



Procedure	Result	Units	Ref Interval	Accession	Collected	Received	Reported/Verified
Respiratory Pathogens by NGS, Source	BAL			17-242-402906	29-Aug-17 00:01:00	30-Aug-17 15:49:34	02-Sep-17 16:08:58
Respiratory Pathogens by NGS	SEE NOTE	f		17-242-402906	29-Aug-17 00:01:00	30-Aug-17 15:49:34	02-Sep-17 16:08:58
EER Respiratory Pathogens by NGS	See Note	f		17-242-402906	29-Aug-17 00:01:00	30-Aug-17 15:49:34	02-Sep-17 16:08:58

29-Aug-17 00:01:00 Respiratory Pathogens by NGS:
 Result Summary
 Respiratory pathogens detected

Analytical Sensitivity: normal

Detected Pathogens:
 Bacteria: Streptococcus intermedius, Corynebacterium pseudodiphtheriticum
 Viruses: None
 Fungi: None

Explify Version: v1.1.0
 29-Aug-17 00:01:00 EER Respiratory Pathogens by NGS:
 Access ARUP Enhanced Report using either link below:

-Direct access:

-Enter Username, Password:
 Username:
 Password:

29-Aug-17 00:01:00 Respiratory Pathogens by NGS:
 INTERPRETIVE INFORMATION: Explify Respiratory
 Pathogens by NGS

This test detects potential respiratory pathogens by unbiased next-generation cDNA and DNA sequencing of viral, bacterial, and fungal transcriptome and genome sequences. Sequencing data are interpreted by the Explify software.

Negative results do not rule out viral, bacterial, or fungal infections. Targeted, PCR-based tests are generally more sensitive and are preferred when specific pathogens are suspected, especially for DNA viruses (Adenovirus, CMV, HHV6, HSV, and VZV), mycobacteria, and fungi.

The analytical sensitivity of this test depends on the cellularity of the sample and the concentration of all microbes present. Analytical sensitivity is assessed using Internal Controls that are added to each sample. Sequencing data for Internal Controls is quantified. Samples with Internal Control values below the validated minimum may have reduced analytical sensitivity or contain inhibitors and are reported as 'Reduced Analytical Sensitivity'. Additional respiratory pathogens to those reported cannot be excluded in samples with 'Reduced Analytical Sensitivity'.

Due to the complexity of next generation sequencing methodologies, there may be a risk of false-positive results. Contamination with organisms from the upper respiratory tract during specimen collection can also occur. The detection of viral, bacterial, and fungal nucleic acid does not imply organisms causing invasive infection. Results from this test need to be interpreted in conjunction with the clinical history, results of other laboratory tests, epidemiologic information, and other available data. Confirmation of positive results by an alternate method may be indicated in select cases.

* 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:
Printed: 18-Sep-17 13:43:34

Test developed and characteristics determined by ARUP Laboratories. See Compliance Statement B: aruplab.com/CS

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