

ACCELERATE YOUR HI-C STUDIES

with the Dovetail® LinkPrep™ Assay



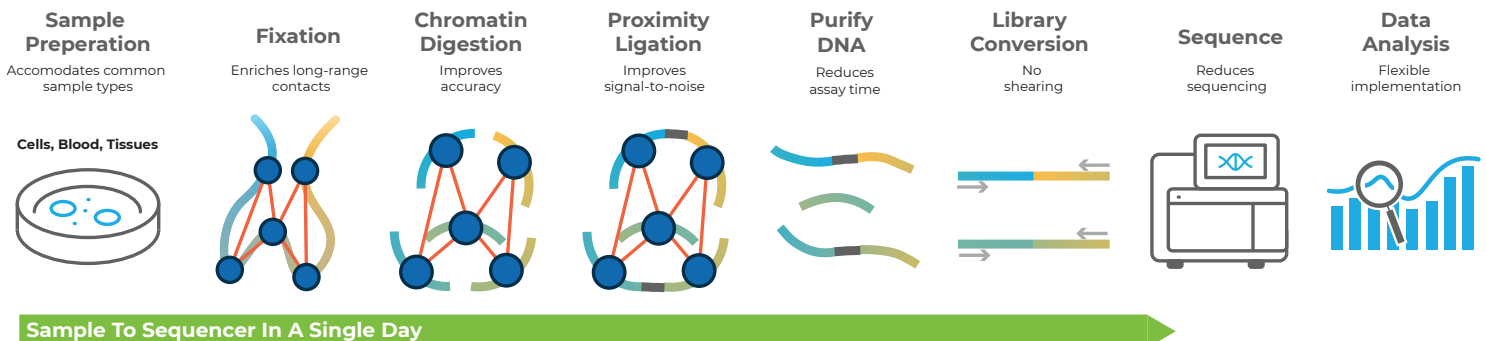
**FASTEST HI-C
WORKFLOW**

**REDUCED
SEQUENCING**

**IMPROVED
ACCURACY**

ACCELERATE YOUR HI-C STUDIES

Dovetail® LinkPrep™ Assay addresses one of the most challenging hurdles in Hi-C data generation – assay length and difficulty. The Dovetail® LinkPrep™ workflow enables users to go from sample to sequence-ready library in less than a day.

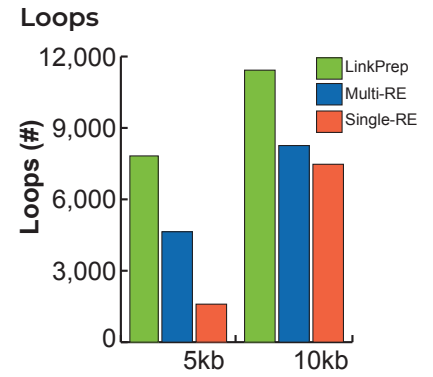
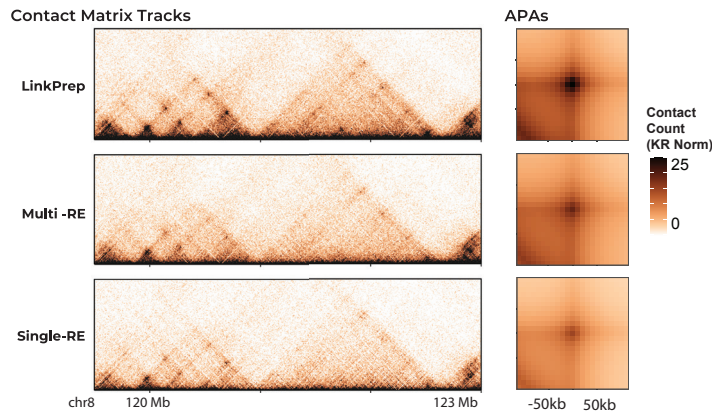


SEE MORE - SEQUENCE LESS

Detect more TADs and loops compared to traditional Hi-C. Moreover, detected features have higher read support resulting in high-confidence feature calling even at reduced sequencing depths. As a result, fewer libraries and less sequencing are required simplifying experimental design and execution.

	LinkPrep	Hi-C
Required Input (cells)	1 Million	2-5 Million
Total Assay Time	1 Day	2-3 Days
Required Proximity Ligation Reactions	1	3 - 4
Required # Libraries	3	6 - 8
Required Read Pairs For Loop Detection	800 Million	1.2 - 1.6 Billion
TADs Called	5,179	2,386
Loops Called	19,253	9,071 - 12,899

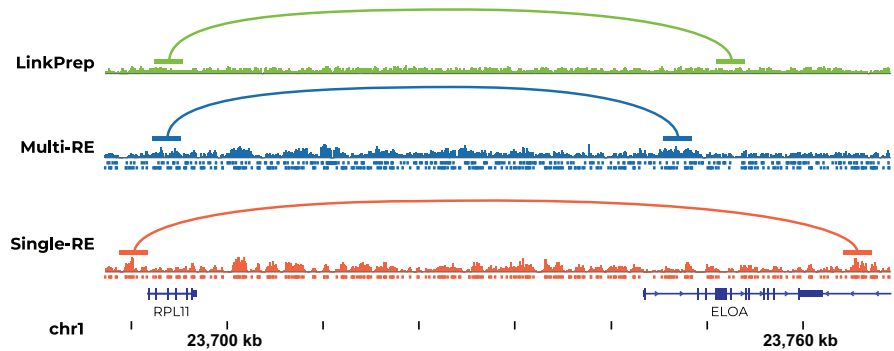
GENERATE HIGH QUALITY CONTACT MATRICES AND IMPROVE FEATURE DETECTION



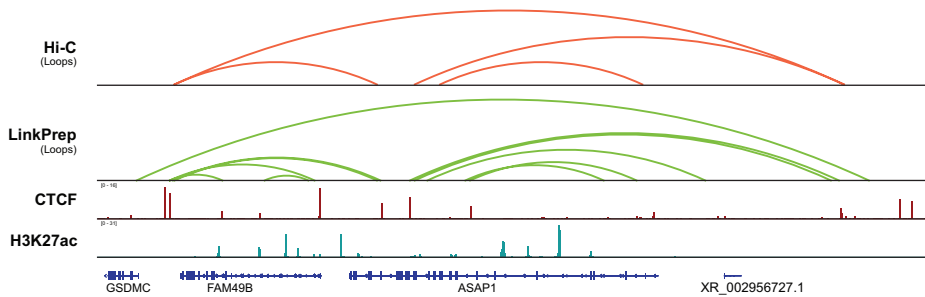
UNBIASED GENOMIC COVERAGE EQUALS IMPROVED ACCURACY

Our uniform sequence coverage produces the most accurate chromatin interaction map possible. Where the non-uniform restriction enzyme site distribution associated with Hi-C methods often skews signals, you can be confident in the position of interactions detected by the Dovetail LinkPrep Assay.

Uneven Sequence Coverage Shifts Loop Position



BUILD MORE COMPLETE REGULATORY NETWORKS



The Dovetail LinkPrep Assay provides the most comprehensive view in regulatory dynamics. Integrate multi-omic data (ATAC-seq, ChiP-seq, RNA-seq, etc.) through the linkages generated by 3D genome folding.

- Quality Control
- Actionable Data
- Integratable Outputs

