



**Figure 11.** Coordinated modification of chromatin. The transition of a naïve chromatin template to active euchromatin (*left*) or the establishment of repressive heterochromatin (*right*) involves a series of coordinated chromatin modifications. In the case of transcriptional activation, this is accompanied by the action of nucleosome remodeling complexes to create a nucleosome-depleted region (NDR) at the promoter for TF binding and the replacement of core histones with histone variants (yellow, namely, H3.3). Also, euchromatin is typically enriched for histone acetylation (Ac), recruiting readers with a bromodomain, and contains ubiquitinated histones and H3K4me3 (green Me hexagons) at the transcriptional start site. Heterochromatin is typically depleted of histone acetylation via HDAC complexes and contains methylated DNA (pink Me hexagons), recruiting methyl-CpG-binding domain (MBD) readers, such as MeCP2. In addition, repressive histone methyllysine marks (red Me hexagons) are placed by KMTs and can recruit readers, such as HP1, via H3K9 methylation.