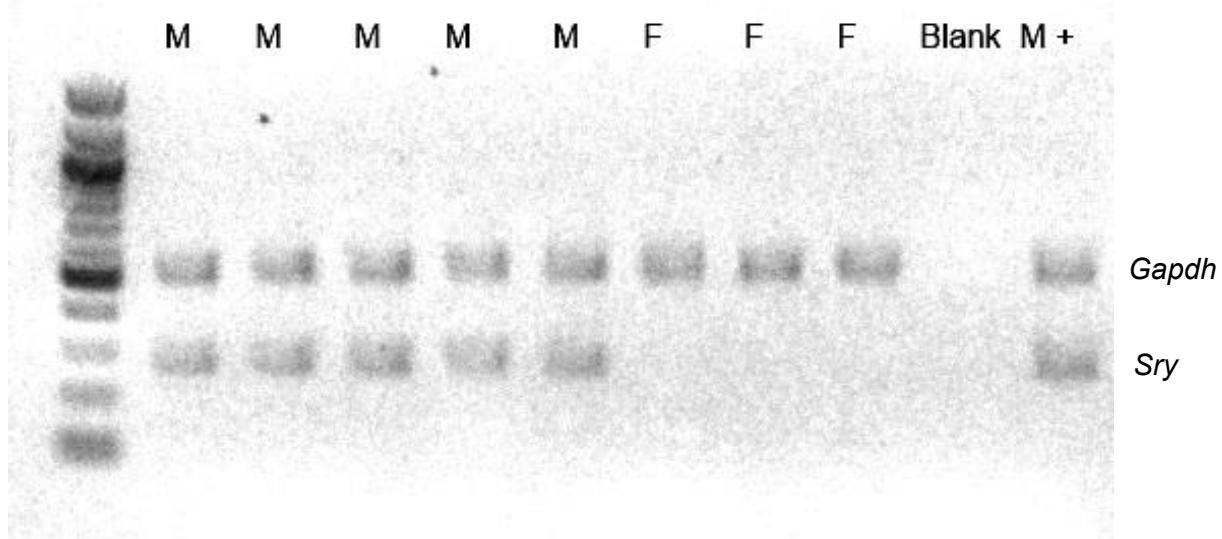
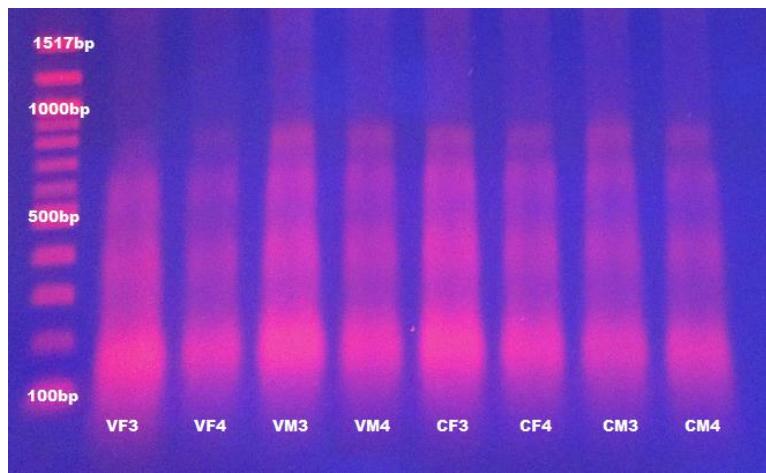


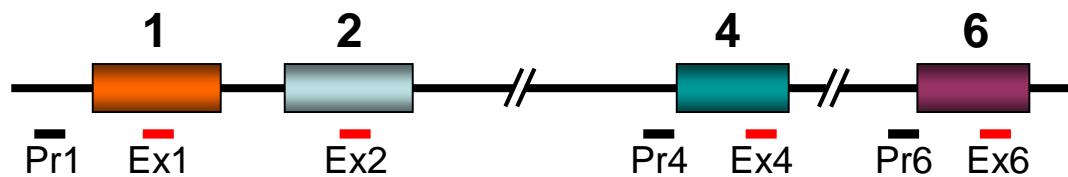
SUPPLEMENTARY MATERIAL
(Konopko *et al.*)



Supplementary Fig. 1. Fetal sex determination. Trunk tissue from each fetus was analyzed by detection of *Sry* RNA by PCR. Primer sequences given in Table S1A. Fetuses expressing *Sry* were designated male; those without, female. Five males and three females are shown on this gel. *Gapdh* was included as a PCR control. Brain tissue from an adult male mouse was used as a positive control (M+)



Supplementary Fig. 2. Chromatin shearing by micrococcal endonuclease. Chromatin was prepared from male and female fetal brains and was treated with micrococcal nuclease as described in Experimental Procedures. A portion of each sample was analyzed by gel electrophoresis prior to ChIP; the gel was stained with ethidium bromide. Figure shows a representative gel analyzing two male and two female fragmented chromatin samples with and without VPA exposure at E12.5. All chromatin samples were consistently reduced to primarily one- (147 bp) and two- (294 bp) nucleosome fragments. The actual chromatin fragments are somewhat larger due to the inclusion of inter-nucleosomal, linker sequences.



