Regence

Medical Policy Manual Genetic Testing, Policy No. 85

Identification of Microorganisms Using Nucleic Acid Probes

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IMPORTANT REMINDER

Medical Policies are developed to provide guidance for members and providers regarding coverage in accordance with contract terms. Benefit determinations are based in all cases on the applicable contract language. To the extent there may be any conflict between the Medical Policy and contract language, the contract language takes precedence.

PLEASE NOTE: Contracts exclude from coverage, among other things, services or procedures that are considered investigational or cosmetic. Providers may bill members for services or procedures that are considered investigational or cosmetic. Providers are encouraged to inform members before rendering such services that the members are likely to be financially responsible for the cost of these services.

DESCRIPTION

Nucleic acid probes are available for the identification of a wide variety of microorganisms and can also be used to quantitate the number of microorganisms present. This technology offers advantages over standard techniques when rapid identification is clinically important, when microbial identification using standard culture is difficult or impossible, and/or when treatment decisions are based on quantitative results.

MEDICAL POLICY CRITERIA

Note: Nucleic acid testing specific to the SARS-CoV-2 virus (COVID-19) is addressed in a separate policy (see Cross References).

Medically Necessary

I. The use of nucleic acid testing using a direct or amplified probe technique (with or without quantification) may be considered **medically necessary** for one or more of the following microorganisms:

   A. BK virus

   B. Cytomegalovirus

C. Hepatitis B virus
D. Hepatitis C virus
E. Hepatitis D virus
F. HIV-1
G. HIV-2
H. Human herpesvirus 6
I. Influenza virus

Not Medically Necessary

II. Respiratory pathogen panels with 12 or more targets are considered **not medically necessary**.

Investigational

III. The use of nucleic acid testing is considered **investigational** for the following (see Policy Guidelines):

A. Testing with quantification or semi-quantification for microorganisms that *are not* included in the list of microorganisms for which probes with or without quantification are considered medically necessary (see Criterion I above)
B. Central nervous system pathogen panels
C. Urinary tract infection pathogen panels
D. Joint infection panels
E. Endometrial pathogen panels
F. Pathogen panels for surgical or chronic wounds
G. Nucleic acid testing for the Hepatitis G virus
H. Oral HPV testing

NOTE: A summary of the supporting rationale for the policy criteria is at the end of the policy.

POLICY GUIDELINES

Table 1. CPT Codes for Nucleic Acid Probes

Pathogen	Direct Probe	Amplified Probe	Quantification
Bartonella henselae or *quintana*		87471	87472 [investigational]
Candida species	87480	87481	87482 [investigational]
Chlamydophila pneumoniae	87485	87486	87487 [investigational]
Chlamydia trachomatis	87490	87491	87492 [investigational]
Cytomegalovirus	87495	87496	87497

Pathogen	Direct Probe	Amplified Probe	Quantification
Gardnerella vaginalis	87510	87511	87512 [investigational]
Hepatitis B virus		87516	87517
Hepatitis C virus	87520	87521	87522
Hepatitis D virus			87523
Hepatitis G virus	87525 [investigational]	87526 [investigational]	87527 [investigational]
Herpes simplex virus	87528	87529	87530 [investigational]
Herpes virus-6	87531	87532	87533
HIV-1	87534	87535	87536
HIV-2	87537	87538	87539
Human papillomavirus		87623-87625	
Human papillomavirus (oral)		0429U [investigational]	
Influenza virus		87501-87503	
Legionella pneumophila	87540	87541	87542 [investigational]
Mycobacteria species	87550	87551	87552 [investigational]
Mycobacterium tuberculosis	87555	87556	87557 [investigational]
Mycobacterium avium-intracellulare	87560	87561	87562 [investigational]
Mycoplasma pneumoniae	87580	87581	87582 [investigational]
Neisseria gonorrhoeae	87590	87591	87592 [investigational]
Streptococcus, group A	87650	87651	87652 [investigational]
Panels			
Central nervous system pathogen panel	87483 [investigational]		
Urinary tract infection panel	0321U, 0371U, 0372U, 0374U, 0590U, 0593U [investigational]		
Joint infection panel	87627 [investigational]		
Endometrial panel	0607U, 0608U [investigational]		
Wound infection panel	0600U [investigational]		
Central nervous system pathogen panel	87483 [investigational]		
Respiratory pathogen panels with 12 or more targets	0115U, 0202U, 0223U, 0225U, 0373U, 0556U, 0563U, 0564U, 87633 [not medically necessary]		

It should be noted that the technique for quantification includes both amplification and direct probes; therefore, simultaneous coding for both quantification with either amplification or direct probes is not warranted.

CROSS REFERENCES

1. COVID-19 Testing, Laboratory, Policy No. 74

BACKGROUND

NUCLEIC ACID PROBES

A nucleic acid probe is used to detect and identify species or subspecies of organisms by identifying nucleic acid sequences in a sample. Nucleic acid probes detect genetic materials, such as RNA or DNA, unlike other tests, which use antigens or antibodies to diagnose organisms.

The availability of nucleic acid probes has permitted the rapid direct identification of microorganism DNA or RNA. Amplification techniques result in exponential increases in copy numbers of a targeted strand of microorganism-specific DNA. The most used amplification technique is polymerase chain reaction (PCR) or reverse transcriptase PCR. In addition to PCR, other nucleic acid amplification techniques have been developed, such as transcription-mediated amplification, loop-mediated isothermal DNA amplification, strand displacement amplification, nucleic acid sequence-based amplification, and branched-chain DNA signal amplification. After amplification, target DNA can be readily detected using a variety of techniques. The amplified product can also be quantified to assess how many microorganisms are present. Quantification of the number of nucleic acids permits serial assessments of response to treatment; the most common clinical application of quantification is the serial measurement of HIV RNA (called viral load).

The direct probe technique, amplified probe technique, and probe with quantification methods vary based on the degree to which the nucleic acid is amplified and the method for measurement of the signal. The direct probe technique refers to detection methods in which nucleic acids are detected without an initial amplification step. The amplified probe technique refers to detection methods in which either target, probe, or signal amplification is used to improve the sensitivity of the assay over direct probe techniques, without quantification of nucleic acid amounts.

- Target amplification methods include PCR (including PCR using specific probes, nested or multiplex PCR), nucleic acid-based sequence amplification, transcription-mediated amplification, and strand displacement amplification. Nucleic acid-based sequence amplification and transcription-mediated amplification involve amplification of an RNA (rather than a DNA) target.
- Probe amplification methods include ligase chain reaction.
- Signal amplification methods include branched DNA (bDNA) probes and hybrid capture methods using an anti-DNA/RNA hybrid antibody.

