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Pathology & Laboratory
2020 CPT Updates
Effective 1/1/2020

Each year the CPT code manual is revised to delete codes and/or guidelines, and to add or revise codes to reflect current technologies, techniques, and services. As a service to our clients, APS Medical Billing has summarized those changes to facilitate accurate reporting of the affected services as of January 1, 2020. The American Medical Association has released that there will be 394 code changes in the new CPT edition to capture and describe the latest scientific and technological advances in medical, surgical and diagnostic services. A big change for Pathology will be to the Molecular Pathology codes.

Below we have also outlined the changes made to these sections. All new codes are highlighted in red and revised/deleted codes are noted:

Therapeutic Drug Assays

New Codes for 2020

80145 Adalimumag
80187 Posaconazole
80230 Infiximab
80235 Lacosmide
80280 Vedolizumab
80285 Voriconazole
87563 Infectious agent detection by nucleic acid (DNA or RNA); Mycoplasma genitalium, amplified probe technique

Molecular Pathology

New Codes for 2020 - Tier 1

81277 Cytogenomic neoplasia (genome-wide) microarray analysis, interrogation of genomic regions for copy number loss-of-heterozygosity variants for chromosomal abnormalities.
81307 PALB2 (partner and localizer of BRCA2) (eg. Breast and Pancreatic cancer) gene analysis; full gene sequence.
81308 PALB2 (partner and localizer of BRACA2) (eg. Breast and Pancreatic cancer) gene analysis; known familial variant.
81309 PIK3CA (phosphatidylinositol-4, 5-diphoshate 3-kinase, catalytic subunit alpha) (eg, Colorectal and Breast cancer) gene analysis, targeted sequence analysis (eg, exons 7, 9, 20)

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81522 Oncology (breast), mRNA, gene expression profiling by RT-PCR of 12 genes (8 content and 4 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as recurrence risk score.

81542 Oncology (prostate), mRNA, microarray gene expression profiling of 22 content genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as metastasis risk score.

81552 Oncology (uveal melanoma), mRNA, gene expression profiling by real-time RT-PCR of 15 genes (12 content and 3 housekeeping), utilizing fine needle aspirate or formalin-embedded tissue, algorithm reported as risk of metastasis.

Revised Codes for 2020

81350 UGT1A1 (UDP glucuronosyltransferase 1 family, polypeptide A1) (eg, drug metabolism, hereditary unconjugated hyperbilirubinemia [Gilbert Syndrome]) gene analysis, common variants (eg *28, *36, *37)

81404 Molecular pathology procedure, Level 5 (eg, analysis of 2-5 exons) by DNA sequence analysis, mutation scanning or duplication/deletion variants of 6-10 exons, or characterization of a dynamic mutation disorder/triplet repeat by southern blot analysis)
~~PIK3CA (phosphatidylinositol 4, 5 bisphosphate 3 kinase, catalytic subunit alpha) (eg, colorectal cancer), targeted sequence analysis (eg, exon 9 and 20)~~
UGT1A1 (UDP glucuronosyltransferase 1 family, polypeptide A1) (eg. Hereditary unconjugated hyperbilirubinemia (Crigler-Najjar syndrome) full gene sequence

81406 Molecular pathology procedure, Level 7 (eg, analysis of 11-25 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of 26-50 exons, ~~cytogenomic array analysis for neoplasia~~
~~Cytogenomic microarray analysis, neoplasia (eg, interrogation of copy number, and loss of heterozygosity via single nucleotide polymorphism [SNP] based comparative genomic hybridization [CGH 1] microarray analysis~~
~~PALB2 (partner and localizer of BRCA2), (eg, breast and pancreatic cancer), full gene sequence~~

81407 Molecular pathology procedure, Level 8 (eg, analysis of 26-50 exons by DNA sequence analysis, mutation scanning or duplication/ deletion variants of >50 exons, sequence analysis of multiple genes on one platform)
APOB (apolipoprotein B) (eg, familial hypercholesterolemia type B) full gene sequence

Multiananlyte Assays with Alogorithmic Analyses

New Codes for 2020

81522 Oncology (breast) mRNA, gene expression profiling by real-time RT-PCR of 12 genes (8 content and 4 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as recurrence risk score

81542 Oncology (prostate), mRNA, microarray gene expression profiling of 22 content genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as metastasis risk score

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81552 Oncology (uveal melanoma), mRMA, gene expression profiling by real-time RT-PCR of 15 genes (12 content and 3 housekeeping), utilizing fine needle aspirate or formalin-fixed paraffin-embedded tissue, algorithm reported as risk of metastasis.

