Centers for Medicare and Medicaid Services

Clinical Laboratory Fee Schedule Annual Laboratory Meeting

June 24, 2021

Meeting Agenda:

8:45 a.m.	Sign In/Connectivity Check
9:00 a.m.	Welcome and Introductions Sarah Harding Meeting Facilitator, Hospital and Ambulatory Policy Group, CMS
9:20 a.m.	**Public Presentations* on CY 2022 New and Reconsidered Codes** ***Note:** This session will contain 10 minute presentations from pre-registered presenters on specific CLFS codes with recommendations for either gap-filling or crosswalking for code payment determinations.
12:00 – 1:00 p.m.	Lunch Break ***Note:** Presenters please reconnect by 12:45pm.
1:00 p.m.	**Public Presentations* on CY 2022 New and Reconsidered Codes (continued)**
5:00 p.m.	Closing / Meeting Adjourns

Annual Laboratory Meeting Overview

Welcome and Introductions

Annual Laboratory Meeting

- New or Substantially Revised Healthcare Common Procedure Coding System (HCPCS) Codes and Reconsidered Codes
- Basis of Payment: Gapfill or Crosswalk to Code on CLFS
- CY 2022 CLFS Code List
  - https://www.cms.gov/Medicare/Medicare-Fee-for-Service-Payment/ClinicalLabFeeSched/Laboratory_Public_Meetings

Format and Flow

Presentations

- Presentation Order Located on Agenda
- Max Time: 10 mins for each presentation

Q/A will occur via Zoom Chat-Box

- Max Time: 5 mins per presenter

Post Meeting Next Steps

CDLT Panel Meeting

- July 28-29, 2021 (Virtual)
- Registration not required for non-speakers

CMS CLFS CY 2022 Proposed Payment Determinations

- September 2021

CMS CLFS CY 2022 Final Payment Determinations

- November 2021

Reconsideration Requests

- Deadline: 60 days from Final Payment Determination Issuance

Housekeeping

Agenda, code list and presentations may be found on our CMS website at: https://www.cms.gov/Medicare/Medicare-Fee-for-Service-Payment/ClinicalLabFeeSched/Laboratory_Public_Meetings

Speaker:

Please speak directly into your microphone, announcing your name before speaking and please place your phone on mute when you are not speaking.

Comments/Questions:

Q/A occurs after each presentations.

Instructions for submitting questions

Type question in the chat-box:

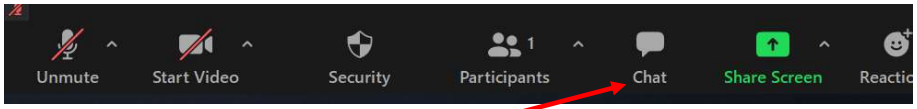
Format:

Your Name and Organization:

Presentation #:

Question:

5-minute limit for comments or questions.



1. Select "Chat" indicator at bottom of your screen

2. Type "Question"

3. Select "Send"

Welcome Remarks

Hospital and Ambulatory Policy Group Leadership

1. Personal Genome Diagnostics (PGDx)

Presenter: Jennifer Dickey, PhD

Code: 0250U

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

Public Comment	**Rationale**
We recommend crosswalk as follows: **81455:** Test for detecting genes associated with cancer (>50 genes)	**0250U** is an FDA cleared test of >50 genes for profiling a solid tumor. Prior to the PLA code, we believe that 81455 would be the appropriate code to describe this test, so it is a clear choice for crosswalking.

2. Plexision

Presenter: Mike Ryan, JD (McDermott Will & Emery LLP)

Code (s): 815X0, 002XM

815X0: Transplantation medicine (allograft rejection, pediatric liver and small bowel), measurement of donor and third-party-induced CD154+T-cytotoxic memory cells, utilizing whole peripheral blood, algorithm reported as a rejection risk score

Public Comment	Rationale

• Gapfill	• No comparable existing test priced on the CLFS
	  • Unique analytic methodology
	  • Unique post-analytic steps

002XM: 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

Public Comment	Rationale

• Gapfill	• No comparable existing test priced on the CLFS
	  • Unique analytic methodology
	  • Unique post-analytic steps

Background

- **Codes report two tests – Pleximmune (815X0) and Pleximark (002XM) – that are run on the same analytic and algorithmic platform**
  - **Methodology/workflow, analytes measured, and underlying algorithm are identical for the two assays**
- Tests only differ with respect to FDA regulatory status, intended use population, and threshold above which the algorithm predicts rejection
  - Pleximmune (815X0) is an FDA-approved humanitarian use device and is used in the evaluation of the risk of acute cellular rejection ("ACR") in patients less than 21 years old with liver or small bowel transplantation
  - Pleximark (002XM) is a laboratory-developed test and is intended for use in the evaluation of the risk of ACR in adult and pediatric patients with renal transplantation

Purpose, methods, and charges (both tests)

- **<u>Purpose (both tests)</u>:**
  - To predict a transplant patient's risk of rejection
    - Algorithm produces numeric score – the IR – that indicates the patient's risk of rejection
- **<u>Method (both tests)</u>:**
  - Algorithmic analysis of results obtained following induction of CD154+T-cytotoxic memory cells in donor culture and reference culture.
  - Process involves (a) isolation, counting and assessment of viability of leukocytes; (b) identification, thawing, counting and assessment of viability of donor and reference stimulators; (c) overnight culture of donor and reference media; (d) counting of both cultures via flow cytometry; and (e) algorithmic analysis

Recommendation:
Gapfill 815X0 and 002XM

Rationale:

As compared to potential crosswalks (e.g., MAAAs), 815X0 and 002XM differ in several key respects:

Pre-analytic differences	Analytic differences	Post-analytic differences
• Test only performed at Plexision (specimen must be shipped to Plexision)	• Unique analyte (CD154+ T-cytotoxic memory cells) • Unique methodology (combination of stimulator, culture, and flow cytometry)	• Unique algorithm • Unique intended use for MAAAs (assessment of rejection status)

3. Clinical Genomics Pathology Inc.

Presenter: Robert Bruce

Code: 0229U: BCAT1 (Branched chain amino acid transaminase 1) or IKZF1 (IKAROS family zinc finger 1) (eg, colorectal cancer) promoter methylation analysis

0229U: BCAT1 (Branched chain amino acid transaminase 1) or IKZF1 (IKAROS family zinc finger 1) (eg, colorectal cancer) promoter methylation analysis

Test Purpose: 0229U detects circulating tumor DNA associated with colorectal cancer tissue. The assay is intended for the detection of Minimal Residual Disease ("MRD") and Recurrent Disease in patients previously treated for primary or recurrent colorectal cancer.

Test Method: Polymerase Chain Reaction detects methylated CPG sites in two target genes (BCAT1 and/or IKZF1).

0229U: BCAT1 (Branched chain amino acid transaminase 1) or IKZF1 (IKAROS family zinc finger 1) (eg, colorectal cancer) promoter methylation analysis

Test Costs: 0229U costs include: sample collection supplies and transport to national laboratory; DNA extraction from plasma; Bisulphite conversion of DNA; DNA purification; BisDNA triplex PCR; direct lab labor; and overhead. Demanding clinical quality standards for 0229U indications for use require automated liquid handling process with substantial direct and indirect resource burden.

Test Charges: The list price of 0229U is $499.00

Current Payment Rate: Novitas Solutions has established a payment rate for 0229U of $384.00

0229U: BCAT1 (Branched chain amino acid transaminase 1) or IKZF1 (IKAROS family zinc finger 1) (eg, colorectal cancer) promoter methylation analysis

Public Comment	**Rationale**
81327 TIMES 2 ($192.00 x 2 = $384.00) SEPT9 (SEPTIN9) (eg, Colorectal cancer) promoter methylation analysis	<u>Similar methodology but significantly more work and resources required</u> • Both are PCR assays to detect circulating tumor DNA associated with colorectal cancer • 0229U detects 21 methylated CPG sites across 2 target genes, versus 8 methylated CPG sites on 1 target gene in 81327 • 0229U requires much greater work and resources to process in order to achieve required clinical performance levels

0229U: Potential cross-walk codes

CPT Code	0229U	81327	0114U
Test Technology	**Promoter Methylation Analysis**	Promoter Methylation Analysis	Methylation Analysis
Sample	**10 mL Blood**	10 mL Blood	Esophageal cells
Target Genes	**2 (BCAT1/IKZF1)**	1 (SEPT9)	2 (VIM/CCNA1)
CPG Sites	**21**	8	31
Target	**Circulating tumor DNA**	Circulating tumor DNA	Pre-cancerous DNA
Test Method	**qPCR**	qPCR	qPCR, then NGS, with algorithm
Disease	**Colorectal Cancer**	Colorectal Cancer	Barrett's Esophagus
Indication	**MRD, Recurrence Surveillance**	Screening	Identification of pts at elevated risk of Esophageal Cancer
Reg. Status	**LDT**	FDA PMA	LDT
NLA	**Recommended - $384.00 (=2 X 81327)**	$192.00	$1,938.01

4. AGENDIA, INC.

For comments from Agendia, Inc regarding CPT 815X1, please contact Vicky Huerta Reyes (Vicky.reyes@agendia.com)

5.HalioDx

Presenter: Paul Gerrard, MD

Code (s): 0X70U

0X70U: 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

Public Comment	**Rationale**
0108U TIMES 1.2 ($3015.90)	Consistent with methodology, amount of tissue material, and clinical risk readout; clinical validation study resources (10X) consistent with multiplier

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HalioDx– Gerrard, Paul

6. BioFire Diagnostics, LLC

Presenter: Brett Barrett, Market Access Manager

Code (s): 8715X

8715X: Culture, typing; identification of blood pathogen and resistance typing, when performed, by nucleic acid (DNA or RNA) probe, multiplexed amplified probe technique including multiplex reverse transcription, when performed, per culture or isolate, 6 or more targets

Public Comment	**Rationale**
Crosswalk: 87506 ($262.99)	87506: Detection test by nucleic acid for digestive tract pathogen, 6 -12 targets • 87506 desriptor most closely aligns with descriptor of proposed code 8715X

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BioFire Diagnostics – Name of Presenter (BARRETT, Brett)

7. Bruce Quinn Associates

Presenter: Dr. Bruce Quinn

Code (s): 812X0

Presenter: Dr Bruce Quinn
Company: INVITAE

812X0

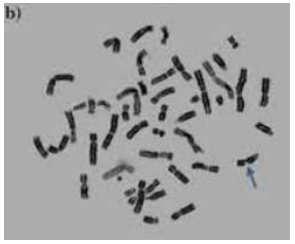
Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and loss-of-heterozygosity variants, low-pass sequencing analysis. Agenda #99.

812X0

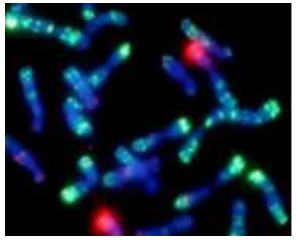
Descriptor:
Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and loss-of-heterozygosity variants, low-pass sequencing analysis

Public Comment	Rationale
Crosswalk **to** 81229	New procedure has same purpose, same indication, same patients, very similar report output New test has similar net resources requirements (including more elaborate capital equipment and informatics) New procedure is more agnostic (unbiased) to racial groups (Martin, Am J Hum Gen, 2021) CMS used 81229 as crosswalk for the most recent update to this code set (81277 in CY2020)

Progress in Technologies for Chromosome Studies

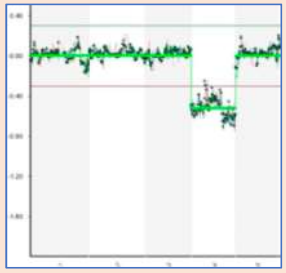


Giemsa Banding
1970s

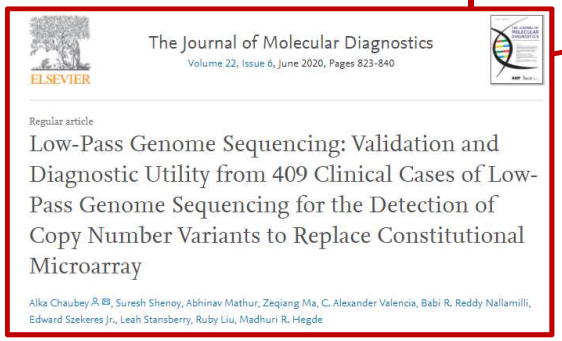


FISH
1990s

Microarrays
2000+
CPT 81228/81229
Codes from 2012



Low Pass NGS
Cytogenomics
2018+
- 812X0-



The Journal of Molecular Diagnostics
Volume 22, Issue 6, June 2020, Pages 823-840

ELSEVIER

Regular article

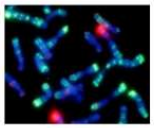
Low-Pass Genome Sequencing: Validation and Diagnostic Utility from 409 Clinical Cases of Low-Pass Genome Sequencing for the Detection of Copy Number Variants to Replace Constitutional Microarray

Alka Chaubey, Suresh Shenoy, Abhinav Mathur, Zeqiang Ma, C. Alexander Valencia, Babi R. Reddy Nallamilli, Edward Szekeres Jr., Leah Stansberry, Ruby Liu, Madhuri R. Hegde

- **Low-pass NGS provides high resolution mapping of chromosome structure but is not intended to provide point mutation analysis**
- **Coverage typically 0.5X-5X**

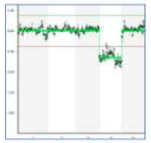
Thompson & Thompson, Genetics in Medicine, 2015, p.57 (1970s)
Speicher, Carter, Nat Rev Genet 6:782, 2005 (transition to Microarray)
Roooney, Brit J Ca, CGH in solid tumors, 80:862, 1999

Giemsa Banding
1970s



FISH
1990s

Microarrays
2000+
CPT 81228/81229
Codes = 2012



Low Pass NGS
Cytogenomics
2018+
- NEW CODE -

Low-Pass Genome Sequencing

Check for updates

Validation and Diagnostic Utility from 409 Clinical Cases of Low-Pass Genome Sequencing for the Detection of Copy Number Variants to Replace Constitutional Microarray

Alka Chaubey, Suresh Shenoy, Abhinav Mathur, Zeqiang Ma, C. Alexander Valencia, Babi R. Reddy Nallamilli, Edward Szekeres, Jr, Leah Stansberry, Ruby Liu, and Madhuri R. Hegde

From PerkinElmer Genomics, Pittsburgh, Pennsylvania

Accepted for publication March 12, 2020.

Address correspondence to Alka Chaubey, Ph.D., PerkinElmer Genomics, 3950 Shackleford Rd., Ste. 195, Duluth, GA 30096. E-mail: alka.chaubey@perkinelmer.com.

