JUN/c-Jun CUTANA™ CUT&RUN Antibody

Catalog No	13-2019	**Type**	Polyclonal
Lot No	22070001-85	**Host**	Rabbit
Pack Size	100 µL	**Concentration**	200 µg/mL
Applications	CUT&RUN, IHC, IP, WB	**Reactivity**	Human, Mouse

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. JUN/c-Jun heterodimerizes with proteins of the FOS family to form an AP-1 transcription complex and binds to the AP-1 consensus motif [1]. JUN/c-Jun antibody produces CUT&RUN peaks above background primarily in intronic, intergenic, and promoter regions (**Figure 1**) that overlap with known JUN/c-Jun DNA-binding motifs (**Figure 2**).

TECHNICAL INFORMATION

Immunogen	Between amino acids 1 and 40
Storage	Stable for 1 year at 4°C from date of receipt
Formulation	Antigen affinity-purified antibody in Tris-buffered saline, 0.1% BSA, 0.09% sodium azide

RECOMMENDED DILUTION

CUT&RUN	0.5 µg per reaction	**Immunoprecipitation**	2 - 5 µg/mg lysate
Immunohistochemistry	1:100 - 1:500	**Western Blot**	1:2,000 - 1:10,000

Epitope retrieval with citrate buffer pH 6.0 is recommended for FFPE tissue sections

GENE & PROTEIN INFORMATION

UniProt ID	P05412
Gene Name	JUN
Protein Name	Transcription factor Jun
Target Size	35 kDa
Alternate Names	transcription factor Jun, activator protein 1, AP1, proto-oncogene c-Jun, transcription factor AP-1 subunit Jun, v-jun avian sarcoma virus 17 oncogene homolog, p39, AP-1, c-Jun, enhancer-binding protein AP1, Jun activation domain binding protein, jun oncogene

REFERENCES

[1] van Dam H, Castellazzi M, Oncogene (2001). PMID: 11402340

VALIDATION DATA

CUT&RUN Methods

CUT&RUN was performed on 500k HeLa cells with 0.5 µg of either JUN/c-Jun 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), 12.1 million reads (JUN/c-Jun), and 6.2 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.

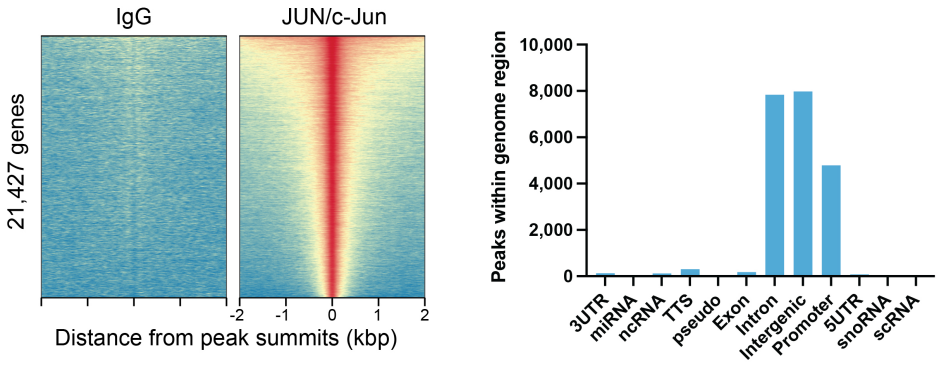

FIGURE 1 JUN/c-Jun peaks in CUT&RUN. CUT&RUN was performed as described above. Peaks were called with MACS2. Heatmaps show JUN/c-Jun peaks relative to IgG negative control antibody in aligned rows ranked by intensity (top to bottom) and colored such that red indicates high localized enrichment and blue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

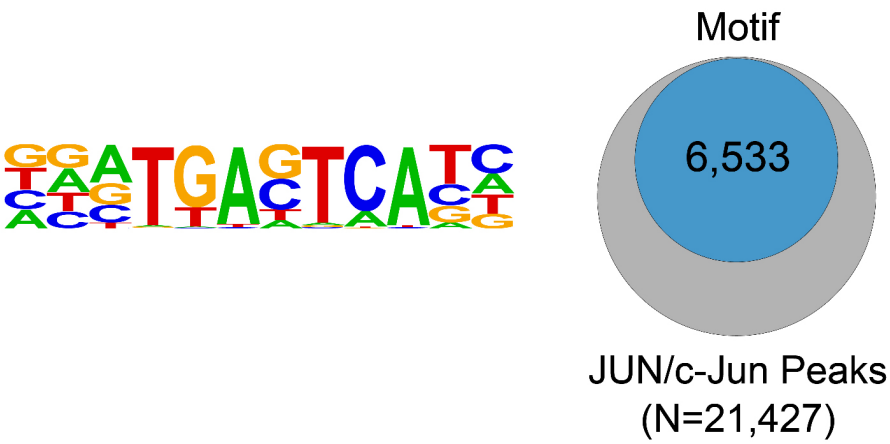

FIGURE 2 JUN/c-Jun transcription factor binding motif analysis in CUT&RUN. Fra1(bZIP)/BT549-Fra1-ChIP-Seq(GSE46166)/Homer consensus motif, represented as a sequence logo position weight matrix, was the top called motif significantly enriched under JUN/c-Jun CUT&RUN peaks (**left**). The number of JUN/c-Jun peaks containing the consensus motif from the left panel is represented by a Venn Diagram (**right**).

