Figure S3  Prominent variables detected by principal components analysis. The first two principal components for the M-values of the 290,577 CpG sites after quantile normalization are plotted, colored by bisulfite conversion batch (A) and array hybridization batch (B). The array hybridization batch appears to be the prominent variable. (C) The M-values of the 290,577 CpG sites were quantile normalized and adjusted for batch effects using COMBAT. Gender is the prominent variable. (D) The M-values of the 283,540 autosomal CpG sites after quantile normalization and batch correction. Population identity is the prominent variable.