New Procedures

Chlamydia/Gonococcus, NAA With Reflex to Trichomonas vaginalis, NAA

CPT 87491; 87591
Use Diagnosis of Chlamydia trachomatis and Neisseria gonorrhoeae infection. If a positive result is obtained for either Chlamydia trachomatis or Neisseria gonorrhoeae, testing for Trichomonas vaginalis is performed.

Limitations Note: Specimens cannot be collected and used for Chlamydia/Neisseria and routine chemistry or urine culture. Chlamydia/Neisseria requires use of a first catch (the initial stream of urine that will wash organisms out of the urethra of men or women). Routine chemistry and bacterial or fungal culture require use of the clean catch midstream collection technique.

Methodology Nucleic acid amplification (NAA)
Specimen Vaginal, endocervical, or male urethral swab, first-void urine (patient should not have urinated for one hour prior to specimen collection), or cervical cells in liquid cytology vial.
Volume One swab, 2 mL of a 20 mL to 30 mL urine collection, or entire liquid cytology vial
Minimum Volume One swab, 2 mL of a 20 mL to 30 mL urine collection, or entire liquid cytology vial
Container Gen-Probe® Aptima® swab or Aptima® urine specimen transport; Cytyc® ThinPrep® or TriPath SurePath™ liquid cytology vial

Collection Vaginal swab collection: Care provider specimen: Collect vaginal fluid sample using the Gen-Probe® Aptima® Vaginal Swab Kit by contacting the swab to the lower third of the vaginal wall, rotating the swab for 10 to 30 seconds to absorb the fluid. Immediately place the swab into the transport tube and carefully break the swab shaft against the side of the tube. Tightly screw on the cap. Patient self-collection instructions: Partially open the package. Do not touch the soft tip or lay the swab down. If the soft tip is touched, the swab is laid down, or the swab is dropped, use a new Aptima® Vaginal Swab Specimen Collection Kit. Remove the swab. Carefully insert the swab into the vagina about 2’ past the introitus and gently rotate the swab for 10 to 30 seconds, making sure the swab touches the walls of the vagina so that moisture is absorbed by the swab. Withdraw the swab without touching the skin. Immediately place the swab into the transport tube and carefully break the swab shaft against the side of the tube. Tightly screw on the cap.

Endocervical swab: Remove excess mucus from the cervical os and surrounding mucosa using the cleaning swab (white-shaft swab in the package with red printing). Discard this swab. Insert the specimen collection swab (blue-shaft swab in the package with green printing) into the endocervical canal. Gently rotate the swab clockwise for 10 to 30 seconds in the endocervical canal to ensure adequate sampling. Withdraw the swab carefully. Remove the cap from the swab specimen transport tube and immediately place the specimen collection swab into the specimen transport tube. Carefully break the swab shaft at the scoreline using care to avoid splashing of contents. Recap the swab specimen transport tube tightly.

Male urethral swab: The patient should not have urinated for at least one hour prior to specimen collection. Insert the specimen collection swab (blue-shaft swab in the package with the green printing) 2 to 4 cm into the urethra. Gently rotate the swab clockwise for two to three seconds in the urethra to ensure adequate sampling. Withdraw the swab carefully. Remove the cap from the swab specimen transport tube and immediately place the specimen collection swab into the specimen transport tube. Carefully break the swab shaft at the scoreline using care to avoid splashing of contents. Recap the swab specimen transport tube tightly.

Urine specimen: The patient should not have urinated for at least one hour prior to specimen collection. Direct patient to provide a first-catch urine (approximately 20 mL to 30 mL of the initial urine stream) into a urine collection cup free of any preservatives. Collection of larger volumes of urine may result in specimen dilution that may reduce test sensitivity; lesser volumes may not adequately rinse organisms into the specimen. Female patients should not cleanse the labial area prior to providing the specimen. Add urine to the Aptima® COMBO 2 urine collection device. The final volume must be between the two black lines on the device (about 2 mL).

