CUT&Tag Kit NPA

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EpiCypher®

Available in Canada from...

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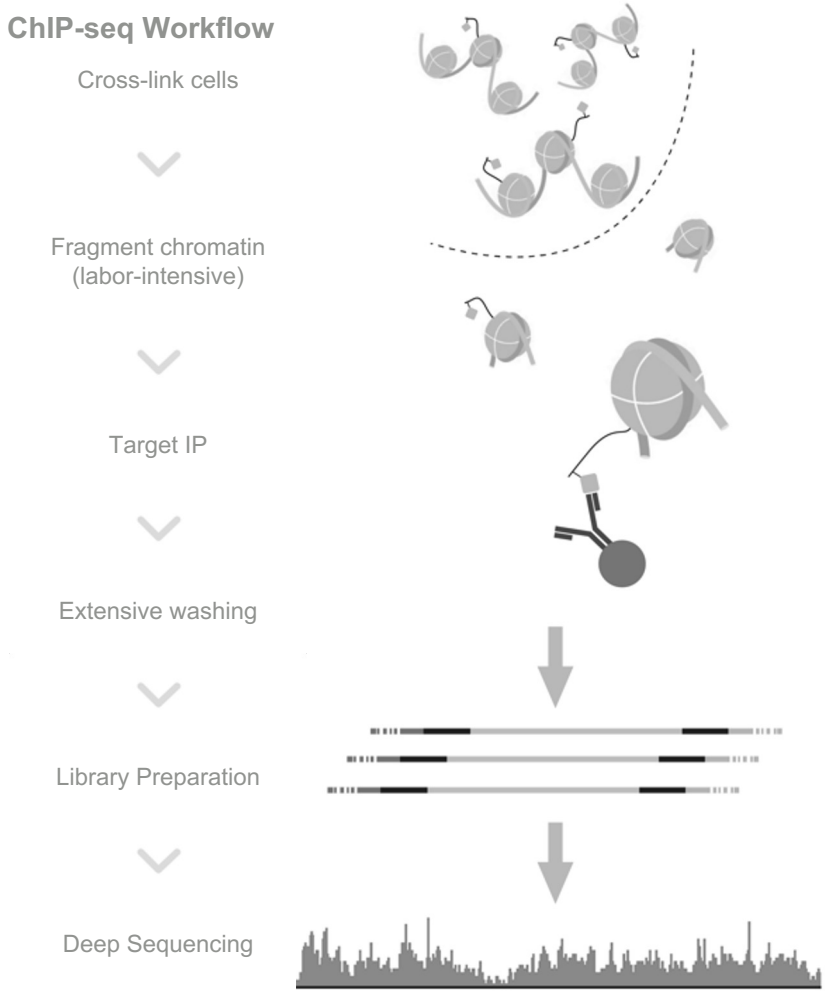
Product Information

ChIP-seq is the most widely used chromatin mapping assay - but has major limitations



Chromatin Immunoprecipitation sequencing fails key metrics for assay selection:

High cell numbers

✗

Low throughput

✗

Technically challenging

✗

High costs – deep sequencing

✗

Poor data quality, highly variable

✗

CUTANA™ CUT&RUN and CUT&Tag assays are replacing ChIP-seq

Streamlined workflows skip challenging steps of ChIP-seq, including chromatin fragmentation and antibody pull down, generating high-resolution data with fewer cells and sequencing reads.

Platform Comparison	ChIP-seq	CUTANA™ CUT&RUN	CUTANA™ CUT&Tag
Required Cells	> 1 million	5,000 - 500,000	1 - 100,000*
Sequencing Depth (Reads)	> 30 million	3-8 million	5-8 million
Experimental Throughput	Low	High	High
Signal-to-Noise	Low	High	High
Assay Automation	Difficult	Yes	Yes

* CUT&Tag has been applied for single-cell chromatin analysis in the literature. However, the recommended input for CUTANA™ CUT&Tag assays is 100,000 to 10,000 nuclei.

