Nucleosome spike-in controls enable reliable next-generation epigenomic mapping

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The Problem: Improved epigenomics assays are needed to advance epigenetics research

- Epigenomic mapping of histone post-translational modifications (PTMs) is crucial for advancing biological research, particularly in the study of the epigenetics of aging.
- Chromatin immunoprecipitation followed by sequencing (ChIP-seq) has been the predominant method for this purpose. However, ChIP-seq presents several significant limitations, such as dependency on PTM antibodies, which are often cross-reactive, and the requirement for large cell numbers, making it unsuitable for clinical or rare cell samples. Additionally, the technique frequently yields poor data quality, characterized by a low signal-to-noise ratio and poor reproducibility.
- A critical shortcoming is the lack of defined controls, which are essential for producing reliable and quantitative results. To address these challenges, Epicypher has developed defined DNA barcoded nucleosomes, known as **SNAP Spike-ins**, for use in chromatin immunoprecipitation assays. These SNAP Spike-ins enable accurate sample normalization and antibody profiling, improving data reliability and reproducibility.

Nucleosome spike-in controls show that most histone PTM antibodies fail in ChIP-seq

(A) Fully defined ChIP controls mimic physiological targets

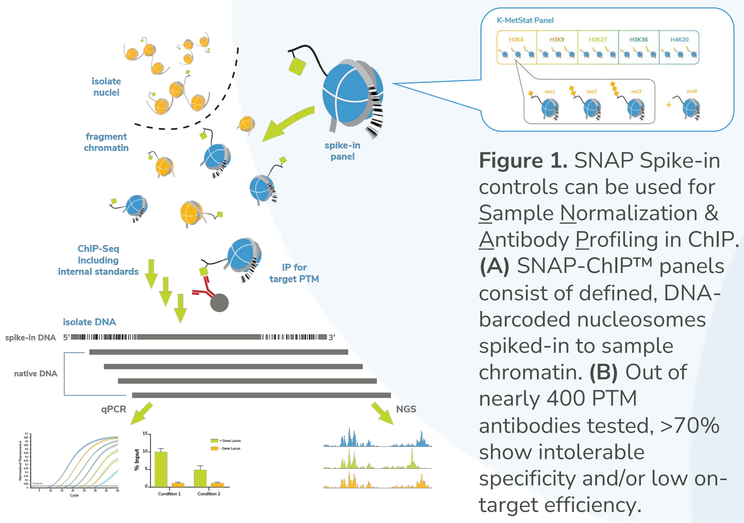


Figure 1. SNAP Spike-in controls can be used for Sample Normalization & Antibody Profiling in ChIP. **(A)** SNAP-ChIP™ panels consist of defined, DNA-barcoded nucleosomes spiked-in to sample chromatin. **(B)** Out of nearly 400 PTM antibodies tested, >70% show intolerable specificity and/or low on-target efficiency.

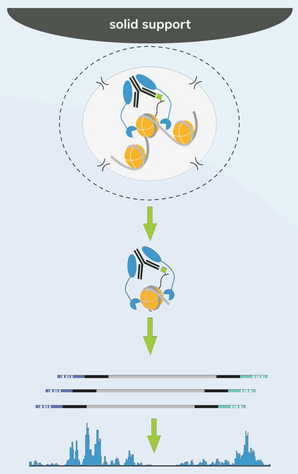
(B) Most commercial antibodies are unfit for epigenomics

Antibodies Tested by SNAP-ChIP™	Lysine Methylation	Lysine Acylation	Total
Total Tested	263	129	392
Failure Rate	74.5%	64.5%	**71.2%**
$ Spent	$105,200	$51,600	$156,800
$ Wasted	$78,374	$33,282	$111,656
Top Cited: Citations w/"ChIP"	3,720 (N=18)	1,031 (N=6)	4,751 (N=24)
Top Cited: Failure Rate	74.5%	64.5%	**79.2%**

Data available at: www.ChromatinAntibodies.com[3]

CUTANA™ CUT&RUN has major advantages over ChIP

(A) CUT&RUN Workflow



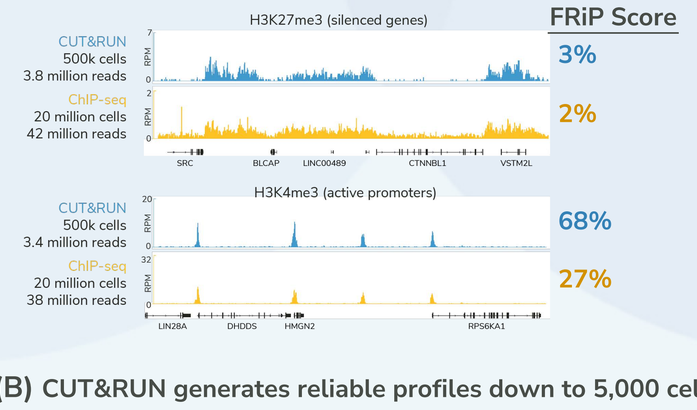
(B) CUT&RUN vs. ChIP-seq

Platform Comparison	ChIP-seq	CUTANA™ CUT&RUN
Required Cells	>1 million	5,000-500,000
Ideal for Profiling	Histone PTMs, TFs	Histone PTMs, TFs & chromatin remodelers
Sequencing Depth (Reads)	>30 million	3-8 million
Experimental Throughput	Low	High
Signal-to-Noise	Low	High
Assay Automation	Difficult	Yes

