LASTNAME, FIRSTNAME	DOB: mm/dd/yyyy	Account Number: 0000000	labcorp 🜔
Patient ID:		Account Number, 0000000	
Specimen ID: 000-000-0000-0	Age: 00	Ordering Physician:	
	Sex: Female		
Date Collected: mm/dd/yyyy	Date Received: mm/dd/yyyy	Date Reported: mm/dd/yyyy	Date Entered: mm/dd/yyyy
Specimen Type: Chorionic Villi	Ethnicity: Not Provided		
Indication: Prenatal Test / Family history	/ - previous affected child		

Spinal Muscular Atrophy (SMA), Fetal Analysis Summary: POSITIVE SAMPLE REPORT

Variants Detected

Disorder (Gene)	Result	Interpretation
Spinal muscular atrophy <i>(SMN1)</i> NM_000344.3	POSITIVE: PREDICT AFFECTED SMN1 copy number: 0 SMN2 copy number: 3	This fetus has no copies of <i>SMN1</i> and is therefore predicted to be affected with spinal muscular atrophy, a disease of variable age of onset and severity. An increase in the number of copies of the <i>SMN2</i> gene correlates with reduced disease severity. Genetic counseling is recommended.

Comparison of maternal and fetal DNA markers indicates that maternal cell contamination is unlikely to have interfered with the reported fetal result (maternal specimen # 00000000000). The result obtained from a multiple gestation pregnancy depends on the successful sampling of the intended fetus.

Recommendations

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 Labcorp Genetic Counselors please visit https://womenshealth.labcorp.com/genetic-counseling or call (855) GC-CALLS (855-422-2557).

Additional Clinical Information

Spinal muscular atrophy (SMA) is an autosomal recessive neurodegenerative disorder with variable age at onset and severity, characterized by progressive degeneration of the lower motor neurons in the spinal cord and brain stem, leading to muscle weakness, and in its most common form, respiratory failure by age two. Complications of SMA may include poor weight gain, sleep difficulties, pneumonia, scoliosis, and joint deformities. In severely affected individuals, abnormal fetal ultrasound findings may include congenital joint contractures, polyhydramnios, and decreased fetal movement. (Korinthenberg, PMID:9307259). Treatment is supportive. Targeted therapies may be available for some individuals. Approximately 94% of affected individuals have 0 copies of the *SMN1* gene; in these individuals, an increase in the number of copies of the *SMN2* gene correlates with reduced disease severity (Feldkotter M, PMID:11791208). Individuals with one copy of the *SMN1* gene are predicted to be carriers of SMA; those with two or more copies have a reduced carrier risk. For individuals with two copies of the *SMN1* gene, the presence or absence of the variant c.*3+80T>G correlates with an increased or decreased risk, respectively, of being a silent carrier (2+0).

Comments

This interpretation is based on the clinical information provided and the current understanding of the molecular genetics of the disorder(s) tested. Information about the disorder(s) tested is available at https://womenshealth.labcorp.com.

Methods/Limitations

Maternal Cell Contamination Analysis: DNA is isolated and amplified by the polymerase chain reaction (PCR). Fifteen polymorphic markers from 14 chromosomes are analyzed by capillary gel electrophoresis and fluorescence detection. Markers analyzed include TPOX, D3S1358, FGA, D5S818, CSF1PO, D7S820, D8S1179, THO1, vWA, D13S317, Penta E, D16S539, D18S51, D21S11, and Penta D. The analytical sensitivity of the assay is approximately 10%; maternal cell contamination present at a lower percentage may not be detected.

Spinal muscular atrophy: The copy number of *SMN1* exon 7 is assessed relative to internal standard reference genes by quantitative polymerase chain reaction (qPCR). A mathematical algorithm calculates 0, 1, 2 and 3 copies with statistical confidence. In fetal specimens and specimens with 0 or 1 copies, the primer and probe binding sites are sequenced to rule out variants that could interfere with copy number analysis. *SMN2* copy number is assessed by digital droplet PCR analysis relative to an internal standard reference gene in samples with no copies of *SMN1*. For carrier screening, when two copies of *SMN1* are detected, allelic discrimination qPCR targeting c.*3+80T>G in *SMN1* is performed.

Limitations: Technologies used do not detect germline mosaicism and do not rule out the presence of large chromosomal aberrations including rearrangements and gene fusions, or variants in regions or genes not included in this test, or possible inter/intragenic interactions between variants, or repeat expansions. 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.

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LASTNAME, FIRSTNAME

DOB: mm/dd/yyyy



Patient ID:

Specimen ID: 000-000-0000-0

Age: **00** Sex: **Female** Ordering Physician:

Spinal Muscular Atrophy (SMA), Fetal Analysis

Information Table

Spinal muscular atrophy detection rates for prenatal testing

Population	Detection rate
African American	90.3%
Ashkenazi Jewish	92.8%
Asian	93.6%
Caucasian	95.0%
Hispanic	92.6%
Mixed or other ethnic background	For counseling purposes, consider using the ethnic background with the most conservative risk estimates.
-	

Feng. PMID 28125085; Luo. PMID 23788250; Sugarman. PMID 21811307

References

Deignan JL, Astbury C, Behlmann A et al. Addendum: Technical standards and guidelines for spinal muscular atrophy testing. Genet Med 23, 2462 (2021). [Addendum to PMID: 21673580]

Prior TW, Leach ME, Finanger E. Spinal Muscular Atrophy. 2000 Feb 24 (Updated 2020 Dec 30). In: Adam MP, Ardinger HH, Pagon RA, et al., editors. GeneReviews[®] [Internet]. PMID: 20301526

Performing Labs

Component Type	Performed at	Laboratory Director		
Technical component, processing	Esoterix Genetic Laboratories, LLC, 3400 Computer Drive, Westborough, MA 01581-1771	Hui Zhu, PhD, FACMG		
Technical component, analysis	Esoterix Genetic Laboratories, LLC, 3400 Computer Drive, Westborough, MA 01581-1771	Hui Zhu, PhD, FACMG		
Professional component	Esoterix Genetic Laboratories, LLC, 3400 Computer Drive, Westborough, MA 01581-1771	Hui Zhu, PhD, FACMG		

For inquiries, the physician may contact the lab at 800-255-7357

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

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Patient Details LASTNAME, FIRSTNAME

Phone: Date of Birth: **mm/dd/yyyy** Age: **00** Sex: **Female** Patient ID: Alternate Patient ID:

Physician Details CLIENT NAME CLIENT ADDRESS

Phone: **00000000** Account Number: **00000000** Physician ID: NPI: Specimen Details Specimen ID: 0000000000 Control ID: Alternate Control Number: Date Collected: mm/dd/yyyy 0000 Local Date Received: mm/dd/yyyy 1428 ET Date Entered: mm/dd/yyyy 1203 ET Date Reported: mm/dd/yyyy 2002 ET

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