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Meeting Background and Purpose

This meeting provides an opportunity for the Medicare Advisory Panel on Clinical Diagnostic Laboratory Tests (the CDLT Panel) to publicly convene and make recommendations to the Secretary of the Department of Health and Services and the Administrator of CMS regarding crosswalking and gapfilling for new and reconsidered laboratory tests discussed during the CLFS Annual Public Meeting for CY 2025. The CDLT Panel may also provide input on any other CY 2025 CLFS issues that are designated in the Panel's charter and specified in this agenda. Notice of this meeting and additional supplemental information regarding the CDLT Panel were published in the Federal Register on April 16, 2024 (CMS-1824-N; 88 FR 23084).

Meeting Format

- *** IMPORTANT NOTE: Please note that although we hoped to facilitate an in-person meeting this year, due to the current building issues, the CLFS CDLT Panel meeting will use a virtual-only platform and will not have in-person attendance. While we are disappointed that we will not be able to interact with attendees and speakers at CMS headquarters, we look forward to hosting an in-person meeting in 2025!
- The CDLT Panel interim Co-Chairs will direct the presentation and discussion of each laboratory test code on the agenda.
- Each laboratory test code under consideration will be introduced and discussed by the CDLT Panel. The focus of discussion is payment of the laboratory test code either through crosswalking the laboratory test code to another existing laboratory test code on the CLFS, or to use the gapfill methodology to determine payment. During the discussion the CDLT Panel and CMS staff may ask questions of the representative of laboratory that owns the test. Once CDLT Panel discussions are concluded, the suggestions from the Panel are summarized and the Panel votes on their recommendation for payment.
- The meeting is divided into two sessions, one session on each date of the meeting. Session times are approximate and subject to change. The codes and order of discussed in each session are provided in Appendix 3.
- On Thursday and Friday (if needed), following lunch, the CDLT Panel will hold a discussion on the overall CDLT rate setting process. This session will be for Panel discussion only, although members of the public will be able to ask questions via the Q&A section of the Zoom chat.

Meeting Connection Instructions and Details

- <u>Listen-in via audio and watch via Zoom connection only</u> details are provided using instructions described in Appendix 1.
- Please note that the video or audio recordings of the meeting will not be immediately available after the conclusion of the meeting.

AGENDA

Thursday July 25 and Friday July 26, 2024

| Time | Topic | Supporting Resource |
|-------------------|--|------------------------|
| 9:30 a.m. | Check-In and Audio/Video Connection Test Check | Itesource |
| 10:00 a.m. | Welcome and Panel Introductions: | |
| | Rasheeda Arthur, PhD, Designated Federal Officer (DFO) and | |
| | Meeting Facilitator from the Division of Ambulatory Services. | |
| | Dr. Chris Chong and Dr. Jochen Lennerz, Interim CDLT Panel Co- | |
| | Chairs | |
| 10:15 -12:30 p.m. | Day 1 and 2 Morning Session: | Appendix 3 |
| | Please view Appendix 3 for exact order of codes. | |
| 12:30- 1:15pm | Lunch Break | |
| | Please Note: All speakers please reconnect by 1:00pm | |
| 1:15- 1:45pm | Day 1 and Day 2: Panel Discussion: CDLT rate setting process | |
| 1:45-4:00 p.m. | Day 1 and 2 Afternoon Session: | Appendix 3 |
| | Please view Appendix 3 for exact order of codes. | |
| 4:00 p.m. | Meeting Adjourns | |

^{***}Please note that the order of the agenda and content of the appendices are subject to change.***

Appendix 1: Audio and/or Video Access: Join the meeting by Zoom.

Step 1: Please click the link below to register for the webinar:

https://cms.zoomgov.com/webinar/register/WN xvGPnLreQ0Kw7VVBVKL-eQ

Note: This link provides attendees the ability to view and listen to the meeting. Only confirmed stand-by speakers will have the ability to speak during the meeting.

Step 2: All attendees and participants will be requested to provide their name and email address before joining the meeting.

Step 3: Click "Register."

Appendix 2: Access to CLFS CY 2025 New and Reconsidered Codes and Other Information.

 For a list of <u>CY 2025 new and reconsidered codes</u> that will be discussed during the CDLT Panel meeting, please go to the CLFS Annual Laboratory Meeting website at: https://www.cms.gov/Medicare/Medicare-Fee-for-Service-Payment/ClinicalLabFeeSched/Laboratory Public Meetings

Scroll down to "Test Code Updates" for access to the CY 2024 new and reconsidered code list.

- 2. For <u>CLFS Annual Laboratory Public meeting agenda</u> from June 25, 2024, please see: https://www.cms.gov/files/document/june-25-2024-clfs-public-meeting-agenda-v3.pdf
- 3. For a recording of the CFLS Annual Laboratory Public Meeting from June 25, 2024, please see links below:
 - a. Recording:
 https://cms.zoomgov.com/rec/share/2jQakqNnZtNNToCNxJxnc62trzrWzmBar60OC5y2zhNgK256MZ3GQODzGyUv23UD.Quqt-jAZ5LoO8IH
 - b. Passcode: v\$Rf7#3J
- 4. For a copy of <u>CY 2024 Clinical Laboratory Fee Schedule Test Codes Final Payment Determinations</u> that were discussed during last year's CLFS Annual Laboratory Meeting and the Medicare Advisory Panel for Clinical Diagnostic Laboratory Tests (CDLT Panel) Meeting, please see link: https://www.cms.gov/files/zip/cy-2024-final-payment-determinations.zip

Appendix 3: Summary of codes

- *Subcommittees: Chemistry, Hematology, Immunology, Microbiology (CHIM); Molecular Pathology, Genomic Sequencing (MoG)

 ** Advanced Diagnostic Laboratory Tests (ADLT) status: code is removed from CDLT Panel discussion

Corrections to order of codes:

a. None currently.

