The document reflects voting results from the Medicare Advisory Panel on Clincal Laboratory Test Meeting that occurred on July 28-29, 2021. For more information on the CDLT Panel, please refer to the following CMS webpage: https://www.cms.gov/Regulations-and-Guidance/Guidance/FACA/AdvisoryPanelonClinicalDiagnosticLaboratoryTests.



| Code: Long Descriptor | Option | Votes | Option | Votes | Option | Votes | Option | Votes | Option | Votes | Total Votes Received |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 0226U: Surrogate viral neutralization test (sVNT), severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]), ELISA, plasma, serum | Crosswalk: 86769 | 12 | Gapfill | | Abstain | | | | | | 12 |
| 86413: Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]) antibody,quantitative | Crosswalk: 86769 x 1.25 | 3 | 86794 x 3.125 | | 86769 x 2 | 8 | Gapfill | | Abstain | 1 | 12 |
| 863X4: Mitochondrial antibody (eg, M2), each | 86146 | 12 | Gapfill | | Abstain | | | | | | 12 |
| 865X0: Voltage-gated calcium channel antibody, each | 84586 | 12 | Gapfill | | Abstain | | | | | | 12 |
| 86XX0: Actin (smooth muscle) antibody (ASMA), each | 86146 | 2 | 83516 | 10 | Gapfill | | Abstain | | | | 12 |
| 86X00: Antineutrophil cytoplasmic antibody (ANCA); screen, each antibody | 86146 | 2 | 86255 | 10 | Gapfill | | Abstain | | | | 12 |
| 86X01: Antineutrophil cytoplasmic antibody (ANCA); titer, each antibody | 86146 | | 86256 | 12 | Gapfill | | Abstain | | | | 12 |
| 0X65U: Hematology (heparin-induced thrombocytopenia) platelet antibody reactivity by flow cytometry, serum | Gapfill | 12 | Abstain | | | | | | | | 12 |
| 0X66U: Hematology (von Willebrand disease [VWD]), von Willebrand factor (VWF) and collagen IV binding by enzyme-linked immunosorbent assays (ELISA), plasma, report of collagen IV binding | 83520 | 11 | Gapfill | | Abstain | 1 | | | | | 12 |
| 0X67U: Hematology (von Willebrand disease [VWD]), von Willebrand propeptide, enzyme-linked immunosorbent assays (ELISA), plasma, diagnostic report of von Willebrand factor (VWF) propeptide antigen level | 83520 | 6 | Gapfill | | Abstain | 1 | Crosswalk: 85246 | 5 | | | 12 |
| 0X68U: von Willebrand factor (VWF), type 2B, platelet-binding evaluation, radioimmunoassay, plasma | 83519 | 11 | Gapfill | | Abstain | 1 | | | | | 12 |
| 0X69U: von Willebrand factor (VWD), type 2N, factor VIII and VWF binding evaluation, enzyme-linked immunosorbent assays (ELISA), plasma | 83520 | 1 | Gapfill | | Abstain | 1 | Crosswalk: 85246 x 1.5 | 4 | Crosswalk: 85246 x 2.0 | 6 | 12 |
| 860XX: Aquaporin-4 (neuromyelitis optica [NMO]) antibody; enzyme-linked immunosorbent immunoassay (ELISA) | 86146 | 11 | Gapfill | | Abstain | 1 | | | | | 12 |
| 860X1: Aquaporin-4 (neuromyelitis optica [NMO]) antibody; cell-based immunofluorescence assay (CBA), each | 86341 | 11 | Gapfill | | Abstain | 1 | | | | | 12 |
| 860X2: Aquaporin-4 (neuromyelitis optica [NMO]) antibody; flow cytometry (ie, fluorescence-activated cell sorting [FACS]), each | 86367 | 11 | Gapfill | | Abstain | 1 | | | | | 12 |
| 863X2: Myelin oligodendrocyte glycoprotein (MOG-IgG1) antibody; cell-based immunofluorescence assay (CBA), each | 86357 | 11 | Gapfill | | Abstain | 1 | | | | | 12 |

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| 863X3: Myelin oligodendrocyte glycoprotein (MOG-IgG1) antibody; flow cytometry (ie, fluorescence-activated cell sorting [FACS]), each | 86367 | 11 | Gapfill | | Abstain | 1 | | | | | 12 |
| 862X0: Endomysial antibody (EMA), each immunoglobulin (Ig) class | 86038 | 5 | 86038 x 2 | 6 | Gapfill | | Abstain | 1 | | | 12 |
| 862XX: Gliadin (deamidated) (DGP) antibody, each immunoglobulin (Ig) class | 86147 | 11 | Gapfill | | Abstain | 1 | | | | | 12 |
| 862X1: Tissue transglutaminase, each immunoglobulin (Ig) class | 86147 | 11 | Gapfill | | Abstain | 1 | | | | | 12 |
