Figure S4

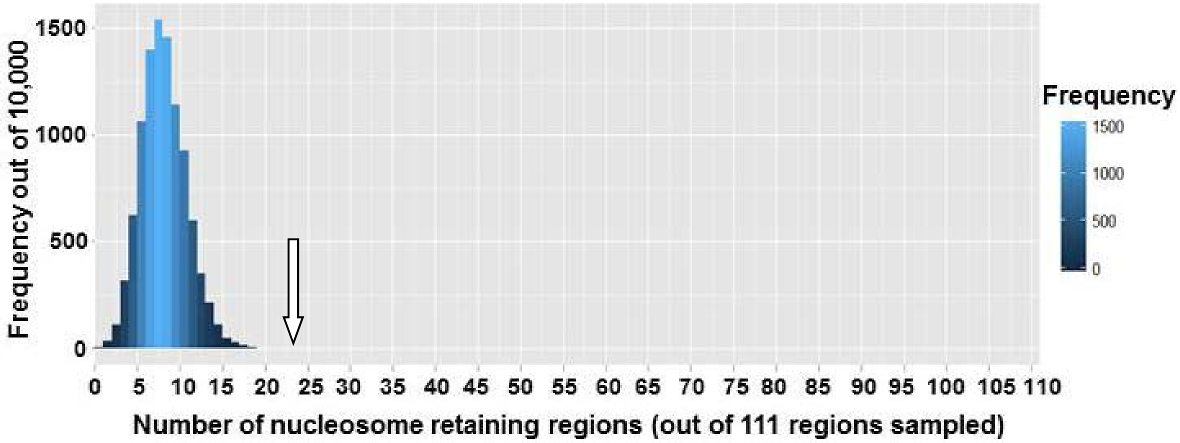

Fig.S4 Bootstrap resampling analysis demonstrates significant enrichment of nucleosome containing regions among hypomethylated DMRs.

111 regions were sampled randomly from all background regions captured by MeDIP-seq and intersected with nucleosome bound regions in sperm (*27*). This process was repeated 10,000 times and the number of intersected regions recorded for each iteration. The above histogram gives the frequency of these intersections. The data are normally distributed, with mean=7.61, median=7 and standard deviation=2.65. Assuming a normal distribution, a p-value of 0.0001 would give a boundary equivalent to a z-statistic score of 3.89 * standard deviations away from the mean:

Mean + (3.89 x standard deviation) = 7.61 + (3.89 x 2.65) = 17.92

23/111 of our hypomethylated DMRs are nucleosome bound regions (white arrow), thus hypomethylated DMRs are significantly enriched in nucleosome occupied regions with p-value < 0.0001.