| FACA Panel Item # | Current Code # | Final Code # | Code Type | Code Category | Subcategory | Subcommittee | Long Code Descriptor |
|-------------------------|-------------------|--------------|--------------|------------------------------------|-------------|--------------|--|
| 1 | 0445U | 0445U | New (PLA) | Immunology | Alzheimer | CHIM | B-amyloid (abeta42) and phospho tau (181p) (ptau181), electrochemiluminescent immunoassay (eclia), cerebral spinal fluid, ratio reported as positive or negative for amyloid pathology |
| 2 | 82XX0 | TBD | New | Immunology | Alzheimer | CHIM | Beta-amyloid; 1-40 (Abeta 40) |
| 3 | 82XX1 | TBD | New | Immunology | Alzheimer | CHIM | Beta-amyloid; 1-42 (Abeta 42) |
| 4 | 83XX0 | TBD | NEW | Immunology | Alzheimer | CHIM | Neurofilament light chain (NfL) |
| 5 | 86XX1 | TBD | NEW | Immunology | Alzheimer | CHIM | Streptococcus pneumoniae antibody (IgG), serotypes, multiplex immunoassay, quantitative |
| 6 | 8X3XX | TBD | New | Immunology | Alzheimer | CHIM | Tau, total (tTau) |
| 7 | XX42U | 0462U | New (PLA) | Chemistry | Alzheimer | CHIM | Melatonin levels test, sleep study, 7 or 9 sample melatonin profile (cortisol optional), enzyme-linked immunosorbent assay (ELISA), saliva, screening/preliminary |
| 8 | XX65U | TBD | NEW | Microbiology Infectious Disease | Alzheimer | CHIM | Infectious disease (bacteria, viruses, fungi, and parasites), cerebrospinal fluid (CSF), metagenomic next-generation sequencing (DNA and RNA), bioinformatic analysis, with positive pathogen identification |
| 9 | 86041 | 86041 | Reconsidered | Immunology | Neurology | CHIM | Recommendation: Crosswalk code: 86341 Islet cell antibody |
| 10 | 86042 | 86042 | Reconsidered | Immunology | Neurology | CHIM | Acetylcholine receptor (AChR); blocking antibody |
| 11 | 86043 | 86043 | Reconsidered | Immunology | Neurology | CHIM | Acetylcholine receptor (AChR); modulating antibody |
| 12 | 86366 | 86366 | Reconsidered | Immunology | Neurology | CHIM | Muscle-specific kinase (MuSK) antibody |
| 13 | 0431U | 0431U | New (PLA) | Immunology | Neurology | CHIM | Glycine receptor alpha1 IgG, serum or cerebrospinal fluid (CSF), live cell-binding assay (LCBA), qualitative |
| 14 | 0432U | 0432U | New (PLA) | Immunology | Neurology | CHIM | Kelch-like protein 11 (KLHL11) antibody, serum or cerebrospinal fluid (CSF), cell-binding assay, qualitative |
| 15 | 0443U | 0443U | New (PLA) | Chemistry | Neurology | CHIM | Neurofilament light chain (nfl), ultra-sensitive immunoassay, serum or cerebrospinal fluid |

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|-------------------------|-------------------|--------------|--------------------|--|------------------|--------------|---|
| 16 | XX32U | 0451U | New (PLA) | Chemistry | Neurology | CHIM | Oncology (multiple myeloma), LCMS/MS, peptide ion quantification, serum, results compared with baseline to determine monoclonal paraprotein abundance |
| 17 | 0394U | 0394U | Reconsidered (PLA) | Chemistry | Chemistry | CHIM | Perfluoroalkyl substances (PFAS) (eg, perfluorooctanoic acid, perfluorooctane sulfonic acid), 16 PFAS compounds by liquid chromatography with tandem mass spectrometry (LCMS/MS), plasma or serum, quantitative |
| 18 | 8X051 | TBD | NEW | Microbiology | Chemistry | CHIM | Infectious agent detection by nucleic acid (DNA or RNA); Mycobacterium tuberculosis, rifampin resistance, amplified probe technique |
| 19 | 8X3X0 | TBD | New | Immunology | Chemistry | CHIM | Tau, phosphorylated (eg, pTau 181, pTau 217), each |
| 20 | 8XX00 | TBD | NEW | Microbiology Infectious Disease & Genome Sequencing Procedure | Chemistry | CHIM | Infectious disease, bacterial vaginosis and vaginitis, real-time PCR amplification of DNA markers for Atopobium vaginae, Atopobium species, and Megasphaera type 1, Bacterial Vaginosis—Associated Bacteria 2 (BVAB-2), utilizing vaginal-fluid specimens, algorithm reported as positive or negative for high likelihood of bacterial vaginosis, includes separate detection of Trichomonas vaginalis and Candida species (C. albicans, C. tropicalis, C. parapsilosis, C. dubliniensis), Candida glabrata/Candida krusei, when reported |
| 21 | 0435U | 0435U | New (PLA) | Molecular Pathology | Chemosensitivity | CHIM | Oncology, chemotherapeutic drug cytotoxicity assay of cancer stem cells (CSCs), from cultured CSCs and primary tumor cells, categorical drug response reported based on cytotoxicity percentage observed, minimum of 14 drugs or drug combinations |
| 22 | XX84U | TBD | NEW | Genomic Sequencing Procedures; Infectious Disease | Chemosensitivity | CHIM | Human papillomavirus (HPV), E6/E7 markers for high-risk types (16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, and 68), cervical cells, branched-chain capture hybridization, reported as negative or positive for high risk for HPV |
| 23 | XX89U | TBD | NEW | Genomic Sequencing Procedures; Infectious Disease | Therapeutic | CHIM | Infectious disease (vaginal infection), identification of 32 pathogenic organisms, swab, real-time PCR, reported as positive or negative for each organism |
| 24 | XX99U | TBD | NEW | Immunology | Therapeutic | CHIM | Gastroenterology (irritable bowel disease [IBD]), immunoassay for the quantitative determination of infliximab (IXL) levels in venous serum in patients undergoing infliximab therapy, results reported as a numerical value as micrograms per milliliter (µg/mL) |
| 25 | XX97U | TBD | NEW | Pharmacogenomics | Therapeutic | CHIM | Oncology (solid tumor), tumor cell culture in 3D microenvironment, 36 or more drug panel, reported as tumor-response prediction for each drug |
| 26 | XX98U | TBD | NEW | Immunology | Therapeutic | CHIM | Gastroenterology (irritable bowel disease [IBD]), immunoassay for the quantitative determination of adalimumab (ADL) levels in venous serum in patients undergoing adalimumab therapy, results reported as a numerical value as micrograms per milliliter (μg/mL) |
| 27 | 0430U | 0430U | New (PLA) | Chemistry | GI | CHIM | Gastroenterology, malabsorption evaluation of alpha-1-antitrypsin, calprotectin, pancreatic elastase and reducing substances, feces, quantitative |

