

Figure S1. Identification of AGO4-bound loci.

- (A, C, E) Graphical representation of AGO4-bound loci identified using ChIP-seq. (A) Actin control and loci with the score of AGO4 binding ranking in the top 20%. (C) Loci with the score of AGO4 binding ranking in the middle 60%. (E) Loci with the score of AGO4 binding ranking in the bottom 20%. The genome browser screenshots show from top genome annotation, ChIP-seq sequencing reads from Col-0 wild type, *nrpe1* and *ago4* strains, CHH DNA methylation (Lister *et al.*, 2008) and total small RNA reads (Lister *et al.*, 2008)
- (B, D, F) ChIP-real time PCR validation of Pol V-dependent AGO4 binding to chromatin on AGO4 peaks identified using ChIP-seq. (B) Actin control and loci with the score of AGO4 binding ranking in the top 20%. (D) Loci with the score of AGO4 binding ranking in the middle 60%. (F) Loci with the score of AGO4 binding ranking in the bottom 20%. Bars represent averages from three independent amplifications. Error bars represent standard deviations.