# Quarterly New Code List Effective Oct. 1, 2026

This list is provided for reference purposes only and may not be all-inclusive. The listing of a code does not imply that the service described by the code is a covered or non-covered health service. Benefit coverage for health services is determined by the member specific benefit plan document and applicable laws that may require coverage for a specific service. The inclusion of a code does not imply any right to reimbursement or guarantee claim payment. Other policies and guidelines may apply. Please refer to Itiliti, the prior authorization tool located in the Availity provider portal, for requirements for outpatient services and procedures. Prior authorization requirements are subject to change.

**KEY: PA=Prior Authorization Required; NPA=No Prior Authorization Required; NC= Not Covered; NC-I&E=Not Covered Investigative & Experimental**

| Procedure Code | Procedure Description | Advantage MD | Priority Partners | USFHP | EHP |
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| 0660U | Human papillomavirus (HPV), genotypes, 18,31,33, and 36, cell-free DNA (cfDNA), whole blood, multiplex digital droplet PCR (ddPCR), quantiative | PA<br>EviCore decision | PA<br>EviCore decision | NC-I&E | NC-I&E |
| 0661U | Human papillomavirus (HPV), genotype 16, cell-free DNA (cfDNA), whole blood, digital droplet PCR (ddPCR), quantitative | PA<br>EviCore decision | PA<br>EviCore decision | NC-I&E | NC-I&E |
| 0662U | Transplantation medicine (kidney allograft rejection), mRNA, gene-expression profiling by real-time quantitative PCR of 12 genes (11 content and 1 housekeeping), urine, algorithm reported as a rejection risk score | PA<br>EviCore decision | PA<br>EviCore decision | NC-I&E | NC-I&E |
| 0663U | Obstetrics (fetal platelet antigen noninvasive prenatal test [NIPT]), cell-free DNA (cfDNA) sequence analysis for detection of fetal presence or absence of 1 human platelet antigen or more (HPA-1a, HPA-1b, HPA-3a, HPA-5b, and others) when performed, reported as maternal/fetal incompatibility detected or not detected per selected antigen. | PA<br>EviCore decision | PA<br>EviCore decision | NC-I&E | NC-I&E |
| 0664U | Transplantation medicine (kidney allograft failure), RNA expression transcriptome by next-generation sequencing (NGS), profiling of 13 genes, post-transplant peripheral blood, algorithm reported as a risk score for predicting progressive fibrosis in the kidney allograft. | PA<br>per EviCore | PA<br>per EviCore | NC-I&E | NC-I&E |
| 0665U | Hepatology (metabolic dysfunction-associated steatohepatitis [MASH]), enzyme-linked immunosorbent assay (ELISA) for YKL40 and quantitative reverse transcription polymerase chain reaction (RT-qPCR) for miR34a-5p, serum, algorithm reported as a single score for MASH activity and fibrosis | NPA<br>per EviCore Claims Mgmt | NC<br>Not priced by MDH | NC-I&E | NC-I&E |
| 0666U | Infectious disease (wound infection), DNA, multiplex realtime PCR, wound swab, detection of 27 microbial targets and 28 antibiotic resistance targets, reported as semiquantitative for bacterial and fungal targets, and qualitative for viral- and antibiotic-resistance targets | NPA<br>per EviCore Claims Mgmt | NC<br>Not priced by MDH | NC-I&E | NC-I&E |
| 0667U | Inborn error of metabolism (primary mitochondrial disease), determination of fibroblast growth factor 21 (FGF21) concentration by enzyme-linked immunosorbent assay (ELISA), serum or plasma, diagnostic quantitative result | NPA<br>per EviCore Claims Mgmt | NC<br>Not priced by MDH | NC-I&E | NC-I&E |
| 0668U | Oncology (pancreas), DNA, genome sequence with 5- hydroxymethylcytosine (5hmC) enrichment and glycan biomarker analysis, whole blood or plasma, algorithm reported as cancer detected or not detected | PA<br>per EviCore | PA<br>per EviCore | NC-I&E | NC-I&E |
| 0669U | Infectious disease (Bartonella species, Borrelia species, and Babesia species), multiplex digital PCR for detection of DNA at the genus level for each species, blood, qualitative reporting of presence or absence of each pathogen at the genus level | NPA<br>per EviCore Claims Mgmt | NC<br>Not priced by MDH | NC-I&E | NC-I&E |
| 0670U | 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 (STR) genes, methylation status of selected regions, blood, saliva, amniocentesis, chorionic villus sample or tissue, identification and categorization of genetic variant, proband and comparator | PA<br>per EviCore | PA<br>per EviCore | NC-I&E | NC-I&E |
| 0671U | 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 (STR) genes, methylation status of selected regions, blood, saliva, amniocentesis, chorionic villus sample or tissue, identification and categorization of genetic variant, proband and 2 comparators | PA<br>per EviCore | PA<br>per EviCore | NC-I&E | NC-I&E |
| 0672U | Rare diseases (constitutional/heritable disorders), whole exome and mitochondrial DNA sequence analysis, including small sequence changes, deletions, duplications, short tandem repeat (STR) gene expansions, and variants in nonuniquely mappable regions, blood or saliva, identification and categorization of genetic variants, proband and comparator | PA<br>per EviCore | PA<br>per EviCore | NC-I&E | NC-I&E |

