



Figure 1- figure supplement 2. Cytosine methylation for functional elements in Wild-type and Dhp1. Cytosine methylation was calculated using weighted methylation (see methods) in the CG, CHG and CHH sequence context in both wild-type (JR2) and Dhp1. DNA methylation was summarized over genes, promoters and TEs as labeled. The individual elements are shown as colored points, along with a violin plot showing the distribution and median as a black line. Methylation levels were determined to be significantly higher in WT, Mann-Whitney U-test with Holm multiple testing correction. Associated p-values are shown.