Passes key assay metrics

Low cell numbers

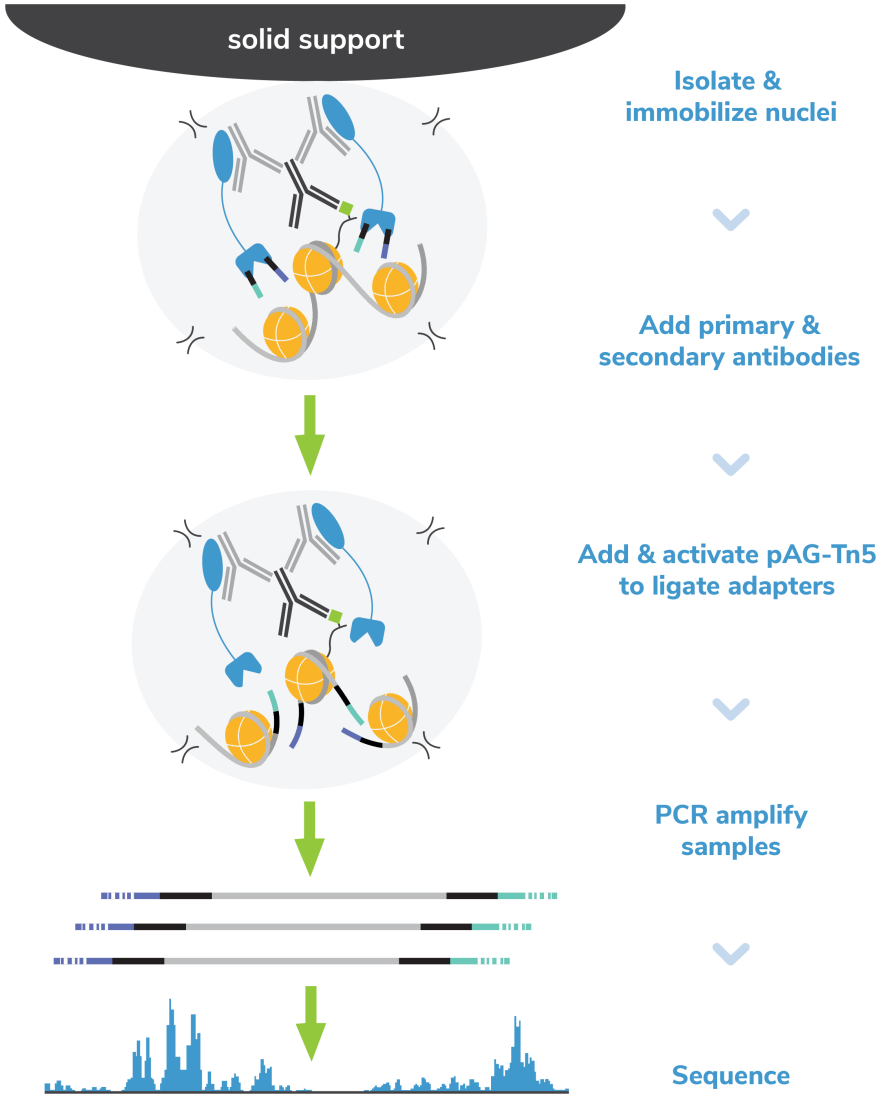
High throughput

Streamlined workflows, less optimization

Low costs – fewer sequencing reads

High-quality & reliable data

What is driving scientists to CUT&Tag?



Compared to ChIP-seq, CUT&Tag has multiple advantages:

