Figure S5  The 118 unrelated samples (60 CEU + 58 YRI) and 16,651 CpG sites that overlapped between this study and GSE27146 (FRASER et al. 2012) were re-processed by the same procedure. Each dataset was then re-analyzed with the linear model: cytosine modification level ~ population + gender + error. The regression coefficients of the two datasets are shown as scatter plot. The x-axis: data from FRASER et al. 2012, y-axis: data from this study.