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|-------------------------|-------------------|--------------|--------------|---|------------------------|--------------|---|
| 28 | 0427U | 0427U | New (PLA) | Hematology | Hematology | CHIM | Monocyte distribution width, whole blood (List separately in addition to code for primary procedure) |
| 20 | ***** | TDD | NEWY | | *** | cym (| (Use 0427U in conjunction with 85004, 85025) |
| 29 | X102U | TBD | NEW | Therapeutic Drug Assay | Hepatology | CHIM | Therapeutic drug monitoring, 200 or more drugs or substances, LC-MS/MS, plasma, qualitative and quantitative therapeutic minimally effective range of prescribed and non-prescribed medications |
| 30 | XX85U | TBD | NEW | Immunology | Monoclonal antibody | СНІМ | Neurology (Alzheimer disease), beta amyloid (Aβ40, Aβ42, Aβ42/40 ratio) and tau-protein (p-tau217, np-tau217, p-tau217/np-tau217 ratio), blood, immunoprecipitation with quantitation by liquid chromatography with tandem mass spectrometry (LC-MS/MS), algorithm score reported as the likelihood of positive or negative for amyloid plaques |
| 31 | XX88U | TBD | NEW | Genomic Sequencing Procedures; Infectious Disease | Monoclonal antibody | CHIM | Infectious disease (urinary tract infection), identification of 17 pathologic organisms, urine, real-time PCR, reported as positive or negative for each organism |
| 32 | 87XX0 | TBD | NEW | Microbiology Infectious Disease | Monoclonal proteins | CHIM | Infectious agent detection by nucleic acid (DNA or RNA); Pneumocystis jirovecii, amplified probe technique |
| 33 | 87XX1 | TBD | NEW | Microbiology Infectious Disease & Genome Sequencing Procedure | Monoclonal proteins | CHIM | Infectious agent detection by nucleic acid (DNA or RNA); Human Papillomavirus (HPV), separately reported high-risk types (eg, 16, 18, 31,45, 51, 52) and high-risk pooled result(s) |
| 34 | XX48U | 0468U | New (PLA) | MAAA | OB | CHIM | Hepatology (nonalcoholic steatohepatitis [NASH]), miR-34a5p, alpha 2-macroglobulin, YKL40, HbA1c, serum and whole blood, algorithm reported as a single score for NASH activity and fibrosis |
| 35 | 0436U | 0436U | New (PLA) | Molecular Pathology | Oncology proteins | CHIM | Oncology (lung), plasma analysis of 388 proteins, using aptamerbased proteomics technology, predictive algorithm reported as clinical benefit from immune checkpoint inhibitor therapy |
| 36 | 0446U | 0446U | New (PLA) | MAAA | Rheumatology | CHIM | Autoimmune diseases (systemic lupus erythematosus [sle]), analysis of 10 cytokine soluble mediator biomarkers by immunoassay, plasma, individual components reported with an algorithmic risk score for current disease activity |
| 37 | 0447U | 0447U | New (PLA) | MAAA | Rheumatology | CHIM | Autoimmune diseases (systemic lupus erythematosus [sle]), analysis of 11 cytokine soluble mediator biomarkers by immunoassay, plasma, individual components reported with an algorithmic prognostic risk score for developing a clinical flare |
| 38 | X103U | TBD | NEW | Therapeutic Drug Assay | Rheumatology | CHIM | Therapeutic drug monitoring, 90 or more pain and mental health drugs or substances, LC-MS/MS, plasma, qualitative and quantitative therapeutic minimally effective range of prescribed and non-prescribed medications |
| 39 | 0429U | 0429U | New (PLA) | Microbiology Infectious Disease | HPV | CHIM | 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) |
| 40 | XX39U | 0458U | New (PLA) | Chemistry | HPV | CHIM | Oncology (breast cancer), S100A8 and S100A9, by enzyme linked immunosorbent assay (ELISA), tear fluid with age, algorithm reported as a risk score |

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|-------------------------|-------------------|--------------|--------------------------|---|-------------|--------------|---|
| 41 | X101U | TBD | NEW | Therapeutic Drug Assay | HPV | CHIM | Therapeutic drug monitoring, 80 or more psychoactive drugs or substances, LC-MS/MS, plasma, qualitative and quantitative therapeutic minimally and maximally effective dose of prescribed and non-prescribed medications |
| 42 | XX63U | TBD | NEW | Chemistry | HPV | CHIM | Obstetrics (preeclampsia), biochemical assay of soluble fms-like tyrosine kinase 1 (sFIT-1) and placental growth factor (PIGF), serum, ratio reported for sFIT-1/PIGF, with risk of progression for preeclampsia with severe features within 2 weeks |
| 43 | 87593 | 87593 | New* Missed from 2022 | Microbiology Infectious Disease | ID | CHIM | Infectious agent detection by nucleic acid (DNA or RNA); Orthopoxvirus (eg, monkeypox virus, cowpox virus, vaccinia virus), amplified probe technique, each |
| 44 | 0442U | 0442U | New (PLA) | Microbiology Infectious Disease | ID | CHIM | Infectious disease (respiratory infection), myxovirus resistance protein a (mxa) and c-reactive protein (crp), fingerstick whole blood specimen, each biomarker reported as present or absent |
| 45 | XX38U | 0457U | New (PLA) | Chemistry | ID | CHIM | Perfluoroalkyl substances (PFAS) (eg, perfluorooctanoic acid, perfluorooctane sulfonic acid), 9 PFAS compounds by LC-MS/MS, plasma or serum, quantitative |
| 46 | X104U | TBD | NEW | Therapeutic Drug Assay | ID | СНІМ | Therapeutic drug monitoring, medications specific to pain, depression, and anxiety, LC-MS/MS, plasma, 110 or more drugs or substances, qualitative and quantitative therapeutic minimally effective range of prescribed, non-prescribed, and illicit medications in circulation |
| 47 | XX31U | 0450U | New (PLA) | Chemistry | ID | CHIM | Oncology (multiple myeloma), liquid chromatography with tandem mass spectrometry (LCMS/MS), monoclonal paraprotein sequencing analysis, serum, results reported as baseline presence or absence of detectable clonotypic peptides |
| 48 | XX36U | 0455U | New (PLA) | Microbiology Infectious Disease | ID | CHIM | Infectious agents (sexually transmitted infection), Chlamydia trachomatis, Neisseria gonorrhoeae, and Trichomonas vaginalis, multiplex amplified probe technique, vaginal, endocervical, gynecological specimens, oropharyngeal swabs, rectal swabs, female or male urine, each pathogen reported as detected or not detected |
| 49 | XX66U | TBD | NEW | MAAA; Microbiology | ID | CHIM | Infectious disease (Neisseria gonorrhoeae), sensitivity, ciprofloxacin resistance (gyrA S91F point mutation), oral, rectal, or vaginal swab, algorithm reported as probability of fluoroquinolone resistance |
| 50 | XX43U | 0463U | New (PLA) | Microbiology Infectious Disease & Genome Sequencing Procedures; RT-PCR | ID | CHIM | Oncology (cervix), mRNA gene expression profiling of 14 biomarkers (E6 and E7 of the highest-risk human papillomavirus [HPV] types 16, 18, 31, 33, 45, 52, 58), by real-time nucleic acid sequence-based amplification (NASBA), exo- or endocervical epithelial cells, algorithm reported as positive or negative for increased risk of cervical dysplasia or cancer for each biomarker |
| 51 | 8X050 | TBD | NEW | Microbiology | ID GU | CHIM | Infectious agent detection by nucleic acid (DNA or RNA); Helicobacter pylori (H. pylori), clarithromycin resistance, amplified probe technique |
| 52 | XX52U | 0472U | New (PLA) | MAAA | ID GU | CHIM | Carbonic anhydrase VI (CA VI), parotid specific/secretory protein (PSP) and salivary protein (SP1) IgG, IgM, and IgA antibodies, |