Supplementary Fig. 3. Locations of primers used for ChIP determination of histone acetylation and methylation.

Supplementary Table 1. Mouse PCR primers used in this study.

Gene	Forward/reverse Primer Sequence (5' → 3')
A. Sex Determination	
<i>Sry</i>	F - TTG TCT AGA GAG CAT GGA GGG CCA TGT C R - CCA CTC CTC TGT GAC ACT TTA GCC CTC CG
<i>Gapdh</i>	F - TGG CCA AGG TCA TCC ATG AC R - GTC CAC CAC CCT GTT GCT GTA G
B. BDNF exon transcript qRT-PCR primers	
<i>Bdnf</i> Exon 1	F - GAG TCT CCA GGA CAG CAA AG
<i>Bdnf</i> Exon 2	F - GGA TTT GTC CGA GGT GGT AGT A
<i>Bdnf</i> Exon 4	F - CTC TGC CTA GAT CAA ATG GAG CTT C
<i>Bdnf</i> Exon 6	F - ATC CGA GAG CTT TGT GTG G
<i>Bdnf</i> All Exons	R - CTT CAT GCA ACC GAA GTA TGA AAT A
<i>Bdnf</i> Exon 9	F - AAA GTC CCG GTA TCC AAA GGC CAA R - TAG TTC GGC ATT GCG AGT TCC AGT
β -actin	F - GGC TGT ATT CCC CTC CAT CG R - CCA GTT GGT AAC AAT GCC ATG T
C. ChIP qRT-PCR primers (see Fig. S3)	
<i>Bdnf</i> Promoter 1	F - GTC CGC TGG AGA CCC TTA GT R - CTG AGC CAG TTA CGT GAC CA
<i>Bdnf</i> Exon 1	F - GCA ATT GGA CAG TCA TTG GTA ACC R - ACG CAA ACG CCC TCA TTC TG
<i>Bdnf</i> Exon 2	F - GGG CTG GAG AGA GAG TCA GA R - CAG CCT ACA CCG CTA GGA AG
<i>Bdnf</i> Promoter 4	F - CTA TTT CGA GGC AGA GGA GGT A R - ATG GGA AAG TGG GTG GGA
<i>Bdnf</i> Exon 4	F - CCC TCC CCC TTT TAA CTG AA R - CAG CTG CTC TGG GGA AGA C
<i>Bdnf</i> Promoter 6	F - CTT TAA GCA GCC ACC CCA AT R - CTC TTC GGT TGA GCT TCG AT
<i>Bdnf</i> Exon 6	F - CTT GGG GCA GAC GAG AAA GC R - GGC AGT GGA GTC ACA TTG TTG TC
D. Methylation (bisulfite converted) PCR primers (forward/reverse M13 tags italicized)	
<i>Bdnf</i> Promoter 1	F - <i>GTA AAA CGA CGG CCA GTG ATT TAY</i> GTA GTT GTT TTT TAG AAT AAG TTA TTT T R - CAG GAA ACA <i>GCT ATGAC</i> CAA TAA CTA TCC AAT TAC CCT ACT ATA TAA
<i>Bdnf</i> Exon 1	F - <i>GTA AAA CGA CGG CCA GTG GTT GGT</i> GTA GAA AAG TAA TAA GTT TTT TAG R - CAG GAA ACA <i>GCT ATGAC</i> CTT AAC GAC TAC AAA AAA CAA AAC AAC TAA
<i>Bdnf</i> Promoter 4	F - <i>GTA AAA CGA CGG CCA GTG TTG TTT AGA</i> TAA TGA TAG GTT TGG TTT T R - CAG GAA ACA <i>GCT ATGAC</i> AAT CTA AAC AAA AAC TAA AAA ATT TCA TAC TAA
<i>Bdnf</i> Exon 4	F - <i>GTA AAA CGA CGG CCA GTG GAG TTT TTT YGT</i> GGA TTT TTA TTT ATT TTT TT R - CAG GAA ACA <i>GCT ATGAC</i> CTA AAA AAA ACC RAT CCC CAA AAT TC
<i>Bdnf</i> Promoter 6	F - <i>GTA AAA CGA CGG CCA GTG ATT ATT TTT TTT AGT</i> AAA GGG TAT TTT G R - CAG GAA ACA <i>GCT ATGAC</i> CA CTA AAA TCA AAC ATT ATT TAA CTC TTC
<i>Bdnf</i> Exon 6	F - <i>GTA AAA CGA CGG CCA GTG TYG TTT TTT TTA AGT AGT TAT TTT AAT GGT AT</i> R - CAG GAA ACA <i>GCT ATGAC</i> CTA CCC CAA AAC AAT AAC AAT TAA AAA

