Dovetail GENOMICS
Part of Cantata Bio LLC

Understand Promoter-Enhancer Dynamics Using Promoter-Targeted Micro-C

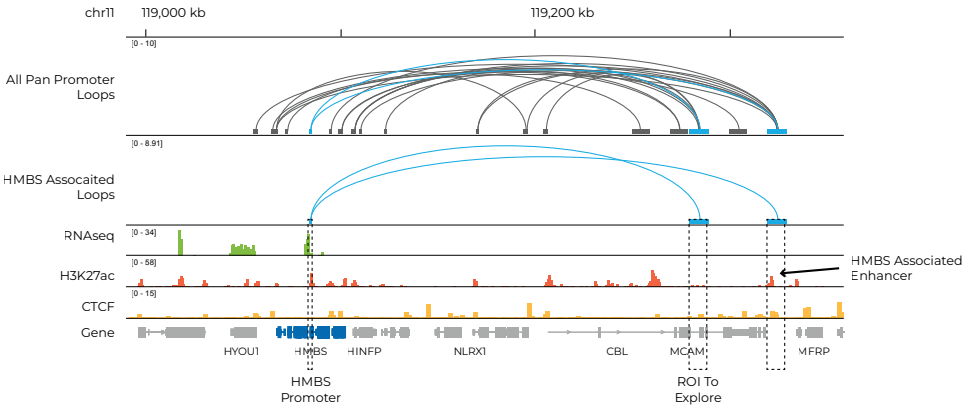
Gain novel insight of how distal regulatory elements interact with promoters

Reduce sequence cost compared to genome wide approaches

Maximize your discovery potential

View Gene Expression in a New Dimension

NGS datatypes such as ChIP-seq and ATAC-seq are blind to the 3D architectural structure that connects promoter and enhancers over long distances. The power of promoter targeted Micro-C data is illustrated below – interactions within vicinity of the HMBS gene identify two HMBS associated interactions spanning >200 kb of sequence. These map to enhancer (H3K27ac) and CTCF marks respectively. Enhancer marks closer to the HMBS gene do not show evidence of interactions.



Sequence Less and Discover More, While Simplifying Data Analysis

Whole genome experiments can require well over 1 billion read pairs to call chromatin interactions. Consequently, many studies are either underpowered or too costly to consider. By anchoring sequenced reads to promoters, sequencing depth requirements are reduced 10-fold and the resulting data is more sensitive. Compared to whole genome data, a greater number of intereactions are detected with virtually all data being informative of promoters. The data generated from the Pan Promoter Panel easily integrates with open-source tools enabling simple, robust analysis.

DTG Pan-Promoter Panel fastqs + CHiCAGO Analysis

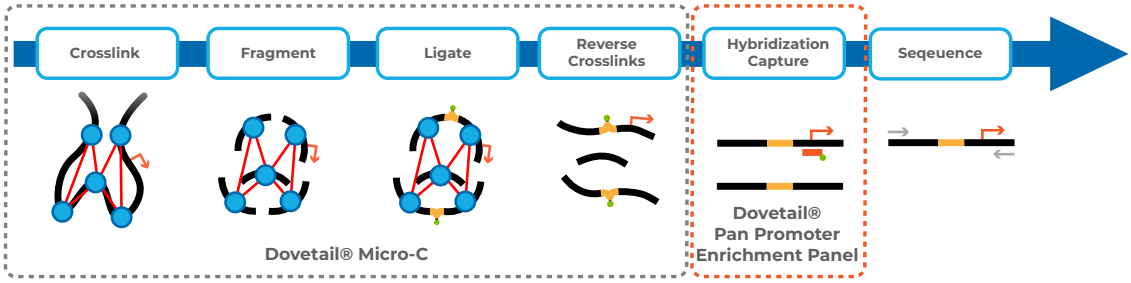
- Quality Control
- Priotized Table of Loops
- Integratable Outputs

	Sequence Less	Call More Loops	Highly Targeted
Assay	**# Read Pairs**	**# Loops***	**% Promoter Loops**
Hi-C	1.6 Billion	7,092	37.5%
Micro-C	800 Million	12,643	43.9%
Pan Promoter Panel	150 Million	21,995	100%

*Hi-C and Micro-C loops were detected with Mustache on default settings at 10kb resolution; Pan Promoter loops were detected with CHiCAGO on default settings at 10kb resolution.

The Promoter Pan Promoter Panel Works in Tandem with Micro-C

Whether you are new to Hi-C or already using Hi-C in your lab, the workflow uses common molecular biology steps and follows a six-step workflow completed over two days. Hybridization capture is performed on the final Micro-C library immediately prior to sequencing and interactions are detected using Illumina paired-end sequencing. Already a Dovetail® Micro-C user? Existing Dovetail Micro-C libraries can be target enriched without the need to create new libraries for this purpose.



Going from Sample to NGS Library through Kits and Services

Kit purchasing information – services please reach out to your regional Cantata Bio sales representative.

Part Name	Catalog #
Dovetail Micro-C Kit	#21007
Pan Promoter Enrichment Kit	#23013 (Human); #25014 (Mouse)
Dovetail Library Module for Illumina	#25004
Dovetail Dual Index Primer Set # 1 for Illumina	#25010

Specifications	
Reaction	4 with up to 8 libs multiplex/rxn
Maximum # of Libraries	32
Validated Samples	Human or Mouse/span
Compatible Kits	Dovetail Micro-C & Omni-C Kits
Labeling	For Research Use Only
Module 1 of 3 – content	Streptabidin Binding Beads DNA Purification Beads Binding Buffer Wash Buffer 1 Wash Buffer 2
Module 1 of 3 – storage	2° - 8° C
Module 2 of 3 – content	Universial Blockers Blocker Solution Hybridization Mix Hybridization Enhancer Amplification Primers Capture Amplification Mix
Module 2 of 3 – storage	-25° - -15° C
Module 3 of 3 – content	Pan Promoter Panel
Module 3 of 3 – storage	-25° - -15° C

Cantata Bio

 www.cantatabio.com
We are Cantata Bio. Delivering powerful, novel NGS-based products and services.