FACA Mtg. Item #	ALM Item #	Code #	Code Type	Category	Code Subcategory	Long Code Descriptor	Panel Recommendation
1	26	0377U	PLA	Chemistry	Chemistry	Cardiovascular disease, quantification of advanced serum or plasma lipoprotein profile, by nuclear magnetic resonance (NMR) spectrometry with report of a lipoprotein profile (including 23 variables)	Crosswalk to 83704 + 80061: 9 2. Crosswalk to (83704 X 2) + 80061: 0
2	30	0381U	PLA	Chemistry	Chemistry	Maple syrup urine disease monitoring by patient-collected blood card sample, quantitative measurement of alloisoleucine, leucine, isoleucine, and valine, liquid chromatography with tandem mass spectrometry (LCMS/MS)	1. Gapfill: 8 2.Abstain: 1
3	31	0382U	PLA	Chemistry	Chemistry	Hyperphenylalaninemia monitoring by patient-collected blood card sample, quantitative measurement of phenylalanine and tyrosine, liquid chromatography with tandem mass spectrometry (LC-MS/MS)	1. Gapfill: 8 2. Abstain: 1
4	32	0383U	PLA	Chemistry	Chemistry	Tyrosinemia type I monitoring by patient-collected blood card sample, quantitative measurement of tyrosine, phenylalanine, methionine, succinylacetone, nitisinone, liquid chromatography with tandem mass spectrometry (LC-MS/MS)	1. Gapfill: 8 2.Abstain: 1
5	47	0394U	PLA	Chemistry	Chemistry	Perfluoroalkyl substances (PFAS) (eg, perfluorooctanoic acid, perfluorooctane sulfonic acid), 16 PFAS compounds by liquid chromatography with tandem mass spectrometry (LC-MS/MS), plasma or serum, quantitative	1. Crosswalk to 0263U: 9 2. Gapfill: 0 3. Abstain: 0
6	54	8X016	NEW	Chemistry	Chemistry	Anti-mullerian hormone (AMH)	1. Crosswalk to 82024: 8 2. Gapfill: 0 3. Abstain: 1
7	70	X074U	NEW	Multianalyte Assays with Algorithmic Analyses	Chemistry	Oncology (breast), semiquantitative measurement of thymidine kinase activity by immunoassay, serum, results reported as risk of disease progression	1. Crosswalk to 0058U: 5 2. Gapfill: 4 3. Abstain: 0
8	25	0376U	PLA	Multianalyte Assays with Algorithmic Analyses	MAAA-DP	Oncology (prostate cancer), image analysis of at least 128 histologic features and clinical factors, prognostic algorithm determining the risk of distant metastases, and prostate cancerspecific mortality, includes predictive algorithm to androgen deprivationtherapy response, if appropriate	1.Crosswalk to 0261U X 0.5: 1 2.Crosswalk to 0220U: 6 3. Gapfill: 1 4. Abstain: 1
9	80	X084U	NEW	Multianalyte Assays with Algorithmic Analyses	MAAA-DP	X084U: Oncology (lung), augmentative algorithmic analysis of digitized whole slide imaging for 8 genes (ALK, BRAF, EGFR, ERBB2, MET, NTRK1-3, RET, ROS1), and KRAS G12C and PD-L1, if performed, formalin-fixed paraffin-embedded (FFPE) tissue, reported as positive or negative for each biomarker [**REVISED by CPT 6-12-2023]	1. Crosswalk to 0220U: 9 2. Gapfill: 0 3. Abstain: 0
10	84	X088U	NEW	Multianalyte Assays with Algorithmic Analyses: Immunology	MAAA-DP	X088U: Oncology (breast), augmentative algorithmic analysis of digitized whole slide imaging of 8 histologic and immunohistochemical features, reported as a recurrence score [**REVISED by CPT 6-12-2023]	1. Crosswalk to 0220U: 9 2. Gapfill: 0 3. Abstain: 0
11	72	X076U	NEW	Multianalyte Assays with Algorithmic Analyses	MAAA	Oncology (lung), flow cytometry, sputum, 5 markers (meso-tetra [4-carboxyphenyl] porphyrin [TCPP], CD206, CD66b, CD3, CD19), algorithm reported as likelihood of lung cancer	1. Crosswalk to 0021U: 8 2. Gapfill: 1 3. Abstain: 0