Rapid workflow with high throughput

- ✓ No chromatin fragmentation or library prep

Compatible with low nuclei numbers

- ✓ Access rare/precious samples

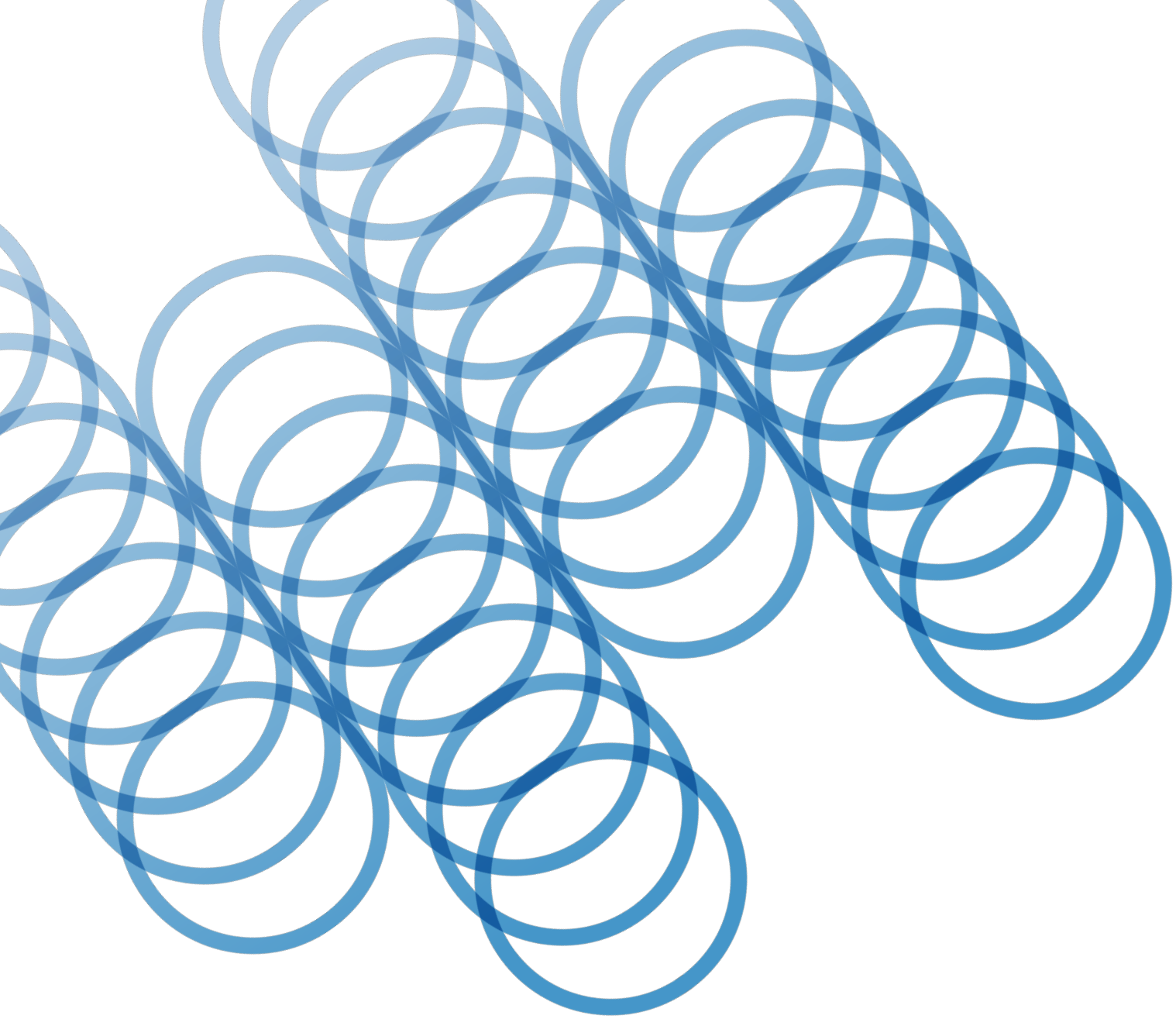
High sensitivity

- ✓ Improved signal over background

Reduced costs

- ✓ Only 5-8 million sequencing reads per reaction

EpiCypher's **exclusive protocol** goes from cells to amplified DNA in one tube and is designed for multi-channel pipetting, streamlining the workflow for high reproducibility and sensitivity

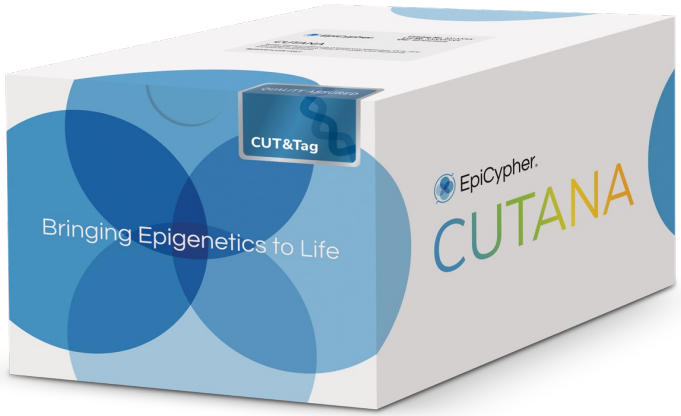


New launch!
CUTANA™ CUT&Tag Kit

KEY NOTES:

- 48-reaction kit
- Best for mapping histone PTMs (not proteins)
- Contains all necessary buffers and reagents for CUT&Tag assays

CUTANA™ CUT&Tag Kits : Powerful assays for epigenomic profiling



Cleavage Under Targets and Tagmentation (CUT&Tag) uses a fusion of protein A, protein G, and Tn5 (pAG-Tn5) to selectively target antibody-labelled chromatin for high-resolution sequencing analysis. EpiCypher is launching a CUT&Tag kit to enable use of this innovative mapping assay.