The probe with quantification techniques refers to quantitative PCR (qPCR) or real-time PCR (rt-PCR) methods that use a reporter at each stage of the PCR to generate absolute or relative amounts of a known nucleic acid sequence in the original sample. These methods may use DNA-specific dyes (ethidium bromide or SYBR green), hybridization probes (cleavage-based [TaqMan] or displaceable), or primer incorporated probes.

Direct assays will generally have lower sensitivity than amplified probes. In practice, most commercially available probes are amplified, with a few exceptions. For this evidence review, indications for direct and/or amplified probes without quantification are considered together, while indications for a probe with quantification are considered separately.

Classically, identification of microorganisms relies either on the culture of body fluids or tissues or identification of antigens, using a variety of techniques including direct fluorescent antibody technique and qualitative or quantitative immunoassays. These techniques are problematic when the microorganism exists in very small numbers or is technically difficult to culture. Indirect identification of microorganisms by immunoassays for specific antibodies reactive with the microorganism is limited by difficulties in distinguishing between past exposure and current infection.

Potential reasons for a nucleic acid probe to be associated with improved clinical outcomes compared with standard detection techniques include the following (note: in all cases, for there to be clinical utility, making a diagnosis should be associated with changes in clinical management, which could include initiation of effective treatment, discontinuation of other therapies, or avoidance of invasive testing.):

- Significantly improved speed and/or efficiency in making a diagnosis.
- Improved likelihood of obtaining any diagnosis in cases where standard culture is difficult. Potential reasons for difficulty in obtaining standard culture include low numbers of the organisms (e.g., HIV), fastidious or lengthy culture requirements (e.g., *Mycobacteria*, *Chlamydia*, *Neisseria* species), or difficulty in collecting an appropriate sample (e.g., herpes simplex encephalitis).
- There is no way to definitively make a diagnosis without nucleic acid testing.
- The use of nucleic acid probe testing provides qualitatively different information than that available from standard cultures, such as information regarding disease prognosis or response to treatment. These include cases where quantification of viral load provides prognostic information or is used to measure response to therapy.

The risks of nucleic acid testing include false-positive and false-negative results; inaccurate identification of pathogens by the device, inaccurate interpretation of test results, or incorrect operation of the instrument.

- False-positive results can lead to unnecessary treatment, with its associated toxicities and side effects, including allergic reaction. In addition, true diagnosis and treatment could be delayed or missed altogether.
- False-negative results could delay diagnosis and initiation of proper treatment.
- It is possible that these risks can be mitigated by the use of a panel of selected pathogens indicated by the clinical differential diagnosis while definitive culture results are pending.

REGULATORY STATUS

A list of current U.S. Food and Drug Administration-approved or cleared nucleic acid-based microbial tests is available online.[1]

Clinical laboratories may develop and validate tests in-house and market them as a laboratory service; laboratory-developed tests must meet the general regulatory standards of the Clinical Laboratory Improvement Amendments. Laboratories that offer laboratory-developed tests must be licensed by the Clinical Laboratory Improvement Amendments for high-complexity testing.

EVIDENCE SUMMARY

Validation of the clinical use of any diagnostic test focuses on three main principles:

1. Analytic validity of the test;
2. Clinical validity of the test (i.e., sensitivity, specificity, and positive and negative predictive values in relevant populations of patients and compared to the gold standard); and
3. Clinical utility of the test (i.e., how the results of the diagnostic test will be used to improve the management of the patient).

This evidence review focuses on the clinical validity and clinical utility of testing that is not covered in this policy.

CENTRAL NERVOUS SYSTEM BACTERIAL AND VIRAL PANELS

The purpose of nucleic acid-based central nervous system pathogen panel is to provide a treatment option that is an alternative to or an improvement on existing therapies in patients with signs and/or symptoms of meningitis and/or encephalitis. The standard approach to the diagnosis of meningitis and encephalitis is culture and pathogen-specific PCR testing of cerebrospinal fluid (CSF) based on clinical characteristics. These techniques have a slow turnaround time, which can delay administration of effective therapies and lead to unnecessary empirical administration of broad-spectrum antimicrobials.

The FilmArray Meningitis/Encephalitis Panel (BioFire Diagnostics) is a nucleic acid-based test that simultaneously detects multiple bacterial, viral, and yeast nucleic acids from CSF specimens obtained via lumbar puncture from patients with signs and/or symptoms of meningitis and/or encephalitis. The test has been cleared for marketing through the U.S. Food and Drug Administration 510(k) process. The test identifies 14 common organisms responsible for community-acquired meningitis or encephalitis:

- Bacteria: *Escherichia coli K1*; *Haemophilus influenzae*; *Listeria monocytogenes*; *Neisseria meningitides*; *Streptococcus agalactiae*; *Streptococcus pneumoniae*;
- Viruses: cytomegalovirus; enterovirus; herpes simplex virus 1 (HSV-1); herpes simplex virus 2 (HSV-2); human herpesvirus 6; human parechovirus; varicella zoster virus (VZV);
- Yeast: *Cryptococcus neoformans/gattii*.

The systematic review and meta-analysis by Tansarli and Chapin (2019) examined the diagnostic accuracy of the BioFire FilmArray Meningitis/Encephalitis (ME) panel.[2] Thirteen prospective and retrospective studies conducted from 2016 through 2019 were reviewed (n=3,764 patients); eight were included in the meta-analysis (n=3,059 patients). Included in the meta-analysis is the study by Leber [2016],[3] which is discussed below. Risk of bias among the studies was mixed but tended toward low risk, with the index test aspect being most questionable. No applicability concerns were found in any studies. To be eligible, studies had to provide sensitivity and specificity data compared with a reference standard. Patients in the studies had infections caused by a variety of components found on the panel (bacterial, viral, Cryptococcus neoformans/gatti). Table 2 summarizes the sensitivity, specificity, and other

measurements of accuracy. The highest proportions of false-positive results were for *Streptococcus pneumoniae* (17.5%) and *Streptococcus agalactiae* (15.4%). The highest proportion of false negatives was seen for Herpes Simplex Virus 1 and 2, *Enterovirus*, and *C. neoformans/gatti*. The rate of false-positive results with the ME panel suggests this method should be used with caution, and additional diagnostic methods should be used to confirm panel results.

Table 2. Accuracy of BioFire FilmArray Meningitis/Encephalitis Panel

Measurement	Sensitivity, mean %	Specificity, mean %	PPV, %	NPV, %	False-Positives Before and After Adjudication[a], %		False-Negatives Before and After Adjudication, %	
					Before	After	Before	After
Value	90.2	97.7	85.1	98.7	11.4	4.0	2.2	1.5
95% CI	86.2-93.1	94.6-99.0	NR	NR	NR	NR	NR	NR
Range	60-100	88-100	NR	NR	NR	NR	NR	NR

Source: Tansarli and Chapin (2019)[2]
CI: confidence interval; NPV: negative predictive value; NR: not reported; PPV: positive predictive value.
[a] Adjudication is further investigation of results, which could include further testing, clinician input, or chart review. In this study it was performed for discordant results between index and reference tests.

