Omni-C™ Technology

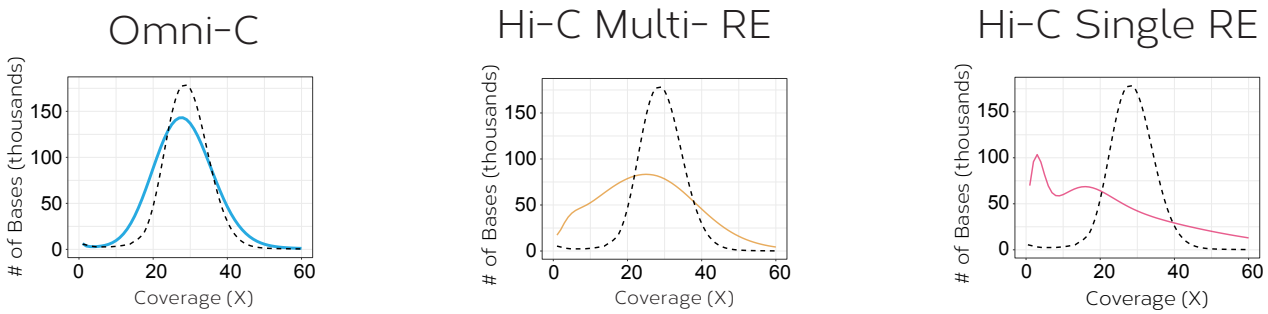
Delivers SNPs to Genome Conformation In a Single Assay

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).

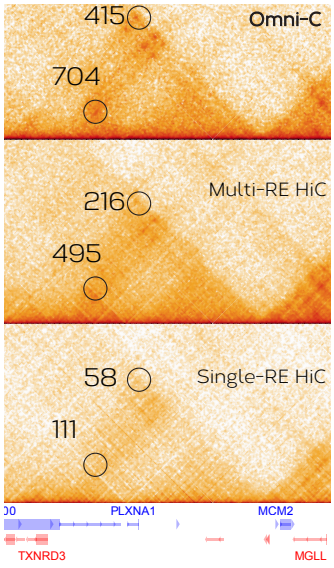
CAPTURE LONG-RANGE INFORMATON

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
Omni-C	5%	95%	73%
Hi-C Multi-RE	20%	80%	69%
Hi-C Single-RE	34%	66%	50%

B.



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.

To place an order or for more information:
visit us at www.dovetailgenomics.com or send an email to 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%
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%

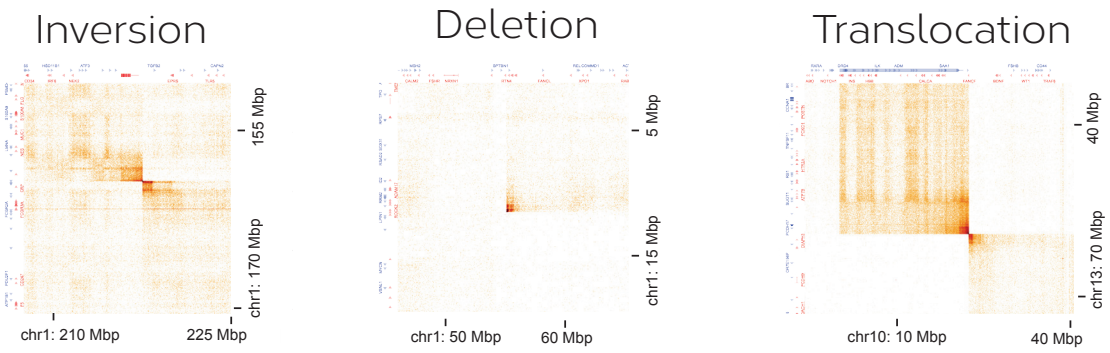
Homozygous SNP calls sampled at 300 M read pairs.

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
Omni-C	**2,299,248**	**84.00%**	**0.0100**	**248.01 Mb**	**23**
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.

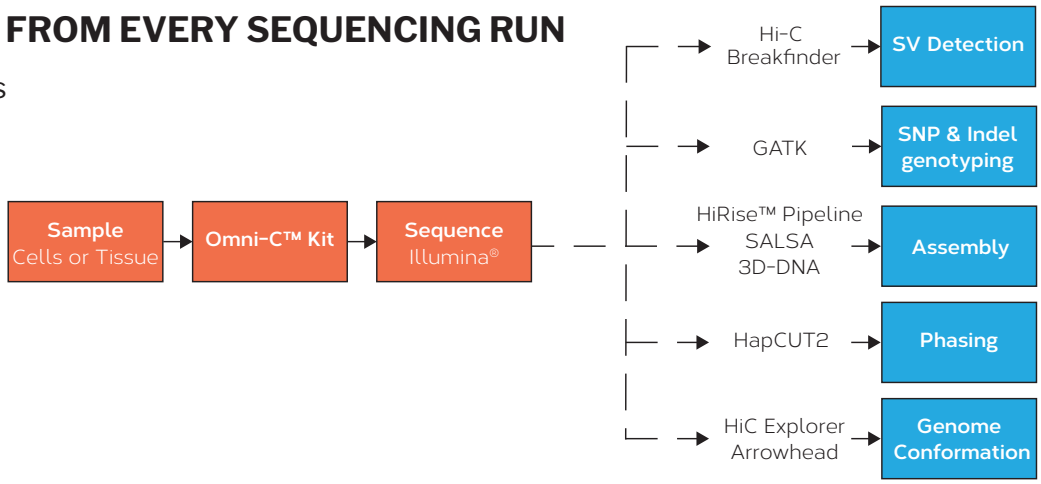


Validated large SVs found in breast cancer cell line HCC1187 representing an inversion, a deletion and inter-chromosomal translocation

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.



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