# Probing Protein Directed Chromatin Architecture
using the Dovetail™ HiChIP Kit.

- Capture ChIP-seq and Hi-C data together in a single library
- Choose from 12 ready-to-use antibodies
- Map protein-mediated chromatin interactions at nucleosome resolution
- Increase you singal-to-noise ratio while reducing your sequencing costs

Integrate ChIP-seq and Hi-C data to view protein-directed topology

Dovetail™ HiChIP MNase combines the power of ChIP-seq with 3-D mapping enabled by Hi-C. For proteins of interest, capture primary DNA binding sites while concomitantly capturing their long-range interactions. Identify transcription factor binding and enhancer/promoter interactions in a single experiment.
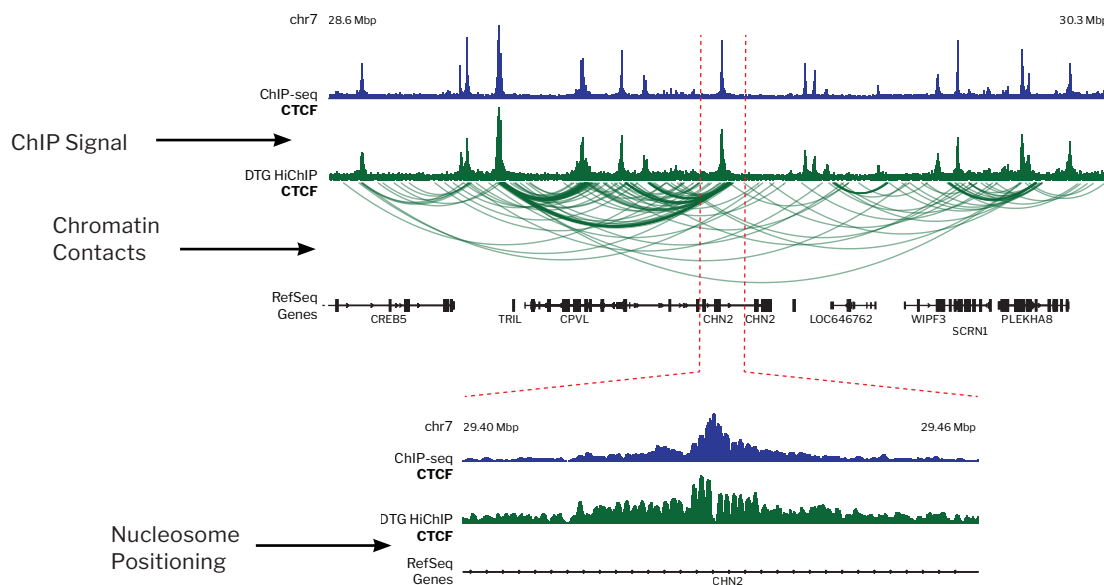

Comparison of CTCF ChIP-seq (blue) and HiChIP (green) showing high concordance in 1-D peaks while capturing the interaction frequency and nucleosome position.
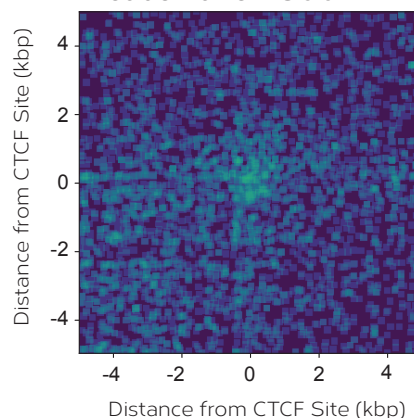
Increase the signal-to-noise and reduce sequencing cost to capture topological features

Dovetail HiChIP efficiently captures topology features with a fraction of the sequencing depth required by tranditional Hi-C approaches.

A) Dovetail HiChIP
S:N = 2.5
Reads Pairs = 150 M
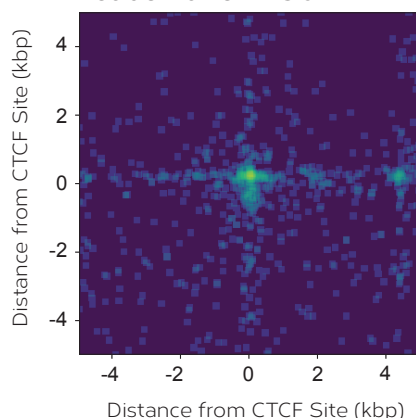
B) Multi-RE Hi-C
S:N = 0.9
Reads Pairs = 800 M

Chromatin contacts averaged around CTCF sites in A) HiChIP and B) Multi-RE Hi-C.

Robust workflow down to 1 M cells

Reduce sample burden to capture both topology and ChIP-seq data in a single library.

Dovetail HiChIP assay is robust down to 1 M cells. HiChIP coverage plots for four antibodies at differing cell inputs.

Generate Informative contact matrices

Discover protein-specific topology features in HiChIP-derived contact matrices.

Contact matrices from different antibodies on the same genomic region of GM12878. Interestingly, the H3K4me3 (a marker for active chromatin) matrix reveals different contact patterns compared to the punctuate features of a CTCF (anchors for chromatin loops) matrix.