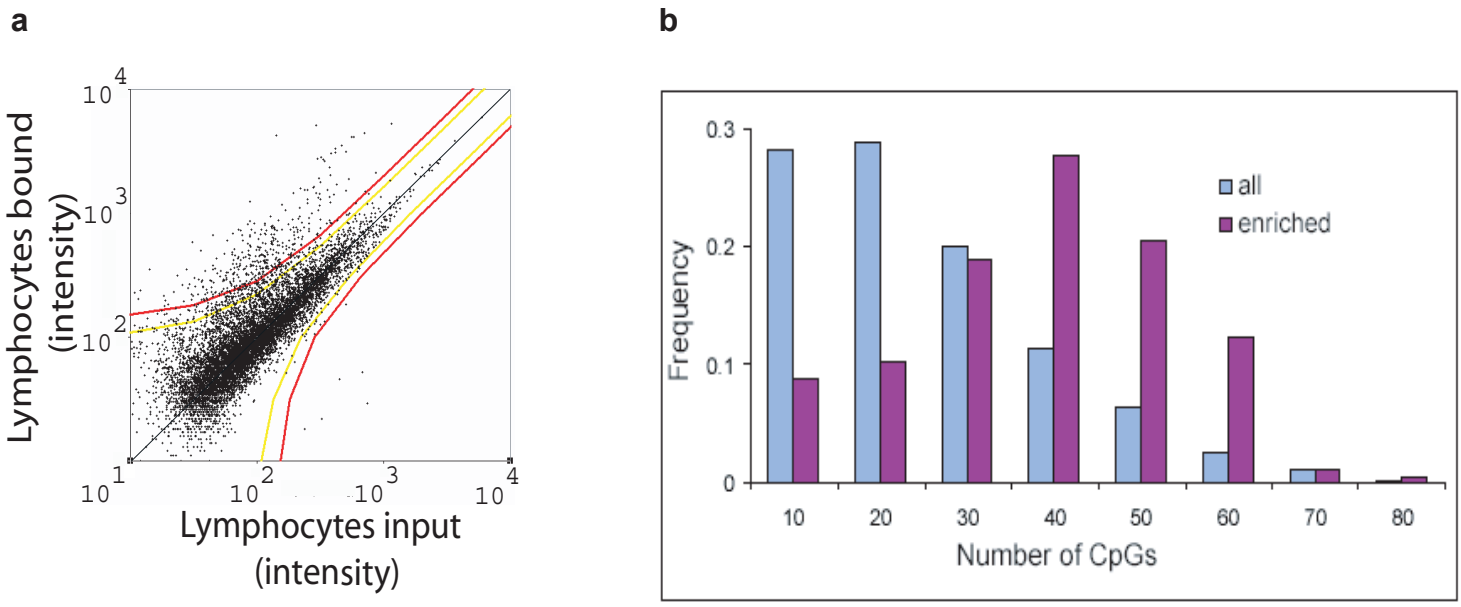

Supplementary Figure 1. Sensitivity of micro-array mDIP for detecting DNA methylation.
a. Lymphoblast DNA was subject to mDIP. Input and bound fractions were labeled by random priming using cy-3 and cy-5, respectively, mixed in equal quantities and hybridized to a microarray chip containing ~10,000 human promoter fragments. The Intensities of cy-3 and cy-5 for each spot is displayed as a scatter plot. Boundary lines indicate confidence limits of $p<0.01$ (yellow) or $p<0.001$ (red). 229 gene promoters were enriched in the bound fraction and therefore deemed methylated ($p<0.001$). b. The number of CpG residues located outside CpG islands on each 1 kb promoter was determined for all genes on the micro-array and this was used to determine the distribution of CpG in the total promoter population and the enriched (methylated) population of genes. Note that in non-CpG island regions having less than 30 CpG, enrichment is very poor, whereas non-CpG island DNA with >30 CpG residues methylated DNA is enriched. These results suggest that a minimal density (~30/1000 = 3%) of methylated CpG residues is necessary in order to be efficiently precipitated by the antibody.