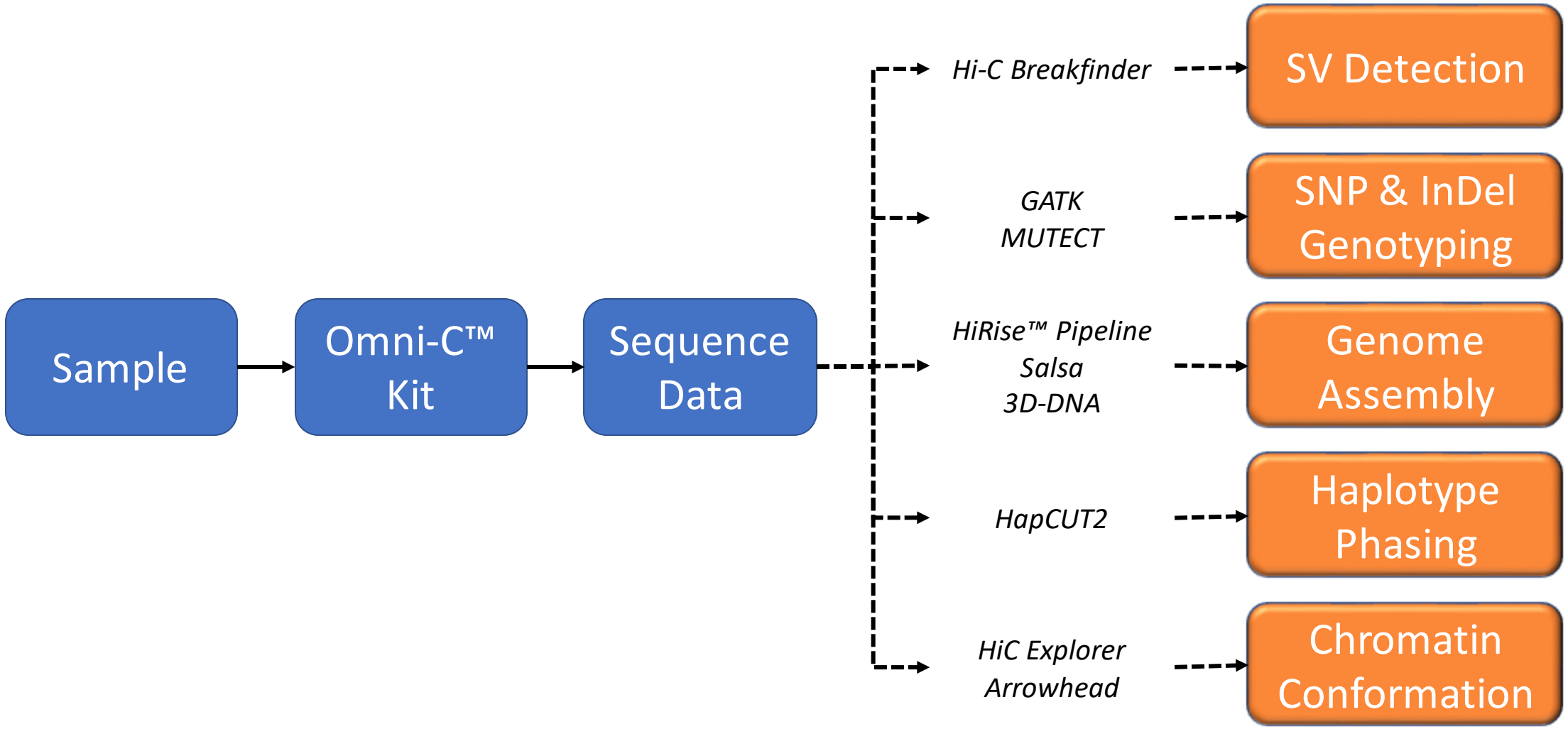
From 3D genome topology to SNPs: Omni-C™ provides a multi-resolution view of the genome in a single library prep

Cory Padilla, Ph.D.

