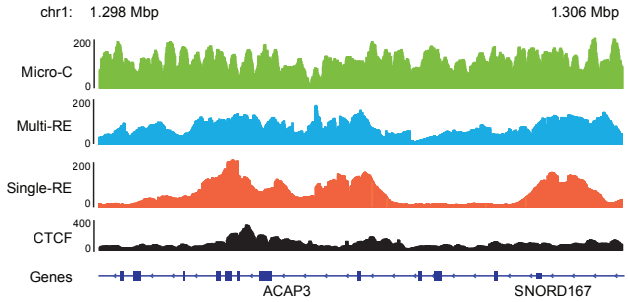
Dovetail GENOMICS
Part of Cantata Bio, LLC

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.

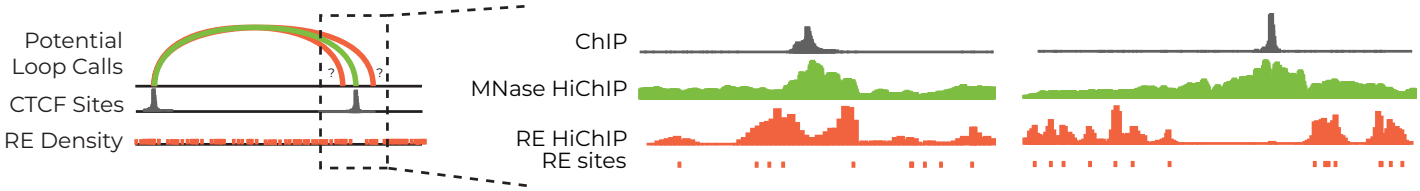
Dovetail Micro-C Captures More of the Genome



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

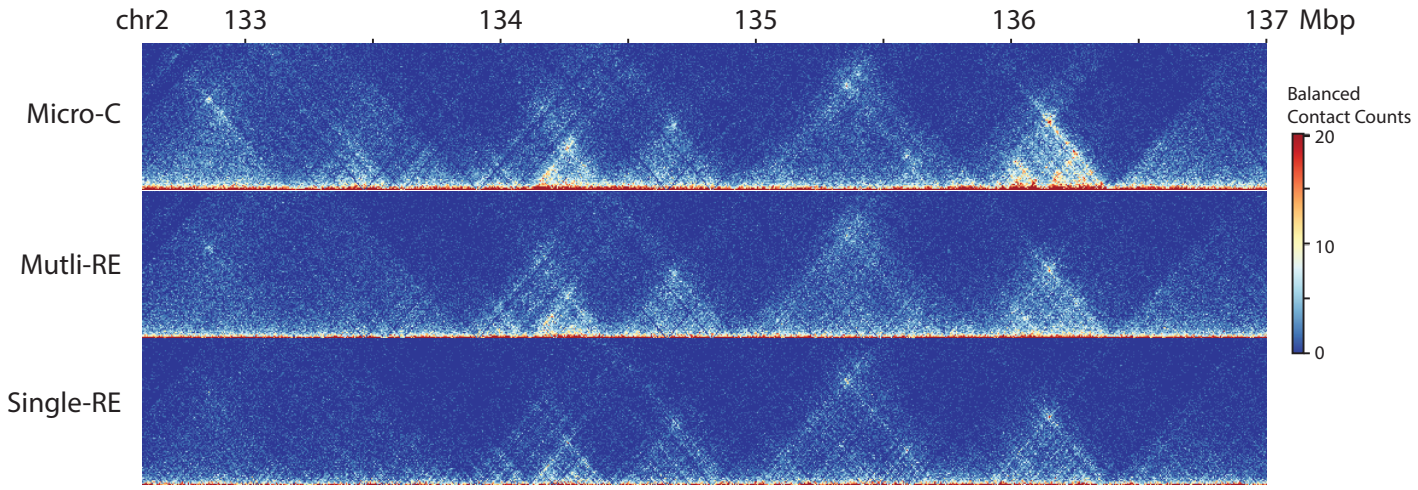
Assay	Total Input (# Cells)	Sequencing (# read pairs)	Total Cost (USD)*	Loops (5 kbp)	Cost per Loop (USD)
Micro-C	**1 Million**	**800 Million**	**$3,900**	**8,649**	**$0.45**
Multi-RE	5-10 Million	1.2 Billion	$4,950	4,639	$1.07
Single-RE	5-10 Million	1.6 Billion	$8,800	1,597	$5.57

*Combines assay cost and sequencing cost

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.

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 Comparments	✓		
TADs	✓		
Chromatin Loops	✓		
Chromatin Ultrastructure	✓		
Protein-Directed Interactions		✓	
Enhancer-Promoter Loops			✓
Hybrid-Capature Compatible	✓		

Publications

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

Publication	Summary
MCM complexes are barriers that restrict cohesin-mediated loop extrusion, Dequeker et al., 2022, https://doi.org/10.1038/s41586-022-04730-0	• The minichromosome maintenance (MCM) complex is a barrier that restricts loop extrusion in G1 phase. • MCM loading reduces CTCF-anchored loops and decreases TAD boundary insulation. • MCMs are physical barriers that frequently constrain cohesin translocation *in vitro*.
Targeting Swi/SNF ATPases in enhancer-addicted prostate cancer, Xiao et al., 2022, https://doi.org/10.1038/s41586-021-04246-z	• The chromatin remodeler SWI/SNF complex is altered in over 20% of cancers and the ATPase subunits can be degreated with PROTAC. • Prostate cancer cells that express AR and FOXA1 are highly sensitive to PROTAC-degredation. • SWI/SNF ATPase degradation disrupts super-enhancer and promoter looping interactions that wire expression of oncogenes.
Loss of epigenetic information as a cause of mammalian aging, Yang et al., 2023, https://doi.org/10.1016/j.cell.2022.12.027	• Cellular responses to double-stranded DNA breaks erode the epigenetic landscape and accelerates the hallmarks of aging. • These changes are reversible by epigenetic reprogramming, including TAD boundaries and E-P interactions. • By manipulating the epigenome, aging can be driven forward and backward.