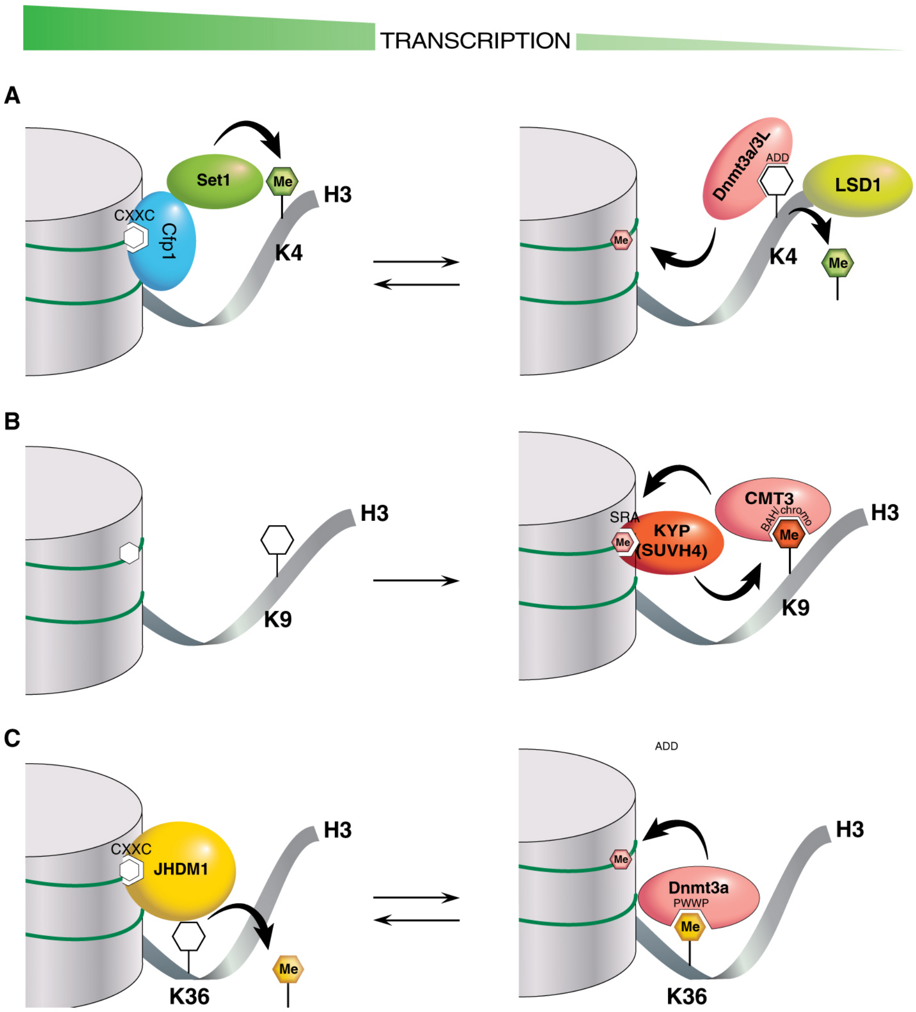

Figure 10. Cartoons of interactions that regulate DNA methylation and associated histone H3 modifications. There are three examples of PTM cross talk between histone and DNA methylation. Chromatin on the *left* represents transcriptionally active states, whereas chromatin on the *right* represents transcriptionally repressive states. The "Me"-labeled filled hexagons indicate one or more methyl groups in DNA (pink) or protein lysine residues (K). The catalytic action of methylation writers and erasers are indicated by curved black arrows. Methylation readers interact via specific labeled domains that fit in a lock-and-key fashion to methylated (filled hexagons) or unmethylated CpGs or lysines (unfilled hexagons). (*A*) Enzymatic reactions by the Dnmt3a-Dnmt3L complex and the SET1/CFP1 complex regulate the inverse correlation of DNA methylation and H3K4 methylation. (*B*) In plants, enzymatic reactions by CMT3 and KYP reinforce the correlation between DNA CHG methylation and H3K9 methylation. (*C*) Enzymatic reactions by Dnmt3a and JHDM1 positively regulate the association of DNA methylation with H3K36 methylation.