TAR and Non-Benefit List: Codes 0001M thru 0999U

Page updated: August 2025

‹‹Medi-Cal has not activated all CPT® Category I or Proprietary Laboratory Analysis (PLA) codes associated with various covered Medi-Cal benefits and services. In these instances, the CPT Category I or PLA codes are classified a "non-benefit" for Medi-Cal and in deny status for the general Medi-Cal population. However, Medi-Cal may provide reimbursement for a CPT code Category I or PLA code with an approved *Treatment Authorization Request* (TAR) if medical necessity is established. Billing codes in non-benefit status should be evaluated and coverage decided on a case-by-case basis for individual Medi-Cal members based upon medical necessity.››

Proprietary Laboratory Analyses (PLA) Codes and Multianalyte Assays with Algorithmic Analyses (MAAA) Codes

This section contains PLA and MAAA codes and descriptions indicating TAR requirement and benefit status. Medi-Cal may provide reimbursement for non-benefit codes with an approved TAR and if medical necessity is established, unless specifically identified. For instructions on submitting an electronic TAR (eTAR) for a non-benefit code, refer to the "eTAR Submission Guidelines" in the TAR Overview section of the Part 1 manual.

Note: Refer to the *TAR and Non-Benefit: Introduction to List* section in this manual for more information about the categories of benefit restrictions.

Note: Inpatient laboratory services are included in the Diagnosis Related Group (DRG) or per diem bundled payment. Please refer to *Diagnosis Related Group Hospital Inpatient Payment Methodology* for inpatient billing.

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement

Code	Description	Benefit Status
0002M	Liver disease, ten biochemical assays (ALT, A2-macroglobulin, apolipoprotein A-1, total bilirubin, GGT, haptoglobin, AST, glucose, total cholesterol and triglycerides) utilizing serum, prognostic algorithm reported as quantitative scores for fibrosis, steatosis and alcoholic steatohepatitis (ash)	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0003M	Liver disease, ten biochemical assays (ALT, A2-macroglobulin, Apolipoprotein A-1, Total Bilirubin, GGT, Haptoglobin, AST, Glucose, Total cholesterol and Triglycerides) utilizing serum, prognostic algorithm reported as quantitative scores for fibrosis, steatosis and nonalcoholic steatohepatitis (NASH)	Non-Benefit
0004M	Scoliosis, DNA analysis of 53 single nucleotide polymorphisms (SNPS), using saliva, prognostic algorithm reported as a risk score	Non-Benefit
0006M	Oncology (hepatic), mRNA expression levels of 161 genes, utilizing fresh hepatocellular carcinoma tumor tissue, with alpha-fetoprotein level, algorithm reported as a risk classifier	Non-Benefit
0007M	Oncology (gastrointestinal neuroendocrine tumors), real-time PCR expression analysis of 51 genes, utilizing whole peripheral blood, algorithm reported as a nomogram of tumor disease index	Non-Benefit
‹‹0009M	Fetal aneuploidy (trisomy 21, and 18) DNA sequence analysis of selected regions using maternal plasma, algorithm reported as a risk score for each trisomy	Non-Benefit››
0011M	Oncology, prostate cancer, mRNA expression assay of 12 genes (10 content and 2 housekeeping), RT-PCR test utilizing blood plasma and/or urine, algorithms to predict high-grade prostate cancer risk	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0012M	Oncology (urothelial), mRNA, gene expression profiling by real-time quantitative PCR of five genes (MDK, HOXA13, CDC2 [CDK1], IGFBP5, and CXCR2), utilizing urine, algorithm reported as a risk score for having urothelial carcinoma	Non-Benefit
0013M	Oncology (urothelial), mRNA, gene expression profiling by real-time quantitative PCR of five genes (MDK, HOXA13, CDC2 [CDK1], IGFBP5, and CXCR2), utilizing urine, algorithm reported as a risk score for having recurrent urothelial carcinoma.	Non-Benefit
0015M	Adrenal cortical tumor, biochemical assay of 25 steroid markers, utilizing 24-hour urine specimen and clinical parameters, prognostic algorithm reported as a clinical risk and integrated clinical steroid risk for adrenal cortical carcinoma, adenoma, or other adrenal malignancy	Non-Benefit
0016M	Oncology (bladder), mRNA, microarray gene expression profiling of 209 genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as molecular subtype (luminal, luminal infiltrated, basal, basal claudin-low, neuroendocrine-like)	Non-Benefit
0018M	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	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0019M	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	Non-Benefit
0020M	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	Non-Benefit
0002U	Oncology (colorectal), quantitative assessment of three urine metabolites (ascorbic acid, succinic acid and carnitine) by liquid chromatography with tandem mass spectrometry (LC-MS/MS) using multiple reaction monitoring acquisition, algorithm reported as likelihood of adenomatous polyps	Non-Benefit
0005U	Oncology (prostate) gene expression profile by real-time RT-PCR of 3 genes (ERG, PCA3, and SPDEF), urine, algorithm reported as risk score	Non-Benefit
0008U	Helicobacter pylori detection and antibiotic resistance, DNA, 16S and 23S rRNA, gyrA, pbp1, rdxA and rpoB, next generation sequencing, formalin-fixed paraffin-embedded or fresh tissue, predictive, reported as positive or negative for resistance to clarithromycin, fluoroquinolones, metronidazole, amoxicillin, tetracycline and rifabutin	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0009U	Oncology (breast cancer), ERBB2 (HER2) copy number by FISH, tumor cells from formalin-fixed paraffin-embedded tissue isolated using image-based dielectrophoresis (DEP) sorting, reported as ERBB2 gene amplified or non-amplified	Non-Benefit
0010U	Infectious disease (bacterial), strain typing by whole genome sequencing, phylogenetic-based report of strain relatedness, per submitted isolate	Non-Benefit
0011U	Prescription drug monitoring, evaluation of drugs present by LC-MS/MS, using oral fluid, reported as a comparison to an estimated steady-state range, per date of service including all drug compounds and metabolites	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0018U	Oncology (thyroid), microRNA profiling by RT-PCR of 10 microRNA sequences, utilizing fine needle aspirate, algorithm reported as a positive or negative result for moderate to high risk of malignancy	Requires TAR
0019U	Oncology, RNA, gene expression by whole transcriptome sequencing, formalin-fixed paraffin embedded tissue or fresh frozen tissue, predictive algorithm reported as potential targets for therapeutic agents.	Non-Benefit
0021U	Oncology (prostate), detection of 8 autoantibodies (ARF 6, NKX3-1, 5'-UTR-BMI1, CEP 164, 3'-UTR-Ropporin, Desmocollin, AURKAIP-1, CSNK2A2), multiplexed immunoassay and flow cytometry serum, algorithm reported as risk score.	Non-Benefit
0022U	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/absence of variants and associated therapy(ies) to consider.	Requires TAR
0024U	Glycosylated acute phase proteins (GlycA), nuclear magnetic resonance spectroscopy, quantitative	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0025U	Tenofovir, by liquid chromatography with tandem mass spectrometry (LC-MS/MS), urine, quantitative	Non-Benefit
0026U	Oncology (thyroid), DNA and mRNA of 112 genes, next-generation sequencing, fine needle aspirate of thyroid nodule, algorithmic analysis reported as a categorical result ("Positive, high probability of malignancy" or "Negative, low probability of malignancy")	Requires TAR
0029U	Drug metabolism (adverse drug reactions and drug response), targeted sequence analysis (ie, CYP1A2, CYP2C19, CYP2C9, CYP2D6, CYP3A4, CYP3A5, CYP4F2, SLCO1B1, VKORC1 and rs12777823).	Non-Benefit
0030U	Drug metabolism (warfarin drug response), targeted sequence analysis (ie, CYP2C9, CYP4F2, VKORC1, rs12777823).	Non-Benefit
0031U	CYP1A2 (cytochrome P450 family 1, subfamily A, member 2)(eg, drug metabolism) gene analysis, common variants (ie, *1F, *1K, *6, *7).	Non-Benefit
0032U	COMT (catechol-O-methyltransferase)(drug metabolism) gene analysis, c.472G>A (rs4680) variant	Non-Benefit
0033U	HTR2A (5-hydroxytryptamine receptor 2A), HTR2C (5-hydroxytryptamine receptor 2C) (eg, citalopram metabolism) gene analysis, common variants (ie, HTR2A rs7997012 [c.614-2211T>C], HTR2C rs3813929 [c.-759C>T] and rs1414334 [c.551-3008C>G]).	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0034U	TPMT (thiopurine S-methyltransferase), NUDT15 (nudix hydroxylase 15)(eg, thiopurine metabolism), gene analysis, common variants (ie, TPMT *2, *3A, *3B, *3C, *4, *5, *6, *8, *12; NUDT15 *3, *4, *5).	Requires TAR
0035U	Neurology (prion disease), cerebrospinal fluid, detection of prion protein by quaking-induced conformational conversion, qualitative	Requires TAR
0036U	Exome (ie, somatic mutations), paired formalin-fixed paraffin-embedded tumor tissue and normal specimen, sequence analyses	Non-Benefit
0037U	Targeted genomic sequence analysis, solid organ neoplasm, DNA analysis of 324 genes, interrogation for sequence variants, gene copy number amplifications gene rearrangements, microsatellite instability and tumor mutational burden.	Requires TAR
0045U	Oncology (breast ductal carcinoma in situ), mRNA, gene expression profiling by real-time RT-PCR of 12 genes (7 content and 5 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as recurrence score	Non-Benefit
0047U	Oncology (prostate), mRNA, gene expression profiling by real-time RT-PCR of 17 genes (12 content and 5 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a risk score	Requires TAR

