

ELF1 CUTANA™ CUT&RUN Antibody

Catalog No	13-2023	Type	Polyclonal
Lot No	22056001-81	Host	Rabbit
Pack Size	100 µL	Concentration	250 µg/mL
Applications	CUT&RUN, IHC	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. ELF1 is a member of the ETS (e26 transformation specific sequence) family of transcription factor proteins. ELF1 antibody produces CUT&RUN peaks above background primarily in intronic and promoter regions (**Figure 1**) that overlap with known ELF1 DNA-binding motifs (**Figure 2**). ELF1 is expressed in B and T cells and has been shown to be involved with the regulation of several T- and B-cell specific genes [1].

TECHNICAL INFORMATION

Immunogen	Between amino acids 569 and 619
Storage	Stable for 1 year at 4°C from date of receipt
Formulation	Antigen affinity-purified antibody in Tris-buffered saline, 0.1% BSA, 0.9% sodium azide

RECOMMENDED DILUTION

CUT&RUN	0.5 µg per reaction
Immunohistochemistry	1:100 - 1:500

GENE & PROTEIN INFORMATION

UniProt ID	P32519
Gene Name	ELF1
Protein Name	ETS-related transcription factor Elf-1
Target Size	67 kDa
Alternate Names	ETS-like factor 1, EFTUD1, RIA1

REFERENCES

[1] Oettgen et al. *Mol Cell Biol* (1996). PMID: 8756667

VALIDATION DATA

CUT&RUN Methods

CUT&RUN was performed on 500k HeLa cells with 0.5 µg of either ELF1 or IgG negative control (EpiCypher 13-0042) 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 5.1 million reads (IgG) and 6.0 million reads (ELF1). Data were aligned to the hg19 genome using Bowtie2. Data were filtered to remove duplicates, multi-aligned reads, and ENCODE DAC Exclusion List regions.

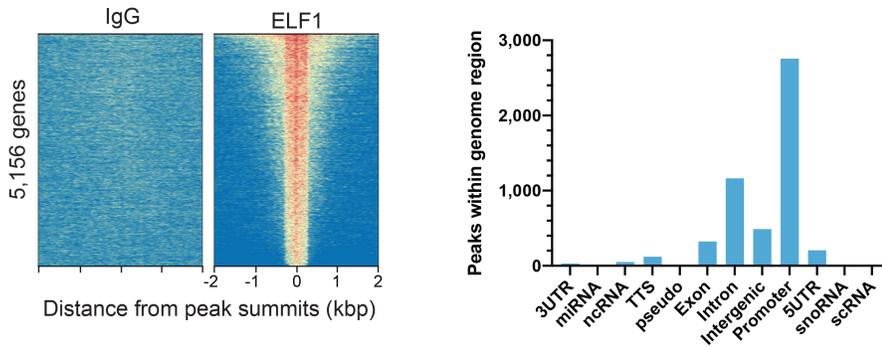


FIGURE 1 ELF1 peaks in CUT&RUN. CUT&RUN was performed as described above. Peaks were called using MACS2. Heatmaps show ELF1 peaks relative to IgG negative control antibody in aligned rows ranked by intensity (top to bottom) and colored such that red indicates high localized enrichment and blue denotes background signal (left). The number of peaks that fall into distinct classes of functionally annotated genomic regions are shown (right).

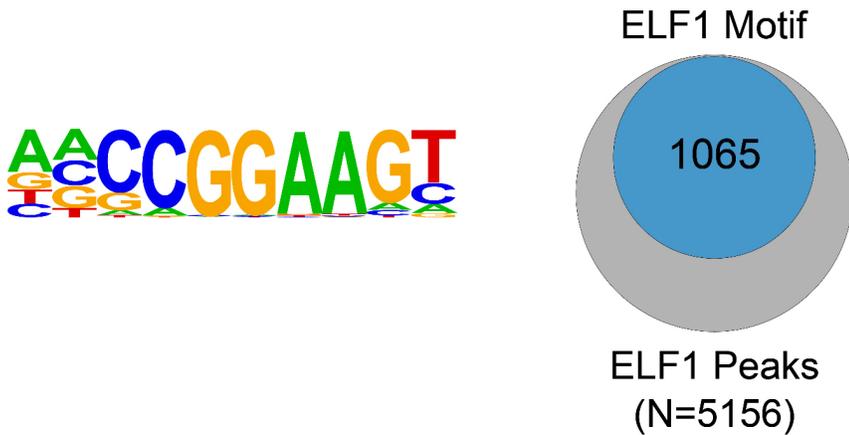


FIGURE 2 ELF1 transcription factor binding motif analysis in CUT&RUN. Homer analysis determined that the ELF1(ETS)/Jurkat-ELF1-ChIP-Seq(SRA014231)/Homer consensus motif, represented as a sequence logo position weight matrix, was significantly enriched under ELF1 CUT&RUN peaks (left). The number of ELF1 peaks containing the consensus motif from the left panel is represented by a Venn Diagram (right).

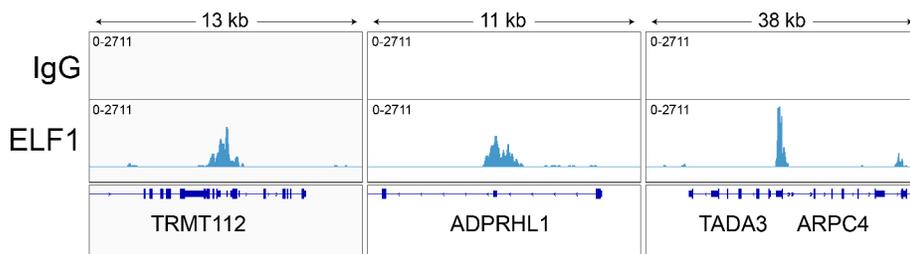


FIGURE 3 ELF1 CUT&RUN representative browser tracks. CUT&RUN was performed as described above. Gene browser shots were generated using the Integrative Genomics Viewer (IGV, Broad Institute). Three representative loci of the top called peaks are shown.

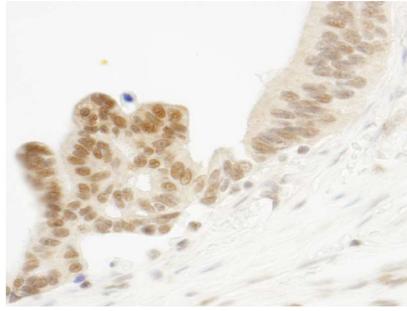
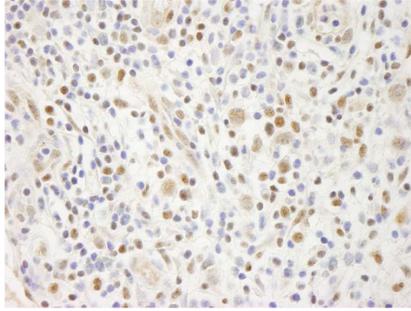


FIGURE 4 Immunohistochemistry data. FFPE sections of human Hodgkin's Lymphoma (**left**) and human ovarian carcinoma (**right**) using ELF1 antibody at a dilution of 1:250.

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