BAYLOR GENETICS

Enhanced Whole Genome Sequencing and Whole Exome Sequencing Reports

Clearer layouts and improved usability designed to deliver actionable insights for confident clinical decisions

Baylor Genetics is introducing newly enhanced Whole Genome Sequencing (WGS) and Whole Exome Sequencing (WES) reports — designed to deliver greater clarity, usability, and clinical relevance. These improvements reflect feedback from healthcare providers and align with national reporting guidelines, reinforcing Baylor Genetics' commitment to precision diagnostics.

In the coming weeks, providers will begin receiving reports in the new format, ensuring timely access to clearer insights for patient care.

What's New

- A streamlined design that consolidates priority information into a single, easy-to-read view
- An updated organizational framework where findings are sorted by result type: Primary Findings, ACMG Secondary Findings, Incidental Findings, and Genes with No Known Disease Association (candidate genes)
- Prioritization of the most clinically relevant management information and removal of redundant variant details

Future Updates

- All other report type, including Panels (e.g., Epilepsy Panel), Chromosomal Microarray Analysis (CMA), and Mitochondrial testing (mtDNA)
- Canceled reports, including WGS and WES
- Clinical content such as indication, summary, and disease description

For questions about this update, your Baylor Genetics regional account executive is ready to help. You may also contact Client Services at 1-800-411-4363 or info@baylorgenetics.com.

01.13.26

New Design Highlights

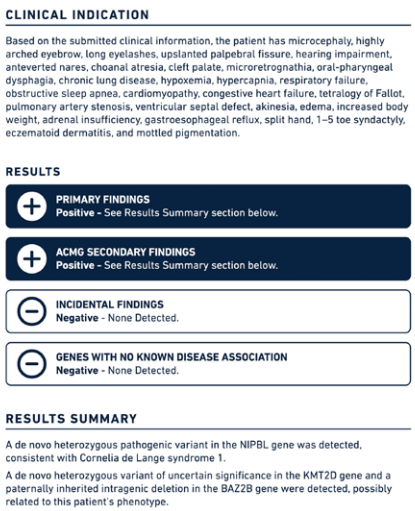
Making Clinical Insights Easier to Interpret

Clinical Findings

All key clinical information is now presented on the front page for quick, confident assessment.

This includes:

1. Clinical Indication
2. Results
3. Results Summary

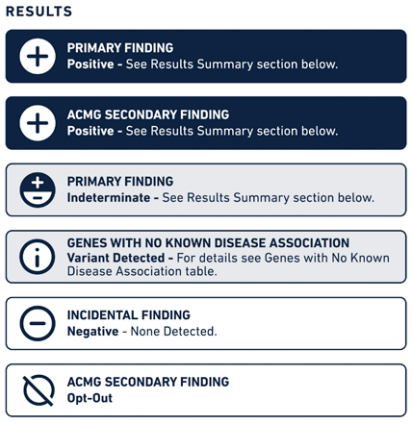


Visual Cues for Faster Interpretation

The new result bars make it easier to interpret findings at a glance, so providers can act quickly and confidently:

This includes:

- Clear shading for results:
  - Dark shading = Positive result
  - Light shading = Indeterminate
  - No shading = Negative or opt-out
- Symbols for clarity:
  - An “i” symbol marks findings in genes with no known disease association
- Opt-in/opt-out indicators:
  - Clearly defined selections, with opt-out shown by a circle and slash



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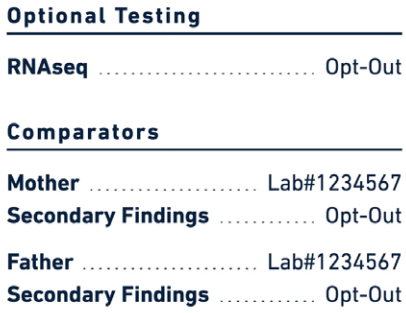
New Informational Column

To make reports easier to navigate, the first page now includes a dedicated informational column with key testing details—so providers can access critical information quickly and confidently.

This column highlights:

- The preferred RNA sequencing (RNAseq) option
- Comparator information for family-based testing



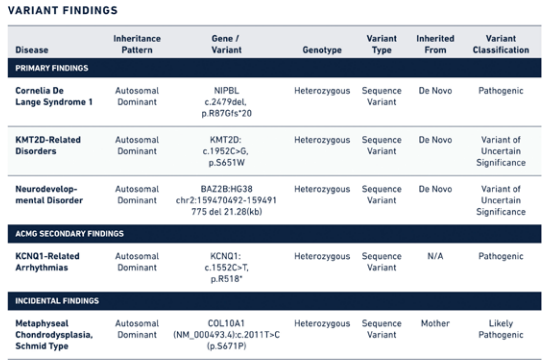
Variant Findings Table

Prioritizing Actionable Insights

To support faster clinical interpretation, the second page now includes a consolidated Variant Findings Table. This table organizes and prioritizes all actionable findings for efficient review, including:

- Primary Findings
- ACMG Secondary Findings
- Incidental Findings

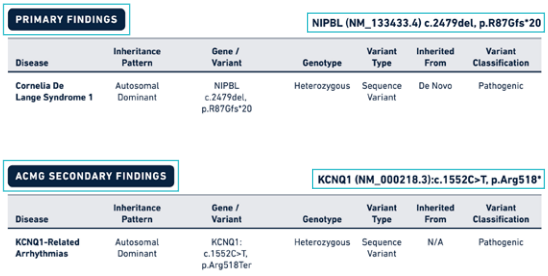
Additionally, variants are listed in order of pathogenicity.



Guideposts for Easier Navigation & Standardized Nomenclature

To make reports more clear, each variant page now includes clear ***guideposts*** that indicate whether a finding is primary, ACMG secondary, or incidental.

Inclusion of reference sequence identifiers to support easier variant look-up and ensure consistency across the field. These enhancements streamline interpretation and reinforce Baylor Genetics' commitment to precision and clarity.



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