



Figure 4. HSVd infection affects the methylation patterns of rRNA genes and TE in pollen grains. (A) Diagram showing the relative (HSVd/Mock) total rDNA methylation levels. Total methylation (paired t-test values) means 0.40 (mock) and 0.37 (HSVd). (B) Analysis of symmetric and asymmetric cytosine methylation levels in analysed rDNA. Symmetric methylation (paired t-test values) means 0.89 (mock) and 0.83 (HSVd). Asymmetric methylation means 0.06 (mock) and 0.05 (HSVd). (C) Position-specific relative methylation levels in CG and CHG context in the analysed rDNA. (D) Relative (HSVd/Mock) total TE methylation. Total methylation (paired t-test values) means 0.055 (mock) and 0.022 (HSVd). (E) Analysis of symmetric and asymmetric cytosine methylation in analysed TE. Symmetric methylation (paired t-test values) means 0.084 (mock) and 0.041 (HSVd). Asymmetric methylation means 0.037 (mock) and 0.018 (HSVd). (F) Position-specific relative methylation levels in CG and CHG context in the analyzed TE. P values are shown in all figure panels.