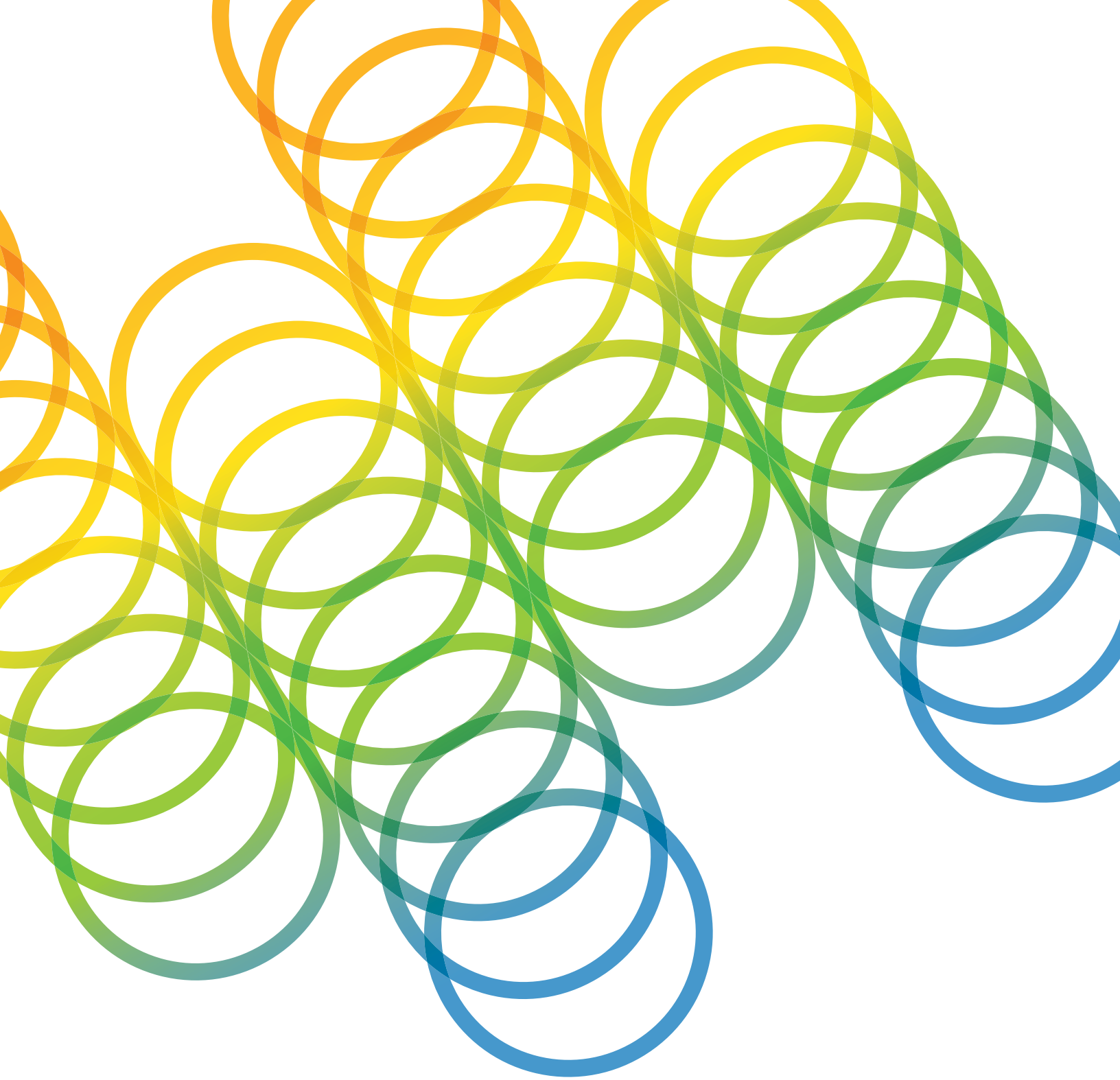


EpiCypher®
Bringing Epigenetics to Life

Stratech

# CUTANA™
## Ultra-sensitive genomic mapping assays for ChIC / CUT&RUN

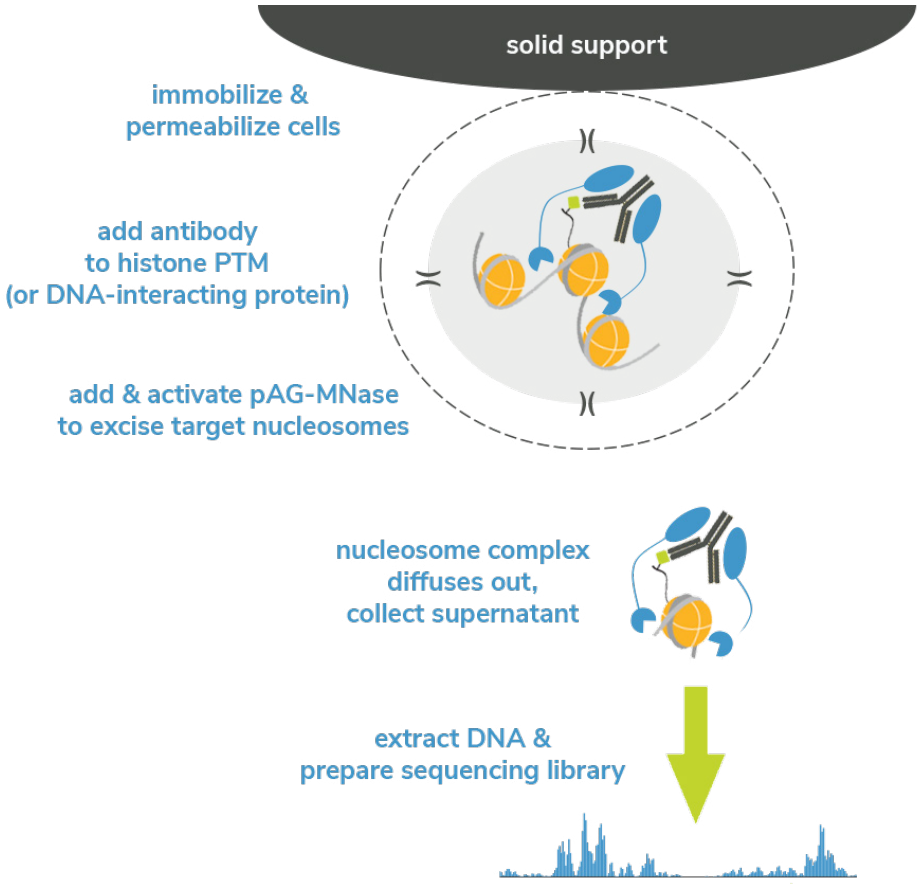
**CUTANA™** Products and Services

# CUTANA™ is an ultra-sensitive genomic mapping assay that uses a proprietary immunotethering approach similar to **Ch**romatin **I**mmuno**C**leavage (**ChIC**) and **C**leavage **U**nder **T**argets and **R**elease **U**sing **N**uclease (**CUT&RUN**) methods.

CUTANA assays are used to map histone post-translational modifications (PTMs) and chromatin interactors with high resolution. This approach leverages a factor specific antibody to tether a fusion of protein A, protein G and micrococcal nuclease (pAG-MNase) to genomic binding sites in intact cells, which is then activated by the addition of calcium to cleave DNA.

