

Specimen Collected: 29-Oct-25 14:19**Spinal Muscular Atrophy(SMA) Copy Number****Received: 29-Oct-25 14:20 Report/Verified: 30-Oct-25 11:23**

Procedure	Result	Units	Reference Interval
SMA Copy Number, Specimen	Whole Blood		
SMA Copy Number, Symptoms	Yes		
SMA Copy Number, SMN1 Copies	0 copies *		
SMA Copy Number, SMN2 Copies	3 copies		
SMA Copy Number, Linked Variant	Not Present		
SMA Copy Number, Int	See Note ^{f1 i1}		

Result Footnote

f1: SMA Copy Number, Int

Indication for testing: Confirm a diagnosis of spinal muscular atrophy (SMA).

Result:

SMN1 gene copies: 0

SMN2 gene copies: 3 copies

Linked variant: not detected

Interpretation: No copies of the SMN1 gene were detected by multiplex ligation-dependent probe amplification (MLPA); therefore, this individual is predicted to be affected with spinal muscular atrophy (SMA). 3 copies of the SMN2 gene was/were detected by MLPA. Although SMN2 copy number inversely correlates with disease severity, it cannot be used to predict phenotype with certainty. Clinical findings and disease severity are variable.

Recommendations: Genetic consultation is indicated, including a discussion of medical screening and management. Adult family members should be offered SMA carrier screening.

This result has been reviewed and approved by [REDACTED]

Test Information

i1: SMA Copy Number, Int

BACKGROUND INFORMATION: Spinal Muscular Atrophy (SMA) Copy Number Analysis

CHARACTERISTICS: Spinal muscular atrophy (SMA) is the most common lethal genetic disease in children and is characterized by progressive muscle weakness due to degeneration of the lower motor neurons. Onset ranges from before birth to adulthood and severity is highly variable. Individuals with SMA have no functioning copies of the SMN1 gene. Most (95 percent) have homozygous loss of SMN1 due to deletion or gene conversion, while a minority (5 percent) have a deletion of SMN1 on one chromosome and a SMN1 sequence variant on the other. The SMN2 gene, adjacent and highly homologous to SMN1, produces lower levels of survival motor neuron protein compared to SMN1. Disease severity has been shown to be modified by SMN2 gene copy number in some cases, though phenotype cannot be predicted with certainty. An SMN1 variant, c.*3+80T>G (rs143838139), that is part of a haplotype associated with SMN1 duplication in silent carriers (two copies of SMN1 on one chromosome and no copies on the other), particularly in Ashkenazi Jews, increases the likelihood that two copies of SMN1 are on the same chromosome.

*=Abnormal, #=Corrected, C=Critical, f=Result Footnote, H-High, i-Test Information, L-Low, t-Interpretive Text, @=Performing lab

Unless otherwise indicated, testing performed at:**ARUP Laboratories**

500 Chipeta Way, Salt Lake City, UT 84108

Laboratory Director: Jonathan R. Genzen, MD, PhD

ARUP Accession: 25-302-900295**Report Request ID:** 20887799**Printed:** 04-Nov-25 14:43

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Test Information

il: SMA Copy Number, Int

INHERITANCE: Autosomal recessive.

CAUSE: Pathogenic variants in the SMN1 gene.

VARIANTS TESTED: For copy number: SMN1 (NM_000344.3) exon 7 c.840C and exon 8 c.*239G, and SMN2 (NM_017411.3) exon 7 c.840T. For haplotype associated with SMN1 duplication (silent carriers): SMN1 c.*3+80T>G (rs143838139).

CLINICAL SENSITIVITY: 95-98 percent in individuals affected with SMA. Detection rate for carrier screening is 90 percent in African Americans, 93 percent in Ashkenazi Jewish, 93 percent in Asians, 95 percent in Caucasians, and 93 percent in Hispanics.

METHODOLOGY: Multiplex ligation-dependent probe amplification (MLPA) to detect SMN1 and SMN2 copy number and presence or absence of the SMN1 linked variant c.*3+80T>G (rs143838139).

ANALYTICAL SENSITIVITY AND SPECIFICITY: 99 percent.

LIMITATIONS: Diagnostic errors can occur due to rare sequence variations. Single base pair substitutions, small deletions/duplications, and regulatory region and deep intronic variants will not be detected. SMN2 copy numbers greater than 3 may not be reliably distinguished. This test is unable to determine chromosomal phase of SMN1 or SMN2 copies. Even if the linked variant associated with SMN1 duplication is detected, the test cannot definitively differentiate between 1+ copies of SMN1 on each chromosome from 2+ copies of SMN1 on one chromosome and none on the other (silent carriers).

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the U.S. Food and Drug Administration. This test was performed in a CLIA- certified laboratory and is intended for clinical purposes.

Counseling and informed consent are recommended for genetic testing. Consent forms are available online.

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