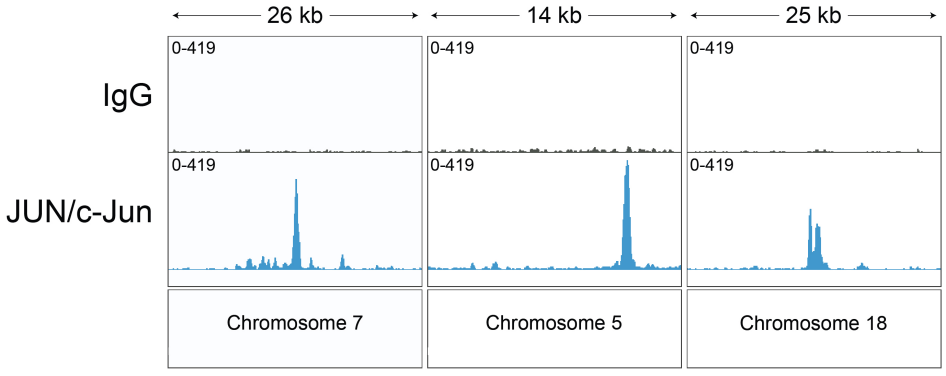

FIGURE 3 JUN/c-Jun CUT&RUN representative browser tracks. CUT&RUN was performed as described above. Gene browser shots were generated using the Integrative Genomics Viewer (IGV, Broad Institute). Three representative loci of the top called peaks are shown.

VALIDATION DATA

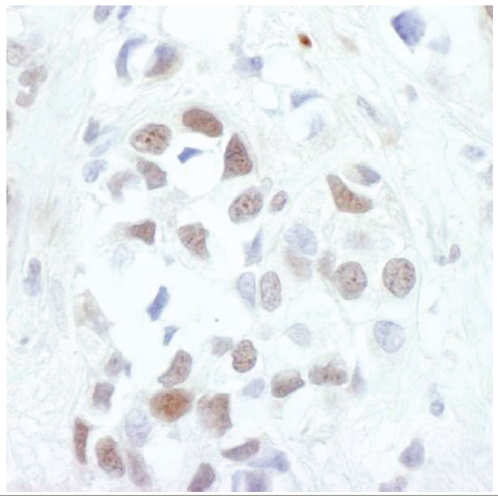

FIGURE 4 Immunohistochemistry data. FFPE section of human breast carcinoma using JUN/c-Jun antibody at a dilution of 1:200.

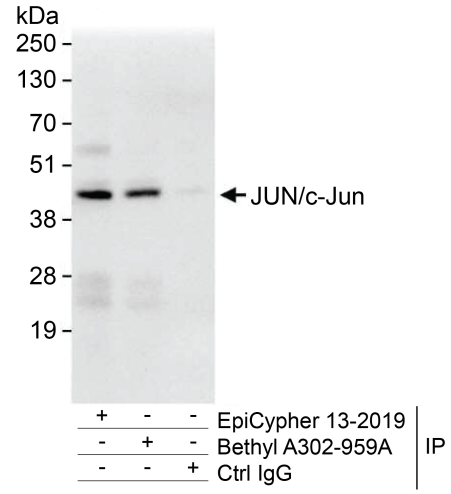

FIGURE 5 Immunoprecipitation data. EpiCypher JUN/c-Jun antibody (3 µg/mg lysate) was used to immunoprecipitate whole cell lysates (1 mg, 20% of IP loaded) isolated from HEK293T cells. A negative control IgG antibody and positive control antibody targeting a different JUN/c-Jun epitope (Bethyl Laboratories) were also used to demonstrate the specificity of the IP. For blotting immunoprecipitates, EpiCypher JUN/c-Jun antibody was used at a dilution of 1:200.

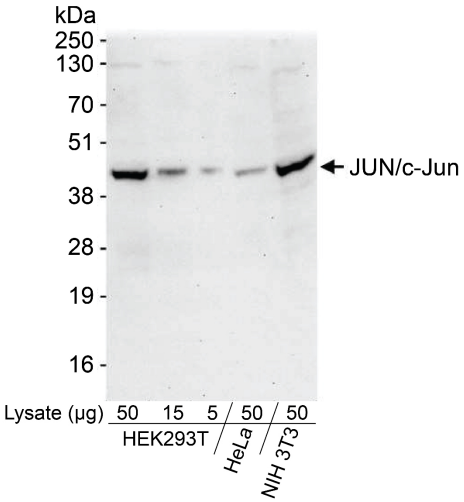

FIGURE 6 Western blot data. Western analysis of JUN/c-Jun in whole cell extracts from HEK293T (5, 15, and 50 µg), HeLa (50 µg), and mouse NIH 3T3 (50 µg) cells. Lysates were resolved via SDS-PAGE and detected with a 1:5,000 dilution of JUN/c-Jun antibody.