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0048U	Oncology (solid organ neoplasia), DNA, targeted sequencing of protein-coding exons of 468 cancer-associated genes, including interrogation for somatic mutations and microsatellite instability, matched with normal specimens, utilizing formalin-fixed paraffin-embedded tumor tissue, report of clinically significant mutation(s)	Non-Benefit
0055U	Cardiology (heart transplant), cell-free DNA, PCR assay of 96 DNA target sequences (94 single nucleotide polymorphism targets and two control targets), plasma	Non-Benefit
0060U	Twin zygosity, genomic targeted sequence analysis of chromosome 2, using circulating cell-free fetal DNA in maternal blood	Non-Benefit
0061U	Transcutaneous measurement of five biomarkers (tissue oxygenation [StO2], oxyhemoglobin [ctHbO2], deoxyhemoglobin [ctHbR], papillary and reticular dermal hemoglobin concentrations [ctHb1 and ctHb2]), using spatial frequency domain imaging (SFDI) and multi-spectral analysis	Non-Benefit
0062U	Autoimmune (systemic lupus erythematosus), IgG and IgM analysis of 80 biomarkers, utilizing serum, algorithm reported with a risk score	Non-Benefit
0063U	Neurology (autism), 32 amines by LC-MS/MS, using plasma, algorithm reported as metabolic signature associated with autism spectrum disorder	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0067U	Oncology (breast), immunohistochemistry, protein expression profiling of 4 biomarkers (matrix metalloproteinase-1 [MMP-1], carcinoembryonic antigen-related cell adhesion molecule 6 [CEACAM6], hyaluronoglucosaminidase [HYAL1], highly expressed in cancer protein [HEC1]), formalin-fixed paraffin-embedded precancerous breast tissue, algorithm reported as carcinoma risk score	Non-Benefit
0069U	Oncology (colorectal), microRNA, RT-PCR expression profiling of miR-31-3p, formalin-fixed paraffin-embedded tissue, algorithm reported as an expression score	Non-Benefit
0070U	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, common and select rare variants (ie, *2, *3, *4, *4N, *5, *6, *7, *8, *9, *10, *11, *12, *13, *14A, *14B, *15, *17, *29, *35, *36, *41, *57, *61, *63, *68, *83, *xN)	Non-Benefit
0071U	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, full gene sequence (List separately in addition to code for primary procedure)	Non-Benefit
0072U	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, CYP2D6-2D7 hybrid gene) (List separately in addition to code for primary procedure)	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0073U	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, CYP2D7-2D6 hybrid gene) (List separately in addition to code for primary procedure)	Non-Benefit
0074U	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, non-duplicated gene when duplication/multiplication is trans) (List separately in addition to code for primary procedure)	Non-Benefit
0075U	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, 5' gene duplication/multiplication) (List separately in addition to code for primary procedure)	Non-Benefit
0076U	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, 3' gene duplication/ multiplication) (List separately in addition to code for primary procedure)	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0079U	Comparative DNA analysis using multiple selected single-nucleotide polymorphisms (SNPs), urine and buccal DNA, for specimen identity verification	Non-Benefit
0080U	Oncology (lung), mass spectrometric analysis of galectin-3-binding protein and scavenger receptor cysteine-rich type 1 protein M130, with five clinical risk factors (age, smoking status, nodule diameter, nodule-spiculation status and nodule location), utilizing plasma, algorithm reported as a categorical probability of malignancy	Non-Benefit
0083U	Oncology, response to chemotherapy drugs using motility contrast tomography, fresh or frozen tissue, reported as likelihood of sensitivity or resistance to drugs or drug combinations	Non-Benefit
0086U	Infectious disease (bacterial and fungal), organism identification, blood culture, using rRNA FISH, 6 or more organism targets, reported as positive or negative with phenotypic minimum inhibitory concentration (MIC)-based antimicrobial susceptibility	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0089U	Oncology (melanoma), gene expression profiling by RTqPCR, PRAME and LINC00518, superficial collection using adhesive patch(es)	Non-Benefit
0090U	Oncology (cutaneous melanoma), mRNA gene expression profiling by RT-PCR of 23 genes (14 content and 9 housekeeping), utilizing formalin-fixed paraffin-embedded ‹‹(FFPE)›› tissue, algorithm reported as a categorical result (ie, benign, indeterminate, malignant)	Non-Benefit
0091U	Oncology (colorectal) screening, cell enumeration of circulating tumor cells, utilizing whole blood, algorithm, for the presence of adenoma or cancer, reported as a positive or negative result.	Non-Benefit
0092U	Oncology (lung), three protein biomarkers, immunoassay using magnetic nanosensor technology, plasma, algorithm reported as risk score for likelihood of malignancy	Non-Benefit
0093U	Prescription drug monitoring, evaluation of 65 common drugs by LC-MS/MS, urine, each drug reported detected or not detected	Non-Benefit
0094U	Genome (eg, unexplained constitutional or heritable disorder or syndrome), rapid sequence analysis	‹‹Non-Benefit †››
0095U	Inflammation (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]), specimen obtained by swallowed nylon string, algorithm reported as predictive probability index for active eosinophilic esophagitis	Non-Benefit
0096U	Human papillomavirus (HPV), high-risk types (ie, 16, 18, 31, 33, 35, 39, 45, 51, 52,56, 58, 59, 66, 68), male urine	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0101U	Hereditary colon cancer disorders (eg, Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis), genomic sequence analysis panel utilizing a combination of NGS, Sanger, MLPA, and array CGH, with MRNA analytics to resolve variants of unknown significance when indicated (15 genes [sequencing and deletion/duplication], EPCAM and GREM1 [deletion/duplication only])	Non-Benefit
0102U	Hereditary breast cancer-related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), genomic sequence analysis panel utilizing a combination of NGS, Sanger, MLPA, and array CGH, with MRNA analytics to resolve variants of unknown significance when indicated (17 genes [sequencing and deletion/duplication])	Non-Benefit
0103U	Hereditary ovarian cancer (eg, hereditary ovarian cancer, hereditary endometrial cancer), genomic sequence analysis panel utilizing a combination of NGS, Sanger, MLPA, and array CGH, with MRNA analytics to resolve variants of unknown significance when indicated (24 genes [sequencing and deletion/duplication], EPCAM [deletion/duplication only])	Non-Benefit
0104U	Hereditary pan cancer (eg, hereditary breast and ovarian cancer, hereditary endometrial cancer, hereditary colorectal cancer), genomic sequence analysis panel utilizing a combination of NGS, Sanger, MLPA, and array CGH, with MRNA analytics to resolve variants of unknown significance when indicated (32 genes [sequencing and deletion/duplication], EPCAM and GREM1 [deletion/duplication only])	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0105U	Nephrology (chronic kidney disease), multiplex electrochemiluminescent immunoassay (ECLIA) of tumor necrosis factor receptor 1A, receptor superfamily 2 (TNFR1, TNFR2), and kidney injury molecule-1 (KIM-1) combined with longitudinal clinical data, including APOL1 genotype if available, and plasma (isolated fresh or frozen), algorithm reported as probability score for rapid kidney function decline (RKFD)	Non-Benefit
0106U	Gastric emptying, serial collection of 7 timed breath specimens, non-radioisotope carbon-13 (13C) spirulina substrate, analysis of each specimen by gas isotope ratio mass spectrometry, reported as rate of 13CO2 excretion.	Non-Benefit
0108U	Gastroenterology (Barrett's esophagus), whole slide–digital imaging, including morphometric analysis, computer-assisted quantitative immunolabeling of 9 protein biomarkers (p16, AMACR, p53, CD68, COX-2, CD45RO, HIF1a, HER-2, K20) and morphology, formalin-fixed paraffin-embedded tissue, algorithm reported as risk of progression to high-grade dysplasia or cancer	Non-Benefit
0110U	Prescription drug monitoring, one or more oral oncology drug(s) and substances, definitive tandem mass spectrometry with chromatography, serum or plasma from capillary blood or venous blood, quantitative report with steady-state range for the prescribed drug(s) when detected	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0111U	Oncology (colon cancer), targeted KRAS (codons 12, 13, and 61) and NRAS (codons 12, 13, and 61) gene analysis utilizing formalin-fixed paraffin-embedded tissue	Non-Benefit
0112U	Infectious agent detection and identification, targeted sequence analysis (16S and 18S rRNA genes) with drug-resistance gene	Non-Benefit
0113U	Oncology (prostate), measurement of PCA3 and TMPRSS2-ERG in urine and PSA in serum following prostatic massage, by RNA amplification and fluorescence-based detection, algorithm reported as risk score	Non-Benefit
0114U	Gastroenterology (Barrett's esophagus), VIM and CCNA1 methylation analysis, esophageal cells, algorithm reported as likelihood for Barrett's esophagus	Non-Benefit
0115U	Respiratory infectious agent detection by nucleic acid (DNA and RNA), 18 viral types and subtypes and 2 bacterial targets, amplified probe technique, including multiplex reverse transcription for RNA targets, each analyte reported as detected or not detected	Non-Benefit
0116U	Prescription drug monitoring, enzyme immunoassay of 35 or more drugs confirmed with LC-MS/MS, oral fluid, algorithm results reported as a patient-compliance measurement with risk of drug to drug interactions for prescribed medications	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0117U	Pain management, analysis of 11 endogenous analytes (methylmalonic acid, xanthurenic acid, homocysteine, pyroglutamic acid, vanilmandelate, 5-hydroxyindoleacetic acid, hydroxymethylglutarate, ethylmalonate, 3-hydroxypropyl mercapturic acid (3-HPMA), quinolinic acid, kynurenic acid), LC-MS/MS, urine, algorithm reported as a pain-index score with likelihood of atypical biochemical function associated with pain	Non-Benefit
0118U	Transplantation medicine, quantification of donor-derived cell-free DNA using whole genome next-generation sequencing, plasma, reported as percentage of donor-derived cell-free DNA in the total cell-free DNA	‹‹Requires TAR››
0119U	Cardiology, ceramides by liquid chromatography–tandem mass spectrometry, plasma, quantitative report with risk score for major cardiovascular events	Non-Benefit
0121U	Sickle cell disease, microfluidic flow adhesion (VCAM-1), whole blood	Non-Benefit
0122U	Sickle cell disease, microfluidic flow adhesion (P-Selectin), whole blood	Non-Benefit
0123U	Mechanical fragility, RBC, shear stress and spectral analysis profiling	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0129U	Hereditary breast cancer–related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), genomic sequence analysis and deletion/duplication analysis panel (ATM, BRCA1, BRCA2, CDH1, CHEK2, PALB2, PTEN, and TP53)	Non-Benefit
0130U	Hereditary colon cancer disorders (eg, Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis), targeted mRNA sequence analysis panel (APC, CDH1, CHEK2, MLH1, MSH2, MSH6, MUTYH, PMS2, PTEN, and TP53) (List separately in addition to code for primary procedure)	Non-Benefit
0131U	Hereditary breast cancer–related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), targeted mRNA sequence analysis panel (13 genes) (List separately in addition to code for primary procedure)	Non-Benefit
0132U	Hereditary ovarian cancer–related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), targeted mRNA sequence analysis panel (17 genes) (List separately in addition to code for primary procedure)	Non-Benefit
0133U	Hereditary prostate cancer–related disorders, targeted mRNA sequence analysis panel (11 genes) (List separately in addition to code for primary procedure)	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0134U	Hereditary pan cancer (eg, hereditary breast and ovarian cancer, hereditary endometrial cancer, hereditary colorectal cancer), targeted mRNA sequence analysis panel (18 genes) (List separately in addition to code for primary procedure)	Non-Benefit
0135U	Hereditary gynecological cancer (eg, hereditary breast and ovarian cancer, hereditary endometrial cancer, hereditary colorectal cancer), targeted mRNA sequence analysis panel (12 genes) (List separately in addition to code for primary procedure)	Non-Benefit
0136U	ATM (ataxia telangiectasia mutated) (eg, ataxia telangiectasia) mRNA sequence analysis (List separately in addition to code for primary procedure)	Non-Benefit
0137U	PALB2 (partner and localizer of BRCA2) (eg, breast and pancreatic cancer) mRNA sequence analysis (List separately in addition to code for primary procedure)	Non-Benefit
0138U	BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) mRNA sequence analysis (List separately in addition to code for primary procedure)	Non-Benefit
0139U	Neurology (autism spectrum disorder [ASD]), quantitative measurements of 6 central carbon metabolites (ie, α-ketoglutarate, alanine, lactate, phenylalanine, pyruvate, and succinate), LC-MS/MS, plasma, algorithmic analysis with result reported as negative or positive (with metabolic subtypes of ASD)	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0152U	Infectious disease (bacteria, fungi, parasites, and DNA viruses), microbial cell-free DNA, plasma, untargeted next-generation sequencing, report for significant positive pathogens	Non-Benefit
0153U	Oncology (breast), mRNA, gene expression profiling by next-generation sequencing of 101 genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a triple negative breast cancer clinical subtype(s) with information on immune cell involvement	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0156U	Copy number (eg, intellectual disability, dysmorphology), sequence analysis	Non-Benefit
0163U	Oncology (colorectal) screening, biochemical enzyme-linked immunosorbent assay (ELISA) of 3 plasma or serum proteins (teratocarcinoma derived growth factor-1 [TDGF-1, Cripto-1], carcinoembryonic antigen [CEA], extracellular matrix protein [ECM]), with demographic data (age, gender, CRC-screening compliance) using a proprietary algorithm and reported as likelihood of CRC or advanced adenomas	Non-Benefit
0164U	Gastroenterology (irritable bowel syndrome [IBS]), immunoassay for anti-CdtB and anti-vinculin antibodies, utilizing plasma, algorithm for elevated or not elevated qualitative results	Non-Benefit
0168U	Fetal aneuploidy (trisomy 21, 18, and 13) DNA sequence analysis of selected regions using maternal plasma without fetal fraction cutoff, algorithm reported as a risk score for each trisomy	Requires TAR