The study by Leber (2016) was the FDA pivotal study, as well as the largest and one of the only prospective studies available.[3] A total of 1,560 samples were tested from children and adults with available CSF, but not limited to those with high pretest probability for an infectious cause for meningitis or encephalitis. (See Table 3 for study characteristics.) Even the most prevalent organisms were present only a small number of times in the samples. The specificities ranged from 98% to 100% and, given the high number of true negatives, the specificities were estimated with tight precision. However, given the small number of true positives, the sensitivities to detect any given organism could not be estimated with precision. A total of 141 pathogens were detected in 136 samples with the FilmArray and 104 pathogens were detected using comparator methods; 43 FilmArray results were “false-positive” compared with the comparator method and six were “false-negative.” For 21 of the 43 “false-positives,” repeat testing of the FilmArray, comparator, or additional molecular testing supported the FilmArray results. The remaining 22 “false positives” (16% of all positives) were unresolved. Codetections were observed in 3.7% (5/136) positive specimens. All five included a bacterial and viral positive result, and all five specimens were found to have a false-positive result demonstrated by comparator testing. The investigators suggested that the discrepancies could have been due to specimen contamination or another problem with the assay configuration or testing process.

The smaller studies were consistent with Leber (2016) in estimating the specificities for all included pathogens to be greater than 98%. However, there were also a very low number of true positives for most pathogens in these studies and thus the estimates of sensitivities were imprecise. Relevance, study design, and trial conduct limitations are shown in Tables 5 and 6.

Cuesta (2024) prospectively evaluated the performance of a multiplex PCR assay (QIAstat-Dx ME panel) compared to conventional diagnostic methods and the Biofire FilmArray ME Panel for diagnosing meningoencephalitis in 50 CSF samples.[4] Conventional methods identified a pathogen in 29 CSF samples (58%), with 41% bacterial and 59% viral etiologies. The QIAstat-Dx ME panel demonstrated a sensitivity of 96.5% (95% confidence interval [CI] 79.8% to 99.8%) and specificity of 95.2% (95% CI 75.2% to 99.7%), with high positive and negative

predictive values (96.4% and 95.2%) and complete agreement (91.8%) with conventional methods based on Cohen's kappa. In contrast, the FilmArray ME panel had a lower sensitivity (85.1%, 95% CI 55.9% to 90.2%), specificity (57.1%, 95 %CI 29.6% to 70.3%), positive and negative predictive values and only moderate agreement (43.5%) with conventional methods. The FilmArray ME panel reported seven single-pathogen and five polymicrobial false positive results, most commonly for HSV-1, while the QIAstat-Dx ME panel had only one false positive (VZV) and one false negative (HSV-1) result. Limitations include the enrichment of positive samples in the QIAstat-Dx ME analysis and the inability to evaluate all panel targets due to a lack of some positive CSF samples.

López (2024) retrospectively reviewed the performance of the Biofire FilmArray ME panel compared to conventional diagnostic methods in 313 patients with suspected ME seen at a single center from 2018 to 2022.[5] FilmArray was positive in 84 cases (26.8%) (HSV-1 [10.9%], VZV [5.1%], enterovirus [2.6%], and *S. pneumonia* [1.9%]). In the 136 cases where both FilmArray and routine methods were performed, there was a 25.7% lack of agreement. In the overall tested population, the sensitivity was estimated to be 81% (95% CI 70.6% to 89%) with a specificity of 89% (95% CI 85.4% to 93.4%). The authors reported a high NPV (93.4%, 95 %CI 89.9% to 95.7%) and modest PPV (73%, 95 %CI 64.6% to 80.1%). While FilmArray had a low false negative rate of 6.6%, it reported a high false positive rate of 28.6%, mainly due to HSV-1. The authors observed that the PPV dropped to 36.9% in cases without pleocytosis and 70.2% in those lacking high CSF protein levels; other test characteristics were less impacted by individual CSF characteristics. Limitations include the retrospective single-center design and that conventional testing could not be performed on all samples due to insufficient volume.

Erinmez (2026) conducted a single-center cohort study of 955 patients at a Turkish tertiary academic hospital to evaluate the real-world diagnostic performance of the BioFire FilmArray ME Panel against CSF culture and a composite clinical-laboratory reference standard.[6] The panel demonstrated an overall sensitivity of 94.8% (95% CI 87.5 to 97.9) and specificity of 99.4% (95% CI 98.6 to 99.7), with consistent performance across pediatric (sensitivity 91.6%, specificity 99.6%) and adult (sensitivity 97.6%, specificity 99.1%) subgroups; positive predictive values were 97.3% for bacterial, 90.0% for viral, and 100% for fungal targets. False-negative results occurred exclusively in culture-confirmed *S. pneumoniae* and *E. coli* meningitis, while clinically discordant false positives involved HHV-6, Enterovirus, and *H. influenzae*; notably, 3.9% of the cohort harbored CSF pathogens outside the panel's coverage—most frequently *Acinetobacter baumannii* and *Stenotrophomonas maltophilia* in healthcare-associated or post-neurosurgical infections. The authors conclude that the ME panel is a highly accurate rapid diagnostic adjunct for community-acquired CNS infections but should complement, not replace, conventional CSF culture and clinical assessment—particularly in patients with neurosurgical hardware, intensive care unit (ICU) exposure, or low pretest probability where latent herpesvirus detection and off-panel organisms remain meaningful limitations.

Table 3. Characteristics of Clinical Validity Studies of CNS Panel

Author (Year)	Study Population	Design	Reference Standard	Timing of Reference and Index Tests	Blinding of Assessors
Leber (2016)[3]	Children and adults from whom a CSF specimen was available from standard care testing for	Nonconcurrent prospective	Culture and PCR	Processed within seven days of collection or	Yes

Author (Year)	Study Population	Design	Reference Standard	Timing of Reference and Index Tests	Blinding of Assessors
	bacterial culture; not limited to those with high pretest probability for an infectious cause for meningitis or encephalitis			immediately frozen for future testing	
Hanson (2016)[7]	Children and adults from whom a CSF specimen was available who had been tested with at least one conventional method	Retrospective, selection method not clear	Culture and PCR with discrepancy resolution LDT PCR	Stored up to two years after collection	Yes
Graf (2017)[8]	Positive samples (children) selected based on positivity of reference method for any of targets on the CNS panel. Negative samples selected based on negativity of reference sample and with preference for samples highly suggestive of meningitis or encephalitis	Retrospective, convenience	Culture and PCR	Stored up to two years after collection	NR

CNS: central nervous system; CSF: cerebrospinal fluid; LDT: laboratory-developed test; NR: not reported; PCR: polymerase chain reaction.

