Specimen ID: 00000000050 **Container ID:** H0655
Control ID: **Acct #:** LCA-BN **Phone:**

SAMPLE REPORT, F-630068

Patient Details		Specimen Details		Physician Details	
DOB:	05/05/1995	**Date Collected:**	08/05/2019 12:00 (Local)	**Ordering:**	
Age (yyy/mm/dd):	024/07/04	**Date Received:**	08/06/2019	**Referring:**	
Gender:	Female	**Date Entered:**	08/06/2019	**ID:**	
Patient ID:	00000000050	**Date Reported:**	08/16/2019 13:21 (Local)	**NPI:**	

Ethnicity: Unknown
Indication: MAN2B1 carrier testing
Specimen Type: Blood
Lab ID: MNEGA
Genetic Counselor:

SUMMARY: POSITIVE

POSITIVE RESULTS

DISORDER *(GENE)*	RESULTS	INTERPRETATION
Alpha-mannosidosis (*MAN2B1*) NMID: NM_000528	POSITIVE Heterozygous for c.2248C>T (p.Arg750Trp), pathogenic Chr19:12760746 (GRCh37)	Predicted to be a carrier. Genetic counseling is recommended. **Risk:** AT INCREASED RISK FOR AFFECTED PREGNANCY. See Additional Clinical Information.

Genetic counseling is recommended to discuss the potential clinical and/or reproductive implications of positive results, as well as recommendations for testing family members and, when applicable, this individual's partner. Genetic counseling services are available. To access Integrated Genetics Genetic Counselors please visit www.integratedgenetics.com/genetic-counselingor call (855) GC-CALLS (855-422-2557).

ADDITIONAL CLINICAL INFORMATION

Alpha-mannosidosis: Alpha-mannosidosis is an autosomal recessive lysosomal storage disorder with variable severity and age at onset. Signs and symptoms may include progressive neurological deterioration, intellectual disability, skeletal and facial abnormalities, immunodeficiency, and hearing impairment. Bone marrow transplant may be an option for some individuals. Treatment is otherwise supportive. (Malm, PMID:18651971). If this individual's reproductive partner is also a carrier of a pathogenic variant in the same gene the risk for an affected fetus is 25%.

COMMENTS

This interpretation is based on the clinical information provided and the current understanding of the molecular genetics of the disorders(s) tested. References and additional information about the disorders tested are available at www.integratedgenetics.com.

Electronically released under the direction of Peter L. Nagy, MD PhD by: Trey Langley, PhD

Testing Performed at Medical Neurogenetics, LLC, 5424 Glenridge Drive. Atlanta, GA 30342. Peter L. Nagy MD PhD, Laboratory Director 1-800-255-7357

Patient: SAMPLE REPORT, F-630068
DOB: 05/05/1995 **Patient ID:** 00000000050 **Control ID:**

Specimen ID: 00000000050
Container ID: H0655
Date Collected: 08/05/2019

METHODS/LIMITATIONS

Single Nucleotide Polymorphism and Small Indel Sequencing Assessment: Genomic regions of interest are selected using a custom capture reagent for target enrichment (Twist Bioscience) and sequenced via the Illumina® next generation sequencing platform. Sequencing reads are aligned with the human genome reference GRCh37/hg19 build. Regions of interest include all exons and intron/exon junctions (+/- 20 nucleotides) for each gene analyzed. A minimum of 99% of bases are covered at >15X. Analytical sensitivity is estimated to be >99% for single nucleotide variants, >97% for insertions/deletions less than six base pairs, and >95% for insertions/deletions between six and fifteen base pairs. Uncovered regions with known pathogenic variants are sequenced in a targeted manner (List based on ClinVar Database: July 2019 release). All reported variants are confirmed by a second method.