Microbiology

New Code for 2020

87563 Mycoplasma genitalium, amplified probe technique

Proprietary Laboratory Analyses

New Codes for 2020

0062U Autoimmune (systemic lupus erythematosus), IgG and IgM analysis of 80 biomarkers, utilizing serum, algorithm reported with a risk score
0063U Neurology (autism), 32 amines by LC-MS/MS, using plasma, algorithm reported as metabolic signature associated with autism spectrum disorder
0064U Antibody, Treponema pallidum, total and rapid plasma reagin (RPR), immunoassay, qualitative
0065U Syphilis test, non-treponemal antibody, immunoassay, qualitative (RPR)
0066U Placental alpha-micro globulin-1 (PAMG-1), immunoassay with direct optical observation, cervico-vaginal fluid, each specimen
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
0068U Candida species panel (C. albicans, C. glabratam C. parapsilosis, C. kruseiim C. tropicalis, and C. auris) amplified probe technique with qualitative report of the presence or absence of each species
0069U Oncology (colorectal), microRNA, RT-PCR expression profiling of miR-31-3p, formalin-fixed paraffin-embedded tissue, algorithm reported as an expression score
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)
+ 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)
➢ Use 0071U in conjunction with 0070U
+ 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)
➢ Use 0072U in conjunction with 0070U

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+ 0073U *CYP2D6 (cytochrome P450, family 2, subfamily D polypeptide 6)* (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, *CYP2D6-2D6* hybrid gene) (List separately in addition to code for primary procedure)
➢ Use 0073U in conjunction with 0070U

+ 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)
➢ Use 0074U in conjunction with 0070U

+ 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)
➢ Use 0075U in conjunction with 0070U

+ 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)
➢ Use 0076U in conjunction with 0070U

0077U Immunoglobulin paraprotein (M-protein), qualitative, immunoprecipitation and mass spectrometry, blood or urine, including isotype

0078U Pain management (opioid-use disorder) genotyping panel, 16 common variants (ie, *ABCB1, COMT, DAT1, DBH, DOR, DRD1, DRD2, DRD4, GABA, GAL, HTR2A, HTTLPR, MTHFR, MUOR, OPRK1, OPRM1*) buccal swab or other germline tissue sample, algorithm reported as positive or negative risk of opioid-use disorder

0079U Comparative DNA analysis using multiple selected single-nucleotide polymorphisms (SNPs), urine and buccal DNA, for specimen identity verification

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

0082U Drug test(s), definitive, 90 or more drugs or substances, definitive chromatography with mass spectrometry, and presumptive, any number of drug classes, by instrument chemistry analyzer (utilizing immunoassay), urine, report of presence or absence of each drug, drug metabolite or substance with description and severity of significant interactions per date of service

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

0084U Red blood cell antigen typing, DNA, genotyping of 10 blood groups with phenotype prediction of 37 red blood cell antigens

0085U Cytolethal distending toxin B (CdtB) and vinculin IgG antibodies by immunoassay (ie, ELISA)

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0086U Infections 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

0087U Cardiology (heart transplant), mRNA gene expression profiling by microarray of 1283 genes, transplant biopsy tissue, allograft rejection and injury algorithm reported as a probability score

0088U Transplantation medicine (kidney allograft rejection), microarray gene expression profiling of 1494 genes, utilizing transplant biopsy tissue, algorithm reported as a probability score for rejection

0089U Oncology (melanoma), gene expression profiling by *RTqPCR, PRAME and LINC00518*, superficial collection using adhesive patch(es)

0090U Oncology (cutaneous melanoma), mRNA gene expression profiling by RT-PCR of 23 genes (14 content and 9 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a categorical result (ie, benign, indeterminate, malignant)

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

0092U Oncology (lung), three protein biomarkers, immunoassay using magnetic nanosensor technology, plasma, algorithm reported as risk score for likelihood of malignancy

0093U Prescription drug monitoring, evaluation of 65 common drugs by LC-MS/MS, urine, each drug reported detected or not detected

0094U Genome (eg, unexplained constitutional or heritable disorder or syndrome, rapid sequence analysis

0095U Inflammation (eosinophilic esophagitis), ELISA analysis of eotaxin-3 (CCL26 *C-C motif chemokine ligand 26])* and major basic protein (*PRG2 [proteoglycans 2, pro eosinophil major basic protein])*, specimen obtained by swallowed nylon string, algorithm reported as predictive probability index for active eosinophilic esophagitis

