Figure S3. Selective amplification of the CGCGCGG sequence.

For each type of sequence, the amplification efficiency is calculated as the average number of mapped reads in the FMG for all of this sequence in the human genome. The amplification efficiency of the CGCGCGG sequence is set as 100%, and the efficiencies of the TG-CG-chimeric sequences, as modeling the partially methylated CGCGCGG sequences, are shown as relative values to the CGCGCGG sequence. Note that the amplification efficiency of the CGCGCGG sequence is about 50-fold higher than the one-TG-chimeric sequences (TGTGCGG, CGTGTGG and TGCGTGG), and 5000-fold higher than the two-TG-chimeric sequences (TGTGCGG, CGTGTGG and TGCGTGG), and 200,000-fold higher than the TGTGTGG sequence.