Table 4. Results of Clinical Validity Studies of CNS Panel

Author (Year)	Initial N	Final N	Excluded Samples	Prevalence of Condition, %	Clinical Validity (95% CI)	
					Sensitivity/ Positive % Agreement	Specificity/ Negative % Agreement
Leber (2016)[3]	1,643	1,560	Insufficient volume, outside the seven-day window, repeat subject, or invalid FilmArray test.			
Bacteria						
Escherichia coli K1				0.1	100 (34 to 100)	99.9 (99.6 to 100)
Haemophilusinfluenzae				0.06	100 (NA)	99.9 (99.6 to 100)
Listeria monocytogenes				0		100 (99.8 to 100)
Neisseria meningitides				0		100 (99.8 to 100)

Author (Year)	Initial N	Final N	Excluded Samples	Prevalence of Condition, %	Clinical Validity (95% CI)	
					Sensitivity/ Positive % Agreement	Specificity/ Negative % Agreement
Streptococcus agalactiae				0.06	0 (NA)	99.9 (99.6 to 100)
Streptococcus pneumoniae				0.3	100 (51 to 100)	99.2 (98.7 to 99.6)
Viruses						
Cytomegalovirus				0.2	100 (44 to 100)	99.8 (99.4 to 99.9)
Enterovirus				2.9	96 (86 to 99)	99.5 (99.0 to 99.8)
Herpes simplex virus 1				0.1	100 (34 to 100)	99.9 (99.5 to 100)
Herpes simplex virus 2				0.6	100 (72 to 100)	99.9 (99.5 to 100)
Human herpesvirus 6				1.3	86 (65 to 95)	99.7 (99.3 to 99.9)
Human parechovirus				0.6	100 (70 to 100)	99.8 (99.4 to 99.9)
Varicella zostervirus				0.3	100 (51 to 100)	99.8 (99.4 to 99.9)
Yeast						
Cryptococcus neoformans/ Cryptococcus gattii				0.06	100 (NA)	99.7 (99.3 to 99.9)
Hanson et al (2016)[7]	342	342	NR			
Bacteria						
Escherichia coli K1				0.3	100 (3 to 100)	100 (98 to 100)
Haemophilus influenza				1.5	100 (48 to 100)	100 (97 to 100)
Listeria monocytogenes				0	NA	100 (98 to 100)
Neisseria meningitides				0.3	100 (3 to 100)	100 (98 to 100)
Streptococcus agalactiae				0.9	67 (9 to 99)	99 (95 to 100)
Streptococcus pneumoniae				1.5	100 (48 to 100)	99 (96 to 100)
Viruses						
Cytomegalovirus				2.0	57 (18 to 90)	100 (91 to 100)
Enterovirus				11.1	97 (86 to 100)	100 (69 to 100)
Herpes simplex virus 1				3.5	93 (66 to 100)	98 (89 to 100)
Herpes simplex virus 2				8.5	100 (88 to 100)	100 (82 to 100)

Author (Year)	Initial N	Final N	Excluded Samples	Prevalence of Condition, %	Clinical Validity (95% CI)	
					Sensitivity/ Positive % Agreement	Specificity/ Negative % Agreement
Human herpesvirus 6				5.6	95 (74 to 100)	100 (93 to 100)
Human parechovirus				0.3	100 (3 to 100)	100 (93 to 100)
Varicella zostervirus				9.4	100 (89 to 100)	100 (79 to 100)
Yeast						
Cryptococcus neoformans/ Cryptococcus gattii				2.6	64 (35 to 87)	NA
Graf (2017)[8]	133	133	NR			
Bacteria						
Haemophilus influenzae				NA[a]	100 (1 to 100)[b]	100 (96 to 100)[b]
Streptococcus agalactiae				NA[a]	100 (1 to 100)[b]	100 (96 to 100)[b]
Streptococcus pneumoniae				NA[a]	100 (28 to 100)[b]	100 (96 to 100)[b]
Viruses						
Enterovirus				NA[a]	95 (82 to 99)[b]	100 (94 to 100)[b]
Herpes simplex virus 1				NA[a]	50 (7 to 93)[b]	100 (96 to 100)[b]
Herpes simplex virus 2				NA[a]	100 (1 to 100)[b]	100 (96 to 100)[b]
Human herpesvirus 6				NA[a]	100 (9 to 100)[b]	100 (96 to 100)[b]
Human parechovirus				NA[a]	94 (70 to 100)[b]	100 (95 to 100)[b]

CI: confidence interval; NA: not available; NR: not reported.
[a] Positives and negatives retrospectively selected from a convenience sample with different selection criteria; prevalence is unknown.
[b] Confidence intervals not provided in publication; estimated based on available information.

Table 5. Relevance Limitations of Studies of CNS Panel

Study	Population[a]	Intervention[b]	Comparator[c]	Outcomes[d]	Duration of Follow-Up[e]
Leber (2016)[3]	4. Participants not limited to those with high pretest probability for an infectious cause for meningitis or encephalitis	3. Used investigational version of test but varies from marketed version only in that Epstein-Barr virus is not available			

Study	Population[a]	Intervention[b]	Comparator[c]	Outcomes[d]	Duration of Follow-Up[e]
		in the marketed version			
Hanson (2016)[7]	3. Selection criteria with respect to clinical characteristics not described	3. Used investigational version (see above)			
Graf (2017)[8]	4. Selection criteria varied for positive and negative samples				

FN: false-negative; FP: false-positive; TN: true negative; TP: true positive.
[a] Population key: 1. Intended use population unclear; 2. Clinical context is unclear; 3. Study population is unclear; 4. Study population not representative of intended use.
[b] Intervention key: 1. Classification thresholds not defined; 2. Version used unclear; 3. Not intervention of interest.
[c] Comparator key: 1. Classification thresholds not defined; 2. Not compared to credible reference standard; 3. Not compared to other tests in use for same purpose.
[d] Outcomes key: 1. Study does not directly assess a key health outcome; 2. Evidence chain or decision model not explicated; 3. Key clinical validity outcomes not reported (sensitivity, specificity and predictive values); 4. Reclassification of diagnostic or risk categories not reported; 5. Adverse events of the test not described (excluding minor discomforts and inconvenience of venipuncture or noninvasive tests).
[e] Follow-Up key: 1. Follow-up duration not sufficient with respect to natural history of disease (true positives, true negatives, false positives, false negatives cannot be determined).