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| Tem # | | | | | | | enzyme-linked immunosorbent assay (ELISA), semiqualitative, blood, reported as predictive evidence of early Sjögren syndrome |
| 53 | XX62U | TBD | NEW | Immunology | ID GU | CHIM | Tau, phosphorylated, pTau217 |
| 54 | XX72U | TBD | NEW | MAAA: Microbiology | ID GU | CHIM | Infectious disease (Mycoplasma genitalium), macrolide sensitivity (23S rRNA point mutation), oral, rectal, or vaginal swab, algorithm reported as probability of macrolide resistance |
| 55 | 0441U | 0441U | New (PLA) | Microbiology Infectious Disease | ID non-mol | СНІМ | Infectious disease (bacterial, fungal, or viral infection), semiquantitative biomechanical assessment (via deformability cytometry), whole blood, with algorithmic analysis and result reported as an index |
| 56 | XX40U | 0459U | New (PLA) | Immunology | ID non-mol | CHIM | β-amyloid (Abeta42) and total tau (tTau), electrochemiluminescent immunoassay (ECLIA), cerebral spinal fluid, ratio reported as positive or negative for amyloid pathology |
| 57 | 0420U | 0420U | New (PLA) | Genome Sequencing Procedures; RT-PCR | Oncology urothelial | СНІМ | Oncology (urothelial), mRNA expression profiling by real-time quantitative PCR of MDK, HOXA13, CDC2, IGFBP5, and CXCR2 in combination with droplet digital PCR ddPCR) analysis of 6 single-nucleotide polymorphisms (SNPs) genes TERT and FGFR3, urine, algorithm reported as a risk score for urothelial carcinoma |
| 58 | XX95U | TBD | NEW | Augmented analysis | AI | MoG | Oncology (prostate), augmentative algorithmic analysis of digitized whole-slide imaging of histologic features for microsatellite instability (MSI) status, formalin-fixed paraffin-embedded (FFPE) tissue, reported as increased or decreased probability of MSI-High (MSI-H) |
| 59 | XX96U | TBD | NEW | Augmented analysis | AI | MoG | Oncology (prostate), augmentative algorithmic analysis of digitized whole-slide imaging of histologic features for microsatellite instability (MSI) and homologous recombination deficiency (HRD) status, formalin-fixed paraffin-embedded (FFPE) tissue, reported as increased or decreased probability of each biomarker |
| 60 | 0439U | 0439U | New (PLA) | Genomic Sequencing Procedures; targeted sequence analysis | Cardiology | MoG | Cardiology (coronary heart disease [chd]), dna, analysis of 5 single-nucleotide polymorphisms (snps) (rs11716050 [loc105376934], rs6560711 [wdr37], rs3735222 [scin/loc107986769], rs6820447 [intergenic], and rs9638144 [esyt2]) and 3 dna methylation markers (cg00300879 [transcription start site {tss200} of cnksr1], cg09552548 [intergenic], and cg14789911 [body of spatc11]), qpcr and digital pcr, whole blood, algorithm reported as a 4-tiered risk score for a 3-year risk of symptomatic chd |
| 61 | 0440U | 0440U | New (PLA) | Genomic Sequencing Procedures; targeted sequence analysis | Cardiology | MoG | Cardiology (coronary heart disease [chd]), dna, analysis of 10 single-nucleotide polymorphisms (snps) (rs710987 [linc010019], rs1333048 [cdkn2b-as1], rs12129789 [kcnd3], rs942317 [ktn1-as1], rs1441433 [ppp3ca], rs2869675 [prex1], rs4639796 [zbtb41], rs4376434 [linc00972], rs12714414 [tmem18], and rs7585056 [tmem18]) and 6 dna methylation markers (cg03725309 [sars1], cg12586707 [cxcl1, cg04988978 [mpo], cg17901584 [dhcr24-dt], cg21161138 [ahrr], and cg12655112 [ehd4]), qpcr and digital pcr, whole blood, algorithm reported as detected or not detected for chd |