0096U Human papillomavirus (HPV),high-risk types (ie, 16,18,31,33,35,39,45,51,52,56,58,59,66,68), male urine

0097U Gastrointestinal pathogen, multiplex reverse transcription and multiplex amplified probe technique, multiple types or subtypes, 22 targets (Campylobacter [C, jejuni/C, coli/C, upsaliensis], Clostridium difficile –C, difficile] toxin A/B, Plesiomonas shingelliodes, Salmonella, Vibrio [V. parahaemolyticus/V. vulnificus/V. cholera], including specific identification of Vibrio cholera, Yersinia enterocolitica, Enteroaggregative Escherichia coli [EAEC], Enteropathogenic Escherichia colie [EPEC], Entertoxigenic Escherichia coli [ETEC] Is/st, Shiga-like toxin-producing Escherichia coli [STEC] stx1/stx2 [including specific identification of the E.coli 0157 serogroup within STEC], Shigella/Enteroinvasive Escherichia coli [EIEC], Cryptosporidium, Cyclospora cayetanenis, Entamoeba, histolytica, Giardia lamblia [also known as G. intestinalis and G. duodenalis], adenovirus F40/41, astrovirus norovirus GI/GII, rotavirus A, sapovirus [Genogroups I, II, IV, and VI])

0098U Respiratory pathogen, multiplex reverse transcription and multiplex amplified probe technique, multiple types or subtypes, 14 targets (adenovirus, coronavirus, human metapneumovirus, influenza A, influenza A subtype H1, influenza A subtype H3, influenza A subtype H1-20019, influenza A, parainfluenza virus, human rhinovirus/enterovirus, respiratory syncytial, virus, Bordetella pertussis, Chlamydophila pneumoniae, Mycoplasma pneumoniae)

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0099U Respiratory pathogen, multiplex reverse transcription and multiplex amplified probe technique, multiple types or subtypes, 20 targets (adenovirus, coronavirus 229E, coronavirus HKU1, coronavirus, coronavirus OC43, human metapneumovirus, influenza A subtype H3, influenza A subtype H1-009, influenza, parainfluenza virus, parainfluenza virus 2, parainfluenza virus 3, parainfluenza virus 4, human rhinovirus/enterovirus, respiratory syncytial virus Bordetella pertussis, Chlamydophila pneumonia Mycoplasma pneumoniae)

0100U Respiratory pathogen, multiplex reverse transcription and multiplex amplified probe technique, multiple types or subtypes, 21 targets (adenovirus, coronavirus 229E, coronavirus HKU1, coronavirus NL3, coronavirus OC43, human metapneumovirus, human rhinovirus/enterovirus, influenza A, including subtypes H1,H1-2009, and H3, influenza B, parainfluenza virus 1, parainfluenza virus 2, parainfluenza virus 3, parainfluenza virus 4, respiratory syncytial virus, Bordetella parapertussis [IS1001], Bordetella pertussis [ptxP], Chlamydia pneumoniae, Mycoplasma pneumoniae)

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 CHG, with mRNA analytics to resolve variants of unknown significance when indicated (15 genes [sequencing and deletion/duplication], *EPCAM* and *GREM1* [deletion/duplication only]

+ 0130U Hereditary colon cancer disorders (eg, Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis), targeted mRNA sequence analysis panel *(APC, CHD1, CHEK2, MLH1, MSH2, MSH6, MUTYH, PMS2, PTEN, and TP53)* (List separately in addition to code for primary procedure)

➢ (Use 0130U in conjunction with 81435, 0101U)

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])

+ 0131U Hereditary breast cancer-related disorder (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)

➢ (Use 0131U in conjunction with 81162, 81432, 0102U)

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])

+ 0132U Hereditary ovarian cancer-related disorder (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)

➢ (Use 0132U in conjunction with 81162, 81432, 0103U)

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0105U Nephrology (chronic kidney disease), multiplex eletrochemiluminescent 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)

0106U Gastric emptying, serial collection of 7 timed breath specimens, non-radioisotope carbon-13 (^{13}C) spirulina substrate, analysis of each specimen by gas isotope ratio mass spectrometry, reported as rate of $^{13}CO_2$ excretion

0107U Clostridium difficile toxin(s) antigen detection by immunoassay technique, stool, qualitative, multiple-step method

0108U Gastroenterology (Barrett's esophagus), whole slide-digital imaging, including morphometric analysis computer-assisted quantitative immune-labeling 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 hyperplasia or cancer

