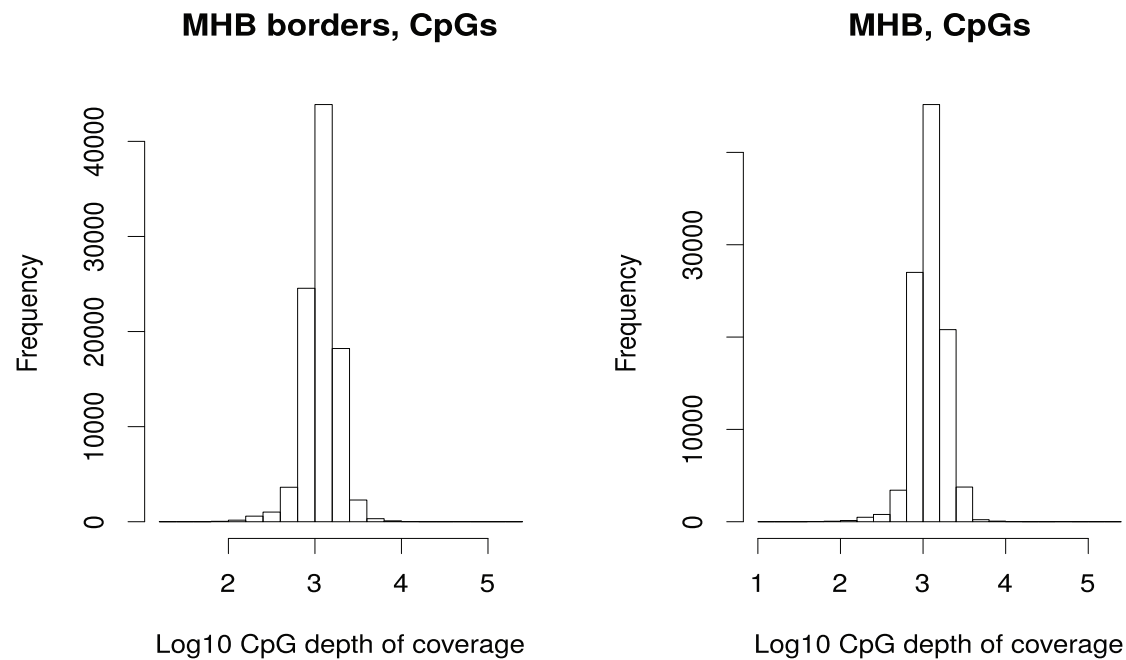


OFR-Figure 1 (Only for Reviewer)

Distribution of sequencing coverage in MHB borders and MHB regions



To show that our MHB boundaries were not defined by lack of coverage, we calculated the total depth of coverage for CpGs which are within a MHB and for CpGs within 100 bp of a MHB. Both sets of CpGs have very high depth of coverages. In fact, we intentionally avoided calling MHBs in regions with low mappability by pre-defining genomic windows with minimum 10 depth of coverage.