12	8	0359U	PLA	Multianalyte Assays with Algorithmic Analyses; Immunoassay	MAAA	Oncology (prostate cancer), analysis of all prostate-specific antigen (PSA) structural isoforms by phase separation and immunoassay, plasma, algorithm reports risk of cancer	1. Crosswalk to 81539: 9 2. Gapfill: 0 3. Abstain: 0
13	9	0360U	PLA	Multianalyte Assays with Algorithmic Analyses; Immunoassay	MAAA	Oncology (lung), enzyme-linked immunosorbent assay (ELISA) of 7 autoantibodies (p53, NY-ESO-1, CAGE, GBU4-5, SOX2, MAGE A4, and HuD), plasma, algorithm reported as a categorical result for risk of malignancy	1. Crosswalk to 81490: 7 2. Crosswalk to 0312U: 2 3. Gapfill: 0 4. Abstain: 0
14	14	0365U	PLA	Multianalyte Assays with Algorithmic Analyses; Immunoassay	MAAA	Oncology (bladder), analysis of 10 protein biomarkers (A1AT, ANG, APOE, CA9, IL8, MMP9, MMP10, PAI1, SDC1 and VEGFA) by immunoassays, urine, algorithm reported as a probability of bladder cancer	1. Crosswalk to 81503: 9 2. Gapfill: 0 3. Abstain: 0
15	15	0366U	PLA	Multianalyte Assays with Algorithmic Analyses; Immunoassay	MAAA	Oncology (bladder), analysis of 10 protein biomarkers (A1AT, ANG, APOE, CA9, IL8, MMP9, MMP10, PAI1, SDC1 and VEGFA) by immunoassays, urine, algorithm reported as a probability of recurrent bladder cancer	1. Crosswalk to 81503: 9 2. Gapfill: 0 3. Abstain: 0

16	16	0367U	PLA	Multianalyte Assays with Algorithmic Analyses; Immunoassay	MAAA	Oncology (bladder), analysis of 10 protein biomarkers (A1AT, ANG, APOE, CA9, IL8, MMP9, MMP10, PAI1, SDC1 and VEGFA) by immunoassays, urine, diagnostic algorithm reported as a risk score for probability of rapid recurrence of recurrent or persistent cancer following transurethral resection	1. Crosswalk to 81503 + 82570: 9 2. Crosswalk to 81503 X 1.5: 0 3. Gapfill: 0 4. Abstain: 0
17	24	0375U	PLA	Multianalyte Assays with Algorithmic Analyses; Immunoassay	MAAA	Oncology (ovarian), biochemical assays of 7 proteins (follicle stimulating hormone, human epididymis protein 4, apolipoprotein A-1, transferrin, beta-2 macroglobulin, prealbumin [ie, transthyretin], and cancer antigen 125), algorithm reported as ovarian cancer risk score	1. Gapfill: 5 2. Abstain: 4
18	33	0384U	PLA	Multianalyte Assays with Algorithmic Analyses	MAAA	Nephrology (chronic kidney disease), carboxymethyllysine, methylglyoxal hydroimidazolone, and carboxyethyl lysine by liquid chromatography with tandem mass spectrometry (LCMS/MS) and HbA1c and estimated glomerular filtration rate (GFR), with risk score reported for predictive progression to high-stage kidney disease	1. Crosswalk to 0247U: 9 2. Gapfill: 0 3. Abstain: 0
19	34	0385U	PLA	Multianalyte Assays with Algorithmic Analyses; Immunoassay	MAAA	Nephrology (chronic kidney disease), apolipoprotein A4 (ApoA4), CD5 antigen-like (CD5L), and insulin-like growth factor binding protein 3 (IGFBP3) by enzyme-linked immunoassay (ELISA), plasma, algorithm combining results with HDL, estimated glomerular filtration rate (GFR) and clinical data reported as a risk score for developing diabetic kidney disease	1.Crosswalk to 0308U: 9 2. Gapfill: 0 3. Abstain: 0