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|-------------------------|-------------------|--------------|--------------------|--|--------------|--------------|--|
| 62 | XX46U | 0466U | New (PLA) | Genomic Sequencing Procedures; targeted sequence analysis | Cardiology | MoG | Cardiology (coronary artery disease [CAD]), DNA, genomewide association studies (564856 single-nucleotide polymorphisms [SNPs], targeted variant genotyping), patient lifestyle and clinical data, buccal swab, algorithm reported as polygenic risk to acquired heart disease |
| 63 | XX73U | TBD | NEW | Genomic Sequencing Procedures | Cellsearch | MoG | Oncology (cutaneous or uveal melanoma), circulating tumor cell selection, morphological characterization and enumeration based on differential CD146, high molecular—weight melanoma-associated antigen, CD34 and CD45 protein biomarkers, peripheral blood |
| 64 | XX75U | TBD | NEW | Genomic Sequencing Procedures | Cellsearch | MoG | Oncology (solid tumor), circulating tumor cell selection, morphological characterization and enumeration based on differential epithelial cell adhesion molecule (EpCAM), cytokeratins 8, 18, and 19, CD45 protein biomarkers, and quantification of estrogen receptor (ER) protein biomarker–expressing cells, peripheral blood |
| 65 | XX74U | TBD | NEW | Genomic Sequencing Procedures | Cellsearch | MoG | Oncology (solid tumor), circulating tumor cell selection, morphological characterization and enumeration based on differential epithelial cell adhesion molecule (EpCAM), cytokeratins 8, 18, and 19, CD45 protein biomarkers, and quantification of PD-L1 protein biomarker–expressing cells, peripheral blood |
| 66 | 0355U | 0355U | Reconsidered (PLA) | Genomic Sequencing Procedures; targeted variant analysis | CKD | MoG | APOL1 (apolipoprotein L1) (eg, chronic kidney disease), risk variants (G1, G2) |
| 67 | XX83U | TBD | NEW | Genomic Sequencing Procedures | Hematology | MoG | Autoinflammatory disease (VEXAS syndrome), DNA, UBA1 gene mutations, targeted variant analysis (M41T, M41V, M41L, c.118-2A>C, c.118-1G>C, c.118-9 118-2del, S56F, S621C) |
| 68 | 0437U | 0437U | New (PLA) | Molecular Pathology | Psychiatry | MoG | Psychiatry (anxiety disorders), mRNA, gene expression profiling by RNA sequencing of 15 biomarkers, whole blood, algorithm reported as predictive risk score |
| 69 | XX37U | 0456U | New (PLA) | MAAA | Rheumatology | MoG | Autoimmune (rheumatoid arthritis), next-generation sequencing (NGS), gene expression testing of 19 genes, whole blood, with analysis of anticyclic citrullinated peptides (CCP) levels, combined with sex, patient global assessment, and body mass index (BMI), algorithm reported as a score that predicts nonresponse to tumor necrosis factor inhibitor (TNFi) therapy |
| 70 | 0428U | 0428U | New (PLA) | Genomic Sequencing Procedures; cell free DNA | Cf breast | MoG | Oncology (breast), targeted hybrid-capture genomic sequence analysis panel, circulating tumor DNA (ctDNA) analysis of 56 or more genes, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability, and tumor mutation burden |
| 71 | XX34U | 0453U | New (PLA) | Genomic Sequencing Procedures; cell free DNA & Genomic Sequencing Procedures; methylation analysis | Cf colon | MoG | Oncology (colorectal cancer), cellfree DNA (cfDNA), methylationbased quantitative PCR assay (SEPTIN9, IKZF1, BCAT1, Septin9-2, VAV3, BCAN), plasma, reported as presence or absence of circulating tumor DNA (ctDNA) |

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|-------------------------|-------------------|--------------|--------------|---|----------------|--------------|---|
| 72 | XX87U | TBD | NEW | Genomic Sequencing Procedures | Cf colon | MoG | Oncology (colorectal), cell-free DNA, 8 genes for mutations, 7 genes for methylation by real-time RT-PCR, and 4 proteins by enzymelinked immunosorbent assay, blood, reported positive or negative for colorectal cancer or advanced adenoma risk |
| 73 | XX80U | TBD | NEW | Genomic Sequencing Procedures | Cf colon | MoG | Oncology (colorectal), blood, quantitative measurement of cell-free DNA (cfDNA) |
| 74 | XX70U | TBD | NEW | Genomic Sequencing Procedures | Cf obstetrics | MoG | Obstetrics (fetal antigen noninvasive prenatal test), cell-free DNA sequence analysis for the detection of the fetal presence or absence of 1 or more of the Rh, C, c, D, E, Duffy (Fya), or Kell (K) antigen in alloimmunized pregnancies, reported as selected antigen(s) detected or not detected |
| 75 | XX76U | TBD | NEW | Genomic Sequencing Procedures | Cf obstetrics | MoG | Obstetrics (single-gene noninvasive prenatal test), cell-free DNA sequence analysis of 1 or more targets (eg, CFTR, SMN1, HBB, HBA1, HBA2) to identify paternally inherited pathogenic variants, and relative mutation-dosage analysis based on molecular counts to determine the fetal inheritance of the maternal mutation, algorithm reported as a fetal risk score for the condition (eg, cystic fibrosis, spinal muscular atrophy, beta hemoglobinopathies [including sickle cell disease], alpha thalassemia) |
| 76 | XX82U | TBD | NEW | Genomic Sequencing Procedures | Cf obstetrics | MoG | Red blood cell antigen (fetal RhD gene analysis), next-generation sequencing of circulating cell-free DNA (cfDNA) of blood in pregnant individuals known to be RhD negative, reported as positive or negative |
| 77 | XX50U | 0470U | New (PLA) | Genomic Sequencing Procedures; targeted sequence analysis | Cf oropharynx | MoG | Oncology (oropharyngeal), detection of minimal residual disease by next-generation sequencing (NGS) based quantitative evaluation of 8 DNA targets, cell-free HPV 16 and 18 DNA from plasma |
| 78 | 81462 | 81462 | Reconsidered | Genomic Sequencing Procedures; cell free DNA | Cf solid tumor | MoG | Solid organ neoplasm, genomic sequence analysis panel, cell-free nucleic acid (eg, plasma), interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants and rearrangements |
| 79 | 81464 | 81464 | Reconsidered | Genomic Sequencing Procedures; cell free DNA | Cf solid tumor | MoG | Solid organ neoplasm, genomic sequence analysis panel, cell-free nucleic acid (eg, plasma), interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants, microsatellite instability, tumor mutation burden, and rearrangements |
| 80 | 0422U | 0422U | New (PLA) | Genomic Sequencing Procedures; cell free DNA | Cf solid tumor | MoG | Oncology (pan-solid tumor), analysis of DNA biomarker response to anti-cancer therapy using cell-free circulating DNA, biomarker comparison to a previous baseline pre-treatment cell-free circulating DNA analysis using next-generation sequencing, algorithm reported as a quantitative change from baseline, including specific alterations, if appropriate |
| 81 | XX41U | 0460U | New (PLA) | Genomic Sequencing Procedures; targeted variant analysis | Cf solid tumor | MoG | Oncology, whole blood or buccal, DNA single-nucleotide polymorphism (SNP) genotyping by real-time PCR of 24 genes, with variant analysis and reported phenotypes |
| 82 | XX69U | TBD | NEW | Genomic Sequencing Procedures | Cf solid tumor | MoG | Oncology (solid tumor), cell-free DNA and RNA by next-generation sequencing, interpretative report for germline mutations, clonal hematopoiesis of indeterminate potential, and tumor-derived single- |

