

# Omni-C™ Technology

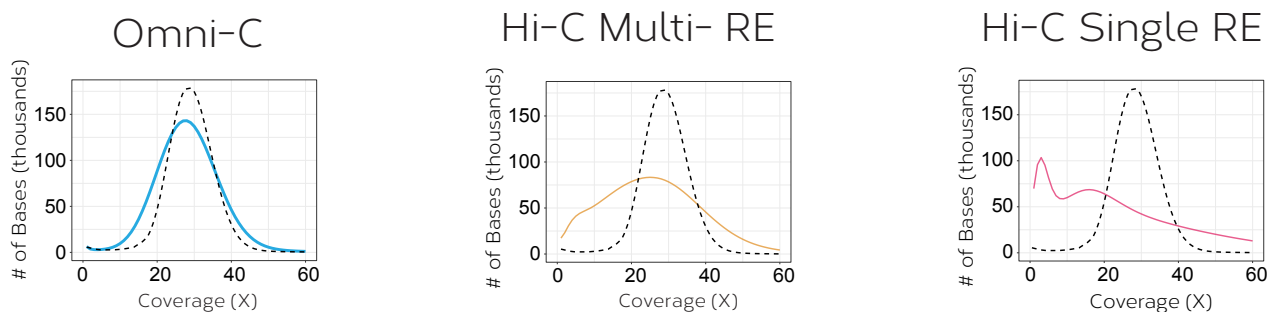
*Delivers SNPs to Genome Conformation In a Single Assay*

Powered by a sequence-independent endonuclease, Omni-C™ technology represents the next-evolution in Hi-C assays delivering unbiased long-range reads and highly uniform sequence coverage.

Gain a comprehensive view of the genome from SNPs to indels, SNVs to phasing, and loops to topologically associated domains (TADs), all from a single NGS library.

## ACHIEVE SHOTGUN-LIKE COVERAGE

Omni-C libraries contain uniform, shotgun-like coverage enabling downstream applications sensitive to variant detection.



Coverage distribution of different Hi-C libraries (colored lines) compared to a shotgun library (dotted line).

## CAPTURE LONG-RANGE INFORMATION

Omni-C libraries offer greater long-range information compared to other Hi-C approaches. The result is greater support for chromatin 3-D interactions such as TADs and loops enabling comprehensive genome conformation mapping.

**A.**

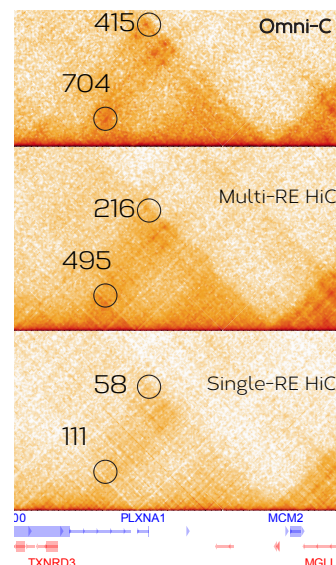
Library Type	% cis <1 kbp	% cis >1 kbp	% unique molecules at 300 M read pairs
<b>Omni-C</b>	<b>5%</b>	<b>95%</b>	<b>73%</b>
Hi-C Multi-RE	20%	80%	69%
Hi-C Single-RE	34%	66%	50%

Comparison of Omni-C libraries with multi-restriction enzyme (RE) and single-RE Hi-C libraries.

A. Proportion of long-range reads for each library type

B. Contact matrices at 4 kb resolution from 800 M total reads per library. Loops are circled with the number of raw reads supporting each contact indicated.

**B.**



To place an order or for more information:

visit us at [www.dovetailgenomics.com](http://www.dovetailgenomics.com) or send an email to [info@dovetail-genomics.com](mailto:info@dovetail-genomics.com)

# GENETIC VARIANTS AND PHASED GENOMES FROM A SINGLE LIBRARY

The shotgun-like characteristics of Omni-C data enable genotyping and haplotype phasing.

