



EpiFinder™ GenomePro

# Epigenica

## A HIGH-THROUGHPUT, MULTIPLEXED, QUANTITATIVE

### Solution for Accelerating Epigenomics with Broader Insights

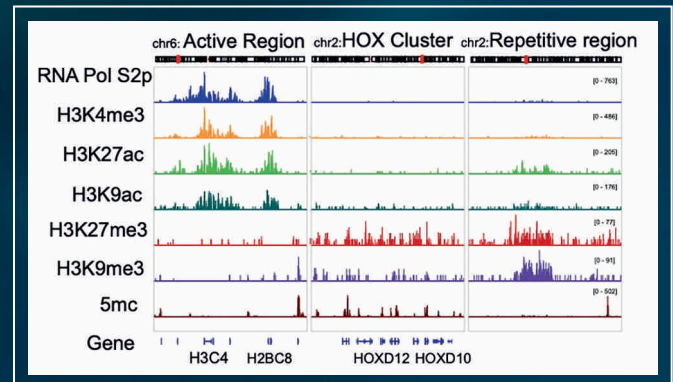
#### Unmatched Epigenomics with Reliable Results

- Extended overview of the epigenetic landscape
- 24 samples per run
- 8 Histone PTMs and DNA methylation
- 192 ChIP-Seq genome-wide profiles in just 3 days
- Standardized, robust quantification without spike-ins

#### Why EpiFinder™ GenomePro?

- Low sample volume: 1M cells/multiple epigenetic marks
- Compatible: live, frozen, or fixed tissues
- Flexible: design your custom epigenetic discovery panel
- Bioinformatics support: Automated Open-source data analysis pipeline
- Cost efficient: Industry-leading price unmatched anywhere
- Scalable: Large studies with incomparable speed

#### EpiFinder™ GenomePro



Data from 15 samples of the K562 leukemia cell line with and without epigenetic inhibitors treatment.

Figure: Genome browser (IGV) tracks displaying enrichment patterns for multiple epigenetic marks, including five histone modifications (H3K4me3, H3K27ac, H3K9ac, H3K27me3, H3K9me3), RNA Polymerase II (RNA Pol S2p), and DNA methylation (5mC), across three different genomic regions.



To learn more, please contact our experts at  
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