Storage Instructions Room temperature
Causes for Rejection Specimen with incorrect patient identification; unlabeled specimen; inappropriate specimen transport conditions; specimens received after prolonged delay (usually >72 hours); specimen leaked in transit; specimen in expired transport or incorrect transport device; specimens with inappropriate source for test requested; specimen with fixative or additives; Aptima® urine transport >30 days from collection; Aptima® urine transport with incorrect specimen volume; <15 mL urine submitted in sterile container; receipt of urine in sterile container >24 hours from collection; Aptima® swab transport >60 days from collection; Aptima® swab specimens with incorrect specimen volume; Aptima® swab specimens without a swab; cleaning swab (white-shaft swab) in Aptima® swab transport; any non—Gen-Probe® swab submitted in Aptima® transport device; wooden-shaft swab in transport device; transport device with multiple swabs; female urethral swab; bloody or grossly mucoid specimens; bacterial swabs; specimen in ProbeTec™ UPT transport; ProbeTec™ Q-swabs; UTM-RT

Hepatitis B Virus (HBV) Evaluation Profile ........ 037215
CPT 86704; 86706; 87340
Synonyms HBV Evaluation Profile
Test Includes Hepatitis B core antibody, total; hepatitis B surface antibody, qualitative; hepatitis B surface antigen
Use Determine HBV infection status in patients prior to initiation of HCV treatment with direct-acting agents
Methodology Immunochemiluminometric assay (ICMA)

These new/revised publications are now available:
- Allergy Test Menu (L3535)
- Women’s Health Test List (L8739)
- Cardiovascular Care Anchor Brochure (L14246)
- Zika Virus and Pregnancy Brochure (L15667)

Please ask your LabCorp service representative for these titles.
Additional biochemical or molecular tests may be performed on

- have abnormal fetal ultrasound findings
- are known carriers of an X-linked disorder
- have a previous child having chromosome abnormality or multiple

Use

- Rapid identification of common prenatal aneuploidy (specific for X, Y, 13, 18, 21). If abnormal, reflex to banded chromosomes to obtain fetal karyotype. This test allows prenatal detection of chromosomal rearrangements, aneuploidy, or mosaicism. Such groups include women who:
  - are age 35 years or older
  - have a previous child having chromosome abnormality or multiple congenital abnormalities
  - have had two or more previous spontaneous abortions
  - have a family history of a chromosome abnormality
  - are known carriers of an X-linked disorder
  - are 31 years of age or older with twin pregnancies
  - have abnormal fetal ultrasound findings
  - have a positive maternal serum marker screen

Additional biochemical or molecular tests may be performed on the cultured amnionctyes. Fetal loss rate at 14 to 18 week sampling is considered to be 0.5%, and 2% to 3% at 10 to 13 weeks. Chorionic villus sampling (CVS) may be safer than early amniocentesis for fetal karyotyping at 10-13 weeks' gestation. CVS than with amniocentesis. Cytogenetic analyses using such samples is 1% to 1.5% but the risk of maternal infection appears to be higher with CVS than with amnioncentesis. Cytogetic analyses using such samples allow for an early gestational testing based on a 10- to 11-week placental biopsy and a 8-day cytogenetic study. Most failures are due to an inappropriate biopsy containing only maternal decidua.

Chromosomal aberration were found in 4.6% of fetuses in women older than 38 to 40 years of age. Trisomy 21 was the most common abnormality (62%). Klinefelter syndrome (11%) and trisomy 18 (11%) were next most frequent in the cases of advanced maternal age. Prenatal diagnosis is possible for more than 1000 inherited diseases. Most are inherited in an autosomal recessive manner. Antenatal molecular diagnosis has become available for cystic fibrosis, muscular dystrophy, sickle cell anemia, hemophilia, and many other genetic abnormalities. This can be done from either cultured amniotic fluid cells or chorionic villous sampling. A normal FISH result reflexes to high resolution SNP microarray which detects genomic imbalance associated with development delay/congenital anomalies and the percentage and location of allele homozogosity associated with uniparental disomy, recessive allele risk and identity by descent.

Limitations FISH detects only the most common aneuploidies found in the second trimester. Abnormal results will reflex to banded chromosome analyses. Although the overall culture success rate is reported as >99%, culture failure can result. Reasons include, but are not limited to lack of amnionctyes in the fluid, and contamination of the fluid with bacteria or yeast. Normal FISH results will reflex to the microarray. FISH and microarray will not detect balanced rearrangements and may not detect low level mosaicism. Extensive maternal cell contamination will limit the sensitivity of the assay.

