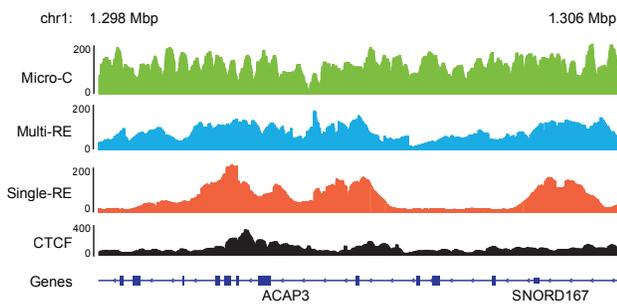


## Not All Hi-C Is Created Equal

### The Micro-C Difference

Hi-C is a powerful tool for understanding 3D chromosome architecture, how chromatin topology influences cellular function and how topological changes contribute to disease. However, traditional Hi-C, relying on sequence biased restriction enzymes, has significant limitations. The Dovetail® Micro-C Assay addresses many of these limitations.

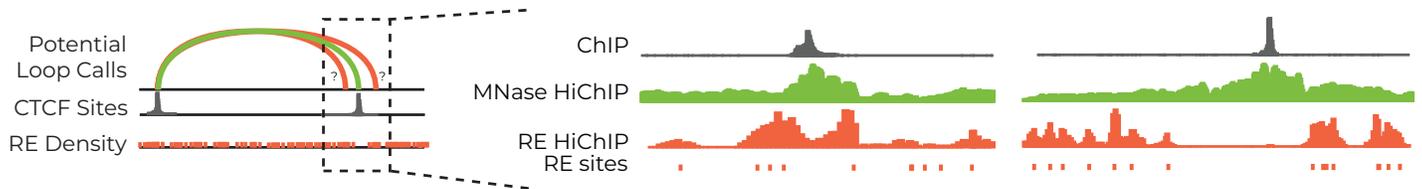
### Dovetail Micro-C Captures More of the Genome



**FEATURE:** Micro-C produces more uniform coverage of the genome overcoming sequence gaps present in traditional Hi-C data due to low restriction site density.

**BENEFIT:** Capture more chromatin topology across more of the genome.

### Dovetail Micro-C More Accurately Captures Biology



**FEATURE:** Traditional Hi-C is biased by restriction enzyme motif location, which can distort identified topological features. Micro-C's use of the sequence independent enzyme, micrococcal nuclease, eliminates this bias.

**BENEFIT:** More accurate calling of topological features such as chromatin loops.

### Dovetail Micro-C Reduces Overall Experiment Cost

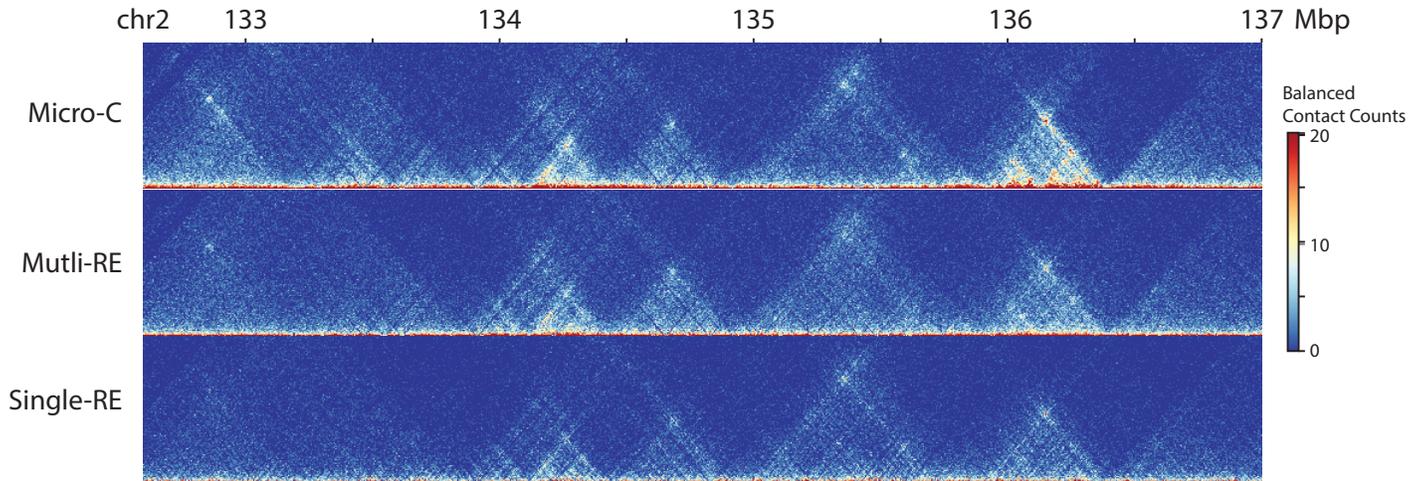
Assay	Total Input (# Cells)	Sequencing (# read pairs)	Total Cost (USD)*	Loops (5 kbp)	Cost per Loop (USD)
Micro-C	1 Million	800 Million	\$3,900	8,649	\$0.45
Multi-RE	5-10 Million	1.2 Billion	\$4,950	4,639	\$1.07
Single-RE	5-10 Million	1.6 Billion	\$8,800	1,597	\$5.57