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0169U	NUDT15 (nudix hydrolase 15) and TPMT (thiopurine S-methyltransferase) (eg, drug metabolism) gene analysis, common variants	Requires TAR
0170U	Neurology (autism spectrum disorder [ASD]), RNA, next-generation sequencing, saliva, algorithmic analysis, and results reported as predictive probability of ASD diagnosis	Non-Benefit
0172U	Oncology (solid tumor as indicated by the label), somatic mutation analysis of BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) and analysis of homologous recombination deficiency pathways, DNA, formalin-fixed paraffin-embedded tissue, algorithm quantifying tumor genomic instability score	Requires TAR
0173U	Psychiatry (ie, depression, anxiety), genomic analysis panel, includes variant analysis of 14 genes	Non-Benefit
0174U	Oncology (solid tumor), mass spectrometric 30 protein targets, formalin-fixed paraffin-embedded tissue, prognostic and predictive algorithm reported as likely, unlikely, or uncertain benefit of 39 chemotherapy and targeted therapeutic oncology agents	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0175U	Psychiatry (eg, depression, anxiety), genomic analysis panel, variant analysis of 15 genes	Non-Benefit
0176U	Cytolethal distending toxin B (CdtB) and vinculin IgG antibodies by immunoassay (ie, ELISA)	Non-Benefit
0177U	Oncology (breast cancer), DNA, PIK3CA (phosphatidylinositol-4, 5-bisphosphate 3-kinase catalytic subunit alpha) gene analysis of 11 gene variants utilizing plasma, reported as PIK3CA gene mutation status	Requires TAR
0179U	Oncology (non-small cell lung cancer), cell-free DNA, targeted sequence analysis of 23 genes (single nucleotide variations, insertions and deletions, fusions without prior knowledge of partner/breakpoint, copy number variations), with report of significant mutation(s)	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0201U	Red cell antigen (Yt blood group) genotyping (YT), gene analysis, ACHE (acetylcholinesterase [Cartwright blood group]) exon 2	Non-Benefit
0203U	Autoimmune (inflammatory bowel disease), mRNA, gene expression profiling by quantitative RT-PCR, 17 genes (15 target and 2 reference genes), whole blood, reported as a continuous risk score and classification of inflammatory bowel disease aggressiveness	Non-Benefit
0205U	Ophthalmology (age-related macular degeneration), analysis of 3 gene variants (2 CFH gene, 1 ARMS2 gene), using PCR and MALDI-TOF, buccal swab, reported as positive or negative for neovascular age-related macular-degeneration risk associated with zinc supplements	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0206U	Neurology (Alzheimer disease); cell aggregation using morphometric imaging and protein kinase C-epsilon (PKCe) concentration in response to amylospheroid treatment by ELISA, cultured skin fibroblasts, each reported as positive or negative for Alzheimer disease	Non-Benefit
0207U	Neurology (Alzheimer disease); quantitative imaging of phosphorylated ERK1 and ERK2 in response to bradykinin treatment by in situ immunofluorescence, using cultured skin fibroblasts, reported as a probability index for Alzheimer disease	Non-Benefit
0209U	Cytogenomic constitutional (genome-wide) analysis, interrogation of genomic regions for copy number, structural changes and areas of homozygosity for chromosomal abnormalities	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0211U	Oncology (pan-tumor), DNA and RNA by next-generation sequencing, utilizing formalin-fixed paraffin-embedded tissue, interpretative report for single nucleotide variants, copy number alterations, tumor mutational burden, and microsatellite instability, with therapy association	Non-Benefit
0212U	Rare diseases (constitutional/heritable disorders), whole genome and mitochondrial DNA sequence analysis, including small sequence changes, deletions, duplications, short tandem repeat gene expansions, and variants in non-uniquely mappable regions, blood or saliva, identification and categorization of genetic variants, proband	‹‹Non-Benefit››
0213U	Rare diseases (constitutional/heritable disorders), whole genome and mitochondrial DNA sequence analysis, including small sequence changes, deletions, duplications, short tandem repeat gene expansions, and variants in non-uniquely mappable regions, blood or saliva, identification and categorization of genetic variants, each comparator genome (eg, parent, sibling)	‹‹Non-Benefit››

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0214U	Rare diseases (constitutional/heritable disorders), whole exome and mitochondrial DNA sequence analysis, including small sequence changes, deletions, duplications, short tandem repeat gene expansions, and variants in non-uniquely mappable regions, blood or saliva, identification and categorization of genetic variants, proband	Non-Benefit
0215U	Rare diseases (constitutional/heritable disorders), whole exome and mitochondrial DNA sequence analysis, including small sequence changes, deletions, duplications, short tandem repeat gene expansions, and variants in non-uniquely mappable regions, blood or saliva, identification and categorization of genetic variants, each comparator exome (eg, parent, sibling)	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0218U	Neurology (muscular dystrophy), DMD gene sequence analysis, including small sequence changes, deletions, duplications, and variants in non-uniquely mappable regions, blood or saliva, identification and characterization of genetic variants	Requires TAR
0220U	Oncology (breast cancer), image analysis with artificial intelligence assessment of 12 histologic and immunohistochemical features, reported as a recurrence score	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
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	Non-Benefit
0229U	‹‹BCAT1 (Branched chain amino acid transaminase 1) and IKZF1 (IKAROS family zinc finger 1) (for example, colorectal cancer) promoter methylation analysis ››	Non-Benefit
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	Requires TAR
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	Requires TAR

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
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	Requires TAR
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	Requires TAR
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	Requires TAR
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	Requires TAR

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
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	Requires TAR
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	Requires TAR
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	Requires TAR

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**››

Code	Description	Benefit Status
‹‹0242U	Targeted genomic sequence analysis panel, solid organ neoplasm, cell-free circulating DNA analysis of 55-74 genes, interrogation for sequence variants, gene copy number amplifications, and gene rearrangements	Requires TAR››
‹‹0243U	Obstetrics (preeclampsia), biochemical assay of placental-growth factor, time-resolved fluorescence immunoassay, maternal serum, predictive algorithm reported as a risk score for preeclampsia	Non-Benefit››
‹‹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	Requires TAR››
‹‹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	Requires TAR››
‹‹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	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**››

Code	Description	Benefit Status
‹‹0248U	Oncology (brain), spheroid cell culture in a 3d microenvironment, 12 drug panel, tumor-response prediction for each drug	Non-Benefit››
‹‹0249U	Oncology (breast), semiquantitative analysis of 32 phosphoproteins and protein analytes, includes laser capture microdissection, with algorithmic analysis and interpretative report	Non-Benefit››
‹‹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	Non-Benefit››
‹‹0251U	Hepcidin-25, enzyme-linked immunosorbent assay (elisa), serum or plasma	Non-Benefit››
‹‹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	Non-Benefit››

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
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)	Non-Benefit
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	Non-Benefit
‹‹0255U	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	Non-Benefit››
‹‹0256U	Trimethylamine/trimethylamine N-oxide (TMA/TMAO) profile, tandem mass spectrometry (MS/MS), urine, with algorithmic analysis and interpretive report	Non-Benefit››
‹‹0257U	Very long chain acyl-coenzyme A (CoA) dehydrogenase (VCLAD), leukocyte enzyme activity, whole blood	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**››

Code	Description	Benefit Status
‹‹0258U	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	Non-Benefit››
‹‹0259U	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, quanititative	Non-Benefit››
‹‹0260U	Rare diseases (constitutional/heritable disorders), identification of copy number variations, inversions, insertions, translocations, and other structural variants by optical genome mapping	Non-Benefit››
‹‹0261U	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	Non-Benefit››
‹‹0262U	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	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**››

Code	Description	Benefit Status
‹‹0263U	Neurology (autism spectrum disorder [ASD]), quantitative measurements of 16 central carbon metabolites (ie, a-ketoglutarate, alanine, lactate, phenylalanine, pyruvate, succinate, carnitine, citrate, fumarate, hypoxanthine, inosine, malate, S-sulfocystein, 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)	Non-Benefit››
‹‹0264U	Rare diseases (constitutional/heritable disorders), identification of copy number variations, inversions, insertions, translocations, and other structural variants by optical genome mapping	Non-Benefit››
‹‹0265U	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	Non-Benefit››
‹‹0266U	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	Non-Benefit››
‹‹0267U	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	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**››

