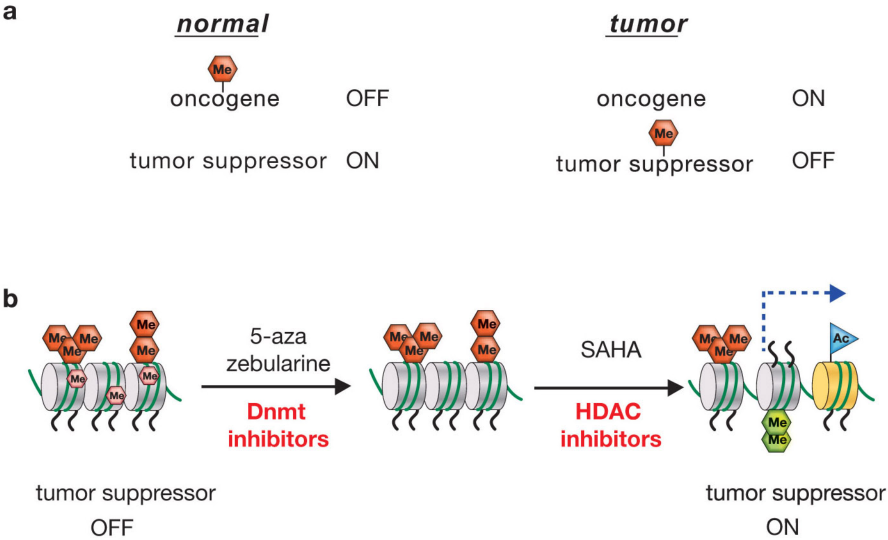

Figure 19. Epigenetic Modifications in Cancer

(*a*) Aberrant epigenetic marks at cancer-causing loci typically involve the derepression of oncogenes or silencing of tumor suppressor genes. Epigenetic marks known to alter a normal cell include DNA methylation, repressive histone methylation, and histone deacetylation. (*b*) The use of epigenetic therapeutic agents for the treatment of cancer has consequences on the chromatin template, illustrated for a tumor suppressor locus. Exposure to Dnmt inhibitors results in a loss of DNA methylation, and exposure to HDAC inhibitors results in the acquisition of histone acetyl marks and subsequent downstream modifications, including active histone methyl marks and the incorporation of histone variants. The cumulative chromatin changes lead to gene re-expression.