Figure 2. Overview of the CUTANA™ CUT&RUN workflow and advantages compared to ChIP-seq. Because CUT&RUN releases antibody-bound fragments into solution (**A**), it has improved signal-to-noise even with significantly reduced cell numbers and sequencing depth (**B**).

CUT&RUN enables ultra-sensitive epigenomic profiling from low cell numbers

(A) CUT&RUN vs. ChIP-seq: better data, low sequencing costs



(B) CUT&RUN generates reliable profiles down to 5,000 cells

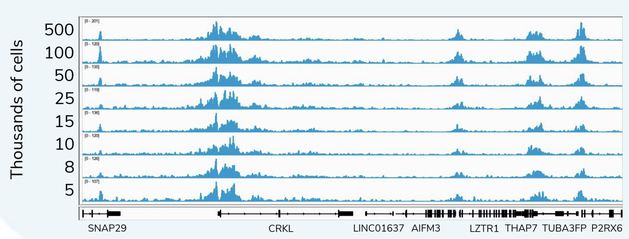
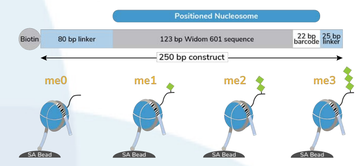


Figure 3. (A) The Fraction of Reads in Peaks (FRiP) score, a measure of signal-to-noise (S:N), is higher in CUT&RUN vs. ChIP-seq, despite using fewer cells and reduced sequencing depths. **(B)** Enrichment profiles are conserved when inputs are titrated from 500k to 5k cells.

SNAP-CUTANA™ Spike-ins are critical controls for reliable chromatin mapping

(A) SNAP Spike-ins for CUT&RUN



(B) SNAP testing identifies specific antibodies for CUT&RUN

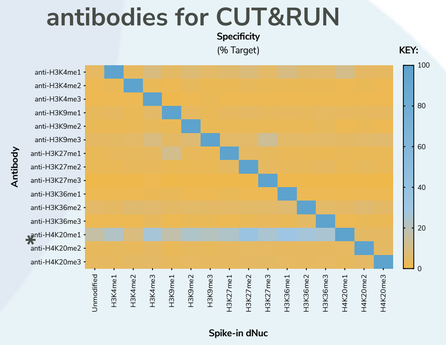
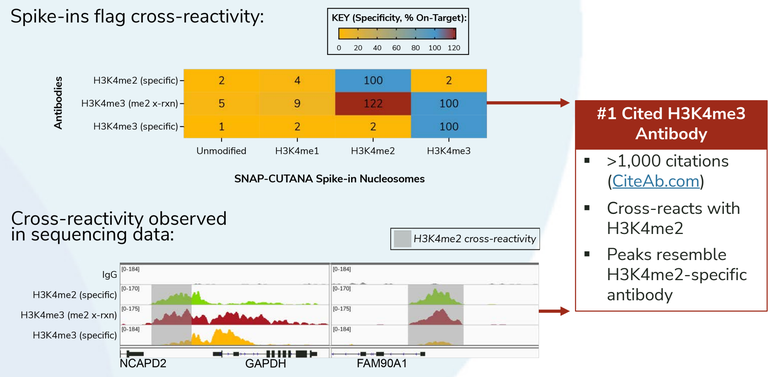


Figure 4. SNAP-CUTANA spike-in controls optimized for use in CUT&RUN (**A**) can be used to identify highly specific antibodies to widely studied histone PTMs (**B**). By spiking them into CUT&RUN workflows just prior to antibody addition, they provide a quantitative readout of on- vs. off-target recovery that predicts non-specific peaks in genomic data (**C**). **Ongoing testing for H4K20me1. Inquire at info@epicypher.com for up-to-date information.*

(C) SNAP Spike-ins predict non-specific recovery in CUT&RUN



Conclusions

- CUTANA™ CUT&RUN is poised to rapidly replace ChIP-seq
- Our data illustrate how CUT&RUN could be applied for epigenomics research, particularly for low sample inputs and/or high-throughput applications
- SNAP Spike-in controls address pervasive antibody specificity problems while enabling a direct readout of assay success and quantitative normalization (*see below!*)

References

1. Shah *et al.* Examining the roles of H3K4 methylation states with systematically characterized antibodies. *Mol. Cell* **72**, 162-177 (2018).
2. Small *et al.* Chromatin Immunoprecipitation (ChIP) to study DNA-Protein Interactions. *Methods Mol. Biol.* **2261**, 323-343 (2021).
3. Maryanski *et al.* Novel nucleosome-based methods for rapid screening and identification of best-in-class antibodies: a community resource to improve genomic mapping. *In preparation*. www.ChromatinAntibodies.com