DNA copy number variants (CNVs) account for approximately 300 Mb of sequence variation in the normal human genome. Significant numbers of pathogenic CNVs contribute toward human genetic disorders. Recent studies suggest a higher diagnostic and clinical significance of low-pass genome sequencing (LP-GS) compared with chromosomal microarrays (CMAs). The performance metrics of the 5X LP-GS was compared with CMA to validate a low-cost and high-throughput method. LP-GS test performed on 409 samples (including 78 validation and 331 clinical) was evaluated using American College of Medical Genetics and Genomics guidelines. The CNV accuracy, precision, specificity, and sensitivity were calculated to be 100% for all previously characterized CNVs by CMA. Samples (n = 6) run at both approximately 30X GS and approximately 5X GS (LP-GS) average depth detected a concordance of 89.43% to 91.8% and 77.42% to 89.86% for overall single-nucleotide variants and insertions/deletions, respectively. In the 331 clinical samples, 17.2% each were classified as pathogenic/likely pathogenic and uncertain clinical significance. In addition, several cases with pathogenic CNVs were detected that were missed by CMA. This study demonstrates that LP-GS (5X GS) was able to reliably detect absence of heterozygosity, microdeletion/microduplication syndromes, and intragenic CNVs with higher coverage and resolution over the genome. Because of lower cost, higher resolution, and greater sensitivity of this test, our study in combination with other reports could be used in an evidence-based review by professional societies to recommend replacing CMAs. *(J Mol Diagn 2020, 22: 823—840; https://doi.org/10.1016/j.jmoldx.2020.03.008)*

Low Pass Genome Sequencing for Chromosome Structure

- **Increasing Adoption; Potentially a replacement technology**
- **VERY HIGH PERFORMANCE AND ACCURACY** *(accurately matching microarrays, see Chaubey 2020 at left, in J Molec Dx, the journal of the AMP)*
- **"Not racially biased" in under-represented populations**

81229 is a Good Crosswalk

Code	Purpose	Source	CLFS
81228	**Molecular cytogenomnics,** microarray	Germline	$900
81229	**Molecular cytogenomics,** microarray, SNPs	Germline	$1160
81277	**Molecular cytogenomics,** microarray, SNPs	Tumor	$1160
812XO	**Molecular cytogenomics,** low pass NGS	Germline	**$1160 CW**

- ✓ Last year, new code 81277 for tumor cytogenomics was added to this series, and directly crosswalked to 81229
- ✓ 81229 is also a good crosswalk for NGS Cytogenomics
- ✓ Exactly the same indications and similar reports as 81229
- ✓ Similar total resource use including higher capital equipment

Other Comparators

- 0012U Germline disorders, gene rearrangements by NGS, Mayo $2516
- 0013U, 0014U, 0056U, gene arrangements, cancer, by NGS, Mayo $2516

Note: 81228, 81229 were new in CY2012, but first priced by PAMA in 2018

8. Mayo Clinic Laboratories (MCL)/Mayo Clinic

Presenter: Cheryl James

New Codes:
0017M, 860X2, 863X3,862X0, 862XX, 862X1, 8715X

Reconsideration Codes:
80151, 80161, 80167, 80181

0017M: Oncology (diffuse large B-cell lymphoma [DLBCL]), mRNA, gene expression profiling by fluorescent probe hybridization of 20 genes, formalin-fixed paraffin-embedded tissue, algorithm reported as cell of origin
Lymph2Cx, Mayo Clinic Arizona Molecular Diagnostics Laboratory

Public Comment	**Rationale**
Crosswalk to 0120U ($2510.21) 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 latter	Both tests use the same methodology and require similar resources to perform

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MCL/Mayo Clinic – James, Cheryl

860X2: Aquaporin-4 (neuromyelitis optica [NMO] antibody; flow cytometry (ie, fluorescence-activated cell sorting [FACS]), each

Public Comment	**Rationale**
86367 ($77.78) Stem cells (ie, CD34), total count	NMO antibody testing and total stem cell count are performed by the same methodology (FACS) and require similar resources to perform. Both tests involve similar processes, including isolating the cells and using antibodies to quantify the cells via flow cytometry. In addition, NMO antibody testing also requires a complex algorithm to determine the ratio of the IgG binding index.

863X3: Myelin oligodendrocyte glycoprotein (MOG-IgG1) antibody; flow cytometry (ie, fluorescence-activated cell sorting [FACS]), each

Public Comment	**Rationale**
86367 ($77.78) Stem cells (ie, CD34), total count	MOG antibody testing and total stem cell count are performed by the same methodology (FACS) and require similar resources to perform. Both tests involve similar processes, including isolating the cells and using antibodies to quantify the cells via flow cytometry. In addition, MOG antibody testing also requires a complex algorithm to determine the ratio of the IgG binding index

862X0: Endomysial antibody (EMA), each immunoglobulin (Ig) class

Public Comment	**Rationale**
86038 x 2 ($24.18) Antinuclear antibodies (ANA)	The EMA test uses a similar methodology as the test for antinuclear antibodies (a substrate is overlaid with dilutions of the patient's serum, incubated and then covered with fluorescein-conjugated IgG antiserum). The resources required to perform the EMA test are higher than those for antinuclear antibodies (EMA test uses a rhesus monkey substrate, which is more expensive than the Hep-2 substrate used for antinuclear antibodies). The x 2 multiplier accounts for the reagent cost difference and additional technologist time required to perform the EMA test.

862XX: Gliadin (deamidated) (DGP) antibody, each immunoglobulin (Ig) class

Public Comment	**Rationale**
86147 ($25.45) Cardiolipin (phospholipid) antibody, each Ig class	Gliadin antibody testing, like Cardiolipin antibody testing, uses the same methodology (ELISA) and requires similar resources to perform. Both codes represent antibody-specific tests to detect antibodies present in autoimmune disorders.

CMS Annual Lab Meeting, June 24, 2021
MCL/Mayo Clinic – James, Cheryl

862X1: Tissue transglutaminase, each immunoglobulin (Ig) class

Public Comment	**Rationale**
86147 ($25.45) Cardiolipin (phospholipid) antibody, each Ig class	Tissue transglutaminase antibody testing, like Cardiolipin antibody testing, uses the same methodology (ELISA) and requires similar resources to perform. Both codes represent antibody-specific tests to detect antibodies present in autoimmune disorders.

8715X: Culture, typing; identification of blood pathogen and resistance typing, when performed, by nucleic acid (DNA or RNA) probe, multiplexed amplified probe technique including multiplex reverse transcription, when performed, per culture or isolate, 6 or more targets

Public Comment	**Rationale**
87506 ($262.99) Infectious agent detection by nucleic acid (DNA or RNA); gastrointestinal pathogen (eg, Clostridium difficile, E. coli, Salmonella, Shigella, norovirus, Giardia), includes multiplex reverse transcription, when performed, and multiplex amplified probe technique, multiple types or subtypes, 6-11 targets	Both tests use a similar methodology (multiplex amplified probe technique) for infectious agent detection of 6 or more target pathogens and require similar resources to perform

Reconsideration:
80151 Amiodarone
80161 Carbamazepine; -10, 11-epoxide
80181 Flecainide

Public Comment	Rationale
80155 ($38.57) Caffeine	Current crosswalk to 80299 (Quantitation of therapeutic drug, not elsewhere specified) does not appropriately account for the complexities involved in testing for these therapeutic drugs. Codes 80151, 80161 and 80181 use the same methodology (LC-MS/MS) as Caffeine testing and require similar resources to perform. Therefore, we maintain a crosswalk to 80155 is most appropriate. A crosswalk to 80155 is consistent with how CMS set payment amounts for therapeutic drug assays on the 2019 CLFS

Reconsideration:
80167 Felbamate

Public Comment	Rationale
80199 ($27.11) Tiagabine	Current crosswalk to 80299 (Quantitation of therapeutic drug, not elsewhere specified) is not appropriate and there is a more specific code available. Code 80167 uses similar methodology and resources to perform as 80199. Additionally, both codes represent quantitative assays for an epileptic drug used to treat epilepsy and seizures. A crosswalk to 80155 is consistent with how CMS set payment amounts for therapeutic drug assays on the 2019 CLFS

9. Interpace Biosciences, Inc.

Presenter: Alidad Mireskandari, Ph.D.

Chief Development Officer Interpace Biosciences, Inc.

Code: 0245U

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

Public Comment	**Rationale**
Crosswalk to 81455	• 0245U includes 51 genes, matching the descriptor for 81455 • Novitas LCD coding article instructed Interpace to bill for the test (ThyGeNEXT) using 81455 in 2020 • **Novitas currently prices 0245U at the same rate as 81455**

Clinical Laboratory Fee Schedule - Annual Laboratory Meeting June 24, 2021

Interpace Biosciences – MIRESKANDARI, Alidad

ThyGeNEXT: Test Purpose

- ThyGeNEXT oncogene panel helps to resolve diagnostic uncertainty in the diagnosis of thyroid nodules and has a high Positive Predictive Value (75%) for ruling in malignancy
- ThyGeNEXT identifies 10 DNA mutations with multiple hotspots, 37 gene fusions, and 4 mRNA markers
- Test includes both diagnostic and prognostic markers as well as markers that are therapeutic targets

ThyGeNEXT® NGS Panel	
DNA mutation panel	**RNA panel (# of fusions)**
ALK	ALK (2)
BRAF	BRAF (3)
GNAS	NTRK (8)
HRAS	PPARg (5)
KRAS	RET (14)
NRAS	THADA (5)
PIK3CA	**mRNA markers** NKX2-1, PAX8, TBP, USP33
PTEN	
RET	
TERT	

ThyGeNEXT: Test Purpose

ThyGeNEXT identifies the DNA mutations and gene fusions most commonly seen across all types of thyroid cancer.

Papillary thyroid carcinoma	Follicular variant of papillary thyroid carcinoma	Follicular carcinoma	Medullary carcinoma
BRAF (V600E)	RAS	RAS	RET
RET/PTC	PAX8/PPARG	PAX8/PPARG	RAS
RAS	BRAF (K601E)	PIK3CA	
NTRK	RET/PTC	PTEN	
TERT		TERT	

Fig. 10.1 Common gene mutations and gene fusions in different thyroid tumors.

Note: Not all available molecular tests include testing for the potentially aggressive TERT Promoter Mutation Markers

Hsiao SJ and Nikiforov YE, Otolaryngology 6/1/2020 https://entokey.com/10-molecular-advances-in-the-diagnosis-and-treatment-of-thyroid-cancer/

ThyGeNEXT: Test Methodology

- The ThyGeNEXT expanded mutation panel utilizes amplicon-based targeted next-generation sequencing (NGS) (MiSeq, Illumina) to detect messenger RNA fusion transcripts and DNA mutation variants
  - For a positive variant determination, a specimen is required to contain at least 3% BRAF V600E, 10% GNAS, or 5% other individual DNA variants in the panel
  - ThyGeNEXT performed only in Interpace's CLIA-certified, CAP-accredited laboratory in Pittsburgh, Pennsylvania
- ThyGeNEXT testing can be performed from a single dedicated fresh FNA (fine needle aspiration) sample or a diagnostic cytology slide containing > 80 follicular cells
  - Note: Not all available molecular tests provide for testing from cytology slides
- Comprehensive test report provides risk of malignancy, allowing physicians customized treatment options for patients. Test results highlight:
  - Location of the nodule
  - Cytology diagnosis
  - Molecular diagnostic results
  - Customized pathology commentary

Crosswalk to Most Comparable Test

- Regulations provide that CMS chooses crosswalk **"if it is determined that a new [test] is comparable to an existing test, multiple existing test codes, or a portion of an existing test code"**
  - New test is assigned the payment rate of the comparable test
- A test is gapfilled when **"no comparable existing [test] is available"**
  - New test is priced by Medicare contractors the following year
- Gapfill appropriate **only** when there are no comparable tests on the CLFS
- If there are **multiple** comparable tests, CMS guidance makes clear that a test should be crosswalked to the **"most appropriate existing test"**

CPT 0245U Most Comparable to 81455

- **CPT 81455** describes a targeted genomic sequence analysis panel of 51 or more genes
  - Includes DNA analysis and RNA analysis “when performed”
- ThyGeNEXT **(0245U)** uses next generation sequencing (NGS) to interrogate 51 genomic markers
  - Targets include, but are not limited to, ALK, BRAF, KRAS, NRAS, PTEN, PIK3CA, and RET, which are included as exemplar genes in the 81455 descriptor
- ThyGeNEXT list price is $2,950

Medicare Contractor Priced ThyGeNEXT at 81455 Payment Rate

- ThyGeNEXT covered by Medicare Administrative Contractor Novitas
  - Local MAC for Interpace's Pennsylvania laboratory
- Novitas instructed Interpace in coding and billing article A52986 to submit claims for ThyGeNEXT with CPT 81455 effective December 13, 2020
  - Predecessor test with fewer genes, ThyGenX, had been billed with 81445
- When ThyGeNEXT was assigned code 0245U effective April 1, 2021, Novitas added 0245U to the coding article at the same payment rate as 81455

Recommendation

Public Comment	Rationale
Crosswalk 0245U to 81455	• 0245U includes 51 genes, matching the descriptor for 81455 • Novitas LCD coding article instructed Interpace to bill for ThyGeNEXT using 81455 in 2020 • Novitas currently prices 0245U at the same rate as 81455

10. Point of Care Testing Association Joined by BD, Hologic, Qiagen, and Quidel

Presenter: Paul Radensky, MD, JD (McDermott+Consulting LLC)

Code (s): 87636, 87637, 0240U, 0241U, 0223U, 87426, 87428, 87811, 86408, 86409, 86413, 835X1, 8352X

Agenda

- COVID-19 amplified probe tests
  - 87636, 87637, 0240U, 0241U, 0223U
- COVID-19 antigen tests
  - 87426, 87428, 87811
- COVID-19 antibody tests
  - 86408, 86409, 86413
- Chemistry tests
  - 835X1, 8352X

87636: Infectious agent detection by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]) and influenza virus types A and B, multiplex amplified probe technique

Public Comment	Rationale
• Crosswalk 87631X1=$142.63	• Same method (multiplexed amplified probe) • Same number of viral targets (3)

87637: Infectious agent detection by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]) and influenza virus types A and B, and respiratory syncytial virus, multiplex amplified probe technique

Public Comment	Rationale
• Crosswalk 87631X1=$142.63	• Same method (multiplexed amplified probe) • Same number of viral targets (4)

0240U: Infectious disease (viral respiratory tract infection), pathogen-specific RNA, 3 targets (severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2], influenza A, influenza B), upper respiratory specimen, each pathogen reported as detected or not detected

Public Comment	Rationale
• Crosswalk 87631X1=$142.63	• Same method (multiplexed amplified probe) • Same number of viral targets (3)

0241U: Infectious disease (viral respiratory tract infection), pathogen-specific RNA, 4 targets (severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2], influenza A, influenza B, respiratory syncytial virus [RSV]), upper respiratory specimen, each pathogen reported as detected or not detected

Public Comment	Rationale
• Crosswalk 87631X1=$142.63	• Same method (multiplexed amplified probe) • Same number of viral targets (4)

0223U: Infectious disease (bacterial or viral respiratory tract infection), pathogen-specific nucleic acid (DNA or RNA), 22 targets including severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), qualitative RT-PCR, nasopharyngeal swab, each pathogen reported as detected or not detected

Public Comment	Rationale
• Crosswalk 87633X1=$416.78	• Same method (multiplexed amplified probe) • Same number of viral targets (22)

87426: Infectious agent antigen detection by immunoassay technique, (eg, enzyme immunoassay [EIA], enzyme-linked immunosorbent assay [ELISA], immunochemiluminometric assay [IMCA]) qualitative or semiquantitative, multiple-step method; severe acute respiratory syndrome coronavirus (eg, SARS-CoV, SARS-CoV-2 [COVID-19])

Public Comment	Rationale
• Crosswalk 87430X2.5=$42.03	• Same method (instrumented immunoassay) • Multiplier to reflect resources required for COVID-19 testing

87428: Infectious agent antigen detection by immunoassay technique, (eg, enzyme immunoassay [EIA], enzyme-linked immunosorbent assay [ELISA], fluorescence immunoassay [FIA], immunochemiluminometric assay [IMCA]) qualitative or semiquantitative; severe acute respiratory syndrome coronavirus (eg, SARS-CoV, SARS-CoV-2 [COVID-19]) and influenza virus types A and B

Public Comment	Rationale
• Crosswalk 87430X2.5+87400X2=$70.29	• Same method (instrumented immunoassay) • 2.5 X Multiplier to reflect resources required for COVID-19 testing • 2 X Multiplier to reflect influenza types A and B (87400=each)

87811: Infectious agent antigen detection by immunoassay with direct optical (ie, visual) observation; severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19])

Public Comment	Rationale
• Crosswalk 87804X2.5=$41.38	• Same method (direct optical [visual] observation immunoassay) • Multiplier to reflect resources required for COVID-19 testing

86408: Neutralizing antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]); screen

Public Comment	Rationale
• Crosswalk 86794X2.5=$42.13	• Same method (antibody immunoassay) • Multiplier to reflect resources required for COVID-19 testing

86409: Neutralizing antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]); titer

Public Comment	Rationale
• Crosswalk 86352X1=$135.86	• Similar method

86413: Severe acute respiratory syndrome coronavirus 2 (SARS CoV-2) (Coronavirus disease [COVID-19]) antibody, quantitative

Public Comment	Rationale
• Crosswalk 86794X3.125=$52.66	• Similar method • Multiplier to reflect resources required to perform procedure

835X1: Interleukin-6 (IL-6)

Public Comment	Rationale
• Crosswalk 83006X1=$75.60	• Similar method (immunoassay) • Similar analyte. ST2 is a member of the IL-1 receptor family.