Table 6. Study Design and Conduct Gaps

Study	Selection[a]	Blinding[b]	Delivery of Test[c]	Selective Reporting[d]	Follow-Up Completeness[e]	Statistical[f]
Leber (2016)[3]			2. Many tests performed on frozen samples			
Hanson (2016)[7]	1. Not clear if participants were consecutive		2. Many tests performed on frozen samples		1. Not clear if there were indeterminate samples	
Graf (2017)[8]	3. Selection not random or consecutive and varied for positive and negatives	1. Not clear if blinded	2. Many tests performed on frozen samples		1. Not clear if there were indeterminate samples	1. Confidence intervals not provided

The evidence limitations stated in this table are those notable in the current review; this is not a comprehensive gaps assessment.
[a] Selection key: 1. Selection not described; 2. Selection not random or consecutive (ie, convenience).
[b] Blinding key: 1. Not blinded to results of reference or other comparator tests.
[c] Test Delivery key: 1. Timing of delivery of index or reference test not described; 2. Timing of index and comparator tests not same; 3. Procedure for interpreting tests not described; 4. Expertise of evaluators not described.

[d] Selective Reporting key: 1. Not registered; 2. Evidence of selective reporting; 3. Evidence of selective publication.
[e] Data Completeness key: 1. Inadequate description of indeterminate and missing samples; 2. High number of samples excluded; 3. High loss to follow-up or missing data.
[f] Statistical key: 1. Confidence intervals and/or p values not reported; 2. Comparison to other tests not reported.

Section Summary: Central Nervous System Bacterial and Viral Panel

The FilmArray ME Panel provides fast diagnoses compared with standard culture and pathogen-specific PCR and, because it combines multiple individual nucleic acid tests, clinicians can test for several potential pathogens simultaneously. The test uses only a small amount of CSF, leaving remaining fluid for additional testing if needed. The test is highly specific for the included organisms. However, due to the low prevalence of these pathogens overall, the sensitivity for each pathogen is not well-characterized. More than 15% of positives in the largest study were reported to be false positives, which could cause harm if used to make clinical decisions. Also, a negative panel result does not exclude infection due to pathogens not included in the panel.

RESPIRATORY PATHOGEN PANELS

Markussen (2024) conducted a prospective, single-center, RCT to evaluate the impact of rapid syndromic PCR testing on pathogen-directed antibiotic treatment in adults presenting to the emergency department with suspected community-acquired pneumonia in Norway.[9] A total of 374 patients were randomized to receive either standard care alone or standard care plus BioFire FilmArray Pneumonia plus Panel testing. At 48 hours, significantly more patients in the PCR group received pathogen-directed treatment (35.3% vs 13.4%, OR 3.53, 95% CI 2.13 to 6.02, p<0.001), with a median 9.4-hour faster time to treatment (HR 3.08, 95% CI 1.95 to 4.89, p<0.001). Among the subset with confirmed CAP, these differences were more pronounced (47.4% vs. 15.5% received pathogen-directed treatment, OR 4.90, p<0.001). No significant differences were observed in hospital length of stay, 30- or 90-day mortality, or readmission.

Cartuliares (2023) conducted a prospective, multicenter, randomized controlled trial to evaluate the impact of point-of-care multiplex PCR on antibiotic prescribing for patients admitted with suspected community-acquired pneumonia in Denmark.[10] Lower respiratory tract samples were collected from 294 patients randomized to either the PCR group (Biofire FilmArray Pneumonia Panel plus added to standard care) or the standard care only group. The primary outcome, prescription of no or narrow-spectrum antibiotics at four hours, did not differ significantly between the PCR (62.8%) and standard of care (59.6%) groups (odds ratio [OR] 1.13, 95% CI 0.96 to 1.34, p=0.134). However, the PCR group had significantly more targeted antibiotic prescriptions at four hours (OR 5.68, 95% CI 2.49 to 12.94, p<0.001) and 48 hours (OR 4.20, 95% CI 1.87 to 9.40, p<0.001), and more adequate prescriptions at 48 hours (OR 2.11, 95% CI 1.23 to 3.61, p=0.006) and day five (OR 1.40, 95% CI 1.18 to 1.66, p<0.001). There were no significant differences in ICU admissions, 30-day readmissions, length of stay, 30-day mortality, or in-hospital mortality.

A secondary analysis of this trial evaluated the diagnostic impact of point-of-care multiplex PCR versus conventional culture in 145 emergency department patients with suspected community-acquired pneumonia (CAP) who had paired lower respiratory tract specimens.[11] PCR identified substantially more pathogens than culture (187 vs. 34), with positive-result agreement of only 31.6% for *Streptococcus pneumoniae* and 26% for *Haemophilus influenzae*; notably, bacterial loads ≥10^7 copies/mL for both pathogens were strongly associated with expert-panel and HRCT-confirmed CAP diagnoses, while concentrations of *M. catarrhalis*, *S.*

aureus, and Enterobacterales showed no such correlation, consistent with upper-airway commensal carriage. Prior antibiotic exposure within 30 days (25% of cohort) markedly reduced *S. pneumoniae* detection by both methodologies, and among patients with *S. pneumoniae* and/or *H. influenzae* identified by POC-PCR, 69% received targeted and 85% received adequate antibiotic therapy within 4 hours of admission. The authors concluded that POC PCR enhances diagnostic yield and may enable a diagnostics-driven antimicrobial stewardship approach in the emergency department, but emphasized that semi-quantitative concentration thresholds and expert interpretive guidance are essential to differentiate true pathogens from colonizing flora and avoid inappropriate broad-spectrum prescribing.

Andrews (2017) published a quasi-randomized study assessing the impact of multiplex PCR on length of stay and turnaround time compared with routine, laboratory-based testing in the treatment of patients aged ≥16 years presenting with influenza-like illness or upper or lower respiratory tract infection.[12] Patients were selected at inpatient and outpatient clinics in three areas of a hospital. FilmArray RP PCR systems were used. Of eligible patients (n=606), 545 (89.9%) were divided into a control arm (n=211) and an intervention arm (n=334). While PCR testing was not associated with a reduction in length of stay, turnaround time was reduced. Limitations of the study included design and patient allocation (patients were allocated to the intervention arm on even days). Additionally, the patients considered in the study were not noted to be high-risk individuals as defined above, only those with pertinent symptoms.

