AACC CY 2024 Crosswalk Recommendations

Code #	Long Code Desciptor	Test Purpose	AACC Crosswalk Recommendation	Rationale	Proposed NLA
Chemistry					
8X016	Anti-mullerian hormone (AMH)	Chemistry	**82024** Adrenocorticotropic hormone (ACTH)	Both tests are performed by immunoassays that use similar work and resources to form antibody sandwich complexes. The results of both tests report out quantitative hormone levels.	$38.62
Immunology					
8X025	Liver disease, analysis of 3 biomarkers (hyaluronic acid [HA], procollagen III amino terminal peptide [PIIINP], tissue inhibitor of metalloproteinase 1 [TIMP-1]), using immunoassays, utilizing serum, prognostic algorithm reported as a risk score and risk of liver fibrosis and liver-related clinical events within 5 years	Immunology	**0014M** Liver disease, analysis of 3 biomarkers (hyaluronic acid [HA], procollagen III amino terminal peptide [PIIINP], tissue inhibitor of metalloproteinase 1 [TIMP-1]), using immunoassays, utilizing serum, prognostic algorithm reported as a risk score and risk of liver fibrosis and liver-related clinical events within 5 years	Consistent with 0014M code descriptor, 8X025 will replace code 0014M January 1, 2024.	$176.19
8X036	Acetylcholine receptor (AChR); binding antibody	Immunology	**86341** Islet cell antibody	Both assays use similar work and resources and measure the radioactivity level of the precipitate and are used to quantitate the antibodies being tested to diagnose autoimmune disorders.	$23.57
8X037	Acetylcholine receptor (AChR); blocking antibody	Immunology	**86341** Islet cell antibody	Both assays use similar work and resources and measure the radioactivity level of the precipitate and are used to quantitate the antibodies being tested to diagnose autoimmune disorders.	$23.57
8X038	Acetylcholine receptor (AChR); modulating antibody	Immunology	**86053** Aquaporin-4 (neuromyelitis optica [NMO]) antibody; flow cytometry (ie, fluorescence-activated cell sorting [FACS]), each	Both antibody assays use flow cytometry to measure the amount of antibody expressed on the surface of live cells. Methodology and resources are similar for these two antibody assays. 86357 was used as the crosswalk in 2023 for 86053 as both are flow cytometry assays.	$37.73
Molecular Pathology					
8X017	Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis, microsatellite instability	Genomic Sequencing Procedures	**81455-Minus-81277** 81455: Targeted genomic sequence analysis panel, solid organ or hematolymphoid neoplasm or disorder, 51 or greater genes (eg, ALK, BRAF, CDKN2A, CEBPA, DNMT3A, EGFR, ERBB2, EZH2, FLT3, IDH1, IDH2, JAK2, KIT, KRAS, MET, MLL, NOTCH1, NPM1, NRAS, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; DNA analysis or combined DNA and RNA analysis 81277: Cytogenomic neoplasia (genome-wide) microarray analysis, interrogation of genomic regions for copy number and loss-of-heterozygosity variants for chromosomal abnormalities	Crosswalk to 81455 minus 81277: removes the copy number work/resources from 81455 to reflect the reduced amount of work by not performing copy number.	81455 ($2919.60) MINUS 81277 (tumor microarray @ $1,160.00) = $1,759.60
8X018	Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis, copy number variants and microsatellite instability	Genomic Sequencing Procedures	**81455** Targeted genomic sequence analysis panel, solid organ or hematolymphoid neoplasm or disorder, 51 or greater genes (eg, ALK, BRAF, CDKN2A, CEBPA, DNMT3A, EGFR, ERBB2, EZH2, FLT3, IDH1, IDH2, JAK2, KIT, KRAS, MET, MLL, NOTCH1, NPM1, NRAS, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; DNA analysis or combined DNA and RNA analysis	Both tests are genomic profiling tests that use similar work and resources. These two assays are designed to analyze tumor alterations (sequence variants, copy number variants and microsatellite instability) to match the patient to the best therapies based on clinical evidence in peer-reviewed literature and professional guidelines. Given the analysis in 8X018 a crosswalk to 81455 represents a comparable test code that most accurately reflects the work in 8X018.	81455: $2919.60 0179U *.8 ($1,943.21 *.8) = $1,554.57

