

## CUTANA™ IgG Negative Control Antibody for CUT&RUN and CUT&Tag

<b>Catalog No</b>	13-0042	<b>Type</b>	Polyclonal
<b>Lot No</b>	24190007-82	<b>Host</b>	Rabbit
<b>Pack Size</b>	100 µg	<b>Concentration</b>	0.5 mg/mL
<b>Applications</b>	CUT&RUN, CUT&Tag	<b>Reactivity</b>	Negative Control

### DESCRIPTION

Cleavage Under Targets & Release Using Nuclease (CUT&RUN) and Cleavage Under Targets and Tagmentation (CUT&Tag) are next generation assays for genomic mapping of chromatin features to replace Chromatin Immunoprecipitation (ChIP-seq) [1]. Unlike in ChIP-seq, where baseline signal is established by sequencing the fragmented input chromatin, reactions performed with this rabbit IgG antibody are used to determine background signal arising from non-specific MNase digestion and Tn5 tagmentation. Pair with the H3K4me3 positive control antibody (EpiCypher 13-0060) for a well-controlled experiment.

### TECHNICAL INFORMATION

<b>Immunogen</b>	None
<b>Storage</b>	Stable for 1 year at 4°C from date of receipt
<b>Formulation</b>	Affinity-purified antibody in PBS pH 7.6

### RECOMMENDED DILUTION

<b>CUT&amp;RUN:</b>	0.5 µg per reaction	<b>CUT&amp;Tag:</b>	0.5 µg per reaction
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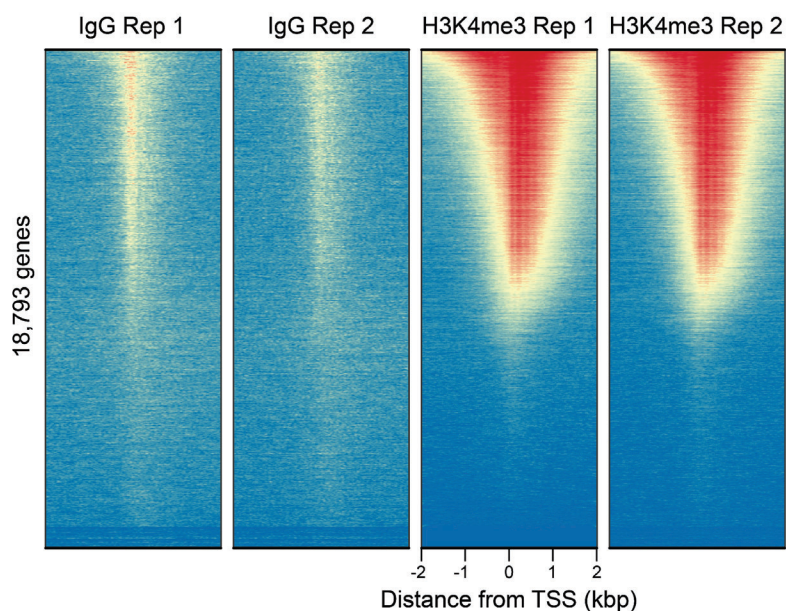
### REFERENCES

[1] Skene & Henikoff eLife (2017). PMID: 28079019

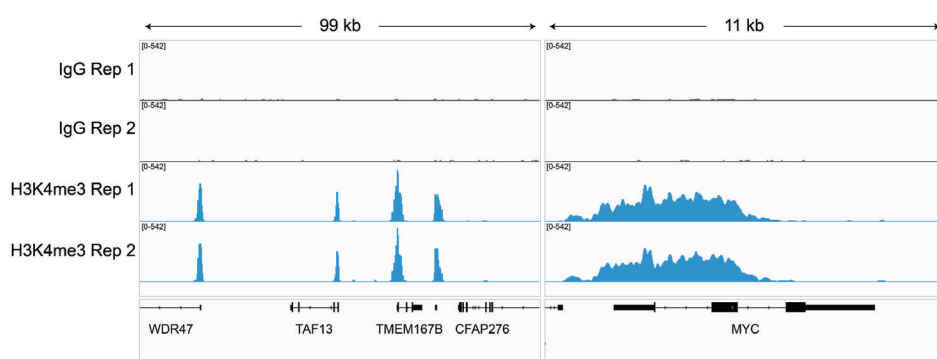
## VALIDATION DATA

### CUT&RUN Methods

CUT&RUN was performed on 500k native K562 cells with 0.5 µg of either IgG or H3K4me3 (EpiCypher 13-0060) antibodies in duplicate using the CUTANA™ ChIC/CUT&RUN Kit v4 (EpiCypher 14-1048). Library preparation was performed with 5 ng of DNA (or the total amount recovered if less than 5 ng) using the CUTANA™ CUT&RUN Library Prep Kit (EpiCypher 14-1001/14-1002). Both kit protocols were adapted for high throughput Tecan liquid handling. Sample sequencing depth was 7.8/6.8 million reads (IgG Rep 1/Rep 2) and 12.6/10.9 million reads (H3K4me3 Rep 1/Rep 2). Data were aligned to the hg19 genome using Bowtie2. Data were filtered to remove duplicates, multi-aligned reads, and ENCODE DAC Exclusion List regions.