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| 0673U | Rare diseases (constitutional/heritable disorders), whole exome and mitochondrial DNA sequence analysis, including small sequence changes, deletions, duplications, short tandem repeat (STR) gene expansions, and variants in nonuniquely mappable regions, blood or saliva, identification and categorization of genetic variants, proband and 2 comparators | PA per EviCore | PA per EviCore | NC-I&E | NC-I&E |
| 0674U | Rare diseases (constitutional/heritable disorders), whole genome and mitochondrial DNA sequence analysis, including small sequence changes insertions/deletions, copy number variants, mobile element insertions, runs of homozygosity, aneuploidy, and inversions, short tandem repeat (STR) gene expansions, blood, saliva, or genomic DNA, identification and categorization of genetic variants, proband and comparator | PA per EviCore | PA per EviCore | NC-I&E | NC-I&E |
| 0675U | Rare diseases (constitutional/heritable disorders), whole genome and mitochondrial DNA sequence analysis, including small sequence changes, insertions/deletions, copy number variants, duplications/deletions, mobile element insertions, runs of homozygosity, aneuploidy, and inversions, short tandem repeat (STR) gene expansions, blood, saliva, or genomic DNA, identification and categorization of genetic variants proband and 2 comparators | PA per EviCore | PA per EviCore | NC-I&E | NC-I&E |
| 0676U | 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 and maternal cell contamination, fetal sample, identification and categorization of genetic variants, proband and maternal comparator | PA per EviCore | PA per EviCore | NC-I&E | NC-I&E |
| 0677U | 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 and maternal cell contamination, fetal sample, identification and categorization of genetic variants, proband and 2 comparators | PA per EviCore | PA per EviCore | NC-I&E | NC-I&E |
| 0678U | Oncology (hereditary cancer),genome sequence for 117 genes (single-nucleotide variants, deletions/insertions, and characterized intronic variants), copy number variants, duplications/deletions, mobile element insertions and inversions, blood, saliva, cultured skin fibroblasts (skin biopsy) or extracted genomic DNA, diagnostic, identification and categorization of genetic variants | PA per EviCore | PA per EviCore | NC-I&E | NC-I&E |
| 0679U | Oncology (hereditary hematologic cancer), genomic DNA, whole genome sequence (single-nucleotide variants, deletions/insertions, and characterized intronic variants), copy number variants, duplications/deletions, mobile element insertions and inversions, analysis of over 105 genes, genomic DNA isolated from blood, saliva, cultured skin fibroblasts (skin biopsy), identification and categorization of genetic variants | PA per EviCore | PA per EviCore | NC-I&E | NC-I&E |
| 0680U | Tobacco use, DNA analysis of 1 methylation marker (cg05575921 [AHRR]),methylation-sensitive digital PCR, whole blood, algorithm reported as quantitative percentage methylation and estimated average cigarette use per day | PA per EviCore | PA per EviCore | NC-I&E | NC-I&E |
| 0681U | Tobacco use, DNA analysis of 2 methylation markers (1 content: cg05575921 [AHRR] and 1 normalizing: cg08141395), methylationsensitive digital PCR, saliva, algorithm reported as quantitative percent methylation and estimated average cigarette use per day | PA per EviCore | PA per EviCore | NC-I&E | NC-I&E |
| 0682U | Oncology (lung cancer), DNA analysis of 1 methylation marker (cg05575921), methylation-sensitive digital PCR, whole blood, algorithm results reported as the 20- year-hazard ratio for lung cancer | PA per EviCore | PA per EviCore | NC-I&E | NC-I&E |
| 0683U | Oncology (lung cancer), DNA analysis of 2 methylation markers (1 content: cg05575921 and 1 normalizing: cg08141395), methylation-sensitive digital PCR, saliva, algorithm results reported as the 20-yearhazard ratio for lung cancer | PA per EviCore | PA per EviCore | NC-I&E | NC-I&E |
| 0684U | Alcohol use disorder, DNA analysis of 4 methylation markers (cg02583484, cg04987734, cg09935388, cg04583842), methylationsensitive digital PCR, whole blood, algorithm reported as a summed T-score | PA per EviCore | PA per EviCore | NC-I&E | NC-I&E |
| 0685U | Alcohol use disorder, DNA analysis of 5 methylation markers (4 content: cg02583484, cg04987734, cg09935388, cg04583842,and 1 normalizing: cg08141395), methylationsensitive digital PCR, whole blood or saliva, algorithm reported as a summed T-score | PA per EviCore | PA per EviCore | NC-I&E | NC-I&E |
| 0686U | Oncology (prostate), mRNA, next-generation sequencing (NGS) gene expression profiling of 22 genes, formalinfixed paraffin-embedded (FFPE) tissue, algorithm reported as risk score | PA per EviCore | PA per EviCore | NC-I&E | PA |
| 0687U | Comparative analysis using short tandem repeat (STR) markers, patient and comparative specimen, DNA, buccal swab and tissue,reported match or mismatch | PA per EviCore | PA per EviCore | NC-I&E | NC-I&E |
| 0688U | Oncology (colorectal cancer), analysis of minimal residual disease (MRD), nextgeneration sequencing (NGS), circulating tumor DNA (ctDNA)analysis in whole blood and tumor for baseline assessment to evaluate current MRD status and for comparisons to subsequent MRD assessments | PA per EviCore | PA per EviCore | NC-I&E | NC-I&E |