Methodology

Fluorescence in situ hybridization (FISH) and in situ chromosome cell culturing of amnionctyes to investigate numerical and/or structural chromosome abnormalities. Whole genome SNP-based copy number microarray analysis targeting 2.695 million copy number and allele-specific genome sites from uncultured cells. If DNA yield on uncultured cells is inadequate, analysis will be performed on cultured cells.

Specimen

- Amniotic fluid

Volume

- 25 mL or greater

Container

- Sterile plastic conical tube

Patient Preparation

- The patient preferably should have had ultrasound studies (to verify fetal life, detect multiple gestation, confirm gestational age, localize fetus/placenta).

Collection

- Discard first 2 mL of fluid aspirated to avoid maternal cell contamination. Specimen is collected in a 20 mL sterile syringe and transferred aseptically to sterile tubes to be transported to LabCorp. Request form is completed and accompanies specimen and miscellaneous slip to the laboratory.

Storage Instructions

- Maintain specimen at room temperature.

Causes for Rejection

- Specimen found not to be amniotic fluid; gross contamination with blood cells; frozen specimen; container with rubber stopper (rubber is toxic to amnionctyes); quantity not sufficient for analysis

Special Instructions

- This test is currently NOT orderable by New York State clients. Pertinent medical findings should accompany request for FISH. A completed Informed Consent and Prenatal Chromosome SNP Microarray Questionnaire should accompany specimens. Call 800-345-4363 to request form. In the case of a reflex to microarray, concurrent maternal contamination (MCC) studies are recommended.

References

The MECP2 gene is located on the X chromosome. Currently, the criteria for clinical diagnosis of Rett syndrome has been used to identify Rett syndrome and to distinguish between classical and atypical Rett syndrome patients. The most clinically defined group is referred to as classic Rett. Of these, the majority are found in both classical and atypical Rett syndrome patients. Rett syndrome is considered to be the first syndrome identified directly related to mutations in a gene controlling gene expression.

Mutations in the gene for methyl-CpG-binding protein 2 (MECP2), which causes Rett syndrome, are found in both classical and atypical Rett syndrome patients. Rett syndrome primarily affects females. It is the second most common cause of mental retardation in females (frequency: 1:15,000 to 1:8,500 births). The risk of development of Rett syndrome seems to be equal among different ethnic groups.

Mutations in the gene for methyl-CpG-binding protein 2 (MECP2) are the most common cause of Rett syndrome. The MECP2 protein is one of the many components involved with the regulation of gene expression. Rett syndrome is considered to be the first syndrome identified directly related to mutations in a gene controlling gene expression.

The MECP2 gene is located on the X chromosome. Currently, the criteria for Rett syndrome diagnosis is completely clinical. A group of standardized clinical benchmarks has been used to identify Rett syndrome and to distinguish between classical and atypical Rett syndrome patients. The most clinically defined group is referred to as classic Rett. Of these, the majority (80%) have MECP2 gene mutations. Although 12 mutations account for 8% to 10% of MECP2 pathogenic variants.

Specimen Whole blood or amniotic fluid or chorionic villus sample (CVS) Volume 7 mL whole blood or 10 mL amniotic fluid or 10 mg CVS Container Lavender top (EDTA) or yellow-top (ACD) or sterile plastic conical tube or two confluent T-25 flasks for fetal testing Storage Instructions Maintain specimen at room temperature

Causes for Rejection Frozen specimen; hemolysis; quantity not sufficient for analysis; improper container

References
**Biotin Interference Affects Some Assays**

LabCorp would like to make clinicians aware that some assays can be affected by high levels of biotin in a patient’s serum/plasma. Thinking it is a contributor to keratin, some people have begun taking large doses of biotin to improve their hair, nails, and skin. Some clinicians prescribe high-dose biotin in the treatment of multiple sclerosis or dermatologic conditions.