8352X: Immunoglobulin light chains (ie, kappa, lambda), free, each

Public Comment	Rationale
• Crosswalk 83520X1=$17.27	• Similar method (immunoturbidometry) • Similar resources

11. Mindera Corporation

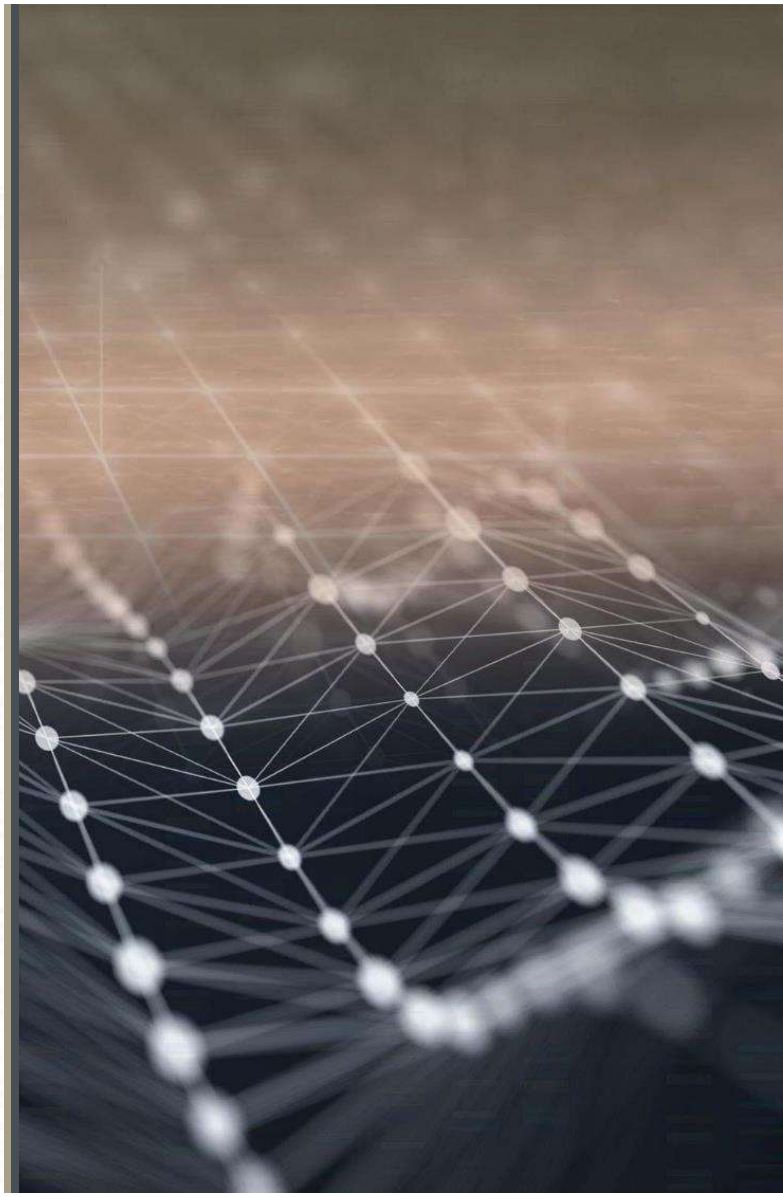
Presenter: Tobin Dickerson

Code (s): 0X59U

Mindera

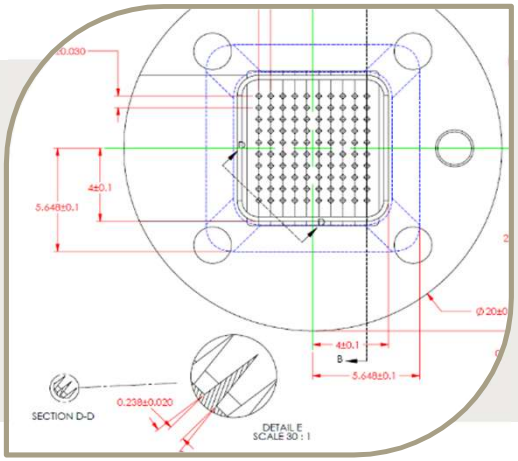
Clinical Laboratory Fee Schedule Public Meeting

PLA Code 0X59U



Mind.Px™: First diagnostic test to utilize Machine Learning to predict psoriasis biologic response with high accuracy

LAB APPLIES BIOMARKER PATCH

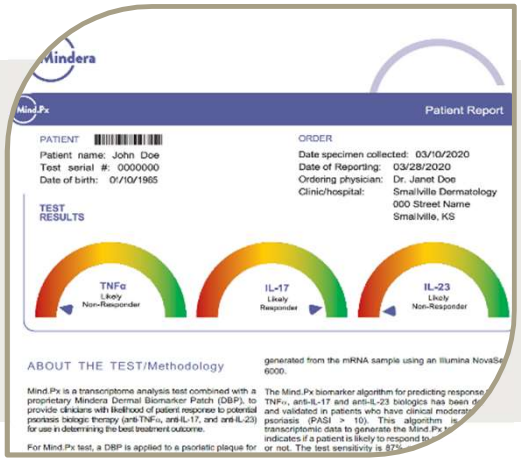


Mindera's proprietary FDA-registered Class I Dermal Biomarker Patch isolates the whole transcriptome from a patient. Developed over 10 years, this versatile platform was designed and optimized for efficient extraction of mRNA from the epidermis and dermis.

MINDERA SEQUENCES

Mind.Px uses Next-Generation Sequencing to analyze a patient's whole dermal transcriptome comprised of 7,000 unique mRNA biomarkers in our CLIA-registered lab.

MIND.PX PREDICTS



Mindera applies artificial intelligence and machine learning methods to a patient data set to create data-driven classifiers through analytics. These sophisticated classifiers are continuously learning from this complex data set and have a high predictive value for patient biologic drug response.

Mindera Mind.Px test PLA 0X59U

Public Comment: Crosswalk to 0019U

	PLA 0X59U	PLA 0019U
Descriptor	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	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.
Next Generation Sequencing technology applied to the RNA of 50+ genes	✓	✓
RNA sequencing yields the whole transcriptome, which is then analyzed for gene expression	✓	✓
Predictive algorithm determining likelihood of response to therapy	✓	✓

12. Association for Molecular Pathology

Presenter: Jay Patel, MD (Alternate: Anthony Sireci, MD)

Code(s): 81279, 81338, 81339, 812X0, 87636, 87637, 0240U, 0241U

81279: JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) targeted sequence analysis (eg, exons 12 and 13)

Public Comment	**Rationale**
81272 ($329.51)	The methodology, resources, and amount of genetic material sequenced are comparable to that of KIT targeted sequence analysis

81338: MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; common variants (eg, W515A, W515K, W515L, W515R)

Public Comment	**Rationale**
81120 - ($193.25)	The methodology, resources, and amount of genetic material sequenced are comparable to that of IDH1 common variants (both are testing of variants in one codon in oncology samples)

81339: MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; sequence analysis, exon 10

Public Comment	Rationale
81310 - ($246.52)	The methodology, resources, and amount of genetic material sequenced are comparable to that of NPM1 gene analysis (both are 1 exon targeted sequencing for oncology samples)

812X0: Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and loss-of-heterozygosity variants, low-pass sequencing analysis

Public Comment	**Rationale**
81229 ($1,160)	The methodology, resources, type of genetic material sequenced, and genomic analysis required are comparable to that of 81229

87636: Infectious agent detection by nucleic acid (DNA or RNA) severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (coronavirus disease [COVID-19]) and influenza virus types A and B, multiplex amplified probe technique

Public Comment	**Rationale**
87631 - ($142.63)	The methodology, resources, and number of viruses sequenced are comparable to that of 87631

87637: Infectious agent detection by nucleic acid (DNA or RNA) severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (coronavirus disease [COVID-19]), influenza virus types A and B, and respiratory syncytial virus, multiplex amplified probe technique

Public Comment	**Rationale**
87631 - ($142.63)	The methodology, resources, and number of viruses sequenced are comparable to that of 87631

0240U: Infectious disease (viral respiratory tract infection), pathogen-specific RNA, 3 targets (severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2], influenza A, influenza B), upper respiratory specimen, each pathogen reported as detected or not detected

Public Comment	**Rationale**
87631 - ($142.63)	The methodology, resources, and number of viruses assessed are comparable to that of 87631

0241U: Infectious disease (viral respiratory tract infection), pathogen-specific RNA, 4 targets (severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2], influenza A, influenza B, respiratory syncytial virus [RSV]), upper respiratory specimen, each pathogen reported as detected or not detected

Public Comment	**Rationale**
87631 - ($142.63)	The methodology, resources, and number of viruses assessed are comparable to that of 87631

13.Variantyx, Inc.

Presenters: Daryl Spinner and Christine Stanley

Codes: 0230U, 0231U, 0232U, 0233U, 0234U, 0235U, 0236U, 0237U, 0238U

Overview of Variantyx, Inc. CPT Code Pricing Recommendations

CPT Code	Test Name	Pricing Approach
0230U	Genomic Unity® AR Gene Analysis	Crosswalk to 81173 + 81204
0231U	Genomic Unity® CACNA1A Gene Analysis	Crosswalk to 81184 + 81185
0232U	Genomic Unity® CSTB Gene Analysis	Crosswalk to 81188 + 81189
0233U	Genomic Unity® FXN Gene Analysis	Crosswalk to 81285 + 81286
0234U	Genomic Unity® MECP2 Gene Analysis	Crosswalk to 81302 + 81304
0235U	Genomic Unity® PTEN Gene Analysis	Crosswalk to 81321 + 81323
0236U	Genomic Unity® SMN1/2 Gene Analysis	Crosswalk to 81329 + 81337
0237U	Genomic Unity® Cardiac Ion Channelopathies Analysis	Crosswalk to 81413 + 81414
0238U	Genomic Unity® Lynch Syndrome Analysis	Crosswalk to 81435 + 81436

Multiple types of genomic variants cause genetic disorders and inherited cancers

Genomic Variant Types/ DNA Changes	**Details**	**Example Indications**
Small sequence changes	Single nucleotide variants (SNVs), insertions or deletions [indels] of less than 35 bp	Hereditary cancers, inherited cardiovascular disorders, neurodevelopmental disorders
Deletions, duplications and copy number variations (CNVs)	Ranging from 35 bp up to whole chromosomes	Spinal muscular atrophy, hereditary cancers, neurodevelopmental disorders
Short tandem repeat (STR) expansions	Short repetitive sequences in genes that expand in number of repeats	Multiple movement disorders, intellectual disability, other neurodevelopmental disorders

Multiple types of genomic variants cause genetic disorders and inherited cancers *(cont.)*

Genomic Variant Types/ DNA Changes	**Details**	**Example Indications**
Inversions	Regions of DNA that are inverted from their normal orientation	Movement disorders, intellectual disability, seizure disorders
Transposable element insertions/ mobile element insertions	Abnormal pieces of DNA that insert and move around the genome causing heritable disease	Movement disorders, intellectual disability, seizure disorders
Loss of heterozygosity (LOH)/ uniparental disomy (UPD)	Changes in the DNA arising from abnormalities in how chromosomes were inherited from mother and father	Intellectual disability, hereditary cancers

These genomic variant types play an important role in the genes/ disorders tested by Variantyx PLAs under consideration

- Neuromuscular disorders, intellectual disability and other neurodevelopmental disorders, inherited cardiac disorders, and inherited cancers*
- Tests that cannot detect the full range of genomic variants leave clinicians with significant uncertainty when negative results are returned
  - True or false negative?
  - Missed definitive genetic diagnosis when one is identifiable?
  - Continued testing/ prolonged diagnostic odyssey → wasted resources/ time
  - Uncertainty and missed diagnoses → reduced actionability
  - Wrong conclusions → reduced clinical utility

** ClinVar: https://www.ncbi.nlm.nih.gov/clinvar/, and numerous peer reviewed studies.*

Variantyx PLAs under consideration comprehensively detect these relevant genomic variant types

- All testing for patients/ probands conducted on a DNA sequencing platform (WGS backbone) with proprietary bioinformatics that detect all these genomic variant types in every test, from single-gene to gene panel to WES to WGS
- Single gene and panel tests conducted on most common sequencing platforms do not detect the full range of genomic variants and thus have reduced:
  - Clinical validity
  - Actionability/ clinical utility
  - Diagnostic yield
- Given the more advanced sequencing platform used in all patient/ proband testing to produce the superior results described, the cost of testing is significantly greater

Detection/ characterization of the full range of genomic variant types were not anticipated in the current Medicare CLFS, especially in a single sequencing test

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Variantyx Inc – SPINNER, Daryl; STANLEY, Christine

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

0230U: Genomic Unity® AR Gene Analysis

Public Comment	Rationale
Crosswalk to: 81173 + 81204 = ($301.35 + $137.00 = $438.35)	• Closest match* for level of resources based on analytes and totality of code descriptors • Increased clinical validity and utility given all relevant DNA changes are detected in one, single platform test (small sequence changes, duplications/ deletions, short tandem repeat expansions, etc.)

* Current CLFS for CPT codes 81173 and 81204 does not anticipate duplications, deletions, CNVs, insertions across exons nor introns (only small sequence changes and STRs are anticipated in current CLFS codes)

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

Variantyx Inc – SPINNER, Daryl; STANLEY, Christine

0231U: Genomic Unity® CACNA1A Gene Analysis

Public Comment	Rationale
Crosswalk to: 81184 + 81185 = ($137.00 + $846.27 = $983.27)	• Closest match* for level of resources based on analytes and totality of code descriptors • Increased clinical validity and utility given all relevant DNA changes are detected in one, single platform test (small sequence changes, duplications/ deletions, short tandem repeat expansions, etc.)

* Current CLFS for CPT codes 81184 and 81185 does not anticipate duplications, deletions, CNVs, insertions, LOH across exons nor introns (only small sequence changes and STRs are anticipated in current CLFS codes)

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

0232U: Genomic Unity® CSTB Gene Analysis

Public Comment	Rationale
Crosswalk to: 81188 + 81189 = ($137.00 + $274.83 = $411.83)	• Closest match* for level of resources based on analytes and totality of code descriptors • Increased clinical validity and utility given all relevant DNA changes are detected in one, single platform test (small sequence changes, duplications/ deletions, short tandem repeat expansions, etc.)

* Current CLFS for CPT codes 81188 and 81189 does not anticipate duplications, deletions, CNVs, insertions across exons nor introns (only small sequence changes and STRs are anticipated in current CLFS codes)

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

0233U: Genomic Unity® FXN Gene Analysis

Public Comment	Rationale
Crosswalk to: 81285 + 81286 = ($274.83 + $274.83 = $549.66)	• Closest match* for level of resources based on analytes and totality of code descriptors • Increased clinical validity and utility given all relevant DNA changes are detected in one, single platform test (small sequence changes, duplications/ deletions, short tandem repeat expansions, etc.)

