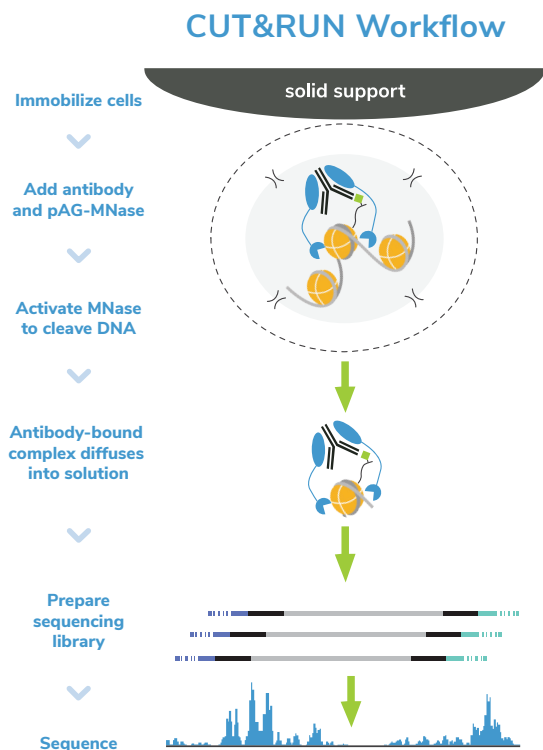# CUTANA™ CUT&RUN Assays
For Ultra-Sensitive Genomic Mapping

Cleavage Under Targets & Release Using Nuclease (CUT&RUN) is a breakthrough method for genomic mapping of protein-DNA interactions and histone post-translational modifications (PTMs). For new users, our CUTANA™ CUT&RUN platform provides everything you need to get started, including user-friendly kits, protocols, validated antibodies, and more.

CUT&RUN Workflow

Immobilize cells

solid support

Add antibody and pAG-MNase

Activate MNase to cleave DNA

Antibody-bound complex diffuses into solution

Prepare sequencing library

Sequence

Advantages

- Save 10x in sequencing costs (vs. ChIP-seq)
- Use fewer cells (down to 5k)
- Works with a diversity of targets & sample types
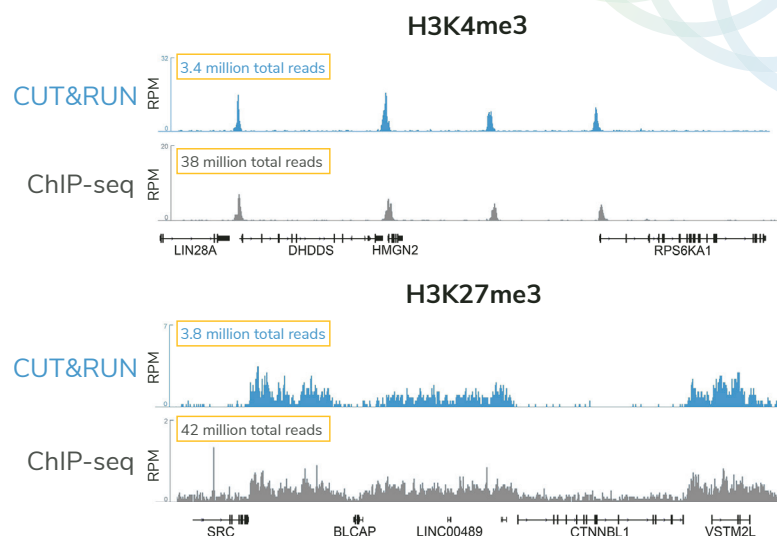- User-friendly workflow with reproducible results

