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Pathology & Laboratory
2019 CPT Update
Effective 1/1/2019

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, 2019. The American Medical Association has released that there will be 335 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 procedure codes for Fine Needle Aspirations. Gone is CPT code 10022 and codes 10004-10012 have been added. Again, the Molecular Pathology Tier 1 subsections include 45+ new codes to conform to the parent code structure and there have been revisions for Tier 2 codes 81400-81406. In addition, there are changes and/or new codes to the Genomic Sequencing Procedure and Other Molecular Multianalyte Assays, the Multianalyte Assays with Algorithmic Analyses, Chemistry, and Proprietary Laboratory Analysis.

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

Fine Needle Aspiration

Revised Code for 2019:

10021 Fine needle aspiration; without imaging guidance; first lesion
(10022 has been deleted. To report see 10005, 10006, 10007, 10008, 10009, 10010, 10011, 10012)

New Codes for 2019:

+10004 Fine needle aspiration biopsy, without imaging guidance; each additional lesion (List separately in addition to code for primary procedure)
(Use 10004 in conjunction with 10021)
(Do not report 10004, 10021 in conjunction with 10005, 10006, 10007, 10008, 10009, 10010, 10011, 10012 for the same lesion)

10005 Fine needle aspiration biopsy, including ultrasound guidance; first lesion

+10006 Fine needle aspiration biopsy, including ultrasound guidance; each additional lesion (List separately in addition to code for primary procedure)
(Use 10006 in conjunction with 10005)
(Do not report 10005, 10006 in conjunction with 76942

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10007 Fine needle aspiration biopsy, including fluoroscopic guidance; first lesion

+10008 Fine needle aspiration biopsy, including fluoroscopic guidance; each additional lesion (List separately in addition to code for primary procedure)
(Use 10008 in conjunction with 10007)
(Do not report 10007, 10008 in conjunction with 77002)

10009 Fine needle aspiration biopsy, including CT guidance; first lesion

+10010 Fine needle aspiration biopsy, including CT guidance; each additional lesion (List separately in addition to code for primary procedure)
(Use 10010 in conjunction with 10009)
(Do not report 10009, 10010 in conjunction with 77012)

10011 Fine needle aspiration biopsy, including MR guidance; first lesion

+10012 Fine needle aspiration biopsy, including MR guidance; each additional lesion (List separately in addition to code for primary procedure)
(Use 10012 in conjunction with 10011)
(Do not report 10011, 10012 in conjunction with 77021)

Fine Needle Aspiration biopsy procedures are performed with or without imaging guidance. Imaging guidance codes (76942, 77002, 77012, 77021) may not be reported separately with new codes 10004, 10005, 10006, 10007, 10008, 10009, 10010, 10011, 10012 or 10021. Codes 10004, 10005, 10006, 10007, 10008, 10009, 10010, 10011, 10012 and 10021 are reported once per lesion taken in a single session.

When more than one FNA biopsy is performed on separate lesions at the same session, same day, same imaging modality, use the appropriate imaging modality add-on code for the second and subsequent lesion(s).

When more than one FNA biopsy is performed on separate lesions, same session, same day, using different imaging modalities, report the corresponding primary code with modifier 59 for each additional imaging modality and corresponding add-on codes for subsequent lesions taken.

This instruction applies regardless of whether the lesions are ipsilateral or contralateral to each other and/or whether they are in the same or different organs/structures.

When FNA biopsy and core needle biopsy both are performed on the same lesion, same session, same day using the same type of imaging guidance, do not separately report the imaging guidance for the core needle biopsy.

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When FNA biopsy is performed on one lesion and core needle biopsy is performed on a separate lesion, same session, same day using the same type of imaging guidance, both the core needle biopsy and the imaging guidance for the core needle biopsy may be reported separately with modifier 59.

When FNA biopsy is performed on one lesion and core needle biopsy is performed on a separate lesion, same session, same day using different types of imaging guidance, both the core needle biopsy and the imaging guidance for the core needle biopsy may be reported with modifier 59.