* Current CLFS for CPT codes 81285 and 81286 does not anticipate duplications, deletions, CNVs, insertions across exons nor introns (only small sequence changes and STRs are anticipated in current CLFS codes)

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

0234U: Genomic Unity® MECP2 Gene Analysis

Public Comment	Rationale
Crosswalk to: 81302 + 81304 = ($527.87 + $150.00 = $677.87)	• Closest match* for level of resources based on analytes and totality of code descriptors • Increased clinical validity and utility given all relevant DNA changes are detected in one, single platform test (small sequence changes, duplications/ deletions, etc.)

* Current CLFS for CPT codes 81302 and 81304 does not anticipate CNVs, insertions across exons nor introns (only small sequence changes and del/ dups are anticipated in current CLFS codes)

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

0235U: Genomic Unity® PTEN Gene Analysis

Public Comment	Rationale
Crosswalk to: 81321 + 81323 = ($600.00 + $300.00 = $900.00)	• Closest match* for level of resources based on analytes and totality of code descriptors • Increased clinical validity and utility given all relevant DNA changes are detected in one, single platform test (small sequence changes, duplications/ deletions, etc.)

* Current CLFS for CPT codes 81321 and 81323 does not anticipate CNVs, inversions, LOH across exons nor introns (only small sequence changes and del/ dups are anticipated in current CLFS codes)

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

0236U: Genomic Unity® SMN1/2 Gene Analysis

Public Comment	Rationale
Crosswalk to: 81329 + 81337 = ($137.00 + $301.35 = $438.35)	• Closest match* for level of resources based on analytes and totality of code descriptors • Increased clinical validity and utility given all relevant DNA changes are detected in one, single platform test (small sequence changes, duplications/ deletions, etc.)

* Current CLFS for CPT codes 81329 and 81337 does not anticipate CNVs, insertions, across exons nor introns (only small sequence changes and del/ dups are anticipated in current CLFS codes)

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

0237U: Genomic Unity® Cardiac Ion Channelopathies Analysis

Public Comment	Rationale
Crosswalk to: 81413 + 81414 = ($584.90 + $584.90 = $1,169.80)	• Closest match* for level of resources based on analytes and totality of code descriptors • Increased clinical validity and utility given all relevant DNA changes are detected in one, single platform test (small sequence changes, duplications/ deletions, etc.)

* Current CLFS for CPT codes 81413 and 81414 does not anticipate CNVs, inversions, insertions, LOH across exons nor introns (only small sequence changes and del/ dups are anticipated in current CLFS codes)

0238U: Oncology (Lynch syndrome), genomic DNA sequence analysis of MLH1, MSH2, MSH6, PMS2, and EPCAM, including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non-uniquely mappable regions

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Variantyx Inc – SPINNER, Daryl; STANLEY, Christine

0238U: Genomic Unity® Lynch Syndrome Analysis

Public Comment	Rationale
Crosswalk to: 81435 + 81436 = ($584.90 + $584.90 = $1,169.80)	• Closest match* for level of resources based on analytes and totality of code descriptors • Increased clinical validity and utility given all relevant DNA changes are detected in one, single platform test (small sequence changes, duplications/ deletions, etc.)

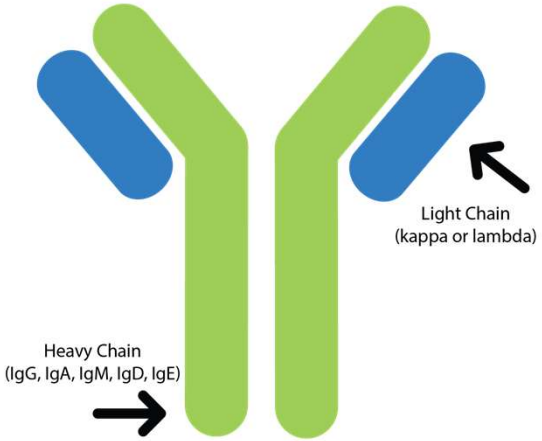
* Current CLFS for CPT codes 81435 and 81436 does not anticipate CNVs, inversions, insertions, LOH across exons nor introns (only small sequence changes and del/ dups are anticipated in current CLFS codes)

14. The Binding Site

Presenter: David Parker, PhD, Precision for Medicine

Code: 8352X, Immunoglobulin Light Chains (i.e., Kappa, Lambda) Free, Each

Measuring Kappa and Lambda Free Light Chains in Multiple Myeloma (MM) and Amyloidosis (AL)



- Plasma cell dyscrasias occur when plasma cells overproduce abnormal immunoglobulin(s) and/or free light chains (FLCs)
- Physicians measure kappa and lambda FLCs and the kappa/lambda FLC ratio to screen for plasma cell dyscrasias, diagnose MM, and monitor response to treatment and disease progression
- Serum free light chain assays are in vitro diagnostic immunoassays that measure serum FLC concentrations
- Two assays are necessary to separately quantify kappa FLC and lambda FLC and to generate a kappa/lambda ratio
- Serum FLC testing is recommended by several national and international guidelines for the diagnosis and monitoring of MM or AL

1. Types of Myeloma. International Myeloma Foundation Website. Available at: https://www.myeloma.org/types-of-myeloma. Last Reviewed August 1, 2019. Accessed May 24, 2021. **2.** Ahlstrom J. Kappa and Lambda Light Chains. Myeloma Crowd Website. Available at: https://www.myelomacrowd.org/kappa-lambda-light-chain/. Published March 6, 2019. Accessed May 24, 2021.

CMS Annual Lab Meeting, June 24, 2021
The Binding Site – Parker, David

Turbidimetry is the Dominant Methodology for Measuring Kappa/Lambda FLCs in the United States

Kit Manufacturer	Kappa/Lambda IVD Kit Name	Analyzer	Methodology	Appropriate CPT Coding*
The Binding Site	Optilite Freelite Kappa Free Kit, Optilite Freelite Lambda Free Kit	Optilite®	Turbidimetry	83520 x 2
	Freelite Human Kappa And Lambda Free Kits For Use On The SPAPLUS Analyzer	SPAPlus®	Turbidimetry	83520 x 2
	Freelite Human Kappa And Lambda Free Diagnostic Test Kits For Use On Roche Cobas Analyzers	Roche Cobas c501	Turbidimetry	83520 x 2
	Freelite Human Kappa And Lambda Free Kits For Use On The Dade Behring Nephelometer II (currently being phased out)	BN Systems BN II	Nephelometry	83883 x 2
Diazyme	Diazyme Human Kappa Free Light Chain Assay; Diazyme Human Lambda Free Light Chain Assay	Hitachi 917	Turbidimetry	83520 x 2
Siemens Healthineers	N Latex FLC Kappa, N Latex FLC Lambda	Atellica® CH	Turbidimetry	83520 x 2
	N Latex FLC Kappa Assay, N Latex FLC Lambda Assay	BN Systems (BN II/ BN ProSpec)	Nephelometry	83883 x 2

- The Binding Site has the leading market share in kappa and lambda FLC tests, and is currently phasing out its kappa/lambda FLC kit on the BN II system due to the market preference for turbidimetric methods
- Turbidimetry does not have a methodology-specific code, and its use for an otherwise unspecified analyte is best described currently by 83520 (Immunoassay for analyte other than infectious agent antibody or infectious agent antigen; quantitative, not otherwise specified)
- 3 of the 4 major national laboratories bill for the individual tests to determine the kappa and lambda FLC ratio using 83520 x 2

* Coding for determination of kappa/lambda ratio; separate measurements of kappa and lambda required

8352X:
Immunoglobulin Light Chains (i.e., Kappa, Lambda) Free, Each

Public Comment	Rationale
Crosswalk: 83520 ($17.27)	• 8352X is a new analyte-specific code for an assay previously described using a methodology code – no changes to current test methodologies or resources are implied • Most kappa and lambda FLC testing is performed with turbidimetric methods • 83520 is the most specific CPT code that describes an NOS immunoassay measured by turbidimetry • 83520 is both appropriate and commonly used by laboratories to bill for each separate test of kappa or lambda FLC • The proposed crosswalk maintains current payment levels for the dominant methodology

15. Presentation removed by lab

16. Theralink Technologies, Inc.

Presenters:

- Kris Weinberg: Theralink Technologies, Inc.
- Emanuel Petricoin, PhD: George Mason University Center for Applied Proteomics and Molecular Medicine

Code: 0249U

0249U: Oncology (breast), semiquantitative analysis of 32 phosphoproteins and protein analytes, includes laser capture microdissection, with algorithmic analysis and interpretative report

Public Comment	**Rationale**
Crosswalk to 0037U ($3,500)	Consistent with code descriptor in terms of level of complexity, resources required and assay output

CMS Annual Lab Meeting, June 24, 2021

Theralink Technologies, Inc., Petricoin, Emanuel, PhD – Weinberg, Kris

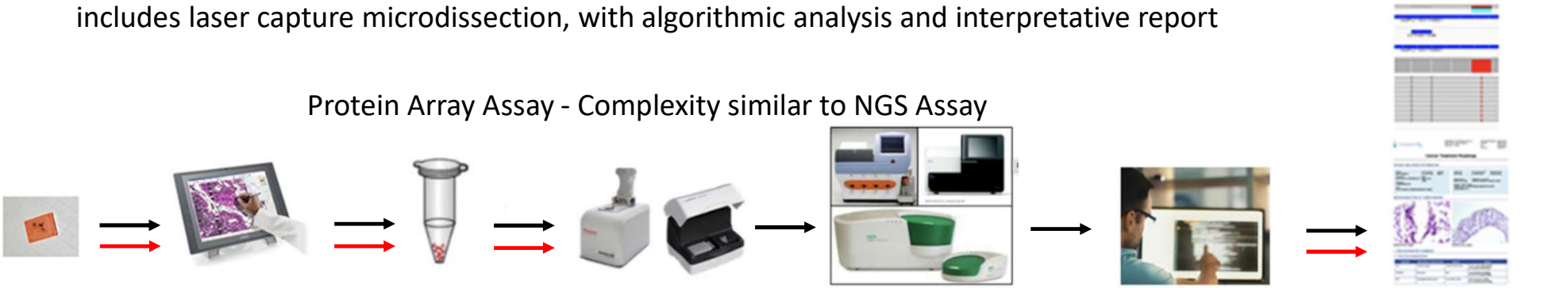
0249U: Oncology (breast), semiquantitative analysis of 32 phosphoproteins and protein analytes, includes laser capture microdissection, with algorithmic analysis and interpretative report

Theralink Protein Array Assay - Overview

Test Overview	Theralink is a novel, quantitative, antibody-based reverse phase protein array assay (RPPA) that measures the abundance of total and activated proteins for therapeutic targeting
Indication	Metastatic breast cancer
Value Proposition	• Panel includes core biological pathways involved in cancer • Informs activation levels of several known, direct targets of FDA-approved therapies: – HER family of receptors – Receptor tyrosine kinases (e.g., EGFR, IGFR, FGFR2, Met, Alk, FLK1 / VEGFR2, etc.) – RTK-associated signaling pathways (e.g., Jak/Stat, Ras/MAPK, Akt/mTOR) • Offers information which is discrete and independent from that provided by other methods • Can predict patient response to therapies such as inhibitors against HER2 (e.g., trastuzumab), EGFR (e.g., cetuximab), VEGFR2 (e.g., bevacizumab), and ALK (e.g., crizotinib) with a high degree of accuracy • Broad patent estate (9 issued patents), intellectual property coverage
Sample	Sample is prepared from routine histopathology sections procured through standard biopsies
Test Output Results	• Based on an algorithmic process, results are presented in a comprehensive report summarizing clinically actionable findings • Test results available within 15 days

0249U: Oncology (breast), semiquantitative analysis of 32 phosphoproteins and protein analytes, includes laser capture microdissection, with algorithmic analysis and interpretative report

Protein Array Assay - Complexity similar to NGS Assay



Tissue Acquisition

Histopathologic Review and Laser Capture Microdissection

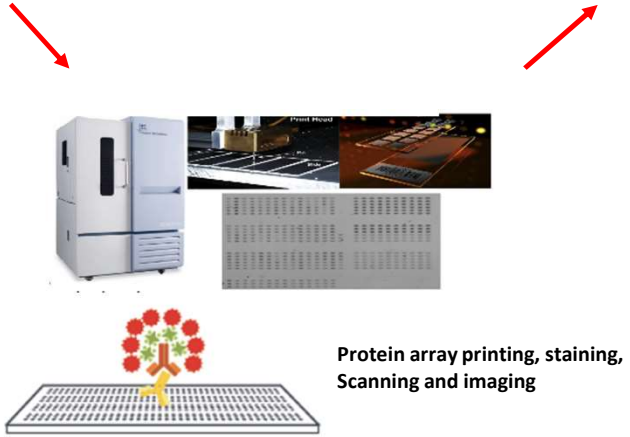
Lysate Preparation Extraction of Analyte

Sample/analyte quantification and qualification

Reaction, library prep and sequencing

Bioinformatic/Algorithm Analysis

Test Result and Report Generation Therapy Matching



Protein array printing, staining, Scanning and imaging

0037U Targeted Genomic Panel Assay

0249U Targeted Protein/Phosphoprotein Panel Assay

Theralink Technologies, Inc. - Petricoin, Emanuel, PhD - Weinberg, Kris

0249U: Oncology (breast), semiquantitative analysis of 32 phosphoproteins and protein analytes, includes laser capture microdissection, with algorithmic analysis and interpretative report

The Theralink Protein/Phosphoprotein Panel

12 CLINICAL PHARMACOLOGY

12.1 Mechanism of Action

Tucatinib is a tyrosine kinase inhibitor of HER2. In vitro, tucatinib inhibits phosphorylation of HER2 and HER3, resulting in inhibition of downstream MAPK and AKT signaling and cell proliferation, and showed anti-tumor activity in HER2 expressing tumor cells. In vivo, tucatinib inhibited the growth of HER2 expressing tumors. The combination of tucatinib and trastuzumab showed increased anti-tumor activity in vitro and in vivo compared to either drug alone.

12 CLINICAL PHARMACOLOGY

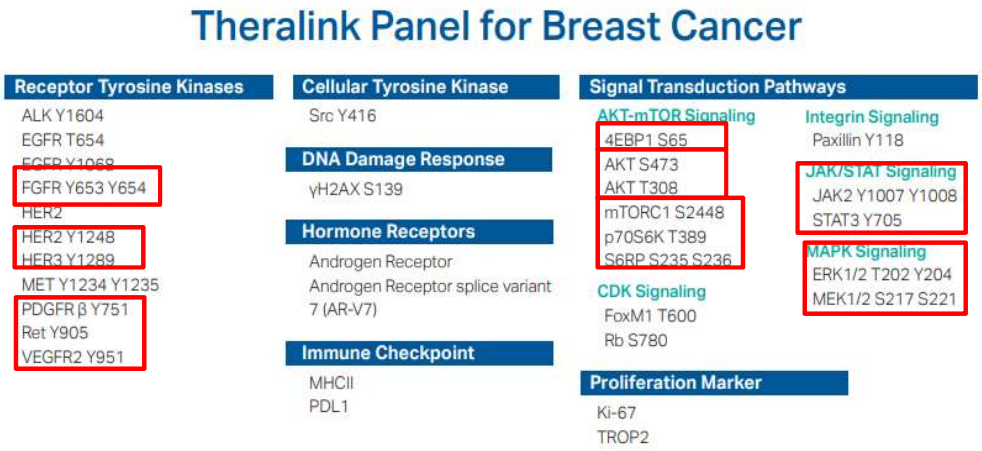
12.1 Mechanism of Action

Erdafitinib is a kinase inhibitor that binds to and inhibits enzymatic activity of FGFR1, FGFR2, FGFR3 and FGFR4 based on *in vitro* data. Erdafitinib also binds to RET, CSF1R, PDGFRA, PDGFRB, FLT4, KIT, and VEGFR2. Erdafitinib inhibited FGFR phosphorylation and signaling and decreased cell viability in cell lines expressing FGFR genetic alterations, including point mutations, amplifications, and fusions. Erdafitinib demonstrated antitumor activity in FGFR-expressing cell lines and xenograft models derived from tumor types, including bladder cancer.

