

3B-NEO, Basic Test

Clinical use

Unique ID: [Unique ID]
3billion ID: [3billion ID]

Comprehensive Genetic Screening for Your Newborn

NEWBORN DETAILS

Unique ID	[Unique ID]	Physician	[Physician]	Sample type	DBS
3billion ID	[3billion ID]	Department	Obstetrics & Gynecology	Collected on	yyyy-mm-dd
DOB* / Sex	yyyy-mm-dd / Male	Institution	[Institution]	Ordered on	yyyy-mm-dd
Ethnicity	Latino/Admixed American			Accessioned on	yyyy-mm-dd

* (YYYY-MM-DD)

RESULT SUMMARY

NOT DETECTED

This test focused on an in-depth analysis of 704 genes selected by 3B-NEO, which are critical for preventing irreversible damage through early intervention. Within this gene set, variants were analyzed across all zygosity types, including heterozygous, homozygous, potential compound heterozygous, and hemizygous. The review encompassed single nucleotide variants (SNVs), small insertions/deletions (Indels), copy number variants (CNVs), and structural variants (SVs). No clinically significant variants were identified at this time.

RESULT INTERPRETATION

This report presents the screening results, which focuses on conditions where early intervention during infancy can prevent irreversible damage and decisively improve prognosis. The fundamental objective of this test is to identify high-risk individuals at a pre-symptomatic stage to facilitate timely clinical management. However, these results do not guarantee the absolute absence of all genetic disorders nor provide a definitive diagnosis for every possible condition.

Due to the technical limitations of current genomic technologies, certain genomic regions may not be fully analyzed. Furthermore, the possibility remains that potential causative variants were not identified due to the existence of novel variants or incomplete knowledge regarding genotype-phenotype correlations. Given that clinical manifestations of genetic disorders can emerge at later stages of growth, we recommend continuous pediatric monitoring and consultation with specialists regarding any developmental changes, independent of these test results.

LIST OF GENES

The 704 genes included in this test provide comprehensive coverage across all clinical specialties, including Metabolism, Immunology, Endocrinology, Hematology, Neurology, Gastroenterology, Nephrology, ENT/Dental, Cardiovascular, Medical Genetics, Pulmonology, Oncology, Ophthalmology, and Dermatology.

For the complete list of genes and associated conditions, please [click here](#).

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RESOURCES

- Online Mendelian Inheritance in Man®: This report contains information from the Online Mendelian Inheritance in Man® (OMIM®) database, which has been obtained under a license from Johns Hopkins University. This report does not represent the entire, unmodified OMIM® database, which is available in its entirety at <http://omim.org/downloads>.
- gnomAD (genome Aggregation Database): gnomad.broadinstitute.org
- ClinVar (National Center for Biotechnology Information ClinVar Database): ncbi.nlm.nih.gov/clinvar
- HGVS (Human Genome Variation Society): varnomen.hgvs.org
- HGMD (The Human Gene Mutation Database) Professional

REFERENCES

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NOTES

1. Results summary: Results are categorized into detected and not detected.

Category	Explanation
Detected	- AD or XL disease: one heterozygous or hemizygous P/LP variant is identified within the curated gene list. - AR disease: one homozygous P/LP variant or two P/LP (potential) compound heterozygous variants are identified within the curated gene list.
Not Detected	No clinically significant variant

2. Variant Classification: A variant is classified according to the ACMG guideline (PMID 25741868) using the type of evidence including population data, computational and predictive data, functional data, segregation data, de novo data, and allelic data.

RECOMMENDATIONS

1. Genetic counseling is warranted to review the test results and interpretation.
2. This test is designed for newborn screening purposes. A 'Detected' result does not necessarily constitute a definitive diagnosis of the associated disorder, nor does a 'Not Detected' result 100% exclude the possibility of a condition (potential for false negatives). If clinical symptoms or a relevant family history are present, a comprehensive clinical evaluation by a specialist and additional confirmatory testing (e.g., biochemical assays) may be required regardless of the test results.
3. This test can detect single nucleotide variants, small insertions/deletions (<50 bp) and large (>=3 consecutive exons) copy number variants with high accuracy in most of the genomic regions. If low level (<20%) mosaicism variants on autosomes and sex chromosomes, small (<3 consecutive exons) copy number variants (CNVs), structural variants (SVs) including inversions and translocations, or low heteroplasmic level mitochondrial genome variants are suspected, it is recommended to perform other tests specifically designed to detect these types of variants. Variants in regions of high sequence homology, such as pseudogenes, may be difficult to detect. Intronic variants, epigenetic factors, or variants in regulatory regions called by being near coding exons may not be interpretable.
- [Technical Limitation Note for Specific Genes] Due to the inherent technical boundaries of short-read NGS, this assay exhibits reduced analytical sensitivity in highly challenging genomic loci. Clinical confirmation via specialized non-NGS assays is strongly recommended regardless of these screening results if the following conditions are suspected: *SMN1 & CYP21A2: High sequence homology with SMN2 (paralogous gene) and CYP21A1P (pseudogene), respectively, combined with frequent gene conversion events, may confound variant calling or mask silent carriers (e.g., 2+0 genotype). Targeted assays such as MLPA or ddPCR are highly recommended. *F8: Large-scale structural rearrangements, specifically the Intron 22 and Intron 1 inversions, cannot be reliably resolved by standard short-read NGS. If hemophilia is clinically suspected or there is a relevant family history, specialized testing (e.g., inverse-shifting PCR or long-range PCR) must be performed.
4. Variant interpretation is based on currently available scientific and medical information that were publicly available at the time the results were reported. Therefore, the referenced data may not be current at the time of genetic counseling.

