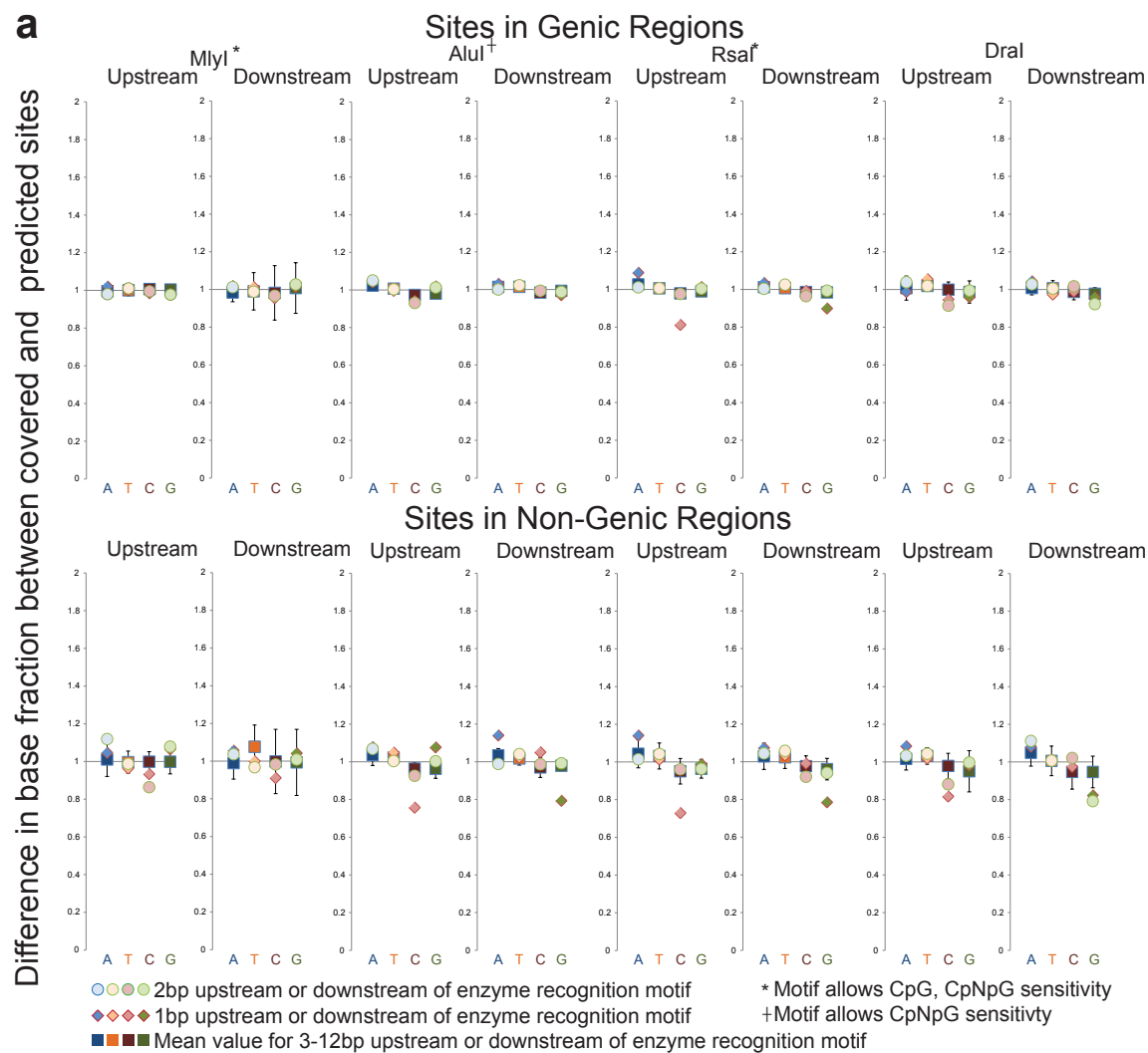
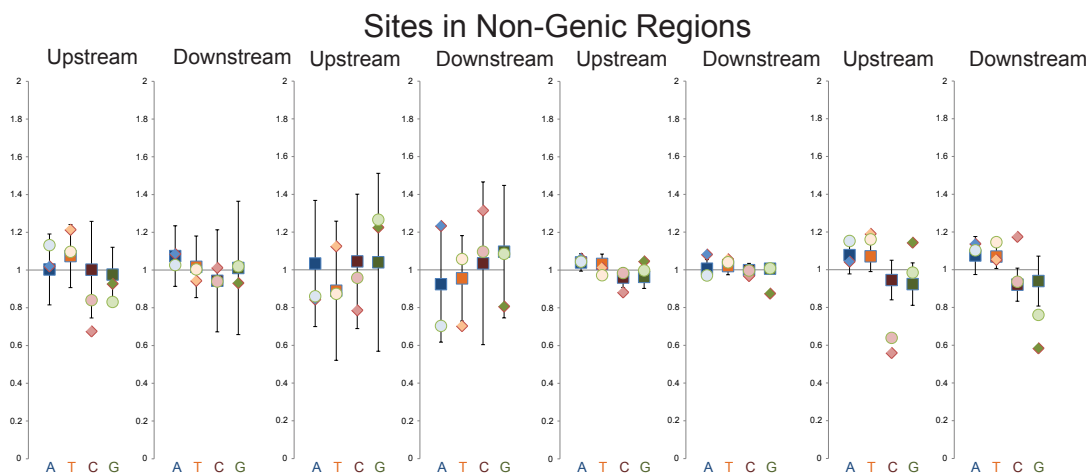