CUT&Tag assays offer unique advantages, including:

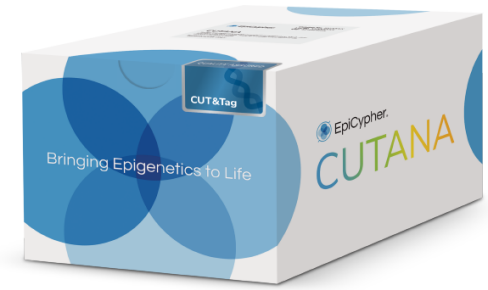
- ✓ Fast: Cells to sequencing in 2 days
- ✓ Streamlined: Exclusive single-tube protocol, no library prep
- ✓ High Sensitivity: Reliable data down to 10,000 cells
- ✓ Dramatic cost savings: Only 5-8 million sequencing reads

How does CUT&Tag work? See this video

Streamlined workflow allows higher throughput - meaning you get data FAST

- ✓ Fewer steps: One-tube workflow bypasses library prep
- ✓ Scalable: Designed for multi-channel pipetting and 8-strip tubes
- ✓ Rapid: Go from cells to sequence-ready libraries in less than 2 days

DAY 1-2

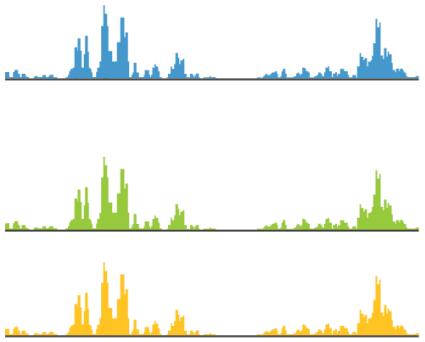


CUTANA™
CUT&Tag Kit

DAY 2-3

Next-Generation
Sequencing

DAY 3



Data
Analysis

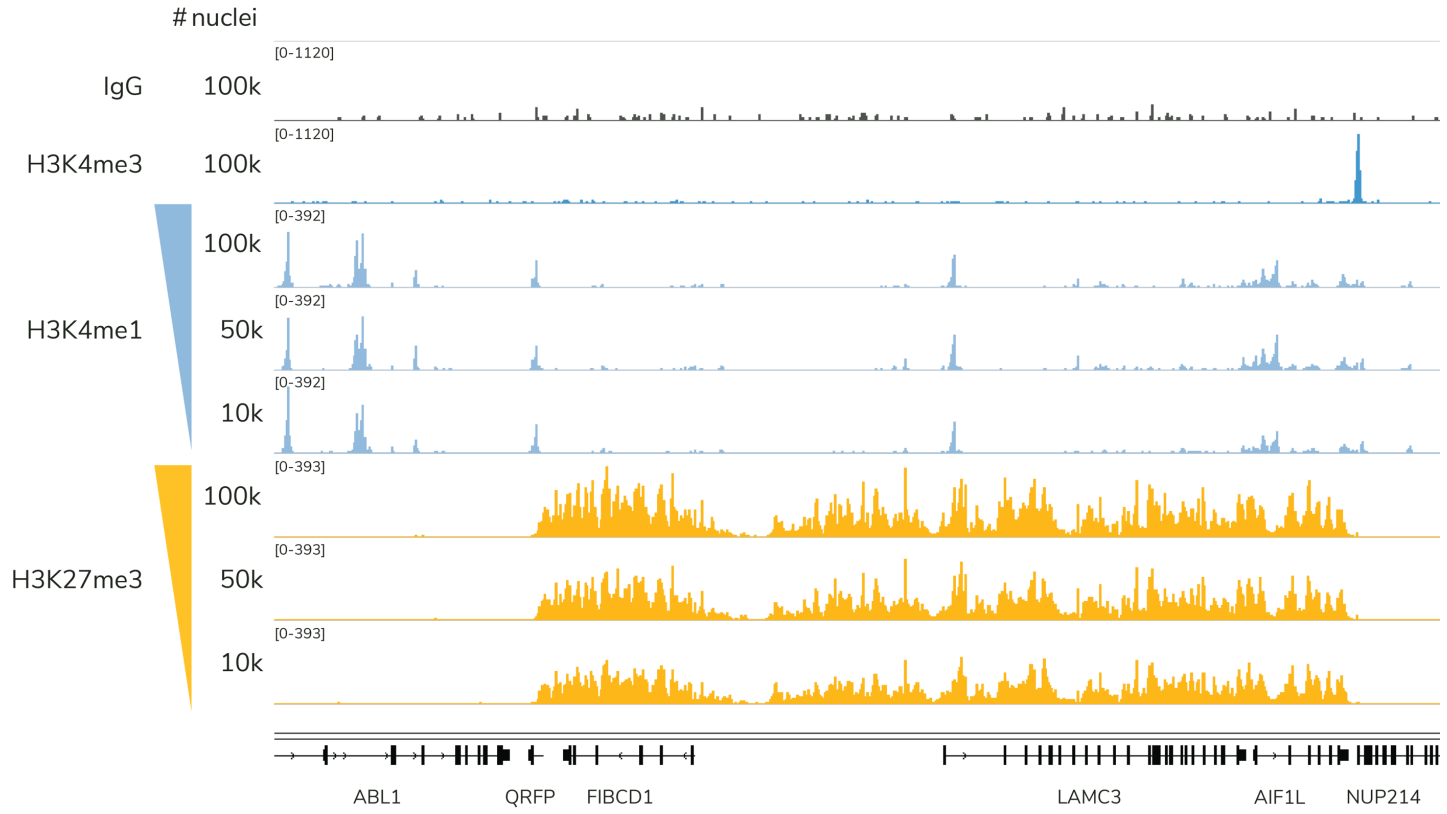
Reliable, cost-effective chromatin mapping using low cell numbers

CUTANA™ CUT&Tag provides high-quality histone PTM mapping data using:

- ✓ 100,000 to 10,000 nuclei
- ✓ 5-8 million sequencing reads

How?

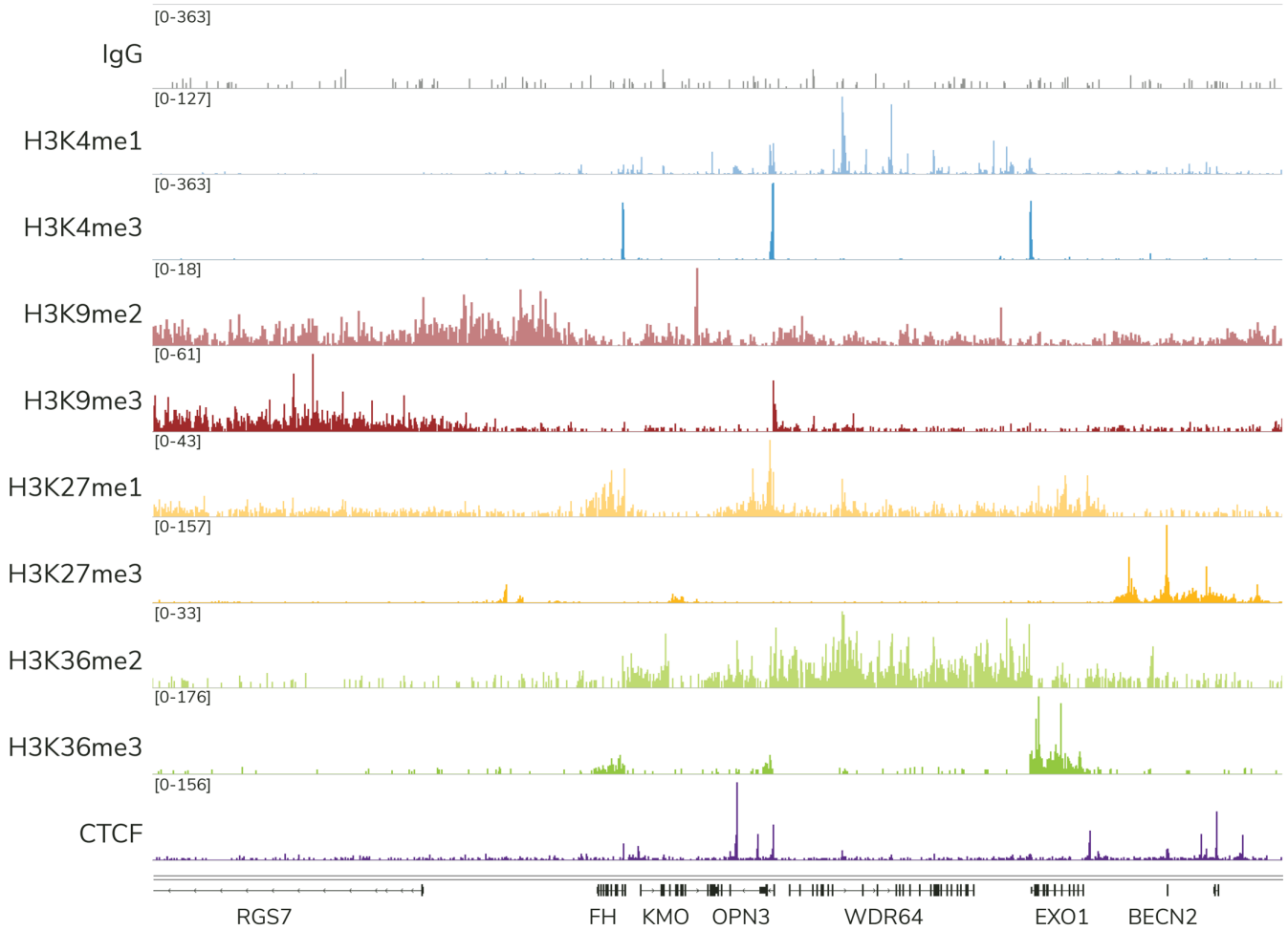
- ✓ One-tube workflow maximizes recovery
- ✓ Low background enable reduced sequencing depths – **providing major cost savings**



