



Supplemental Fig S1. False positive m⁶dA calls before and after correction for multiple hypothesis testing. The analysis was conducted on a well characterized native *Clostridium difficile* (*C. diff*) methylome (right) and its WGA sample (left; negative control without methylation). Red dots: known m⁶dA sites (CAAAAA); black dots: non-methylated adenine sites. At $p < 0.01$ (student's t -test, unadjusted), 10,870 sites are called as false positive m⁶dA even from the WGA sample. In the native sample, 11,942 of 12,195 (97.9%) true m⁶dA sites remain significant after Bonferroni correction (corrected $p < 0.01$). In contrast, none of the 10,870 false positive calls in WGA survives the Bonferroni correction.