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| Tem # | | | | | | | nucleotide variants, small insertions/deletions, copy number alterations, fusions, microsatellite instability, and tumor mutational burden |
| 83 | XX77U | TBD | NEW | Genomic Sequencing Procedures | Cf solid tumor | MoG | Oncology (pan-solid tumor), next-generation sequencing analysis of tumor methylation markers present in cell-free circulating tumor DNA, algorithm reported as quantitative measurement of methylation as a correlate of tumor fraction |
| 84 | 8156X | TBD | New | Genome Sequencing Procedures; RT-PCR | Cf transplantation | MoG | Transplantation medicine (allograft rejection, kidney), mRNA, gene expression profiling by quantitative polymerase chain reaction (qPCR) of 139 genes, utilizing whole blood, algorithm reported as a binary categorization as transplant excellence, which indicates immune quiescence, or not transplant excellence, indicating subclinical rejection |
| 85 | XX78U | TBD | NEW | Genomic Sequencing Procedures | Cf transplantation | MoG | Transplantation medicine, quantification of donor-derived cell-free DNA using next-generation sequencing, plasma, reported as percentage of donor-derived cell-free DNA (cfDNA) |
| 86 | XX93U | TBD | NEW | Molecular Pathology | Cf transplantation | MoG | Transplantation medicine, quantification of donor-derived cell-free DNA using 40 single-nucleotide polymorphism (SNPs), plasma, and urine, initial evaluation reported as percentage of donor-derived cell-free DNA with risk for active rejection |
| 87 | XX94U | TBD | NEW | Molecular Pathology | Cf transplantation | MoG | Transplantation medicine, quantification of donor-derived cell-free DNA using up to 12 single-nucleotide polymorphism (SNPs) previously identified, plasma, reported as percentage of donor-derived cell-free DNA with risk for active rejection |
| 88 | 0425U | 0425U | New (PLA) | Genome Sequencing Procedures | Genomic sequencing | MoG | Genome (eg, unexplained constitutional or heritable disorder or syndrome), rapid sequence analysis, each comparator genome (eg, parents, siblings) |
| 89 | 0426U | 0426U | New (PLA) | Genome Sequencing Procedures | Genomic sequencing | MoG | Genome (eg, unexplained constitutional or heritable disorder or syndrome), ultra-rapid sequence analysis |
| 90 | 0449U | 0449U | New (PLA) | Genomic Sequencing Procedures; targeted sequence analysis | Genomic sequencing | MoG | Carrier screening for severe inherited conditions (eg, cystic fibrosis, spinal muscular atrophy, beta hemoglobinopathies [including sickle cell disease], alpha thalassemia), regardless of race or self-identified ancestry, genomic sequence analysis panel, must include analysis of 5 genes (cftr, smn1, hbb, hba1, hba2) |
| 91 | XX49U | 0469U | New (PLA) | Genome Sequencing Procedures | Genomic sequencing | MoG | Rare diseases (constitutional/heritable disorders), whole genome sequence analysis for chromosomal abnormalities, copy number variants, duplications/deletions, inversions, unbalanced translocations, regions of homozygosity (ROH), inheritance pattern that indicate uniparental disomy (UPD), and aneuploidy, fetal sample (amniotic fluid, chorionic villus sample, or products of conception), identification and categorization of genetic variants, diagnostic report of fetal results based on phenotype with maternal sample and paternal sample, if performed, as comparators and/or maternal cell contamination |

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| 92 | 0417U | 0417U | Reconsidered | Genomic Sequencing Procedures; mitochondrial | Genomic sequencing | MoG | Rare diseases (constitutional/heritable disorders), whole mitochondrial genome sequence with heteroplasmy detection and deletion analysis, nuclear-encoded mitochondrial gene analysis of 335 nuclear genes, including sequence changes, deletions, insertions, and copy number variants analysis, blood or saliva, identification and categorization of mitochondrial disorder-associated genetic variants |
| 93 | 0X00M | 0020M | New | Genomic Sequencing Procedures; methylation analysis | Oncology brain | MoG | Oncology (central nervous system), analysis of 30000 DNA methylation loci by methylation array, utilizing DNA extracted from tumor tissue, diagnostic algorithm reported as probability of matching a reference tumor subclass |
| 94 | XX67U | TBD | NEW | Genomic Sequencing Procedure | Oncology brain | MoG | Isocitrate dehydrogenase 1 (IDH1), isocitrate dehydrogenase 2 (IDH2), and telomerase reverse transcriptase (TERT) promoter (eg, central nervous system [CNS] tumors), next-generation sequencing (single-nucleotide variants [SNV], deletions, and insertions) |
| 95 | 0421U | 0421U | New (PLA) | Genome Sequencing Procedures; RT-PCR | Oncology colorectal | MoG | Oncology (colorectal) screening, quantitative real-time target and signal amplification of 8 RNA markers (GAPDH, SMAD4, ACY1, AREG, CDH1, KRAS, TNFRSF10B, GLN2) and fecal hemoglobin, algorithm reported as a positive or negative for colorectal cancer risk |
| 96 | XX44U | 0464U | New (PLA) | Genomic Sequencing Procedures; methylation analysis | Oncology colorectal | MoG | Oncology (colorectal) screening, quantitative real-time target and signal amplification, methylated DNA markers, including LASS4, LRRC4 and PPP2R5C, a reference marker ZDHHC1, and a protein marker (fecal hemoglobin), utilizing stool, algorithm reported as a positive or negative result |
| 97 | XX51U | 0471U | New (PLA) | Genomic Sequencing Procedures; targeted sequence analysis | Oncology colorectal | MoG | Oncology (colorectal cancer), qualitative real-time PCR of 35 variants of KRAS and NRAS genes (exons 2, 3, 4), formalinfixed paraffin-embedded (FFPE), predictive, identification of detected mutations |
| 98 | XX68U | TBD | NEW | Genomic Sequencing Procedures | Oncology colorectal | MoG | Oncology (colorectal), next-generation sequencing for mutation detection in 43 genes and methylation pattern in 45 genes, blood, and formalin-fixed paraffin-embedded (FFPE) tissue, report of variants and methylation pattern with interpretation |
| 99 | XX86U | TBD | NEW | Genomic Sequencing Procedures | Oncology colorectal | MoG | Oncology (colorectal and lung), DNA from formalin-fixed paraffin- embedded (FFPE) tissue, next-generation sequencing of 8 genes (NRAS, EGFR, CTNNB1, PIK3CA, APC, BRAF, KRAS, and TP53), mutation detection |
| 100 | XX90U | TBD | NEW | Genomic Sequencing Procedures | Oncology esophagus | MoG | Gastroenterology (Barrett's esophagus), esophageal cells, DNA methylation analysis by next-generation sequencing of at least 89 differentially methylated genomic regions, algorithm reported as likelihood for Barrett's esophagus |
| 101 | XX54U | 0475U | New (PLA) | Genomic Sequencing Procedures; targeted sequence analysis | Oncology hereditary | MoG | Hereditary prostate cancerrelated disorders, genomic sequence analysis panel using next-generation sequencing (NGS), Sanger sequencing, multiplex ligation-dependent probe amplification (MLPA), and array comparative genomic hybridization (CGH), evaluation of 23 genes and duplications/deletions when indicated, pathologic mutations reported with a genetic risk score for prostate cancer |

