3D Genomics: An Essential Part of Any Multi-Omic Approach

Key Takeaways

- The vast majority of NGS approaches detect linear DNA sequence ignoring the 3D context of the genome.
- 3D chromatin structure can be effectively captured alongside primary sequence.
- A deeper functional understanding can be achieved by adding 3D genomic data to any NGS multi-omic approach.

Complete Your Multi-Omic Picture

Integrating 3D genomics into multi-omic studies unleashes a powerful synergy, elevating our understanding of cell function. Reveal connections across one-dimensional datasets by overlaying the 3-dimensional (3D) organization of genes and their regulatory elements. This spatial context uncovers relationships missed by linear sequencing, revealing long-range physical interactions that influence gene function. A deeper 3-D multi-omic view offers new insights into complex diseases and regulatory mechanisms, ultimately providing a more holistic representation of key biological systems.

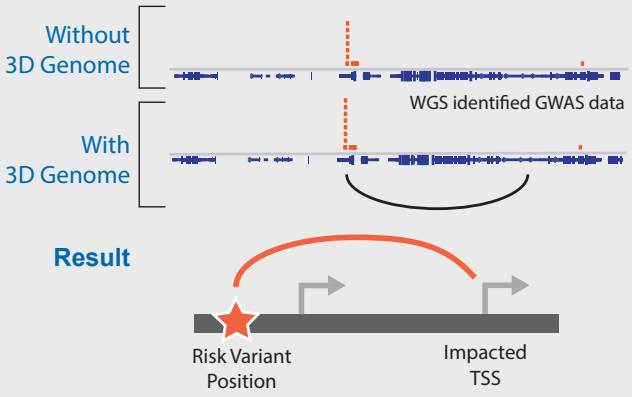
Integrate with WGS To Annotate Risk Variants

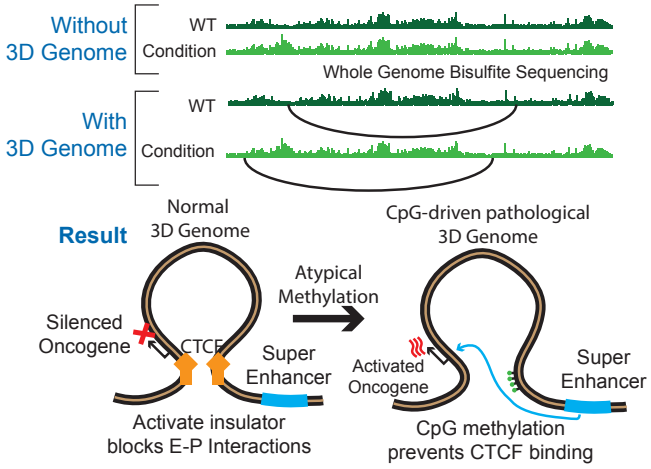
Benefit – Annotate gene and disease associated variants through 3D interaction mapping.

- Contextualize genetic variants in their 3D environment.
- Aid in assembly and gap filling of WGS data
- Identify genomic haplotypes.

Research Areas – Genome assembly, cancer genomics, precision medicine.

Example Publication – Zhang *et al.* (2023). DOI: 10.1016/j.xgen.2023.100399.





Integrate with DNA Methylation Analysis

Benefit – Understand the interplay between 3D chromatin structure and DNA methylation patterns.

- Link methylation patterns to genes and regulatory elements.
- Elucidate links between disease and DNA methylation.

Research Areas – Epigenetics, Chromatin Biology, Stem Cell Research, Developmental Biology, Cancer & Disease Research

Example Publication – Flavahan *et al.* (2019). DOI: 10.1038/s41586-019-1668-3.

