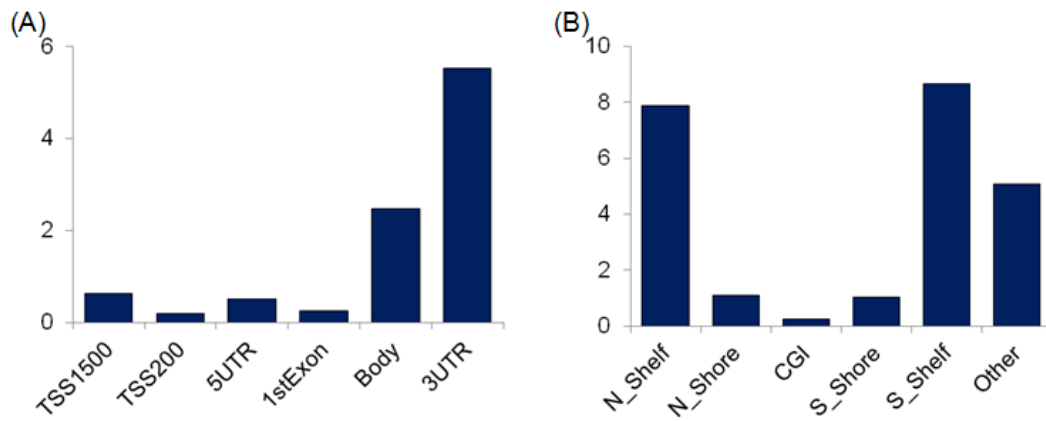


SUPPLEMENTARY INFORMATION

DNA Methylation Profiles of Blood Cells Are Distinct between Early-Onset Obese and Control Individuals

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Supplementary Fig. 1. Hyper-vs.-hypomethylated CpGs ratio with respect to nearby genes and CGIs. (A) The hyper-vs.-hypo-methylated CpGs are shown for six gene-based CpG categories. (B) Similarly shown for CGI-based CpG categories. The y-axis is calculated as the number of the hypermethylated CpGs divided by the number of hypomethylated CpGs. TSS1500, 1,500 bp regions upstream of the transcription start site; TSS200, 200 bp regions upstream of the transcription start site; UTR, untranslated region; CGI, CpG island.