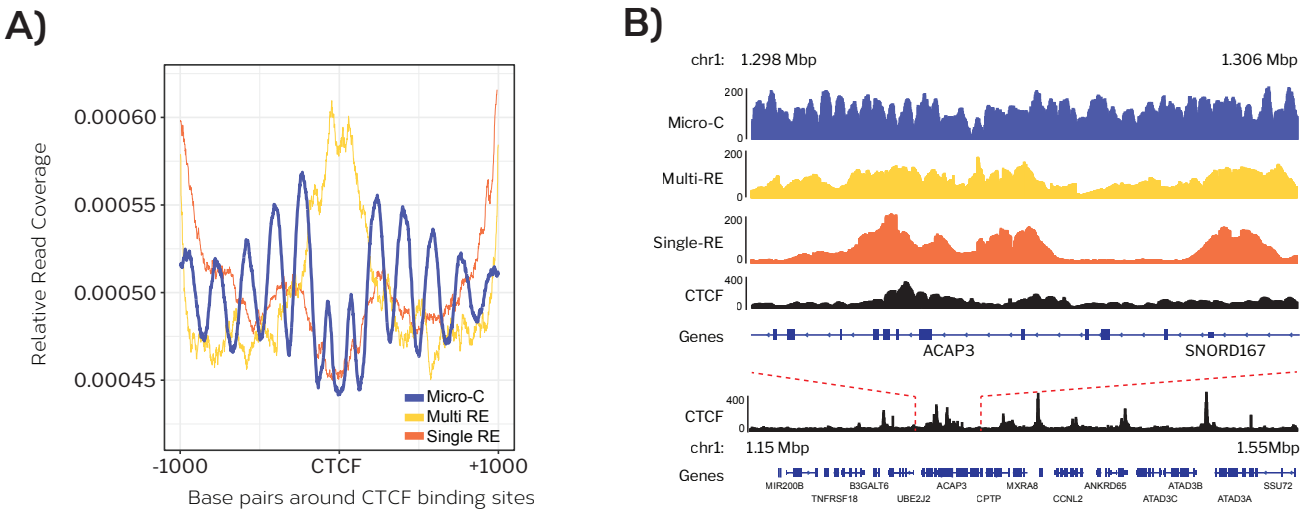
Map Chromatin Topology at Ultrahigh-Resolution

with the Dovetail™ Micro-C Kit, an *MNase* Hi-C approach.

- Generate the highest resolution data through an MNase based Hi-C approach
- Capture more information from A/B compartments to chromatin loops to nucleosome interactions
- Produce higher confidence data
- Generate more read-support per topological feature
- Reduce required depth of sequencing for cost savings

Phase Nucleosomes

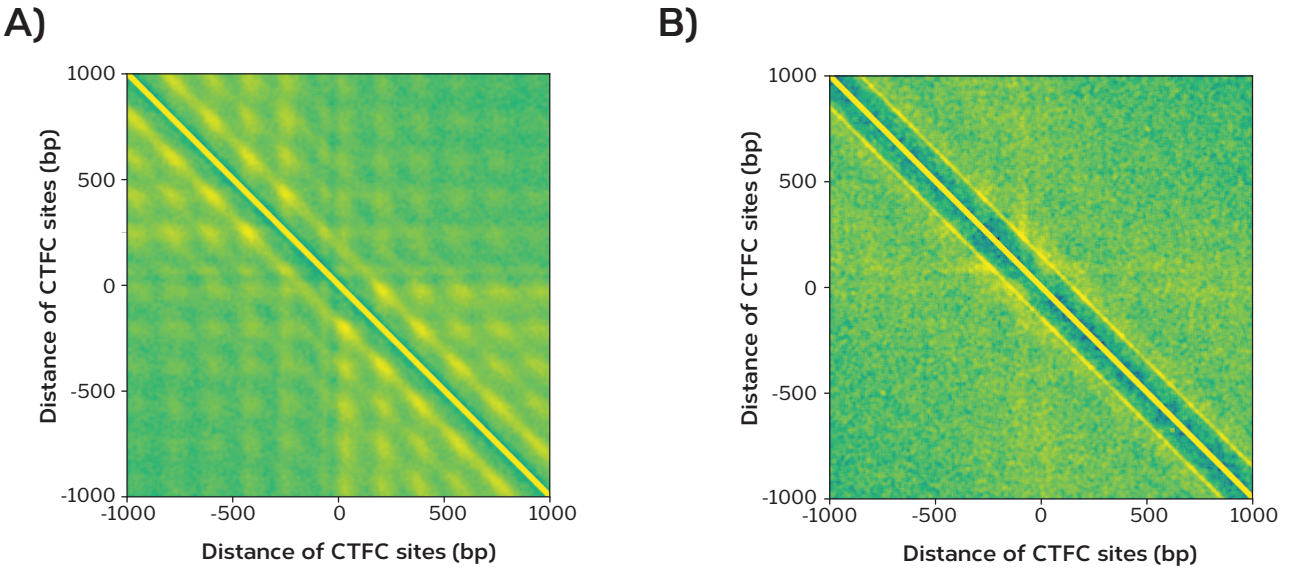
Dovetail Micro-C libraries are enriched for DNA protected by nucleosomes enabling detection of nucleosome position.



