Comprehensive insights, unprecedented simplicity

Illumina Constellation mapped read technology

On-flow cell library prep and cluster proximity information unlock long-distance genomic information and novel insights.

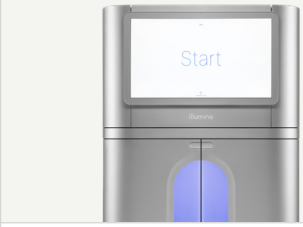
- Elimate most **traditional library prep** steps
- Resolve **challenging-to-map regions** and large structural variations
- Generate **phased sequencing data** for deeper genomic insights

Prep for sequencing with unparalleled ease

DNA templates, extracted from samples using standard or high molecular weight methods, are introduced directly to the flow cell surface, where they are captured, tagmented into clusters, and sequenced.

Minimal prep for sequencing

Add diluted DNA and two reagents to the sequencing system cartridge



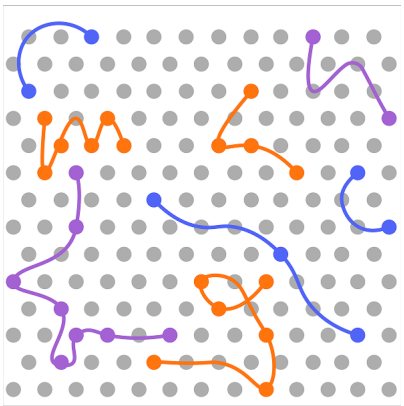
Prep library on flow cell and sequence

Analyze using novel DRAGEN™ algorithms

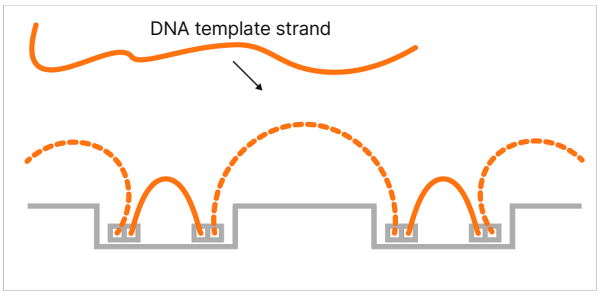
The power of proximity

The highly simplified workflow results in neighboring clusters having a high probability of mapping to the same DNA template strand, enabling the use of proximity information to determine genomic location with high accuracy.

DNA attaches to the flow cell in a constellation pattern



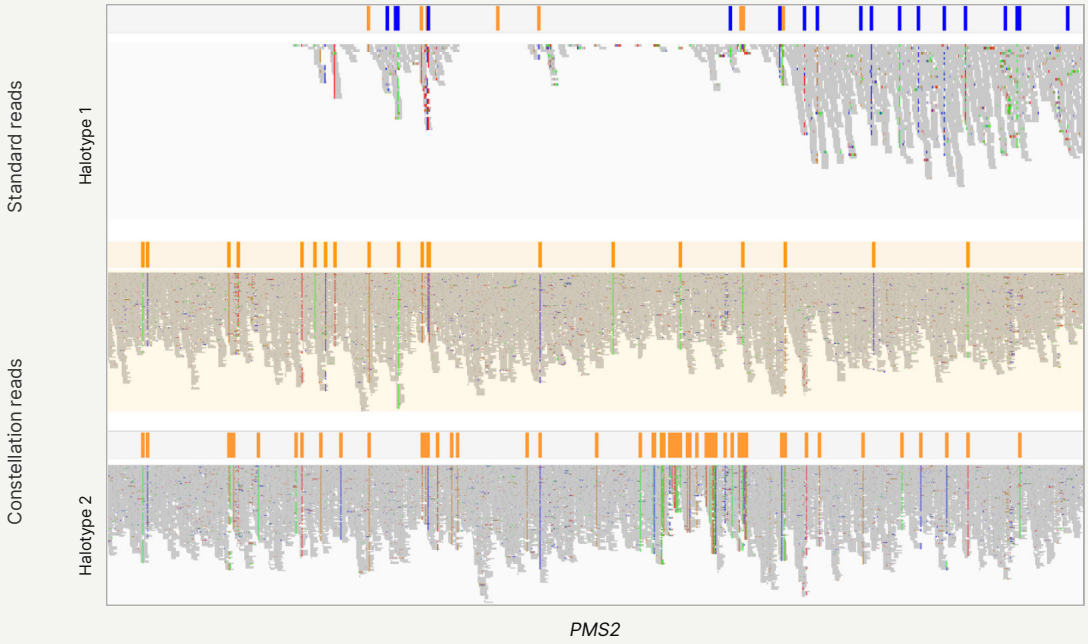
Top view of DNA strands across the flow cell surface. Image represents a small percentage of the tile.



Side view of the template DNA undergoing tagmentation on the flow cell.

Resolve challenging-to-map regions

The *PMS2* gene has a highly homologous pseudogene, *PMS2A*, with 99% similarity, making it difficult to correctly identify using traditional sequencing techniques. Proximity information allows for accurate mapping of these ambiguous regions with a high degree of confidence.

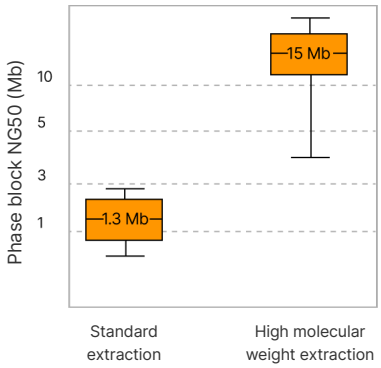


Highly homologous regions can be challenging to map and lead to gaps in coverage.

Adding proximity information enables assignment of reads to the correct genomic location and mapping of the unique region.

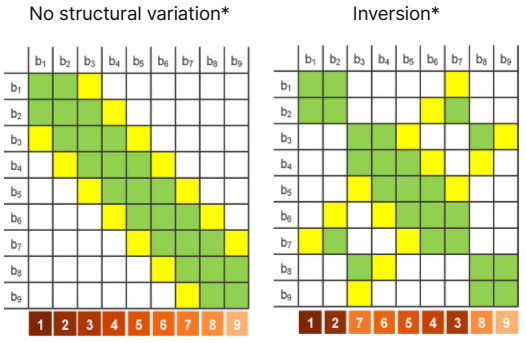
Generate megabase-length phase blocks

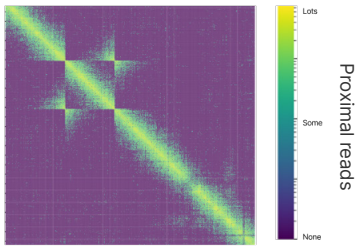
Constellation reads are defined by the length of the native DNA template and can extend from hundreds of kilobases up to several megabases, contributing to larger phase blocks for greater insights into haplotypes and compound heterozygotes.



Novel visualization of structural variation

By extracting information about reads from proximal clusters, Constellation technology can produce high-resolution "colocation plots" that depict large structural variations.





Courtesy of Rady Children's Hospital, San Diego.

Colocation plots plot the genome position of a reference vs sample. No large variations will generate a straight diagonal line. Samples with large structural variation create a distinct visual pattern.

*These are example plots and do not represent real data.

A new foundation for genomic sequencing

Greatly simplify your NGS workflow and generate novel genomic insights, even when working through traditionally challenging regions, with Constellation mapped read technology.†

† Broad commercial availability is slated for H1 2026.

Learn more →

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