NEURAZON
WELLNESS STARTS WITH YOU

From:
Neurazon INC.
Precision Health Analysis Department - Children with Autism and Developmental Disorders
Quebec, Canada

Case no: 572216390
First Name: Kenz
Last Name: Haddadin
DOB: 24.11.2019
Sex: Male

Test requested: Precision Health Analysis®

Results:
True Autism Spectrum Disorder Variants: NEGATIVE
Acquired Autism Spectrum Disorder Variants: POSITIVE
Attention-Deficit/Hyperactivity Disorder Variants: NEGATIVE
Information Processing and Brain Development Variants: NEGATIVE
White Matter Delays Variants: POSITIVE
Methylation Variants: NEGATIVE
Metabolic and Mitochondrial Function Variants: NEGATIVE
Neurotransmitters, Synaptic Health, and Behavior Variants: POSITIVE
Immune System Variants: NEGATIVE
Potential Digestive System Variants: POSITIVE
Epigenetic Regulation Variants: NEGATIVE
Potential Uncontrolled Electrical Activity: NEGATIVE

Recommended Interpretation:

- Please note any clinically relevant variants detected that are associated with the described phenotype, if present.
- Review all variants listed in the attached report, if applicable.
- We recommend reevaluating the sequence dataset every 12 months or when there are changes in the phenotype.
- Reassessment by a multidisciplinary team is advised every 3 months to monitor any observed phenotypic changes using artificial intelligence.
- A tailored intervention plan should be developed and supervised by a multidisciplinary team.

ADDITIONAL INFORMATION

This assessment was developed and validated using the AI model of NEURAZON, based on the findings outlined in the attached report. The U.S. Food and Drug Administration (FDA) has determined that clearance or approval for this method is not required; therefore, neither has been sought. All test results are thoroughly reviewed, interpreted, and reported by our team of scientific and medical experts. For full details, please refer to the attached report.

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Tel.: +1 438-497 4440
customer.support@neurazon.com
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Recommended Homeopathy Plan

Step: 1st
step Name: Kenz Haddadin
DOB: 24.11.2019

Please refer to external plan

ADDITIONAL INFORMATION

Recommendations: The provided guidance includes safe, non-drug, natural treatments intended to support the child's development. These recommendations are not a replacement for professional rehabilitation and training sessions and should always be followed under the supervision of a qualified specialist. Progress and improvement depend on the individual child, the underlying causes, and their response to the interventions, with recommendations adjusted based on regular evaluations every three months. If any signs of an allergic reaction occur, discontinue the treatment immediately and consult with a healthcare provider to modify the treatment plan accordingly.

Reevaluation: A reevaluation is necessary after the specified duration to reassess development using the AI model or as recommended by the professional team.

Next Steps: Begin the second phase of the protocol after the timeframe indicated in the treatment plan.

This assessment was developed and its performance validated using the AI model of NEURAZON, as detailed in the attached report. Based on the U.S. Food and Drug Administration (FDA) guidelines, this method does not require clearance or approval, and none has been pursued. This test is intended for clinical purposes. All results are thoroughly reviewed, interpreted, and reported by our team of scientific and medical experts. Please refer to the attached report for comprehensive details.

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Order no: 572216390
Report Type: Final report

Case no: 572216390
First Name: KENZ
Last Name: HADDADIN
DOB: 24.11.2019
Sex: Male

Requested Test: WES (Whole Exome Sequencing)
Clinical Information/Indication: The analysis was performed according to the demand of referal center to identify variants in relevant genes associated with neurological disorders.
Result:
Table:

Main Findings:
A Class 1 mutation; c.2977T>C / p.Cys993Arg in the FBN1 gene was identified.
A Class 3 variant; c.3700G>A / p.Asp1234Asn in the CDC42BPB gene was identified.

Gene (Transcript)	Location	Nucleotide (protein) dbSNP	Zygosity	Variant Classification	Disease (OMIM#, Inheritance)
FBN1 NM_000138.5	Exon 25	c.2977T>C p.Cys993Arg rs1206813753	Heterozygous	Class 1	FBN1 Related Disease OMIM: 134797 Autosomal Dominant
CDC42BPB NM_006035.4	Exon 28	c.3700G>A p.Asp1234Asn rs747398820	Heterozygous	Class 3	Chilton-Okur-Chung Neurodevelopmental Syndrome OMIM: 619841 Autosomal Dominant

Details About Gene and Variants:
FBN1: This gene encodes a member of the fibrillin family of proteins. The encoded preproprotein is proteolytically processed to generate two proteins including the extracellular matrix component fibrillin-1 and the protein hormone asprosin. Fibrillin-1 is an extracellular matrix glycoprotein that serves as a structural component of calcium-binding microfibrils. These microfibrils provide force-bearing structural support in elastic and nonelastic connective tissue throughout the body. Asprosin, secreted by white adipose tissue, has been shown to regulate glucose homeostasis. Mutations in this gene are associated with Marfan syndrome and the related MASS phenotype, as well as ectopia lentis syndrome, Weill-Marchesani syndrome, Shprintzen-Goldberg syndrome and neonatal progeroid syndrome. [provided by RefSeq, Apr 2016]

The FBN1 variant c.2977T>C / p.Cys993Arg was detected in heterozygous state. It is classified as Pathogenic (P/Class 1) according to the recommendations of ACMG. This variant is associated with autosomal dominant FBN1 Related Diseases (OMIM: 134797).