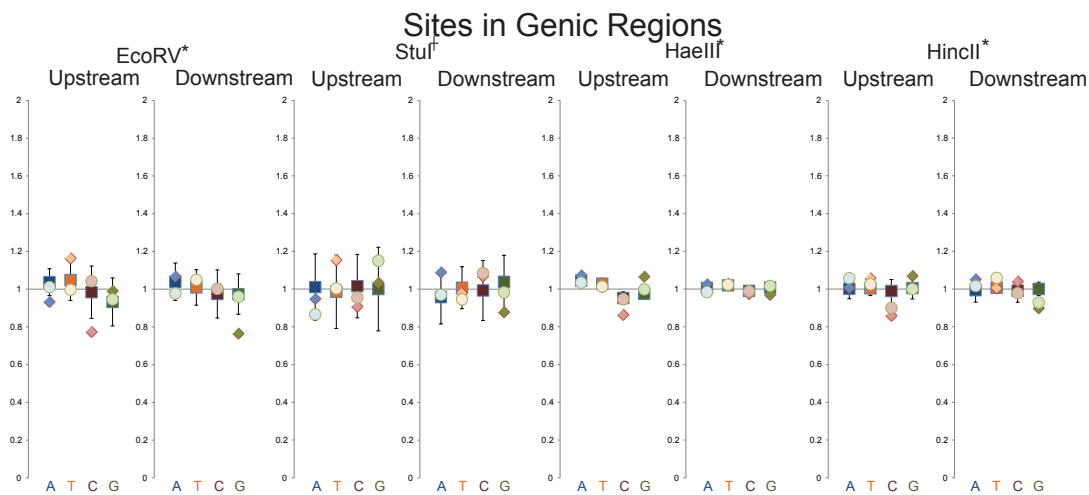


