



Figure 4. Boxplot of pyrosequencing data obtained from the cerebral cortex (CTX), hippocampus (HIP) and hypothalamus (HYP) brDMRs. We assessed and validated percent DNA methylation of five unique DMRs from each pair of brain tissues compared by CHARM. For each brDMR, the number of CpGs assayed varied from 4 to 16 CpGs, thus a small subset of the region assayed by the CHARM array. Average percent methylation was determined from all of the assayed CpGs for each brDMR in each brain tissue type and displayed as a boxplot. Stippled horizontal lines represent the percent DNAm predicted by CHARM for the particular brain tissue for the entire brDMR region. Types of brain tissues being compared and the nearest genes associated with the brDMRs are indicated below the X-axis.

Table 6. Differentially methylated regions in the cerebral cortex vs. hypothalamus comparison

Genome Browser Coordinates	Gene Symbol	Distance to Gene	CpG Islands	Higher DNAm	%DNAm Diff.	p-value	FDR
Chr2: 224,889,548–224,894,316	Neurog2	1.4 kb 5'	2	Cortex	19.2	0.0	0.0
Chr14: 100,710,575–100,715,363	<i>Spred2</i>	Inside	1.0 kb	Hypo	24.2	0.0	0.0
Chr6: 130,607,715–130,610,889	<i>Vrk1</i>	358.4 kb 3'	2	Hypo	31.2	0.0	0.0
Chr18: 74,158,499–74,161,968	<i>St8sia5</i>	2.0 kb 5'	0.3 kb	Hypo	26.5	0.0	0.0
Chr17: 17,246,672–17,249,804	<i>Msx2</i>	3' Overlap	2	Cortex	24.6	0.0	0.0
Chr17: 7,137,629–7,140,331	<i>Ptch1</i>	Inside	2	Cortex	26.9	0.0	0.0
Chr1: 23,780,028–23,782,977	<i>Sgk1</i>	270.9 kb 5'	2	Hypo	23.4	0.0	0.0
Chr12: 6,564,480–6,566,824	Rpl35a	7.3 kb 3'	1	Hypo	33.0	0.0	0.0
Chr19: 38,428,535–38,432,257	Zfhx3	2.6 kb 5'	1.9 kb	Cortex	20.7	3.131E-06	0.00267
Chr4: 8,969,556–8,972,220	<i>Lrrc17</i>	Inside	0.3 kb	Hypo	25.1	6.263E-06	0.00400
Chr2: 177,162,376–177,164,873	Fdps	77.9 kb 3'	1	Hypo	26.4	6.263E-06	0.00400
Chr2: 35,033,638–35,035,978	<i>Sgtb</i>	Inside	1	Hypo	28.5	9.394E-06	0.00400
Chr8: 74,211,291–74,213,781	<i>Foxb1</i>	8.4 kb 5'	1	Hypo	19.9	9.394E-06	0.00400
Chr1: 95,646,663–95,648,875	<i>Slc17a7</i>	Inside	0.1 kb	Hypo	29.9	9.394E-06	0.00400
Chr3: 38,867,965–38,870,218	<i>Nr4a2</i>	Inside	4	Cortex	31.7	9.394E-06	0.00400
Chr10: 31,085,071–31,088,230	<i>Thg1l</i>	0.7 kb 3'	2	Hypo	25.6	9.394E-06	0.00400
Chr1: 232,594,738–232,597,692	<i>RGD1310039</i>	Inside	0.7 kb	Hypo	23.2	9.394E-06	0.00400
Chr2: 83,442,269–83,445,183	<i>Ankrd33b</i>	Inside	0.3 kb	Hypo	20.1	1.253E-05	0.00400
Chr17: 82,655,805–82,658,235	<i>Cugbp2</i>	50.1 kb 5'	10.7 kb	Hypo	24.4	1.253E-05	0.00400
Chr13: 44,182,429–44,185,020	<i>Rassf5</i>	Inside	1.1 kb	Hypo	21.8	1.253E-05	0.00400

Numbers in the CpG Islands column indicate either the number of CpG islands that overlap the DMR, or if zero, the distance to the closest CpG island. Gene names marked in bold indicate genes annotated in the UCSC Genome Browser only for the human and mouse, but presumed to exist in the rat.

-
31. Hansen KD, Timp W, Bravo HC, Sabunciyan S, Langmead B, McDonald OG, et al. Increased methylation variation in epigenetic domains across cancer types. *Nat Genet* 2011; 43:768-75.
 32. Colella S, Shen L, Baggerly KA, Issa JP, Krahe R. Sensitive and quantitative universal Pyrosequencing methylation analysis of CpG sites. *Biotechniques* 2003; 35:146-50.
 33. Aryee MJ, Wu Z, Ladd-Acosta C, Herb B, Feinberg AP, Yegnasubramanian S, et al. Accurate genome-scale percentage DNA methylation estimates from microarray data. *Biostatistics* 2011; 12:197-210.

©2011 Landes Bioscience.
Do not distribute.