Copy Number Variant Assessment: Next Generation Sequencing is performed and the data are assessed with Illumina's DRAGEN (Dynamic Read Analysis for GENomics) Bio-IT Platform. Genes listed in ClinVar with pathogenic deletions less than 10 exons in size are padded with additional intronic probes to allow single exon resolution CNV detection (List based on ClinVar Deletion Database: January 2019 release; see list below). For other genes, large deletions (>10 exons) can be detected. The c.1263_1317del55 variant in *GBA* is assessed by targeted PCR and gel electrophoresis. The resolution of this analysis can vary depending on region-specific features. Reported variants are confirmed by a second method. Analytical sensitivity is estimated to be >95%. Padded genes: *ABCA12, ABCD1, ACADM, ACOX1, ADAMTS2, ADGRV1, AGL, AGPAT2, AGXT, AHI1, AIRE, ALDOB, ALMS1, AP3B1, ARL6, ARSA, ARSB, ATM, ATP7A, ATRX, BBS1, BBS2, BBS4, BBS5, BBS7, BBS9, BCKDHB, BLM, BRIP1, CAPN3, CBS, CDH23, CFTR, CLCN5, CLN3, CLN5, CLN8, CNTNAP2, COL4A5, CP, CPT1A, CTNS, CYBB, DBT, DCLRE1C, DHCR7, DMD, DOCK8, DOK7, DYSF, EIF2B5, ELP1, EMD, ERCC4, ETHE1, EYS, FA2H, FAM126A, FANCA, FANCC, FANCD2, FANCI, FKRP, FKTN, GAA, GALC, GALNS, GALT, GBE1, GLDC, GNE, GNPTAB, GUSB, HBB, HEXA, HEXB, HINT1, HJV, HPD, HSD17B4, IDS, IFT140, IL7R, ITPA, KCTD7, L1CAM, LAMA2, LAMP2, MCOLN1, MEGF8, MKKS, MKS1, MLC1, MMAB, MTM1, NBN, NCF2, NDUFAF2, NDUFS6, NEB, NPHP1, NR0B1, NTRK1, OAT, OCRL, OTC, PAH, PANK2, PCCA, PCDH15, PDHX, PEX1, PEX6, PHKA1, PHKA2, PHKB, PKHD1, PLA2G6, PMM2, POLH, POMGNT1, RAPSN, RDH12, RPGRIP1, RPS6KA3, SGCD, SGCG, SLC25A20, SLC26A4, SLC2A10, SLC35A3, SLC7A7, SPG11, STRC, STX11, SYNE4, TAZ, TMEM231, TMEM237, TMEM38B, TMEM70, TRIM32, USH2A, VLDLR, VPS13B, VRK1, WRN.*

Reported variants: Pathogenic variants, likely pathogenic variants, and variants of uncertain significance are reported after confirmation by an appropriate technology. *NEB* variants occurring in exons 82-105 may not be reliably detected by this analysis and are not reported. Nondeletion variants are specified using the numbering and nomenclature recommended by the Human Genome Variation Society (HGVS, http://www.hgvs.org/). Benign and likely benign variants are not reported. Variant classification is consistent with ACMG standards and guidelines (Richards, PMID:25741868). Detailed variant classification information is available upon request.

Limitations: Technologies used do not detect germline mosaicism and do not rule out the presence of large chromosomal aberrations, including rearrangements, gene fusions, or variants in regions or genes not included in this test, or possible inter/intragenic interactions between variants. Variant classification and/or interpretation may change over time if more information becomes available. False positive or false negative results may occur for reasons that include: rare genetic variants, sex chromosome abnormalities, pseudogene interference, blood transfusions, bone marrow transplantation, somatic or tissue-specific mosaicism, mislabeled samples, or erroneous representation of family relationships.

This test was developed and its performance characteristics determined by Medical Neurogenetics, LLC. It has not been cleared or approved by the Food and Drug Administration.

Medical Neurogenetics, LLC is a wholly-owned subsidiary of Laboratory Corporation of America Holdings.

Electronically released under the direction of Peter L. Nagy, MD PhD by: Trey Langley, PhD

Testing Performed at Medical Neurogenetics, LLC, 5424 Glenridge Drive. Atlanta, GA 30342. Peter L. Nagy MD PhD, Laboratory Director 1-800-255-7357