ARUP Laboratories
500 Chipeta Way – Salt Lake City, UT 84108
(800)522-2787 - www.aruplab.com
Julio C. Delgado, M.D. M.S., Director of Laboratories

*****Example Report*****

Patient Age/Gender: 33 years Female
Printed: 20-Mar-17 12:39:43

Procedure	Result	Units	Ref Interval	Accession	Collected	Received	Reported/ Verified
Ordering Physician Name	@			17-030-104297	30-Jan-17 10:34:00	31-Jan-17 10:00:00	31-Jan-17 15:30:09
Ordering Physician Phone Number	@			17-030-104297	30-Jan-17 10:34:00	30-Jan-17 10:53:00	01-Feb-17 13:57:28
JAG1 Sequencing and Microarray	NEGATIVE f@			17-030-104297	30-Jan-17 10:34:00	31-Jan-17 10:00:00	31-Jan-17 15:30:09
EER Alagille Syndrome (JAG1)	See Note f			17-030-104297	30-Jan-17 10:34:00	30-Jan-17 10:53:00	01-Feb-17 13:57:28

30-Jan-17 10:34:00 JAG1 Sequencing and Microarray:
Date Test(s) Started: 1/31/2017 14:18:00
Test(s) Requested: JAG1 Gene / Tier 1 Analysis / Alagille Syndrome (AGS)
Result: NEGATIVE
No pathogenic variant was identified in exons 1-6, 9, 12, 16-17, 20, and 23-24 of the JAG1 gene in the submitted specimen of this individual. Concurrent targeted array CGH analysis with exon-level resolution (ExonArrayDx) did not reveal a deletion or duplication of JAG1.
Interpretation: No pathogenic variant or gene deletion/duplication known to be associated with Alagille syndrome (AGS) was identified by this Tier 1 analysis of the JAG1 gene. Germline pathogenic variants in JAG1 have been found in 94% of patients with AGS who meet the published diagnostic criteria (Warthen DM et al., 2006). About 88% of Alagille patients have a small intragenic DNA pathogenic variant detectable by sequencing, while 6% harbor larger genomic deletions detectable by FISH or other deletion detection methods. Using our testing approach, this Tier 1 sequencing analysis of selected exons of the JAG1 gene and exon-level array CGH analysis (ExonArrayDx) is expected to identify about 77% of DNA pathogenic variants, including a complete or partial gene deletion/duplication. Analysis of the rest of the JAG1 gene (Tier 2) would detect the remainder of pathogenic variants identifiable by sequencing, if one exists.
Follow-up Testing: Tier 2 analysis of the JAG1 gene is available and may be considered using the specimen already at GeneDx.
Recommendation: Genetic counseling is recommended to discuss the implications of this test report.
Resources: GenomeConnect is an NIH initiative created to enable individuals and families with the same genetic variant or medical history to connect and share de-identified information. If you are interested in participating, please visit www.genomeconnect.org.
Methods: Using genomic DNA from the submitted specimen, exons 1-6, 9, 12, 16-17, 20, and 23-24 and their splice junctions were PCR amplified and capillary sequencing was performed. Bi-directional sequence was assembled, aligned to reference gene sequences based on human genome build GRCh37/UCSC hg19, and analyzed for sequence variants. Capillary sequencing or another appropriate method was used to confirm all potentially pathogenic variants. If present, apparently homozygous variants were confirmed using alternate primer pairs to significantly reduce the possibility of allele drop-out. Concurrent deletion/duplication testing was performed for most, if not all, of the coding exons using exon-level oligo array CGH (ExonArrayDx), and data analysis was performed using gene-specific filtering. Probe sequences and locations were based on human genome build GRCh37/UCSC hg19. Confirmation of copy number changes was performed by MLPA, qPCR, or repeat array CGH analysis. Sequence alterations were reported according to the Human Genome Variation Society (HGVS) nomenclature guidelines. Benign and likely benign variants, if present, are not included in this report but are available upon request. The methods used by GeneDx are expected to be greater than 99% sensitive in detecting variants identifiable by sequencing.
Report electronically signed by: Chris Lauricella M.S., CGC
Report electronically signed by: Val Zvereff MD, PhD, FACMG
Coding DNA RefSeq: NM_000214.2, counting from the ATG initiation codon.
References: Warthen DM et al., (2006) Hum Mutat. 27: 436-443
Limitations: Genetic testing using the methods applied at GeneDx is expected to be highly accurate. Normal findings do not rule out the diagnosis of a genetic disorder since some genetic abnormalities may be undetectable with this test. This test cannot reliably detect mosaicism. Exon-level array CGH test (ExonArrayDx) also cannot reliably detect chromosomal aberrations and deletions/insertions of less than 500 bp. Rarely incidental findings of large chromosomal rearrangements (>3Mb) outside the gene of interest may be identified. Some genes have inherent sequence properties (for example: repeat, homology, or pseudogene regions, high GC content, rare polymorphisms) that may result in suboptimal data, and variants in those regions may not be reliably identified. False negative results may also occur in the setting of bone marrow transplantation, recent blood transfusion, or suboptimal DNA quality. The chance of a false positive or false negative result due to laboratory errors incurred during any phase of testing cannot be completely excluded. Interpretations are made with the assumption that any information provided on family relationships is accurate. Consultation with a genetics professional is recommended for interpretation of results.
Disclaimer: This test was developed and its performance characteristics determined by GeneDx. It has not been cleared or approved by the U.S. Food and Drug Administration. The laboratory is regulated under CLIA as qualified to perform high-complexity testing. This test is used for clinical purposes. It should not be regarded as investigational or for research.

***** Abnormal, **#** = Corrected, **C** = Critical, **f** = Footnote, **H** = High, **L** = Low, **t** = Interpretive Text, **@** = Reference Lab

ARUP Laboratories
500 Chipeta Way – Salt Lake City, UT 84108
(800)522-2787 - www.aruplab.com
Julio C. Delgado, M.D. M.S., Director of Laboratories

*****Example Report*****

Patient Age/Gender: 33 years Female
Printed: 20-Mar-17 12:39:43

30-Jan-17 10:34:00 EER Alagille Syndrome (JAG1):
Access ARUP Enhanced Report using either link below:

-Direct access:

-Enter Username, Password:
Username:
Password:
30-Jan-17 10:34:00 Ordering Physician Name,Ordering Physician Phone Number,JAG1 Sequencing and Microarray:
Performed at: GeneDx Inc.,207 Perry Parkway, Gaithersburg, MD 20877