Representative genome browser tracks from H3K4me1 and H3K27me3 CUT&Tag experiments using decreasing amounts of K562 nuclei and 5-8 million sequencing reads.

High-quality chromatin profiling across active and repressed chromatin

- ✓ CUT&Tag is ideal for histone post-translational modifications (PTMs) in both repressed and actively transcribed regions
- X CUT&Tag is **NOT** recommended for chromatin-associated proteins, such as transcription factors



Representative genome browser tracks from CUT&Tag experiments mapping diverse histone PTMs and the transcription factor CTCF. Each reaction used 100,000 K562 nuclei and 5-8 million reads.

CUTANA™ CUT&Tag Kit – inside the box!

	Component	CUTANA™ CUT&Tag Kit
Key Assay Components	ConA	✓
	pAG-Tn5	✓
	Secondary antibody	✓
	Indexing primers 96 unique libraries	✓
	DNA purification beads	✓
Controls	- Control antibody	IgG
	+ Control antibody	H3K27me3
	Assay control	Nucleosome spike-ins
Features	Single-tube workflow	✓
	Cells to sequence-ready DNA in 2 days	✓

*Blue rows are reagents and features unique to our CUT&Tag Kit

The user-friendly kit includes CUT&Tag assay essentials and all the controls you need for successful experiments:

