Dovetail GENOMICS
Part of Cantata Bio, LLC

Explore Promoter-Enhancer Dynamics Using Promoter-Targeted Linked-Reads

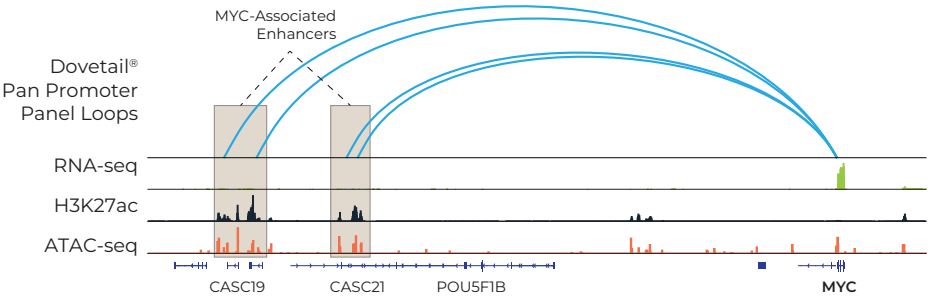
Gain novel insight of how distal regulatory elements interact with promoters

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 promoters and enhancers over long distances. The power of promoter targeted linked-read data is illustrated in the figure. Interactions anchored at the MYC proto-oncogene promoter span >700 kb of sequence and identify upstream regulatory regions. These regions map to enhancer (H3K27ac) and open chromatin (ATAC-seq) marks. Enhancer marks closer to the MYC 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 compared to non-targeted approaches and the resulting data is more sensitive. Compared to whole genome data, a greater number of interactions are detected with all data being informative of promoters. The data generated from the Pan Promoter Panel easily integrates with open-source tools enabling simple, robust analysis.

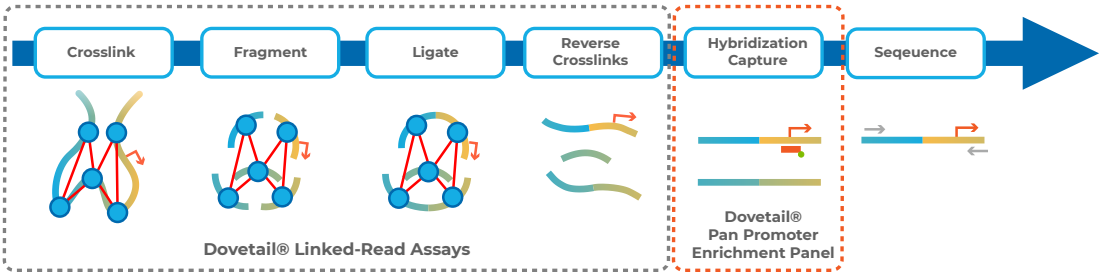
- Quality Control
- Priotized Table of Loops
- Integratable Outputs

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

*Non-targeted assays were analyzed with Mustache on default settings at 10kb resolution; Pan Promoter loops were detected with CHiCAGO on default settings at 10kb resolution.

The Pan Promoter Panel Works in Tandem with Dovetail Linked-Read Kits

The workflow uses common molecular biology steps and follows a six-step workflow completed over two days. Hybridization capture is performed on the final linked-read library immediately prior to sequencing and interactions are detected using Illumina paired-end sequencing. Already a Dovetail® Kit user? Existing Dovetail libraries can be target enriched without the need to create new libraries for this purpose.

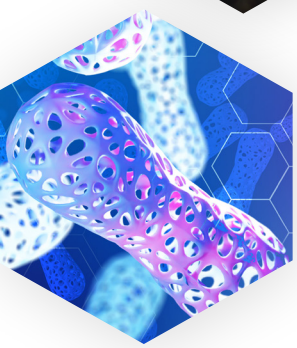


Capture Promoter-Driven Interactions With Comprehensive Panel Contents

The panels are optimized to capture all promoter content in either human or mouse genomes. This enables researches to directly link ChIP-seq, ATAC-seq, or GWAS derived data to cognate promoters, accelerating research while simplifying conclusions.

Human *Ensembl: GRCh38 v.86*	**Coverage**
Genes	27,375
Coding Genes	19,725
LncRNA	7,630
Promoters	84,643
Coding Genes	72,043
LncRNA	12,353
Probes	161,144

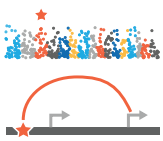
Mouse *Ensembl: GRChm38 v.79*	**Coverage**
Genes	24,141
Coding Genes	21,676
LncRNA	2,469
Promoters	47,739
Coding Genes	44,372
LncRNA	3,369
Probes	117,974



Power Your Applications Through Targeted Genomic Interactions

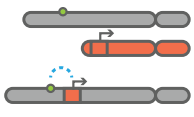
Targeted genomic interactions provide novel insight into several applications. Link non-coding variants and VUS in GWAS data to gene content. Expand your view into oncogenic gene regulation through discovery of enhancer hijacking. Reduced sequencing requirments enable scalable 3D genomics experiments to increased sample sizes or for more rigorous statistical analyses.

GWAS



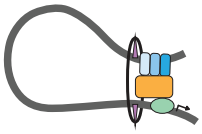
Illuminate genomic dark matter

Oncology



Uncover enhancer-hijacking

3D Genomics



Increase sensitivity with reduced sequencing

Learn more at dovetailgenomics.com