**FIGURE 1 CUT&RUN genome wide enrichment.** CUT&RUN was performed as described above. Heatmaps show H3K4me3 peaks relative to IgG antibody in aligned rows ranked by intensity (top to bottom) and colored such that red indicates high localized enrichment and blue denotes background signal. H3K4me3 antibody showed expected enrichment around the TSS. Despite some observable background in the IgG control, differential enrichment with the target antibody is as expected.

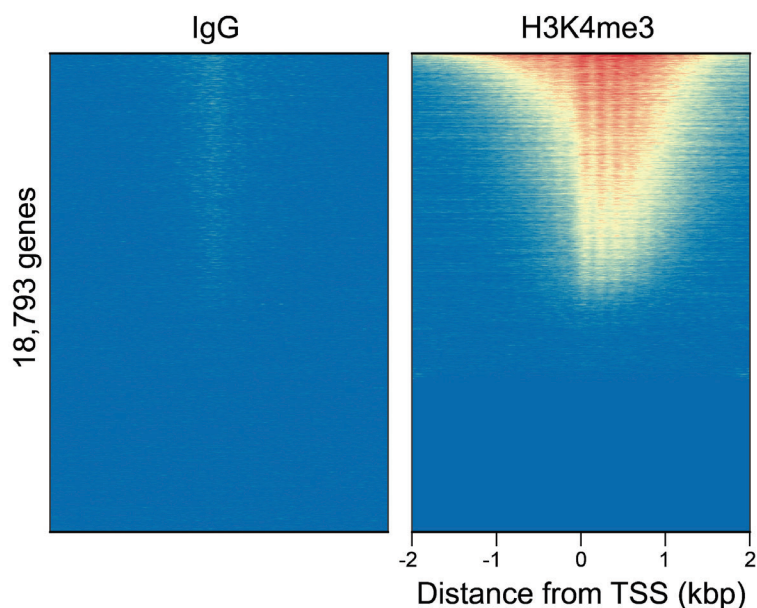


**FIGURE 2 Rabbit IgG CUT&RUN tracks.** CUT&RUN was performed as described above. Gene browser shots were generated using the Integrative Genomics Viewer (IGV, Broad Institute). Two gene loci show H3K4me3 peaks and minimal background in the IgG track, as expected.

## VALIDATION DATA

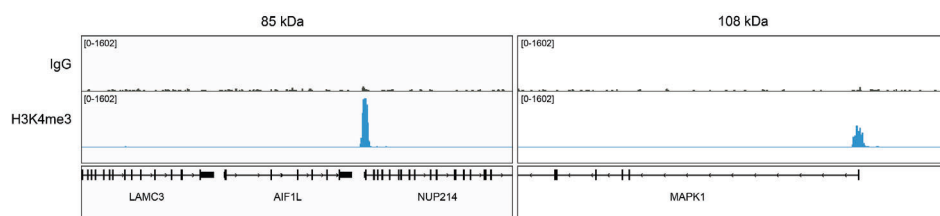
### CUT&Tag Methods

CUT&Tag was performed on 100k native K562 nuclei with 0.5  $\mu$ g of either IgG or H3K4me3 (EpiCypher 13-0041) antibodies in singlicate using the CUTANATM CUT&Tag Kit v1 (EpiCypher 14-1102/14-1103). Libraries were run on an Illumina NextSeq2000 with paired-end sequencing (2x50bp). Sample sequencing depth was 0.9 million reads (IgG) and 2.9 million reads (H3K4me3). Data were aligned to the hg19 genome using Bowtie2. Data were filtered to remove duplicates, multi-aligned reads, and ENCODE DAC Exclusion List regions.



**FIGURE 3** CUT&Tag genome wide enrichment.

CUT&Tag was performed as described above. Representative (not lot-specific) heatmaps show H3K4me3 peaks relative to IgG antibody in aligned rows ranked by intensity (top to bottom) and colored such that red indicates high localized enrichment and blue denotes background signal. H3K4me3 antibody showed expected enrichment around the TSS. Despite some observable background in the IgG control, differential enrichment with the target antibody as expected.



**FIGURE 4** Rabbit IgG CUT&Tag tracks.

CUT&Tag was performed as described above. Representative (not lot-specific) gene browser shots were generated using the Integrative Genomics Viewer (IGV, Broad Institute). Two gene loci show H3K4me3 peaks and minimal background in the IgG track, as expected.