| 0X85U: Hematology (von Willebrand disease [VWD]), von Willebrand factor (VWF) and collagen III binding by enzyme-linked immunosorbent assays (ELISA), plasma, report of collagen III binding | 83520 | 4 | 85246 | 7 | Gapfill | | Abstain | 1 | | | 12 |
| 86408: Neutralizing antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]); screen | 86769 | 1 | 86794 x 2.5 | | Gapfill | 11 | Abstain | | | | 12 |
| 86409: Neutralizing antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]); titer | 86769 x 3 | | 86352 | | Gapfill | 12 | Abstain | | | | 12 |
| 87426: Infectious agent antigen detection by immunoassay technique, (eg, enzyme immunoassay [EIA], enzyme-linked immunosorbent assay [ELISA], immunochemiluminometric assay [IMCA]) qualitative or semiquantitative, multiple-step method; severe acute respiratory syndrome coronavirus (eg, SARS-CoV, SARS-CoV-2 [COVID-19]) | 87430 x 2.5 | 1 | 87430 x 2 | 11 | Gapfill | | Abstain | | | | 12 |
| 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 | 87633 | 12 | Gapfill | | Abstain | | | | | | 12 |
| 0224U: Antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]), includes titer(s), when performed | 86769 | 11 | Gapfill | | Abstain | 1 | | | | | 12 |
| 0240U: Infectious disease (viral respiratory tract infection), pathogen-specific RNA, 3 targets (severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2], influenza A, influenza B), upper respiratory specimen, each pathogen reported as detected or not detected | 87631 | 11 | Gapfill | | Abstain | 1 | | | | | 12 |
| 0241U: Infectious disease (viral respiratory tract infection), pathogen-specific RNA, 4 targets (severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2], influenza A, influenza B, respiratory syncytial virus [RSV]), upper respiratory specimen, each pathogen reported as detected or not detected | 87631 | 11 | Gapfill | | Abstain | 1 | | | | | 12 |
| 87636: Infectious agent detection by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]) and influenza virus types A and B, multiplex amplified probe technique | 87631 | 11 | Gapfill | | Abstain | 1 | | | | | 12 |

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| 87637: Infectious agent detection by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]), influenza virus types A and B, and respiratory syncytial virus, multiplex amplified probe technique | 87631 | 11 | Gapfill | | Abstain | 1 | | | | | 12 |
| 87811: Infectious agent antigen detection by immunoassay with direct optical (ie, visual) observation; Streptococcus, group B severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)<br>(Coronavirus disease [COVID-19]) | 87804 x 2.5 | 1 | 87804 x 2 | 11 | Gapfill | | Abstain | | | | 12 |
| 8715X: Culture, typing; identification of blood pathogen and resistance typing, when performed, by nucleic acid (DNA or RNA) probe, multiplexed amplified probe technique including multiplex reverse transcription, when performed, per culture or isolate, 6 or more targets | 87632 | | 87506 | 11 | Gapfill | 1 | Abstain | | | | 12 |
| 87428: Infectious agent antigen detection by immunoassay technique, (eg, enzyme immunoassay [EIA], enzyme-linked immunosorbent assay [ELISA], fluorescence immunoassay [FIA], immunochemiluminometric assay [IMCA]) qualitative or semiquantitative; severe acute respiratory syndrome coronavirus (eg, SARS-CoV, SARS-CoV-2 [COVID-19]) and influenza virus types A and B | 87430 x2.5 + 87400 x 2 | 2 | 87430 x 2 + 87400 x 2 | 10 | Gapfill | | Abstain | | | | 12 |
| 0227U: Drug assay, presumptive, 30 or more drugs or metabolites, urine, liquid chromatography with tandem mass spectrometry (LC-MS/MS) using multiple reaction monitoring (MRM), with drug or metabolite description, includes sample validation | 80307 | 12 | Gapfill | | Abstain | | | | | | 12 |
| 81338: MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; common variants (eg, W515A, W515K, W515L, W515R) | 81120 | 12 | 81402 | | Gapfill | | Abstain | | | | 12 |
| 81339: MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; sequence analysis, exon 10 | 81310 | 12 | 81403 | | Gapfill | | Abstain | | | | 12 |
