EpiCypher®

Anti-Mouse Secondary Antibody for CUTANA™ CUT&Tag

Catalog No	13-0048	**Type**	Mixed Monoclonal*
Lot No	24264004-82	**Host**	Goat
Pack Size	50 Reactions	**Concentration**	1 mg/mL
Applications	CUT&Tag	**Reactivity**	Anti-Mouse

DESCRIPTION

Anti-Mouse Secondary Antibody for CUTANA™ CUT&Tag is affinity purified and specific for mouse immunoglobulins. Minimal cross reactivity with rabbit, rat, human, bovine, guinea pig, and donkey IgG is observed. Use of a secondary antibody in CUT&Tag aids in signal amplification by increasing bound IgG per target epitope [1]. For best results, use with CUTANA™ pAG-Tn5 (EpiCypher 15-1017 & 15-1117). For detailed instructions for use, see EpiCypher's CUTANA™ CUT&Tag protocol: epicypher.com/protocols.

*Mixed Monoclonal: a pool of multiple recombinant monoclonal antibodies.

TECHNICAL INFORMATION

Immunogen	Recombinant full-length mouse immunoglobulin protein
Storage	Store at 4°C short term. For long term storage, store at -20°C. Avoid freeze/thaw cycles.
Formulation	Protein G affinity-purified antibody in PBS pH 7.2, 0.09% sodium azide.

RECOMMENDED DILUTION

CUT&Tag	0.5 µg per reaction

REFERENCES

[1] Kaya-Okur et al. Nat. Commun. (2019). PMID: 31036827

VALIDATION DATA

CUT&Tag Methods CUT&Tag was performed on 100k K562 nuclei with 0.5 µg of either IgG (Invitrogen 10400C) or H3K27me3 (Abcam ab6002) antibodies, followed by 0.5 µg of anti-mouse secondary antibody for CUTANA™ CUT&Tag. The EpiCypher Direct-to-PCR CUT&Tag protocol (epicypher.com/protocols) was used. Libraries were run on an Illumina NextSeq2000 with paired-end sequencing (2x50 bp). Sample sequencing depth was 4.3 million reads (IgG) and 6.8 million reads (H3K27me3). Data were aligned to the hg19 genome using Bowtie2. Data were filtered to remove duplicates, multi-aligned reads, and ENCODE DAC Exclusion List regions.
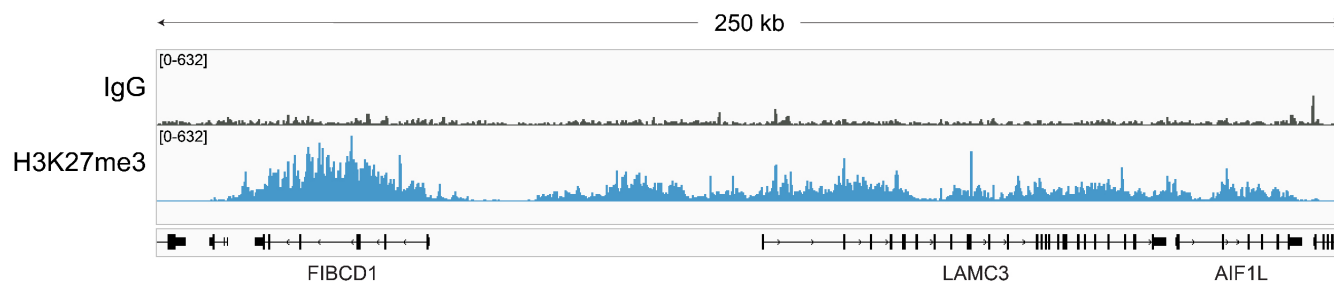

FIGURE 1 CUT&Tag data. CUT&Tag was performed as described above. Gene browser shots generated using the Integrative Genomics Viewer (IGV, Broad Institute) show a representative 250 kb window centered at the *LAMC3* gene. The genomic distribution pattern was consistent with that expected for H3K27me3.