FIGURE 1

*Overview of the CUTANA approach. Cells (or nuclei) are immobilized on lectin-coated magnetic beads, permeabilized, and incubated with an antibody to a chromatin target (e.g. histone PTM or chromatin / DNA binding protein). Next, pAG-MNase is added and activated via Ca2+. The clipped chromatin fragments diffuse out, followed by DNA purification and next-generation sequencing. CUTANA assays vastly outperform those using chromatin immunoprecipitation, the current gold-standard genomic mapping assay.*




## CUTANA vastly outperforms leading ChIP-seq approaches

TABLE 1

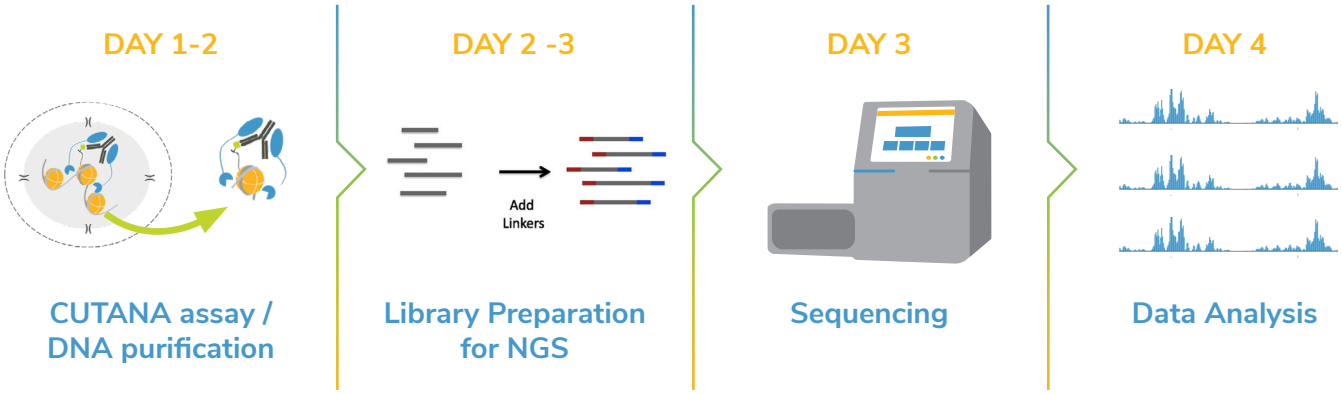
*Comparison of CUTANA assays with ChIP-seq. Low sequencing requirements, improved Signal : Noise, and reduced assay time make CUTANA far superior to ChIP-seq.*

