

H3K36me2 CUTANA™ CUT&RUN and CUT&Tag Antibody

Catalog No	13-0056	Type	Monoclonal [2527-1B4]
Lot No	22207001-62	Host	Rabbit
Pack Size	100 µg	Concentration	0.5 mg/mL
Applications	CUT&RUN, CUT&Tag	Reactivity	Human, Wide Range (Predicted)

DESCRIPTION

This H3K36me2 antibody is validated for chromatin profiling of histone H3 lysine 36 dimethylation (H3K36me2), an epigenetic mark deposited primarily by the histone methyltransferase NSD2 (WHSC1/MMSET). H3K36me2 is broadly enriched downstream of transcription start sites across gene bodies and intergenic chromatin [1], where it contributes to chromatin accessibility, transcriptional regulation, and enhancer activity [2]. Dysregulation of NSD2-mediated H3K36me2 deposition drives oncogenic transcriptional programs in multiple cancers, making H3K36me2 antibodies essential tools for studying NSD2 biology and epigenetic drug discovery. **Key advantages include:**

- **Target specific enrichment in CUT&Tag** – This antibody meets EpiCypher’s SNAP-Certified™ criteria in CUT&Tag, demonstrating <20% cross-reactivity to related histone PTMs when tested with SNAP-CUTANA™ controls, the gold standard for quantitative specificity assessment in chromatin profiling assays (**Figure 1**).
- **Knockout tested** – Antibody-generated CUT&Tag enrichment is depleted following NSD2 knockout, confirming that the observed signal reflects NSD2-dependent H3K36me2 deposition (see product page: epicypher.com/13-0056).
- **Best-in-class performance in CUT&RUN** – While SNAP-CUTANA™ spike-in analysis indicates this antibody does not meet EpiCypher specificity thresholds for CUT&RUN, it delivers substantially stronger and more reproducible genomic enrichment than alternative commercial antibodies (see product page).
- **Reliable lot-to-lot performance** – Each production lot undergoes rigorous quality control, including direct testing in genomic mapping assays, to ensure consistent performance.
- **Validated in drug discovery research** – This antibody was used to profile changes following treatment with a novel NSD2 inhibitor, helping reveal the epigenomic consequences of NSD2 inhibition, demonstrating its utility for studying NSD2 biology, and evaluating epigenetic therapeutics [3].

TECHNICAL INFORMATION

Immunogen	A synthetic peptide corresponding to histone H3 dimethylated at lysine 36
Storage	Stable for 1 year at 4°C from date of receipt
Formulation	Protein A affinity-purified recombinant monoclonal antibody in borate buffered saline pH 8.0, 0.09% sodium azide
Target Size	15 kDa

RECOMMENDED DILUTION

CUT&Tag:	0.5 µg per reaction
CUT&RUN:	0.5 µg per reaction

GENE & PROTEIN INFORMATION

UniProt ID	H3.1 - P68431
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REFERENCES

[1] Kuo et al. *Mol Cell* (2011) PMID: 22099308
[2] Fang et al. *Nucleic Acids Res.* (2021) PMID: 34107030

[3] Jeong et al. *Nature* (2026) PMID: 40770093

VALIDATION DATA

CUT&Tag Methods

CUT&Tag was performed on 100k K562 nuclei with the SNAP-CUTANA™ K-MetStat Panel (EpiCypher 19-1002) spiked-in prior to the addition of 0.5 µg of either IgG negative control (EpiCypher 13-0042), H3K4me3 positive control (EpiCypher 13-0060), or H3K36me2 antibodies. The experiment was performed using the CUTANA™ CUT&Tag Kit v4 (EpiCypher 14-1102). Libraries were run on an Illumina NextSeq2000 with paired-end sequencing (2x50 bp). Sample sequencing depth was 11.8 million reads (IgG), 10 million reads (H3K4me3), 8.4 million reads (H3K36me2). Data were aligned to the hg38 genome using Bowtie2. Data were filtered to remove duplicates, multi-aligned reads, and ENCODE DAC Exclusion List regions.