20	36	0095U	Substantially Revised (PLA)	Multianalyte Assays with Algorithmic Analyses; Immunoassay	MAAA	Eosinophilic esophagitis),ELISA analysis of (Eotaxin-3 ([CCL26 [{C-C motif chemokine ligand 26}]) and major basic protein ([PRG2 [{proteoglycan 2, pro eosinophil major basic protein}]), enzyme-linked immunosorbent assays (ELISA), specimen obtained by esophageal string test device, algorithm reported as probability of active or inactive eosinophilic esophagitis	1. Crosswalk to 0095U: 9 2. Gapfill: 0 3. Abstain: 0
21	43	0390U	PLA	Multianalyte Assays with Algorithmic Analyses; Immunoassay	MAAA	Obstetrics (preeclampsia), kinase insert domain receptor (KDR), Endoglin (ENG), and retinol-binding protein 4 (RBP4), by immunoassay, serum, algorithm reported as a risk score	1. Crosswalk to 0243U x 3: 8 2. Gapfill: 1 3. Abstain: 0
22	61	8X025	NEW	Immunology	MAAA	Liver disease, analysis of 3 biomarkers (hyaluronic acid [HA], procollagen III amino terminal peptide [PIIINP], tissue inhibitor of metalloproteinase 1 [TIMP-1]), using immunoassays, utilizing serum, prognostic algorithm reported as a risk score and risk of liver fibrosis and liver-related clinical events within 5 years	1. Crosswalk to 0014M: 9 2. Gapfill: 0 3. Abstain: 0
23	67	00X6M	NEW	Multianalyte Assays with Algorithmic Analyses	MAAA	Cardiovascular disease, plasma, analysis of protein biomarkers by aptamer-based microarray and algorithm reported as 4-year likelihood of coronary event in high-risk populations	1. Gapfill: 9 2. Abstain: 0
24	73	X077U	NEW	Multianalyte Assays with Algorithmic Analyses	MAAA	Nephrology (diabetic chronic kidney disease [CKD]), multiplex electrochemiluminescent immunoassay (ECLIA) of soluble tumor necrosis factor receptor 1 (sTNFR1), soluble tumor necrosis receptor 2 (sTNFR2), and kidney injury molecule 1 (KIM-1) combined with clinical data, plasma, algorithm reported as risk for progressive decline in kidney function	1. Crosswalk to 0105U: 8 2. Gapfill: 1 3. Abstain: 0
25	81	X085U	NEW	Multianalyte Assays with Algorithmic Analyses: Immunology	MAAA	Cardiovascular disease (acute coronary syndrome [ACS]), IL-16, FAS, FASLigand, HGF, CTACK, EOTAXIN, and MCP-3 by immunoassay combined with age, sex, family history, and personal history of diabetes, blood, algorithm reported as a 5-year (deleted risk) score for ACS	1. 0309U: 9 2. Gapfill: 0 3. Abstain: 0
26	40	0387U	PLA	Immunology	IHC	Oncology (melanoma), autophagy and beclin 1 regulator 1 (AMBRA1) and loricrin (AMLo) by immunohistochemistry, formalinfixed paraffin-embedded (FFPE) tissue, report for risk of progression (Do not report 0387U in conjunction with 88341, 88342)	1. Crosswalk to 0067U*0.5: 9 2. Gapfill: 0 3. Abstain: 0
27	42	0389U	PLA	Genome Sequencing Procedures; RT-PCR	PCR	Pediatric febrile illness (Kawasaki disease [KD]), interferon alphainducible protein 27 (IFI27) and mast cell-expressed membrane protein 1 (MCEMP1), RNA, using reverse transcription polymerase chain reaction (RT-qPCR), blood, reported as a risk score for KD	1. Gapfill: 9 2. Abstain: 0
28	50	0398U	PLA	Genomic Sequencing Procedures; methylation analysis	PCR	Gastroenterology (Barrett esophagus), P16, RUNX3, HPP1, and FBN1 DNA methylation analysis using PCR, formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reported as risk score for progression to high-grade dysplasia or cancer	1. Crosswalk to 0108U: 2 2. Crosswalk to 0114U: 6 4. Gapfill: 1 5. Abstain: 0
29	3	0348U	Reconsideration (PLA)	Genomic Sequencing Procedures	SEQ	Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 25 gene report, with variant analysis and reported phenotypes	1. Gapfill: 4 2. Abstain: 0 3. Crosswalk to 0029U (CMS): 5