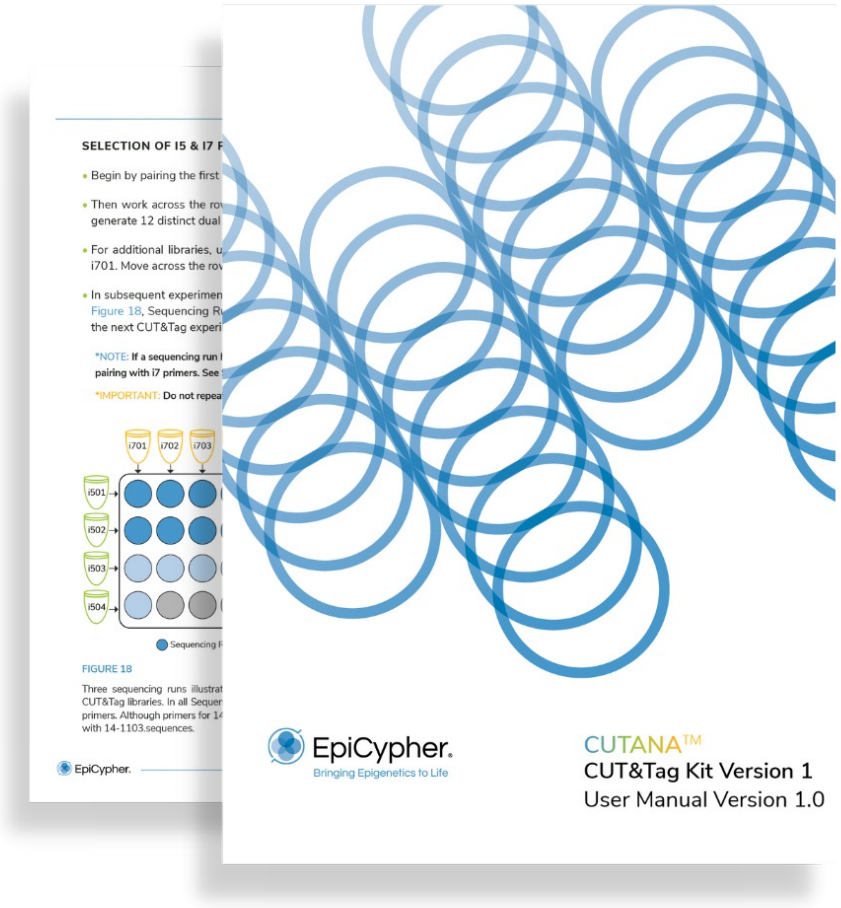
- ✓ Control antibodies
- ✓ Nucleosome spike-in controls
- ✓ Detailed quality control metrics
- ✓ Troubleshooting tips

The CUTANA™ CUT&Tag Kit Manual

The CUTANA™ CUT&Tag Manual is a complete guide to CUT&Tag experiments. Contents include:

- Validated CUT&Tag protocol
- Quality control metrics
- Guidance on experimental design
- Troubleshooting tables

The kit also comes with a protocol quick card to keep at your bench for easy access.

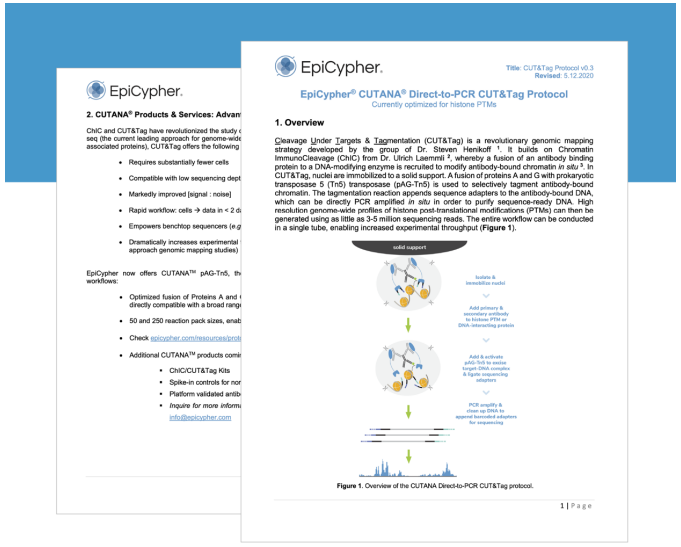


Links to Key Resources

Technical Information

CUTANA™ CUT&Tag Kit links

- Product Page
- Technical Datasheet
- CUTANA™ CUT&Tag Protocol



EpiCypher

CUTANA®
CUT&Tag Protocol

Marketing Material

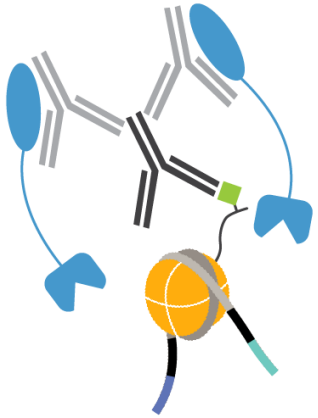
Learn the basics of CUT&Tag

- CUTANA™ Assays Overview
- CUTANA™ CUT&Tag Technology Page
- CUTANA™ CUT&Tag Product Category Page