Supplementary Table 2

	Sex		Treat		SxT		Treat w/in	
	F	P	F	P	F	P	M	F
<i>Bdnf9</i>	0.149	0.709	128.04	<0.001	2.07	0.188	<0.001	<0.001
<i>Bdnf1</i>	0.661	0.426	44.03	<0.001	6.61	0.018	0.010	<0.001
<i>Bdnf4</i>	10.367	0.004	28.97	<0.001	10.68	0.004	<0.001	0.151
<i>Bdnf6</i>	0.104	0.750	362.23	<0.001	1.69	0.209	<0.001	<0.001

Statistics for Figure 1: F and P values for Two-Way ANOVA. Sources of variation: Sex = Difference between Male & Female. Treat = Difference between Control & VPA. SxT = Interaction between Sex & Treatment groups. Final 2 columns are P values of effect of treatment within males (M) and Females (F).

Supplementary Table 3

	H3K9/14Ac								H4Ac								H3K27ac							
	Sex		Treat		SxT		Treat w/in		Sex		Treat		SxT		Treat w/in		Sex		Treat		SxT		Treat w/in	
	F	P	F	P	F	P	M	F	F	P	F	P	F	P	M	F	F	P	F	P	F	P	M	F
Pr1	0.25	0.629	18.44	0.003	0.23	0.646	0.027	0.010	0.01	0.919	35.64	<0.001	0.05	0.829	0.003	0.004	0.63	0.449	52.42	<0.001	0.14	0.719	<0.001	0.001
Ex1	1.56	0.247	35.56	<0.001	1.45	0.263	0.010	0.001	0.07	0.798	46.34	<0.001	0.06	0.810	0.001	0.002	1.09	0.327	59.60	<0.001	0.16	0.698	<0.001	0.001
Pr4	0.08	0.395	45.55	<0.001	0.72	0.421	0.003	<0.001	0.36	0.567	91.53	<0.001	0.46	0.515	<0.001	<0.001	0.70	0.428	95.03	<0.001	0.02	0.900	<0.001	<0.001
Ex4	2.71	0.138	73.30	<0.001	2.31	0.167	0.001	<0.001	0.44	0.528	114.89	<0.001	0.49	0.503	<0.001	<0.001	0.01	0.910	131.30	<0.001	0.38	0.557	<0.001	<0.001
Pr6	8.70	0.018	52.34	<0.001	5.67	0.044	0.009	<0.001	5.31	0.050	93.46	<0.001	2.03	0.192	<0.001	<0.001	0.03	0.574	81.16	<0.001	1.51	0.254	<0.001	<0.001
Ex6	5.94	0.041	50.02	<0.001	4.31	0.071	0.008	<0.001	3.41	0.102	151.82	<0.001	1.87	0.209	<0.001	<0.001	1.67	0.232	190.68	<0.001	6.60	0.033	<0.001	<0.001
Ex2	0.66	0.441	20.83	0.002	0.08	0.784	0.017	0.009	0.01	0.931	53.30	<0.001	0.04	0.845	0.001	<0.001	0.60	0.461	55.46	<0.001	0.02	0.883	0.001	<0.001

Statistics for Figure 2. Sources of variation: Sex = Difference between Male & Female. Treat = Difference between Control & VPA. SxT = Interaction between Sex & Treatment groups. Final 2 columns within each modification are P values for effect of treatment within males (M) and Females (F).

Supplementary Table 4

	H3K27me3						H3K4me3							
	Sex		Treat		SxT		Sex		Treat		SxT		Treat w/in	
	F	P	F	P	F	P	F	P	F	P	F	P	M	F
Pr1	0.595	0.463	0.167	0.693	0.491	0.503	1.788	0.196	23.74	<0.001	5.31	0.032	0.085	<0.001
Ex1	1.044	0.337	0.404	0.543	2.317	0.166	1.152	0.296	29.26	<0.001	2.57	0.125	0.014	<0.001
Pr4	3.057	0.119	0.089	0.773	0.961	0.356	2.045	0.168	39.90	<0.001	6.98	0.016	0.017	<0.001
Ex4	1.588	0.243	0.853	0.383	2.777	0.134	2.511	0.129	43.77	<0.001	5.31	0.032	0.007	<0.001
Pr6	0.496	0.501	0.086	0.777	2.209	0.175	2.318	0.144	2.993	0.099	5.18	0.034	0.703	0.010
Ex6	0.428	0.531	0.837	0.387	2.492	0.153	1.743	0.202	8.70	0.008	5.88	0.025	0.714	0.001
Ex2	1.451	0.263	0.134	0.724	0.913	0.367	1.527	0.231	39.05	<0.001	2.93	0.102	0.005	<0.001

Statistics for Figure 4. Sources of variation: Sex = Difference between Male & Female. Treat = Difference between Control & VPA. SxT = Interaction between Sex & Treatment groups. Final 2 columns within each modification are P values of effect of treatment within males (M) and Females (F).