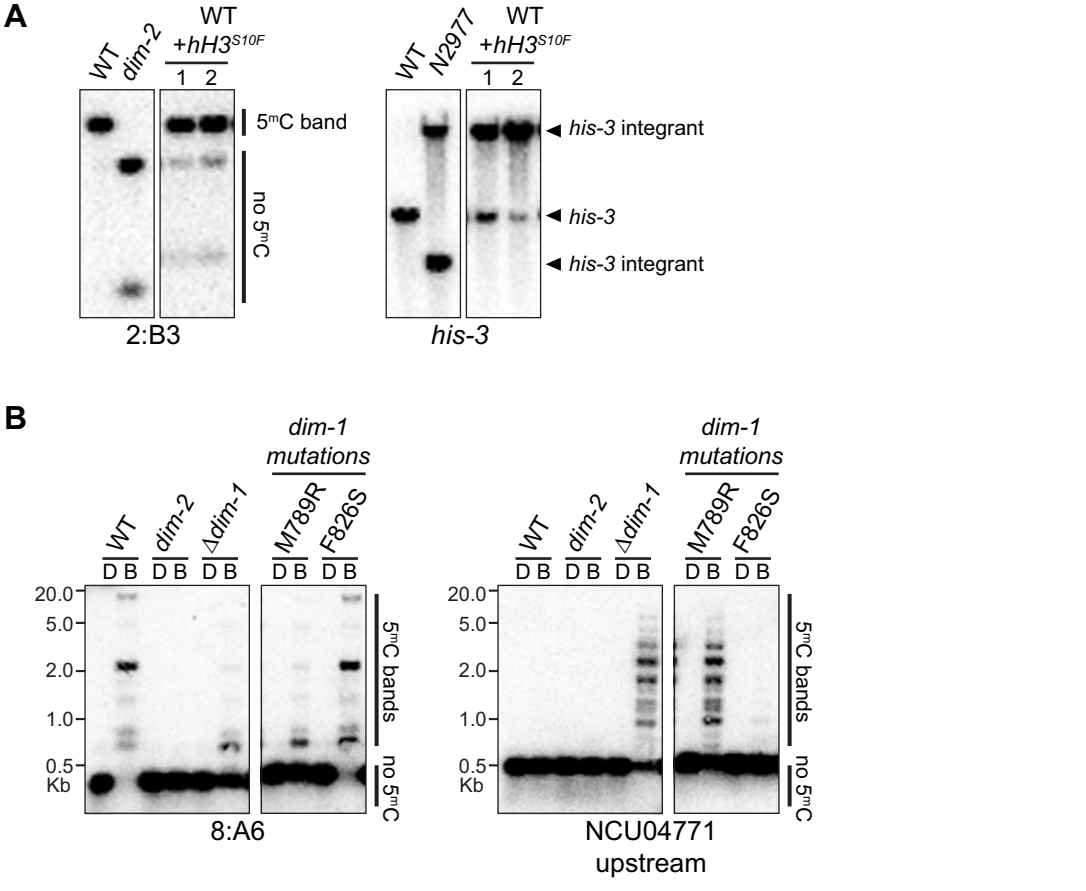

Supplemental Figure 5: Partial dominance of a histone H3 allele and aberrant cytosine methylation in *dim-1* alleles. (A) Southern hybridizations of genomic DNA from the indicated wildtype strains, in which a mutant histone H3 (hH3S10F) allele isolated from our *dim* mutant selection has been integrated at the *his-3* locus, digested with either the 5mC-sensitive AvaII and probed for a constitutive heterochromatin region (2:B3, left) (Selker et al. 2003) or the enzyme NdeI and probed for the his-3 locus (*his-3*, right) to examine construct integration. Two independent colonies ("1" and "2") are displayed; six independent colonies were examined in total. **(B)** Southern hybridizations of genomic DNA from the indicated *dim-1* isolated allele strains or control strains digested with either the 5mC-resistant restriction enzyme DpnII (D) or its 5mC-sensitive isoschizomer BfuCI (B) and probed for a constitutive heterochromatin region (8:A6, left) (Selker et al. 2003) or an intergenic region (NCU04771 upstream, right). The control strains and *dim-1* mutant experimental strains were analyzed on the same blot; both control images are also presented in (Klocko et al. 2019).