

**Supplementary Figure 4.** Histograms of  $d_i$ 's and the posterior mean differential methylation between two groups (see Methods), obtained by ABBA using data from  $d_i$ 's from a contiguous 45,300 CpG stretch of the genome (red) and the corresponding  $d_i$ 's which were obtained by ABBA using the same stretch broken down into smaller chunks (blue).

### Whole data vs chunked data analysis