Over-the-counter formulations are available in a variety of names, including vitamin B7, vitamin H, and coenzyme R. These formulations can contain nearly 1,000 times as much of the Institute of Medicine-recommended daily dose of 30 mcg.

Many modern immunoassays contain biotin along with streptavidin. Samples from patients taking megadoses of biotin can produce falsely high or falsely low results, depending on the assay mechanism. As such, it is important for physicians to remind patients to refrain from taking megadoses of biotin for at least 72 hours prior to immunoassay test collection.

**References:**


Service Announcements

CAP Publishes Revised Guidelines for Specimen Labeling

Recently published guidelines by the College of American Pathologists (CAP) has recommended changes regarding proper specimen labeling. Below is an excerpt from the CAP All Common Checklist, revised August 17, 2016:

All primary specimen containers are labeled with at least two patient-specific identifiers.

NOTE: A primary specimen container is the innermost container that holds the original specimen prior to processing and testing. This may be in the form of a specimen collection tube, cup, syringe, swab, slide or other form of specimen storage.

For prepared slides submitted to the laboratory, if the slides only contain one identifier, they must be securely submitted in a container labeled with two identifiers.

In limited situations, a single identifier may be used if it can uniquely identify the specimen. For example, in a trauma situation where a patient’s identification is not known, a specimen may be submitted for testing labeled with a unique code that is traceable to the trauma patient. Other examples may include forensic specimens, coded or de-identified research specimens, or donor specimens labeled with a unique code decryptable only by the submitting location.

For specimens where site of origin is critical to the analysis (e.g. site specific cultures, surgical and cytology specimens), the primary specimen container and/or the requisition must clearly identify the site of origin, and as appropriate, the laterality of the specimen (right versus left).

Pursuant to recent changes in CAP guidelines, all primary specimen containers must be labeled with two patient-specific identifiers at the time of collection. The identifiers must correspond to information on the patient's test request form.

Prepared slide(s) submitted to the laboratory with only one identifier must be securely submitted in a container labeled with two identifiers. Each specimen must be clearly labeled with the patient’s first and last name as they appear on the test request form. The preferred second identifier is the date of birth.

The specimen container also should include the following information: date and time of collection; specimen type; and site of origin for specimens where site of origin is critical to analysis (e.g. site-specific cultures and surgical and cytology specimens). The name on the test request form must exactly match the patient's name on the specimen submitted. If there are any questions, please contact your LabCorp service representative.

Reference:
College of American Pathologists, Accreditation Programs, All Common Checklist. Laboratory Accreditation Program. Northfield, Ill; CAP 2016.

Updates to the Directory of Services and Interpretive Guide (DoS)

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<tr>
<th>Test Name</th>
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<th>Field/Change (Only fields that change are included here.)</th>
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<tbody>
<tr>
<td>Acid-fast (Mycobacteria) Smear and Culture With Reflex to Identification and Susceptibility Testing</td>
<td>183764</td>
<td>Special Instructions Specimen processing (ie, N-acetyl-L-cystine-sodium hydroxide treatment or equivalent, concentration, grinding, both or neither), mycobacterial culture, and smear when appropriate (smears are not performed on blood or when there is less than 2 mL of fluid). Identification by DNA probes or sequencing will be performed at an additional charge. This culture will often detect Nocardia species and other aerobic actinomycetes, and identification appropriate for these organisms will be included.</td>
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<tr>
<td>Allergen Profile, Pediatric, Birth to Three Years</td>
<td>671935</td>
<td>Volume 0.5 mL</td>
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<tr>
<td>C-Telopeptide (Endocrine Sciences)</td>
<td>500089</td>
<td>Stability</td>
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<tr>
<td></td>
<td></td>
<td>Temperature</td>
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<tr>
<td></td>
<td>Room temperature</td>
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<td></td>
<td>Refrigerated</td>
<td>14 days</td>
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<tr>
<td></td>
<td>Frozen</td>
<td>2 years</td>
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<td></td>
<td>Freeze/thaw cycles</td>
<td>Stable x6</td>
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</table>

Note: For the most current test information, please consult the online Directory of Services and Interpretive Guide at https://www.labcorp.com/wps/portal/provider/testmenu.
## Updates to the Directory of Services and Interpretive Guide (DoS)