a

Difference in base ratio between covered and predicted sites



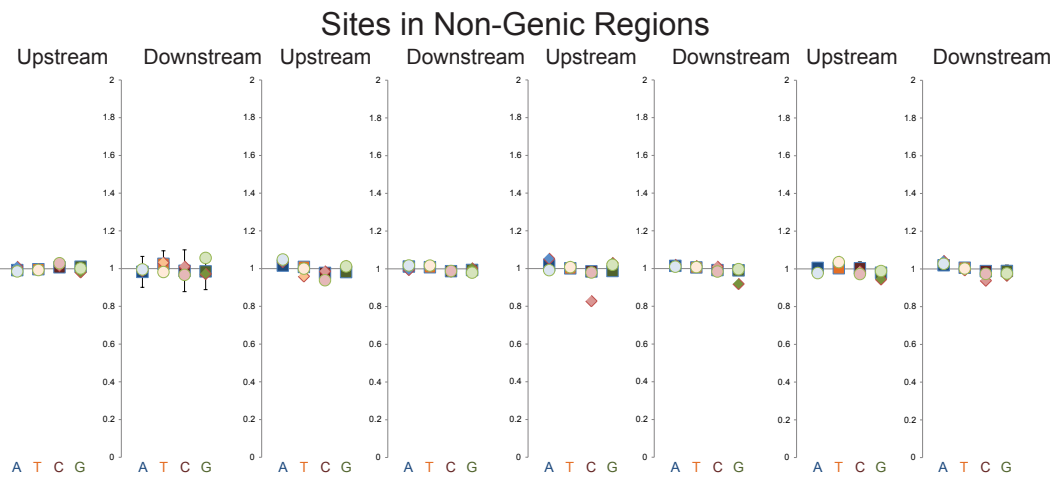
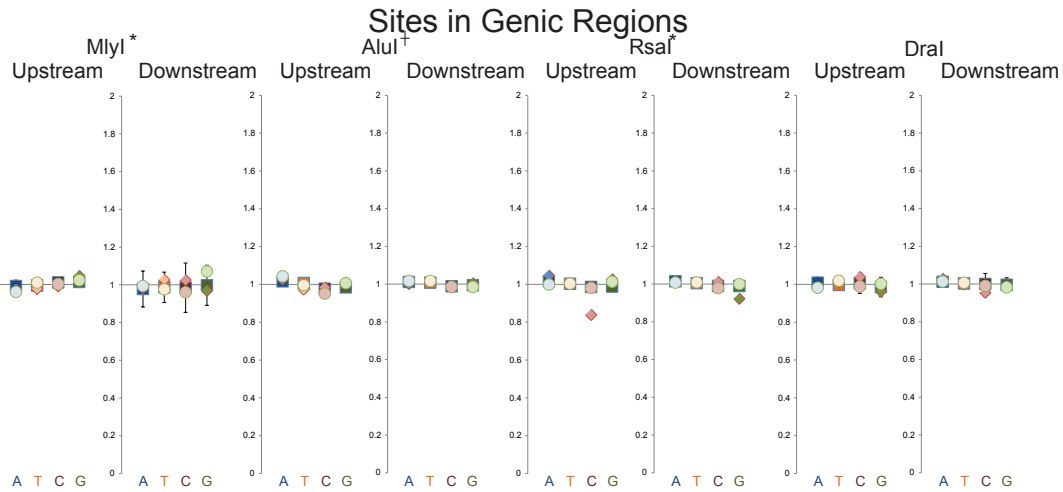
○●●● 2bp upstream or downstream of enzyme recognition motif
 ◆◆◆◆ 1bp upstream or downstream of enzyme recognition motif

