

PATIENT

Name: **Patient, Sample**
 Accession #: 00-324513
 DOB: 01/01/1901
 Sex at Birth: Male
 MRN: N/A
 Indication: Diagnostic

TEST INFORMATION

Portal Order #: 0000000
 Family #: 0000000
 Specimen #: N/A
 Specimen type: Blood EDTA
 Collection date: 01/01/2023
 Received date: 01/01/2023
 Test Started: 01/01/2023
 Final Report: 02/20/2023

MEDICAL PROFESSIONAL

Sample Doctor
 Sample Facility

ADDITIONAL RECIPIENTS

Sample GC

UNCERTAIN: Alteration(s) of Uncertain Clinical Relevance Detected

Reportable Findings

Single gene alterations	Contiguous gene deletions/duplications	Mitochondrial genome
1(1)*	None	Not Ordered

* genes(alterations)

Indication for Testing

Speech and language delays, concern for autism

Results

Gene (RefSeq ID)	Characterized/ Uncharacterized Gene	Relevant Associated Syndrome	Mode of Inheritance	Genotype	Alteration	Alteration Classification
<i>TCF20</i> (NM_005650)	Characterized	<i>TCF20</i> -related neurodevelopmental disorder	Autosomal dominant	Heterozygous	c.1591G>A (p.G531S)	Variant of Uncertain Significance

Interpretation

- Overall, the evidence suggests it is uncertain if the identified *TCF20* alteration is the cause of the patient's clinical symptoms. Clinical correlation is recommended.

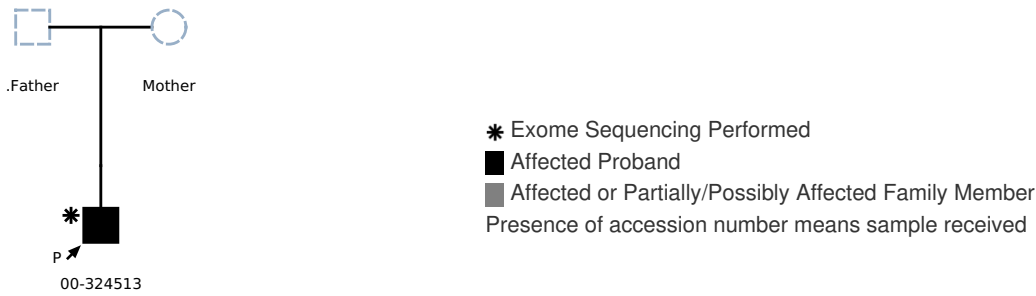
Notes

- Secondary findings were issued in a separate report.
- Please note this assay is not intended to confirm previously detected copy number variants.
- Genetic counseling is a recommended option for all patients undergoing genetic testing.
- Any tests on hold, previously reported, and those that have been cancelled (including reflex testing steps cancelled due to a positive result in a preceding test) have not been included in this report. For additional information, please contact Ambry Genetics.

Electronically Signed By Sample Director, on 2/20/2023 at 0:00:00 PM

All content hereafter is supplemental information to the preceding report.

Family Pedigree



Analyses Performed

- i) Full exome sequencing, bioinformatics, filtering and manual review based on autosomal and X-linked dominant and recessive and Y-linked inheritance models of the proband was performed. Medical review of characterized genetic etiologies revealed an alteration with uncertain clinical relevance.
- ii) Because fewer than three informative individuals in this family were available for sequencing and a characterized finding was identified, medical review of uncharacterized genes* and gene-disease relationships for potential candidate gene findings was not performed.

*Uncharacterized genes are not currently established to underlie Mendelian genetic conditions. An uncharacterized gene will be classified as a "candidate" or "suspected candidate" when sufficient evidence, based on Ambry's comprehensive, rule-based scoring criteria, is available (Farwell Hagman, 2017) (<http://www.ambrygen.com/candidate-gene-reporting>).

Raw Data

A table with additional variant filtering details can be found with the raw data filtered variant list (if requested). This list includes clinically irrelevant characterized genes and uncharacterized genes which could not be ruled out (if analyzed); these alterations are not systematically confirmed via Sanger sequencing. The filtered variant list can be requested via this form (www.ambrygen.com/file/material/view/1262/Raw_Sequence_Data_Consent_0619_final.pdf).

Metrics and Coverage

The values below represent metrics from the proband's exome sequencing. Complete coverage data for this proband can be e-mailed or made available for download through AmbryPort by request.