30	4	0350U	Reconsideration (PLA)	Genomic Sequencing Procedures	SEQ	Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 27 gene report, with variant analysis and reported phenotypes	1. Gapfill: 4 2. Abstain: 0 3. Crosswalk to 0175U (CMS): 5

31	5	0355U	PLA	Molecular Pathology	SEQ	APOL1 (apolipoprotein L1) (eg, chronic kidney disease), risk variants (G1, G2)	1. Crosswalk to 81120: 9 2. Gapfill: 0 3. Abstain: 0
32	6	0356U	PLA	Multianalyte Assays with Algorithmic Analyses	SEQ	Oncology (oropharyngeal), evaluation of 17 DNA biomarkers using droplet digital PCR (ddPCR), cell-free DNA, algorithm reported as a prognostic risk score for cancer recurrence	1. Gapfill: 9 2. Abstain: 0
33	27	0378U	PLA	Molecular Pathology	SEQ	RFC1 (replication factor C subunit 1), repeat expansion variant analysis by traditional and repeat-primed PCR, blood, saliva, or buccal swab	1. Crosswalk 81181: 7 2. Crosswalk 81401: 2 3. Gapfill: 0 4. Abstain: 0
34	69	X073U	NEW	Multianalyte Assays with Algorithmic Analyses	SEQ	Oncology (prostate), mRNA, gene expression profiling of 18 genes, first-catch post-digital rectal examination urine (or processed first-catch urine), algorithm reported as percentage of likelihood of detecting clinically significant prostate cancer	1. Crosswalk to 0011M: 9 2. Crosswalk to 0113U: 0 3. Gapfill: 0 4. Abstain: 0
35	79	X083U	NEW	Genomic Sequencing Procedures; optical genome mapping	SEQ	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	1. Crosswalk to 0260U X 1.5: 2 2. Crosswalk 0260U: 6 3. Gapfill: 1 4. Abstain: 0
36	2	0324U	Reconsideration (PLA)	Microbiology	Micro	Oncology (ovarian), spheroid cell culture, 4-drug panel (carboplatin, doxorubicin, gemcitabine, paclitaxel), tumor chemotherapy response prediction for each drug	1. Crosswalk to 81535 + 81536*3 (also CMS decision last year): 9 2. Gapfill: 0 3. Abstain: 0
37	18	0369U	PLA	Microbiology; Infectious Disease	Micro	Infectious agent detection by nucleic acid (DNA and RNA), gastrointestinal pathogens, 31 bacterial, viral, and parasitic organisms and identification of 21 associated antibiotic-resistance genes, multiplex amplified probe technique	1. Crosswalk to 87507 x 2: 9 2. Gapfill: 0 3. Abstain: 0
38	19	0370U	PLA	Microbiology; Infectious Disease	Micro	Infectious agent detection by nucleic acid (DNA and RNA), surgical wound pathogens, 34 microorganisms and identification of 21 associated antibioticresistance genes, multiplex amplified probe technique, wound swab	1. Crosswalk to 87633 x 2: 9 2. Gapfill: 0 3. Abstain: 0
39	20	0371U	PLA	Microbiology; Infectious Disease	Micro	Infectious agent detection by nucleic acid (DNA or RNA), genitourinary pathogen, semiquantitative identification, DNA from 16 bacterial organisms and 1 fungal organism, multiplex amplified probe technique via quantitative polymerase chain reaction (qPCR), urine	1. Crosswalk to 87633: 9 2. Gapfill: 0 3. Abstain: 0
40	21	0372U	PLA	Microbiology	Micro	Infectious disease (genitourinary pathogens), antibiotic-resistance gene detection, multiplex amplified probe technique, urine, reported as an antimicrobial stewardship risk score	1. Crosswalk to 87633: 9 2. Gapfill: 0 3. Abstain: 0
41	22	0373U	PLA	Microbiology; Infectious Disease	Micro	Infectious agent detection by nucleic acid (DNA and RNA), respiratory tract infection, 17 bacteria, 8 fungus, 13 virus, and 16 antibiotic-resistance genes, multiplex amplified probe technique, upper or lower respiratory specimen	1. Crosswalk to 87633 x 2: 9 2. Gapfill: 0 3. Abstain: 0