Mean value for 3-12bp upstream or downstream of enzyme recognition motif

* Motif allows CpG, CpNpG sensitivity
 † Motif allows CpNpG sensitivity

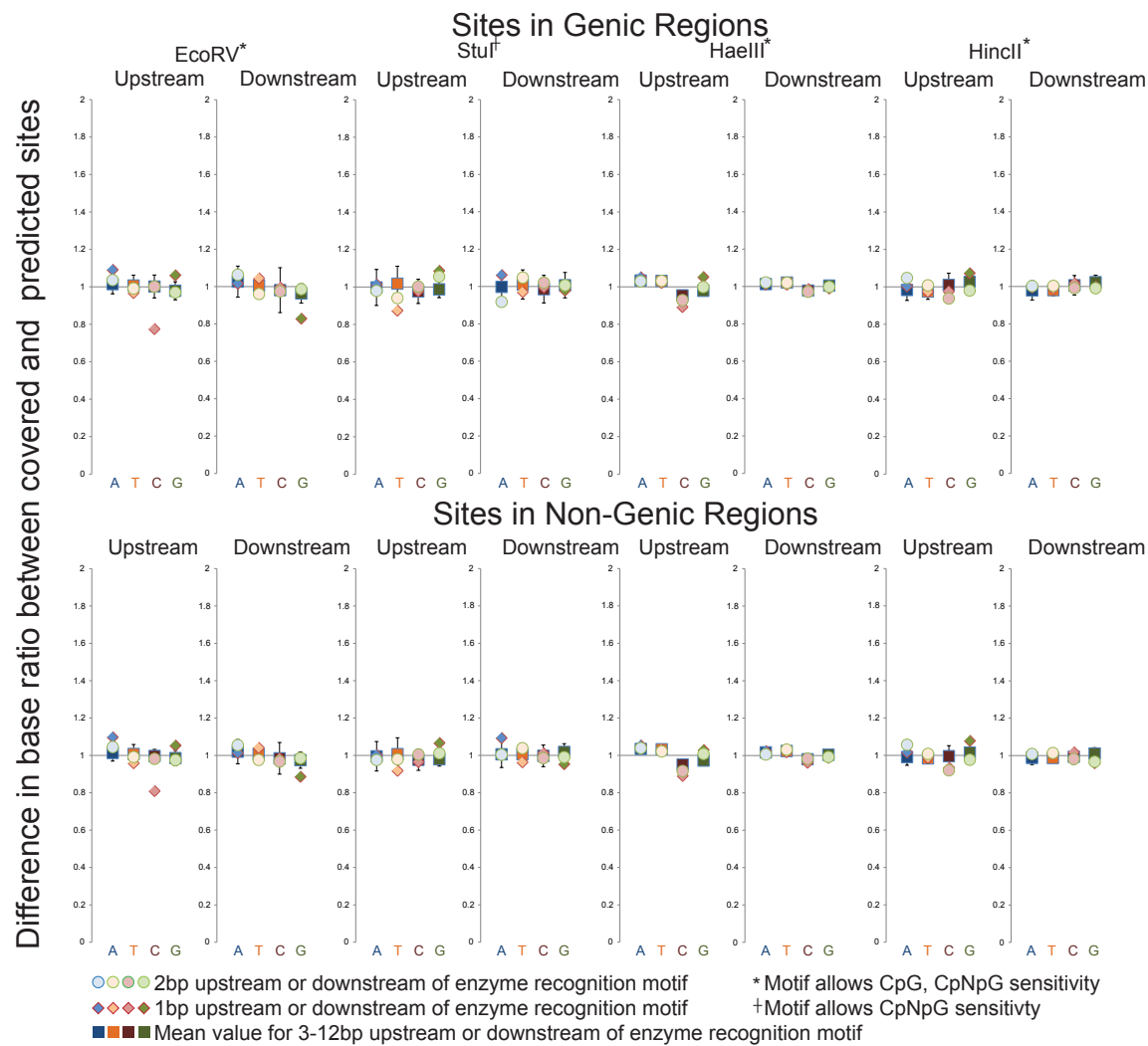
b

Difference in base fraction between covered and predicted sites



○○○○ 2bp upstream or downstream of enzyme recognition motif
 ◇◇◇◇ 1bp upstream or downstream of enzyme recognition motif
 ■■■■ Mean value for 3-12bp upstream or downstream of enzyme recognition motif

* Motif allows CpG, CpNpG sensitivity
 † Motif allows CpNpG sensitivity



Additional File 4 Supplementary Figure 4: Inferred methylation sensitivity of restriction enzymes.

Methylation sensitivity was inferred through changes between predicted and covered sites one to two bases upstream and guanine one to two bases downstream for A) maize and B) rice. Error bars represent two standard deviations based on nucleotide ratios three through twelve bases upstream and downstream.