Relationship	Depth of coverage	
	% Bases ≥ 10x	% Bases ≥ 20x
Proband	98.7	98.4

TCF20 Gene Details

Gene Symbol	RefSeq ID	Genomic Coordinates (GRCh37)	Genomic Size (bp)	Total Exons	Coding Exons	Number of Amino Acids
TCF20	NM_005650	chr22:42556019-42611445	55427	5	4	1960 aa

The *TCF20* gene is located on chromosome 22q13.2 and encodes the transcription factor 20 protein. Pathogenic alterations in this gene are known to cause *TCF20*-related neurodevelopmental disorder, which is an autosomal dominant condition that generally occurs *de novo*, but in a minority of cases has been inherited from an affected parent. *TCF20*-related neurodevelopmental disorder is characterized by developmental delay, intellectual disability, autism spectrum disorder or autistic features, attention disorders or hyperactivity, hypotonia, dysmorphic craniofacial features, and gastrointestinal abnormalities (Torti, 2019; Vetrini, 2019). Mechanism of disease is unclear for *TCF20*-related neurodevelopmental disorder.

TCF20 c.1591G>A (p.G531S)

Alteration description:

The c.1591G>A (p.G531S) alteration is located in exon 1 (coding exon 1) of the *TCF20* gene. This alteration results from a G to A substitution at nucleotide position 1591, causing the glycine (G) at amino acid position 531 to be replaced by a serine (S).

Population frequency:

This variant was not reported in population-based cohorts in the Genome Aggregation Database (gnomAD).

Conservation:

This amino acid position is well conserved in available vertebrate species.

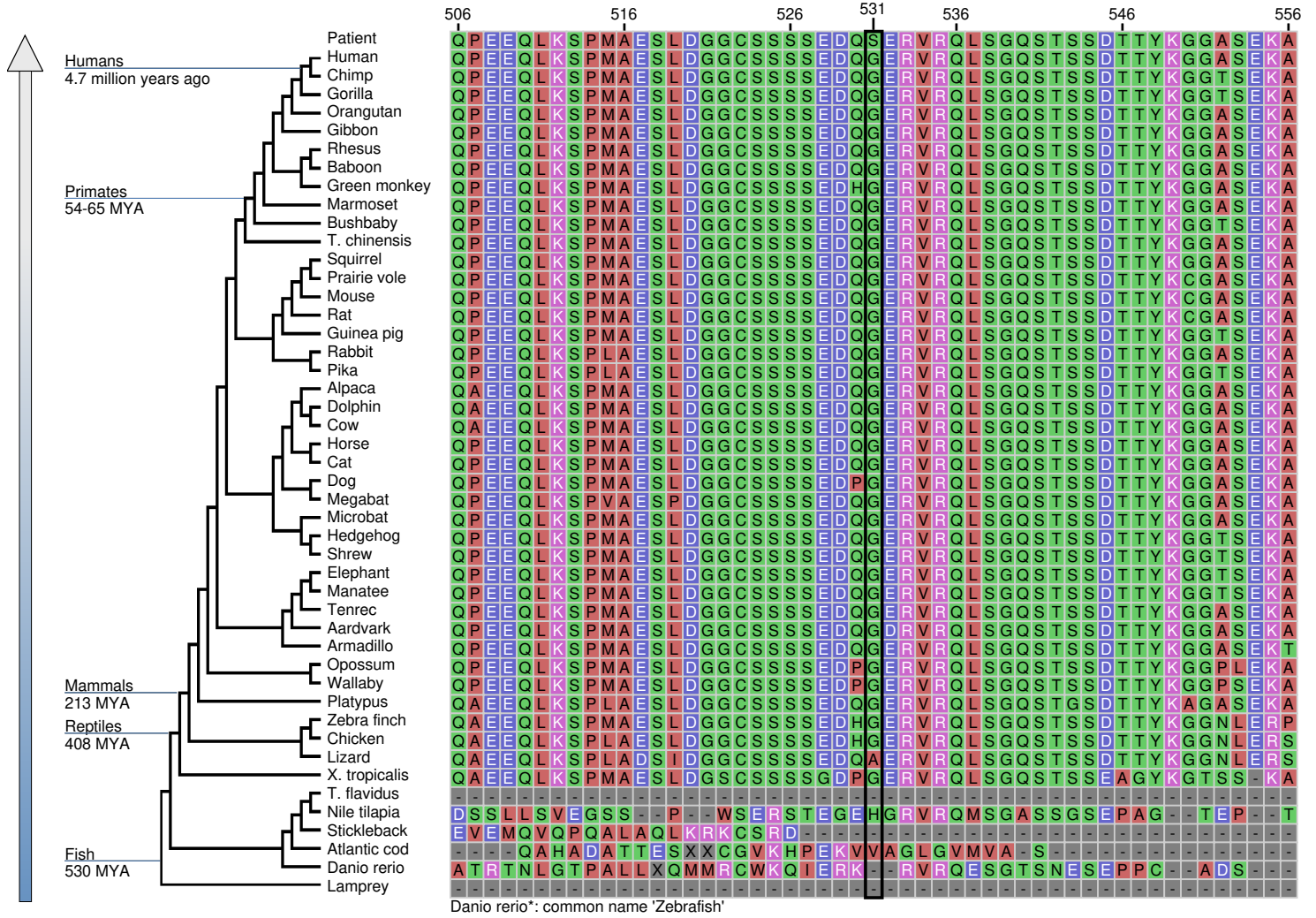
In silico:

This alteration is predicted to be tolerated by *in silico* analysis.

