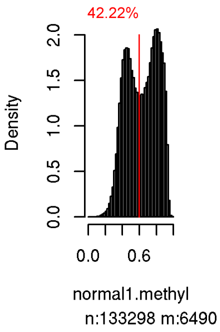
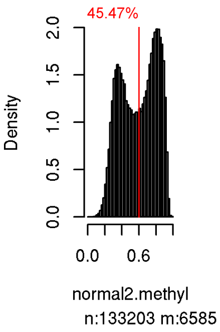
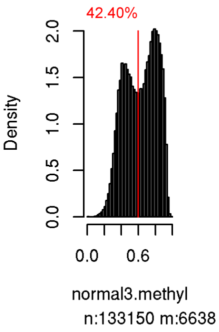
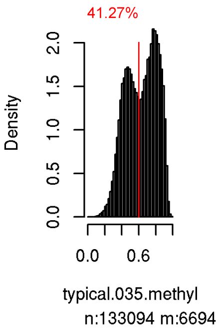
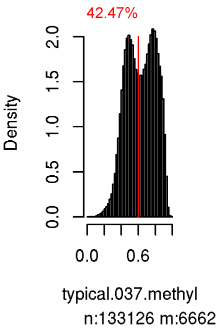
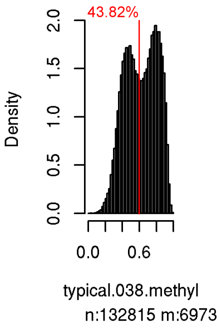

42.22%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
normal1.methyl
n:133298 m:6490

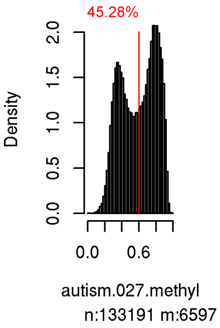

45.47%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
normal2.methyl
n:133203 m:6585

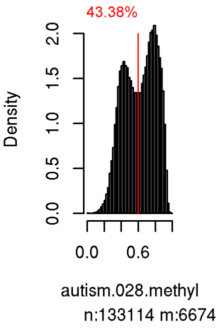

42.40%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
normal3.methyl
n:133150 m:6638

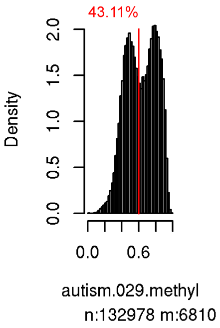

41.27%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
typical.035.methyl
n:133094 m:6694

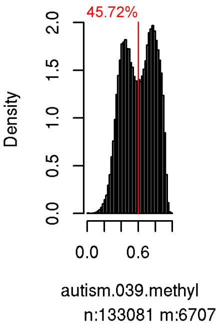

42.47%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
typical.037.methyl
n:133126 m:6662

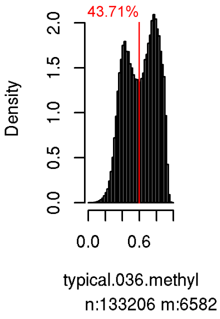

43.82%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
typical.038.methyl
n:132815 m:6973

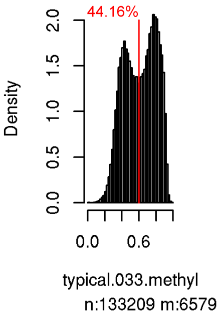

45.28%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
autism.027.methyl
n:133191 m:6597

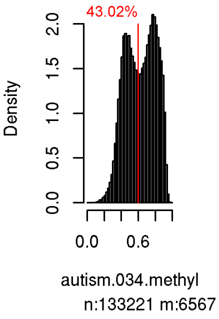

43.38%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
autism.028.methyl
n:133114 m:6674

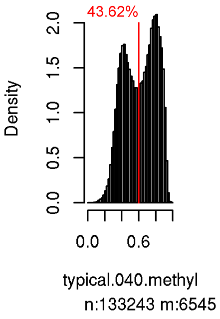

43.11%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
autism.029.methyl
n:132978 m:6810

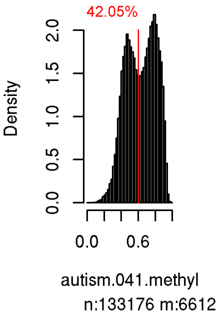

45.72%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
autism.039.methyl
n:133081 m:6707

