

# Epigenetics antibodies

Covering 90% of epigenetic targets and transcription factors

## Epigenetics

Epigenetics is the study of heritable changes in gene expression that modify DNA, RNA, and protein but do not alter the nucleotide sequence. Posttranslational modifications (PTMs) are among the most important types of epigenetic states that apply to proteins. PTMs are marks that provide an extensive regulatory mechanism for cells to signal which genes to turn on and off. Many types and families of proteins are subject to PTMs, but one of the most highly decorated is the histone family of proteins. Some examples of PTMs are methylation, acetylation, phosphorylation, and ubiquitination.

It is essential to use an antibody specific to an individual histone modification because each one represents a unique signal for gene expression. For example, Lys9 on H3 can be acetylated or methylated. Acetylation is an activating mark, whereas methylation has different effects depending on the number of methyl groups. H3K9me1 is found to be enriched at transcription start sites, whereas H3K9me2 and H3K9me3 are associated with gene repression. Further, H3K9me2 is specifically associated with X-chromosome inactivation. Thus, each modification on H3K9 has a distinct effect on the cell, and knowing the identity of the modification is essential for accurately characterizing expression (Figure 1).

Graphical representation of selectivity of H3K9me2 antibody

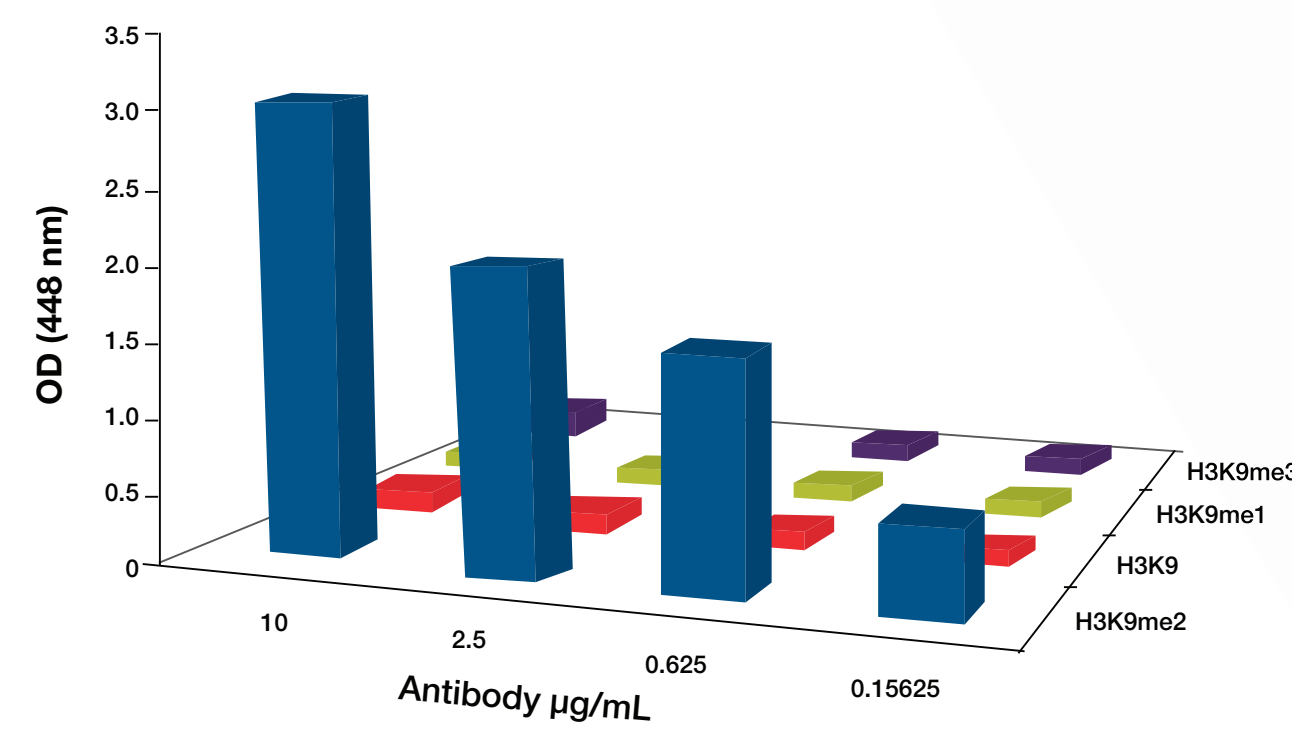
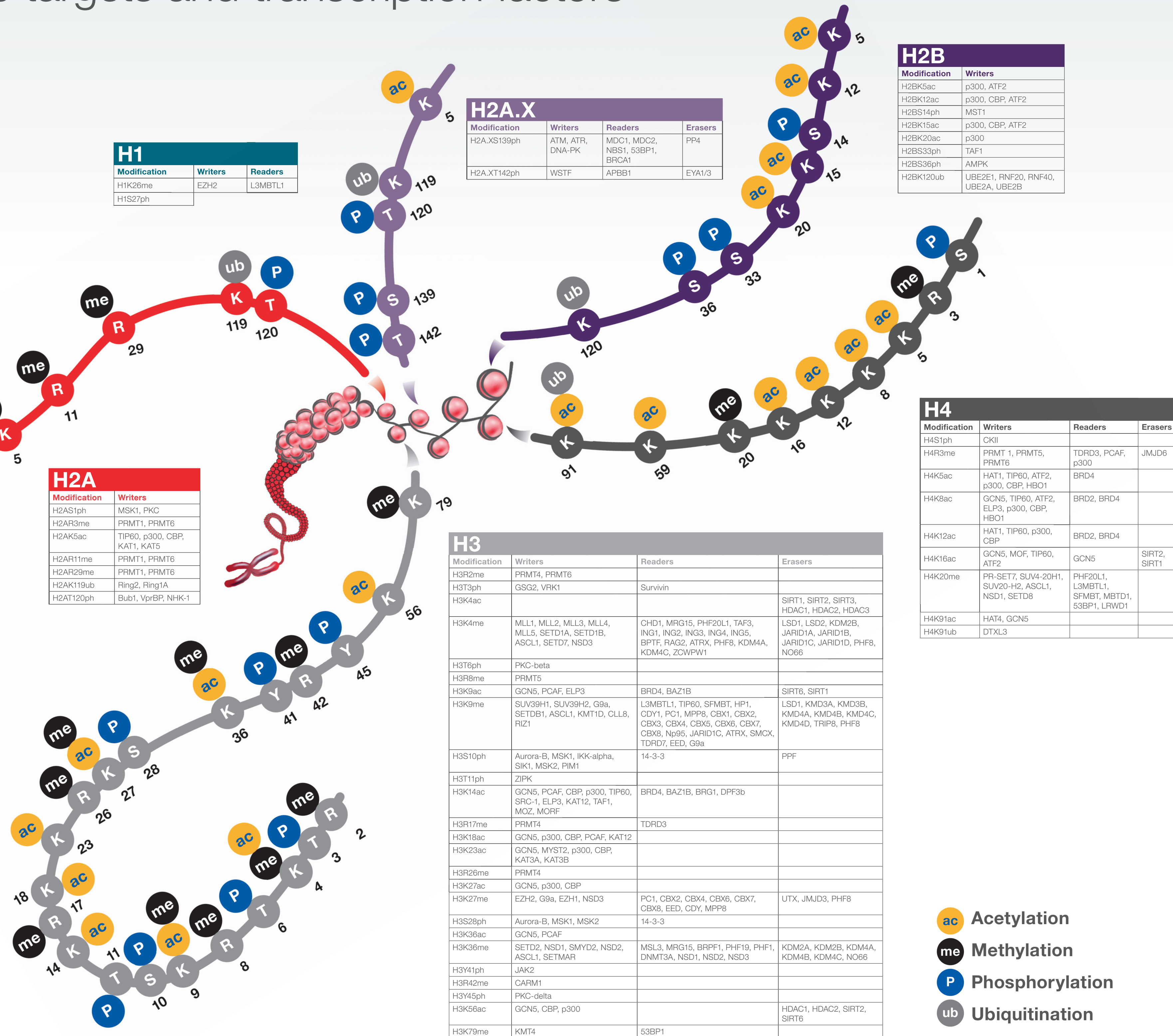


Figure 1. Cross-reactivity in ELISA for Invitrogen™ ABfinity™ anti-H3K9me2 rabbit recombinant monoclonal antibody (Cat. No. 701783).