Code	Description	Benefit Status
‹‹0268U	Hematology (atypical hemolytic uremic syndrome [aHUS]), genomic sequence analysis of 15 genes, blood, buccal swab, or amniotic fluid	Requires TAR››
‹‹0269U	Hematology (autosomal dominant congenital thrombocytopenia), genomic sequence analysis of 14 genes, blood, buccal swab, or amniotic fluid	Requires TAR››
‹‹0270U	Hematology (congenital coagulation disorders), genomic sequence analysis of 20 genes, blood, buccal swab, or amniotic fluid	Non-Benefit››
‹‹0272U	Hematology (genetic bleeding disorders), genomic sequence analysis of 51 genes, blood, buccal swab, or amniotic fluid, comprehensive	Non-Benefit››
‹‹0273U	Hematology (genetic hyperfibrinolysis, delayed bleeding), genomic sequence analysis of 8 genes (F13A1, F13B, FGA, FGB, FGG, SERPINA1, SERPINF1, SERPINF2, PLAU), blood, buccal swab, or amniotic fluid	Non-Benefit››

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0274U	Hematology (genetic platelet disorders), genomic sequence analysis of 43 genes, blood, buccal swab, or amniotic fluid	Non-Benefit
0276U	Genomic sequence analysis of 42 genes for detection of abnormalities associated with inherited thrombocytopenia (low platelet count)	Requires TAR
0277U	Hematology (genetic platelet function disorder), genomic sequence analysis of 31 genes, blood, buccal swab, or amniotic fluid	Non-Benefit
0278U	Hematology (genetic thrombosis), genomic sequence analysis of 12 genes, blood, buccal swab, or amniotic fluid	Non-Benefit
0285U	‹‹Oncology, disease progression and response monitoring to radiation, chemotherapy, or other systematic cancer treatments, cell-free DNA, quantitative branched chain DNA amplification, plasma, reported in ng/mL››	Non-Benefit
0286U	CEP72 (centrosomal protein, 72-KDa), NUDT15 (nudix hydrolase 15) and TPMT (thiopurine S-methyltransferase) (e.g., drug metabolism) gene analysis, common variants	Requires TAR
0287U	Oncology (thyroid), DNA and mRNA, next-generation sequencing analysis of 112 genes, fine needle aspirate or formalin-fixed paraffin-embedded (FFPE) tissue, algorithmic prediction of cancer recurrence, reported as a categorical risk result (low, intermediate, high)	Requires TAR
0288U	Oncology (lung), mRNA, quantitative PCR analysis of 11 genes (BAG1, BRCA1, CDC6, CDK2AP1, ERBB3, FUT3, IL11, LCK, RND3, SH3BGR, WNT3A) and 3 reference genes (ESD, TBP, YAP1), formalin-fixed paraffin-embedded (FFPE) tumor tissue, algorithmic interpretation reported as a recurrence risk score	Non-Benefit

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**››

Code	Description	Benefit Status
‹‹0289U	Neurology (Alzheimer disease), mRNA, gene expression profiling by RNA sequencing of 24 genes, whole blood, algorithm reported as predictive risk score	Non-Benefit››
‹‹0290U	Pain management, mRNA, gene expression profiling by RNA sequencing of 36 genes, whole blood, algorithm reported as predictive risk score	Non-Benefit››
‹‹0291U	Psychiatry (mood disorders), mRNA, gene expression profiling by RNA sequencing of 144 genes, whole blood, algorithm reported as predictive risk score	Non-Benefit››
‹‹0292U	Psychiatry (stress disorders), mRNA, gene expression profiling by RNA sequencing of 72 genes, whole blood, algorithm reported as predictive risk score	Non-Benefit››
‹‹0293U	Psychiatry (suicidal ideation), mRNA, gene expression profiling by RNA sequencing of 54 genes, whole blood, algorithm reported as predictive risk score	Non-Benefit››
‹‹0294U	Longevity and mortality risk, mRNA, gene expression profiling by RNA sequencing of 18 genes, whole blood, algorithm reported as predictive risk score	Non-Benefit››
‹‹0295U	Oncology (breast ductal carcinoma in situ), protein expression profiling by immunohistochemistry of 7 proteins (COX2, FOXA1, HER2, Ki-67, p16, PR, SIAH2), with 4 clinicopathologic factors (size, age, margin status, palpability), utilizing formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reported as a recurrence risk score	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**››

Code	Description	Benefit Status
‹‹0296U	Oncology (oral and/or oropharyngeal cancer), gene expression profiling by RNA sequencing at least 20 molecular features (eg, human and/or microbial mRNA), saliva, algorithm reported as positive or negative for signature associated with malignancy	Non-Benefit››
‹‹0297U	Oncology (pan tumor), whole genome sequencing of paired malignant and normal DNA specimens, fresh or formalin-fixed paraffin-embedded (FFPE) tissue, blood or bone marrow, comparative sequence analyses and variant identification	Non-Benefit››
‹‹0298U	Oncology (pan tumor), whole transcriptome sequencing of paired malignant and normal RNA specimens, fresh or formalin-fixed paraffin-embedded (FFPE) tissue, blood or bone marrow, comparative sequence analyses and expression level and chimeric transcript identification	Non-Benefit››
‹‹0299U	Oncology (pan tumor), whole genome optical genome mapping of paired malignant and normal DNA specimens, fresh frozen tissue, blood, or bone marrow, comparative structural variant identification	Non-Benefit››
‹‹0300U	Oncology (pan tumor), whole genome sequencing and optical genome mapping of paired malignant and normal DNA specimens, fresh tissue, blood, or bone marrow, comparative sequence analyses and variant identification	Non-Benefit››

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0303U	Hematology, red blood cell (RBC) adhesion to endothelial/subendothelial adhesion molecules, functional assessment, whole blood, with algorithmic analysis and result reported as an RBC adhesion index; hypoxic	Non-Benefit
0304U	Hematology, red blood cell (RBC) adhesion to endothelial/subendothelial adhesion molecules, functional assessment, whole blood, with algorithmic analysis and result reported as an RBC adhesion index; normoxic	Non-Benefit
0305U	Hematology, red blood cell (RBC) functionality and deformity as a function of shear stress, whole blood, reported as a maximum elongation index	Non-Benefit
‹‹0306U	Oncology (minimal residual disease [mrd]), next-generation targeted sequencing analysis, cell-free dna, initial (baseline) assessment to determine a patient specific panel for future comparisons to evaluate for mrd	Non-Benefit
0307U	Oncology (minimal residual disease [mrd]), next-generation targeted sequencing analysis of a patient-specific panel, cell-free dna, subsequent assessment with comparison to previously analyzed patient specimens to evaluate for mrd	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**

Code	Description	Benefit Status
0308U	Cardiology (coronary artery disease [cad]), analysis of 3 proteins (high sensitivity [hs] troponin, adiponectin, and kidney injury molecule-1 [kim-1]), plasma, algorithm reported as a risk score for obstructive cad	Non-Benefit
0309U	Cardiology (cardiovascular disease), analysis of 4 proteins (nt-probnp, osteopontin, tissue inhibitor of metalloproteinase-1 [timp-1], and kidney injury molecule-1 [kim-1]), plasma, algorithm reported as a risk score for major adverse cardiac event	Non-Benefit
0310U	Pediatrics (vasculitis, kawasaki disease [kd]), analysis of 3 biomarkers (nt-probnp, c-reactive protein, and t-uptake), plasma, algorithm reported as a risk score for kd	Non-Benefit
0313U	Oncology (pancreas), dna and mrna next-generation sequencing analysis of 74 genes and analysis of cea (ceacam5) gene expression, pancreatic cyst fluid, algorithm reported as a categorical result (ie, negative, low probability of neoplasia or positive, high probability of neoplasia)	Non-Benefit
0315U	Oncology (cutaneous squamous cell carcinoma), mrna gene expression profiling by rt-pcr of 40 genes (34 content and 6 housekeeping), utilizing formalin-fixed paraffin-embedded (ffpe) tissue, algorithm reported as a categorical risk result (ie, class 1, class 2a, class 2b)	Non-Benefit››

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0316U	Borrelia burgdorferi (lyme disease), ospa protein evaluation, urine	Non-Benefit
0317U	Oncology (lung cancer), four-probe fish (3q29, 3p22.1, 10q22.3, 10cen) assay, whole blood, predictive algorithm-generated evaluation reported as decreased or increased risk for lung cancer	Non-Benefit
0318U	Pediatrics (congenital epigenetic disorders), whole genome methylation analysis by microarray for 50 or more genes, blood	Non-Benefit
0319U	Nephrology (renal transplant), rna expression by select transcriptome sequencing, using pretransplant peripheral blood, algorithm reported as a risk score for early acute rejection	Non-Benefit
0320U	Nephrology (renal transplant), rna expression by select transcriptome sequencing, using posttransplant peripheral blood, algorithm reported as a risk score for acute cellular rejection	Non-Benefit
0322U	Neurology (autism spectrum disorder [asd]), quantitative measurements of 14 acyl carnitines and microbiome-derived metabolites, liquid chromatography with tandem mass spectrometry (lc-ms/ms), plasma, results reported as negative or positive for risk of metabolic subtypes associated with asd	Non-Benefit
‹‹0326U	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	Requires TAR››