Based on the available evidence, the clinical significance of the *TCF20* c.1591G>A (p.G531S) alteration is uncertain.

Ambry Genetics offers complimentary genetic studies for variants meeting specific criteria in appropriate family members. Review of clinical information is required. Additional information, application instructions and required forms, and patient education materials are available at <http://ambrygen.com/family-studies-program>. For additional information, please email us at clinicalassistants@ambrygen.com or call 949-900-5500 and ask to speak with a genetic counselor specializing in exome analysis.

TCF20 c.1591G>A (p.G531S)



Trait	Gly (G)	Ser (S)
Amino Acid Name	Glycine	Serine
Polarity/Charge	non-polar	polar
pH	neutral	neutral
Residue Weight	57	87
Hydrophobicity Score	-0.4	-0.8
Hydrophilicity Score	0	0.3
Secondary Structure Propensity	strong α breaker / β breaker	α indifferent / β breaker

Report References

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Resources Used for Bioinformatics, Medical Review Filtering, and Reporting

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- Exome Variant Server, NHLBI Exome Sequencing Project (ESP) [Internet]: Seattle, WA. Available from: <http://evs.gs.washington.edu/EVS>.
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ExomeNext® Assay Information

General Information: Ambry's ExomeNext® is a cost-effective, comprehensive, integrated exome sequencing assay designed to increase the diagnostic yield for genetic disorders that have eluded definitive delineation using traditional diagnostic approaches. The exome represents all the exons, which are the regions in the human genome that are translated into proteins. It is estimated that the protein-coding regions of the human genome contain about 85% of the disease-causing mutations. Whole-exome sequencing has been successfully applied to identify both inherited and de novo mutations in a diverse variety of autosomal dominant, recessive, and X-linked disorders. In addition to the primary analysis, which is performed with the purpose of uncovering the underlying genetic cause for a given clinical presentation, the clinical diagnostic exome may also be utilized to provide secondary findings, which are pathogenic or likely pathogenic alterations in genes that lead to diseases unrelated to the patient's present clinical presentation or reason for referral.

Result Reports: A primary clinical report will only be generated for the proband regardless of number of family members submitted. However, it may be possible to infer information about family member's results based on the proband's report. Pathogenic mutation(s) likely to factor into the patient's current clinical condition are always reported. Since new scientific information becomes available on a regular basis, this could alter the interpretation of previously reported results. In the event of a change in interpretation, an unsolicited reclassification/amended report may be issued to the ordering clinician. Pathogenic mutations or likely pathogenic variants identified within the ACMG secondary findings gene list are reported separately unless opted out (Kalia, 2016; Miller, 2023). Expanded childhood onset secondary findings are available in a separate report for prenatal exome testing orders.

Test Limitations: This test was developed and its performance characteristics were determined by Ambry Genetics. It has not been cleared or approved by the US Food and Drug Administration. The FDA does not require this test to go through premarket FDA review. It should not be regarded as investigational or for research. This test should be interpreted in context with other clinical findings. This report does not represent medical advice. Any questions, suggestions, or concerns regarding interpretation of results should be referred to a genetic counselor, medical geneticist, or physician skilled in evaluating the relevant medical literature. This laboratory is certified under the Clinical Laboratory Improvement Amendments (CLIA) as qualified to perform high complexity clinical laboratory testing. The following types of mutations are detectable: nucleotide substitutions, small deletions, small insertions, small indels, and gross deletions and duplications. The overall coverage of each gene varies and each individual may have slightly different coverage yield. Accurate exon-level gross deletion and duplication detection by exome sequencing is dependent on several factors such as inherent sequence properties of the targeted regions, including shared homology and exon size, depth-of-coverage, efficiency of capture, and degree of read depth variation in the selected reference samples. Therefore, the specificity and sensitivity of gross deletion and duplication detection by exome sequencing may be reduced. Exome sequencing is not intended to analyze the following types of mutations: gross rearrangements, deep intronic variations, long repeat sequences, portions of genes with highly homologous pseudogenes, trinucleotide repeat sequences, mutations involved in tri-allelic inheritance, certain mitochondrial genome mutations, epigenetic effects, oligogenic inheritance, and X-linked recessive mutations in females who manifest disease due to skewed X-inactivation and other unknown abnormalities. A negative result from the analysis cannot rule out the possibility that the tested individual carries a rare unexamined mutation or mutations in an undetectable region. Ambry's ExomeNext® detection rate is 30% for positive or likely positive relevant findings identified in established disease-gene associations, and an additional 7% for candidate gene findings (Farwell, 2015; Farwell Hagman, 2017). Although molecular tests are highly accurate, rare diagnostic errors may occur. Possible diagnostic errors include sample mix-up, erroneous paternity identification, technical errors, clerical errors, and genotyping errors. Genotyping errors can result from trace contamination of PCR reactions, from rare genetic variants that may interfere with analysis, or from other sources.