12 CLINICAL PHARMACOLOGY

12.1 Mechanism of Action

Everolimus is an inhibitor of mammalian target of rapamycin (mTOR), a serine-threonine kinase, downstream of the PI3K/AKT pathway. The mTOR pathway is dysregulated in several human cancers. Everolimus binds to an intracellular protein, FKBP-12, resulting in an inhibitory complex formation (mTORC1) and thus inhibition of mTOR kinase activity. Everolimus reduced the activity of S6 ribosomal protein kinase (S6K1) and eukaryotic elongation factor 4E-binding protein (4E-BP1), downstream effectors of mTOR, involved in protein synthesis. In addition, everolimus inhibited the expression of hypoxia-inducible factor (e.g., HIF-1) and reduced the expression of vascular endothelial growth factor (VEGF). Inhibition of mTOR by everolimus has been shown to reduce cell proliferation, angiogenesis, and glucose uptake in *in vitro* and/or *in vivo* studies.



12.1 Mechanism of Action

Ruxolitinib, a kinase inhibitor, inhibits Janus Associated Kinases (JAKs) JAK1 and JAK2 which mediate the signaling of a number of cytokines and growth factors that are important for hematopoiesis and immune function. JAK signaling involves recruitment of STATs (signal transducers and activators of transcription) to cytokine receptors, activation and subsequent localization of STATs to the nucleus leading to modulation of gene expression.

Jakafi inhibits cytokine induced STAT3 phosphorylation in whole blood from patients with MF and PV. Jakafi administration resulted in maximal inhibition of STAT3 phosphorylation 2 hours after dosing which returned to near baseline by 10 hours in patients with MF and PV.

0249U: Oncology (breast), semiquantitative analysis of 32 phosphoproteins and protein analytes, includes laser capture microdissection, with algorithmic analysis and interpretative report

The Theralink Protein/Phosphoprotein Assay: Select examples of patent estate

US010690672B2

(12) **United States Patent**
Petricoin et al.

(10) **Patent No.: US 10,690,672 B2**
(45) **Date of Patent: Jun. 23, 2020**

(54) **METHODS FOR BREAST CANCER TREATMENT**

(71) Applicant: **GEORGE MASON UNIVERSITY**, Fairfax, VA (US)

(72) Inventors: **Emanuel Petricoin**, Gainsville, VA (US); **Julia Wulfkuhle**, Columbia, MD (US)

(73) Assignee: **George Mason Research Foundation, Inc.**, Fairfax, VA (US)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 23 days.

(58) **Field of Classification Search**
CPC G01N 33/57415; G01N 2800/52; G01N 2800/56
See application file for complete search history.

(56) **References Cited**

FOREIGN PATENT DOCUMENTS

WO WO 2016/094373 6/2016

OTHER PUBLICATIONS

International Preliminary Report on Patentability for PCT/US2015/064437, published as WO2016/094373, dated Jun. 13, 2017.
International Search Report for PCT/US2015/064437, published as

US008628931B2

(12) **United States Patent**
Liotta et al.

(10) **Patent No.: US 8,628,931 B2**
(45) **Date of Patent: Jan. 14, 2014**

(54) **MTOR PATHWAY THERANOSTIC**

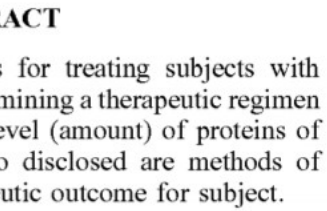
(75) Inventors: **Lance A. Liotta**, Rockville, MD (US); **Emanuel F. Petricoin, III**, Rockville, MD (US); **Virginia Espina**, Rockville, MD (US)

(73) Assignee: **George Mason Intellectual Properties, Inc.**, Fairfax, VA (US)

WO WO 2005/037071 A 4/2005
WO WO 2005/064343 A 7/2005
WO WO 2005/097107 A2 10/2005

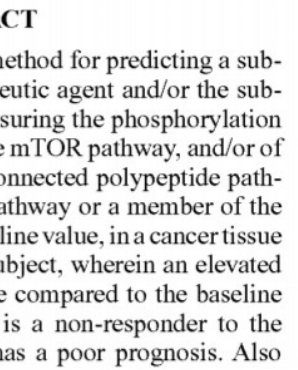
OTHER PUBLICATIONS

Nathan, C.-A. O., et al. Clinical Cancer Research, 10: 5820-5827, Sep. 1, 2004.*
Zhou, X., et al., Clinical Cancer Research, 10: 6779-6788, Oct. 15, 2004.*
Bellisco, C., et al. Clinica Chimica Acta, 357: 180-183, 2005.*



(57) **ABSTRACT**

Disclosed herein are methods for treating subjects with breast cancer, comprising determining a therapeutic regimen for cancer by measuring the level (amount) of proteins of one or more biomarkers. Also disclosed are methods of predicting or assessing therapeutic outcome for subject.

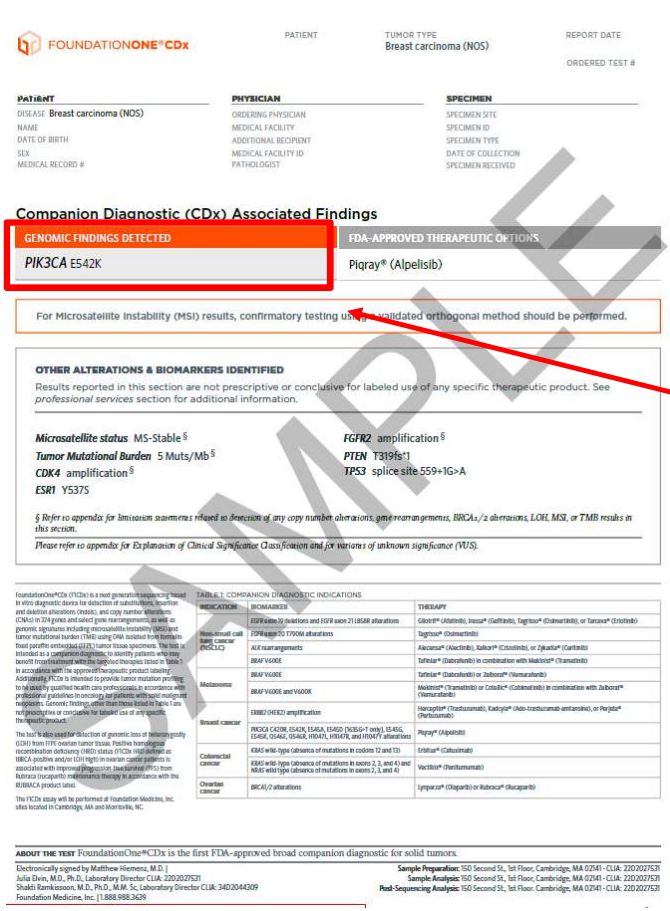


(57) **ABSTRACT**

This invention relates, e.g., to a method for predicting a subject's response to a chemotherapeutic agent and/or the subject's prognosis, comprising measuring the phosphorylation state of at least one member of the mTOR pathway, and/or of at least one member of an interconnected polypeptide pathway (e.g. a member of the Akt pathway or a member of the IRS pathway), compared to a baseline value, in a cancer tissue or cancer cell sample from the subject, wherein an elevated level of the phosphorylation state compared to the baseline value indicates that the subject is a non-responder to the chemotherapeutic agent and/or has a poor prognosis. Also

0249U: Oncology (breast), semiquantitative analysis of 32 phosphoproteins and protein analytes, includes laser capture microdissection, with algorithmic analysis and interpretative report

Theralink Assay Results - CGP



FOUNDATIONONE®CDx

PATIENT

TUMOR TYPE
Breast carcinoma (NOS)

REPORT DATE

ORDERED TEST #

PATIENT
DISEASE Breast carcinoma (NOS)
NAME
DATE OF BIRTH
SEX
MEDICAL RECORD #

PHYSICIAN
ORDERING PHYSICIAN
MEDICAL FACILITY
ADDITIONAL RECIPIENT
MEDICAL FACILITY ID
PATHOLOGIST

SPECIMEN
SPECIMEN SITE
SPECIMEN ID
SPECIMEN TYPE
DATE OF COLLECTION
SPECIMEN RECEIVED

Companion Diagnostic (CDx) Associated Findings

GENOMIC FINDINGS DETECTED	FDA-APPROVED THERAPEUTIC OPTIONS
PIK3CA E542K	Piqray® (Alpelisib)

For Microsatellite Instability (MSI) results, confirmatory testing using a validated orthogonal method should be performed.

OTHER ALTERATIONS & BIOMARKERS IDENTIFIED

Results reported in this section are not prescriptive or conclusive for labeled use of any specific therapeutic product. See *professional services* section for additional information.

Microsatellite status MS-Stable §
Tumor Mutational Burden 5 Muts/Mb §
CDK4 amplification §
ESR1 Y537S
FGFR2 amplification §
PTEN T319fs*1
TP53 splice site 559+1G>A

§ Refer to appendix for limitation statements related to detection of any copy number alterations, gene rearrangements, BRCA1/2 alterations, LOH, MSI, or TMB results in this section.

Please refer to appendix for Explanation of Clinical Significance Classification and for variants of unknown significance (VUS).

FoundationOne®CDx (F1CDx) is a next generation sequencing based in vitro diagnostic device for detection of substitutions, insertion and deletion alterations (indels), and copy number alterations (CNAs) in 324 genes and select gene rearrangements, as well as genomic signatures including microsatellite instability (MSI) and tumor mutational burden (TMB) using DNA isolated from formalin-fixed paraffin-embedded (FFPE) tumor tissue specimens. The test is intended as a companion diagnostic, to identify patients who may benefit from treatment with the approved therapies listed in Table 1 in accordance with the approved therapeutic product labeling. Additionally, F1CDx is intended to provide tumor mutation profiling to be used by qualified health care professionals in accordance with professional guidelines in oncology for patients with solid malignant neoplasms. Genomic findings, other than those listed in Table 1 are not prescriptive or conclusive for labeled use of any specific therapeutic product.

The test is also used for detection of genomic loss of heterozygosity (LOH) from FFPE ovarian tumor tissue. Positive homologous recombination deficiency (HRD) status (F1CDx+ HRD positive) as BRCA-positive and/or LOH high) in ovarian cancer patients is associated with improved progression. (see further PFS) from Rubraca (rucaparib) maintenance therapy in accordance with the RUBRACA product label.

The F1CDx assay will be performed at Foundation Medicine, Inc. sites located in Cambridge, MA and Morrisville, NC.

TABLE 1: COMPANION DIAGNOSTIC INDICATIONS

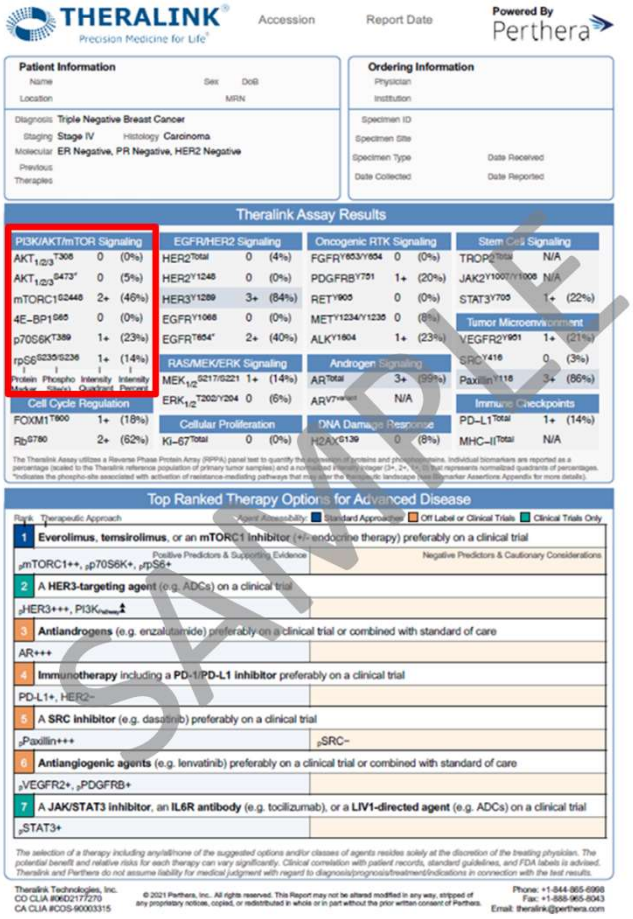
INDICATION	BIOMARKER	THERAPY
Non-small cell lung cancer (NSCLC)	EGFR exon 19 deletions and EGFR exon 21 L858R alterations	Gilotrif® (Afatinib), Iressa® (Gefitinib), Tagrisso® (Osimertinib), or Tarceva® (Erlotinib)
	EGFR exon 20 T790M alterations	Tagrisso® (Osimertinib)
	ALK rearrangements	Alecensa® (Alectinib), Xalkori® (Crizotinib), or Zykadia® (Ceritinib)
Melanoma	BRAF V600E	Tafinlar® (Dabrafenib) in combination with Mekinist® (Trametinib)
	BRAF V600E	Tafinlar® (Dabrafenib) or Zelboraf® (Vemurafenib)
	BRAF V600E and V600K	Mekinist® (Trametinib) or Cotellic® (Cobimetinib) in combination with Zelboraf® (Vemurafenib)
Breast cancer	ERBB2 (HER2) amplification	Herceptin® (Trastuzumab), Kadcyla® (Ado-trastuzumab emtansine), or Perjeta® (Pertuzumab)
	PIK3CA C420R, E542K, E545A, E545D (V659>T only), E545G, E545K, I546K, I546R, H1047L, H1047R, and H1047Y alterations	Piqray® (Alpelisib)
Colorectal cancer	KRAS wild-type (absence of mutations in codons 12 and 13)	Erbitux® (Cetuximab)
	KRAS wild-type (absence of mutations in exons 2, 3, and 4) and NRAS wild type (absence of mutations in exons 2, 3, and 4)	Vectibix® (Panitumumab)
Ovarian cancer	BRCA1/2 alterations	Lynparza® (Olaparib) or Rubraca® (Rucaparib)

ABOUT THE TEST FoundationOne®CDx is the first FDA-approved broad companion diagnostic for solid tumors.