Rich Data Type Enables Multiple Applications



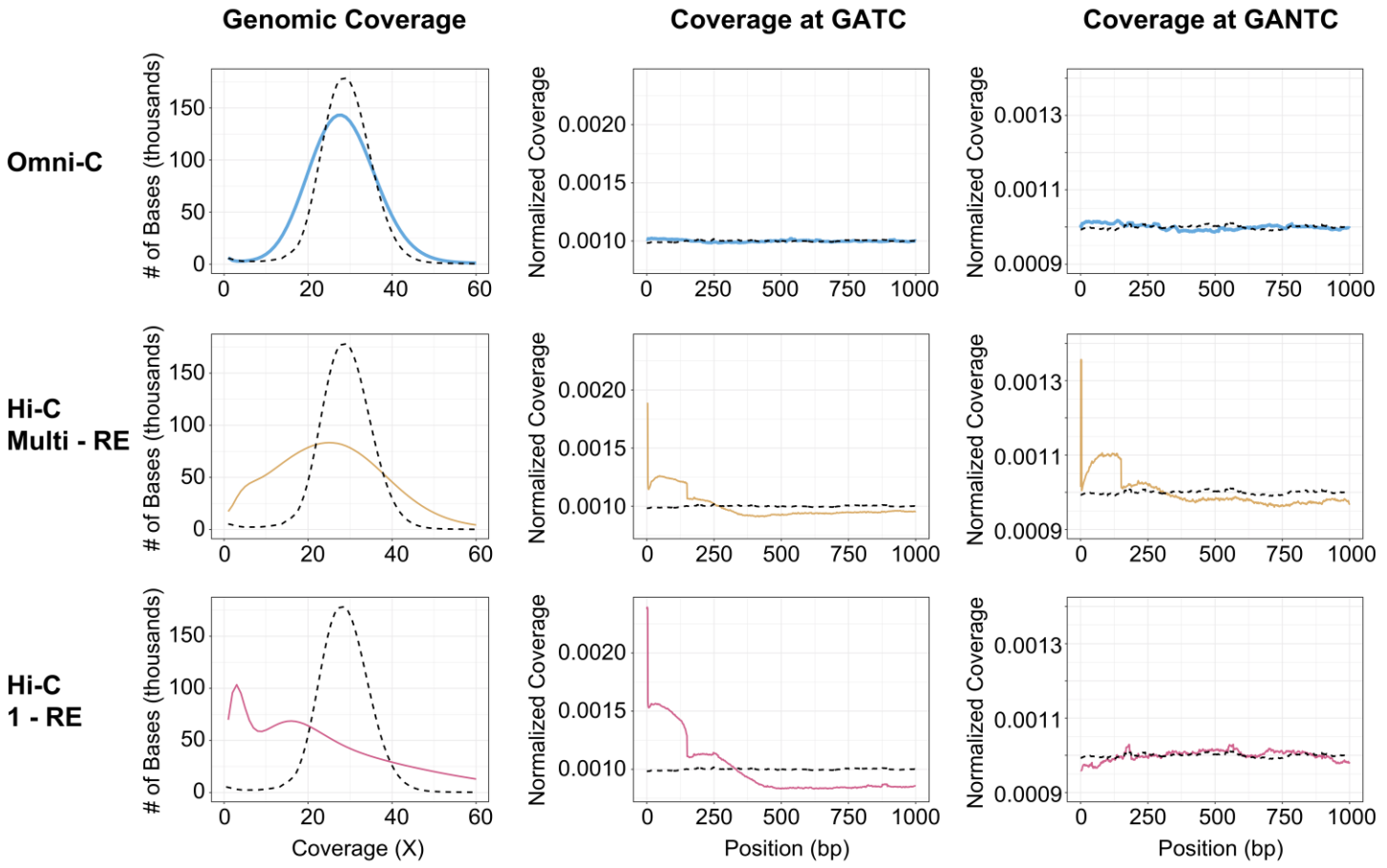
Omni-C™ an sequence-independent approach to Hi-C that provides uniform coverage

Exhibits shotgun-like genomic coverage

Reduces sequence burden to cover genome

Exhibits no sequence bias

Analyses are no longer limited to RE sites



Improved SNP detection combined with long-range information leads to superior chromosome phasing

Dovetail GENOMICS
An EdenRoc Sciences Company

SNPs identified in GM12878 by GATK

Library Type	True Positive	False Positive	False Negative	Sensitivity	Precision
Shotgun	2,696,291	9,270	6,814	99.7%	99.7%
Omni-C	**2,666,339**	**20,081**	**36,766**	**98.6%**	**99.3%**
RE Based Hi-C	2,387,235	33,554	315,870	88.3%	98.6%