| 801XX: Hydroxychloroquine | 80204 | 12 | Gapfill | | Abstain | | | | | | 12 |
| 0248U: Oncology (brain), spheroid cell culture in a 3D microenvironment, 12 drug panel, tumor-response prediction for each drug | Gapfill | 12 | Abstain | | | | | | | | 12 |
| 80151: Amiodarone | 80155 | 12 | 80299 | | Gapfill | | Abstain | | | | 12 |
| 80161: Carbamazepine; 10,11-epoxide | 80155 | 12 | 80299 | | Gapfill | | Abstain | | | | 12 |
| 80167: Felbamate | 80199 | 12 | 80299 | | Gapfill | | Abstain | | | | 12 |
| 80181: Flecainide | 80193 | 2 | 80155 | 10 | 80299 | | Gapfill | | Abstain | | 12 |
| 81279: JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) targeted sequence analysis (eg, exons 12 and 13) | 81272<br>- last year's xwalk | 11 | 81403 | 1 | Gapfill | | Abstain | | | | 12 |

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| 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 | 87633 | 12 | Gapfill | | Abstain | | | | | | 12 |
| 0228U: Oncology (prostate), multianalyte molecular profile by photometric detection of macromolecules adsorbed on nanosponge array slides with machine learning, utilizing first morning voided urine, algorithm reported as likelihood of prostate cancer | Gapfill | 11 | Abstain | | | | | | | | 11 |
| 815X0: Transplantation medicine (allograft rejection, pediatric liver and small bowel), measurement of donor and third-party-induced CD154+T-cytotoxic memory cells, utilizing whole peripheral blood, algorithm reported as a rejection risk score | Gapfill | 11 | Abstain | | | | | | | | 11 |
| 815X1: Oncology (breast), mRNA, next-generation sequencing gene expression profiling of 70 content genes and 31 housekeeping genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as index related to risk to distant metastasis | 81521 | 11 | Gapfill | | Abstain | | | | | | 11 |
| 0017M: Oncology (diffuse large B-cell lymphoma [DLBCL]), mRNA, gene expression profiling by fluorescent probe hybridization of 20 genes, formalin-fixed paraffin-embedded tissue, algorithm reported as cell of origin | 0120U | 11 | Gapfill | | Abstain | | | | | | 11 |
| 0243U: Obstetrics (preeclampsia), biochemical assay of placental-growth factor, time-resolved fluorescence immunoassay, maternal serum, predictive algorithm reported as a risk score for preeclampsia | 82731 | 11 | Gapfill | | Abstain | | | | | | 11 |
| 002XM: Transplantation medicine (allograft rejection, renal), measurement of donor and third-party-induced CD154+T-cytotoxic memory cells, utilizing whole peripheral blood, algorithm reported as a rejection risk score | Gapfill | 11 | Abstain | | | | | | | | 11 |
| 0X56U: Andrology (infertility), sperm-capacitation assessment of ganglioside GM1 distribution patterns, fluorescence microscopy, fresh or frozen specimen, reported as percentage of capacitated sperm and probability of generating a pregnancy score | Gapfill | 11 | Abstain | | | | | | | | 11 |
| 0X59U: Autoimmune (psoriasis), mRNA, next-generation sequencing, gene expression profiling of 50-100 genes, skin-surface collection using adhesive patch, algorithm reported as likelihood of response to psoriasis biologics | 0019U | 6 | Gapfill | 5 | Abstain | | | | | | 11 |
| 0245U: Oncology (thyroid), mutation analysis of 10 genes and 37 RNA fusions and expression of 4 mRNA markers using next-generation sequencing, fine needle aspirate, report includes associated risk of malignancy expressed as a percentage | 81455 | 9 | Gapfill | 2 | Abstain | | | | | | 11 |

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| 0247U: Obstetrics (preterm birth), insulin-like growth factor–binding protein 4 (IBP4), sex hormone– binding globulin (SHBG), quantitative measurement by LC-MS/MS, utilizing maternal serum, combined with clinical data, reported as predictive-risk stratification for spontaneous preterm birth | 0080U X 0.2 | 10 | Gapfill | 1 | Abstain | | | | | | 11 |