| FEATURES | CUTANA™ | ChIP-Seq |
|---|---|---|
| Cells required | 100 | 10,000* |
| Protocol time (cells - DNA) | < 1 day | > 2 days |
| Sequencing reads required | 3 million | 30 million |
| Signal : Noise | High | Low |

*Source: Dirks et al., Clin Epigenetics. 2016 Nov 21;8:122

CUTANA is proprietary technology based on ChIC (US20070009937A1; *Schmid et. al, Mol Cell 2004*) and CUT&RUN (patent pending; *Skene and Henikoff, eLIFE 2017*) methodology.

## The CUTANA workflow - From cells to data in less than 4 days




## CUTANA saves you nearly 5-10 fold in sequencing requirements.

CUTANA assays generate superior quality data compared to ChIP-seq using as little as 3 million sequencing reads.

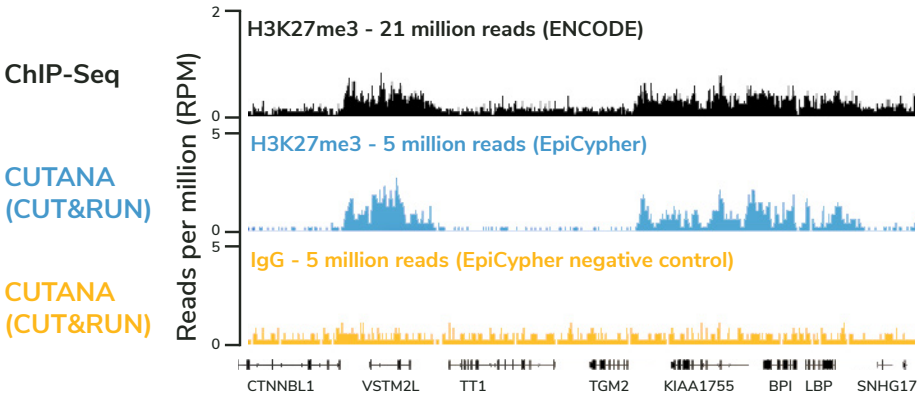



FIGURE 2

*A representative region on chromosome 20 of H3K27me3 from K-562 cells is shown, comparing standard ChIP-seq methods and sequencing depth (black) vs CUTANA (blue). H3K27me3 ChIP-Seq data was sourced from ENCODE. Negative control data (yellow) was generated using a Rabbit IgG antibody in CUTANA. Each dataset of CUTANA was acquired using 0.5 million cells.*

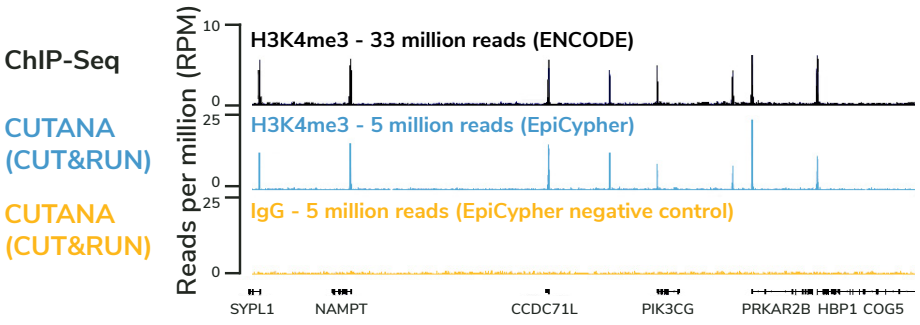



FIGURE 3

*Representative tracks of H3K4me3 on chromosome 7 from K-562 cells, comparing data generated from standard ChIP-seq methods and sequencing depth (black) to CUTANA (blue). H3K4me3 ChIP-seq data was sourced from ENCODE. Negative control data (yellow) was generated using a Rabbit IgG antibody in CUTANA. Each dataset of CUTANA was acquired using 0.5 million cells.*