42	23	0374U	PLA	Microbiology; Infectious Disease	Micro	Infectious agent detection by nucleic acid (DNA or RNA), genitourinary pathogens, identification of 21 bacterial and fungal organisms and identification of 21 associated antibiotic-resistance genes, multiplex amplified probe technique, urine	1. Crosswalk to 0321U: 9 2. Gapfill: 0 3. Abstain: 0
43	38	87467	Reconsideration	Microbiology	Micro	Hepatitis B surface antigen (HBsAg), quantitative	1. Crosswalk to 87340 X 2: 1 2. Gapfill: 5 3. Abstain: 1 4. Crosswalk 84702 (CMS): 2
44	66	8X041	NEW	Microbiology	Micro	Infectious agent detection by nucleic acid (DNA or RNA); hepatitis D (delta), quantification, including reverse transcription, when performed	1. Crosswalk to 87522: 9 2. Gapfill: 0 3. Abstain: 0
45	68	X072U	NEW	Immunology	Micro	Infectious agent (sexually transmitted infection), Chlamydia trachomatis, Neisseria gonorrhoeae, Trichomonas vaginalis, Mycoplasma genitalium, multiplex amplified probe technique, vaginal, endocervical, or male urine, each pathogen reported as detected or not detected	1. Crosswalk to 87631: 9 2. Gapfill: 0 3. Abstain: 0
46	74	X078U	NEW	Immunology	Micro	Infectious agent antigen detection by bulk acoustic wave biosensor immunoassay, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (coronavirus disease [COVID-19])	1. Gapfill: 9 2. Abstain: 0
47	82	X086U	NEW	Microbiology	Micro	Infectious agent detection by nucleic acid (DNA), genitourinary pathogens, identification of 20 bacterial and fungal organisms, including identification of 20 associated antibiotic-resistance genes, if performed, multiplex amplified probe technique, urine	1. 0321U: 9 2. Gapfill: 0 3. Abstain: 0
48	29	0380U	PLA	Genomic Sequencing Procedures; targeted sequence analysis	SEQ 5-50	Drug metabolism (adverse drug reactions and drug response), targeted sequence analysis, 20 gene variants and CYP2D6 deletion or duplication analysis with reported genotype and phenotype	1. Crosswalk 0070U: 9 2. Gapfill: 0 3. Abstain: 0
49	35	0022U	Substantially Revised (PLA)	Genomic Sequencing Procedures	SEQ 5-50	Targeted genomic sequence analysis panel, non- small cell lung neoplasia, DNA and RNA analysis, 23 genes, interrogation for sequence variants and rearrangements, reported as presence/ or absence of variants and associated therapy(ies) to consider	1. Crosswalk 81450: 6 2. No Action: 0 3. Gapfill: 2 4. Abstain: 1

50	41	0388U	PLA	Genomic Sequencing Procedures	SEQ 5-50	Oncology (non-small cell lung cancer), next-generation sequencing with identification of single nucleotide variants, copy number variants, insertions and deletions, and structural variants in 37 cancer-related genes, plasma, with report for alteration detection	1. Crosswalk to 0242U: 8 2. Gapfill: 1 3. Abstain: 0
51	45	0392U	PLA	Genome Sequencing Procedures; dup/del analysis	SEQ 5-50	Drug metabolism (depression, anxiety, attention deficit hyperactivity disorder [ADHD]), gene-drug interactions, variant analysis of 16 genes, including deletion/duplication analysis of CYP2D6, reported as impact of gene-drug interaction for each drug	1. Crosswalk to 0345U: 9 2. Gapfill: 0 3. Abstain: 0