0109U Infectious disease (Aspergillus species), real-time PCR for detection of DNA from 4 species (*A. fumigatus, A. terreus, A niger, and A. Flavus)* blood, lavage fluid, or tissue, qualitative reporting of presence or absence of each species

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

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

0112U Infectious agent detection and identification, targeted sequence analysis (16S and 18S rRNA genes) with drug-resistance gene

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

0114U Gastroenterology (Barrett's esophagus). *VIM* and *CCNA1* methylation analysis, esophageal cells, algorithm reported as likelihood for Barrett's esophagus

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

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

0117U Pain management, analysis of 11 endogenous analystes (methylmalonic acid, xanthurenic acid, homocysteine, pyroglutamic acid, vanilmandelate, 5-hydroxyindoleacetic acid, hydroxymethylglutarate, ethylmalonate, 3-hydroxyporpyl 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

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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

0119U Cardiology, ceramides by liquid chromatography-tandem mass spectrometry, plasma, quantitative report with risk score for major cardiovascular events

0120U Oncology (B-cell lymphoma classification) mRNA, gene expression profiling by fluorescent probe hybridization of 58 genes (45 content and 13 housekeeping genes), formalin-fixed paraffin-embedded tissue, algorithm reported as likelihood for primary mediastinal B-cell lymphoma (PMBCL) and diffuse large B-cell lymphoma (DLBCL) with cell of origin subtyping in the letter

0121U Sickle cell disease, microfluidic flow adhesion (VCAM-1), whole blood

0122U Sickle cell disease, microfluidic flow adhesion (P-Selectin, whole blood

0123U Mechanical fragility, RBC, shear stress and spectral analysis profiling

0124U Fetal congenital abnormalities, biochemical assays of 3 analytes (free beta-hCG, PAPPA-A, AFP), time resolved fluorescence immunoassay, maternal dried blood spot, algorithm reported as risk scores for fetal trisomies 13/18 and 21

0125U Fetal congenital abnormalities and perinatal complications, biochemical assays of 5 analytes (free beta-hCG, PAPP-A, AFP, placental growth factor, and inhibin-A), time resolved fluorescence immunoassay, maternal serum, algorithm reported as risk scores for fetal trisomies 12/18, 21 and preeclampsia

0126U Fetal congenital abnormalities and perinatal complications, biochemical assays of 5 analytes (free beta-hCG, PAPP-A, AFP, placental growth factor and inhibin-A), time-resolved fluorescence immunoassay, includes qualitative assessment of Y chromosome in cell-free fetal DNA, maternal serum and plasma, predicative algorithm reported as risk scores for fetal trisomies 12/18, 21 and preeclampsia

0127U Obstetrics (preeclampsia), biochemical assays of 3 analytes (PAPP-A, AFP, and placental growth factor), time-resolved fluorescence immunoassay, maternal serum, predictive algorithm reported as a risk score for preeclampsia

0128U Obstetrics (preeclampsia), biochemical assays of 3 analytes (PAPP-A, AFP, and placental growth factor), time-resolved fluorescence immunoassay, includes qualitative assessment of Y chromosome in cell-free fetal DNA, maternal serum and plasma, predictive algorithm reported as a risk score for preeclampsia

0129U Hereditary breast cancer-related disorder (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)*

+ 0133U Hereditary prostate cancer-related disorders, targeted mRNA sequence analysis panel (11 genes) (List separately in addition to code for primary procedure)

- (Use 0133U in conjunction with 81162)

+ 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)

- (Use 0134U in conjunction with 88162, 81432, 81435)

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+ 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)
- (Use 01315 in conjunction with 81162)

+ 0136U *ATM (ataxia telangiectasia mutated)* (eg, ataxia telangiectasia) mRNA sequence analysis (List separately in addition to code for primary procedure)
- (Use 0136U in conjunction with 81408)

+ 0137U PALB2 *(partner and localizer of BRCA2)* (eg, breast and pancreatic cancer) mRNA sequence analysis **(**List separately in addition to code for primary procedure)
- (Use 0137U in conjunction with 81307)

+ 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)
- (Use 0138U in conjunction with 81162)

Deleted Codes for 2020

0081U Oncology (uveal melanoma). mRNA, gene-expression profiling by real-time RT-PCR of 15 genes (12, content and 3 housekeeping genes), utilizing fine needle aspirate or formalin-fixed paraffin-embedded tissue, algorithm reported as a risk of metastasis. **Deleted crosswalk CPT 81552**

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]).

The following resources were used in the preparation of this document: the AMA's *Current Procedural Terminology (CPT) 2020, and CPT 2020 Changes-An Insider's View.*