Deleted Code for 2019:

10022-Fine Needle Aspiration; with imaging guidance

Molecular Pathology

Revised Codes for 2019:

81162 BRCA1 (BRACA1, DNA repair associated), BRCA2 (BRCA2 (BRCA2 DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis and full duplication/deletion analysis (ie, detection of large gene rearrangements)

81212 185delAG, 5385insC, 6174delT variants

81215 known familial variant

81216 BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis

81217 known familial variant

81244 characterization of alleles (eg, expanded size and promoter methylation status)

81287 MGMT (0-6-methylguanine-DNA methyltransferase) (eg, glioblastoma multiforme) promoter methylation analysis

81327 SEPT9 (Septin9) (eg, colorectal cancer) promoter methylation analysis

New Codes for 2019:

Tier I
81171 AFF2 (AF4/FMR2 family, member 2 [FMR2]) (eg, fragile X mental retardation 2 [FRAXE]) gene analysis; evaluation to detect abnormal (eg, expanded) alleles

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81172 AFF2 (AF4/FMR2 family, member 2 [FMR2]) (eg, fragile X mental retardation 2 [FRAXE]) gene analysis; characterization of alleles (eg, expanded size and methylation status)

81204 AR (androgen receptor) (eg, spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation) gene analysis; characterization of alleles (eg, expanded size or methylation status)

81173 AR (androgen receptor) (eg, spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation) gene analysis; full gene sequence

81174 AR (androgen receptor) (eg, spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation) gene analysis; known familial variant

81177 ATN1 (atrophin 1) (eg, dentatorubral-pallidoluysian atrophy) gene analysis, evaluation to detect abnormal (eg, expanded) alleles

81178 ATXN1 (ataxin 1) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles

81179 ATXN2 (ataxin 2) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles

81180 ATXN3 (ataxin 3) (eg, spinocerebellar ataxia, Machado-Joseph disease) gene analysis, evaluation to detect abnormal (eg, expanded) alleles

81181 ATXN7 (ataxin 7) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles

81182 ATXN8OS (ATXN8 opposite strand [non-protein coding]) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles

81183 ATXN10 (ataxin 10) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles

81163 BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis

81164 BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full duplication/deletion analysis (ie, detection of large gene rearrangements)

81165 BRCA1 (BRCA1, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis

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81166 BRCA1 (BRCA1, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full duplication/deletion analysis (ie, detection of large gene rearrangements)

81167 BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full duplication/deletion analysis (ie, detection of large gene rearrangements)

81233 BTK (Bruton's tyrosine kinase) (eg, chronic lymphocytic leukemia) gene analysis, common variants (eg, C481S, C481R, C481F)

81184 CACNA1A (calcium voltage-gated channel subunit alpha1 A) (eg, spinocerebellar ataxia) gene analysis; evaluation to detect abnormal (eg, expanded) alleles

81185 CACNA1A (calcium voltage-gated channel subunit alpha1 A) (eg, spinocerebellar ataxia) gene analysis; full gene sequence

81186 CACNA1A (calcium voltage-gated channel subunit alpha1 A) (eg, spinocerebellar ataxia) gene analysis; known familial variant

81187 CNBP (CCHC-type zinc finger nucleic acid binding protein) (eg, myotonic dystrophy type 2) gene analysis, evaluation to detect abnormal (eg, expanded) alleles

81188 CSTB (cystatin B) (eg, Unverricht-Lundborg disease) gene analysis; evaluation to detect abnormal (eg, expanded) alleles

81189 CSTB (cystatin B) (eg, Unverricht-Lundborg disease) gene analysis; full gene sequence

81190 CSTB (cystatin B) (eg, Unverricht-Lundborg disease) gene analysis; known familial variant(s)

81234 DMPK (DM1 protein kinase) (eg, myotonic dystrophy type 1) gene analysis; evaluation to detect abnormal (expanded) alleles

81239 DMPK (DM1 protein kinase) (eg, myotonic dystrophy type 1) gene analysis; characterization of alleles (eg, expanded size)

81236 EZH2 (enhancer of zeste 2 polycomb repressive complex 2 subunit) (eg, myelodysplastic syndrome, myeloproliferative neoplasms) gene analysis, full gene sequence

81237 EZH2 (enhancer of zeste 2 polycomb repressive complex 2 subunit) (eg, diffuse large B-cell lymphoma) gene analysis, common variant(s) (eg, codon 646)

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81284 FXN (frataxin) (eg, Friedreich ataxia) gene analysis; evaluation to detect abnormal (expanded) alleles

81285 FXN (frataxin) (eg, Friedreich ataxia) gene analysis; characterization of alleles (eg, expanded size)

81286 FXN (frataxin) (eg, Friedreich ataxia) gene analysis; full gene sequence

81289 FXN (frataxin) (eg, Friedreich ataxia) gene analysis; known familial variant(s)

81271 HTT (huntingtin) (eg, Huntington disease) gene analysis; evaluation to detect abnormal (eg, expanded) alleles

81274 HTT (huntingtin) (eg, Huntington disease) gene analysis; characterization of alleles (eg, expanded size)

81305 MYD88 (myeloid differentiation primary response 88) (eg, Waldenstrom's macroglobulinemia, lymphoplasmacytic leukemia) gene analysis, p.Leu265Pro (L265P) variant