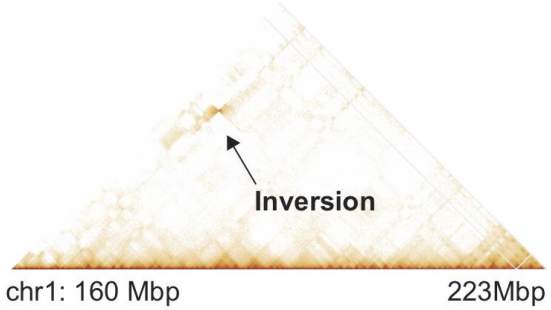
Phasing results with HapCUT2

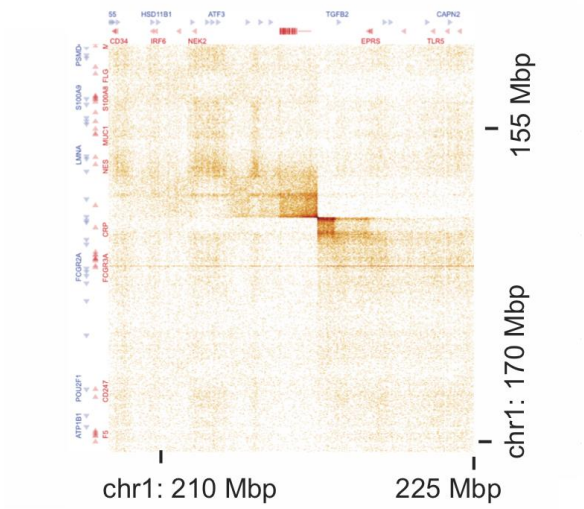
Library Type	#Variants Phased	% Heterozygous SNPs phased	Switch Error Rate	#Chromosomes phased end to end
Shotgun	2,229,492	81.44%	0.0036	0
Omni-C	**2,299,248**	**84%**	**0.0100**	**23**
RE Based Hi-C	1,986,467	72.6%	0.0357	23

Capture Structural Variants

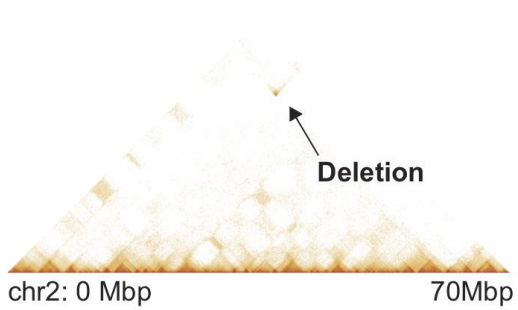
Examples of validated SVs in the cancer cell line HCC1187