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<tbody>
<tr>
<td><strong>Drugs of Abuse Profile (Routine), Urine (Five Drugs) (MS Confirmation Included)</strong></td>
<td>739078</td>
<td><strong>Use</strong> Detect the presence of prescribed and illicit drugs. <strong>Volume</strong> 30 mL. <strong>Container</strong> Use plastic urine drug bottle and evidence tape or tamper-evident container for forensic specimen. <strong>Collection</strong> Urine temperature monitoring is recommended for samples to be tested for medicolegal purposes. <strong>Causes for Rejection</strong> Quantity not sufficient for analysis; improper specimen (serum, plasma, blood); incomplete chain-of-custody documentation; incomplete specimen identification; improper or missing tamper-evident seals.</td>
</tr>
</tbody>
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**GeneSeq™: Cardio Familial Aortopathy Profile** | 451432 | **Use** Confirm a clinical diagnosis of Aortopathy and identify presymptomatic family members, guiding prophylactic measures. |

**GeneSeq™: Cardio Familial Arrhythmia Profile** | 451412 | **Use** Confirm a clinical diagnosis of Arrhythmia and identify presymptomatic family members, guiding prophylactic measures. **Additional Information** Cardiac arrhythmias are generally characterized by abnormal electrical activity in the heart that puts patients at high risk for embolic stroke and/or sudden cardiac death (SCD). Commonly recognized arrhythmic disorders include atrial fibrillation (AF), long QT syndrome (LQTS), catecholaminergic polymorphic ventricular tachycardia (CPVT), arrhythmogenic right ventricular dysplasia/cardiomyopathy (ARVD/C), and Brugada syndrome (BrS). Genetic testing for mutations in genes known to be associated with LQTS, CPVT, ARVD/C, AF, and BrS can be used in conjunction with standard cardiac testing to help: - Confirm a diagnosis. - Differentiate between arrhythmic disorders. - Clarify the prognosis, alerting patients and physicians to the most common arrhythmia triggers, which may be specific to the underlying genetic cause. - Guide therapeutic strategies. - Identify family members who are at increased risk for arrhythmic disorder and may benefit from cardiac screening. An estimated 30% to 50% of arrhythmia cases are familial. Mutations responsible for arrhythmias are typically acquired in an autosomal-dominant manner. Carrier screening for mutations in at-risk family members may help identify individuals - particularly those who do not have clinical signs or symptoms of disease - who would benefit from early intervention to reduce the risk of cardiac events. **References** (additions only included here; visit Test Menu at www.labcorp.com for complete list) Ackerman MJ, Priori SG, Willems S, et al. HRS/EHRA expert consensus statement on the state of genetic testing for the channelopathies and cardiomyopathies. This document was developed as a partnership between the Heart Rhythm Society (HRS) and the European Heart Rhythm Association (EHRA) Heart Rhythm. 2011;8(8):1308-1339. PubMed 21787999 Priori SG, Blomstrom-Lundqvist C, Mazzanti A, et al. 2015 ESC Guidelines for the management of patients with ventricular arrhythmias and the prevention of sudden cardiac death: the Task Force for the Management of Patients with Ventricular Arrhythmias and the Prevention of Sudden Cardiac Death of the European Society of Cardiology (ESC) Endorsed by: Association for European Paediatric and Congenital Cardiology (AEPC). Eur Heart J. 2015;36:2793-2867. PubMed 26320108 |

