

Figure 1. Histone writers, erasers, and readers in cancer. Histone H3 tail lysine residues, frequently subject to posttranslational modifications (PTMs), are indicated along the *left* side. The typical distribution of these H3 PTMs is also indicated along the length of gene loci (including distal enhancers) as shaded blocks. Green (methylation) or cyan (acetylation) indicates histone marks associated with active genes, whereas red shading is indicative of silent genes. A few examples of writers, erasers, and readers that may propagate a mark or act as an effector protein are listed on the *right* side of the figure. For a more complete listing of these proteins, see Appendices A–D at the end of this chapter.

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