52	48	0395U	PLA	Immunology	SEQ 5-50	Oncology (lung), multi-omics (microbial DNA by shotgun nextgeneration sequencing and carcinoembryonic antigen and osteopontin by immunoassay), plasma, algorithm reported as malignancy risk for lung nodules in early-stage disease	1. Crosswalk 81546: 2 2. Crosswalk 0026U: 0 3. Crosswalk (0112U + 0164U) X 1.2: 2 4. Gapfill: 5 5. Abstain: 0
53	53	0401U	PLA	Genomic Sequencing Procedures; targeted variant analysis	SEQ 5-50	Cardiology (coronary heart disease [CAD]), 9 genes (12 variants), targeted variant genotyping, blood, saliva, or buccal swab, algorithm reported as a genetic risk score for a coronary event	1. Crosswalk to 0011M: 9 2. Gapfill: 0 3. Abstain: 0
54	77	X081U	NEW	Genomic Sequencing Procedures	SEQ 5-50	Psychiatry (eg, depression, anxiety, attention deficit hyperactivity disorder [ADHD]), genomic analysis panel, variant analysis of 15 genes, including deletion/duplication analysis of CYP2D6	1. Crosswalk to 0345U: 9 2. Gapfill: 0 3. Abstain: 0
55	85	X089U	NEW	Genomic Sequencing Procedures	SEQ 5-50	Neuropsychiatry (eg, depression, anxiety), genomic sequence analysis panel, variant analysis of 13 genes, saliva or buccal swab, report of each gene phenotype	1. Crosswalk to 0345U: 9 2. Gapfill: 0 3. Abstain: 0
56	28	0379U	PLA	Genomic Sequencing Procedures	SEQ 50+	Targeted genomic sequence analysis panel, solid organ neoplasm, DNA (523 genes) and RNA (55 genes) by nextgeneration sequencing, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability, and tumor mutational burden	1. Crosswalk to 0244U: 8 2. Crosswalk 81455: 1 3. Gapfill: 0 4. Abstain: 0
57	37	0329U	Reconsideration (PLA)	Genomic Sequencing Procedures; exome	SEQ 50+	Oncology (neoplasia), exome and transcriptome sequence analysis for sequence variants, gene copy number amplifications and deletions, gene rearrangements, microsatellite instability and tumor mutational burden utilizing DNA and RNA from tumor with DNA from normal blood or saliva for subtraction, report of clinically significant mutation(s) with therapy associations	1. Crosswalk to 0211U: 7 2. Gapfill (cms): 2 3. Abstain: 0
58	39	0334U	Reconsideration (PLA)	Genomic Sequencing Procedures; targeted sequence analysis	SEQ 50+	Oncology (solid organ), targeted genomic sequence analysis, formalin-fixed paraffin-embedded (FFPE) tumor tissue, DNA analysis, 84 or more genes, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability and tumor mutational burden	1. Crosswalk to 0244U: 6 2. Gapfill: 0 3. Abstain: 0 4. Crosswalk 81455 (CMS): 3
59	52	0400U	PLA	Genomic Sequencing Procedures	SEQ 50+	Obstetrics (expanded carrier screening), 145 genes by nextgeneration sequencing, fragment analysis and multiplex ligationdependent probe amplification, DNA, reported as carrier positive or negative	1. Gapfill: 9 2. Abstain: 0
60	55	8X017	NEW	Genomic Sequencing Procedures	SEQ 50+	Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis, microsatellite instability	1. Crosswalk to 81455 MINUS 81277: 9 2. Gapfill: 0 3. Abstain: 0
61	56	8X018	NEW	Genomic Sequencing Procedures	SEQ 50+	Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis, copy number variants and microsatellite instability	1. Crosswalk to 81455: 9 2. Gapfill: 0 3. Abstain: 0
62	57	8X019	NEW	Genomic Sequencing Procedures	SEQ 50+	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	1. Crosswalk to 0244U: 9 2. Gapfill: 0 3. Abstain: 0