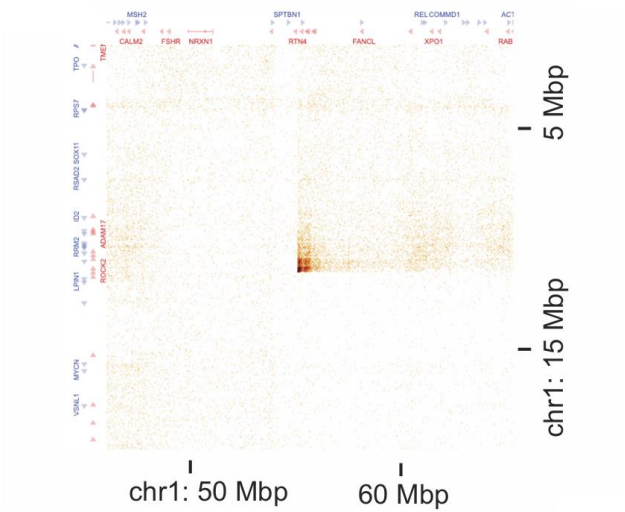
Inversion
chr1: 157,389,509-215,513,024



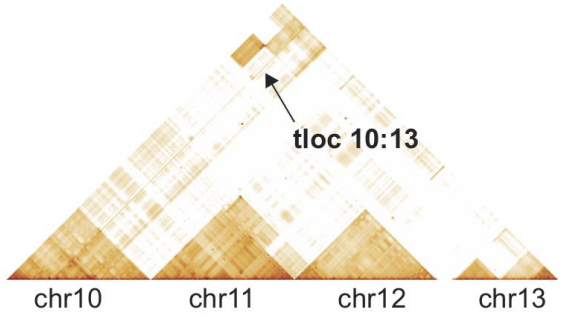


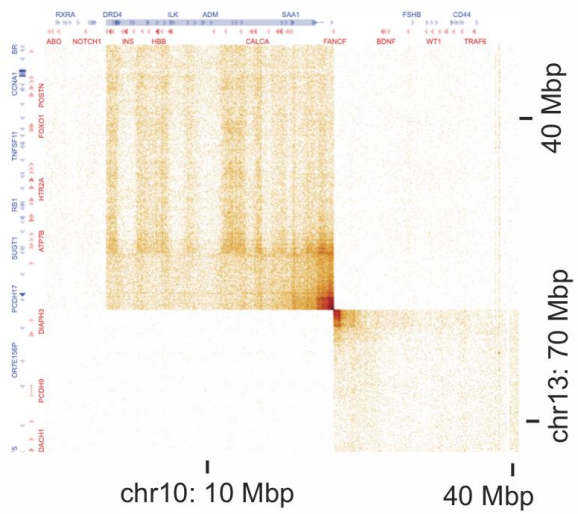
Deletion
chr2: 11,257,650-54,932,039



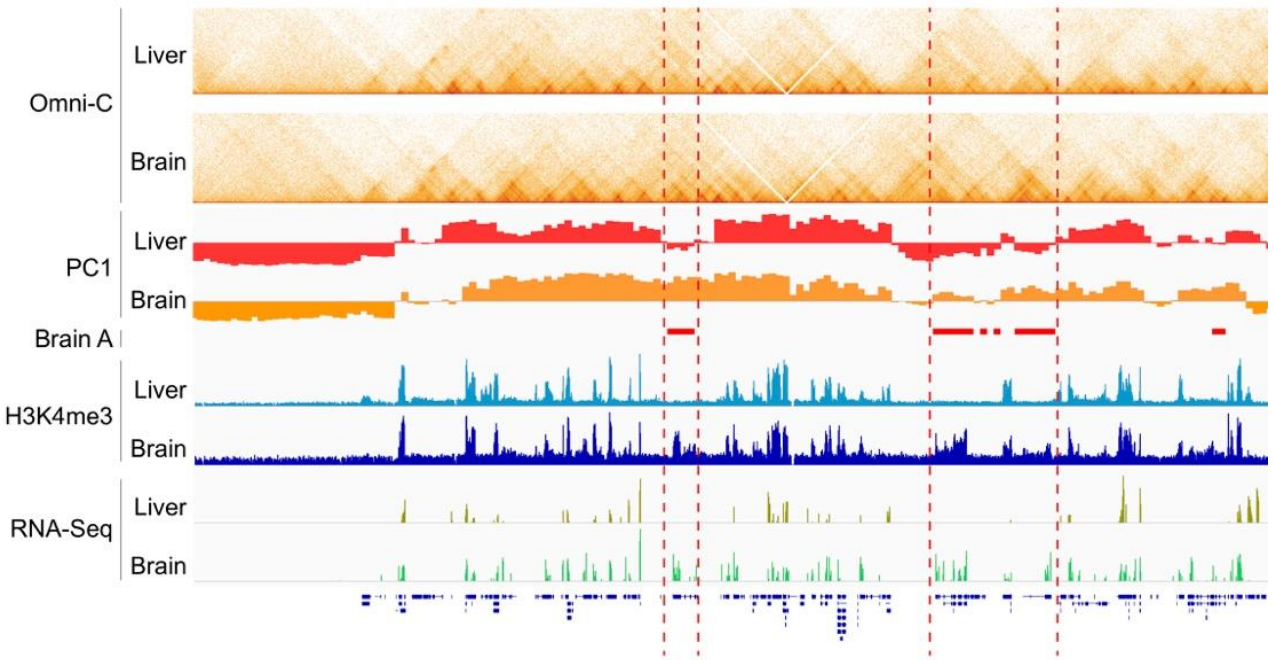


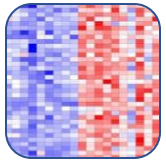
Interchromosomal Translocation
chr10:chr13





Powerful Multi-Dimensional NGS Datatype





Gene Expression

Biomarker Discovery

Genome Phasing

Resequencing

Population Genetics