Redefining the Hi-C toolbox
*New high-resolution approaches for genome-wide applications and protein-directed chromatin architecture*

Cory Padilla, Ph.D.
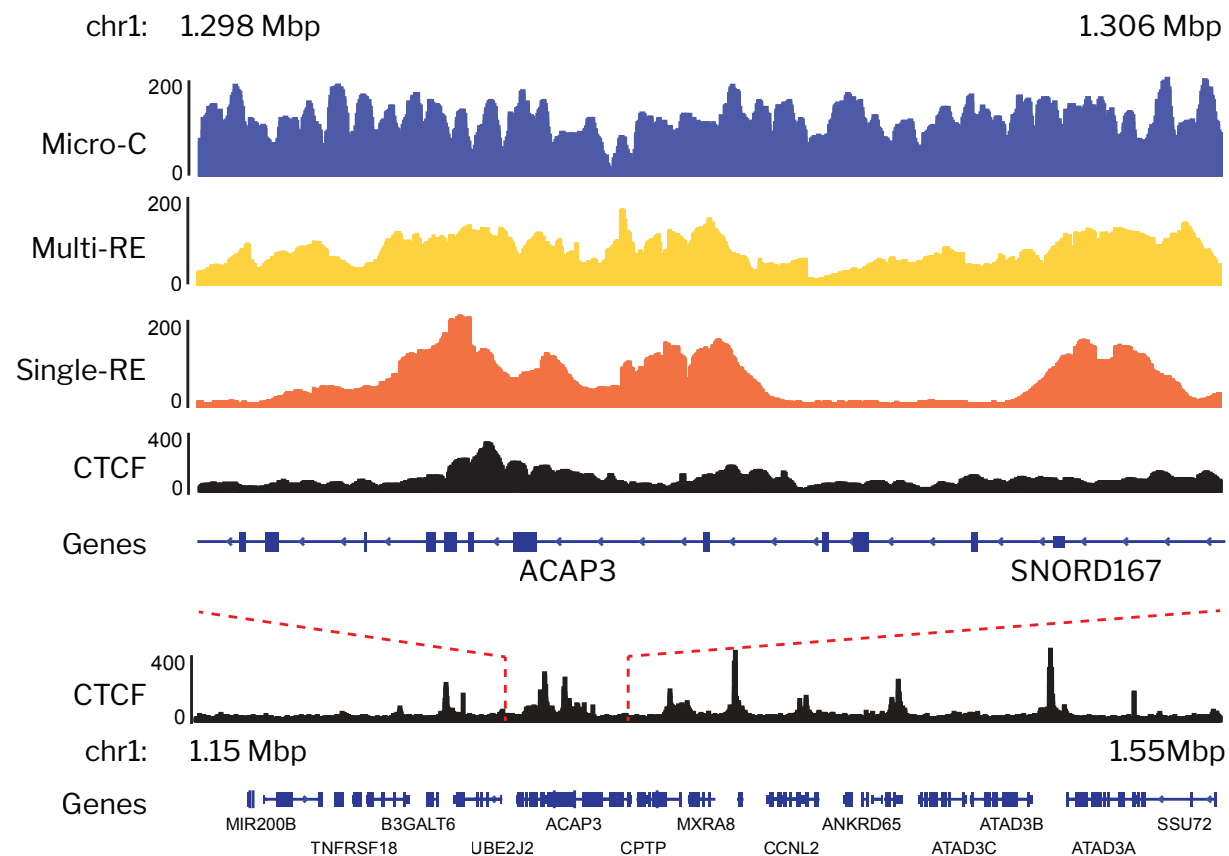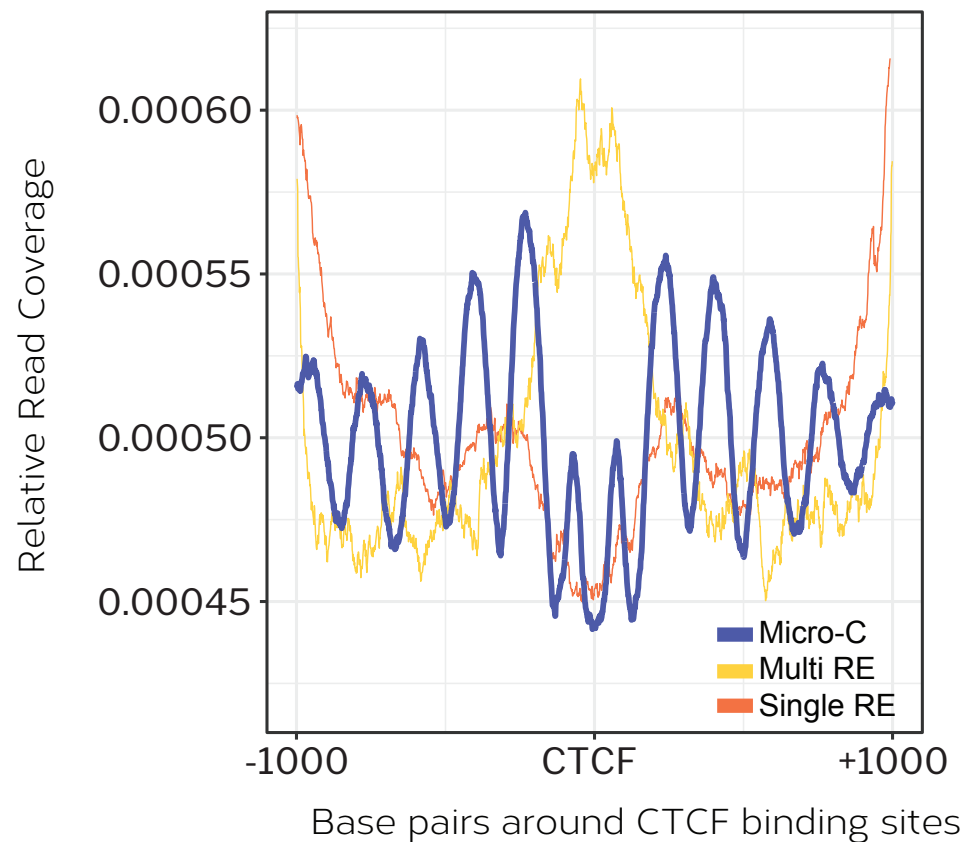Scientific Affairs, Dovetail Genomics