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| 102 | XX55U | 0474U | New (PLA) | Genomic Sequencing Procedures; targeted sequence analysis | Oncology hereditary | MoG | Hereditary pan-cancer (eg, hereditary sarcomas, hereditary endocrine tumors, hereditary neuroendocrine tumors, hereditary cutaneous melanoma), genomic sequence analysis panel of 88 genes with 20 duplications/deletions using nextgeneration sequencing (NGS), Sanger sequencing, blood or saliva, reported as positive or negative for germline variants, each gene |
| 103 | 81432 | TBD | REVISED | Genomic Sequencing Procedures | Oncology hereditary | MoG | Hereditary breast cancer-related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer, hereditary pancreatic cancer, hereditary prostate cancer);, genomic sequence analysis panel, 5 or more genes, interrogation for sequence variants and copy number variants must include sequencing of at least 10 genes, always including BRCA1, BRCA2, CDH1, MLH1, MSH2, MSH6, PALB2, PTEN, STK11, and TP53 |
| 104 | 81435 | TBD | REVISED | Genomic Sequencing Procedures | Oncology hereditary | MoG | Hereditary colon cancer <u>-related</u> disorders (eg, Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis); genomic sequence analysis panel, <u>5 or more genes</u> , interrogation for sequence variants and copy number <u>variants</u> must include sequencing of at least 10 genes, including APC, BMPR1A, CDH1, MLH1, MSH2, MSH6, MUTYH, PTEN, SMAD4, and STK11 |
| 105 | 81437 | TBD | REVISED | Genomic Sequencing Procedures | Oncology hereditary | MoG | Hereditary neuroendocrine tumor-related disorders (eg, medullary thyroid carcinoma, parathyroid carcinoma, malignant pheochromocytoma or paraganglioma); genomic sequence analysis panel, 5 or more genes, interrogation for sequence variants and copy number variants must include sequencing of at least 6 genes, including MAX, SDHB, SDHC, SDHD, TMEM127, and VHL |
| 106 | 0448U | 0448U | New (PLA) | Genomic Sequencing Procedures; targeted variant analysis | Oncology lung | MoG | Oncology (lung and colon cancer), dna, qualitative, nextgeneration sequencing detection of single-nucleotide variants and deletions in egfr and kras genes, formalin-fixed paraffinembedded (ffpe) solid tumor samples, reported as presence or absence of targeted mutation(s), with recommended therapeutic options |
| 107 | XX61U | TBD | NEW | Molecular Pathology | Oncology lung | MoG | Oncology (non-small cell lung cancer), DNA and RNA, digital PCR analysis of 9 genes (EGFR, KRAS, BRAF, ALK, ROS1, RET, NTRK 1/2/3, ERBB2, and MET) in formalin-fixed paraffinembedded (FFPE) tissue, interrogation for single nucleotide variants, insertions/deletions, gene rearrangements, and reported as actionable detected variants for therapy selection |
| 108 | XX91U | TBD | NEW | Genomic Sequencing Procedures | Oncology ovarian | MoG | Oncology (ovarian), DNA, whole-genome sequencing with 5-hydroxymethylcytosine (5hmC) enrichment, using whole blood or plasma, algorithm reported as cancer detected or not detected |
| 109 | XX92U | TBD | NEW | Augmented analysis | Oncology pancreas | MoG | Oncology (pancreatic cancer), augmentative algorithmic analysis of 16 genes from previously sequenced RNA whole-transcriptome data, reported as probability of predicted molecular subtype |
| 110 | 81457 | 81457 | Reconsidered | Genomic Sequencing Procedures | Oncology solid tumor | MoG | Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis, microsatellite instability |