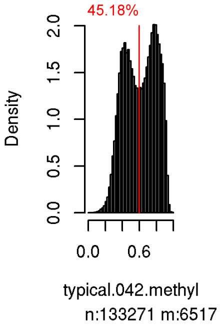

43.71%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
typical.036.methyl
n:133206 m:6582

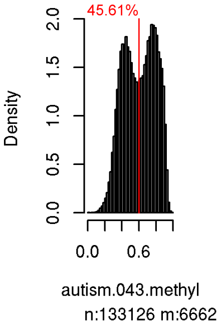

44.16%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
typical.033.methyl
n:133209 m:6579

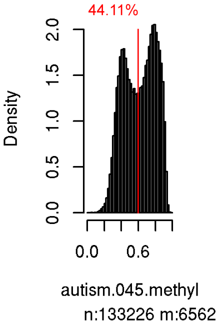

43.02%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
autism.034.methyl
n:133221 m:6567

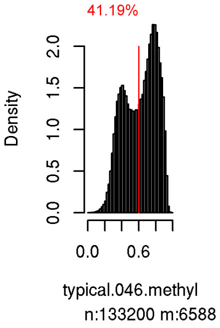

43.62%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
typical.040.methyl
n:133243 m:6545

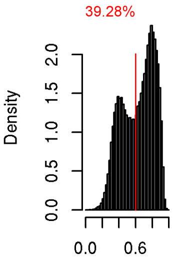

42.05%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
autism.041.methyl
n:133176 m:6612


45.18%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
typical.042.methyl
n:133271 m:6517

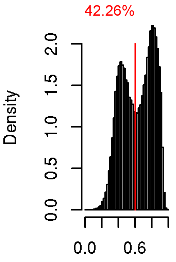

45.61%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
autism.043.methyl
n:133126 m:6662


44.11%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
autism.045.methyl
n:133226 m:6562

