American Society for Microbiology

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Codes:
87635
0140U
0141U
0142U
0151U
0152U
86328
86769
81XX4

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87635: Infectious agent detection by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]), amplified probe technique

Public Comment	Rationale
Crosswalk to U003 for high throughput SARS-CoV-2 testing;	We recommend waiting until the codes for COVID-19 are more stable to revisit.

0140U: Infectious disease (fungi), fungal pathogen identification, DNA (15 fungal targets), blood culture, amplified probe technique, each target reported

Public Comment	Rationale
Crosswalk to 87633 *Infectious agent detection by nucleic acid (DNA or RNA); 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*	This code uses a similar technique and number of targets as 87633.

0141U: Infectious disease (bacteria and fungi), gram-positive organism identification and drug resistance element detection, DNA (20 gram-positive bacterial targets, 4 resistance genes, 1 pan gram-negative bacterial target, 1 pan Candida target), blood culture, amplified probe technique, each target reported as detected or not detected

Public Comment	Rationale
Gap fill to: 87633 *Infectious agent detection by nucleic acid (DNA or RNA); 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* **+ 87481** *Infectious agent detection by nucleic acid (DNA or RNA); Candida species, amplified probe technique*	These two codes comprise both similar nucleic acid techniques and the appropriate number of targets (12-25 + 1 targets).

0142U: Infectious disease (bacteria and fungi), gram-negative bacterial identification and drug resistance element detection, DNA (21 gram-negative bacterial targets, 6 resistance genes, 1 pan gram-positive bacterial target, 1 pan Candida target), amplified probe technique, each target reported as detected or not detected

Public Comment	**Rationale**
Gap fill to 87633 *Infectious agent detection by nucleic acid (DNA or RNA); 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* **+ 87631** *Infectious agent detection by nucleic acid (DNA or RNA); 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, 3-5 targets*	These two codes comprise both similar nucleic acid techniques and the appropriate number of targets (12-25 + 3-5 targets).

0151U: Infectious disease (bacterial or viral respiratory tract infection), pathogen specific nucleic acid (DNA or RNA), 33 targets, real-time semi-quantitative PCR, bronchoalveolar lavage, sputum, or endotracheal aspirate, detection of 33 organismal and antibiotic resistance genes with limited semi-quantitative results

Public Comment	Rationale
Gap fill to **87633** *Infectious agent detection by nucleic acid (DNA or RNA); 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* **+ 87632**, *Infectious agent detection by nucleic acid (DNA or RNA); 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, 6-11 targets*	These two codes comprise both similar nucleic acid techniques and the appropriate number of targets (12-25 + 6-11 targets).

0152U: Infectious disease (bacteria, fungi, parasites, and DNA viruses), DNA, PCR and next-generation sequencing, plasma, detection of >1,000 potential microbial organisms for significant positive pathogens

Public Comment	Rationale
This number of targets (>1,000) does not correspond to any other infectious disease diagnostic test on the CLFS.	We recommend that this number of targets has no precedence and should be gap filled as determined by the Panel

86328: Immunoassay for infectious agent antibody(ies), qualitative or semiquantitative, single step method (eg, reagent strip); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19])

Public Comment	Rationale
Crosswalk to 86794 *Antibody, Zika Virus, IgM* (x 2.5)	This decision follows a CMS decision.

86769: Antibody; severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19])

Public Comment	Rationale
Crosswalk to 86710 *Antibody; influenza virus*	This is a similar methodology and respiratory virus

81XX4: Infectious disease, bacterial vaginosis, quantitative real-time amplification of RNA markers for *Atopobium vaginae*, *Gardnerella vaginalis*, and *Lactobacillus* species, utilizing vaginal fluid specimens, algorithm reported as a positive or negative result for bacterial vaginosis

Public Comment	Rationale
Crosswalk to 87631 *Infectious agent detection by nucleic acid (DNA or RNA); 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, 3-5 targets*	Although this test includes an algorithm, it utilizes similar methodology to 87631.