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METHODS

Genomic DNA was extracted from DBS specimen using standard protocol. Exome capture was performed using xGen Exome Research Panel v2, supplemented with xGen human mtDNA panel and xGen Custom Hyb Panel v1 (Integrated DNA Technologies, Coralville, Iowa, USA). Sequencing was performed using NovaSeq X (Illumina, San Diego, CA, USA). In total, 11,458,836,111 bases of sequence were generated and uniquely aligned to a modified version of the Genome Reference Consortium Human Build 38 (GRCh38), in which falsely duplicated regions of chromosome 21 were masked to N's based on the masking file developed in collaboration with the GRC (Genome Reference Consortium) (Nat Biotechnol. 2022;40:672-680) and Revised Cambridge Reference Sequence (rCRS) of the mitochondrial genome, generating 168.58 mean depth-of-coverage within the 34,212,647 bases of the captured region, which is approximately 99.3% of the RefSeq protein coding region. Approximately 99.40% of the targeted bases were covered to a depth of $\geq 20\times$. Despite the insufficient coverage across 0.60% of the bases (see below for details), these metrics are consistent with high quality exome sequencing data and deemed adequate for analysis. Gene or exon level depth-of-coverage (DOC) information is available upon request. In total, [[snp]] single nucleotide variants (SNV) and [[indel]] small insertions and deletions (INDEL) were identified. Sequencing data analysis and variant interpretation were performed using 3billion's proprietary system, EVIDENCE v4.2 (Clin Genet. 2020;98:562-570). EVIDENCE incorporates bioinformatics pipeline for calling SNV/INDEL based on the GATK best practices (GATK v3.8, Genome Res. 2010;20:1297-303), Manta (Bioinformatics. 2016;32:1220-2) for structural variant calling including CNV (copy number variants) based on paired-end information, and 3bCNV v23.0818, an internally developed tool, for calling CNV including aneuploidy based on the DOC information. It also incorporates Mutect2 (Genome Res. 2010;20:1297-303) for calling lower level heteroplasmic SNV/INDEL in the mitochondrial genome, ExpansionHunter v5.0.0 (Bioinformatics. 2019;35:4754-6) for calling repeat expansion variants, MELT v2.2.2 (Genome Res. 2017;27:1916-29) for calling mobile element insertion variants, AutoMap v1.2 (Nat Commun. 2021;12:518) for detecting regions of homozygosity (ROH). Variant Effect Predictor v104.2 (VEP, Ensembl, Genome Biology 2016;17:122) is used for variant annotation. Variants were prioritized based on the guideline recommended by the American College of Medical Genetics and Genomics (ACMG) and the Association for Molecular Pathology (AMP) (Genet Med. 2015;17:405-424, Genet Med. 2020;22:245-257, and Hum Mutat. 2020;41:2028-2057). Only variants deemed clinically significant and relevant to the patient's clinical indications at the time of variant interpretation are reported. Based on internal studies validating the accuracy of the SNVs and INDELs called with high quality scores, only low quality variants are confirmed by Sanger sequencing. SVs with breakpoints identified were attempted to be confirmed by Sanger sequencing.

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DISCLAIMER

This test was developed by 3billion for the purpose of identifying single nucleotide variants, small insertions and deletions, and structural variants from the [exome/genome] sequence. This laboratory is certified under the College of American Pathologists (CAP#: 8750906) and Clinical Laboratory Improvement Amendments (CLIA#: 99D2274041) as qualified to perform high complexity clinical laboratory testing. Assay validation and clinical validation were performed following the Korea Institute of Genetic Testing Evaluation, the American College of Medical Genetics and Genomics (ACMG) Technical Standards and Guidelines Section G (<https://www.acmg.net/PDFLibrary/Standards-Guidelines-Clinical-Molecular-Genetics.pdf>) and the CAP Next Generation Sequencing (NGS) Worksheets (Santani A et al. J Mol Diagn. 2019 May;21(3):369-374; <https://www.cap.org/member-resources/precision-medicine/next-generation-sequencing-ngs-worksheets>). This test is designed for newborn screening purposes only and is not intended as a standalone diagnostic tool. If low-level mosaicism or variants within regions that are incompletely sequenced due to technical difficulties with amplification, sequencing, or alignment are suspected, it is recommended to perform appropriate testing specifically designed to detect such variants. This report may not be copied or reproduced except in its totality.

ACCREDITATIONS AND CERTIFICATIONS

CAP License #

8750906, AU-ID# 2052626

CLIA ID #

99D2274041

This case has been comprehensively reviewed by our clinical team of physicians, geneticists and informaticists.

Report electronically signed by:



Go Hun Seo, M.D, Ph.D.

Chief Medical Officer & Laboratory Director