The parallel-group, open-label, randomized trial by Brendish (2017) evaluated the routine use of molecular point-of-care testing (POCT) for respiratory viruses in adults presenting to a hospital with acute respiratory illness.[13] In a large U.K. hospital, over two winter seasons, investigators enrolled adults within 24 hours of presenting to the emergency department or acute medical unit with acute respiratory illness or fever >37.5°C, or both. A total of 720 patients were randomized (1:1) to either molecular POCT for respiratory viruses (FilmArray Respiratory Panel, n=362) or routine care (n=358), which included diagnosis based on clinical judgment and testing by laboratory PCR at the clinical team's discretion. All patients in the POCT group were tested for respiratory viruses; 158 (45%) of 354 patients in the control group were tested. Because patients presenting with symptoms are often put on antibiotics before tests can be run, the results of the POCTs were unable to influence the outcome in many patients; therefore, a subgroup analysis was performed for those who were only given antibiotics after test results were available. The results of the analysis showed antibiotics were prescribed for 61 (51%) of 120 patients in the POCT group and for 107 (64%) of 167 in the control group (difference, -13.2%, 95% CI -24.8% to -1.7%, p=0.0289). Mean test turnaround time for POCT was 2.3 hours (SD 1.4) versus 37.1 hours (SD 21.5) in the control group. The percentage of patients prescribed a neuraminidase inhibitor who tested positive for influenza was significantly higher for the POCT group than the control group (82% vs. 47%), and it was significantly lower for the percentage who tested negative for influenza (18% vs. 53%). In addition, the time to first dose was 8.8 hours (SD 15.3) for POCT and 21.0 hours (SD 28.7) for the control group. Blinding of the clinical teams to which group a patient had been randomized to was not possible because the purpose of the study was to inform the clinical team of POCT results. In addition, the limit of the study to the winter months means the findings cannot be extrapolated to the rest of the year.

Section Summary: Respiratory Pathogen Panels

The evidence for the clinical validity or clinical utility of respiratory pathogen panels in diagnosing respiratory infections includes a systematic review and two randomized controlled

trials. The systematic review reported that all three reviewed multiplex PCR systems were highly accurate, compared to the reference tests used. The clinical utility demonstrated by the trials showed some benefits in test results turnaround time, time to receive treatment, targeted antibiotic prescriptions, and length of hospital stay, however significant differences were not seen in readmission or mortality.

JOINT INFECTION PATHOGEN PANELS

Joint infection pathogen panels are intended to diagnose infections related to joint arthroplasty and septic arthritis. The most studied test is the Biofire® Joint Infection (JI) Panel, which has been evaluated in retrospective and prospective studies reporting on diagnostic metrics, such as sensitivity and specificity compared with other techniques (mainly culture methods) in various patient populations.[14-24] Limitations in this evidence include heterogeneous study designs and patient populations, variable reference standards, and limited long-term outcome data. No studies were identified that prospectively evaluated the impact of the panel testing on patient health outcomes.

ENDOMETRIAL PATHOGEN PANELS

No studies were identified that evaluated the clinical validity or utility of endometrial pathogen panels.

WOUND PATHOGEN PANELS

No studies were identified that evaluated the clinical validity or utility of wound pathogen panels.

PRACTICE GUIDELINE SUMMARY

AMERICAN UROLOGICAL ASSOCIATION (AUA)

The AUA, in conjunction with the Canadian Urological Association (CUA) and the Society of Urodynamics, Female Pelvic Medicine and Urogenital Reconstruction (SUFU), published guidelines on recurrent uncomplicated UTIs in women in 2019,[25] which were updated in 2022.[26] These guidelines included the following recommendations:

- To make a diagnosis of [recurrent] UTI, clinicians must document positive urine cultures associated with prior symptomatic episodes. (Clinical Principle)
- Clinicians should obtain urinalysis, urine culture and sensitivity with each symptomatic acute cystitis episode prior to initiating treatment in patients with rUTIs. (Moderate Recommendation; Evidence Level: Grade C)

The guideline update specifically addresses nucleic acid testing, stating:[26]

“To date, more evidence is needed before these technologies become incorporated into the guideline, as there is concern that adoption of this technology in the evaluation of lower urinary tract symptoms may lead to overtreatment with antibiotics.”

CENTERS FOR DISEASE CONTROL AND PREVENTION (CDC)

The CDC has published a number of recommendations and statements regarding the use of nucleic acid amplification testing (NAAT) to diagnose viruses and infections.

In 2019, the CDC published guidance for laboratory testing for Cytomegalovirus (CMV), the guideline stated that the standard laboratory test for congenital CMV is PCR on saliva, with confirmation via urine test to avoid false-positive results from ingesting breast milk from CMV seropositive mothers. Serologic tests were recommended for person >12 months of age.[27]

Currently, the CDC does not recommend oral screening for human papillomavirus (HPV).[28]

INFECTIOUS DISEASE SOCIETY OF AMERICA (IDSA)

In 2017, the IDSA published clinical practice guidelines for the management of healthcare-associated ventriculitis and meningitis.[29] When making diagnostic recommendations, the IDSA notes cultures as the standard of care in diagnosing healthcare-associated ventriculitis and meningitis, but that "nucleic acid amplification tests, such as PCR, on CSF may both increase the ability to identify a pathogen and decrease the time to making a specific diagnosis (strength of recommendation: weak, quality of evidence: low)."

In 2018, the IDSA's published an evidence-based clinical practice guideline for seasonal influenza, which indicated that timely diagnosis of influenza may reduce the inappropriate use of antibiotics.[30] The guideline included the following recommendations:

- Clinicians should use rapid molecular assays (i.e., nucleic acid amplification tests) over rapid influenza diagnostic tests (RIDTs) in outpatients to improve detection of influenza virus infection (recommendation strength: A, quality of evidence: II).
- Clinicians should use multiplex RT-PCR assays targeting a panel of respiratory pathogens, including influenza viruses, in hospitalized immunocompromised patients (recommendation strength: A, quality of evidence: III).
- Clinicians can consider using multiplex RT-PCR assays targeting a panel of respiratory pathogens, including influenza viruses, in hospitalized patients who are not immunocompromised if it might influence care (e.g., aid in cohorting decisions, reduce testing, or decrease antibiotic use) (recommendation strength: B, quality of evidence: III).

IDSA AND AMERICAN THORACIC SOCIETY (ATS)

The IDSA and the ATS published a guideline on the diagnosis and treatment of community-acquired pneumonia (CAP) in 2019, which did not recommend pathogen panel testing for this purpose.[31] The guideline included the following statements:

- Newer nucleic acid amplification systems for sputum, urine, and blood are being developed and require rigorous testing to assess the impact on treatment decisions and clinical outcomes for patients with CAP, as well as the public health benefit in terms of prevention of additional cases and informing primary prevention strategies.
- As bacterial pathogens often coexist with viruses and there is no current diagnostic test accurate enough or fast enough to determine that CAP is due solely to a virus at the time of presentation (*see below*), our recommendations are to initially treat empirically for possible bacterial infection or coinfection.