Ultra-sensitive epigenomics drives biological discovery

Uncover novel biology with highly specific antibodies

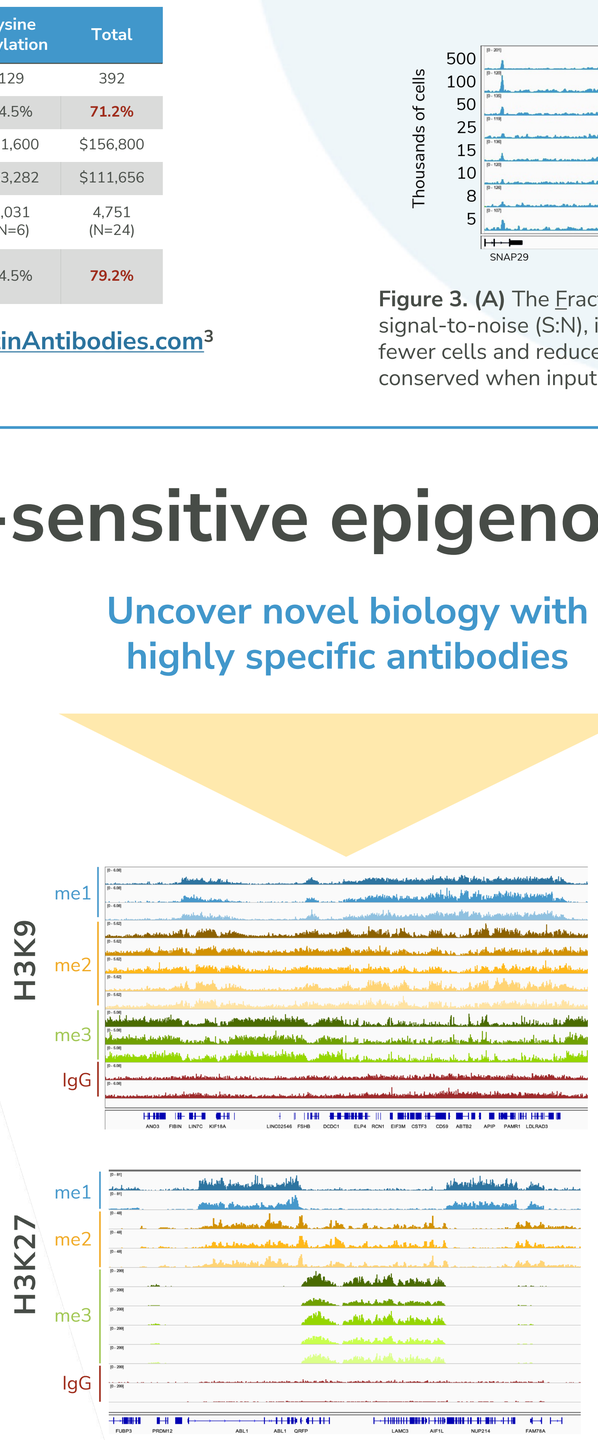


Figure 5. GENOMICALLY DISTINCT = FUNCTIONALLY DISTINCT. The use of highly specific histone PTM antibodies in CUT&RUN (**Figure 4B**) enables novel insights into the histone code. Distinct genomic profiles observed by mono-, di– and tri-methyl states imply distinct biological functions not previously appreciated.

Quantitative readout enables drug & clinical development applications

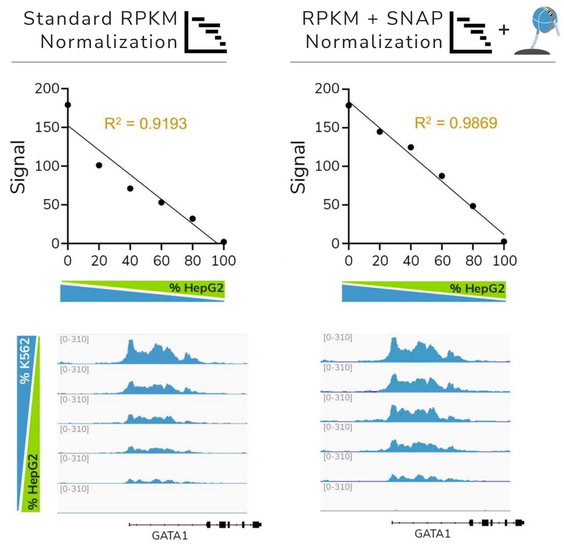


Figure 6. CUT&RUN linearity is improved by SNAP normalization. Cells with distinct lineages were mixed at defined intervals. Linear regression analysis of an H3K4me3 peak shows that SNAP normalization (**right**) shows improved linearity of a K562 cell-specific peak over standard RPKM normalization (**left**).

K562 cells (mesodermal) **HepG2 cells** (ectodermal)