CUT&Tag Blog posts

- Complete Step-by-Step Guide to CUT&Tag
- How to select the best histone PTM antibody for CUT&RUN and CUT&Tag
- ChIP-seq vs. CUT&RUN vs. CUT&Tag: Which should you use?
- Starting CUT&RUN or CUT&Tag for a new target - what you need to know
- Single-cell CUT&Tag: Pushing the Boundaries of Epigenomic Profiling

Companion products for CUTANA™ CUT&Tag assays



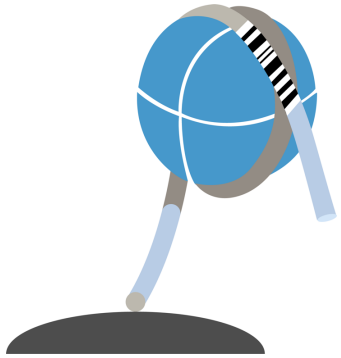
Antibodies

Target-specific antibodies for robust CUT&Tag profiles.

- H3K27me3 (Cat No. 13-0055)
- H3K4me1 (Cat No 13-0057)
- Many CUTANA CUT&RUN antibodies work for CUT&Tag: See the collection

Secondary antibodies

- Anti-mouse (Cat No. 13-0048)
- Anti-rabbit (included with kit; Cat No. 13-0047)



Spike-in Controls

SNAP-CUTANA™ Panels of nucleosome spike-ins to help determine antibody specificity and experimental success.

- SNAP-CUTANA K-MetStat Panel (Cat No. 19-1002): Use for histone lysine methylation PTMs
- Other histone PTM panels in development:
  - Lysine acylation (K-AcylStat)
  - Ubiquitylation (K-UbStat)

Magnetic racks

Immobilize samples bound to magnetic beads. Useful for CUT&Tag and other genomics workflows.

- 0.2 mL tube (Cat No. 10-0008): Streamline your workflow for increased throughput and reproducibility
- 1.5 mL tube (Cat No. 10-0012): Allows batch sample processing during ConA bead activation and sample prep

CUTANA™ CUT&Tag assays: diverse sample types and novel applications

Key cell / tissue	Application notes	Targets	Citation
Frozen human PBMCs	Single cell analysis and integration with 10X Genomics technology	H3K4me1, H3K4me2, H3K4me3, H3K27ac, H3K27me3, H3K9me3, phospho-Rpb1	Zhang et al. Characterizing cellular heterogeneity in chromatin state with scCUT&Tag-pro. *Nature Biotechnology* (2022). PMID: 35332340
K562 cells (native and cross-linked)	Single cell analysis	H3K4me3, H3K27me3, H3K36me3	Kaya-Okur et al. Efficient low-cost chromatin profiling with CUT&Tag. *Nature Protocols* (2020). PMID: 32913232
K562 cells	Characterized molecular phenotypes from CRISPR-Cas9 screens	H3K4me3 H3K27me3 H2AK119ub	Sparbier et al. Targeting Menin disrupts the KMT2A/B and polycomb balance to paradoxically activate bivalent genes. *Nature Cell Biology* (2023). PMID: 36635503
Primary spinal cord from human subjects	Used spinal cord obtained from ALS and healthy human patients	H3K27ac, H3K4me1, phospho-S166 RIPK1, SMARCC2, SMARCA4	Li et al. Nuclear RIPK1 promotes chromatin remodeling to mediate inflammatory response. *Cell Research* (2022). PMID: 35661830
FACS-sorted human T cells, exhausted T cells	Highlights CUT&Tag application in rare immune cell types	H3K4me3, H3K27me3	Ford et al. Tumor microenvironmental signals reshape chromatin landscapes to limit the functional potential of exhausted T cells. *Science Immunology* (2022). PMID: 35930654
Primary human macrophages	Primary macrophages with and without siRNA knockdown of SP140	TOP1, TOP2A	Amatullah et al. Epigenetic reader SP140 loss of function drive Crohn's disease due to uncontrolled macrophage topoisomerases. *Cell* (2022). PMID: 35952671
Drosophila embryos	Used 12-15 mouse embryos per reaction	Histone H1, H2AK9ac, H2BK16ac, H3K4me3, H3K27ac, H3K27me3, H3K36me2, total RNA Pol II, phospho-S2 RNA Pol II	Mühlen et al. Recycling of parental histones preserves the epigenetic landscape during embryonic development. *Science Advances* (2023). PMID: 36724233