**GeneSeq™: Cardio Familial Cardiomyopathy Profile** | 451422 | **Use** Confirm a clinical diagnosis of Cardiomyopathy and identify presymptomatic family member, guiding prophylactic measures. **Additional Information** Cardiomyopathies are generally characterized by weakening and impaired contractile function of the myocardium that leads to ventricular hypertrophy or dilation. Myocardial dysfunction associated with cardiomyopathy can either be of mechanical or electrical etiology. The four major types of cardiomyopathy include dilated cardiomyopathy (DCM), hypertrophic cardiomyopathy (HCM), arrhythmogenic right ventricular dysplasia/cardiomyopathy (ARVD/C), and restrictive cardiomyopathy (RCM). Rarer types include left ventricular noncompaction (LVNC) and the amyloid-associated cardiomyopathies, such as transthyretin (TTR) amyloidosis and apolipoprotein A-1 amyloidosis (AApoA-1). Many cardiomyopathies are now recognized as familial conditions that may be transmitted in an autosomal dominant, autosomal recessive, X-linked, or mitochondrial manner. Genetic testing for the presence of germline mutations in the genes known to be associated with cardiomyopathy may: - Confirm a diagnosis of familial cardiomyopathy. - Identify which subtype of a particular cardiomyopathy. - Identify family members of an index patient who harbor the familial mutation and may wish to undergo cardiac screening at regular intervals. - Facilitate appropriate genetic counseling for family members. **Note:** For the most current test information, please consult the online Directory of Services and Interpretive Guide at https://www.labcorp.com/wps/portal/provider/testmenu.
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<tbody>
<tr>
<td>Hepatitis B Virus (HBV) DNA, Quantitative Real-time PCR With Reflex to HBV Genotype</td>
<td>551722</td>
<td>Limitations: The quantitative test has a range of 10 IU/mL to 1,000,000,000 IU/mL. The genotype assay is only triggered when the quantitative test result is ≥500 IU/mL. Methodology: Quantitative test: cobas® HBV for use on the cobas® 6800/8800 system</td>
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<tr>
<td>Hepatitis B Virus (HBV), Quantitative, DNA Real-time PCR, (Graphical)</td>
<td>551620</td>
<td>Synonyms: HBV Quantitation Limitations: The HBV quantitative real-time PCR assay has a quantitative range of 10 to 1,000,000,000 IU/mL. Methodology: cobas® HBV for use on the cobas® 6800/8800 system</td>
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<tr>
<td>Hepatitis B Virus (HBV), Quantitative, DNA Real-time PCR, (Non-graphical)</td>
<td>551610</td>
<td>Storage Instructions: Freeze (preferred) or refrigerate. Stable at room temperature for 24 hours or refrigerated for six days. Stable frozen for 12 weeks.</td>
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| Hepatitis C Virus (HCV) FibroSure*                          | 550123  | Reference Interval: See tables. METAVIR Group Scoring System

