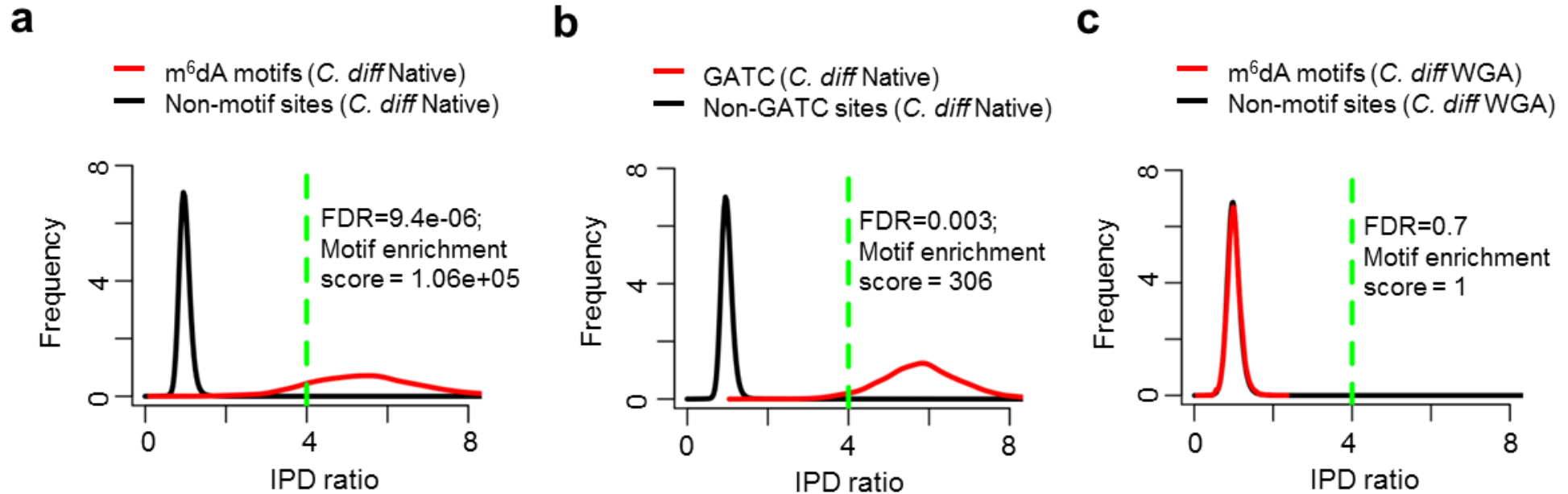


Non-m⁶dA motif sites work well as faux-WGA for motif calling



Supplemental Fig S2. SMRT-seq data from native DNA can be used for reliable motif calling, as illustrated using a *C. diff* methylome. (a) The IPD ratio distribution of all *C. diff* m⁶dA motifs (CAAAAA, GATC, GCMGAAG, GAANNNNNNCTG, and CAGNNNNNNNTTC) were compared with that of all non-motif sites in the same native sample, giving a significant methylation enrichment score of 1.06e+05 (IPD ratio>4), highly consistent with the methylation enrichment score calculated using both native and WGA data (Fig. 2d). (b) GATC motif sites were compared with all the remaining sites (including other m⁶dA sites) in the same native sample, also giving a significant enrichment score of 306. (c) As a negative control, the IPD ratio distribution of all *C. diff* m⁶dA motifs is compared with that of all non-motif sites in the same WGA sample, giving an insignificant enrichment score of 1.