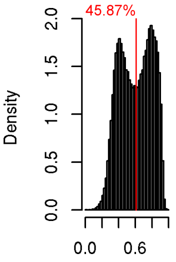

41.19%
Density
2.0
1.5
1.0
0.5
0.0
0.0
0.6
typical.046.methyl
n:133200 m:6588



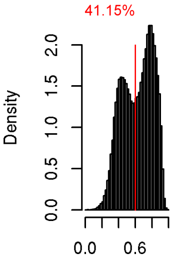
typical.047.methyl
n:133169 m:6619



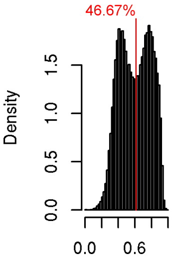
autism.049.methyl
n:133231 m:6557



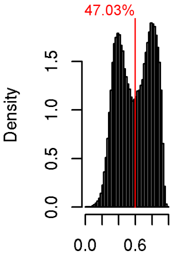
autism.050.methyl
n:133253 m:6535



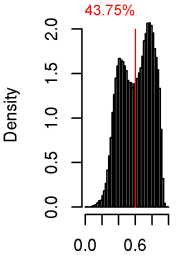
autism.051.methyl
n:133140 m:6648



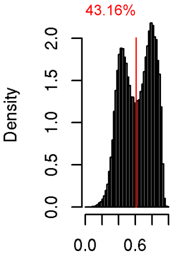
typical.052.methyl
n:133177 m:6611



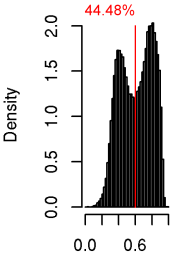
autism.053.methyl
n:133149 m:6639



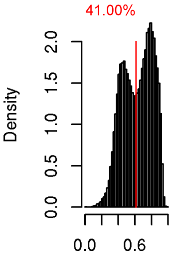
autism.054.methyl
n:133277 m:6511



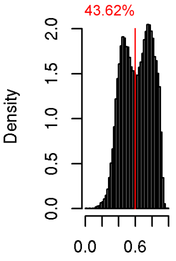
autism.055.methyl
n:133281 m:6507



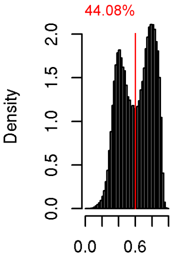
autism.056.methyl
n:133255 m:6533



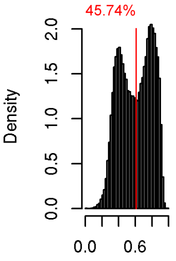
autism.057.methyl
n:133269 m:6519



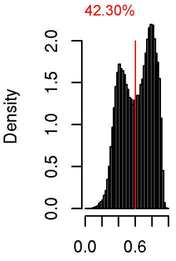
autism.058.methyl
n:133269 m:6519



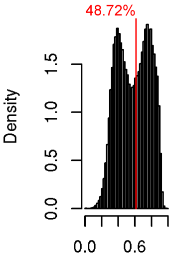
typical.063.methyl
n:133283 m:6505



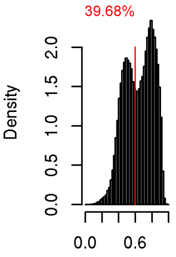
typical.064.methyl
n:133313 m:6475



