ARUP LABORATORIES
800-522-2787 | aruplab.com
500 Chipeta Way, Salt Lake City, UT 84108-1221
Jonathan R. Genzen, MD, PhD, Chief Medical Officer

Client: Example Client ABC123
123 Test Drive
Salt Lake City, UT 84108
UNITED STATES

Physician: Doctor, Example

Patient: Patient, Example

DOB	9/30/1987
Gender:	Female
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	00/00/0000 00:00

Noonan Spectrum Disorders Panel, Sequencing, Fetal

ARUP test code 2010769

Maternal Contamination Study Fetal Spec	Unknown Origin Single genotype. A maternal specimen was not submitted for correlation. The fetal sample was tested using STR markers to rule out maternal cell contamination. Only a single genotype was detected. Testing a maternal sample can confirm that this genotype is from the fetus.
Maternal Contam Study, Maternal Spec	Not Received For quality assurance purposes, ARUP Laboratories will confirm the above result at no charge following delivery. Order Confirmation of Fetal Testing and include a copy of the original fetal report (or the mother's name and date of birth) with the test submission. Please contact an ARUP genetic counselor at (800) 242-2787 extension 2141 prior to specimen submission.
Noonan Disorders Seq. Specimen, Fetal	Cultured CVS
Noonan Disorders Seq. Interp, Fetal	Negative

H=High, L=Low, *=Abnormal, C=Critical

INDICATION FOR TESTING
Increased nuchal translucency.

RESULT
No pathogenic variants were detected in any of the genes tested.

INTERPRETATION
No pathogenic variants were identified by massively parallel sequencing of the coding regions and exon-intron boundaries of the genes tested in this prenatal sample. This result decreases the likelihood of, but does not exclude, a diagnosis of a Noonan spectrum disorder. Please refer to the background information included in this report for a list of the genes analyzed and limitations of this test.

RECOMMENDATIONS
This test does not detect all variants associated with Noonan spectrum disorders. Medical screening and management should rely on clinical findings and family history. Genetic consultation is recommended.

COMMENTS
Likely benign and benign variants are not reported.

This result has been reviewed and approved by [redacted]

BACKGROUND INFORMATION: Noonan Spectrum Disorders Panel, Sequencing, Fetal

CHARACTERISTICS: Group of disorders caused by variants in genes involved in the Ras/mitogen activated protein kinase (MAPK) pathway. Common symptoms include short stature, heart defect, developmental delay, coagulation defects, lymphatic dysplasia and undescended testes. Disorders tested include Noonan syndrome (NS), cardiofaciocutaneous (CFC) syndrome, Costello syndrome (CS), LEOPARD syndrome, Legius syndrome, and Noonan-like syndrome with loose anagen hair.

EPIDEMIOLOGY: Prevalence is 1 in 1,000 to 1 in 2,500 for NS.

CAUSE: Pathogenic germline variants in genes involved in the MAPK pathway.

INHERITANCE: Autosomal dominant for all analyzed genes.

CLINICAL SENSITIVITY: Approximately 99 percent for CFC, 80-90 percent for CS, 95 percent for LEOPARD syndrome and 75 percent for NS.

GENES TESTED: BRAF, CBL, HRAS, KRAS, LZTR1, MAP2K1, MAP2K2, NRAS, PTPN11, RAF1, RASA2, RIT1, SHOC2, SOS1, SOS2, SPRED1

METHODOLOGY: Targeted capture of all coding exons and exon-intron junctions of the targeted genes, followed by massively parallel sequencing. Sanger sequencing was performed as necessary to fill in regions of low coverage and confirm reported variants. Human genome build 19 (Hg 19) was used for data analysis.

ANALYTICAL SENSITIVITY: The analytical sensitivity of this test is approximately 99 percent for single nucleotide variants (SNVs) and greater than 93 percent for insertions/duplications/deletions from 1-10 base pairs in size. Variants greater than 10 base pairs may be detected, but the analytical sensitivity may be reduced.

LIMITATIONS: A negative result does not exclude a diagnosis of a MAPK pathway disorder. This test only detects variants within the coding regions and intron-exon boundaries of the targeted genes. Regulatory region variants and deep intronic variants will not be identified. Deletions/duplications/insertions of any size may not be detected by massive parallel sequencing. Diagnostic errors can occur due to rare sequence variations. In some cases, variants may not be identified due to technical limitations in the presence of pseudogenes, repetitive, or homologous regions. This assay may not detect low-level somatic variants associated with disease. Interpretation of this test result may be impacted if this patient has had an allogeneic stem cell transplantation. Non-coding transcripts were not analyzed.

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the US 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.

H=High, L=Low, *=Abnormal, C=Critical

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
Maternal Contamination Study Fetal Spec	22-012-403372	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Maternal Contam Study, Maternal Spec	22-012-403372	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Noonan Disorders Seq. Specimen, Fetal	22-012-403372	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Noonan Disorders Seq. Interp, Fetal	22-012-403372	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00

END OF CHART

H=High, L=Low, *=Abnormal, C=Critical