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| 111 | 81458 | 81458 | Reconsidered | Genomic Sequencing Procedures | Oncology solid tumor | MoG | Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis, copy number variants and microsatellite instability |
| 112 | 81459 | 81459 | Reconsidered | Genomic Sequencing Procedures | Oncology solid tumor | MoG | Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants, microsatellite instability, tumor mutation burden, and rearrangements |
| 113 | 0444U | 0444U | New (PLA) | Genomic Sequencing Procedures; targeted variant analysis | Oncology solid tumor | MoG | Oncology (solid organ neoplasia), targeted genomic sequence analysis panel of 361 genes, interrogation for gene fusions, translocations, or other rearrangements, using dna from formalin-fixed paraffin-embedded (ffpe) tumor tissue, report of clinically significant variant(s) |
| 114 ** | XX53U** | 0473U** | New (PLA) | Genomic Sequencing Procedures; targeted sequence analysis | Oncology solid tumor | MoG | Oncology (solid tumor), next generation sequencing (NGS) of DNA from formalin-fixed paraffin embedded (FFPE) tissue with comparative sequence analysis from a matched normal specimen (blood or saliva), 648 genes, interrogation for sequence variants, insertion and deletion alterations, copy number variants, rearrangements, microsatellite instability, and tumor-mutation burden |
| 115 | XX71U | TBD | NEW | Genomic Sequencing Procedures | Oncology solid tumor | MoG | Oncology (solid tumor), cell-free circulating DNA, targeted genomic sequence analysis panel of 84 genes, interrogation for sequence variants, aneuploidy-corrected gene copy number amplifications and losses, gene rearrangements, and microsatellite instability |
| 116 | 0424U | 0424U | New (PLA) | Genome Sequencing Procedures; RT-PCR | Oncology urothelial | MoG | Oncology (prostate), exosome-based analysis of 53 small noncoding RNAs (sncRNAs) by quantitative reverse transcription polymerase chain reaction (RTqPCR), urine, reported as no molecular evidence, low-, moderate- or elevated-risk of prostate cancer |
| 117 | 0433U | 0433U | New (PLA) | Genome Sequencing Procedures; RT-PCR | Oncology urothelial | MoG | Oncology (prostate), 5 DNA regulatory markers by quantitative PCR, whole blood, algorithm, including prostate-specific antigen, reported as likelihood of cancer |
| 118 | XX33U | 0452U | New (PLA) | Genomic Sequencing Procedures; methylation analysis | Oncology urothelial | MoG | Oncology (bladder), methylated PENK DNA detection by linear target enrichment-quantitative methylation-specific real-time PCR (LTE-qMSP), urine, reported as likelihood of bladder cancer |
| 119 | XX45U | 0465U | New (PLA) | Genomic Sequencing Procedures; methylation analysis | Oncology urothelial | MoG | Oncology (urothelial carcinoma), DNA, quantitative methylation specific PCR of 2 genes (ONECUT2, VIM), algorithmic analysis reported as positive or negative |
| 120 | XX47U | 0467U | New (PLA) | Genomic Sequencing Procedures; targeted sequence analysis | Oncology urothelial | MoG | Oncology (bladder), DNA, next generation sequencing (NGS) of 60 genes and whole genome aneuploidy, urine, algorithms reported as minimal residual disease (MRD) status positive or negative and quantitative disease burden |
| 121 | XX79U | TBD | NEW | Genomic Sequencing Procedures | Oncology urothelial | MoG | Oncology (prostate), analysis of circulating plasma proteins (tPSA, fPSA, KLK2, PSP94, and GDF15), germline polygenic risk score (60 variants), clinical information (age, family history of prostate cancer, prior negative prostate biopsy), algorithm reported as risk of likelihood of detecting clinically significant prostate cancer |
| 122 | XX81U | TBD | NEW | Genomic Sequencing Procedures | Oncology urothelial | MoG | Oncology (prostate), mRNA gene-expression profiling by real-time RT-PCR of 6 genes (FOXM1, MCM3, MTUS1, TTC21B, ALAS1, |

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| | | | | | | | and PPP2CA), utilizing formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reported as a risk score for prostate cancer |
| 123 | 88XX0 | TBD | NEW | Molecular Pathology; Optical Genome Mapping | Optical genome | MoG | Cytogenomic genome-wide analysis, hematologic malignancy, structural variations and copy number variations, optical genome mapping (OGM) |
| 124 | 0413U | 0413U | Reconsidered | Genomic Sequencing Procedures; optical genome mapping | Optical genome | MoG | Oncology (hematolymphoid neoplasm), optical genome mapping for copy number alterations, aneuploidy, and balanced/complex structural rearrangements, dna from blood or bone marrow, report of clinically significant alterations |
| 125 | XX35U | 0454U | New (PLA) | Genome Sequencing Procedures; dup/del analysis | Optical genome | MoG | Rare diseases (constitutional/heritable disorders), identification of copy number variations, inversions, insertions, translocations, and other structural variants by optical genome mapping |
| 126 | 0423U | 0423U | New (PLA) | Genomic Sequencing Procedures; targeted variant analysis | Pharmacogenetics | MoG | Psychiatry (eg, depression, anxiety), genomic analysis panel, including variant analysis of 26 genes, buccal swab, report including metabolizer status and risk of drug toxicity by condition |
| 127 | 0434U | 0434U | New (PLA) | Genomic Sequencing Procedures; targeted variant analysis | Pharmacogenetics | MoG | Drug metabolism (adverse drug reactions and drug response), genomic analysis panel, variant analysis of 25 genes with reported phenotypes |
| 128 | 0438U | 0438U | New (PLA) | Genomic Sequencing Procedures; targeted sequence analysis | Pharmacogenetics | MoG | Drug metabolism (adverse drug reactions and drug response), buccal specimen, gene-drug interactions, variant analysis of 33 genes, including deletion/duplication analysis of CYP2D6, including reported phenotypes and impacted gene drug interactions |
| 129 | XX30U | 0461U | New (PLA) | Genomic Sequencing Procedures; targeted sequence analysis | Pharmacogenetics | MoG | Oncology, pharmacogenomic analysis of single-nucleotide polymorphism (SNP) genotyping by real-time PCR of 24 genes, whole blood or buccal swab, with variant analysis, including impacted gene-drug interactions and reported phenotypes |
| 130 | XX64U | TBD | NEW | Molecular Pathology, Pharmacogenomics | Pharmacogenetics | MoG | Drug metabolism, psychiatry (eg, major depressive disorder, general anxiety disorder, attention deficit hyperactivity disorder [ADHD], schizophrenia), whole blood, buccal swab, pharmacogenomic genotyping of 14 genes and CYP2D6 copy number variant analysis, and reported phenotypes |
| 131 | XX60U | TBD | NEW | Molecular Pathology, Pharmacogenomics | Pharmacogenetics | MoG | Drug metabolism, psychiatry (eg, major depressive disorder, general anxiety disorder, attention deficit hyperactivity disorder [ADHD], schizophrenia), whole blood, buccal swab, pharmacogenomic genotyping of 14 genes and CYP2D6 copy number variant analysis, including impacted gene-drug interactions and reported phenotypes |
| 132 | X100U | TBD | NEW | Immunology | Pharmacogenetics | MoG | Drug metabolism, whole blood, pharmacogenomic genotyping of 40 genes and CYP2D6 copy number variant analysis, reported as metabolizer status |