CDC42BPB: This gene encodes a member of the serine/threonine protein kinase family. The encoded protein contains a Cdc42/Rac-binding p21 binding domain resembling that of PAK kinase. The kinase domain of this protein is most closely related to that of myotonic dystrophy kinase-related ROK. Studies of the similar gene in rat suggested that this kinase may act as a downstream

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effector of Cdc42 in cytoskeletal reorganization. [provided by RefSeq, Jul 2008]

The CDC42BPB variant c.3700G>A / p.Asp1234Asn was detected in heterozygous state. It is classified as Variant of Unknown Significance (VUS/Class 3) according to the recommendations of ACMG. This variant is associated with Autosomal Dominant, Chilton-Okur-Chung neurodevelopmental syndrome (OMIM: 619841).

Recommendations:
- It is recommended to evaluate this patient's result together with clinical and laboratory findings.
- Genetic screening and clinical evaluation are recommended for family members.
- Genetic counseling is recommended.

Additional Findings:
The variants reported as additional findings refer to pathogenic changes that are not related to the referred phenotype but can cause additional phenotype thus require genetic counseling and further clinical evaluation.

Gene (transcript)	Location	Nucleotide (protein) dbSNP	Zygosity	Variant Classification	Disease (OMIM#, Inheritance)
CFTR NM_000492.4	Exon 12	c.1661C>G p.Ala554Gly	Homozygous	Class 3	Cystic Fibrosis OMIM: 219700 Autosomal Recessive

ACMG Findings (ACMG 81 Genes):
According to the ACMG guidelines (Genetics in Medicine, 2023; PMID: PMID: 37347242), Class 1 or 2 incidental changes in proposed diseases and genes are reported. Variants in the BRCA1/2, MLH1, MSH2, MSH6, PMS2, TMEM127, MAX and MUTYH genes associated with adult onset diseases in children (under 15 years of age) are not reported.

Carriership Findings:
Class 1 and class 2 variants in genes selected according to OMIM phenotypes associated with severe or early-onset diseases have been reported. The variants reported as carriership findings refer to pathogenic changes that are not related to the reported phenotype and require family screening in conjunction with genetic counseling due to potential carrier risk.

Table:

Gene (Transcript)	Location	Nucleotide (protein) dbSNP	Zygosity	Variant Classification	Disease (OMIM#, Inheritance)

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NPHP1 NM_001128178.3	Intron 1	c.69+1del rs1435671751	Heterozygous	Class 2	NPHP1 Related Disease OMIM: 607100 Autosomal Recessive
SLC12A3 NM_001126108.2	Exon 1	c.237_238dup p.Arg80Profs*35 rs780299444	Heterozygous	Class 1	Gitelman Syndrome OMIM: 263800 Autosomal Recessive
AAAS NM_015665.6	Exon 6	c.470_471del p.Phe157Cysfs*16	Heterozygous	Class 1	Achalasia-Addisonianism-Alacrimia Syndrome OMIM: 231550 Autosomal Recessive

Method:
Whole Exome Sequencing is performed by DiagnoSeq using Twist Biosciences technology. First, approximately 36.5 Mb of Consensus Coding Sequences (CCS) (targeting> 98% of RefSeq and Gencode v28 regions derived from the human genome) are replicated from fragmented genomic DNA with the Twist Human Core Exome Plus kit. The generated library is sequenced on the Illumina Novaseq NGS platform to achieve a minimum reading depth of 20x for>98% of the targeted bases. As a result of sequencing, raw data is obtained in FASTQ and VCF formats. Whole Exome Sequencing analysis is performed on FASTQ data using the Franklin by Genoox analysis program. In addition to all disease-causing variants reported in the HGMD®, ClinVar, and CentoMD® databases as well as all variants with a Minor Allele Frequency (MAF) of less than 1% in the gnomAD database are considered. The research for related variables has focused on coding exons and surrounding +/- 20 intronic bases. All potential inheritance patterns are covered. In addition, the family history and clinical information provided are used to evaluate pathogenicity and variables defined by their cause of disease and are classified in Class 1 - 5 scoring **. All variables related to the patient's phenotype are reported, except for benign or possible benign variants. Low-quality single nucleotide variants and all related deletion/insertion variants are validated by Sanger sequencing.

Analysis Statistics:

Average Depth (RefSeq Exome)	121
Variant Quality	99%

Method Limitations:
Polymorphisms in primary binding and regions, CNV duplications and somatic microsatellite variations, tissue mosaic, high GC nucleotide content can lead to false positive / negative results. False positive findings may occur due to large deletion / point mutation combined heterozygosity. Variants in transcripts other than canonical transcripts cannot be eliminated, and differences may occur between exon numbers and mutation positions depending on the transcript type sequenced. This method does not show heterozygous deletions and duplications in rare exons and nucleotide changes in other regions of the gene.

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Variants with the allele fraction below 30% for regions with a sensitivity of this test of 50X read count are not reported. Additionally, due to technology limitations, some regions may be either not covered or poorly covered. Variables in these regions cannot be reliably detected. Areas with extremely low readings are considered artifacts as a result of validation studies, and they were not taken into account during the analysis. Copy number changes, inversions, translocations and repeat sequence increases cannot be detected by the NGS method.

The genetic results are interpreted in the context of the provided clinical findings, family history, and other laboratory data. Only variants in genes potentially related to the proband's medical condition are reported. Misinterpretation of results may occur if the provided information is inaccurate and/or incomplete. If the obtained genetic results do not concur with the clinical findings, additional testing should be considered.

****Variant Classification (According to American College of Medical Genetics ACMG)**
Class 1 – Pathogenic
Class 2 – Likely pathogenic
Class 3 – Variant of Unknown Significance -VUS
Class 4 – Likely benign
Class 5 – Benign

This test was analyzed by Neurazon, Canada.

Digitally Approved by:

Dr. Carmel Katz

Lead Scientist and Geneticist

Lead Bioinformatics Specialist

At Neurazon

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