

Dovetail® Epigenetics Services



Dovetail Genomics offers a one-stop solution for sample-to-data processing. Jump start your studies with data ready for downstream analysis and interpretation.

Benefits

- Save time on optimization
- Ease of mind
- Obtain analysis ready data
- Fast turn-around-time
- Project consultation with the Dovetail scientific experts

Dovetail® Micro-C Service For Genome-Wide Analysis

Dovetail Genomics employs micrococcal nuclease (*MNase*) in our Dovetail® Micro-C Assay. The resulting highly uniform, short fragments enable nucleosome-level resolution of chromatin contacts, a theoretical resolution maximum. Choose from one of two resolutions (TADs or loops calling) to meet your study objectives.

Features

- Data free of restriction enzyme bias
- Highest resolution Hi-C data
- Improved coverage over nucleosomes
- Detect nucleosome-to-nucleosome interactions

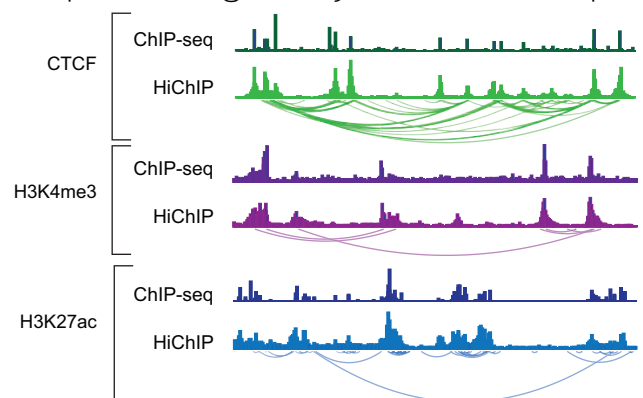


Dovetail® HiChIP *MNase* Service

Combines standard ChIP-seq approaches with Hi-C, an approach that captures long-range 3D genomic interactions, to offer a consolidated view of important regulatory interactions impacting gene expression.

Features

- Available for CTCF, H3K4me3, or H3K27ac
- Map chromatin interactions at nucleosome level resolution
- Capture ChIP-seq & Hi-C data in a single library

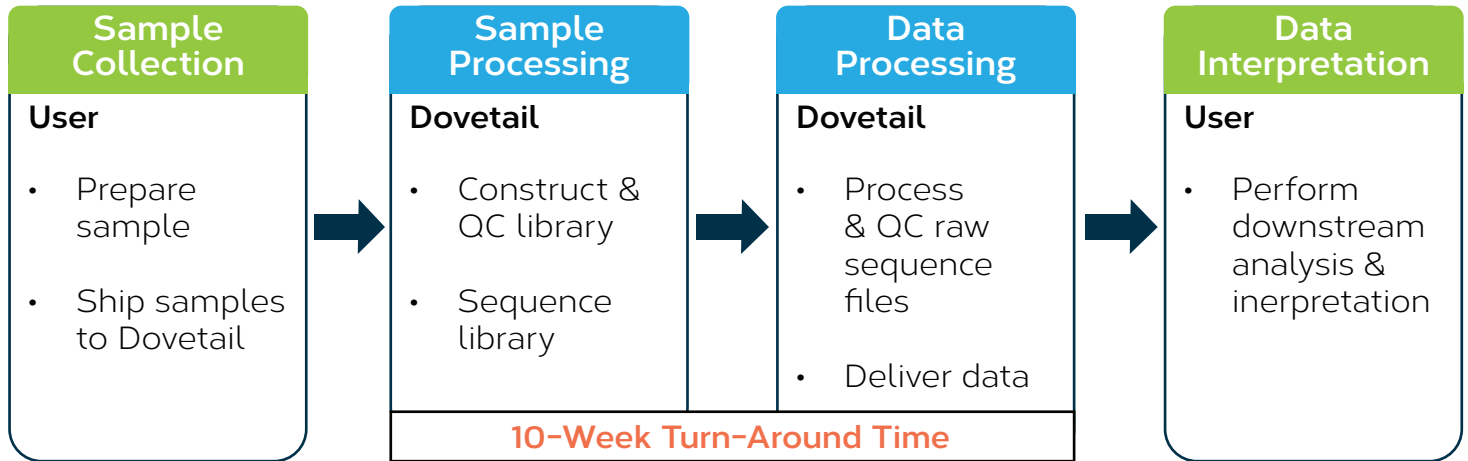


Power your HiChIP by adding *MNase* based ChIP-seq. Designed to augment a HiChIP service project, our ChIP-seq service uses the same chromatin fragmentation strategy as HiChIP ensuring the highest data concordance.

To place an order or for more information:

visit us at www.dovetailgenomics.com or send an email to info@dovetail-genomics.com

Sample To Data Overview



Sample Type and requirement

Service is available for human, mouse and rat for both tissues and cell lines. Contact Dovetail Genomics for sample requirement and shipping guidelines.

Sample To Data Overview

File Description	File Type	Description
Summary statistics	PairTools output	Alignment & proximity-ligation metrics
Sequence data	Fastq file format	Micro-C (Loops): 800 M read-pairs / sample Micro-C (TADs): 330 M read-pairs / sample HiChIP: 200 M read-pairs / sample
Alignment file	*.bam & *.bw files	Linear coverage assessment
Pairs coordinates	*.pairs file	4D Nucleome standard format
Contact matrices	*.mcool, *.cool & *.hic files	Ready for downstream feature calling

Data delivered to you through secure FTP

Custom Project Offerings

Does your project not match our offerings? We would love to discuss your research and see if a customized project could be a solution.

Ordering Information

Product Name	Product Code
Dovetail® HiChIP <i>MNase</i> Service	20117
ChIP-seq Service	20018

Product Name	Product Code
Dovetail® Micro-C Project, TADs	20119
Dovetail® Micro-C Project, Loops	20020
Tissue Prep	1008

Let Dovetail Scientists take on your epigenetic experiment so that you can focus on the findings from your research.