63	75	X079U	NEW	Genomic Sequencing Procedures	SEQ 50+	Oncology (solid tumor), DNA (80 genes) and RNA (36 genes), by next-generation sequencing from plasma, including single nucleotide variants, insertions/deletions, copy number alterations, microsatellite instability, and fusions, report showing identified mutations with clinical actionability	1. Crosswalk to 81455 X 1.25: 9 2. Gapfill: 0 3. Abstain: 0
64	83	X087U	NEW	Genomic Sequencing Procedures; mitochondrial	SEQ 50+	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	1. Crosswalk to 81460 + 81465: 3 2. Gapfill: 6 3. Abstain: 0
65	7	0358U	PLA	Chemistry	Neuroimmunology	Neurology (mild cognitive impairment), analysis of β-amyloid 1-42 and 1-40, chemiluminescence enzyme immunoassay, cerebral spinal fluid, reported as positive, likely positive, or negative	1. Crosswalk to 81500: 8 2. Gapfill: 0 3. Abstain: 1
66	10	0361U	PLA	Immunology	Neuroimmunology	Neurofilament light chain, digital immunoassay, plasma, quantitative	1. Gapfill: 8 2. Abstain: 1
67	46	0393U	PLA	Chemistry	Neuroimmunology	Neurology (eg, Parkinson disease, dementia with Lewy bodies), cerebrospinal fluid (CSF), detection of misfolded α-synuclein protein by seed amplification assay, qualitative	1. Crosswalk to 0035U: 9 2. Gapfill: 0 3. Abstain: 0

68	51	0399U	PLA	Immunology	Neuroimmu nology	Neurology (cerebral folate deficiency), serum, detection of anti-human folate receptor IgGbinding antibody and blocking autoantibodies by enzyme-linked immunoassay (ELISA), qualitative, and blocking autoantibodies, using a functional blocking assay for IgG or IgM, quantitative, reported as positive or not detected	1. Gapfill: 9 2. Abstain: 0
69	62	8X036	NEW	Immunology	Neuroimmu nology	Acetylcholine receptor (AChR); binding antibody	1. Crosswalk to 86341: 8 2. Gapfill: 0 3. Abstain: 1
70	63	8X037	NEW	Immunology	Neuroimmu nology	Acetylcholine receptor (AChR); blocking antibody	1. Crosswalk to 86341: 9 2. Gapfill: 0 3. Abstain: 0
71	64	8X038	NEW	Immunology	Neuroimmu nology	Acetylcholine receptor (AChR); modulating antibody	1.Crosswalk to 86053: 8 2. Gapfill: 0 3. Abstain: 1
72	65	8X039	NEW	Immunology	Neuroimmu nology	Muscle-specific kinase (MuSK) antibody	1. Crosswalk to 84586: 8 2. Gapfill: 0 3. Abstain: 1
73	78	X082U	NEW	Immunology	Neuroimmu nology	Beta amyloid, Aβ42/40 ratio, immunoprecipitation with quantitation by liquid chromatography with tandem mass spectrometry (LC-MS/MS) and qualitative ApoE isoform-specific proteotyping, plasma combined with age, algorithm reported as presence or absence of brain amyloid pathology	1. Gapfill: 9 2. Abstain: 0
74	49	0396U	PLA	Multianalyte Assays with Algorithmic Analyses; Microarray	SEQ+MAA A	Obstetrics (pre-implantation genetic testing), evaluation of 300000 DNA single-nucleotide polymorphisms (SNPs) by microarray, embryonic tissue, algorithm reported as a probability for single-gene germline conditions	1. Crosswalk 0254U X 1.2: 2 2. Crosswalk 81229: 2 3. Gapfill: 5 4. Abstain: 0
75	76	X080U	NEW	Multianalyte Assays with Algorithmic Analyses	SEQ+MAA A	Oncology (pancreatic), DNA, whole genome sequencing with 5-hydroxymethylcytosine enrichment, whole blood or plasma, algorithm reported as cancer detected or not detected	1. Crosswalk to 81349: 8 2. Gapfill: 1 3. Abstain: 0
76	1	0326U	Reconsid eration (PLA)	Multianalyte Assays with Algorithmic Analyses	SEQ+MAA A	Targeted genomic sequence analysis panel, solid organ neoplasm, cell-free circulating DNA analysis of 83 or more genes, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability and tumor mutational burden	1. Crosswalk to 0242U: 3 2. Crosswalk to 81455 X 1.25: 4 3. Gapfill (CMS): 2 4. Abstain: 0
