

Histone modification or variant	Peak or Region	Putative functions
H2A.Z	Peak	Histone protein variant (H2A.Z) associated with regulatory elements with dynamic chromatin
H3K4me1	Peak/Region	Mark of regulatory elements associated with enhancers and other distal elements, but also enriched downstream of transcription starts
H3K4me2	Peak	Mark of regulatory elements associated with promoters and enhancers
H3K4me3	Peak	Mark of regulatory elements primarily associated with promoters/transcription starts
H3K9ac	Peak	Mark of activate regulatory elements with preference for promoters
H3K9me1	Region	Loosely associated with transcription, with preference for 5 end of genes
H3K9me3	Peak/Region	Repressive mark associated with constitutive heterochromatin, repetitive elements and certain broad repressive domains
H3K27ac	Peak	Mark of active regulatory elements; may distinguish active enhancers and promoters from their inactive counterparts
H3K27me3	Region	Repressive mark established by polycomb complex activity associated with repressive domains and silent developmental genes
H3K36me3	Region	Elongation mark associated with transcribed portions of genes, with preference for 3 regions after intron 1
H3K79me2	Region	Transcription-associated mark, with preference for 5 end of genes
H4K20me1	Region	Loosely associated with transcription, with preference for 5 end of genes