H3K4me3

CUT&RUN — 3.4 million total reads

ChIP-seq — 38 million total reads

LIN28A   DHDDS   HMGN2   RPS6KA1

H3K27me3

CUT&RUN — 3.8 million total reads

ChIP-seq — 42 million total reads

SRC   BLCAP   LINC00489   CTNNBL1   VSTM2L

FIGURE 1 *CUTANA CUT&RUN outperforms ChIP-seq using fewer sequencing reads.*

CUTANA™ CUT&RUN Profiles Diverse Targets

CUT&RUN enables investigation of a wide variety of target classes, including transcription factors, chromatin-interacting proteins, and histone modifications. CUT&RUN also provides access to challenging targets like chromatin remodelers.
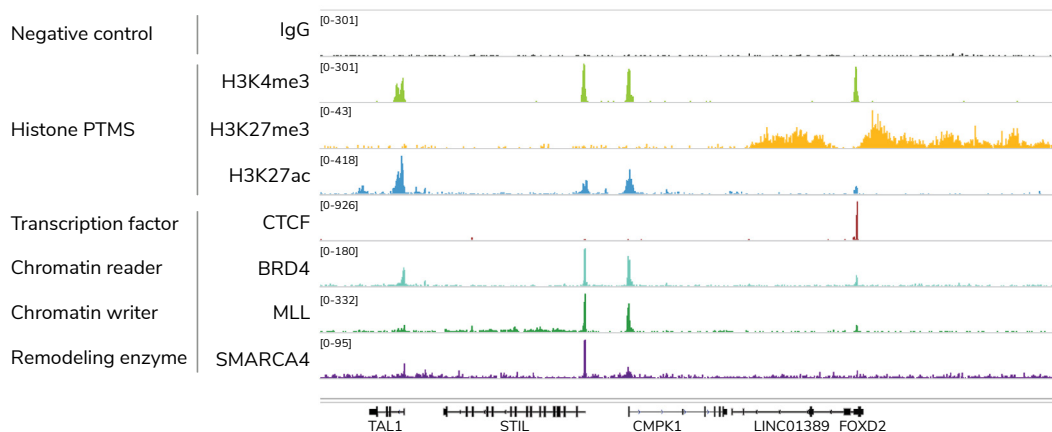
Negative control	IgG	[0-301]
Histone PTMS	H3K4me3	[0-301]
	H3K27me3	[0-43]
	H3K27ac	[0-418]
Transcription factor	CTCF	[0-926]
Chromatin reader	BRD4	[0-180]
Chromatin writer	MLL	[0-332]
Remodeling enzyme	SMARCA4	[0-95]

TAL1   STIL   CMPK1   LINC01389   FOXD2

FIGURE 2 *Representative genome browser tracks show CUTANA CUT&RUN results using K562 cells. Clear peaks with the expected distribution profile are observed using 3-8 million sequencing reads per sample for a variety of epigenetic targets.*

EpiCypher®
Bringing Epigenetics to Life

New Users: Where to Start?
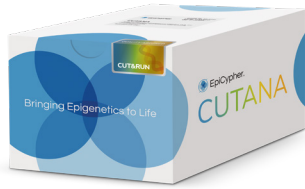
CUTANA™ CUT&RUN AND LIBRARY PREP KITS

- Together, our CUT&RUN and Library Prep Kits offer an all-inclusive workflow from cells to sequencing
- Compatible with fresh, frozen, or cross-linked cells or nuclei
- We recommend these kits to start setting up CUT&RUN in your laboratory!

CUTANA™ REAGENTS

- Design and execute custom CUT&RUN experiments
- Individual components include ConA beads, pAG-MNase, *E. coli* spike-in DNA, a DNA purification kit, and more
- All reagents tested and validated for our optimized CUTANA™ CUT&RUN workflow

CUTANA™ CUT&RUN ANTIBODIES

- Available for various chromatin targets including histone PTMs, transcription factors, and chromatin remodelers.
- Lot-validated by EpiCypher scientists for robust performance in CUTANA™ CUT&RUN assays.
- Check regularly for new targets!

SNAP Spike-ins: Quantitative Nucleosome Controls for Epigenomics

SNAP Spike-ins use panels of DNA-barcoded nucleosomes carrying widely-studied histone PTMs as quantitative spike-in controls for epigenomics assays. These controls improve assay reliability and enable accurate sample normalization. SNAP Spike-ins are now available for CUT&RUN, CUT&Tag, and ChIP-seq.
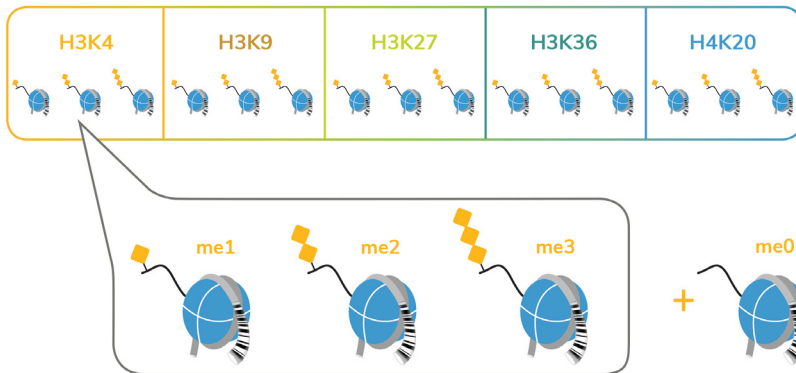
SNAP Spike-ins are useful for:

- *In situ* validation of antibody specificity
- Monitoring assay performance
- Quantitative sample comparisons
- Troubleshooting experiments

THE SNAP-CUTANA™ K-METSTAT PANEL comprises 15 DNA-barcoded dNucs carrying disease relevant methyl-lysine PTMs and an unmodified control.

EpiCypher®

epicypher.com

CUT&RUN Kit & Reagents

epicypher.com/cutana-cut-and-run-kit
epicypher.com/cut-and-run-assays

CUTANA CUT&RUN Antibodies

epicypher.com/cut-and-run-antibodies

SNAP-CUTANA Spike-in Controls

epicypher.com/snap-spike-ins