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| 0689U | Oncology (colorectal cancer), analysis of minimal residualdisease (MRD) using patientspecific assays, reported as amount of circulating tumor DNA (ctDNA) detection and trend over time | PA<br>per EviCore | PA<br>per EviCore | NC-I&E | NC-I&E |
| 0690U | Transplantation medicine (allograft rejection), quantification of donor-derived cell-free DNA (cfDNA) using digital PCR analysis of 45 single-nucleotide polymorphisms, plasma, reported as quantity of donorderived cfDNA in plasma to determine the probability of allograft rejection | PA<br>per EviCore | PA<br>per EviCore | NC-I&E | NC-I&E |
| 0691U | Carrier screening (cystic fibrosis, spinal muscular atrophy, beta hemoglobinopathies [including sickle cell disease], alpha thalassemia, and Duchenne muscular dystrophy), genomic sequence analysis panel, 6 genes (CFTR, SMN1, HBB, HBA1, HBA2, DMD) | NPA<br>per EviCore Claims Mgmt | NC<br>Not priced by MDH | NC-I&E | NC-I&E |
| 0692U | Cardiology (peripheral artery disease [PAD]), analysis of 3 proteins (midkine, angiopoietin-1, and kidney injury molecule-1 [KIM-1]), immunoassay, plasma, algorithm reported as a risk score for obstructive PAD | NPA<br>per EviCore Claims Mgmt | NC<br>Not priced by MDH | NC-I&E | NC-I&E |
| 0693U | Oncology (head and neck), circulating tumor DNA (ctDNA), tumor-informed nextgeneration sequencing (NGS) analysis for 699 genes of patient-specific somatic variants identified from primary tumor tissue, ostoperative<br>lymphatic exudate specimen, algorithm reported as presence or absence of ctDNA | PA<br>per EviCore | PA<br>per EviCore | NC-I&E | NC-I&E |
| 0694U | Oncology (monoclonal gammopathy), immunoprecipitation and matrix-assisted laser desorption/ionization time-offlight (MALDI-TOF) mass spectrometry, identification of intact monoclonal immunoglobulin isotypes (IgG, IgA, IgM, kappa, lambda), and M-protein concentrations in conjunction with turbidimetry, blood, semiquantitative | NPA<br>per EviCore Claims Mgmt | NC<br>Not priced by MDH | NC-I&E | NC-I&E |
| 0695U | Oncology (central nervous system), low-pass whole genome sequence analysis of cerebrospinal fluid, interrogation for chromosome arm-level and focal losses and gains | PA<br>per EviCore | PA<br>per EviCore | NC-I&E | NC-I&E |
| 0696U | Oncology (solid organ), targeted genomic sequence analysis, formalin-fixed paraffin-embedded (FFPE) tumor tissue, RNA analysis, 350 or more genes for RNA alterations (eg, gene rearrangements and splice isoforms) | PA<br>per EviCore | PA<br>per EviCore | NC-I&E | NC-I&E |
| 0697U | Obesity, DNA genotyping, analysis of up to 41 genes, buccal swab or blood specimen, patient biometrics, risk-score algorithm to identify a predisposition to up to 4 phenotypes, reported as likelihood to benefit from therapeutics | PA<br>per EviCore | PA<br>per EviCore | NC-I&E | NC-I&E |
| 0698U | Neurology (traumatic brain injury), analysis of glial fibrillary acidic protein (GFAP) and ubiquitin carboxy-terminal hydrolase L1 (UCHL1), immunoassay, serum or plasma, individual components reported with the overall result of positive or negative based on threshold comparison | NPA<br>per EviCore Claims Mgmt | NC<br>Not priced by MDH | NPA | NPA |