



Supplemental Figure 5. Supplementary information on Class II genes. **A.** Representative views of genes that gain H3K9m2 in *met1* and are H3K27m3-marked in wild-type; however, these genes were not recovered among Class II genes due to their low levels of H3K27m3 in wild-type. This shows that the number of true Class II genes (H3K27m3 in wild type and ectopic H3K9m2 in *met1*) maybe underestimated by our stringencies. Representative IGB view of genes marked with H3K27m3 marks that do not gain ectopic H3K9m2 in *met1*. **B.** Representative views of genes that are marked with H3K27m3 in WT but do not gain ectopic H3K9m2 in *met1*, suggesting that there are additional features that contribute to ectopic H3K9m2 in *met1*. **C.** Representative genome-browser views of two paralogous or related genes that were not retrieved as dispersed repeats by 'Repeat Masker', CITRATE SYNTHASE 1 and 2 genes (At3g58740 and At3g58750). These examples suggest that in the genome-wide analysis shown in Figure 2F, the proportion of genes H3K9m2 hypermethylated in *met1* that correspond to duplicated/paralogous/related genes is underestimated and must be larger than 40%. Yellow horizontal bars in IGB views: protein-coding genes; blue horizontal bars: transposable elements; green bars: dispersed repeats (regions with sequence of homology); orange bars: small RNA clusters (MPSS). **D.** Average distribution of small RNA-seq reads [16] across Class II genes.