



Fig S1: Metaplots of CG methylation levels, α and β rates along gbM genes in *A. thaliana* wildtype and mCHG methylation mutants.

(A) Metaplots of predicted and observed steady state CG methylation levels in a core set of ~5000 gbM from Zhang et al. [52]. Shown are the profiles of wildtype, cmt3 and suv4/5/6 mutants. The mutants deviate from wildtype both within gbM genes as well as in upstream and downstream regions. While steady state methylation levels are decreased within intergenic regions in cmt3 and suv4/5/6, they are increased within gbM genes. **(B)** Metaplots of the gain rate α including 95% confidence intervals along gbM genes. All genotypes show an increase in the α rate within gbM genes. Although similar in steady state methylation, the α rate of suv4/5/6 is significantly lower than that of cmt3, which is compensated by a likewise lower β rate. Windows in which the difference in gain rate α between any pair of genotypes is significant are marked with a gray bar. **(C)** Metaplots of the loss rate β and 95% confidence intervals along gbM genes. Similar to Fig. 3B, β rates are approximately constant within gbM genes compared to up- and downstream sequences. Mutant and wildtype samples show similar rate of methylation loss, with suv4/5/6 being slightly lower than cmt3 and wildtype. For all samples, α is the primary driver of steady state methylation change. Significance of differences in loss rate β indicated as in (B).