77	11	0362U	PLA	Multianalyte Assays with Algorithmic Analyses	SEQ+MAA A	Oncology (papillary thyroid cancer), gene-expression profiling via targeted hybrid capture–enrichment RNA sequencing of 82 content genes and 10 housekeeping genes, formalin-fixed paraffin embedded (FFPE) tissue, algorithm reported as one of three molecular subtypes	1. Crosswalk to 0287U: 9 2. Gapfill: 0 3. Abstain: 0
78	12	0363U	PLA	Multianalyte Assays with Algorithmic Analyses	SEQ+MAA A	Oncology (urothelial), mRNA, geneexpression profiling by real-time quantitative PCR of 5 genes (MDK, HOXA13, CDC2 [CDK1], IGFBP5, and CXCR2), utilizing urine, algorithm incorporates age, sex, smoking history, and macrohematuria frequency, reported as a risk score for having urothelial carcinoma	1. Crosswalk to 0012M: 8 2. Crosswalk to 0013M: 1 3. Gapfill: 0 4. Abstain: 0
79	13	0364U	PLA	Multianalyte Assays with Algorithmic Analyses	SEQ+MAA A	Oncology (hematolymphoid neoplasm), genomic sequence analysis using multiplex (PCR) and next-generation sequencing with algorithm, quantification of dominant clonal sequence(s), reported as presence or absence of minimal residual disease (MRD) with quantitation of disease burden, when appropriate	1. Crosswalk 0171U: 4 2. Gapfill: 5 3. Abstain: 0
80	17	0368U	PLA	Multianalyte Assays with Algorithmic Analyses	SEQ+MAA A	Oncology (colorectal cancer), evaluation for mutations of APC, BRAF, CTNNB1, KRAS, NRAS, PIK3CA, SMAD4, and TP53, and methylation markers (MYO1G, KCNQ5, C9ORF50, FLI1, CLIP4, ZNF132 and TWIST1), multiplex quantitative polymerase chain reaction (qPCR), circulating cell-free DNA (cfDNA), plasma, report of risk score for advanced adenoma or colorectal cancer	1. Crosswalk to 0055U X 0.18: 8 2. Gapfill: 1 3. Abstain: 0
81	71	X075U	NEW	Multianalyte Assays with Algorithmic Analyses	SEQ 50+ MAAA	Oncology (pancreatic), 59 methylation haplotype block markers, next-generation sequencing, plasma, reported as cancer signal detected or not detected	1. Crosswalk to 0318U: 8 2. Gapfill: 1 3. Abstain: 0
82	44	0391U	PLA	Multianalyte Assays with Algorithmic Analyses	SEQ 50+ MAAA	Oncology (solid tumor), DNA and RNA by next-generation sequencing, utilizing formalin-fixed paraffin-embedded (FFPE) tissue, 437 genes, interpretive report for single nucleotide variants, splicesite variants, insertions/deletions, copy number alterations, gene fusions, tumor mutational burden, and microsatellite instability, with algorithm quantifying immunotherapy response score	1. Crosswalk to 0250U: 4 2. Crosswalk to 0287U: 3 3. Gapfill: 2 4. Abstain: 0
83	58	8X020	NEW	Genomic Sequencing Procedures; cell free DNA	SEQ-CF	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	1. Crosswalk to 81455 X 1.25: 9 2. Gapfill: 0 3. Abstain: 0
84	59	8X021	NEW	Genomic Sequencing Procedures; cell free DNA	SEQ-CF	Solid organ neoplasm, genomic sequence analysis panel, cell-free nucleic acid (eg, plasma), interrogation for sequence variants; DNA analysis, copy number variants, and microsatellite instability	1. Crosswalk to 81455 X 1.25: 9 2. Gapfill: 0 3. Abstain: 0

| 85 | 60 | 8X022 | NEW | Genomic Sequencing Procedures; cell free DNA | SEQ-CF | 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 | 1. Crosswalk to 81455 X 1.25: 7
2. Crosswalk to 0244U X 1.25: 2
3. Gapfill: 0
4. Abstain: 0 |