Dovetail™ Micro-C: An MNase-Based Proximity Ligation Kit

Enhanced resolution of chromatin contacts down to mono-nucleosome levels

- Highest achievable contact matrix resolution (146 bp)

- Unparalleled capture of long-range information (> 90% of *cis* reads are > 1 kb)
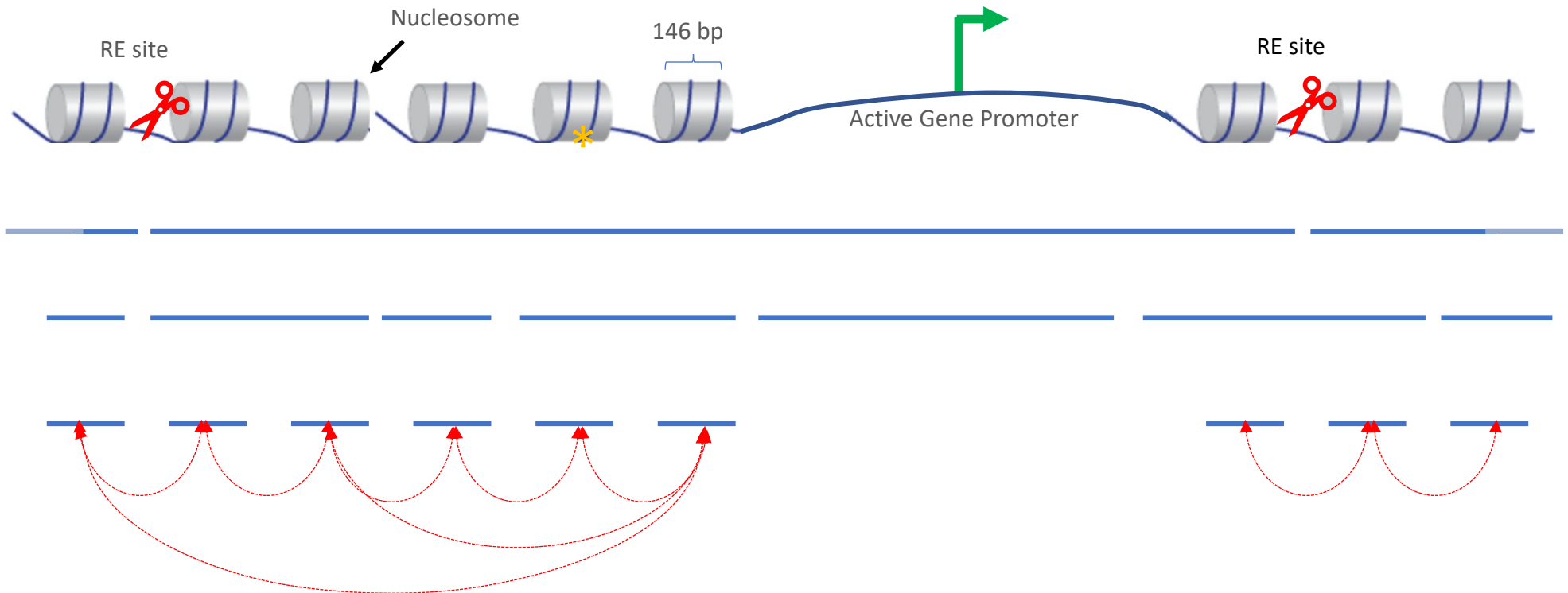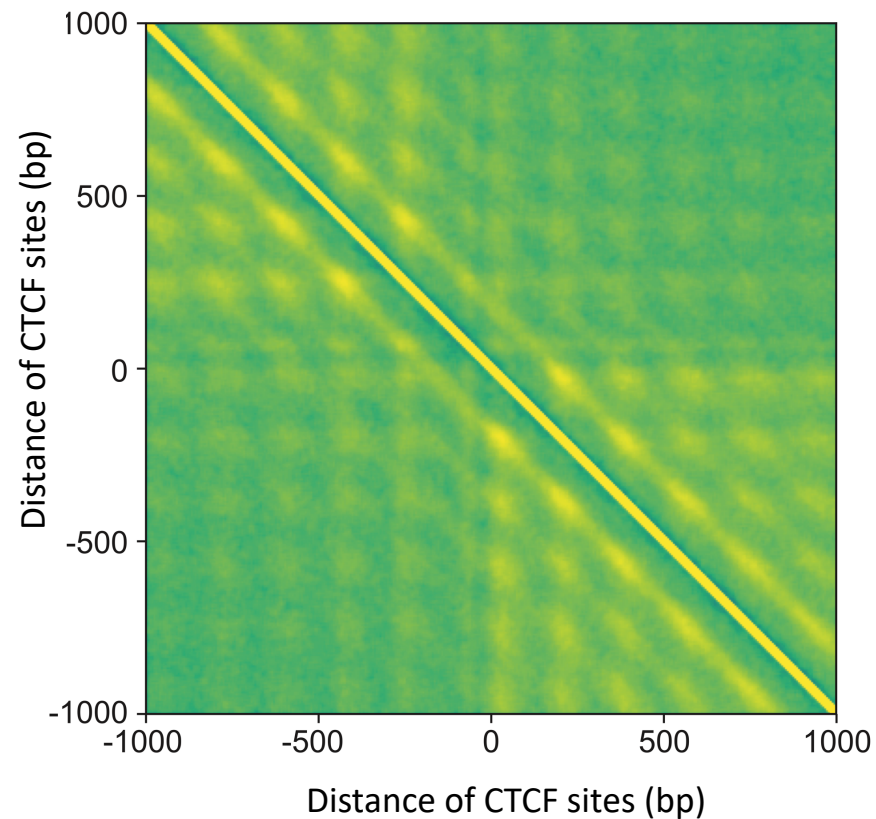
Capture nucleosome position during proximity-ligation
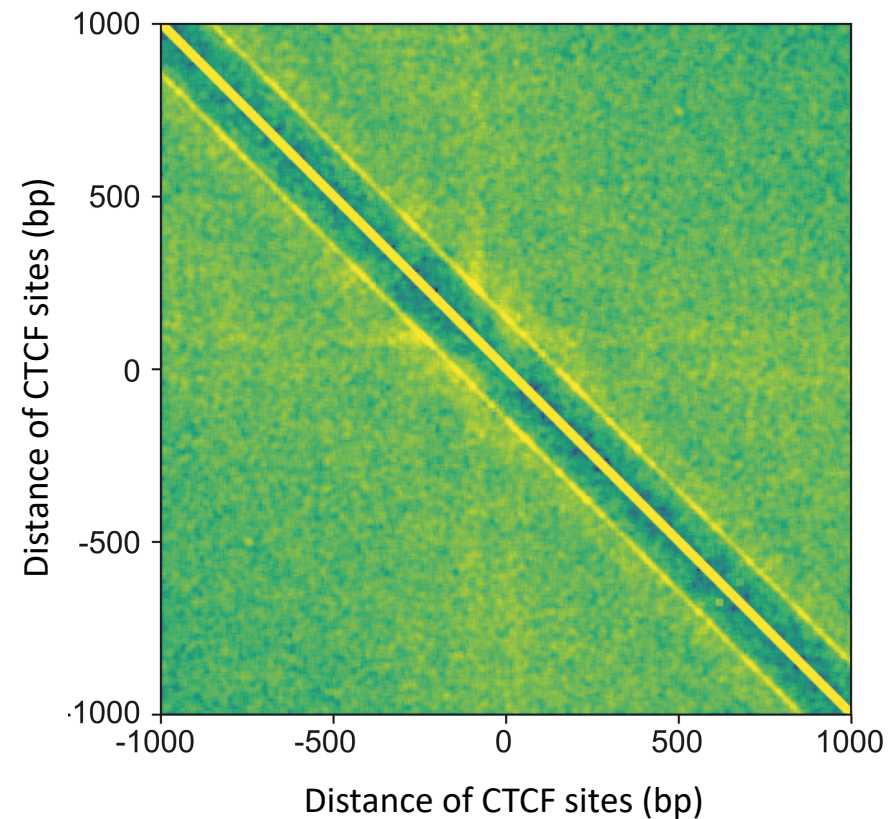