81306 NUDT15 (nudix hydrolase 15) (eg, drug metabolism) gene analysis, common variant(s) (eg, *2, *3, *4, *5, *6)

81312 PABPN1 (poly[A] binding protein nuclear 1) (eg, oculopharyngeal muscular dystrophy) gene analysis, evaluation to detect abnormal (eg, expanded) alleles

81320 PLCG2 (phospholipase C gamma 2) (eg, chronic lymphocytic leukemia) gene analysis, common variants (eg, R665W, S707F, L845F)

81343 PPP2R2B (protein phosphatase 2 regulatory subunit Bbeta) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles

81329 SMN1 (survival of motor neuron 1, telomeric) (eg, spinal muscular atrophy) gene analysis; dosage/deletion analysis (eg, carrier testing), includes SMN2 (survival of motor neuron 2, centromeric) analysis, if performed

81336 SMN1 (survival of motor neuron 1, telomeric) (eg, spinal muscular atrophy) gene analysis; full gene sequence

81337 SMN1 (survival of motor neuron 1, telomeric) (eg, spinal muscular atrophy) gene analysis; known familial sequence variant(s)

81344 TBP (TATA box binding protein) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles

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81345 TERT (telomerase reverse transcriptase) (eg, thyroid carcinoma, glioblastoma multiforme) gene analysis, targeted sequence analysis (eg, promoter region)

81333 TGFBI (transforming growth factor beta-induced) (eg, corneal dystrophy) gene analysis, common variants (eg, R124H, R124C, R124L, R555W, R555Q)

Revised Tier 2 for 2019:

Tier 2 codes are used to report procedures not listed in the Tier 1 molecular pathology codes (81161, 81200-81383). They represent medically useful procedures that are generally performed in lower volumes than Tier 1 procedures. With the addition of many new Tier 1 codes, which many of the new codes are tests that were Tier 2 but have now been given a specific code in Tier 1, the following Tier 2 codes have been revised: 81400, 81401, 81403, 81404, 81405 and 81407.

Genomic Sequencing Procedures and Other Molecular Multianalyte Assays

New Codes for 2019:

81443 Genetic testing for severe inherited conditions (eg, cystic fibrosis, Ashkenazi Jewish-associated disorders [eg, Bloom syndrome, Canavan disease, Fanconi anemia type C, mucolipidosis type VI, Gaucher disease, Tay-Sachs disease], beta hemoglobinopathies, phenylketonuria, galactosemia), genomic sequence analysis panel, must include sequencing of at least 15 genes (eg, ACADM, ARSA, ASPA, ATP7B, BCKDHA, BCKDHB, BLM, CFTR, DHCR7, FANCC, G6PC, GAA, GALT, GBA, GBE1, HBB, HEXA, IKBKAP, MCOLN1, PAH)

Multianalyte Assays with Algorithmic Analyses

New Codes for 2019:

81518 Oncology (breast), mRNA, gene expression profiling by real-time RT-PCR of 11 genes (7 content and 4 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithms reported as percentage risk for metastatic recurrence and likelihood of benefit from extended endocrine therapy

81596 Infectious disease, chronic hepatitis C virus (HCV) infection, six biochemical assays (ALT, A2-macroglobulin, apolipoprotein A-1, total bilirubin, GGT, and haptoglobin) utilizing serum, prognostic algorithm reported as scores for fibrosis and necroinflammatory activity in liver

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Chemistry

New Codes for 2019:

82642 Dihydrotestosterone (DHT)

83722 Lipoprotein, direct measurement; small dense LDL cholesterol

Proprietary Laboratory Analysis

New Codes for 2019:

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

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

0020U Drug test(s), presumptive, with definitive confirmation of positive results, any number of drug classes, urine, with specimen verification including DNA authentication in comparison to buccal DNA, per date of service

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

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

0023U Oncology (acute myelogenous leukemia), DNA, genotyping of internal tandem duplication, p.D835, p.I836, using mononuclear cells, reported as detection or non-detection of FLT3 mutation and indication for or against the use of midostaurin

0024U Glycosylated acute phase proteins (GlycA), nuclear magnetic resonance spectroscopy, quantitative

