illumina®

More with Genomics and Transcriptomics

Discovering the functional consequences of genetic variation using the power of multiomics

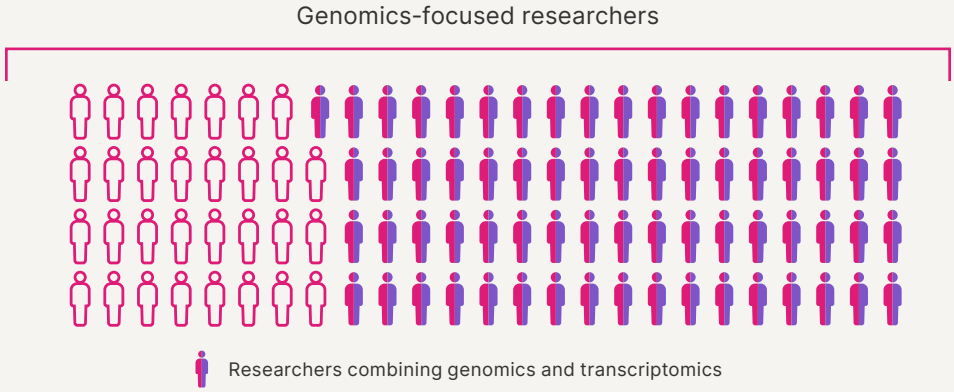
The power of genomics + transcriptomics

Studying multiple "omes" in one experiment can help researchers gain valuable insight into the movement of information from gene to protein to better understand life's complexity.[1] Many multiomic combinations are possible, each with a unique benefit. Specifically, the combination of genomics and transcriptomics can reveal a more complete picture of genetic variation and its consequences. While the genome stays the same from cell-to-cell, the transcriptome can vary, expanding the researcher's view when the two are combined.[2]

> By associating transcriptomics data with genomics data, we may be able to identify which mutation will be the driving mutation for a particular cancer.

Dr. Bernard Lam
Associate Director,
Translational Genomics Laboratory
Ontario Institute of Cancer Research
Watch Video

69%
of genomics researchers also use transcriptomics[3]



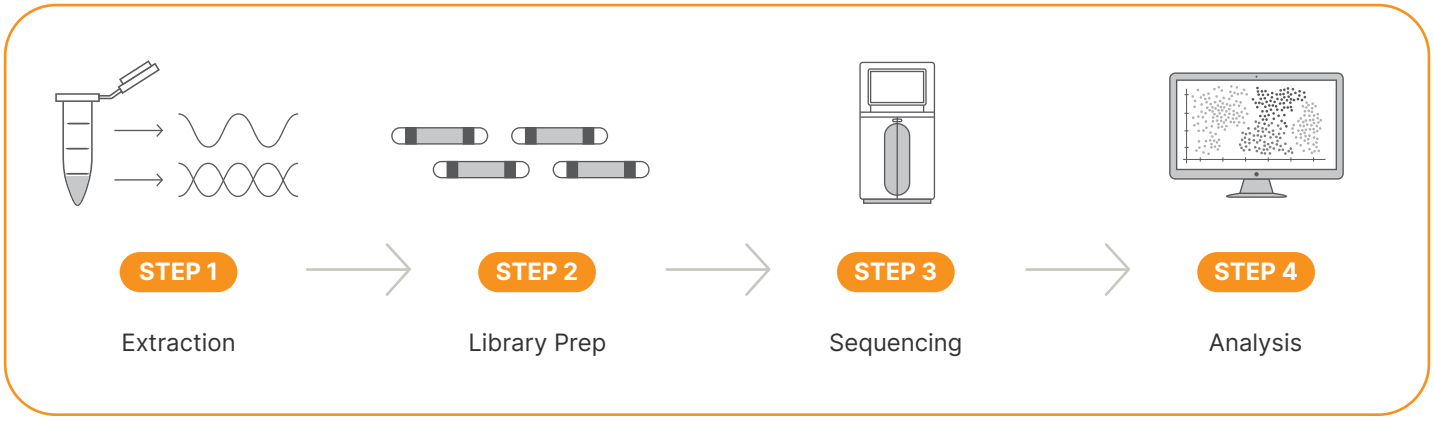
Gaining insights into pediatric cancer

In a recent study, researchers harnessed multiomics to gain insights into tumor and germline genomes from an unbiased cohort of pediatric cancer patients. Using a three-platform sequencing pipeline that included **whole-genome sequencing (WGS), whole-exome sequencing, and RNA sequencing** of paired normal and tumor tissues, researchers acquired a more detailed genetic picture. This included **identifying and confirming novel gene fusions and variants with clinical utility in 86% of patients.**[4]

Read more about the potential of multiomics in cancer research.

Genomics + transcriptomics with a single workflow

There are many ways to combine genomics and transcriptomics, but regardless of which method combination a researcher wants to use, each multiomics experiment follows a similar well-established workflow, supported by Illumina solutions. Even if a researcher has never performed a multiomic workflow before, hundreds of Core Labs offering Illumina Sequencing are available to provide assistance and guidance along the way.



Multiomics with the NovaSeq™ X

With NovaSeq X and the new 25B flow cell, researchers now have **16 billion more reads*** and access to powerful bioinformatics software with DRAGEN™.

You can sequence:

40 more WGS + WTS samples at a **62%** lower cost*

2x faster with **3x** higher accuracy*

*Compared to the S4 flow cell on the NovaSeq™ 6000

Learn how to combine DNA and RNA sequencing

Explore the Genomics and Transcriptomics Workflow eBook
https://ilmn.ly/multiomics-gt-ebook

References

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3. Percepta Associates, Inc. *Global Multiomics Practices Final Report*. 2022.
4. Newman S, Nakitandwe J, Kesserwan CA, et al. Genomes for kids: the scope of pathogenic mutations in pediatric cancer revealed by comprehensive DNA and RNA sequencing. *Cancer Discov*. 2021;11(12):3008-3027. doi:10.1158/2159-8290.CD-20-1631