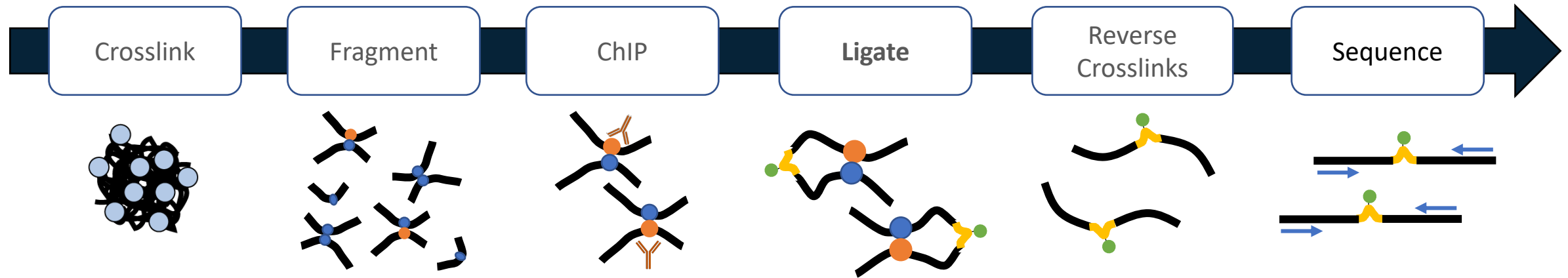# Dovetail™ Micro-C: Nucleosome Positioning Generates The Highest Resolution View of Conformation

Dovetail™ Micro-C

Multi-RE Hi-C

Dovetail™ HiChIP Workflow Combines Hi-C and ChIP-seq

Crosslink	Fragment	ChIP	**Ligate**	Reverse Crosslinks	Sequence
Down to 1 M mammalian cell input. Dual cross-linking maximizes long-range information	Dovetail *MNase* fragmentation eliminates any sonication & enables nucleosome level resolution	8 pre-validated antibodies available with more to come. Alternatively, validate your own antibodies	Optimized proximity ligation for efficient conversion of free ends to ligation products	Efficient cross-link reversal with biotin enrichment to minimize target molecule loss	Standard paired-end sequencing using any Illumina NGS instrument

Input down to 1 M cells	No sonication required	Pre-validated or validate your own antibodies	Standard proximity-ligation and library preparation methods

Capture ChIP-seq Data & Hi-C Long-range Information In A Single Library