8X019	Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants, microsatellite instability, tumor mutation burden, and rearrangements	Genomic Sequencing Procedures	**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	The methodologies for 8X019 and 0244U are genomic profiling tests that use similar work and resources. These two assays are designed to analyze tumor alterations (copy number variants/alterations, sequence variants, rearrangements, microsatellite instability, and tumor mutational burden) to match the patient to the best therapies based on clinical evidence in peer-reviewed literature. The tumor mutational burden analysis in 8X019, a complex biomarker analysis that requires significant bioinformatics and development/validation requirements, which requires additional work and resources beyond test code 81455.	0244U: $3500
8X020	Solid organ neoplasm, genomic sequence analysis panel, cell-free nucleic acid (eg, plasma), interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants and rearrangements	Genomic Sequencing Procedures; cell free DNA	**81455 *1.25** Targeted genomic sequence analysis panel, solid organ or hematolymphoid neoplasm or disorder, 51 or greater genes (eg, ALK, BRAF, CDKN2A, CEBPA, DNMT3A, EGFR, ERBB2, EZH2, FLT3, IDH1, IDH2, JAK2, KIT, KRAS, MET, MLL, NOTCH1, NPM1, NRAS, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; DNA analysis or combined DNA and RNA analysis	Both tests are genomic profiling tests that use similar work and resources. These two assays are designed to analyze tumor alterations (sequence variants, copy number variants and rearrangements) to match the patient to the best therapies based on clinical evidence in peer-reviewed literature and professional guidelines. Given the analysis in 8X020 a crosswalk to 81455 represents a comparable test code that most accurately reflects the work in 8X020. We recommend a multiplier of *1.25. This refects the increased work and resources needed to sequence ctDNA from plasma at 10,000X (compared to FFPE tumor DNA that is sequenced at 100-1000X).	81455 *1.25 ($2919.60 *1.25) = $3649.50
8X021	Solid organ neoplasm, genomic sequence analysis panel, cell-free nucleic acid (eg, plasma), interrogation for sequence variants; DNA analysis, copy number variants, and microsatellite instability	Genomic Sequencing Procedures; cell free DNA	**81455 *1.25** Targeted genomic sequence analysis panel, solid organ or hematolymphoid neoplasm or disorder, 51 or greater genes (eg, ALK, BRAF, CDKN2A, CEBPA, DNMT3A, EGFR, ERBB2, EZH2, FLT3, IDH1, IDH2, JAK2, KIT, KRAS, MET, MLL, NOTCH1, NPM1, NRAS, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; DNA analysis or combined DNA and RNA analysis	Both tests are genomic profiling tests that use similar work and resources. These two assays are designed to analyze tumor alterations (sequence variants, copy number variants and microsatellite instability) to match the patient to the best therapies based on clinical evidence in peer-reviewed literature and professional guidelines. Given the analysis in 8X021 a crosswalk to 81455 represents a comparable test code that most accurately reflects the work in 8X021. We believe the resources for microsatellite instability andrearrangments is the same amount of work and resources. We recommend a multiplier of *1.25. This refects the increased work and resources needed to sequence ctDNA from plasma at 10,000X (compared to FFPE tumor DNA that is sequenced at 100-1000X).	81455 *1.25 ($2919.60 *1.25) = $3649.50
8X022	Solid organ neoplasm, genomic sequence analysis panel, cell-free nucleic acid (eg, plasma), interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants, microsatellite instability, tumor mutation burden, and rearrangements	Genomic Sequencing Procedures; cell free DNA	**0244U *1.25** 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	The methodologies for 8X022 and 0244U are genomic profiling tests that use similar work and resources. These two assays are designed to analyze tumor alterations (copy number variants/alterations, sequence variants, rearrangements, microsatellite instability, and tumor mutational burden) to match the patient to the best therapies based on clinical evidence in peer-reviewed literature. The tumor mutational burden analysis in 8X022, a complex biomarker analysis that requires significant bioinformatics and development/validation requirements, which requires additional work and resources beyond test code 81455. We recommend a multiplier of *1.25. This refects the increased work and resources needed to sequence ctDNA from plasma at 10,000X (compared to FFPE tumor DNA that is sequenced at 100-1000X).	0244U * 1.25 ($3500 *1.25) = $4,375.00