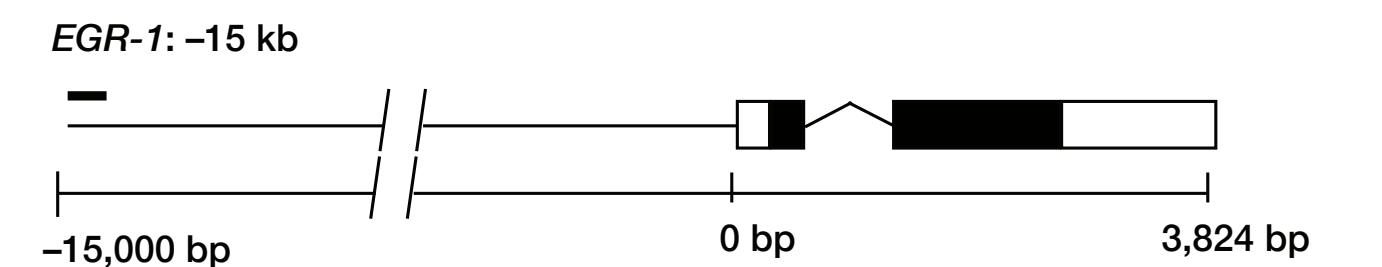


- ac Acetylation
- me Methylation
- P Phosphorylation
- ub Ubiquitination

## Writers, readers, and erasers

Epigenetic regulation is a dynamic process and includes writers, readers, and erasers. Writers place a PTM mark on a specific amino acid on histones or other proteins. These include histone acetyltransferases (HATs), histone methyltransferases (HMTs), protein arginine methyltransferases (PRMTs), and kinases. Readers bind to the epigenetic marks and include proteins with bromodomains, chromodomains, and tudor domains. Epigenetic erasers remove such marks and include histone deacetylases (HDACs), lysine demethylases (KDMs), and phosphatases. The writing, reading, and erasing of these posttranslational marks lead to changes in chromatin structure that can promote or antagonize gene expression. The identification of writers, readers, and erasers is continually growing.

**EGR-1: -15 kb**  
 Forward: GAGGCACTCTGCTCACAAA  
 Reverse: GATGCCTGCGAGGATGGAAA



**HIV gag**  
 Forward: GCTGAGCTGAGCTTCGGTTC  
 Reverse: TCGCCGCTACTCAGTAGGTA

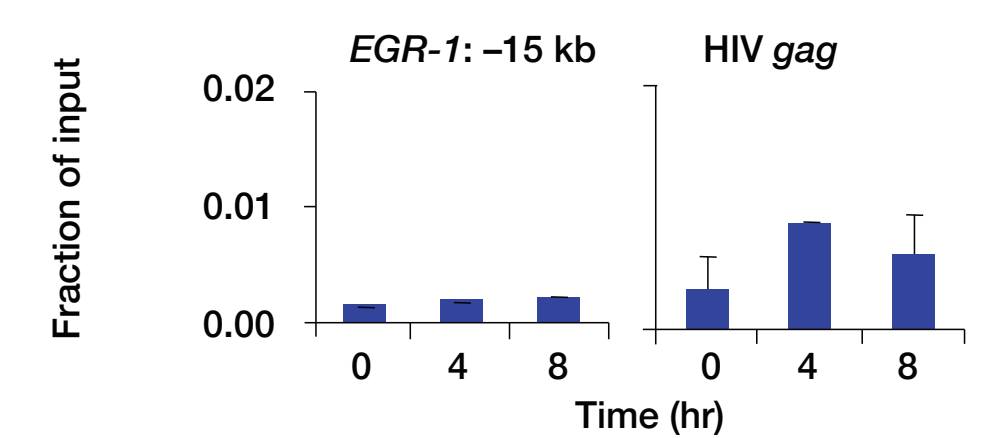
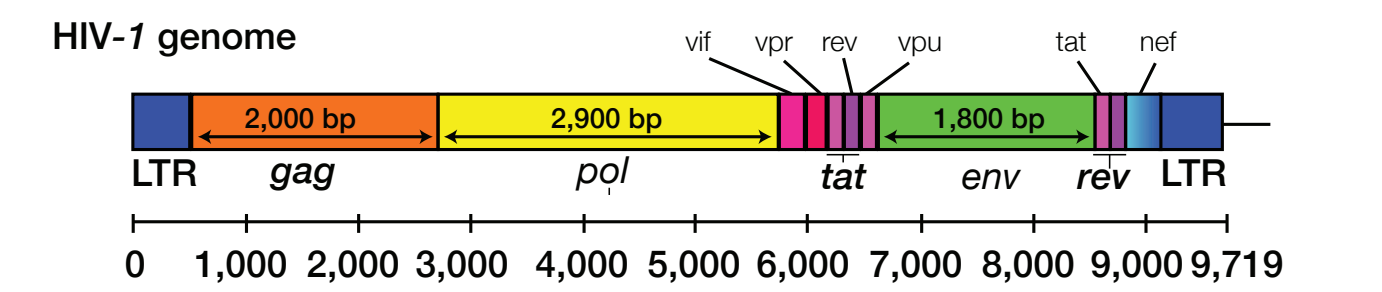


Figure 2. Matrix ChIP analysis using Invitrogen™ GCN5 Antibody (Cat. No. MA3-046) performed on a culture of human 5A8 J-lat T lymphocytes latently infected with HIV-1 and treated with 10 µg/mL phytohemagglutinin (PHA) for the indicated times.

Find out more at [thermofisher.com/epigeneticantibodies](http://thermofisher.com/epigeneticantibodies)