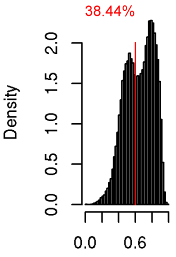
typical.065.methyl
n:133318 m:6470



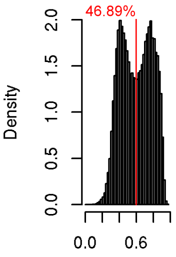
typical.066.methyl
n:133259 m:6529



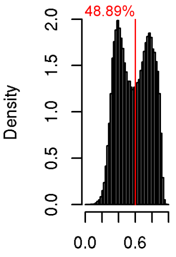
typical.067.methyl
n:133291 m:6497



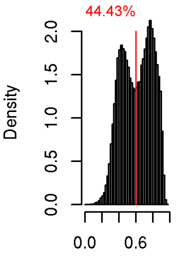
typical.068.methyl
n:132998 m:6790



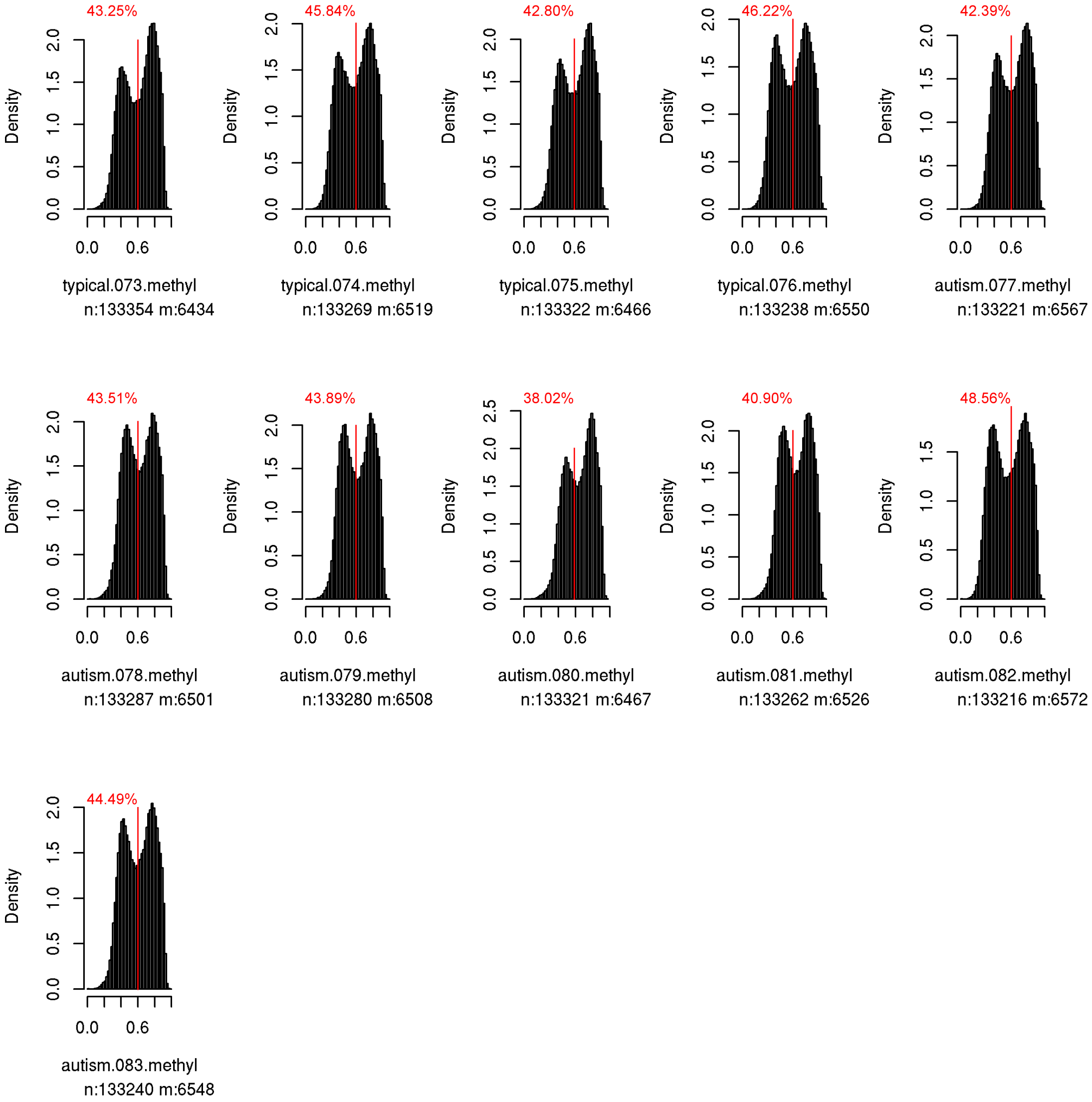
typical.070.methyl
n:133245 m:6543



typical.071.methyl
n:133196 m:6592



typical.072.methyl
n:133252 m:6536



Figures S1: Histograms of average methylation in 20 kb windows for each placenta sample.

Individual histograms (no smoothing) for each MARBLES typical and autism placenta as well as three biological replicates of "normal" non-MARBLES placentas which no known pathologies (Schroeder DI et al., 2013). Methylation data was omitted if a window had fewer than 20 covered CpG sites. Red vertical lines show the arbitrary 60% methylation cutoff between windows with low and high methylation. Percentage of 20 kb windows with average methylation below 60% also shown in red (excluding omitted windows). n=number of windows with required CpG coverage, m=number of windows omitted due to insufficient coverage