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
‹‹0330U	Infectious agent detection by nucleic acid (DNA or RNA), vaginal pathogen panel, identification of 27 organisms, amplified probe technique, vaginal swab	Non-Benefit››
0331U	Oncology (hematolymphoid neoplasia), optical genome mapping for copy number alterations and gene rearrangements utilizing DNA from blood or bone marrow, report of clinically significant alterations	Non-Benefit
0332U	Oncology (pan-tumor), genetic profiling of 8 dna-regulatory (epigenetic) markers by quantitative polymerase chain reaction (qpcr), whole blood, reported as a high or low probability of responding to immune checkpoint-inhibitor therapy	Non-Benefit
0335U	Rare diseases (constitutional/heritable disorders), whole genome sequence analysis, including small sequence changes, copy number variants, deletions, duplications, mobile element insertions, uniparental disomy (UPD), inversions, aneuploidy, mitochondrial genome sequence analysis with heteroplasmy and large deletions, short tandem repeat (str) gene expansions, fetal sample, identification and categorization of genetic variants	Non-Benefit
0336U	Rare diseases (constitutional/heritable disorders), whole genome sequence analysis, including small sequence changes, copy number variants, deletions, duplications, mobile element insertions, uniparental disomy (UPD), inversions, aneuploidy, mitochondrial genome sequence analysis with heteroplasmy and large deletions, short tandem repeat (str) gene expansions, blood or saliva, identification and categorization of genetic variants, each comparator genome (e.g., parent)	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0337U	Oncology (plasma cell disorders and myeloma), circulating plasma cell immunologic selection, identification, morphological characterization, and enumeration of plasma cells based on differential cd138, cd38, cd19, and cd45 protein biomarker expression, peripheral blood	Non-Benefit
0338U	Oncology (solid tumor), circulating tumor cell selection, identification, morphological characterization, detection and enumeration based on differential epcam, cytokeratins 8, 18, and 19, and cd45 protein biomarkers, and quantification of her2 protein biomarker-expressing cells, peripheral blood	Non-Benefit
0340U	Oncology (pan-cancer), analysis of minimal residual disease (mrd) from plasma, with assays personalized to each patient based on prior next-generation sequencing of the patient's tumor and germline DNA, reported as absence or presence of mrd, with disease-burden correlation, if appropriate	‹‹Requires TAR››
0342U	Oncology (pancreatic cancer), multiplex immunoassay of C5, C4, cystatin C, factor B, osteoprotegerin (OPG), gelsolin, IGFBP3, CA125 and multiplex electrochemiluminescent immunoassay (ECLIA) for CA19-9, serum, diagnostic algorithm reported qualitatively as positive, negative, or borderline	Non-Benefit
0343U	Oncology (prostate), exosome-based analysis of 442 small noncoding RNAs (sncRNAs) by quantitative reverse transcription polymerase chain reaction (RT-qPCR), urine, reported as molecular evidence of no-, low-, intermediate- or high-risk of prostate cancer	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0344U	Hepatology (nonalcoholic fatty liver disease [nafld]), semiquantitative evaluation of 28 lipid markers by liquid chromatography with tandem mass spectrometry (lc-ms/ms), serum, reported as at-risk for nonalcoholic steatohepatitis (nash) or not nash	Non-Benefit
0345U	Psychiatry (e.g., depression, anxiety, attention deficit hyperactivity disorder [ADHD]), genomic analysis panel, variant analysis of 15 genes, including deletion/duplication analysis of cyp2d6	‹‹Requires TAR››
0347U	Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 16 gene report, with variant analysis and reported phenotypes	Non-Benefit
0348U	Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 25 gene report, with variant analysis and reported phenotypes	Non-Benefit
0349U	Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 27 gene report, with variant analysis, including reported phenotypes and impacted gene-drug interactions	Non-Benefit
0350U	Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 27 gene report, with variant analysis and reported phenotypes	Non-Benefit
0351U	Infectious disease (bacterial or viral), biochemical assays, tumor necrosis factor related apoptosis-inducing ligand (trail), interferon gamma-induced protein-10 (ip10), and c-reactive protein, serum, algorithm reported as likelihood of bacterial infection	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0355U	APOL1 (apolipoprotein L1) (eg, chronic kidney disease), risk variants (G1, G2)	Non-Benefit
0356U	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	Non-Benefit
0358U	Neurology (mild cognitive impairment), analysis of B-amyloid 1-42 and 1-40, chemiluminescence enzyme immunoassay, cerebral spinal fluid, reported as positive, likely positive, or negative	Non-Benefit
0360U	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	Non-Benefit
0361U	Neurofilament light chain, digital immunoassay, plasma, quantitative	Non-Benefit
0362U	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	Non-Benefit
0363U	Oncology (urothelial), mRNA, gene-expression 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	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0365U	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	Non-Benefit
0366U	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	Non-Benefit
0367U	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	Non-Benefit
0368U	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	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0375U	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	Non-Benefit
0376U	Oncology (prostate cancer), image analysis of at least 128 histologic features and clinical factors, prognostic algorithm determining the risk of distant metastases, and prostate cancer-specific mortality, includes predictive algorithm to androgen deprivation-therapy response, if appropriate	Non-Benefit
0377U	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)	Non-Benefit
0384U	Nephrology (chronic kidney disease), carboxymethyllysine, methylglyoxal hydroimidazolone, and carboxyethyl lysine by liquid chromatography with tandem mass spectrometry (lc-ms/ms) and hba1c and estimated glomerular filtration rate (gfr), with risk score reported for predictive progression to high-stage kidney disease	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0385U	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	Non-Benefit
‹‹0387U	Oncology (melanoma), autophagy and beclin 1 regulator 1 (AMBRA1) and loricrin (AMLo) by immunohistochemistry, formalin-fixed paraffin-embedded (FFPE) tissue, report for risk of progression	Non-Benefit››
‹‹0388U	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	Requires TAR››
‹‹0389U	Pediatric febrile illness (Kawasaki disease [KD]), interferon alpha-inducible 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	Non-Benefit››
‹‹0390U	Obstetrics (preeclampsia), kinase insert domain receptor (KDR), Endoglin (ENG), and retinol-binding protein 4 (RBP4), by immunoassay, serum, algorithm reported as a risk score	Non-Benefit››

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
‹‹0392U	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	Non-Benefit››
‹‹0393U	Neurology (eg, Parkinson disease, dementia with Lewy bodies), cerebrospinal fluid (CSF), detection of misfolded a-synuclein protein by seed amplification assay, qualitative	Non-Benefit››
‹‹0394U	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	Non-Benefit››
‹‹0395U	Oncology (lung) multi-omics (microbial DNA by shotgun next-generation sequencing and carcinoembryonic antigen and osteopontin by immunoassay), plasma, algorithm reported as malignancy risk for lung nodules in early-stage disease	Non-Benefit››

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
‹‹0398U	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	Non-Benefit››
‹‹0399U	Neurology (cerebral folate deficiency), serum, detection of anti-human folate receptor IgG-binding 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	Non-Benefit››
‹‹0400U	Obstetrics (expanded carrier screening), 145 genes by nextgeneration sequencing, fragment analysis and multiplex ligationdependent probe amplification, DNA, reported as carrier positive or negative	Non-Benefit››
‹‹0401U	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	Non-Benefit››

