BAYLOR GENETICS

Whole Genome Sequencing

More Answers to Guide Patient Care and Outcomes

What If Your Clinical Genome Test Could Do More?

Now Updated with New Modalities

GOLD 2024 STEVIE WINNER FOR TECHNOLOGY EXCELLENCE

More Informed Results with Multimodal Data Analysis

Baylor Genetics' Whole Genome Sequencing (WGS) includes a range of modalities and analysis methods that extend beyond standard sequencing. This strategy offers a broader analysis and deeper insight into disease mechanisms, helping to inform accurate diagnosis and support clinical care decisions.

Genome Analysis

Enables the detection of clinically relevant genetic variants across the genome

RNA Sequencing (RNA-Seq) Analysis

Supplemental targeted RNA analysis to support clearer result interpretation of patient specific variants.

Complex Structural Variant (SV) Analysis

Clarify large or complex genomic rearrangements related to a wide spectrum of rare diseases

NEW

Short Tandem Repeat (STR) Analysis

Detect expansions in 58 STRs to identify neurological, neuromuscular, and other genetic disorders

ENHANCED

Methylation Analysis of *FMR1*

Detect *FMR1* gene methylation status in Fragile X-associated conditions

NEW

Mitochondrial DNA (mtDNA) Analysis

Full mtDNA genome sequencing for disorders with neurological and multisystem involvement

Uniparental Disomy (UPD) Analysis

Detection of disorders where both chromosome copies originate from one parent

Metabolomic Analysis

Identify and clarify findings associated with heritable metabolic conditions

Ordered as a separate test Global Metabolomic Assisted Pathway Screen (Global MAPS®) and reported separately from WGS

Restrictions apply. See back cover for details.

New Updates to Whole Genome Sequencing (WGS)

By adding complementary methods such as targeted Long-Read Sequencing and Optical Genome Mapping to our platform, Baylor Genetics' WGS can expand the analysis of clinically significant short tandem repeats, structural variants, and methylation changes that can be challenging to interpret or detect.

Complex Structural Variants (SV) Characterization Analysis

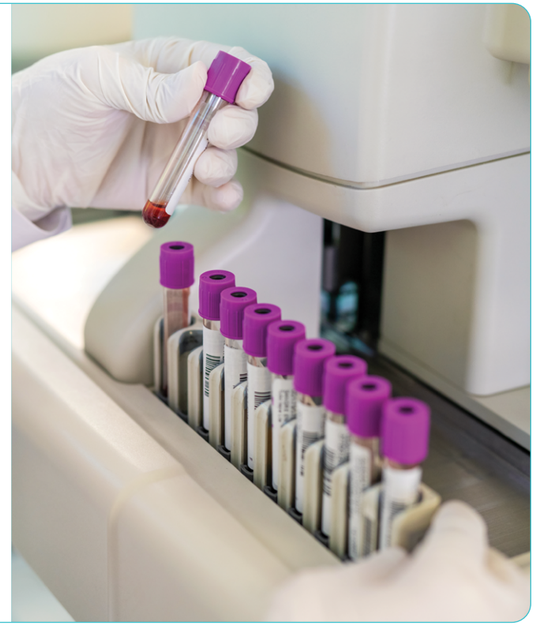
WGS can now provide better clarity for patients with rare disease who have complex SVs using Optical Genome Mapping's unmatched high-resolution detail.

Enhanced Short Tandem Repeat (STR) Analysis

WGS can now support interpretation of even more neurological and neuromuscular repeat-associated conditions by including an additional 29 STRs using targeted Long-Read Sequencing.

Methylation Analysis of *FMR1*

WGS can now detect *FMR1* gene methylation changes with targeted Long-Read Sequencing, providing critical information about gene expression in Fragile X–associated conditions to guide patient diagnosis and prognosis.



Together with RNA sequencing, these insights bring greater clarity to complex genomic findings, supporting care decisions for every patient.

Get started with WGS that does more.

Contact your Baylor Genetics regional account executive or reach out to us at **info@baylorgenetics.com** for more information.

45+ YEARS OF INNOVATION

4 MILLION+ CLINICAL TESTS PERFORMED

1 MILLION+ FAMILIES HELPED

1 MISSION EMPOWERING YOU WITH ANSWERS THAT MATTER

Baylor Genetics pioneered the history of genetic testing. Now, we're leading the way in precision diagnostics.

A pioneer of precision medicine for over 45 years, Baylor Genetics is a leading diagnostic genomics partner offering a full spectrum of clinically relevant genetic testing, including Whole Genome Sequencing, Whole Exome Sequencing, and focused panels. Baylor Genetics couples the fastest and most comprehensive precision diagnostics options with the support of genetic counselors to help clinicians and patients avoid a lengthy diagnostic odyssey, guide medical management, and make sure no patient with a genetic disorder gets left behind. Our test menu spans from family planning, pregnancy, neonatal and pediatric testing, oncology, and beyond.

Baylor Genetics is located in Houston's Texas Medical Center.

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It is important to understand that genetic tests, even if negative, cannot rule out every variant. Genetic testing, while highly accurate, might not detect a variant present in the gene(s) tested. This can be due to limitations of the information available about the gene(s) being tested, or limitations of the testing technology. It is not possible to exclude risks for all genetic diseases for patients or their family members. It is possible that even if the test identifies the underlying genetic cause for a disease, this information may not help in predicting the progression of disease or change management or treatment of disease.

Note: When appropriate, Baylor Genetics may supplement Whole Genome Sequencing (WGS) with RNA Sequencing (RNA-Seq) for variant classification and/or Optical Genome Mapping (OGM) for complex structural variant analysis. A final report will be issued prior to initiating RNA-Seq or OGM, with any resulting updates provided through an addended report. Additional specimens may be requested as needed. Complex SV analysis (with OGM) as well as STR and methylation analysis using long-read sequencing are not approved in New York State. Comparator samples are excluded from RNA-Seq, complex SV (with OGM), and STR analyses. RNA-Seq analysis, complex SV analysis (with OGM), methylation analysis and some STR analysis are not available as stand-alone tests.

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