Electronically signed by Matthew Hiemenz, M.D.]
Julia Elvin, M.D., Ph.D., Laboratory Director CLIA: 22D2027521
Shakti Ramkissoon, M.D., Ph.D., M.M. Sc., Laboratory Director CLIA: 34D2044309
Foundation Medicine, Inc. | 1.888.988.3639

Sample Preparation: 150 Second St., 1st Floor, Cambridge, MA 02141 - CLIA: 22D2027531
Sample Analysis: 150 Second St., 1st Floor, Cambridge, MA 02141 - CLIA: 22D2027531
Post-Sequencing Analysis: 150 Second St., 1st Floor, Cambridge, MA 02141 - CLIA: 22D2027531

Single genetic mutation found in FoundationOne CDx corresponds to altered phosphorylation in the same protein signaling pathway when measured by the Theralink Assay



THERALINK®
Precision Medicine for Life®

Accession

Report Date

Powered By Perthera

Patient Information
Name
Sex
DoB
Location
MRN
Diagnosis Triple Negative Breast Cancer
Staging Stage IV
Histology Carcinoma
Molecular ER Negative, PR Negative, HER2 Negative
Previous Therapies

Ordering Information
Physician
Institution
Specimen ID
Specimen Site
Specimen Type
Date Received
Date Collected
Date Reported

Theralink Assay Results

PI3K/AKT/mTOR Signaling				EGFR/HER2 Signaling				Oncogenic RTK Signaling				Stem Cell Signaling			
$AKT_{1/2/3}^{T308}$	0	(0%)		$HER2^{Total}$	0	(4%)		$FGFR^{Y653/Y654}$	0	(0%)		$TROP2^{Total}$	N/A		
$AKT_{1/2/3}^{S473}$	0	(5%)		$HER2^{Y1248}$	0	(0%)		$PDGFRB^{Y751}$	1+	(20%)		$JAK2^{Y1007/Y1008}$	N/A		
$mTORC1^{S2448}$	2+	(46%)		$HER3^{Y1289}$	3+	(84%)		RET^{Y905}	0	(0%)		$STAT3^{Y705}$	1+	(22%)	
4E-$BP1^{S65}$	0	(0%)		$EGFR^{Y1068}$	0	(0%)		$MET^{Y1234/Y1235}$	0	(8%)		**Tumor Microenvironment**			
$p70S6K^{T389}$	1+	(23%)		$EGFR^{T654*}$	2+	(40%)		ALK^{Y1604}	1+	(23%)		$VEGFR2^{Y951}$	1+	(21%)	
$rpS6^{S235/S236}$	1+	(14%)		**RAS/MEK/ERK Signaling**				**Androgen Signaling**				SRC^{Y416}	0	(3%)	
Protein Marker	Phospho Site(s)	Intensity Quadrant	Intensity Percent	$MEK_{1/2}^{S217/S221}$	1+	(14%)		AR^{Total}	3+	(99%)		$Paxillin^{Y118}$	3+	(86%)	
Cell Cycle Regulation				$ERK_{1/2}^{T202/Y204}$	0	(6%)		AR^{V7}	N/A			**Immune Checkpoints**			
$FOXM1^{T600}$	1+	(18%)		**Cellular Proliferation**				**DNA Damage Response**				$PD\text{-}L1^{Total}$	1+	(14%)	
Rb^{S780}	2+	(62%)		$Ki\text{-}67^{Total}$	0	(0%)		$H2AX^{S139}$	0	(8%)		$MHC\text{-}I^{Total}$	N/A		

The Theralink Assay utilizes a Reverse Phase Protein Array (RPPA) panel test to quantify the expression of proteins and phosphoproteins. Individual biomarkers are reported as a percentage (scaled to the Theralink reference population of primary tumor samples) and a normalized intensity/ranger (3+, 2+, 1+, 0) that represents normalized quadrants of percentages. *Indicates the phospho-site associated with activation of resistance-mediating pathways that may alter the therapeutic landscape (see Biomarker Assertions Appendix for more details).

Top Ranked Therapy Options for Advanced Disease

Rank Therapeutic Approach — Agent Accessibility: Standard Approved / Off Label or Clinical Trials / Clinical Trials Only

		Positive Predictors & Supporting Evidence	Negative Predictors & Cautionary Considerations
1	**Everolimus, temsirolimus**, or an **mTORC1 inhibitor** (+/- endocrine therapy) preferably on a clinical trial	$pmTORC1^{++}$, $pp70S6K^{+}$, $ppS6^{+}$	
2	A **HER3-targeting agent** (e.g. ADCs) on a clinical trial	$pHER3^{+++}$, $PI3K_{H1047R}$ ‡	
3	**Antiandrogens** (e.g. enzalutamide) preferably on a clinical trial or combined with standard of care	AR+++	
4	**Immunotherapy** including a **PD-1/PD-L1 inhibitor** preferably on a clinical trial	PD-L1+, HER2-	
5	A **SRC inhibitor** (e.g. dasatinib) preferably on a clinical trial	$pPaxillin^{+++}$	$pSRC^{-}$
6	**Antiangiogenic agents** (e.g. lenvatinib) preferably on a clinical trial or combined with standard of care	$pVEGFR2^{+}$, $pPDGFRB^{+}$	
7	A **JAK/STAT3 inhibitor**, an **IL6R antibody** (e.g. tocilizumab), or a **LIV1-directed agent** (e.g. ADCs) on a clinical trial	$pSTAT3^{+}$	

The selection of a therapy including any/all/none of the suggested options and/or classes of agents resides solely at the discretion of the treating physician. The potential benefit and relative risks for each therapy can vary significantly. Clinical correlation with patient records, standard guidelines, and FDA labels is advised. Theralink and Perthera do not assume liability for medical judgment with regard to diagnosis/prognosis/treatment/indications in connection with the test results.

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Email: theralink@perthera.com

Theralink Technologies, Inc. - Petricoin, Emanuel, PhD - Weinberg, Kris

17. San Diego Blood Bank

Presenter: Jeffrey Bush

Code: 0246U

0246U: Red blood cell antigen typing, DNA, genotyping of at least 16 blood groups with phenotype prediction of at least 51 red blood cell antigens

Public Comment	Rationale
Crosswalk to 0001U	Code 0246U is substantially similar to code 0001U with description, “Red blood cell antigen typing, DNA, human erythrocyte antigen gene analysis of 35 antigens from 11 blood groups, utilizing whole blood, common RBC alleles reported.”

CMS Annual Lab Meeting June 24, 2021
San Diego Blood Bank, Bush, Jeffrey

Purpose and Value of the Test

PrecisionBlood™

- Intended for at-risk patients; e.g., patients undergoing transfusion
- Initial, apparently minor transfusion reactions can evolve into more severe reactions as the patient develops a heightened immune response to alloantigens
- Severe reactions may occur hours, days and weeks after a transfusion, causing patient morbidity through inflammatory injury
- These reactions can be predicted and avoided using the test
- Prophylactic matching of blood may prevent unnecessary transfusions and additional adverse events

Accuracy of the PrecisionBlood Assay (Compared to 0001U Assay)

Concordance

- 30,452 concordant observations between PrecisionBlood and the RHD + RHCE BeadChips from Immucor (99.9% agreement)

Discordance

- 19 discordant results between PrecisionBlood and BeadChips
- All discordances attributable to BeadChips (arrays) having lower resolution than PrecisionBlood (NGS)
- BeadChips were unable to detect certain distinguishing variants

0246U: Red blood cell antigen typing, DNA, genotyping of at least 16 blood groups with phenotype prediction of at least 51 red blood cell antigens

Public Comment	Rationale
Crosswalk to 0001U	Code 0246U is substantially similar to code 0001U with description, “Red blood cell antigen typing, DNA, human erythrocyte antigen gene analysis of 35 antigens from 11 blood groups, utilizing whole blood, common RBC alleles reported.”

CMS Annual Lab Meeting June 24, 2021
San Diego Blood Bank, Bush, Jeffrey

18. Labtech Diagnostics

Presenter: Dr. Wade Katrangi, PhD, CEO of Labtech Diagnostics

Code: 0X60U

0X60U: 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, serum, quantitative

Public Comment	**Rationale**
83704 ($34.19) TIMES 2 + 82610 ($18.52)	Twice the NMR resources measuring metabolites rather than lipoproteins (complex pulse program, number of scans, QC/QA) plus the immunoassay quantification of cystatin C

CMS Annual Lab Meeting, June 24, 2021
Labtech Diagnostics – Katrangi, Wade)

0X60U: 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, serum, quantitative

Despite use in dosing several common drugs, and kidney disease risk classification and monitoring, current GFR estimates, which are based on creatinine and/or cystatin C, have important limitations

- Estimates have a negative bias, and accuracy is reduced by extremes of muscle mass, body size, high protein diets, and particular conditions such as reduced liver function
- Estimates are also not ethnicity neutral, and race is used in the calculation, significantly altering apparent kidney function

GFR(NMR) shows little bias and is more accurate

	meanGFR (SD)	MAE [95% CI]	p30 [95% CI]	RMSE [95% CI]
mGFR	55.8 (20.3)	ref	ref	ref
GFR(NMR)	55.7 (19.1)	7.4 [6.4 – 8.5]	91.7 [87.2 – 97.2]	9.4 [8.3 – 10.6]
eGFR Cr	51.8 (19.8)	9.5 [8.1 – 10.9]	80.7 [74.3 – 88.1]	12.2 [10.6 – 13.9]
eGFR Cr-CysC	49.0 (19.87)	9.4 [8.1 – 10.8]	87.2 [80.7 – 93.6]	11.8 [10.4 – 13.3]

MAE: mean absolute error P30: Percentage of samples within 30% deviation from mGFR RMSE: root mean squared error

CMS Annual Lab Meeting, June 24, 2021
Labtech Diagnostics – Katrangi, Wade)

0X60U: 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, serum, quantitative

	Comparison of methods	
Methods: Analytes used in GFR(NMR)	*Existing*	*0X60U: NMR(GFR)*
NMR: Creatinine, valine, myo-inositol	83704: 8-scan NMR spectrum quantification of lipoprotein particle count.	16-scan spectrum with complex pulse program to suppress lipoprotein signals and fitter to quantify analytes reduces throughput by more than half. More complex QA and QC.
Immunoassay: Cystatin C	82610 immunoassay for cystatin C	Same as 82610
Algorithm	Not applicable	Proprietary, machine-learning-derived algorithm combining 4 analytes into GFR estimate

CMS Annual Lab Meeting, June 24, 2021
Labtech Diagnostics – Katrangi, Wade)

19. Stemina Biomarker Discovery

Presenter: Elizabeth LR Donley

Code (s): 0X77U: Neurology (autism spectrum disorder [ASD]), quantitative measurements of 16 central carbon metabolites (ie, α-ketoglutarate, alanine, lactate, phenylalanine, pyruvate, succinate, carnitine, citrate, fumarate, hypoxanthine, inosine, malate, S-sulfocysteine, 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)

0X77U: Neurology (autism spectrum disorder [ASD]), quantitative measurements of 16 central carbon metabolites (ie, α-ketoglutarate, alanine, lactate, phenylalanine, pyruvate, succinate, carnitine, citrate, fumarate, hypoxanthine, inosine, malate, S-sulfocysteine, 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)

Public Comment	**Rationale**
Crosswalk to 0063U (CY2021 NLA rate $750)	The platform/method and resources are substantially similar. Employing LC-MS/MS analytical methods with proprietary algorithm.

0X77U: Neurology (autism spectrum disorder [ASD]), quantitative measurements of 16 central carbon metabolites liquid chromatography tandem mass spectrometry (LC-MS/MS), plasma, algorithmic analysis with result reported as negative or positive (with metabolic subtypes of ASD)

- **Background**:
  - Quantitate 16 central carbon metabolites using clinically validated methods
  - Uses essentially the same LC-MS/MS resources as required for 0063U
  - Algorithm employs LC-MS/MS data and proprietary thresholds and ratios based on ASD clinical study (the Children's Autism Metabolome Project) of the metabolism of 1,100 children ages 18 to 48 months used for 0063U
  - Determine likely presence or absence of metabolic dysregulation associated with autism spectrum disorder in children with ASD
  - Positive test:
    - Refer to neurodevelopmental specialist for behavioral assessment
    - Inform more precise treatment based on differences in metabolism

0X77U: Neurology (autism spectrum disorder [ASD]), quantitative measurements of 16 central carbon metabolites liquid chromatography tandem mass spectrometry (LC-MS/MS), plasma, algorithmic analysis with result reported as negative or positive (with metabolic subtypes of ASD)

- **Test Method Substantially Similar to 0063U**:
  - ***Pre-Analytical***

    Collect a minimum of 3 mL of blood in sodium heparin tube

    Prepare plasma and transfer to cryotube

    Place sample on dry ice or in -70C freezer within one hour

    Ship on dry ice to Stemina's CLIA laboratory (NeuroPointDX™) in Madison, Wisconsin
  - ***Analytical***

    LC-MS/MS on Agilent 6490A QQQ Mass Spectrometer

    Isotopically labeled internal standards, 8-point calibration & 4 controls for each metabolite
  - ***Post-Analytical***

    Data Quality Review & Expert Algorithm Reporting

    Repeat Analysis Following Clinical Evaluation

0X77U: Neurology (autism spectrum disorder [ASD]), quantitative measurements of 16 central carbon metabolites liquid chromatography tandem mass spectrometry (LC-MS/MS), plasma, algorithmic analysis with result reported as negative or positive (with metabolic subtypes of ASD)

Supporting Data: Selected Publications

- Alan M. Smith , Marvin R. Natowicz , Daniel Braas, Michael A. Ludwig, Denise M. Ney, Elizabeth L. R. Donley, Robert E. Burrier, and David G. Amaral et al. (2020) A Metabolomics Approach to Screening for Autism Risk in the Children's Autism Metabolome Project, *Autism Res* 2020, 00: 1–16.
- Smith, Alan M. et al. (2019). "Amino Acid Dysregulation Metabotypes: Potential Biomarkers for Diagnosis and Individualized Treatment for Subtypes of Autism Spectrum Disorder." *Biological Psychiatry* 85(4): 345–54.
- West PR, Amaral DG, Bais P, Smith AM, Egnash LA, Ross ME, et al. (2014): Metabolomics as a tool for discovery of biomarkers of autism spectrum disorder in the blood plasma of children. *PLoS One*. 9:e112445.

20. Exact Sciences

Presenter: Rick Baehner, MD

Code: 0244U

Exact Sciences

Rick Baehner, MD

Chief Medical Officer, Genomic Health, Inc. (a wholly-owned subsidiary of Exact Sciences)

Assistant Professor, Clinical Pathology, University of California San Francisco

A leading provider of cancer screening and diagnostic tests, Exact Sciences relentlessly pursues smarter answers to give people the clarity to take life-changing action, earlier. Building on the success of Cologuard® and Oncotype® tests, Exact Sciences is investing in its product pipeline to support patients throughout their cancer diagnosis and treatment. We have laboratories in Arizona, California, Maryland, Massachusetts and Wisconsin.

New Code 0244U: Oncotype MAP™ Pan Cancer Tissue Test

Code Descriptor

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.

Test Purpose

The Oncotype MAP Pan-Cancer Tissue test delivers rapid, comprehensive tumor profiling to aid therapy selection for patients with advanced, metastatic, refractory, relapsed, or recurrent cancer. The test identifies actionable genomic alterations to guide timely treatment decisions including FDA approved and NCCN guideline-recommended therapies.

Test Method

Next-generation sequencing panel of 257 genes and proteins including the analysis of all clinically actionable gene single nucleotide variants, insertion/deletion mutations, copy number variations, fusions/structural variants, and specific protein expressions. In addition, the test provides assessments of TMB, a quantitative measure represented as the number of mutations per megabase of DNA shown to be important for predicting responsiveness to immune checkpoint inhibitors.

New Code 0244U: Recommendation

Recommendation:

Gapfill

Rationale for Gapfill

- The Oncotype Map Pan-Cancer Tissue is a proprietary test performed only by Exact Sciences.
- Given the proprietary nature (and uniqueness) of the test, the most appropriate basis for establishing a payment amount is gapfill. This will allow CMS and its contractors the opportunity to gather current information about the unique manner in which this assay is performed and the resources necessary to provide it. There is not currently a comparable test on the Medicare Clinical Laboratory Fee Schedule.