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0402U	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	Non-Benefit
0403U	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	Non-Benefit
0404U	Oncology (breast), semiquantitative measurement of thymidine kinase activity by immunoassay, serum, results reported as risk of disease progression	Non-Benefit
0405U	Oncology (pancreatic), 59 methylation haplotype block markers, next-generation sequencing, plasma, reported as cancer signal detected or not detected	Non-Benefit
0406U	Oncology (lung), flow cytometry, sputum, 5 markers (meso-tetra [4-carboxyphenyl] porphyrin [TCPP], CD206, CD66b, CD3, CD19), algorithm reported as likelihood of lung cancer	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0407U	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	Non-Benefit
0410U	Oncology (pancreatic), DNA, whole genome sequencing with 5-hydroxymethylcytosine enrichment, whole blood or plasma, algorithm reported as cancer detected or not detected	Non-Benefit
0411U	Psychiatry (eg, depression, anxiety, attention deficit hyperactivity disorder [ADHD]), genomic analysis panel, variant analysis of 15 genes, including deletion/duplication analysis of CYP2D6	Non-Benefit
0412U	Beta amyloid, AB42/40 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	Non-Benefit
0413U	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	Non-Benefit
0414U	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	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0415U	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	Non-Benefit
0417U	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	Non-Benefit
0418U	Oncology (breast), augmentative algorithmic analysis of digitized whole slide imaging of 8 histologic and immunohistochemical features, reported as a recurrence score	Non-Benefit
0419U	Neuropsychiatry (eg, depression, anxiety), genomic sequence analysis panel, variant analysis of 13 genes, saliva or buccal swab, report of each gene phenotype	Non-Benefit
0420U	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	Non-Benefit
0421U	Oncology (colorectal) screening, quantitative real-time target and signal amplification of 8 RNA markers (GAPDH, SMAD4, ACY1, AREG, CDH1, KRAS, TNFRSF10B, EGLN2) and fecal hemoglobin, algorithm reported as a positive or negative for colorectal cancer risk	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0422U	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	Non-Benefit
0423U	Psychiatry (e.g., depression, anxiety), genomic analysis panel, including variant analysis of 26 genes, buccal swab, report including metabolizer status and risk of drug toxicity by condition	Non-Benefit
0424U	Oncology (prostate), exosome-based analysis of 53 small noncoding RNAs (sncRNAs) by quantitative reverse transcription polymerase chain reaction (RT-qPCR), urine, reported as no molecular evidence, low-, moderate- or elevated-risk of prostate cancer	Non-Benefit
0425U	Genome (e.g., unexplained constitutional or heritable disorder or syndrome), rapid sequence analysis, each comparator genome (eg, parents, siblings)	‹‹Non-Benefit †››
0426U	Genome (e.g., unexplained constitutional or heritable disorder or syndrome), ultra-rapid sequence analysis	‹‹Non-Benefit †››
0427U	Monocyte distribution width, whole blood (List separately in addition to code for primary procedure)	Non-Benefit
0429U	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)	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0430U	Gastroenterology, malabsorption evaluation of alpha-1-antitrypsin, calprotectin, pancreatic elastase and reducing substances, feces, quantitative	Non-Benefit
0431U	Glycine receptor alpha1 IgG, serum or cerebrospinal fluid (CSF), live cell-binding assay (LCBA), qualitative	Non-Benefit
0432U	Kelch-like protein 11 (KLHL11) antibody, serum or cerebrospinal fluid (CSF), cell-binding assay, qualitative	Non-Benefit
0433U	Oncology (prostate), 5 DNA regulatory markers by quantitative PCR, whole blood, algorithm, including prostate-specific antigen, reported as likelihood of cancer	Non-Benefit
0434U	Drug metabolism (adverse drug reactions and drug response), genomic analysis panel, variant analysis of 25 genes with reported phenotypes	Non-Benefit
0435U	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	Non-Benefit
0436U	Oncology (lung), plasma analysis of 388 proteins, using aptamer-based proteomics technology, predictive algorithm reported as clinical benefit from immune checkpoint inhibitor therapy	Non-Benefit
0437U	Psychiatry (anxiety disorders), mRNA, gene expression profiling by RNA sequencing of 15 biomarkers, whole blood, algorithm reported as predictive risk score	Non-Benefit
0438U	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	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0439U	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 SPATC1L]), qPCR and digital PCR, whole blood, algorithm reported as a 4-tiered risk score for a 3-year risk of symptomatic CHD	Non-Benefit
0440U	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	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0441U	Infectious disease (bacterial, fungal, or viral infection), semiquantitative biomechanical assessment (via deformability cytometry), whole blood, with algorithmic analysis and result reported as an index	Non-Benefit
0442U	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	Non-Benefit
0443U	Neurofilament light chain (NfL), ultra-sensitive immunoassay, serum or cerebrospinal fluid	Non-Benefit
0444U	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)	Non-Benefit
0445U	B-amyloid (Abeta42) and phospho tau (181P) (pTau181), electrochemiluminescent immunoassay (ECLIA), cerebral spinal fluid, ratio reported as positive or negative for amyloid pathology	Non-Benefit
0446U	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	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0447U	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	Non-Benefit
0449U	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)	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0452U	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	Non-Benefit
0453U	Oncology (colorectal cancer), cell-free DNA (cfDNA), methylation-based quantitative PCR assay (SEPTIN9, IKZF1, BCAT1, Septin9-2, VAV3, BCAN), plasma, reported as presence or absence of circulating tumor DNA (ctDNA)	Non-Benefit
0454U	Rare diseases (constitutional/heritable disorders), identification of copy number variations, inversions, insertions, translocations, and other structural variants by optical genome mapping	Non-Benefit
0455U	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	Non-Benefit
0457U	Perfluoroalkyl substances (PFAS) (eg, perfluorooctanoic acid, perfluorooctane sulfonic acid), 9 PFAS compounds by LC-MS/MS, plasma or serum, quantitative	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0458U	Oncology (breast cancer), S100A8 and S100A9, by enzyme-linked immunosorbent assay (ELISA), tear fluid with age, algorithm reported as a risk score	Non-Benefit
0459U	B-amyloid (Abeta42) and total tau (tTau), electrochemiluminescent immunoassay (ECLIA), cerebral spinal fluid, ratio reported as positive or negative for amyloid pathology	Non-Benefit
0460U	Oncology, whole blood or buccal, DNA single-nucleotide polymorphism (SNP) genotyping by real-time PCR of 24 genes, with variant analysis and reported phenotypes	Non-Benefit
0461U	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	Non-Benefit
0462U	Melatonin levels test, sleep study, 7 or 9 sample melatonin profile (cortisol optional), enzyme-linked immunosorbent assay (ELISA), saliva, screening/preliminary	Non-Benefit
0463U	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	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0464U	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	Non-Benefit
0465U	Oncology (urothelial carcinoma), DNA, quantitative methylation-specific PCR of 2 genes (ONECUT2, VIM), algorithmic analysis reported as positive or negative	Non-Benefit
0466U	Cardiology (coronary artery disease [CAD]), DNA, genome-wide 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	Non-Benefit
0467U	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"	Non-Benefit
0468U	Hepatology (nonalcoholic steatohepatitis [NASH]), miR-34a-5p, alpha 2-macroglobulin, YKL40, HbA1c, serum and whole blood, algorithm reported as a single score for NASH activity and fibrosis	Non-Benefit
0469U	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	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0470U	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	Non-Benefit
0471U	Oncology (colorectal cancer), qualitative real-time PCR of 35 variants of KRAS and NRAS genes (exons 2, 3, 4), formalin-fixed paraffin-embedded (FFPE), predictive, identification of detected mutations	Requires TAR
0472U	Carbonic anhydrase VI (CA VI), parotid specific/secretory protein (PSP) and salivary protein (SP1) IgG, IgM, and IgA antibodies, enzyme-linked immunosorbent assay (ELISA), semiqualitative, blood, reported as predictive evidence of early Sjogren syndrome	Non-Benefit
0473U	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	Requires TAR
0474U	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 next-generation sequencing (NGS), Sanger sequencing, blood or saliva, reported as positive or negative for germline variants, each gene	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0475U	Hereditary prostate cancer-related 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	Requires TAR
‹‹0476U	Drug metabolism, psychiatry (eg, major depressive disorder, general anxiety disorder, attention deficit hyperactivity disorder [adhd], schizophrenia), whole blood, buccal swab and pharmacogenomic genotyping of 14 genes and cyp2d6 copy number variant analysis and reported phenotypes	Non-Benefit
0477U	Drug metabolism, psychiatry (eg, major depressive disorder, general anxiety disorder, attention deficit hyperactivity disorder [adhd], schizophrenia), whole blood, buccal swab and pharmacogenomic genotyping of 14 genes and cyp2d6 copy number variant analysis, including impacted gene-drug interactions and reported phenotypes	Non-Benefit
0478U	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 paraffin-embedded (ffpe) tissue, interrogation for single-nucleotide variants, insertions/deletions, gene rearrangements and reported as actionable detected variants for therapy selection	Non-Benefit››

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0479U	Tau, phosphorylated, ptau217	Non-Benefit
0480U	Infectious disease (bacteria, viruses, fungi and parasites), cerebrospinal fluid (csf), metagenomic next-generation sequencing (dna and rna), bioinformatic analysis, with positive pathogen identification	Non-Benefit
0481U	Idh1 (isocitrate dehydrogenase 1 [nadp+]), idh2 (isocitrate dehydrogenase 2 [nadp+]) and tert (telomerase reverse transcriptase) promoter (eg, central nervous system [cns] tumors), next-generation sequencing (single-nucleotide variants [snv], deletions, and insertions)	Non-Benefit
0482U	Obstetrics (preeclampsia), biochemical assay of soluble fms-like tyrosine kinase 1 (sflt-1) and placental growth factor (plgf), serum, ratio reported for sflt1/plgf, with risk of progression for preeclampsia with severe features within 2 weeks	Non-Benefit
0483U	Infectious disease (neisseria gonorrhoeae), sensitivity, ciprofloxacin resistance (gyra s91f point mutation), oral, rectal or vaginal swab, algorithm reported as probability of fluoroquinolone resistance	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0484U	Infectious disease (mycoplasma genitalium), macrolide sensitivity (23s rrna point mutation), oral, rectal or vaginal swab, algorithm reported as probability of macrolide resistance	Non-Benefit
0485U	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-nucleotide variants, small insertions/deletions, copy number alterations, fusions, microsatellite instability and tumor mutational burden	Non-Benefit
0486U	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	Non-Benefit
0487U	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	Non-Benefit
0488U	Obstetrics (fetal antigen noninvasive prenatal test), cell-free dna sequence analysis for detection of 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	Requires TAR

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0489U	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 fetal inheritance of 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)	Non-Benefit
0490U	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	Non-Benefit
0491U	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	Non-Benefit
0492U	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	Non-Benefit
0493U	Transplantation medicine, quantification of donor-derived cell-free dna (cfdna) using next-generation sequencing, plasma, reported as percentage of donor-derived cell-free dna	‹‹Requires TAR››

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0494U	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	Requires TAR
0495U	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	Non-Benefit
0496U	Oncology (colorectal), cell-free dna, 8 genes for mutations, 7 genes for methylation by real-time rt-pcr and 4 proteins by enzyme-linked immunosorbent assay, blood, reported positive or negative for colorectal cancer or advanced adenoma risk	Non-Benefit
0497U	Oncology (prostate), mrna gene-expression profiling by real-time rt-pcr of 6 genes (foxm1, mcm3, mtus1, ttc21b, alas1 and ppp2ca), utilizing formalin-fixed paraffin-embedded (ffpe) tissue, algorithm reported as a risk score for prostate cancer	Non-Benefit
0498U	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	Non-Benefit
0499U	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	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0500U	Autoinflammatory disease (vexas syndrome), dna, uba1 gene mutations, targeted variant analysis (m41t, m41v, m41l, c.118-2a>c, c.118-1g>c, c.1189_118-2del, s56f, s621c)	Non-Benefit
0501U	Oncology (colorectal), blood, quantitative measurement of cell-free dna (cfdna)	Non-Benefit
0502U	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	Non-Benefit
0503U	Neurology (alzheimer disease), beta amyloid (ab40, ab42, ab42/40 ratio) and tau-protein (ptau217, np-tau217, ptau217/nptau217 ratio), blood, immunoprecipitation with quantitation by liquid chromatography with tandem mass spectrometry (lc-ms/ms), algorithm score reported as likelihood of positive or negative for amyloid plaques	Non-Benefit
0504U	Infectious disease (urinary tract infection), identification of 17 pathologic organisms, urine, real-time pcr, reported as positive or negative for each organism	Non-Benefit
0505U	Infectious disease (vaginal infection), identification of 32 pathogenic organisms, swab, real-time pcr, reported as positive or negative for each organism	Non-Benefit
0506U	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	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0507U	Oncology (ovarian), dna, whole-genome sequencing with 5hydroxymethylcytosine (5hmc) enrichment, using whole blood or plasma, algorithm reported as cancer detected or not detected	Non-Benefit
0508U	Transplantation medicine, quantification of donor-derived cell-free dna using 40 single-nucleotide polymorphisms (snps), plasma and urine, initial evaluation reported as percentage of donor-derived cell-free dna with risk for active rejection	Non-Benefit
0509U	Transplantation medicine, quantification of donor-derived cell-free dna using up to 12 single-nucleotide polymorphisms (snps) previously identified, plasma, reported as percentage of donor-derived cell-free dna with risk for active rejection	Non-Benefit
0510U	Oncology (pancreatic cancer), augmentative algorithmic analysis of 16 genes from previously sequenced rna whole-transcriptome data, reported as probability of predicted molecular subtype	Non-Benefit
0511U	Oncology (solid tumor), tumor cell culture in 3d microenvironment, 36 or more drug panel, reported as tumor-response prediction for each drug	Non-Benefit
0512U	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)	Non-Benefit
0513U	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	Non-Benefit

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0514U	Gastroenterology (irritable bowel disease [ibd]), immunoassay for quantitative determination of adalimumab (adl) levels in venous serum in patients undergoing adalimumab therapy, results reported as a numerical value as micrograms per milliliter (g/ml)	Non-Benefit
0515U	Gastroenterology (irritable bowel disease [ibd]), immunoassay for quantitative determination of infliximab (ifx) levels in venous serum in patients undergoing infliximab therapy, results reported as a numerical value as micrograms per milliliter (g/ml)	Non-Benefit
0516U	Drug metabolism, whole blood, pharmacogenomic genotyping of 40 genes and cyp2d6 copy number variant analysis, reported as metabolizer status	Non-Benefit
0517U	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	Non-Benefit
0518U	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	Non-Benefit
0519U	Therapeutic drug monitoring, medications specific to pain, depression and anxiety, lcms/ms, plasma, 110 or more drugs or substances, qualitative and quantitative therapeutic minimally effective range of prescribed, non-prescribed and illicit medications in circulation	Non-Benefit
0520U	Therapeutic drug monitoring, 200 or more drugs or substances, lcms/ms, plasma, qualitative and quantitative therapeutic minimally effective range of prescribed and non-prescribed medications	Non-Benefit

