**CUTANA™ CUT&Tag : Powerful Platform for Streamlined, Ultra-Sensitive Epigenomics**

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**Improved assays and reagents are needed to advance epigenetic research.**

- Epigenomic mapping for histone post-translational modifications (PTMs) is essential for driving biological discovery.
- ChIP-seq is the most widely used epigenomic mapping assay, but has major limitations:
  - Depends on PTM antibodies, which are notoriously cross-reactive.
  - Requires large cell numbers, unsuitable for clinical or rare cell samples.
  - Poor data quality—low signal to noise ratio, poor reproducibility.
  - Lacks defined control—crucial for reliable, quantitative results.
- Compared to ChIP-seq, CUT&Tag² provides higher quality sequencing data with improved sensitivity and dramatically reduced background.

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**Advantages of CUTANA™ CUT&Tag over ChIP-seq**

<table>
<thead>
<tr>
<th>Platform Comparison</th>
<th>ChIP-seq</th>
<th>CUT&amp;Tag</th>
<th>CUT&amp;Run™ CUT&amp;Tag</th>
<th>CUT&amp;Tag</th>
</tr>
</thead>
<tbody>
<tr>
<td>Required Cells</td>
<td>≥1 million</td>
<td>1,000-5,000,000</td>
<td>10,000-100,000</td>
<td></td>
</tr>
<tr>
<td>Ideal for Profiling</td>
<td>Histone PTMs, TEs</td>
<td>Histone PTMs, TEs &amp; remainders</td>
<td>Histone PTMs</td>
<td></td>
</tr>
<tr>
<td>Sequencing Depth</td>
<td>&gt;30 million</td>
<td>3-8 million</td>
<td>3-8 million</td>
<td></td>
</tr>
<tr>
<td>Experimental Throughput</td>
<td>Low</td>
<td>High</td>
<td>High</td>
<td></td>
</tr>
<tr>
<td>Signal-to-Noise</td>
<td>Low</td>
<td>High</td>
<td>High</td>
<td></td>
</tr>
<tr>
<td>Library Prep</td>
<td>Standard</td>
<td>Standard</td>
<td>Streamlined Direct-in-PCR</td>
<td></td>
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</tbody>
</table>

**Figure 1.** Overview of the CUTANA™ CUT&Tag workflow and advantages compared to ChIP-seq. Because CUTANA™ technologies release antibody-bound fragments into solution (A), it has improved signal-to-noise even with significantly reduced cell numbers and sequencing depth (B). In CUT&Tag, pAC-TnX inserts sequencing adapters at antibody-bound chromatin in intact nuclei, streamlining library preparation.

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**CUTANA™ CUT&Tag is ideal for mapping histone PTMs**

- (A) CUT&Tag delivers robust data across diverse PTM targets.
- (B) TSS Enrichment
- (C) Standard Enrichment

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

- (A) SNAP Spike-ins for CUT&Tag Technologies
- (B) SNAP testing identifies specific antibodies
- (C) Spike-In Workflow

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**CUTAC : Identifying Open Chromatin with Modified CUT&Tag**

- (A) CUTAC conditions differ from CUT&Tag
- (B) CUTAC releases smaller genomic fragments than CUT&Tag
- (C) CUTAC shows stronger signal than Omni-ATAC
- (D) CUTAC, CUT&Tag, and Omni-ATAC enrichment relative to TSS
- (E) Peak calling comparisons across CUTAC, CUT&Tag, and Omni-ATAC

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**Conclusions**

- CUTANA™ technologies (CUT&RUN and CUT&Tag) are poised to rapidly replace ChIP-seq.
- CUT&Tag uses a streamlined protocol to produce high quality data for diverse targets with low cell number requirements and reduced sequencing costs.
- SNAP Spike-ins control inform antibody specificity and monitor assay success.
- CUTAC recapitulates published ATAC-seq datasets but with significantly improved sensitivity and signal-to-noise.

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**References**

4. Wen Sun et al. CUT&Tag: Efficient chromatin accessibility mapping in chry</n>