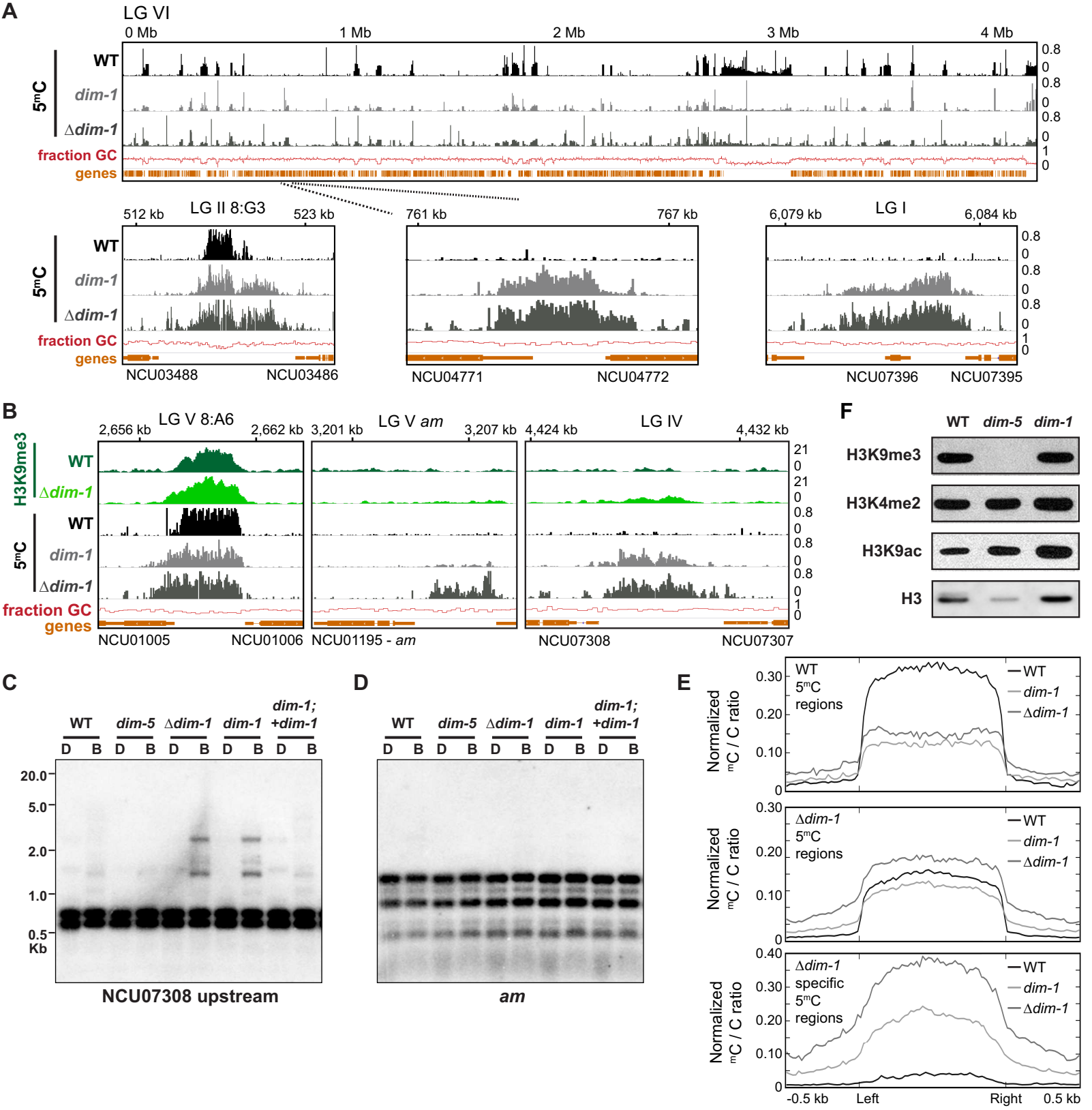

Figure S3: A* dim-1 *deletion strain phenocopies a UV-generated* dim-1 *strain and a wildtype copy of* dim-1 *complements the defect. A. Tracks of BS-seq show cytosine methylation (black / gray) for WT, *dim-1*, and Δ*dim-1* strains. The G:C content ("fraction GC") is shown as in Figure 2A. Name, chromosome, and position of expanded regions are listed. B. Tracks of ChIP-seq (green) for H3K9me3, BS-seq for cytosine methylation (black / gray) for WT, *dim-1*, and Δ*dim-1* strains, or G:C content ("fraction GC") for specific regions. Name, chromosome, and position of these expanded regions are listed. C-D. Southern blots of genomic DNA digested with either DpnII (D) or its 5^{m}C-sensitive isoschizomer BfuCI (B) from the indicated strains and probed for the labeled regions, as in Figures 1A, 2B. The *am* gene is not methylated and therefore shows complete BfuCI digestion. E. Average enrichment profiles of BS-seq data for WT or *dim-1* strains showing the ratio of methylated to unmethylated cytosines across 5^{m}C-marked constitutive heterochromatic regions defined in a Δ*dim-1* strain (n = 557), which include H3K9me3 peaks common in a WT strain and new peaks observed in a Δ*dim-1* strain. F. Western blots on isolated histones for the indicated histone marks or histone H3 from WT, *dim-5*, and *dim-1* strains.