‹‹Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0521U	Rheumatoid factor iga and igm, cyclic citrullinated peptide (ccp) antibodies, and scavenger receptor a (sr-a) by immunoassay, blood	Non-Benefit
0522U	Carbonic anhydrase vi, parotid specific/secretory protein and salivary protein 1 (sp1), igg, igm, and iga antibodies, chemiluminescence, semiqualitative, blood	Non-Benefit
0523U	Oncology (solid tumor), dna, qualitative, next-generation sequencing (ngs) of single-nucleotide variants (snv) and insertion/deletions in 22 genes utilizing formalin-fixed paraffin-embedded tissue, reported as presence or absence of mutation(s), location of mutation(s), nucleotide change, and amino acid change	Requires a TAR
0524U	Obstetrics (preeclampsia), sflt-1/plgf ratio, immunoassay, utilizing serum or plasma, reported as a value	Non-Benefit
0525U	Oncology, spheroid cell culture, 11-drug panel (carboplatin, docetaxel, doxorubicin, etoposide, gemcitabine, niraparib, olaparib, paclitaxel, rucaparib, topotecan, veliparib) ovarian, fallopian, or peritoneal response prediction for each drug	Non-Benefit
0526U	Nephrology (renal transplant), quantification of cxcl10 chemokines, flow cytometry, urine, reported as pg/ml creatinine baseline and monitoring over time	Non-Benefit››

Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0527U	Herpes simplex virus (hsv) types 1 and 2 and varicella zoster virus (vzv), amplified probe technique, each pathogen reported as detected or not detected	Non-Benefit
0529U	Hematology (venous thromboembolism [vte]), genome-wide single-nucleotide polymorphism variants, including f2 and f5 gene analysis, and leiden variant, by microarray analysis, saliva, report as risk score for vte	Non-Benefit
0530U	Oncology (pan-solid tumor), ctdna, utilizing plasma, next-generation sequencing (ngs) of 77 genes, 8 fusions, microsatellite instability, and tumor mutation burden, interpretative report for single-nucleotide variants, copy-number alterations, with therapy association	Non-Benefit
‹‹0531U	Infectious disease (acid-fast bacteria and invasive fungi), DNA (673 organisms), nextgeneration sequencing, plasm	Non-Benefit››
‹‹0532U	Rare diseases (constitutional disease/hereditary disorders), rapid whole genome and mitochondrial DNA sequencing for singlenucleotide variants, insertions/deletions, copy number variations, peripheral blood, buffy coat, saliva, buccal or tissue sample, results reported as positive or negative	Non-Benefit †››
‹‹0533U	Drug metabolism (adverse drug reactions and drug response), genotyping of 16 genes (ie, ABCG2, CYP2B6, CYP2C9, CYP2C19, CYP2C, CYP2D6, CYP3A5, CYP4F2, DPYD, G6PD, GGCX, NUDT15, SLCO1B1, TPMT, UGT1A1, VKORC1), reported as metabolizer status and transporter function	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**

Code	Description	Benefit Status
0534U	Oncology (prostate), microRNA, single-nucleotide polymorphisms (SNPs) analysis by RT-PCR of 32 variants, using buccal swab algorithm reported as a risk score	Non-Benefit
0535U	Perfluoroalkyl substances (PFAS) (eg, perfluorooctanoic acid, perfluorooctane sulfonic acid), by liquid chromatography with tandem mass spectrometry (LC-MS/MS), plasma or serum, quantitative	Non-Benefit
0536U	Red blood cell antigen (fetal RhD), pcr analysis of exon 4 of RHD gene and housekeeping control gene GADPH from whole blood in pregnant individuals at 10 plus weeks gestation known to be RHD negative, reported as fetal RhD status	Non-Benefit
0537U	Oncology (colorectal cancer), analysis of cell-free DNA for epigenomic patterns, next-generation sequencing, greater than2500 differentially methylated regions (DMRs), plasma, algorithm reported as positive or negative	Non-Benefit
0538U	Oncology (solid tumor), next-generation targeted sequencing analysis, formalin-fixed paraffin-embedded (FFPE) tumor tissue, DNA analysis of 600 genes, interrogation for single-nucleotide variants, insertions/deletions, gene rearrangements, and copy number alterations, microsatellite instability, tumor mutation burden, reported as actionable variant	Non-Benefit
0539U	Oncology (solid tumor), cell-free circulating tumor DNA (ctDNA), 152 genes, next-generation sequencing, interrogation for single-nucleotide variants, insertions/deletions, gene rearrangements, copy number alterations, and microsatellite instability, using whole-blood samples, mutations with clinical actionability reported as actionable variant	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**

Code	Description	Benefit Status
0540U	Transplantation medicine, quantification of donor-derived cell-free DNA using next-generation sequencing analysis of plasma, reported as percentage of donor-derived cell-free DNA to determine probability of rejection	Requires TAR
0541U	Cardiovascular disease (HDL reverse cholesterol transport), cholesterol efflux capacity, LC-MS/MS, quantitative measurement of 5 distinct HDL-bound apolipoproteins (apolipoproteins A1, C1, C2, C3, and C4), serum, algorithm reported as prediction of coronary artery disease (pCAD) score	Non-Benefit
0542U	Nephrology (renal transplant), urine, nuclear magnetic resonance (NMR) spectroscopy measurement of 84 urinary metabolites, combined with patient data, quantification of BK virus (human polyomavirus 1) using real-time PCR and serum creatinine, algorithm reported as a probability score for allograft injury status	Non-Benefit
0543U	Oncology (solid tumor), next-generation sequencing of DNA from formalin-fixed paraffin-embedded (FFPE) tissue of 517 genes, interrogation for single-nucleotide variants, multi-nucleotide variants, insertions and deletions from DNA, fusions in 24 genes and splice variants in 1 gene from RNA, and tumor mutational burden	Requires TAR
0544U	Nephrology (transplant monitoring), 48 variants by digital PCR, using cell-free DNA from plasma, donor-derived cell-free DNA, percentage reported as risk for rejection	Non-Benefit››

‹‹Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0545U	Acetylcholine receptor (AChR), antibody identification by immunofluorescence, using live cells, reported as positive or negative	Non-Benefit
0546U	Low-density lipoprotein receptor-related protein 4 (LRP4), antibody identification by immunofluorescence, using live cells, reported as positive or negative	Non-Benefit
0547U	Neurofilament light chain (NfL), chemiluminescent enzyme immunoassay, plasma, quantitative	Non-Benefit
0548U	Glial fibrillary acidic protein (GFAP), chemiluminescent enzyme immunoassay, using plasma	Non-Benefit
0549U	Oncology (urothelial), DNA, quantitative methylated real-time PCR of TRNA-Cys, SIM2, and NKX1-1, using urine, diagnostic algorithm reported as a probability index for bladder cancer and/or upper tract urothelial carcinoma (UTUC)	Non-Benefit
0550U	Oncology (prostate), enzyme linked immunosorbent assays (ELISA) for total prostate specific antigen (PSA) and free PSA, serum, combined with age, previous negative prostate biopsy status, digital rectal examination findings, prostate volume, and image and data reporting of the prostate, algorithm reported as a risk score for the presence of high-grade prostate cancer	Non-Benefit
0551U	Tau, phosphorylated, pTau217, by single-molecule array (ultrasensitive digital protein detection), using plasma	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**

Code	Description	Benefit Status
0552U	Reproductive medicine (preimplantation genetic assessment), analysis for known genetic disorders from trophectoderm biopsy, linkage analysis of disease-causing locus, and when possible, targeted mutation analysis for known familial variant, reported as low-risk or high-risk for familial genetic disorder	Non-Benefit
0553U	Reproductive medicine (preimplantation genetic assessment), analysis of 24 chromosomes using DNA genomic sequence analysis from embryonic trophectoderm for structural rearrangements, aneuploidy, and a mitochondrial DNA score, results reported as normal/balanced (euploidy/balanced), unbalanced structural rearrangement, monosomy, trisomy, segmental aneuploidy, or mosaic, per embryo tested	Non-Benefit
0554U	Reproductive medicine (preimplantation genetic assessment), analysis of 24 chromosomes using DNA genomic sequence analysis from trophectoderm biopsy for aneuploidy, ploidy, a mitochondrial DNA score, and embryo quality control, results reported as normal (euploidy), monosomy, trisomy, segmental aneuploidy, triploid, haploid, or mosaic, with quality control results reported as contamination detected or inconsistent cohort when applicable, per embryo tested	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**

Code	Description	Benefit Status
0555U	Reproductive medicine (preimplantation genetic assessment), analysis of 24 chromosomes using DNA genomic sequence analysis from embryonic trophectoderm for structural rearrangements, aneuploidy, ploidy, a mitochondrial DNA score, and embryo quality control, results reported as normal/balanced (euploidy/balanced), unbalanced structural rearrangement, monosomy, trisomy, segmental aneuploidy, triploid, haploid, or mosaic, with quality control results reported as contamination detected or inconsistent cohort when applicable, per embryo tested	Non-Benefit
0556U	Infectious disease (bacterial or viral respiratory tract infection), pathogen-specific DNA and RNA by real-time PCR, 12 targets, nasopharyngeal or oropharyngeal swab, including multiplex reverse transcription for RNA targets, each analyte reported as detected or not detected	Non-Benefit
0557U	Infectious disease (bacterial vaginosis and vaginitis), real-time amplification of DNA markers for Atopobium vaginae, Gardnerella vaginalis, Megasphaera types 1 and 2, bacterial vaginosis associated bacteria-2 and -3 (BVAB-2, BVAB-3), Mobiluncus species, Trichomonas vaginalis, Neisseria gonorrhoeae, Candida species (C. albicans, C. tropicalis, C. parapsilosis, C. glabrata, C. krusei), Herpes simplex viruses 1 and 2, vaginal fluid, reported as detected or not detected for each organism	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**

