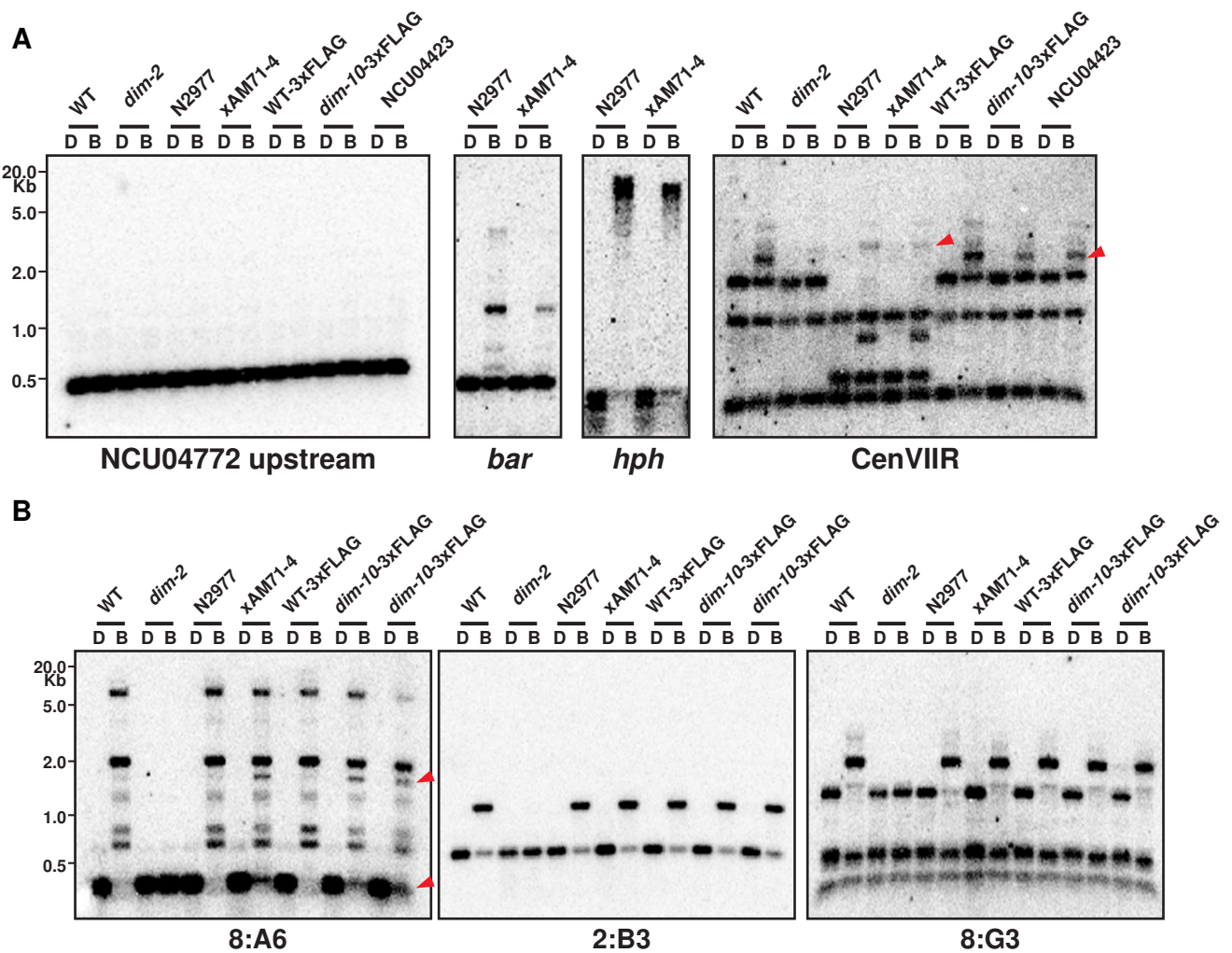

Supplemental Figure 7: Cytosine methylation of strains encoding mutant a dim-10 gene is reduced and not aberrantly localized. (A) Southern hybridizations, as in Figure 6B, of genomic DNA from the indicated control or dim-10 strains digested with either the 5mC-resistant restriction enzyme DpnII ("D") and its 5mC-sensitive isoschizomer BfuCI ("B") and re-probed for a intergenic region (NCU04771 upstream, left) that has little to no cytosine methylation in a wildtype strain but gains cytosine methylation in a genetic background exhibiting nucleosome disorder (a dim-1 strain) (Klocko et al. 2019), the bar (***bi****a*laphos ***r***esistance, conferring resistance to basta; middle) or hph (***h***ygromycin ***ph***osphotransferase, conferring resistance to hygromycin; right) antibiotic genes, which are flanked by RIP'd A:T-rich repetitive sequences in strains used as the parent for (N2977), or derived from (xAM71-4), our dim mutant selection, or CenVIIR, a region of the centromere on Linkage Group VII that exhibits cytosine methylation (Honda et al. 2012). Red arrowheads highlight bands that subtly lose cytosine methylation. **(B)** Southern hybridizations of genomic DNA from the indicated control or dim-10 strains digested with either the 5mC-resistant restriction enzyme DpnII ("D") and its 5mC-sensitive isoschizomer BfuCI ("B") and probed for the interspersed cytosine methylated regions 8:A6 (as in Figure 6B), 2:B3, or 8:G3 (Selker et al. 2003). Red arrowheads highlight bands that subtly lose cytosine methylation.