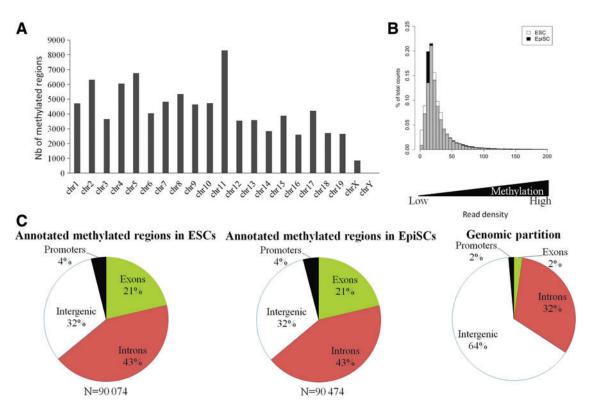
Supplementary Data



SUPPLEMENTARY FIG. S1. Global view of MethylCap-sequencing results. (A) Number of methylated regions on each chromosome. The lower number of regions on chromosome X reflects the fact that all cell lines besides EpiSC2 are male. (B) Distribution of read density for ESCs and EpiSCs. (C) Genomic distribution of methylated regions in ESCs and in EpiSCs (read density >0), compared to the genomic distribution.