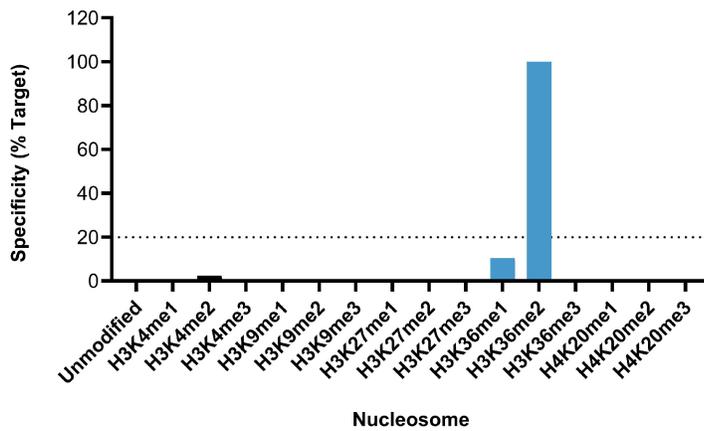


FIGURE 1 SNAP specificity analysis in CUT&Tag. CUT&Tag was performed as described above. CUT&Tag sequencing reads were aligned to the unique DNA barcodes corresponding to each nucleosome in the K-MetStat panel (x-axis). Data are expressed as a percent relative to on-target recovery (H3K36me2 set to 100%). Dotted line represents the 20% cross reactivity threshold for SNAP-certification.

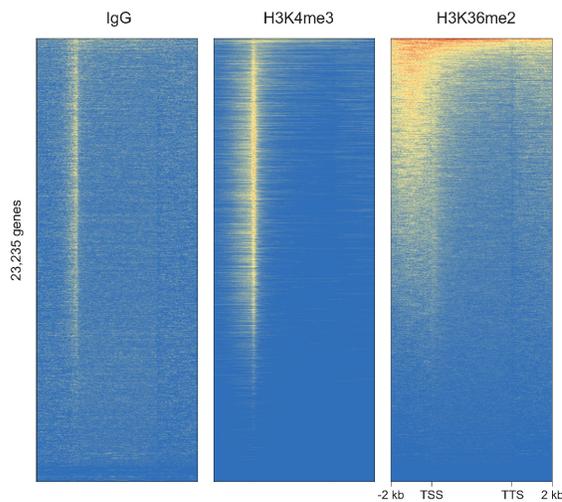


FIGURE 2 CUT&Tag genome-wide enrichment. CUT&Tag was performed as described above. Sequence reads were aligned to 23,235 annotated genes and heatmaps were generated across gene bodies from TSS to TTS extending 2kbp upstream from the TSS and 2kbp downstream from the TTS. Signal enrichment was sorted from highest to lowest (top to bottom) relative to the H3K36me2 sample (all gene rows aligned). High, medium, and low intensity are shown in red, yellow, and blue, respectively. H3K4me3 positive control and H3K36me2 antibodies produced the expected enrichment patterns, which were higher than those observed with the IgG negative control.

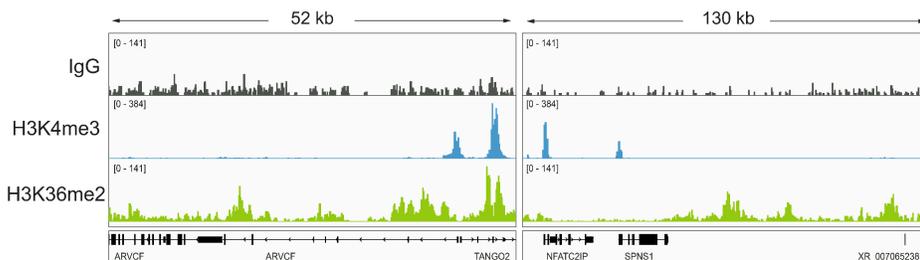


FIGURE 3 H3K36me2 CUT&Tag representative browser tracks. CUT&Tag was performed as described above. Gene browser shots were generated using the Integrative Genomics Viewer (IGV, Broad Institute). H3K36me2 antibody tracks display the characteristic enrichment known to be consistent with the function of this PTM [1].