0025U Tenofovir, by liquid chromatography with tandem mass spectrometry (LC-MS/MS), urine, quantitative

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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")

0027U JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) gene analysis, targeted sequence analysis exons 12-15

0028U CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism) gene analysis, copy number variants, common variants with reflex to targeted sequence analysis

0029U Drug metabolism (adverse drug reactions and drug response), targeted sequence analysis (ie, CYP1A2, CYP2C19, CYP2C9, CYP2D6, CYP3A4, CYP3A5, CYP4F2, SLCO1B1, VKORC1 and rs12777823)

0030U Drug metabolism (warfarin drug response), targeted sequence analysis (ie, CYP2C9, CYP4F2, VKORC1, rs12777823)

0031U CYP1A2 (cytochrome P450 family 1, subfamily A, member 2)(eg, drug metabolism) gene analysis, common variants (ie, *1F, *1K, *6, *7)

0032U COMT (catechol-O-methyltransferase)(drug metabolism) gene analysis, c.472G>A (rs4680) variant

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])

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)

0035U Neurology (prion disease), cerebrospinal fluid, detection of prion protein by quaking-induced conformational conversion, qualitative

0036U Exome (ie, somatic mutations), paired formalin-fixed paraffin-embedded tumor tissue and normal specimen, sequence analyses

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

0038U Vitamin D, 25 hydroxy D2 and D3, by LC-MS/MS, serum microsample, quantitative

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0039U Deoxyribonucleic acid (DNA) antibody, double stranded, high avidity

0040U BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis, major breakpoint, quantitative

0041U Borrelia burgdorferi, antibody detection of 5 recombinant protein groups, by immunoblot, IgM

0042U Borrelia burgdorferi, antibody detection of 12 recombinant protein groups, by immunoblot, IgG

0043U Tick-borne relapsing fever Borrelia group, antibody detection to 4 recombinant protein groups, by immunoblot, IgM

0044U Tick-borne relapsing fever Borrelia group, antibody detection to 4 recombinant protein groups, by immunoblot, IgG

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

0046U FLT3 (fms-related tyrosine kinase 3) (eg, acute myeloid leukemia) internal tandem duplication (ITD) variants, quantitative

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

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)

0049U NPM1 (nucleophosmin) (eg, acute myeloid leukemia) gene analysis, quantitative

0050U Targeted genomic sequence analysis panel, acute myelogenous leukemia, DNA analysis, 194 genes, interrogation for sequence variants, copy number variants or rearrangements

0051U Prescription drug monitoring, evaluation of drugs present by LC-MS/MS, urine, 31 drug panel, reported as quantitative results, detected or not detected, per date of service

0052U Lipoprotein, blood, high resolution fractionation and quantitation of lipoproteins, including all five major lipoprotein classes and subclasses of HDL, LDL, and VLDL by vertical auto profile ultracentrifugation

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0053U Oncology (prostate cancer), FISH analysis of 4 genes (ASAP1, HDAC9, CHD1 and PTEN), needle biopsy specimen, algorithm reported as probability of higher tumor grade

0054U Prescription drug monitoring, 14 or more classes of drugs and substances, definitive tandem mass spectrometry with chromatography, capillary blood, quantitative report with therapeutic and toxic ranges, including steady-state range for the prescribed dose when detected, per date of service

0055U Cardiology (heart transplant), cell-free DNA, PCR assay of 96 DNA target sequences (94 single nucleotide polymorphism targets and two control targets), plasma

0056U Hematology (acute myelogenous leukemia), DNA, whole genome next-generation sequencing to detect gene rearrangement(s), blood or bone marrow, report of specific gene rearrangement(s)

0057U Oncology (solid organ neoplasia), mRNA, gene expression profiling by massively parallel sequencing for analysis of 51 genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a normalized percentile rank

0058U Oncology (Merkel cell carcinoma), detection of antibodies to the Merkel cell polyoma virus oncoprotein (small T antigen), serum, quantitative

0059U Oncology (Merkel cell carcinoma), detection of antibodies to the Merkel cell polyoma virus capsid protein (VP1), serum, reported as positive or negative

0060U Twin zygosity, genomic targeted sequence analysis of chromosome 2, using circulating cell-free fetal DNA in maternal blood

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

Prepared by APS Medical Billing and Professional Consulting, Toledo, OH.

The following resources were used in the preparation of this document: the AMA's *Current Procedural Terminology (CPT) 2019, and CPT 2019 Changes-An Insider's View.*