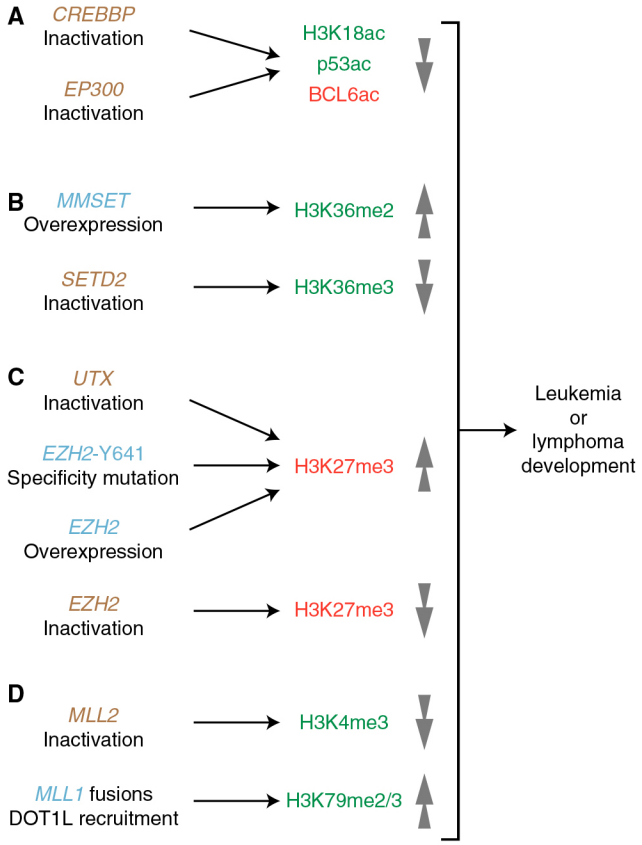

Figure 7. Role of histone-modifying enzymes in leukemia and lymphoma. (*A*) Monoallelic mutation of the *CREBBP* (CBP) or *EP300* (p300) gene results in reduced acetylation of BCL6, p53, and histone H3 in B-cell lymphoma. (*B*) Overexpression of the H3K36 dimethylase MMSET (NSD2, WHSC1) in multiple myeloma and loss of the H3K36 trimethylase SETD2 in early T-cell precursor acute lymphoblastic leukemia (ETP-ALL) contribute to tumorigenesis by altering the methylation state of lysine 36 of histone H3. (*C*) Loss of the H3K27 demethylase UTX as well as an altered specificity mutation and overexpression of the H3K27 methyltransferase EZH2 are implicated in the formation of B-cell malignancies by increasing the abundance of the repressive histone mark H3K27me3, whereas loss of EZH2 is associated with T-ALL. (*D*) Inactivation of the H3K4 methyltransferase MLL2 results in decreased levels of the active modification H3K4me3 in B-cell lymphoma, whereas MLL1 fusion proteins recruit the methyltransferase DOT1L to focally increase H3K79 methylation in *MLL1*-rearranged leukemias. The following color code is used: oncogenes (blue), tumor-suppressor genes (brown), active (green), and repressive (red) protein modifications.