21. ACLA

Presenter: Joan Kegerize, JD

Codes: 80151, 80161, 80167, 80181, 81279, 81338, 86408, 86409, 86413, 87636, 87637, 860XX, 860X1, 86X02, 863X2, 863X3, 862X0, 862XX, 862X1, 863X4, 865X0, 86XX0, 86X00, 86X01, 8715X, 801XX, 812X0, 815X1, 0017M, 835X1, 8352X, 826X0, 0229U, 0244U, 0245U

ACLA Payment Recommendations CY2022 Codes

Clinical Lab Fee Schedule Public Meeting

June 24, 2021

Presented by Joan Kegerize, JD

Vice President, Reimbursement & Scientific Affairs

ACLA

AMERICAN CLINICAL LABORATORY ASSOCIATION

ACLA Recommendations Reconsideration Codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
Reconsideration					
80151	Amiodarone	80155	Caffeine	Suggested crosswalk to 80155 (Caffeine) recommendation, which more accurately represents the methodology, work and resources for testing. Current crosswalk to 80299 (Quantitation of therapeutic drug, not elsewhere specified) doesn't account for the complexities involved with laboratory testing for this therapeutic drug. The crosswalk chosen represents more appropriately the work and resources required for the testing compared to 80299. This code is performed by LC-MS/MS methodology and has similar work and resources as 80155. The crosswalk to Caffeine code 80155 more accurately represents the methodology, work and resources for testing of this new therapeutic drug code. This crosswalk aligns with the method CMS and the CDLT Panel used to crosswalk the drug codes for the 2019 CLFS.	$38.57

ACLA Recommendations Reconsideration Codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
Reconsideration					
80161	Carbamazepine; -10, 11-epoxide	80155	Caffeine	Suggested crosswalk to 80155 (Caffeine) recommendation, which more accurately represents the methodology, work and resources for testing. Current crosswalk to 80299 (Quantitation of therapeutic drug, not elsewhere specified) doesn't account for the complexities involved with laboratory testing for this therapeutic drug. The crosswalk chosen represents more appropriately the work and resources required for the testing compared to 80299. This code is performed by LC-MS/MS methodology and has similar work and resources as 80155. The crosswalk to Caffeine code 80155 more accurately represents the methodology, work and resources for testing of this new therapeutic drug code. This crosswalk aligns with the method CMS and the CDLT Panel used to crosswalk the drug codes for the 2019 CLFS.	$38.57

ACLA Recommendations Reconsideration Codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
Reconsideration					
80167	Felbamate	80199	Tiagabine	Suggested crosswalk to 80199 (Tiagabine) recommendation, which represents similar methodology and resources to perform the testing and is also used to treat seizures/epilepsy. ACLA recommends a crosswalk for the new therapeutic drug code 80167 (Felbamate) to code 80199 (Tiagabine). This code represents similar methodology and resources to perform the testing and is also used to treat seizures/epilepsy. We do not agree with a crosswalk to the unspecified therapeutic drug code 80299, especially in light of the fact that code 80199 is a quantitative assay for an epileptic drug used to treat epilepsy and seizures. The CDLT Panel vote was a tie for 80199 and 80299 and we urge CMS to adopt the analyte specific approach for a crosswalk to Tiagabine code 80199. This crosswalk aligns with the method CMS and the CDLT Panel used to crosswalk the drug codes for the 2019 CLFS.	$27.11

ACLA Recommendations Reconsideration Codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
Reconsideration					
80181	Flecainide	80155	Caffeine	Suggested crosswalk to 80155 (Caffeine) recommendation, which more accurately represents the methodology, work and resources for testing. Current crosswalk to 80299 (Quantitation of therapeutic drug, not elsewhere specified) doesn't account for the complexities involved with laboratory testing for this therapeutic drug. The crosswalk chosen represents more appropriately the work and resources required for the testing compared to 80299. This code is performed by LC-MS/MS methodology and has similar work and resources as 80155. The crosswalk to Caffeine code 80155 more accurately represents the methodology, work and resources for testing of this new therapeutic drug code. This crosswalk aligns with the method CMS and the CDLT Panel used to crosswalk the drug codes for the 2019 CLFS.	$38.57

ACLA Recommendations Reconsideration Codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
Reconsideration					
81279	JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) targeted sequence analysis (eg, exons 12 and 13)	81272	KIT (v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog) (eg, gastrointestinal stromal tumor [GIST], acute myeloid leukemia, melanoma), gene analysis, targeted sequence analysis (eg, exons 8, 11, 13, 17, 18)	Suggested crosswalk to 81272, an analyte specific code. The JAK2 targeted sequence analysis methodology, resources, and amount of genetic material sequenced are comparable to that of KIT targeted sequence analysis. ACLA recommends CMS reconsider its Final Determination and crosswalk 81279 to an analyte specific code 81272, KIT (v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog) (eg, gastrointestinal stromal tumor [GIST], acute myeloid leukemia, melanoma), gene analysis, targeted sequence analysis (eg, exons 8, 11, 13, 17, 18). The JAK2 targeted sequence analysis methodology, resources, and amount of genetic material sequenced are comparable to that of KIT targeted sequence analysis. We believe using the Tier 1 CPT 81272 is a more appropriate crosswalk for code 81279 as the work and resources align with exons studied in the JAK2 targeted gene sequence analysis. We do not agree with the CMS rationale that the crosswalk approach to a Tier 2 code is more transparent than an analyte specific Tier 1 code. ACLA takes issue with this crosswalk approach. A more transparent method is to crosswalk a new Tier 1 code to an analyte specific Tier 1 code and we urge CMS to reconsider its approach and crosswalk the JAK2 code 81279 to the KIT code 81272.	$329.51

ACLA Recommendations Reconsideration Codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
Reconsideration					
81338	MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; common variants (eg, W515A, W515K, W515L, W515R)	81120	IDH1 (isocitrate dehydrogenase 1 [NADP+], soluble) (eg, glioma), common variants (eg, R132H, R132C)	Suggested crosswalk to 81120, an analyte specific code. The MPL common variants methodology, resources and amount of genetic material sequence are comparable to that of IDH1 common variants. Both assess genes for an oncology disorder and both are 1 exon targeted sequencing for oncology samples. ACLA recommends CMS reconsider its Final Determinations and crosswalk 81338 to an analyte specific code 81120, IDH1 (isocitrate dehydrogenase 1 [NADP+], soluble) (eg, glioma), common variants (eg, R132H, R132C). The methodology, resources, and amount of genetic material sequenced are comparable to that of IDH1 common variants. Both assess genes for an oncology disorder and both are 1 exon targeted sequencing for oncology samples. We believe using the Tier 1 CPT 81120 is a more appropriate crosswalk for code 81338 as the IDH1 work and resources align with exons studied in the MPL gene analysis for common variants. We do not agree with the CMS rationale that the crosswalk approach to a Tier 2 code is more transparent than an analyte specific Tier 1 code. ACLA takes issue with this crosswalk approach. A more transparent method is to crosswalk a new Tier 1 code to an analyte specific Tier 1 code and we urge CMS to reconsider its approach and crosswalk the MPL code 81338 to the IDH1 code 81120.	$193.25

ACLA Recommendations on SARS-CoV-2 Immunology codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
SARS-CoV-2 Immunology					
86408	Neutralizing antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]); screen	86794 x 2.5	Antibody; Zika virus, IgM	ACLA recommends crosswalking code 86408 to CPT code 86794 (Zika antibody test) with a multiplier of 2.5. This is appropriate in light of the significant additional resources required to perform this test. The Zika antibody test code 86794 86769 represents the methodology and resources required to perform the assay. 86769, SARS-CoV-2 antibody test code is similar to the new SARS-CoV-2 neutralizing antibody screen test code 86408. Both tests detect antibodies for an infectious agent SARS-CoV-2. These tests are technically similar in that both 86794 and 86408 are qualitative assays that are confirming the presence of an antibody detected against an infectious pathogen SARS-CoV-2 — the difference being 86794 86769 measures binding and 86408 would be neutralization. The SARS-CoV-2 neutralizing antibody screen test uses similar technology and methodology as a Zika antibody test, yet it involves a myriad of factors that increase its costs over the Zika antibody test and other routine immunology tests. The limited factors that normally are used to establish Medicare reimbursement do not fully account for the increased costs of this testing. Some of the additional factors that must be taken into account when establishing reimbursement for SARS CoV-2 serologic testing include: • Phlebotomists need additional PPE because of the high transmissibility of the coronavirus. • Reagent costs are several times what they were prior to the pandemic. • Patient service centers will need additional shifts/expanded hours, resulting in higher labor costs. o Waiting rooms cannot be crowded with individuals who may be infectious. o Appointments must be spread further apart to allow for social distancing and collection station sterilization. • The entire cost of the specimen collection – already higher than normal – will be attributed to the SARS CoV-2 test alone. o Oftentimes the cost of specimen collection is spread among several tests for which specimens are collected at once (e.g., CBC, cholesterol, HbA1c). o In most cases a specimen will be collected only for the SARS CoV-2 test. • Laboratories have far greater public health reporting demands now than with typical immunology tests. o Laboratories are reporting different information to multiple public health agencies in different states and different levels of government. o There are additional labor costs for IT specialists to extract data from the laboratory information system and interface with multiple public health agency reporting systems, including to provide real time reporting.. It is critical that reimbursement for SARS-CoV-2 neutralizing antibody screen testing accounts for the many additional expenses associated with the testing and the expectations and demands placed on laboratories that can perform the testing.	86794 x 2.5/($16.85 x 2.5) = $42.13

ACLA Recommendations on SARS-CoV-2 Immunology codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
SARS-CoV-2 Immunology					
86409	Neutralizing antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]); titer	86352	Cellular function assay involving stimulation (eg, mitogen or antigen) and detection of biomarker (eg, ATP)	Test code 86352 (Cellular function assay involving stimulation (eg, mitogen or antigen) and detection of biomarker (eg, ATP))represents most closely the assay method and resources required to perform the assay. The titer assay involves stimulating the cells with pseudotyped virus, which induces membrane fusion, after which substrate (enduren) is added which is then read as the biomarker readout (luminescence). Serum samples are serially diluted from 1:80 to 1:2,560, and the additional resources needed to perform the serial dilution series account for the additional costs in performing such testing. Therefore, 86352 represents the resources and materials required for the titer.	$135.86

ACLA Recommendations on SARS-CoV-2 Immunology codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
SARS-CoV-2 Immunology					
86413	Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]) antibody, quantitative	86794 x 3.125	Antibody; Zika virus, IgM	ACLA recommends crosswalking code 86413 to CPT code 86794 (Zika qualitative antibody test) with a multiplier of 3.125. This is appropriate in light of the additional resources required to perform this test. The quantitative assay code 86413 represents the quantitative detection of antibodies for SARS-CoV-2. There are additional resources needed to perform the quantitative assay compared to the qualitative assay. The quantitative assay requires higher complexity laboratory-based testing methods as compared to current qualitative assays. Therefore, we recommend a multiplier of 3.125 that represents the additional work, resources and cost. The quantitative assay procedure includes the following steps- Incubate and wash patient serum and diluent added to a SARS-CoV-2 spike protein receptor binding domain (RBD)-complexed solid-phase surface, followed by adding antihuman-signal antibodies to detect bound anti-RBD antibodies. The relative amount of signal measured is directly proportional to the anti-RBD antibody concentration in the specimen and is interpreted using a standards-generated calibration curve with results reported in quantitative units.	86794 x 3.125/($16.85 x 3.125) = $52.66

ACLA Recommendations on SARS-CoV-2 Microbiology codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
SARS-CoV-2 Microbiology					
87636	Infectious agent detection by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]) and influenza virus types A and B, multiplex amplified probe technique	87631	Infectious agent detection by nucleic acid (DNA or RNA); respiratory virus (eg, adenovirus, influenza virus, coronavirus, metapneumovirus, parainfluenza virus, respiratory syncytial virus, rhinovirus), includes multiplex reverse transcription, when performed, and multiplex amplified probe technique, multiple types or subtypes, 3-5 targets	CPT code 87631 represents the methodology and resources required to perform the multiplex assay for the detection of respiratory viral targets. The SARS-CoV-2 multiplex assay code 87636 represents the detection of SARS-CoV-2, influenza A and influenza B. The new COVID-19 multiplex CPT code 87636 represents a 3 target multiplex respiratory viral assay specific for the SARS-CoV-2, influenza virus A and influenza virus B targets. A straight crosswalk to code 87631 is most appropriate for the new code 87636. Code 87631 is already priced for 3 to 5 targets and represents a multiplex respiratory viral target assay. Therefore, code 87631 is the most appropriate crosswalk and represents the same methodology and number of targets tested.	$142.63

ACLA Recommendations on SARS-CoV-2 Microbiology codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
SARS-CoV-2 Microbiology					
87637	Infectious agent detection by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]), influenza virus types A and B, and respiratory syncytial virus, multiplex amplified probe technique	87631	Infectious agent detection by nucleic acid (DNA or RNA); respiratory virus (eg, adenovirus, influenza virus, coronavirus, metapneumovirus, parainfluenza virus, respiratory syncytial virus, rhinovirus), includes multiplex reverse transcription, when performed, and multiplex amplified probe technique, multiple types or subtypes, 3-5 targets	CPT code 87631 represents the methodology and resources required to perform the multiplex assay for the detection of respiratory viral targets. The SARS-CoV-2 multiplex assay code 87637 represents the detection of SARS-CoV-2, influenza A and influenza B and respiratory syncytial virus (RSV). The new COVID-19 multiplex CPT code 87637 represents a 4 target multiplex respiratory viral assay specific for the SARS-CoV-2, influenza virus A, influenza virus B and RSV targets. A straight crosswalk to code 87631 is most appropriate for the new code 87637. Code 87631 is already priced for 3 to 5 targets and represents a multiplex respiratory viral target assay. Therefore, code 87631 is the most appropriate crosswalk and represents the same methodology and number of targets tested.	$142.63

ACLA Recommendations on Immunology codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
Immunology					
860XX	Aquaporin-4 (neuromyelitis optica [NMO]) antibody; enzyme-linked immunosorbent immunoassay (ELISA)	86146	Beta 2 Glycoprotein I antibody, each	Crosswalk to 86146 which is an analyte specific antibody code for antibodies for autoimmune disorders that use an ELISA technique for detection, so methodology is the same with similar work and resources.	$25.45
860X1	Aquaporin-4 (neuromyelitis optica [NMO] antibody; cell-based immunofluorescence assay (CBA), each	86341	Islet cell antibody	Crosswalk to 86341. Aquaporin-4 antibody CBA is performed by a cell binding IFA assay. This antibody is found in patients with the autoimmune disease, neuromyelitis optica. Islet cell antibodies are produced in Type 1 diabetes which is an autoimmune disease and is also performed by an IFA assay. We suggest a crosswalk to the islet cell antibody code based on a similar methodology and disease indication.	$23.57

ACLA Recommendations on Immunology codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
Immunology					
86X02	Aquaporin-4 (neuromyelitis optica [NMO] antibody; flow cytometry (ie, fluorescence-activated cell sorting [FACS]), each	86367	Stem cells (ie, CD34), total count	Crosswalk to 86367. NMO antibody, by fluorescence-activated cell sorting (FACS) uses flow cytometry with a single marker to measure the antibody using flow cytometry and a complex algorithm is applied to calculate the ratio of IgG binding or NMO antibody, by fluorescence-activated cell sorting (FACS) uses very similar resources and methods to a total stem cell count. This test has various steps such as isolating the cells, using antibodies to quantify the cells using flow cytometry and a complex algorithm to determine the ratio of the IgG binding index	$77.78
863X2	Myelin oligodendrocyte glycoprotein (MOG-IgG1) antibody; cell-based immunofluorescence assay (CBA), each	86357	Natural killer (NK) cells, total count	MOG antibody CBA is performed by a cell binding IFA assay. We suggest a crosswalk to CPT 86357 that describes Natural Killer cells. The NK test includes various steps, such as a fluorescent marker to detect the antigen-antibody complex for autoimmune disorders and is similar to the methodology and resources performed in the MOG assay.	$37.73