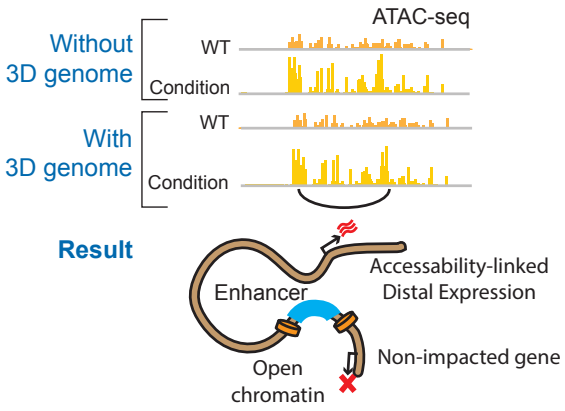
Integrate with ATAC-seq To Understand Accessibility Linked Chromatin Structure

Benefit – Develop insights into how chromatin accessibility shapes gene function and regulation.

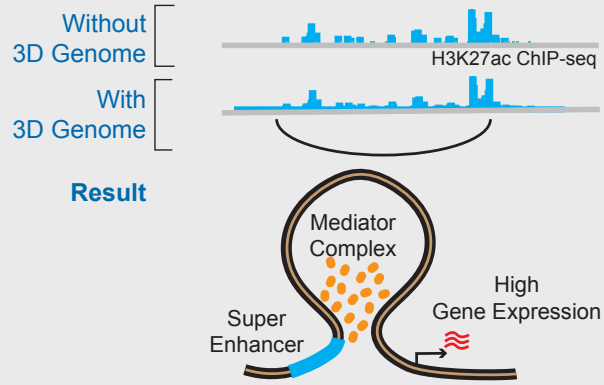
- Classify open chromatin regions contained within topologically associated domains (TADs).
- Uncover regulatory landscapes linking enhancers, promoters, and insulators, providing key insights into gene regulation.

Research Areas – Gene Regulation, Functional Annotation, Developmental Biology, Cancer & Disease Research.

Example Publication – Xiao *et al.* (2021). DOI: 10.1038/s41586-021-04246-z.



Integrate with ChIP-seq To Understand Super Enhancer Function



Benefit – Visualize protein-DNA interactions and the long-range interactions they affect.

- Link transcription factor and enhancer (e.g. H3K27ac) ChIP-seq peaks to the distal genes they regulate.
- Link promoter ChIP-seq peaks to their cognate enhancers.

Research Areas – Gene Regulation, Functional Annotation, Developmental Biology, Cancer & Disease Research.

Example Publication – Asante *et al.* (2023). DOI: 10.1038/s41467-023-43780-4.

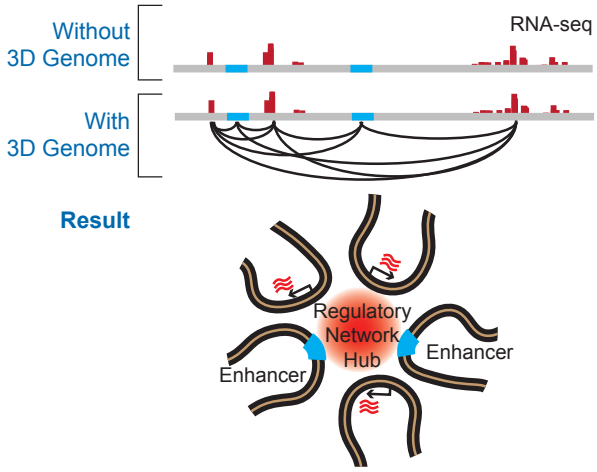
Integrate with RNA-seq To Capture Co-regulatory Networks

Benefit – Decipher long-range regulatory networks and mechanisms of gene expression.

- Elucidate interactions between promoters and distal regulatory elements and their influence on gene expression.
- Identify genes in physical proximity that exhibit similar expression patterns, revealing potential regulatory relationships and functional modules.

Research Areas – Gene Regulation, Systems Biology, Developmental Biology, Cancer & Disease Research.

Example Publication – Sanalkumar *et al.* (2023). DOI: 10.1126/sciadv.abo37.



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