



Figure 1- figure supplement 1. Genome-wide cytosine methylation in Wild-type and  $\Delta hp1$ . (A) Cytosine methylation was calculated using weighted methylation (see methods) in the CG, CHG and CHH sequence context in both wild-type (WT) and  $\Delta hp1$ . Methylation levels were determined to be significantly higher in WT using the Mann-Whitney U-test. The symbol (\*\*\*) indicates  $p < 2.2e-16$ . (B) Similar to (A), but the genome-wide methylation level was calculated using fractional methylation. All data were summarized in 10 kb bins.