| 0252U: Fetal aneuploidy short tandem–repeat comparative analysis, fetal DNA from products of conception, reported as normal (euploidy), monosomy, trisomy, or partial deletion/duplications, mosaicism, and segmental aneuploidy | 0168U | | Gapfill | 11 | Abstain | | | | | | 11 |
| 0249U: Oncology (breast), semiquantitative analysis of 32 phosphoproteins and protein analytes, includes laser capture microdissection, with algorithmic analysis and interpretative report | 0037U | 2 | Gapfill | 9 | Abstain | | | | | | 11 |
| 0253U: Reproductive medicine (endometrial receptivity analysis), RNA gene expression profile, 238 genes by next-generation sequencing, endometrial tissue, predictive algorithm reported as endometrial window of implantation (eg, pre-receptive, receptive, post-receptive) | Gapfill | 11 | Abstain | | | | | | | | 11 |
| 0254U: Reproductive medicine (preimplantation genetic assessment), analysis of 24 chromosomes using embryonic DNA genomic sequence analysis for aneuploidy, and a mitochondrial DNA score in euploid embryos, results reported as normal (euploidy), monosomy, trisomy, or partial deletion/duplications, mosaicism, and segmental aneuploidy, per embryo tested | Gapfill | 11 | Abstain | | | | | | | | 11 |
| 0X71U: Oncology (solid tumor), gene expression profiling by real-time RT-PCR of 7 gene pathways (ER, AR, PI3K, MAPK, HH, TGFB, Notch), formalin-fixed paraffin-embedded (FFPE), algorithm reported as gene pathway activity score | 0011M | 8 | Gapfill | 3 | Abstain | | | | | | 11 |
| 0X70U: Oncology (colorectal cancer), image analysis with artificial intelligence assessment of 4 histologic and immunohistochemical features (CD3 and CD8 within tumor-stroma border and tumor core), tissue, reported as immune response and recurrence-risk score | 0108U | 3 | 0108U x 1.2 | 4 | Gapfill | 3 | Abstain | 1 | | | 11 |
| 826X0: Elastase, pancreatic (EL-1), fecal; quantitative | 82715 | 10 | Gapfill | | Abstain | | | | | | 10 |
| 0X57U: Trimethylamine/trimethylamine N-oxide (TMA/TMAO) profile, tandem mass spectrometry (MS/MS), urine, with algorithmic analysis and interpretive report | Gapfill | 11 | Abstain | | | | | | | | 11 |
| 0X58U: Very long chain acyl- coenzyme A (CoA) dehydrogenase (VLCAD), leukocyte enzyme activity, whole blood | Gapfill | 11 | Abstain | | | | | | | | 11 |

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| 0X60U: Nephrology (chronic kidney disease), nuclear magnetic resonance spectroscopy measurement of myo-inositol, valine, and creatinine, algorithmically combined with cystatin C (by immunoassay) and demographic data to determine estimated glomerular filtration rate (GFR), serum, quantitative | (83704 x2) + (82610) | 2 | 83704 + 82610 | 6 | Gapfill | 1 | Abstain | | | | 9 |
| 0251U: Hepcidin-25, enzyme-linked immunosorbent assay (ELISA), serum or plasma | 83520 | 11 | Gapfill | | Abstain | | | | | | 11 |
| 835X1: Interleukin-6 (IL-6) | 83006 | 10 | Gapfill | | Abstain | 1 | | | | | 11 |
| 8352X: Immunoglobulin light chains (ie, kappa, lambda), free, each | 83520 | 11 | Gapfill | | Abstain | | | | | | 11 |
| 0X77U: Neurology (autism spectrum disorder [ASD]), quantitative measurements of 16 central carbon metabolites (ie, ?-ketoglutarate, alanine, lactate, phenylalanine, pyruvate, succinate, carnitine, citrate, fumarate, hypoxanthine, inosine, malate, S-sulfocysteine, taurine, urate, and xanthine), liquid chromatography tandem mass spectrometry (LC-MS/MS), plasma, algorithmic analysis with result reported as negative or positive (with metabolic subtypes of ASD) | 0063U | 10 | Gapfill | | Abstain | | | | | | 10 |
| 0229U: BCAT1 (Branched chain amino acid transaminase 1) or IKZF1 (IKAROS family zinc finger 1) (eg, colorectal cancer) promoter methylation analysis | 81327 x 2 | 9 | Gapfill | | Abstain | | | | | | 9 |
| 0230U: AR (androgen receptor) (eg, spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation), full sequence analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, short tandem repeat (STR) expansions, mobile element insertions, and variants in non-uniquely mappable regions | 81173 + 81204 | 9 | Gapfill | | Abstain | | | | | | 9 |
