CHD1 CUTANA™ CUT&RUN Antibody

Catalog No	13-2008	**Type**	Polyclonal
Lot No	21013001-42	**Host**	Rabbit
Pack Size	100 µL	**Concentration**	1000 µg/mL
Applications	CUT&RUN, IP	**Reactivity**	Human

DESCRIPTION

This antibody meets EpiCypher's "CUTANA Compatible" criteria for performance in Cleavage Under Targets and Release Using Nuclease (CUT&RUN) and/or Cleavage Under Targets and Tagmentation (CUT&Tag) approaches to genomic mapping. Every lot of a CUTANA Compatible antibody is tested in the indicated approach using EpiCypher optimized protocols (epicypher.com/protocols) and determined to yield peaks that show a genomic distribution pattern consistent with reported function(s) of the target protein. CHD1 antibody produces CUT&RUN peaks above background (**Figure 1**) that overlap with H3K4me3 (**Figures 1-2**), consistent with CHD1 tandem chromodomains that mediate H3K4me3 binding and SWI/SNF complex nucleosome remodeling [1].

TECHNICAL INFORMATION

Immunogen	Between amino acids 1500 to 1550
Storage	Stable for 1 year at 4°C from date of receipt
Formulation	Antigen affinity-purified antibody in Tris-citrate/phosphate buffer pH 7-8, 0.09% sodium azide

RECOMMENDED DILUTION

CUT&RUN	0.5 µg per reaction	**Immunoprecipitation**	2 - 5 µg/mg lysate

REFERENCES

[1] Flanagan et al. *Nature* (2005). PMID: 16372014

VALIDATION DATA

CUT&RUN Methods

CUT&RUN was performed on 500k K562 cells with either CHD1 (0.1 µg), H3K4me3 positive control (EpiCypher 13-0041; 0.5 µg), or IgG negative control (EpiCypher 13-0042; 0.5 µg) antibodies using the CUTANA™ ChIC/CUT&RUN Kit v2.0 (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. Libraries were run on an Illumina NextSeq2000 with paired-end sequencing (2x50 bp). Sample sequencing depth was 2.4 million reads (IgG), 4.1 million reads (H3K4me3), and 4.9 million reads (CHD1). Data were aligned to the hg19 genome using Bowtie2. Data were filtered to remove duplicates, multi-aligned reads, and ENCODE DAC Exclusion List regions.

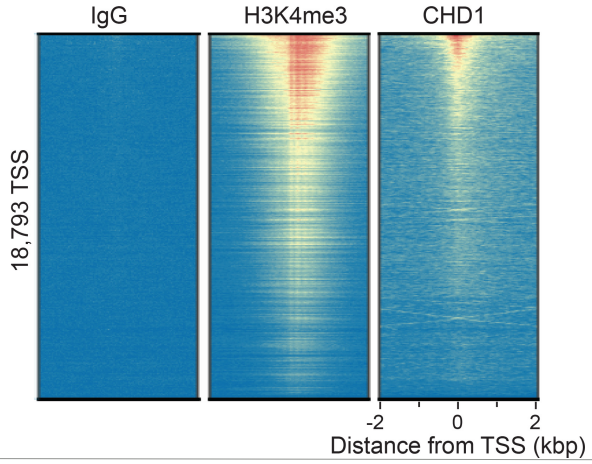

FIGURE 1 CHD1 peaks in CUT&RUN. CUT&RUN was performed as described above. Peaks were called using MACS2. Heatmaps show CHD1 peaks relative to IgG negative control antibody and H3K4me3 positive control antibody in aligned rows ranked by intensity (top to bottom) and colored such that red indicates high localized enrichment and blue denotes background signal.

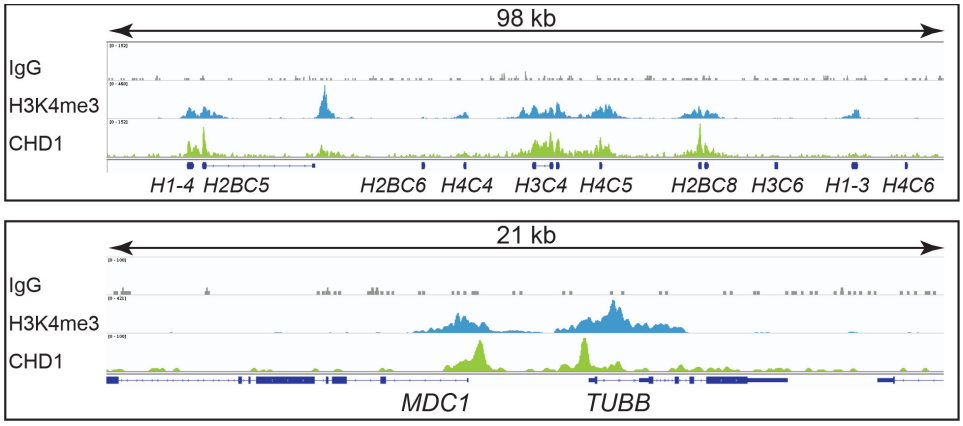

FIGURE 2 CHD1 CUT&RUN representative browser tracks. CUT&RUN was performed as described above. Gene browser shots were generated using the Integrative Genomics Viewer (IGV, Broad Institute). Two gene loci show overlap of CHD1 and H3K4me3 peaks, consistent with the CHD1 double chromodomain recognition of this PTM [1].

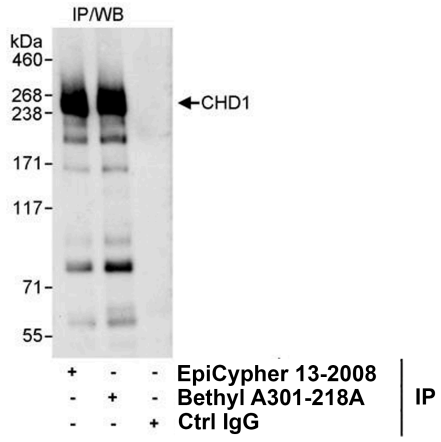

FIGURE 3 Immunoprecipitation data. EpiCypher CHD1 antibody (3 µg) was used to immunoprecipitate whole cell lysates isolated from HeLa cells using NETN lysis buffer (1.0 mg per IP). A negative control IgG antibody and positive control antibody to a different CHD1 epitope (Bethyl Laboratories) were also used to demonstrate specificity of the IP. Immunoprecipitates were loaded onto a 4-8% SDS-PAGE gel (20% of IP loaded) and probed via western blot with Bethyl A301-218A antibody (1.0 µg/mL).