<table>
<thead>
<tr>
<th>Fibrosis Stage (FibroTest)</th>
<th>Range</th>
<th>Activity Stage (ActiTest)</th>
<th>Range</th>
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<tbody>
<tr>
<td>F0—No fibrosis</td>
<td>0.00—0.21</td>
<td>A0—No activity</td>
<td>0.00—0.17</td>
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<tr>
<td>F0—F1</td>
<td>&gt;0.21—0.27</td>
<td>A0—A1</td>
<td>&gt;0.17—0.29</td>
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<tr>
<td>F1—Portal fibrosis</td>
<td>&gt;0.27—0.31</td>
<td>A1—Minimal activity</td>
<td>&gt;0.29—0.36</td>
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<tr>
<td>F1—F2</td>
<td>&gt;0.31—0.48</td>
<td>A1—A2</td>
<td>&gt;0.36—0.52</td>
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<tr>
<td>F2—Bridging fibrosis with few septa</td>
<td>&gt;0.48—0.58</td>
<td>A2—Moderate activity</td>
<td>&gt;0.52—0.60</td>
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<tr>
<td>F3—Bridging fibrosis with many septa</td>
<td>&gt;0.58—0.72</td>
<td>A2—A3</td>
<td>&gt;0.60—0.63</td>
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<tr>
<td>F3—F4</td>
<td>&gt;0.72—0.74</td>
<td>A3—Severe activity</td>
<td>&gt;0.63—1.00</td>
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<tr>
<td>F4—Cirrhosis</td>
<td>&gt;0.74—1.00</td>
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<tr>
<td>Hepatitis C Virus (HCV), Quantitative, RNA PCR (Graphical) With Reflex to Hepatitis C Virus (HCV) NS5B Drug Resistance Assay</td>
<td>550554</td>
<td>Specimen Plasma (preferred) or serum, frozen Container Ship in plasma preparation tube (PPT™) or screw-capped polypropylene frozen transport tubes. Collection Collect specimen in two PPT™ tubes, gel-barrier tubes, or lavender-top (EDTA) tubes. Do not use green-top (heparin) tubes. Centrifuge specimen within six hours of collection, remove serum/plasma, and transfer specimen to polypropylene screw-capped tubes, and freeze. Specimens drawn into PPT™ tubes need to be centrifuged within six hours and frozen. Ship frozen. To avoid delays in turnaround time when requesting multiple tests on frozen samples, please submit separate frozen specimens for each test requested.</td>
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<td>Hepatitis C Virus (HCV), Quantitative, RNA PCR (Nongraphical) With Reflex to Hepatitis C Virus (HCV) NS5B Drug Resistance Assay</td>
<td>550577</td>
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<td>High-density Lipoprotein Cholesterol (HDL-C)</td>
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<td>HLA B*58:01, Allopurinol Hypersensitivity</td>
<td>167351</td>
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<tr>
<td>Mycobacterium tuberculosis Detection, NAA With Acid-fast Smear and Culture and Reflex to Identification</td>
<td>183641</td>
<td>Special Instructions Specimen processing (ie, N-acetyl-L-cystine-sodium hydroxide treatment or equivalent, concentration, grinding, both or neither), mycobacterial culture, and smear when appropriate (smears are not performed on blood or when there is less than 2 mL of fluid). Identification by DNA probes or sequencing will be performed at an additional charge. This culture will often detect Nocardia species and other aerobic actinomyces, and identification appropriate for these organisms will be included.</td>
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<td>Mycobacterium tuberculosis Detection, NAA With Acid-fast Smear and Culture and Reflex to Identification and Susceptibility Testing</td>
<td>183656</td>
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<tr>
<td>Thyroglobulin, Lymph Node Aspirate (Endocrine Sciences)</td>
<td>502380</td>
<td>Stability</td>
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<td>Tricyclic Antidepressants Confirmation, Urine (Pain Management)</td>
<td>739070</td>
<td>Methodology Mass Spectrometry (MS)</td>
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<tr>
<td>Zika Virus Comprehensive Profile, NAA, Serum and Urine</td>
<td>139600</td>
<td>Methodology Nucleic acid amplification (NAA) Specimen Serum, frozen or refrigerated, and urine, frozen or refrigerated Volume 1.2 mL serum and 3 mL urine Minimum Volume 0.7 mL serum and 2 mL urine. Note: This volume does not allow for repeat testing. Container Red-top tube or gel-barrier tube and Aptima® urine transport tube Collection Transfer serum to a plastic transport tube; transfer urine to Aptima® urine transport tube; freeze both serum and urine preferred. Causes for Rejection Specimen not shipped frozen or refrigerated; specimen greater than 5 days from collection at refrigerated temperature; whole blood; quantity not sufficient for analysis; gross specimen contamination; urine specimen in preservative other than Aptima® urine transport tube; leaking or broken tube; submission of only one of the two required specimen types</td>
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Deleted Procedures

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<tr>
<td>Drug Screen and Confirmation (Seven Drug Classes) With Benzodiazepines, Whole Blood</td>
<td>791608</td>
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CPT Code Updates

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<td>BRAF Gene Mutation Analysis</td>
<td>481030</td>
<td>81210; 88381</td>
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<tr>
<td>Fragile X Syndrome, PCR With Reflex to Southern Blot</td>
<td>511919</td>
<td>81243</td>
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</table>

The CPT codes listed are in accordance with the current edition of Current Procedural Terminology, a publication of the American Medical Association. CPT codes are provided for the convenience of our clients; however, correct coding often varies from one carrier to another. Consequently, the codes presented here are intended as general guidelines and should not be used without confirming with the applicable payer that their use is appropriate in each case.

LOINC® Map. The Logical Observation Identifiers Names and Codes (LOINC®) corresponding to the individual LabCorp published assays is updated on a regular basis at [www.labcorp.com](http://www.labcorp.com).

For LabCorp clients that need an Excel version of the LOINC® Map, please contact the Corporate Coding Resources department at CCR@labcorp.com.