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

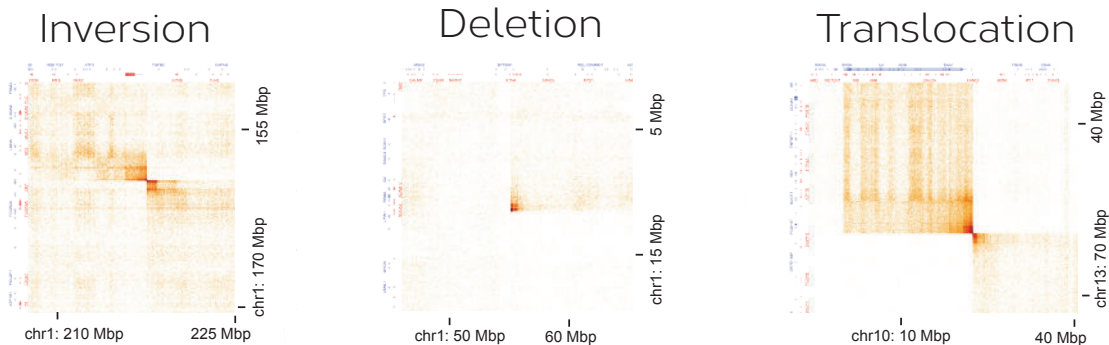
*Homozygous SNP calls sampled at 300 M read pairs.*

Library Type	#Variants Phased	% Heterozygous SNPs phased	Switch Error Rate	Largest Phase Block Size	#Chromosomes phased end to end
Shotgun	2,229,492	81.44%	0.0036	28.2 kb	0
<b>Omni-C</b>	<b>2,299,248</b>	<b>84.00%</b>	<b>0.0100</b>	<b>248.01 Mb</b>	<b>23</b>
RE Based Hi-C	1,986,467	72.60%	0.0357	247.95 Mb	23

*GM12878 haplotype assembly metrics using high confidence heterozygous SNPs from the Illumina Platinum Genome.*

## EXPLORE THE LANDSCAPE OF STRUCTURAL VARIANTS

Omni-C libraries capture large structural (>1 Mbp) variant information such as indels, inversions and chromosomal translocations.

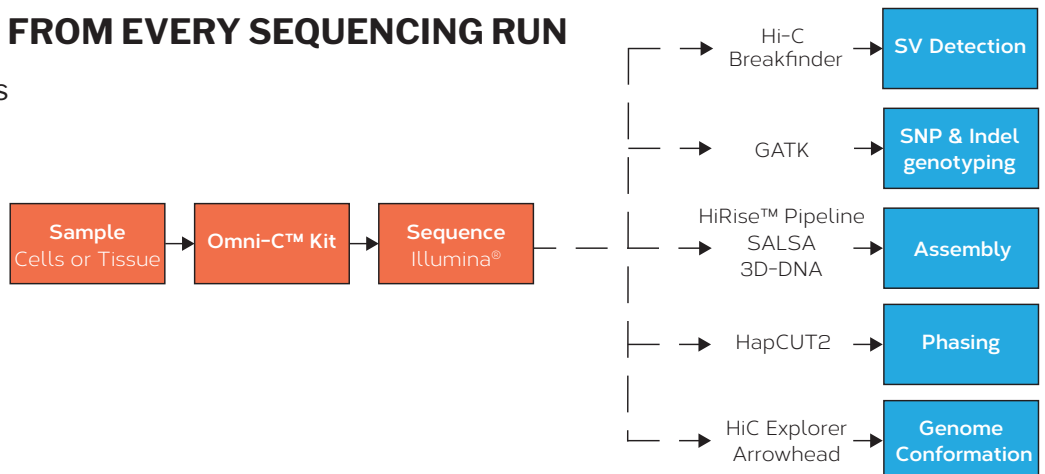


*Validated large SVs found in breast cancer cell line HCC1187 representing an inversion, a deletion and inter-chromosomal translocation*

## EXTRACT MORE DATA FROM EVERY SEQUENCING RUN

Omni-C technology captures genome-wide topology at single nucleotide resolution in a single library prep.

Therefore, in addition to being ideal for the study of 3-D genome conformation, it is suitable for applications traditionally addressed by whole genome sequencing.



To place an order or for more information:

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