| 0231U: CACNA1A (calcium voltage-gated channel subunit alpha 1A) (eg, spinocerebellar ataxia), full gene analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, short tandem repeat (STR) gene expansions, mobile element insertions, and variants in non-uniquely mappable regions | 81184 + 81185 | 9 | Gapfill | | Abstain | | | | | | 9 |
| 0232U: CSTB (cystatin B) (eg, progressive myoclonic epilepsy type 1A, Unverricht-Lundborg disease), full gene analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, short tandem repeat (STR) expansions, mobile element insertions, and variants in non-uniquely mappable regions | 81188 + 81189 | 9 | Gapfill | | Abstain | | | | | | 9 |
| 0233U: FXN (frataxin) (eg, Friedreich ataxia), gene analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, short tandem repeat (STR) expansions, mobile element insertions, and variants in non-uniquely mappable regions | 81285 + 81286 | 9 | Gapfill | | Abstain | | | | | | 9 |

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| 0234U: MECP2 (methyl CpG binding protein 2) (eg, Rett syndrome), full gene analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non-uniquely mappable regions | 81302 + 81304 | 9 | Gapfill | | Abstain | | | | | | 9 |
| 0235U: PTEN (phosphatase and tensin homolog) (eg, Cowden syndrome, PTEN hamartoma tumor syndrome), full gene analysis, including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non-uniquely mappable regions | 81321 + 81323 | 9 | Gapfill | | Abstain | | | | | | 9 |
| 0236U: SMN1 (survival of motor neuron 1, telomeric) and SMN2 (survival of motor neuron 2, centromeric) (eg, spinal muscular atrophy) full gene analysis, including small sequence changes in exonic and intronic regions, duplications and deletions, and mobile element insertions | 81329 + 81337 | 9 | Gapfill | | Abstain | | | | | | 9 |
| 0237U: Cardiac ion channelopathies (eg, Brugada syndrome, long QT syndrome, short QT syndrome, catecholaminergic polymorphic ventricular tachycardia), genomic sequence analysis panel including ANK2, CASQ2, CAV3, KCNE1, KCNE2, KCNH2, KCNJ2, KCNQ1, RYR2, and SCN5A, including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non-uniquely mappable regions | 81413 + 81414 | 9 | Gapfill | | Abstain | | | | | | 9 |
| 0238U: Oncology (Lynch syndrome), genomic DNA sequence analysis of MLH1, MSH2, MSH6, PMS2, and EPCAM, including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non-uniquely mappable regions | 81435 + 81436 | 9 | Gapfill | | Abstain | | | | | | 9 |
| 0239U: Targeted genomic sequence analysis panel, solid organ neoplasm, cell-free DNA, analysis of 311 or more genes, interrogation for sequence variants, including substitutions, insertions, deletions, select rearrangements, and copy number variations | 81455 | 5 | Gapfill | 6 | Abstain | | | | | | 11 |
| 0X62U: Rare constitutional and other heritable disorders, whole- genome and mitochondrial DNA sequence analysis, blood, frozen and formalin-fixed paraffin-embedded (FFPE) tissue, saliva, buccal swabs or cell lines, identification of single nucleotide and copy number variants | 81425+81460 | 5 | Gapfill | 4 | Abstain | | | | | | 9 |
| 0250U: Oncology (solid organ neoplasm), targeted genomic sequence DNA analysis of 505 genes, interrogation for somatic alterations (SNVs [single nucleotide variant], small insertions and deletions, one amplification, and four translocations), microsatellite instability and tumor-mutation burden | 81455 | 11 | Gapfill | | Abstain | | | | | | 11 |

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| 0X63U: Unexplained constitutional or other heritable disorders or syndromes, tissue-specific gene expression by whole-transcriptome and next-generation sequencing, blood, formalin-fixed paraffin-embedded (FFPE) tissue or fresh frozen tissue, reported as presence or absence of splicing or expression changes | 81425 | 1 | Gapfill | 1 | Abstain | | 81415 | 6 | | | 8 |
