



**Figure S6. AGO4 binding mediates DNA methylation.**

(A-B) AGO4 binding sites are enriched in DNA methylation, especially at CHH sites. The graphs show the average levels of CG (green portion of bars), CHG (red portion of bars), and CHH (purple portion of bars) per kilobase (kb) of the *Arabidopsis* genome overall (left bar) or within AGO4 peaks (right bar). Methylation data is previously published (Lister *et al.*, 2008) for *ros1 dml2 dml3* (A) and *met1* (B) mutant plants. \*\*\* denotes p-value  $\rightarrow 0$ . (C) AGO4 and Pol V are required for CHH DNA methylation on AGO4 binding sites. DNA methylation analysis using *AluI*, *Sau3AI*, *HaeIII* and *DdeI* DNA methylation-sensitive restriction endonucleases. Digested genomic DNA was amplified using PCR. Sequence lacking *Sau3AI* and *DdeI* sites (AT2G36490) or *HaeIII* (AT2G27860) were used as loading controls. More loci and a control for *AluI* are shown in Fig. 4E.