- Unfortunately, microbiological testing has yet to deliver fast, accurate, and affordable testing that result in proven benefit for patients with CAP in terms of more rapid delivery of targeted therapy or safe de-escalation of unnecessary therapy. Exceptions include rapid testing for MRSA [methicillin-resistant Staphylococcus aureus] and influenza. Until we have such widely available (and affordable) tests, therapy for many or most patients with CAP will remain empiric. Therefore, clinicians need to be aware of the spectrum of local pathogens, especially if they care for patients at a center where infection with antibiotic-resistant pathogens such as MRSA and *P. aeruginosa* are more common.

SOCIETY OF HOSPITAL MEDICINE

Levin (2024) published guidance for the Choosing Wisely™ program recommending against routine respiratory pathogen panel testing in the emergency department and hospital settings, noting concerns about positive results in asymptomatic patients due to leftover genetic material, the lack of specific treatment available for most of the included pathogens, and studies showing no difference in clinically relevant outcomes between broad pathogen panels and more targeted tests.[32]

UNITED STATES PREVENTIVE SERVICES TASK FORCE (USPSTF)

In 2013, the USPSTF published a final recommendation statement concluding that the current evidence was insufficient to assess the balance of benefits and harms of screening for oral cancer, including HPV testing, in asymptomatic adults.[33] A review of new evidence in 2023 did not result in any changes.[34]

WORLD HEALTH ORGANIZATION (WHO)

In global meningitis guidelines from the WHO (2025), PCR-based NAAT on cerebrospinal fluid is strongly recommended for pathogen identification in all individuals with suspected acute community-acquired meningitis (strong recommendation, low certainty of evidence), with loop-mediated isothermal amplification (LAMP) recognized as an emerging alternative molecular modality.[35] NAAT is positioned as a complement to — not a replacement for — CSF culture with antimicrobial susceptibility testing, which remains the diagnostic gold standard, and results must be interpreted alongside CSF cytochemistry, Gram stain, and clinical presentation, including

SUMMARY

Medically Necessary

There is enough research to show that nucleic acid probe testing with quantification can help improve health outcomes for individuals with BK virus, cytomegalovirus, hepatitis B, hepatitis C, hepatitis D, HIV-1, HIV-2, human herpesvirus 6, and influenza virus. In many cases, this testing is considered standard of care for monitoring treatment for affected individuals. Therefore, the use of nucleic acid testing using a direct or amplified probe technique (with or without quantification of viral load) may be considered medically necessary for these viruses.

Not Medically Necessary

There is enough research to show that nucleic acid-based pathogen panel testing for 12 or more respiratory pathogens does not improve clinically important health outcomes for

individuals who have signs and/or symptoms of a respiratory infection, compared to other types of testing. In addition, there are no clinical guidelines based on research that specifically recommend these expanded tests. Therefore, respiratory pathogen panel tests that include 12 or more targets are considered not medically necessary.

Investigational

There is not enough research to show that nucleic acid probe testing with quantification or semi-quantification for microorganisms other than cytomegalovirus, hepatitis B, hepatitis C, hepatitis D, HIV-1, HIV-2, human herpesvirus 6, and influenza virus can improve health outcomes for individuals. Therefore, nucleic acid testing with quantification or semi-quantification is considered investigational when medical necessity criteria are not met.

There is not enough research to show that nucleic acid probe testing for hepatitis G can improve health outcomes in individuals who have hepatitis. In addition to the lack of evidence on the test performance, the clinical implications of these tests are unclear. Also, there are no clinical guidelines based on research that recommend nucleic acid probe testing for hepatitis G. Therefore, this testing, either with or without quantification, is considered investigational.

There is not enough research to show that a nucleic acid-based central nervous system pathogen panel testing can improve health outcomes for individuals who have signs and/or symptoms of meningitis and/or encephalitis. The available central nervous system panel is highly specific for the included organisms, but the sensitivity for each pathogen is not well-characterized. In addition, the false-positive rate for this panel was more than 15%, and a negative test result does not exclude infection due to pathogens not included in the panel. Also, there are no clinical guidelines based on research that recommend nucleic acid-based central nervous system pathogen panel testing. Therefore, this testing is considered investigational.

There is not enough research to show that a nucleic acid-based pathogen panel testing for urinary tract infections (UTIs) can improve health outcomes for individuals who have signs and/or symptoms of a UTI. In addition, there are no clinical guidelines based on research that recommend nucleic acid-based testing for UTI diagnosis or treatment. Therefore, this testing is considered investigational.

There is not enough research to show that nucleic acid-based pathogen panel testing for joint infections can improve health outcomes for individuals suspected of having this condition. In addition, there are no clinical guidelines based on research that recommend nucleic acid-based testing for this purpose. Therefore, this testing is considered investigational.

There is not enough research to show that nucleic acid-based endometrial pathogen panels can improve health outcomes, including fertility outcomes, for any individuals. In addition, there are no clinical guidelines based on research that recommend endometrial pathogen panel testing. Therefore, this testing is considered investigational.

There is not enough research to show that nucleic acid-based pathogen panels can improve health outcomes for individuals with surgical or chronic wounds. In addition, there are no

clinical guidelines based on research that recommend nucleic acid-based testing for these wounds. Therefore, this testing is considered investigational.

There is not enough research to show that oral screening for human papillomavirus (HPV) can improve health outcomes for any individuals. It is not clear how the results of oral HPV testing would be used to guide healthcare decisions. In addition, there are no clinical guidelines that recommend oral HPV testing. Therefore, this testing is considered investigational.

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CODES

NOTE: CPT codes for quantification include both amplification and direct probes; therefore, simultaneous coding for both quantification with either amplification or direct probes is not warranted.

Codes	Number	Description
CPT	0115U	Respiratory infectious agent detection by nucleic acid (DNA and RNA), 18 viral types and subtypes and 2 bacterial targets, amplified probe technique, including multiplex reverse transcription for RNA targets, each analyte reported as detected or not detected