Methodology: Genomic deoxyribonucleic acid (gDNA) is isolated from the patient's whole blood. Samples are prepared using the IDT xGen Exome Research Panel V1.0 (IDT). Each DNA sample is sheared, adaptor ligated, PCR-amplified and incubated with the exome baits. Captured DNA is eluted and PCR amplified. Final quantified libraries are seeded onto an Illumina flow cell and sequenced using paired-end, 150 cycle chemistry on the Illumina NovaSeq, NextSeq or HiSeq. Initial data processing, base calling, alignments and variant calls are generated by various bioinformatics tools using genome assembly GRCh 37/hg19. Data is annotated with the Ambry Variant Analyzer tool (AVA), including: nucleotide and amino acid conservation, biochemical nature of amino acid substitutions, population frequency, and predicted functional impact. Data analysis is focused on small insertions and deletions, canonical splice site alterations, and non-synonymous alterations. Gross deletion/duplication analysis is assessed for proband only for all genes within the targeted exome using a custom pipeline based on coverage and/or breakpoint analysis from NGS data and is followed by a confirmatory orthogonal method, as needed. The following sites are used to search for previously described gene mutations and polymorphisms: the Human Gene Mutation Database (HGMD), the Single Nucleotide Polymorphism database (dbSNP), ExAC, ESP, 1000 genomes, and online search engines (e.g., PubMed). Variants are then filtered further based on applicable inheritance models. Co-segregation studies are performed if family members are available. All relevant findings undergo manual review by molecular geneticists using integrated genomics software (IGV) and/or undergo confirmation either by automated fluorescence dideoxy (aka "Sanger") sequencing or via trio exome sequencing with coverage and alternate read ratios above established confidence thresholds. Additionally, gross deletions/duplications are confirmed by SNP Microarray (Affymetrix® CytoScan™ HD Array), in-house targeted array, MLPA, or Sanger sequencing. Co-segregation results may be confounded by many factors which cannot be completely ruled out including haploinsufficiency, reduced penetrance, age-of-onset, and/or variable expressivity. Relevant findings are evaluated from among the genes in Ambry's internal, dynamic gene database which classifies genes as characterized or uncharacterized Mendelian disease genes based on clinical validity (Smith, 2017). Characterized genes are those currently known to underlie at least one Mendelian genetic condition. Uncharacterized genes are those not currently known or with insufficient evidence to be associated with a Mendelian genetic condition. Characterized genes are analyzed first. If no positive findings are identified, reflex analysis of uncharacterized genes occurs for potential identification of a candidate gene finding. The analysis of candidate gene findings is only performed when an informative trio is received for testing and focuses on de novo, autosomal recessive, or X-linked inherited alterations. Each alteration remaining after inheritance model filtering is analyzed and/or reviewed by board certified molecular geneticists to identify the most likely causative alteration(s). Interpretation is based on the clinical, family, and test information provided by the referring provider and the current knowledge of genes and alterations at the time of reporting. Screening and analysis of known mtDNA mutations related to the proband's clinical phenotype is included if ordered. Amplification of the entire mitochondrial genome is carried out by long distance PCR and sequencing of mitochondrial DNA (mtDNA) is performed separately on Illumina MiSeq.

Analysis of Alterations: The following lines of evidence are used to assess the pathogenic nature of an alteration: presence in affected and healthy populations, co-segregation information, functional studies, alteration type, conservation, *in silico* predictions, and presence in a functional protein domain. The absence of a particular line of evidence implies that no information was found or it does not apply for that alteration type (e.g. *in silico* for truncating alterations).

Analytical range: Approximately 75% of the bases are expected to have quality scores of Q30 or higher, which translates to an expected base-calling error rate of 1:1000, or an expected base-calling accuracy of 99.9%. Additionally, 90% and 95% of the exome will be covered at $\geq 20\times$ and $\geq 10\times$ respectively under current run conditions, generally sufficient for high quality heterozygous and homozygous variant calling for germline variants. For any given individual ~ 10% of the targeted exome is not sequenced well enough to make a confident call. Each individual may have slightly different coverage yield distributions within the exome. Exons plus at least 6 bases into the 5' and 3' ends of all the introns are analyzed and reported. The pipeline detects deletions and duplications >5 exons in size in sequences with sufficient resolution. The minimum depth of coverage for targeted mitochondrial bases is greater than 1,000X.