| 0X64U: Rare constitutional and other heritable disorders, identification of copy number variations, inversions, insertions, translocations, and other structural variants by optical genome mapping and whole-genome sequencing | 81425 + 81229 | 7 | Gapfill | 1 | Abstain | | | | | | 8 |
| 0X73U: Hematology (atypical hemolytic uremic syndrome [aHUS]), genomic sequence analysis of 15 genes, blood, buccal swab, or amniotic fluid | 81432 | 5 | Gapfill | | Abstain | | 81443 | 5 | | | 10 |
| 0X74U: Hematology (autosomal dominant congenital thrombocytopenia), genomic sequence analysis of 14 genes, blood, buccal swab, or amniotic fluid | 81432 + 81433 | 2 | 81432 | | Gapfill | | Abstain | | 81443 | 8 | 10 |
| 0X75U: Hematology (congenital coagulation disorders), genomic sequence analysis of 20 genes, blood, buccal swab, or amniotic fluid | 81432 + 81433 | | 81432 | 2 | Gapfill | | Abstain | | 81443 | 8 | 10 |
| 0X76U: Hematology (genetic bleeding disorders), genomic sequence analysis of 51 genes, blood, buccal swab, or amniotic fluid, comprehensive | 81443 | | Gapfill | | Abstain | | 81430 | 10 | | | 10 |
| 0X78U: Hematology (genetic platelet disorders), genomic sequence analysis of 43 genes, blood, buccal swab, or amniotic fluid | 81443 | 2 | Gapfill | | Abstain | | 81430 | 7 | | | 9 |
| 0X79U: Hematology (congenital neutropenia), genomic sequence analysis of 23 genes, blood, buccal swab, or amniotic fluid | 81443 | 8 | Gapfill | 1 | Abstain | | | | | | 9 |
| 0X80U: Hematology (genetic hyperfibrinolysis, delayed bleeding), genomic sequence analysis of 8 genes (F13A1, F13B, FGA, FGB, FGG, SERPINA1, SERPINE1, SERPINF2, PLAU) blood, buccal swab, or amniotic fluid | 81443 | 4 | Gapfill | | Abstain | | 81432 | 6 | | | 10 |
| 0X81U: Hematology (inherited thrombocytopenia), genomic sequence analysis of 23 genes, blood, buccal swab, or amniotic fluid | 81443 | 9 | Gapfill | 1 | Abstain | | | | | | 10 |
| 0X82U: Hematology (genetic platelet function disorder), genomic sequence analysis of 31 genes, blood, buccal swab, or amniotic fluid | 81443 | 3 | Gapfill | | Abstain | | 81430 | 7 | | | 10 |
| 0X83U: Hematology (genetic thrombosis), genomic sequence analysis of 12 genes, blood, buccal swab, or amniotic fluid | 81443 | 9 | Gapfill | 1 | Abstain | | | | | | 10 |
| 0X84U: Red blood cell antigen typing, DNA, genotyping of 12 blood group system genes to predict 44 red blood cell antigen phenotypes | 0001U | 10 | Gapfill | | Abstain | | | | | | 10 |
| 0X61U: Rare diseases (constitutional/heritable disorders), identification of copy number variations, inversions, insertions, translocations, and other structural variants by optical genome mapping | Gapfill | 1 | Abstain | 1 | 81229 | 9 | | | | | 11 |

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| 0244U: Oncology (solid organ), DNA, comprehensive genomic profiling, 257 genes, interrogation for single-nucleotide variants, insertions/deletions, copy number alterations, gene rearrangements, tumor-mutational burden and microsatellite instability, utilizing formalin-fixed paraffin-embedded tumor tissue | 0037U | 8 | Gapfill | 1 | Abstain | | | | | | 9 |
| 0246U: Red blood cell antigen typing, DNA, genotyping of at least 16 blood groups with phenotype prediction of at least 51 red blood cell antigens | 0001U | 10 | Gapfill | | Abstain | | | | | | 10 |
| 0X72U: Rare diseases (constitutional/heritable disorders), identification of copy number variations, inversions, insertions, translocations, and other structural variants by optical genome mapping | 81229 | 9 | Gapfill | 1 | Abstain | 1 | | | | | 11 |
| 812X0: Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and loss-of-heterozygosity variants, low-pass sequencing analysis | 81277 | 4 | 81229 | 6 | Gapfill | | Abstain | | | | 10 |
| G0327: Colorectal cancer screening; blood-based biomarker Colon ca scrn;bld-bsd biomrk | Gapfill | | Abstain | | | | | | | | No Vote occurred |