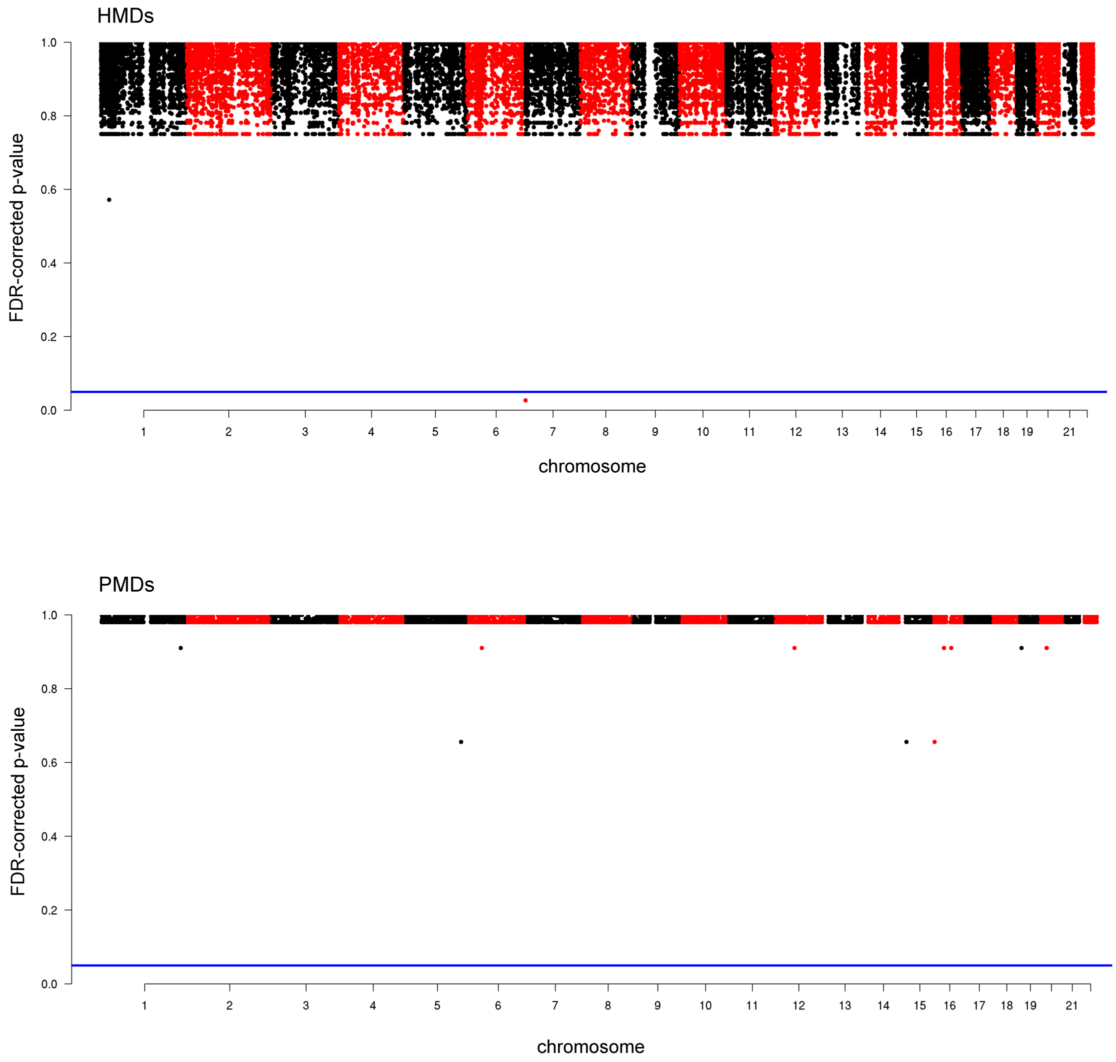


Figure S2: Plots showing location and statistical significance of differential methylation in HMDs and PMDs.

Each point shows the FDR-corrected probability of that HMD/PMD being differentially methylated between autism and typical MARBLES placentas. Chromosomes are alternately colored red and black for clarity. The blue line shows the 0.05 cutoff for statistical significance.

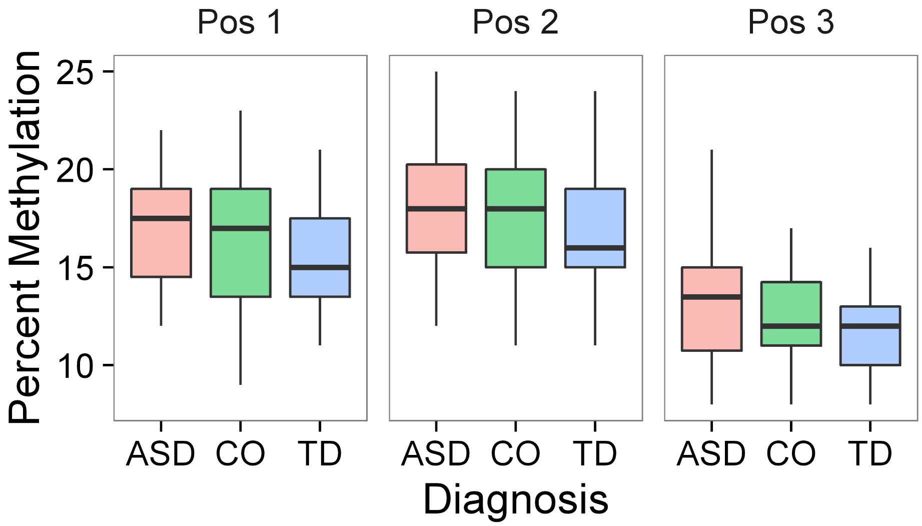


Figure S3: *DLL1* Pyrosequencing results by individual CpG position. Three CpG sites corresponding to the H3K27ac/H3K4me1 peaks were assayed by pyrosequencing on the same samples analyzed by MethylC-seq (region shown by grey bar in Figure 4A within circled HMD).