Code	Description	Benefit Status
0558U	Oncology (colorectal), quantitative enzyme-linked immunosorbent assay (ELISA) for secreted colorectal cancer protein marker (BF7 antigen), using serum, result reported as indicative of response/no response to therapy or disease progression/regression	Non-Benefit
0559U	Oncology (breast), quantitative enzyme-linked immunosorbent assay (ELISA) for secreted breast cancer protein marker (BF9 antigen), serum, result reported as indicative of response/no response to therapy or disease progression/regression	Non-Benefit
0560U	Oncology (minimal residual disease [MRD]), genomic sequence analysis, cell-free DNA, whole blood and tumor tissue, baseline assessment for design and construction of a personalized variant panel to evaluate current MRD and for comparison to subsequent MRD assessments	Non-Benefit
0561U	Oncology (minimal residual disease [MRD]), genomic sequence analysis, cell-free DNA, whole blood, subsequent assessment with comparison to initial assessment to evaluate for MRD	Non-Benefit
0562U	Oncology (solid tumor), targeted genomic sequence analysis, 33 genes, detection of single-nucleotide variants (SNVs), insertions and deletions, copy-number amplifications, and translocations in human genomic circulating cell-free DNA, plasma, reported as presence of actionable variants	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**

Code	Description	Benefit Status
0565U	Oncology (hepatocellular carcinoma), next-generation sequencing methylation pattern assay to detect 6626 epigenetic alterations, cell-free DNA, plasma, algorithm reported as cancer signal detected or not detected	Non-Benefit
0566U	Oncology (lung), qPCR-based analysis of 13 differentially methylated regions (CCDC181, HOXA7, LRRC8A, MARCHF11, MIR129-2, NCOR2, PANTR1, PRKCB, SLC9A3, TBR1_2, TRAP1, VWC2, ZNF781), pleural fluid, algorithm reported as a qualitative result	Non-Benefit
0567U	Rare diseases (constitutional/heritable disorders), whole-genome sequence analysis combination of short and long reads, for single-nucleotide variants, insertions/deletions and characterized intronic variants, copy-number variants, duplications/deletions, mobile element insertions, runs of homozygosity, aneuploidy, and inversions, mitochondrial DNA sequence and deletions, short tandem repeat genes, methylation status of selected regions, blood, saliva, amniocentesis, chorionic villus sample or tissue, identification and categorization of genetic variants	Non-Benefit
0568U	Neurology (dementia), beta amyloid (AB40, AB42, AB42/40 ratio), tau-protein phosphorylated at residue (eg, pTau217), neurofilament light chain (NfL), and glial fibrillary acidic protein (GFAP), by ultra-high sensitivity molecule array detection, plasma, algorithm reported as positive, intermediate, or negative for Alzheimer pathology	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**

Code	Description	Benefit Status
0569U	Oncology (solid tumor), next-generation sequencing analysis of tumor methylation markers (>20000 differentially methylated regions) present in cell-free circulating tumor DNA (ctDNA), whole blood, algorithm reported as presence or absence of ctDNA with tumor fraction, if appropriate	Non-Benefit
0570U	Neurology (traumatic brain injury), analysis of glial fibrillary acidic protein (GFAP) and ubiquitin carboxyl-terminal hydrolase L1 (UCH-L1), immunoassay, whole blood or plasma, individual components reported with the overall result of elevated or non-elevated based on threshold comparison	Non-Benefit
0571U	Oncology (solid tumor), DNA (80 genes) and RNA (10 genes), by next-generation sequencing, plasma, including single-nucleotide variants, insertions/deletions, copy-number alterations, microsatellite instability, and fusions, reported as clinically actionable variants	Non-Benefit
0572U	Oncology (prostate), high-throughput telomere length quantification by FISH, whole blood, diagnostic algorithm reported as risk of prostate cancer	Non-Benefit
0573U	Oncology (pancreas), 3 biomarkers (glucose, carcinoembryonic antigen, and gastricsin), pancreatic cyst lesion fluid, algorithm reported as categorical mucinous or non-mucinous	Non-Benefit
0574U	Mycobacterium tuberculosis, culture filtrate protein-10-kDa (CFP-10), serum or plasma, liquid chromatography mass spectrometry (LC-MS)	Non-Benefit››

‹‹Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0575U	Transplantation medicine (liver allograft rejection), miRNA gene expression profiling by RT-PCR of 4 genes (miR-122, miR-885, miR-23a housekeeping, spike-in control), serum, algorithm reported as risk of liver allograft rejection	Non-Benefit
0576U	Transplantation medicine (liver allograft rejection), quantitative donor-derived cell-free DNA (cfDNA) by whole genome next-generation sequencing, plasma and mRNA gene expression profiling by multiplex real-time PCR of 56 genes, whole blood, combined algorithm reported as a rejection risk score	Non-Benefit
0577U	Oncology (ovarian), serum, analysis of 39 glycoproteins by liquid chromatography with tandem mass spectrometry (LC-MS/MS) in multiple reaction monitoring mode, reported as likelihood of malignancy	Non-Benefit
0578U	Oncology (cutaneous melanoma), RNA, gene expression profiling by real-time qPCR of 10 genes (8 content and 2 housekeeping), utilizing formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reports a binary result, either low-risk or high-risk for sentinel lymph node metastasis and recurrence	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**

Code	Description	Benefit Status
0579U	Nephrology (diabetic chronic kidney disease), enzyme-linked immunosorbent assay (ELISA) of apolipoprotein A4 (APOA4), CD5 antigen-like (CD5L) combined with estimated glomerular filtration rate (GFR), age, plasma, algorithm reported as a risk score for kidney function decline	Non-Benefit
0581U	Transplantation medicine, antibody to non-human leukocyte antigens (non-HLA), blood specimen, flow cytometry, single-antigen bead technology, 39 targets, individual positive antibodies reported	Non-Benefit
0582U	Rare diseases (constitutional disease/hereditary disorders), rapid whole genome DNA sequencing for single-nucleotide variants, insertions/deletions, copy number variations, blood, saliva, tissue sample, variants reported	Non-Benefit †
0583U	Rare diseases (constitutional disease/hereditary disorders), rapid whole genome comparator DNA sequencing for single-nucleotide variants, insertions/deletions, copy number variations, blood, saliva, tissue sample, variants reported with proband results (List separately in addition to code for primary procedure)	Non-Benefit †
0584U	Neurology (prion disease), cerebrospinal fluid, detection of prion protein by quaking-induced conformational conversion, qualitative	Non-Benefit
0585U	Targeted genomic sequence analysis panel, solid organ neoplasm, circulating cell-free DNA (cfDNA) analysis from plasma of 521 genes, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, and microsatellite instability, report shows identified mutations, including variants with clinical actionability	Non-Benefit››

‹‹Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)

Code	Description	Benefit Status
0586U	Oncology, mRNA, gene expression profiling of 216 genes (204 targeted and 12 housekeeping genes), RNA expression analysis, formalin-fixed paraffin-embedded (FFPE) tissue, quantitative, reported as log2 ratio per gene	Non-Benefit
0587U	Therapeutic drug monitoring, 60-150 drugs and metabolites, urine, saliva, quantitative liquid chromatography with tandem mass spectrometry (LC-MS/MS), specimen validity, and algorithmic analyses for presence or absence of drug or metabolite, risk score predicted for adverse drug effects	Non-Benefit
0588U	Infectious disease (bacterial or viral), 32 genes (29 informative and 3 housekeeping), immune response mRNA, gene expression profiling by split-well multiplex reverse transcription loop-mediated isothermal amplification (RT-LAMP), whole blood, reported as continuous risk scores for likelihood of bacterial and viral infection and likelihood of severe illness within the next 7 days	Requires TAR
0589U	Perfluoroalkyl substances (PFAS) (eg, perfluorooctanoic acid, perfluorooctane sulfonic acid), 24 PFAS compounds by high-performance liquid chromatography with tandem mass spectrometry (LC-MS/MS), plasma or serum, quantitative	Non-Benefit
0590U	Infectious disease (bacterial and fungal), DNA of 44 organisms (34 bacteria, 10 fungi), urine, next-generation sequencing, reported as positive or negative for each organism	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**

Code	Description	Benefit Status
0591U	Oncology (prostate cancer), biochemical analysis of 3 proteins (total PSA, free PSA, and HE4), plasma, serum, prognostic algorithm incorporating 3 proteins and digital rectal examination, results reported as a probability score for clinically significant prostate cancer	Non-Benefit
0592U	Oncology (hematolymphoid neoplasms), DNA, targeted genomic sequence of 417 genes, interrogation for gene fusions, translocations, rearrangements, utilizing formalin-fixed paraffin-embedded (FFPE) tumor tissue, results report clinically significant variant(s)	Non-Benefit
0593U	Infectious disease (genitourinary pathogens), DNA, 46 targets (28 pathogens, 18 resistance genes), RT-PCR amplified probe technique, urine, each analyte reported as detected or not detected	Non-Benefit
0594U	Infectious disease (sepsis), semiquantitative measurement of pancreatic stone protein concentration, whole blood, reported as risk of sepsis	Non-Benefit
0596U	Neurology (Alzheimer disease), plasma, 3 distinct isoform-specific peptides (APOE2, APOE3, and APOE4) by liquid chromatography with tandem mass spectrometry (LC-MS/MS), reported as an APOE prototype	Non-Benefit››

‹‹**Table of PLA and MAAA Codes in Non-Benefit Status or with TAR Requirement (continued)**

Code	Description	Benefit Status
0597U	Oncology (breast), RNA expression profiling of 329 genes by targeted next-generation sequencing and 20 proteins by multiplex immunofluorescence, formalin-fixed paraffin-embedded (FFPE) tissue, algorithmic analyses to determine tumor-recurrence risk score	Non-Benefit
0598U	Gastroenterology (irritable bowel syndrome), IgG antibodies to 18 food items by microarray-based immunoassay, whole blood or serum, report as elevated (positive) or normal (negative) antibody levels	Non-Benefit
0599U	Oncology (pancreatic cancer), multiplex immunoassay of ICAM1, TIMP1, CTSD, THBS1, and CA 19-9, serum, diagnostic algorithm reported as positive or negative	Non-Benefit››

Legend

Symbols used in the document above are explained in the following table.

Symbol	Description
‹‹	This is a change mark symbol. It is used to indicate where on the page the most recent change begins.
››	This is a change mark symbol. It is used to indicate where on the page the most recent change ends.
†	Per Assembly Bill (AB) 133, Rapid Whole Genome Sequencing, including individual sequencing, trio sequencing for a parent or parents and their baby, and ultra-rapid sequencing, is a covered benefit for any Medi-Cal beneficiary who is one year of age or younger and is receiving inpatient hospital services in an intensive care unit. These codes cannot be used for the purpose of inpatient billing as inpatient laboratory services are bundled under DRG or per diem payment. For inpatient billing, please refer *to Diagnosis Related Group Hospital Inpatient Payment Methodology*.