Codes	Number	Description
	0202U	Infectious disease (bacterial or viral respiratory tract infection), pathogen-specific nucleic acid (DNA or RNA), 22 targets including severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), qualitative RT-PCR, nasopharyngeal swab, each pathogen reported as detected or not detected
	0223U	Infectious disease (bacterial or viral respiratory tract infection), pathogen-specific nucleic acid (DNA or RNA), 22 targets including severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), qualitative RT-PCR, nasopharyngeal swab, each pathogen reported as detected or not detected
	0225U	Infectious disease (bacterial or viral respiratory tract infection) pathogen-specific DNA and RNA, 21 targets, including severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), amplified probe technique, including multiplex reverse transcription for RNA targets, each analyte reported as detected or not detected
	0321U	Infectious agent detection by nucleic acid (DNA or RNA), genitourinary pathogens, identification of 20 bacterial and fungal organisms and identification of 16 associated antibiotic-resistance genes, multiplex amplified probe technique
	0323U	Infectious agent detection by nucleic acid (DNA and RNA), central nervous system pathogen, metagenomic next-generation sequencing, cerebrospinal fluid (CSF), identification of pathogenic bacteria, viruses, parasites, or fungi
	0371U	Infectious agent detection by nucleic acid (DNA or RNA), genitourinary pathogen, semiquantitative identification, DNA from 16 bacterial organisms and 1 fungal organism, multiplex amplified probe technique via quantitative polymerase chain reaction (qPCR), urine
	0372U	Infectious disease (genitourinary pathogens), antibiotic-resistance gene detection, multiplex amplified probe technique, urine, reported as an antimicrobial stewardship risk score
	0429U	Human papillomavirus (HPV), oropharyngeal swab, 14 high-risk types (ie, 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, and 68)
	0480U	Infectious disease (bacteria, viruses, fungi and parasites), cerebrospinal fluid (CSF), metagenomic next generation sequencing (DNA and RNA), bioinformatic analysis, with positive pathogen identification
	0504U	Infectious disease (urinary tract infection), identification of 17 pathologic organisms, urine, real-time PCR, reported as positive or negative for each organism
	0528U	Lower respiratory tract infectious agent detection, 18 bacteria, 8 viruses, and 7 antimicrobial resistance genes, amplified probe technique, including reverse transcription for RNA targets, each analyte reported as detected or not detected with semiquantitative results for 15 bacteria
	~~0556U~~	~~Infectious disease (bacterial or viral respiratory tract infection), pathogen-specific DNA and RNA by real-time PCR, 12 targets, nasopharyngeal or oropharyngeal swab, including multiplex reverse transcription for RNA targets, each analyte reported as detected or not detected~~ (Deleted 10/01/2026)
	0563U	Infectious disease (bacterial and/or viral respiratory tract infection), pathogen-specific nucleic acid (DNA or RNA), 11 viral targets and 4 bacterial targets, qualitative RT-PCR, upper respiratory specimen, each pathogen reported as positive or negative
	0564U	Infectious disease (bacterial and/or viral respiratory tract infection), pathogen-specific nucleic acid (DNA or RNA), 10 viral targets and 4 bacterial targets, qualitative RT-PCR, upper respiratory specimen, each pathogen reported as positive or negative

Codes	Number	Description
	0590U	Infectious disease (bacterial and fungal), DNA of 44 organisms (34 bacteria, 10 fungi), urine, next-generation sequencing, reported as positive or negative for each organism
	0593U	Infectious disease (genitourinary pathogens), DNA, 46 targets (28 pathogens, 18 resistance genes), RT-PCR amplified probe technique, urine, each analyte reported as detected or not detected
	0600U	Infectious disease (wound infection), identification of 65 organisms and 30 antibiotic resistance genes, wound swab, real-time PCR, reported as positive or negative for each organism
	0607U	Reproductive medicine (endometrial microbiome assessment), real-time PCR analysis for 31 bacterial DNA targets from endometrial biopsy, reported with quantified levels of bacterial presence and targeted treatment recommendations
	0608U	Reproductive medicine (endometrial microbiome assessment), real-time PCR analysis for 10 bacterial DNA targets from endometrial biopsy, reported with quantified levels of bacterial presence and targeted treatment recommendations (Do not report 0608U in conjunction with 0607U)
	0660U	Human papillomavirus (HPV), genotypes 18, 31, 33, and 35, cell-free DNA (cfDNA), whole blood, multiplex digital droplet PCR (ddPCR), quantitative
	0661U	Human papillomavirus (HPV), genotype 16, cell-free DNA (cfDNA), whole blood, digital droplet PCR (ddPCR), quantitative
	0666U	Infectious disease (wound infection), DNA, multiplex real-time PCR, wound swab, detection of 27 microbial targets and 28 antibiotic resistance targets, reported as semiquantitative for bacterial and fungal targets, and qualitative for viral- and antibiotic-resistance targets
	87472	Infectious agent detection by nucleic acid (DNA or RNA); Bartonella henselae and Bartonella quintana, quantification
	87482	;Candida species, quantification
	87483	;central nervous system pathogen (eg, Neisseria meningitidis, Streptococcus pneumoniae, Listeria, Haemophilus influenzae, E. coli, Streptococcus agalactiae, enterovirus, human parechovirus, herpes simplex virus type 1 and 2, human herpesvirus 6, cytomegalovirus, varicella zoster virus, Cryptococcus), includes multiplex reverse transcription, when performed, and multiplex amplified probe technique, multiple types or subtypes, 12-25 targets
	87487	;Chlamydia pneumoniae, quantification
	87492	;Chlamydia trachomatis, quantification
	87497	;cytomegalovirus, quantification
	87501	;influenza virus, includes reverse transcription, when performed, and amplified probe technique, each type or subtype
	87502	;influenza virus, for multiple types or sub-types, includes multiplex reverse transcription, when performed, and multiplex amplified probe technique, first 2 types or sub-types
	87503	;influenza virus, for multiple types or sub-types, includes multiplex reverse transcription, when performed, and multiplex amplified probe technique, each additional influenza virus type or sub-type beyond 2 (List separately in addition to code for primary procedure)
	87512	;Gardnerella vaginalis, quantification
	87517	;hepatitis B virus, quantification
	87522	;hepatitis C, quantification, includes reverse transcription when performed
	87523	;hepatitis D (delta), quantification, including reverse transcription, when performed
	87525	;hepatitis G, direct probe technique
	87526	;hepatitis G, amplified probe technique

Codes	Number	Description
	87527	;hepatitis G, quantification
	87530	;Herpes simplex virus, quantification
	87533	;Herpes virus-6, quantification
	87536	;HIV-1, quantification, includes reverse transcription when performed
	87539	;HIV-2, quantification, includes reverse transcription when performed
	87542	;Legionella pneumophila, quantification
	87552	;Mycobacteria species, quantification
	87557	;Mycobacteria tuberculosis, quantification
	87562	;Mycobacteria avium-intracellulare, quantification
	87582	;Mycoplasma pneumoniae, quantification
	87592	;Neisseria gonorrhoeae, quantification
	87627	;joint space pathogens and drug resistance genes, multiplex amplified probe technique, 26 or more targets
	87633	;respiratory virus (eg, adenovirus, influenza virus, coronavirus, metapneumovirus, parainfluenza virus, respiratory syncytial virus, rhinovirus), includes multiplex reverse transcription, when performed, and multiplex amplified probe technique, multiple types or subtypes, 12-25 targets
	87652	;Streptococcus, group A, quantification
	87799	Infectious agent detection by nucleic acid (DNA or RNA), not otherwise specified; quantification, each organism
HCPCS	None	

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