



Figure 32. Epigenetic modifications in cancer. (A) Aberrant epigenetic marks at cancer-causing loci typically involve the derepression of oncogenes or silencing of tumor-suppressor genes. These epigenetic alterations often include perturbed DNA methylation and histone modifications. (B) The use of epigenetic agents for cancer therapy has consequences on the chromatin template, illustrated for a promoter of a tumor-suppressor locus. Exposure to DNMT inhibitors (DNMTi) results in a loss of DNA methylation and treatment with HDAC inhibitors (HDACi) increases histone acetylation, and subsequent downstream modifications, including active histone methylation marks, induction of a nucleosome-free region, and the incorporation of histone variants. These cumulative chromatin changes lead to gene reexpression.