**With CUTANA you can do more, faster, cheaper**

# CUTANA assays have low background and are highly reproducible! Cut through the noise with CUTANA

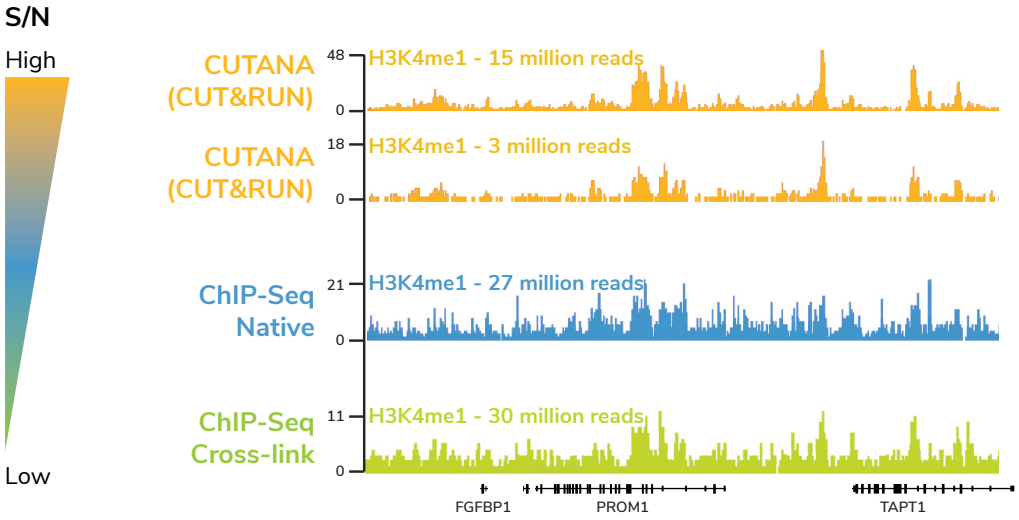



**FIGURE 4**

*A representative 350 kb region of an H3K4me1 profile in K-562 cells, generated using CUTANA (yellow panels), native ChIP-seq (blue panels), or cross-linked ChIP-seq (green panels). All data were generated by EpiCypher and are expressed as reads per million (RPM). Color-coded gradient (to left) represents signal/noise (S/N) ratios determined by genome-wide analysis (bamFingerprint data, not shown).*

## Get inspiration to design your next experiment!

Check out these papers to see validated approaches for your ChIC/CUT&RUN workflows

### ChIC workflows

- Schmid et. al, Mol. Cell 2004 (PMID : 15469830)
- Ku et. al, Nat. Methods 2019 (PMID : 30923384) **Single Cell**

### CUT&RUN workflows

- Skene and Henikoff, eLIFE 2017 (PMID : 28079019)
- Thakur and Henikoff, G&D 2018 (PMID : 29386331)
- Liu et. al, Cell 2018 (PMID : 29606353)
- Skene et. al, Nat. Protoc. 2018 (PMID : 29651053)
- Janssens et. al, Epi. Chromatin 2018 (PMID : 30577869)
- Brahma and Henikoff, Mol. Cell 2019 (PMID : 30554944)
- Oomen et. al, Genome Res. 2019 (PMID : 30655336)
- Zheng and Gehring, Plant Reprod. 2019 (PMID : 30719569)
- Ernst et. al, Nat. Commun. 2019 (PMID : 30890697)
- Hainer et. al, Cell, 2019 (PMID : 30955888)
- Meers et. al, eLIFE 2019 (PMID : 31232687)*

  * Paper describes optimized protocol using pAG-MNase*
- Meers et. al, Mol. Cell 2019 (In Press)

## ORDERING INFO

### CUTANA pAG-MNase for ChIC/CUT&RUN

Catalog No 15-1016

### Coming Soon

CUTANA pAG-MNase assay kit for ChIC/CUT&RUN

CUTANA pAG-Tn5 for ChIC/CUT&TAG

CUTANA pAG-Tn5 assay kit for ChIC/CUT&TAG

### Services

**New to CUT&RUN? Lack the resources to perform assay internally?**
**We can help!**
Inquire at **info@stratech.co.uk** to learn more about EpiCypher's 'end-to-end' assay services for ChIC/CUT&RUN

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