Coverage comparison of different Hi-C libraries A) averaged around CTCF sites and B) along a genomic region

Build the highest resolution contact matrices

Capture topology features from A/B compartments down to nucleosome interactions. Only Dovetail Micro-C enables detection of nucleosome positions and interactions

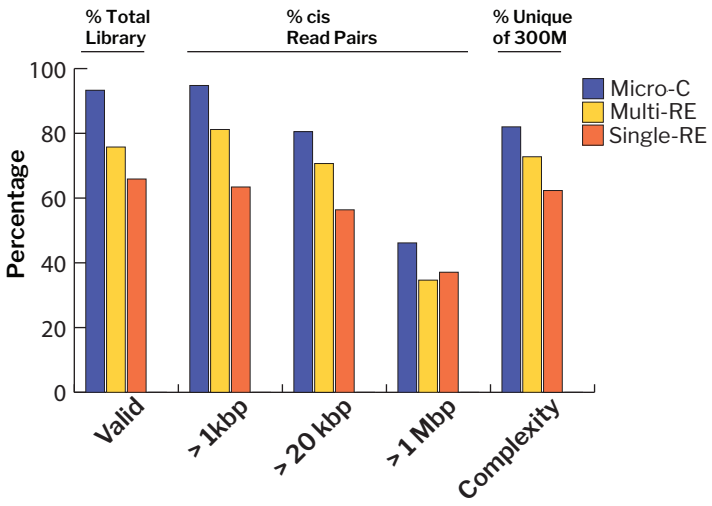


Nucleosome-level resolution of chromatin contacts average across CTCF sites in A) Micro-C and B) Multi-RE Hi-C.

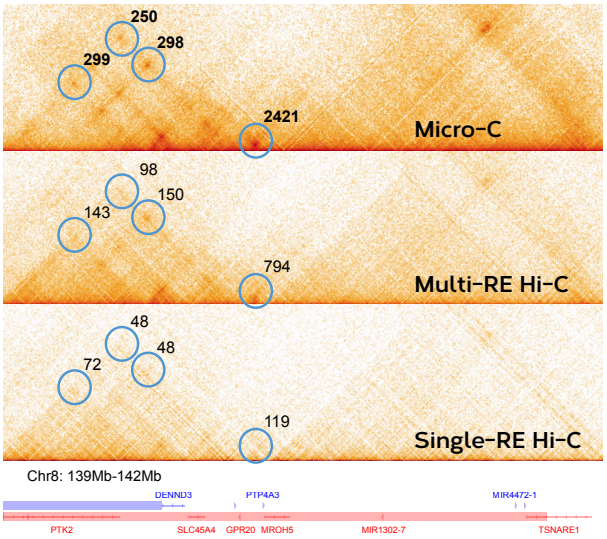
Maximize long-range data and read-support for topology features to save on sequencing cost

Micro-C libraries offer greater long-range information compared to other Hi-C approaches which, in turn, provides greater read-support per feature than other Hi-C approaches. The result is a reduction in sequencing cost for your topological studies.

A)



B)

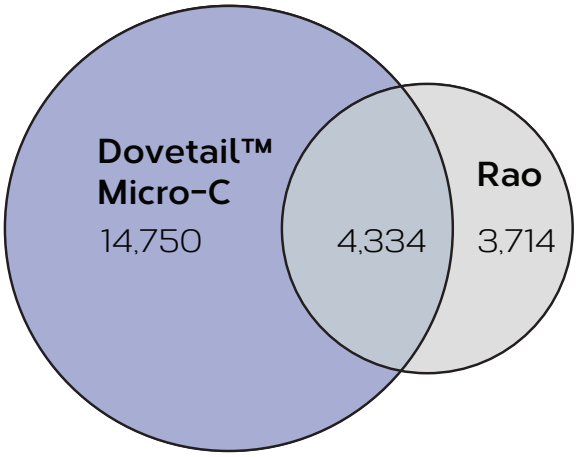


A) Comparison of valid reads (cis > 1kbp + trans) and percentage of long-range inserts captured in cis reads at <1kb, <20 kb, and <1 Mbp. Complexity is shows as percent of unique molecules sequenced at 300 million read pairs. B) Contact matrix at 4 kbp resolution at known loops from Rao et al., 2014. All libraries sequenced to 800 million read pairs.

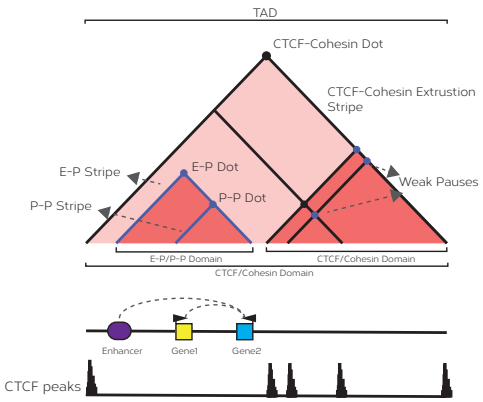
Explore the anatomy of TAD

Micro-C's nucleosome level resolution captures the full scale of chromatin conformation from A/B compartments to ultrastructure nucleosome-nucleosome folding. Call ~3-5 times more loops with only 800M paired-end reads including enhancer (E) and promoter (P) interactions.

A)



B) **Micro-C reveals the anatomy of the TAD**



A) Venn diagram comparing Juicer detected loops between Rao et al., 2014 and Dovetail Micro-C. B) Explore the ultrastructure of topology by capturing sub-TAD features exclusive to Micro-C (blue features) including E-P/P-P stripes and dots, and extrusion weak pause sites, as well as the features captured in Hi-C (black features) of A/B compartments, TADs, CTCF-mediated loops and CTCF-cohesin mediated extrusion stripes.