**FEATURE:** Micro-C bolstered signal-to-noise reduces sequencing cost and requires less sample compared to traditional Hi-C.

**BENEFIT:** Significant savings on sequencing and sample preparation costs without compromising experimental discoveries; in fact, even at lower sequencing coverage, Micro-C detects more loops than traditional Hi-C.

\*Combines assay cost and sequencing cost

# Micro-C Generates the Best-in-Class Contact Matrices



**FEATURE:** Contact matrices show an enrichment of contacts compared to traditional Hi-C approaches due to Micro-C's greater signal-to-noise. All matrices were generated from 800 million total read pairs and contacts were balanced.

**BENEFIT:** Increased sensitivity for topological features at lower sequencing depths.

## Dovetail Solutions

Leveraging the advantages of the Dovetail Micro-C Assay in Genome-wide or Targeted Approaches.

Application	Micro-C	HiChIP	Pan Promoter Panel
A/B Compartments	✓		
TADs	✓		
Chromatin Loops	✓		
Chromatin Ultrastructure	✓		
Protein-Directed Interactions		✓	
Enhancer-Promoter Loops			✓
Hybrid-Capture Compatible	✓		

## Publications

The Dovetail Micro-C Assay is enabling new discoveries in fields such as gene regulation, developmental biology and human disease.

Publication	Summary
<p><b>MCM complexes are barriers that restrict cohesin-mediated loop extrusion.</b>                      Dequeker et al. 2022.  <a href="https://doi.org/10.1038/s41586-022-04730-0">https://doi.org/10.1038/s41586-022-04730-0</a></p>	<ul style="list-style-type: none"> <li>The minichromosome maintenance (MCM) complex is a barrier that restricts loop extrusion in G1 phase.</li> <li>MCM loading reduces CTCF-anchored loops and decreases TAD boundary insulation.</li> <li>MCMs are physical barriers that frequently constrain cohesin translocation <i>in vitro</i>.</li> </ul>
<p><b>Targeting Swi/SNF ATPases in enhancer-addicted prostate cancer.</b>                      Xiao et al. 2022.  <a href="https://doi.org/10.1038/s41586-021-04246-z">https://doi.org/10.1038/s41586-021-04246-z</a></p>	<ul style="list-style-type: none"> <li>The chromatin remodeler SWI/SNF complex is altered in over 20% of cancers and the ATPase subunits can be degraded with PROTAC.</li> <li>Prostate cancer cells that express AR and FOXA1 are highly sensitive to PROTAC-degradation.</li> <li>SWI/SNF ATPase degradation disrupts super-enhancer and promoter looping interactions that wire expression of oncogenes.</li> </ul>
<p><b>Loss of epigenetic information as a cause of mammalian aging.</b>                      Yang et al. 2023.  <a href="https://doi.org/10.1016/j.cell.2022.12.027">https://doi.org/10.1016/j.cell.2022.12.027</a></p>	<ul style="list-style-type: none"> <li>Cellular responses to double-stranded DNA breaks erode the epigenetic landscape and accelerates the hallmarks of aging.</li> <li>These changes are reversible by epigenetic reprogramming, including TAD boundaries and E-P interactions.</li> <li>By manipulating the epigenome, aging can be driven forward and backward.</li> </ul>