ACLA Recommendations on Immunology codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
Immunology					
863X3	Myelin oligodendrocyte glycoprotein (MOG-IgG1) antibody; flow cytometry (ie, fluorescence-activated cell sorting [FACS]), each	86367	Stem cells (ie, CD34), total count	Crosswalk to 86367. MOG antibody, by fluorescence-activated cell sorting (FACS) uses flow cytometry with a single marker to measure the antibody using flow cytometry and a complex algorithm is applied to calculate the ratio of IgG binding or NMO antibody, by fluorescence-activated cell sorting (FACS) uses very similar resources and methods to a total stem cell count. This test has various steps such as isolating the cells, using antibodies to quantify the cells using flow cytometry and a complex algorithm to determine the ratio of the IgG binding index.	$77.78
862X0	Endomysial antibody (EMA), each immunoglobulin (Ig) class	86038 (x2)	Antinuclear antibodies (ANA)	We suggest a crosswalk to 86038, antinuclear antibody, using immunofluorescence antibody, with an x 2 multiplier. The EMA test uses a rhesus monkey esophagus substrate that is overlaid with dilutions of the patient's serum, incubated and then covered with fluorescein-conjugated IgG antiserum, which accounts for the x 2 multiplier to cover the more costly reagents and additional technologist time for the testing. The methodology is the same and includes similar work and resources.	86038 x 2/($12.09 x 2) =$24.18

ACLA Recommendations on Immunology codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
Immunology					
862XX	Gliadin (deamidated) (DGP) antibody, each immunoglobulin (Ig) class	86147	Cardiolipin (phospholipid) antibody, each Ig class	We suggest a crosswalk to 86147 which is an analyte specific antibody code for antibodies for autoimmune disorders that use an ELISA technique for detection. The methodology is the same and includes similar work and resources.	$25.45
862X1	Tissue transglutaminase, each immunoglobulin (Ig) class	86147	Cardiolipin (phospholipid) antibody, each Ig class	We suggest a crosswalk to 86147 which is an analyte specific antibody code for antibodies for autoimmune disorders that use an ELISA technique for detection. The methodology is the same and includes similar work and resources.	$25.45
863X4	Mitochondrial antibody (eg, M2), each	86146	Beta 2 Glycoprotein I antibody, each	We suggest a crosswalk to 86146 which is an analyte specific antibody code for antibodies for autoimmune disorders that use an ELISA technique for detection. The methodology is the same and includes similar work and resources.	$25.45
865X0	Voltage-gated calcium channel antibody, each	84586	Vasoactive intestinal peptide (VIP)	We recommend a crosswalk to CPT 84586. The vasoactive intestinal peptide test may be performed by radioimmunoassay and uses similar methodology and resources.	$35.33

ACLA Recommendations on Immunology codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
Immunology					
86XX0	Actin (Smooth Muscle) Antibody (ASMA), each	86146	Beta 2 Glycoprotein I antibody, each	We suggest a crosswalk to 86146 which is an analyte specific antibody code for antibodies for autoimmune disorders that use an ELISA technique for detection. The methodology is the same and includes similar work and resources.	$25.45
86X00	Antineutrophil cytoplasmic antibody (ANCA); screen, each antibody	86146	Beta 2 Glycoprotein I antibody, each	We suggest a crosswalk to 86146 which is an analyte specific antibody code for antibodies for autoimmune disorders. The tests include similar work and resources.	$25.45
86X01	Antineutrophil cytoplasmic antibody (ANCA); titer, each antibody	86146	Beta 2 Glycoprotein I antibody, each	We suggest a crosswalk to 86146 which is an analyte specific antibody code for antibodies for autoimmune disorders. The tests include similar work and resources.	$25.45

ACLA Recommendations on Microbiology codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
Microbiology					
8715X	Culture, typing; identification of blood pathogen and resistance typing, when performed, by nucleic acid (DNA or RNA) probe, multiplexed amplified probe technique including multiplex reverse transcription, when performed, per culture or isolate, 6 or more targets	87632	Infectious agent detection by nucleic acid (DNA or RNA); respiratory virus (eg, adenovirus, influenza virus, coronavirus, metapneumovirus, parainfluenza virus, respiratory syncytial virus, rhinovirus), includes multiplex reverse transcription, when performed, and multiplex amplified probe technique, multiple types or subtypes, 6-11 targets	Crosswalk to 87632; both use same methodology for detecting multiple pathogen targets simultaneously with targets being 6 or greater.	$218.06

ACLA Recommendations on Therapeutic Drug and Molecular Pathology codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
Therapeutic Drug					
801XX	Hydroxychloroquine	80204	Methotrexate	Crosswalk to 80204 Methotrexate. Same methodology of LC/MS/MS and is also used in treatment of lupus. 80299 which is currently used is a not elsewhere specified code, and doesn't represent the similarity in method, resources and use of the therapeutic drug.	$38.57
Molecular Pathology					
812X0	Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and loss-of-heterozygosity variants, low-pass sequencing analysis	81229	Cytogenomic constitutional (genome-wide) microarray analysis; interrogation of genomic regions for copy number and single nucleotide polymorphism (SNP) variants for chromosomal abnormalities	Code 81277 for tumor cytogenomics was a new code for the 2021 CLFS. The CMS final determination for 81277 was to crosswalk this code to 81229, molecular cytogenomics for microarray and SNP's. Code 81229 is also a good crosswalk for the new code 812X0, molecular cytogenomics using next generation sequencing. These are both germline assays used for the same indications with similar work and resources.	$1,160.00

ACLA Recommendations on Multianalyte Assays with Algorithmic Analysis (MAAA) codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
MAAA					
815X1	Oncology (breast), mRNA, next-generation sequencing gene expression profiling of 70 content genes and 31 housekeeping genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as index related to risk to distant metastasis	81521	Oncology (breast), mRNA, microarray gene expression profiling of 70 content genes and 465 housekeeping genes, utilizing fresh frozen or formalin-fixed paraffin-embedded tissue, algorithm reported as index related to risk of distant metastasis	Crosswalk to 81521. Gene expression (quantifying levels of mRNA) based, same 70 genes, same algorithm, same intended use, same result but using RNAseq instead of microarray.	$3,873.00

ACLA Recommendations on Administrative Multianalyte Assays with Algorithmic Analysis (MAAA) codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
Administrative MAAA					
0017M	Oncology (diffuse large B-cell lymphoma [DLBCL]), mRNA, gene expression profiling by fluorescent probe hybridization of 20 genes, formalin-fixed paraffin-embedded tissue, algorithm reported as cell of origin **Lymph2Cx**, **Mayo Clinic Arizona Molecular Diagnostics Laboratory**	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 latter	Suggested crosswalk to 0120U recommendation was obtained for same platform, same testing, different algorithm for outcome	$2,510.21

ACLA Recommendations on Chemistry codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
Chemistry					
835X1	Interleukin-6 (IL-6)	83006	Growth stimulation expressed gene 2 (ST2, Interleukin 1 receptor like-1)	Crosswalk to 83006 which is an analyte specific code for ST2. This is a member of the IL-1 receptor family. Resources and work would be similar and also is an ELISA method.	$75.60
8352X	Immunoglobulin light chains (ie, kappa, lambda), free, each	83520	Immunoassay for analyte other than infectious agent antibody or infectious agent antigen; quantitative, not otherwise specified	Suggested crosswalk to 83520. The methodology is immunoturbidimetry which measures the absorbance of light by the sample. The level of analyte is determined by comparison of know concentration.	$17.27
826X0	Elastase, pancreatic (EL-1), fecal; quantitative	82715	Fat differential, feces, quantitative	Crosswalk to 82715. Both use similar methodology to determine an analyte that is associated with a comparable diagnostic condition. Work and resources are similar.	$22.97

ACLA Recommendations on Proprietary Laboratory Analysis (PLA) codes

2022 AMA Placeholder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
PLA Codes					
0229U	BCAT1 (Branched chain amino acid transaminase 1) or IKZF1 (IKAROS family zinc finger 1) (eg, colorectal cancer) promoter methylation analysis **Colvera®, Clinical Genomics Pathology Inc**	81327 x 2	SEPT9 (Septin9) (eg, colorectal cancer) promoter methylation analysis	Suggested crosswalk to two times 81327, based on similar methodology but additional required work and resources for 0229U CPT code. 81327 represents the methodology and resources to perform the assay. 81327 represents a PCR test that detects promoter methylation in one gene (SEPT9) that is associated with colorectal cancer ("CRC"), and which is used to screen for CRC. 0229U also represents a PCR test that detects promoter methylation associated with CRC, however it detects promoter methylation in two genes (BCAT1 and IKZF1) and more than double the number of CPG sites targeted in 81327 (21 in 0229U versus 8 in 81327). 0229U is not a screening assay, but rather is used post-treatment to detect Minimal Residual Disease and recurrent CRC. 0229U requires substantially more resources and materials to achieve the required assay performance levels than 81327. The multiplier of 2 represents the additional work and resources required for this new CRC MRD and recurrence surveillance test.	81327 x 2/($192.00 x 2) = $384.00

ACLA Recommendations on on Proprietary Laboratory Analysis (PLA) codes

2022 AMA Place-holder	2022 Long Code Descriptor	ACLA Crosswalk Recommendation	Descriptor	ACLA Rationale for CLFS Crosswalk or Gapfill requests	2022 NLA
PLA Codes					
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 **Oncotype MAP™ PanCancer Tissue Test, Paradigm Diagnostics, Inc, Paradigm Diagnostics, Inc**	Gapfill			
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 **ThyGeNEXT® Thyroid Oncogene Panel, Interpace Diagnostics, Interpace Diagnostics**	81455	Targeted genomic sequence analysis panel, solid organ or hematolymphoid neoplasm, DNA analysis, and RNA analysis when performed, 51 or greater genes (eg, ALK, BRAF, CDKN2A, CEBPA, DNMT3A, EGFR, ERBB2, EZH2, FLT3, IDH1, IDH2, JAK2, KIT, KRAS, MLL, NPM1, NRAS, MET, NOTCH1, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, if performed	ThyGeNEXT contains 10 genes, 37 fusions, and 4 mRNA for a total of 51 markers. Suggested crosswalk to 81455 recommendation, which more accurately represents the methodology, work and resources for this testing.	$2,919.60

Thank you

22. American Association for Clinical Chemistry (AACC)

- Presenter: Jason Park, MD, PhD, DABCC
- Codes: 80151, 80161, 80167, 80181, 81279, 81338, 86408, 86409, 86413, 87636, 87637, 860XX, 860X1, 860X2, 863X2, 863X3, 862X0, 862XX, 862X1, 863X4, 865X0, 86XX0, 86X00, 8715X, 801XX, 812X0, 815X1, 835X1, 8352X, 826X0

80151: Amiodarone

Public Comment	Rationale
80155, $38.57	Recommended crosswalk to 80155 (Caffeine) more accurately represents the methodology, work and resources for testing.

80161: Carbamazepine; -10, 11-epoxide

Public Comment	Rationale
80155, $38.57	Recommended crosswalk to 80155 (Caffeine) more accurately represents the methodology, work and resources for testing.

80167: Felbamate

Public Comment	Rationale
80199, $27.11	Recommended crosswalk to 80199 (Tiagabine) which represents similar methodology and resources to perform the testing and is also used to treat seizures/epilepsy.

80181: Flecainide

Public Comment	Rationale
80193, $38.57	Crosswalk to 80193 (leflunomide), which more accurately represents the methodology, work and resources for testing.

81279: JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) targeted sequence analysis (eg, exons 12 and 13)

Public Comment	Rationale
81272 , $329.51	The JAK2 targeted sequence analysis methodology, resources, and amount of genetic material sequenced are comparable to that of KIT (81272) targeted sequence analysis.

81338: MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; common variants (eg, W515A, W515K, W515L, W515R)

Public Comment	Rationale
81120, $193.25	The MPL common variants methodology, resources and amount of genetic material sequence are comparable to that of IDH1 common variants (81120). Both assess genes for an oncology disorder, and both are targeted sequencing of a single exon for oncology samples.

86408: Neutralizing antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]); screen

Public Comment	Rationale
86769, $42.13	This code represents similar methodology and resources to perform the testing.

86409: Neutralizing antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]); titer

Public Comment	Rationale
86769 x3/($42.13 x3) = $126.39	This code represents similar methodology and resources to perform the testing. The multiplier (x3) reflects additional work to perform a serial dilution titer.

86413: Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]) antibody, quantitative

Public Comment	Rationale
86769 x1.25/($42.13 x 1.25) = $52.66	This code represents similar methodology and resources to perform the testing. An additional multiplier (x1.25) reflects a quantitative assay

87636: Infectious agent detection by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]) and influenza virus types A and B, multiplex amplified probe technique

Public Comment	Rationale
87631, $142.63	This code represents the methodology and resources required to perform the multiplex assay for the detection of respiratory viral targets.

87637: Infectious agent detection by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]), influenza virus types A and B, and respiratory syncytial virus, multiplex amplified probe technique

Public Comment	Rationale
87631, $142.63	This code represents the methodology and resources required to perform the multiplex assay for the detection of respiratory viral targets.

860XX: Aquaporin-4 (neuromyelitis optica [NMO]) antibody; enzyme-linked immunosorbent immunoassay (ELISA)

Public Comment	Rationale
86146, $25.45	Crosswalk is an analyte specific antibody code for autoimmune disorders that use an ELISA technique for detection, so methodology is the same with similar work and resources.

860X1: Aquaporin-4 (neuromyelitis optica [NMO] antibody; cell-based immunofluorescence assay (CBA), each

Public Comment	Rationale
86341, $23.57	Crosswalk to the islet cell antibody code based on a similar methodology and disease indication.

860X2: Aquaporin-4 (neuromyelitis optica [NMO] antibody; flow cytometry (ie, fluorescence-activated cell sorting [FACS]), each

Public Comment	Rationale
86367, $77.78	This code represents similar methodology and resources to perform the testing.

863X2: Myelin oligodendrocyte glycoprotein (MOG-IgG1) antibody; cell-based immunofluorescence assay (CBA), each

Public Comment	Rationale
86357, $37.73	This code represents similar methodology and resources to perform the testing.

863X3: Myelin oligodendrocyte glycoprotein (MOG-IgG1) antibody; flow cytometry (ie, fluorescence-activated cell sorting [FACS]), each

Public Comment	Rationale
86367, $77.78	This code represents similar methodology and resources to perform the testing.

862X0: Endomysial antibody (EMA), each immunoglobulin (Ig) class

Public Comment	Rationale
86038, $12.09	Crosswalk to 86038 antinuclear antibody, IFA screen, methodology and similar work and resources as ANA.

862XX: Gliadin (deamidated) (DGP) antibody, each immunoglobulin (Ig) class

Public Comment	Rationale
86147, $25.45	Crosswalk is an analyte specific antibody code for antibodies for autoimmune disorders that use an ELISA technique for detection. The methodology is the same and includes similar work and resources.

862X1: Tissue transglutaminase, each immunoglobulin (Ig) class

Public Comment	Rationale
86147, $25.45	Crosswalk is an analyte specific antibody code for antibodies for autoimmune disorders that use an ELISA technique for detection. The methodology is the same and includes similar work and resources.

863X4: Mitochondrial antibody (eg, M2), each

Public Comment	Rationale
86146, $25.45	Crosswalk to 86146 which is an analyte specific antibody code for antibodies for autoimmune disorders that use an ELISA technique for detection. The methodology is the same and includes similar work and resources.

865X0: Voltage-Gated Calcium Channel Antibody, each

Public Comment	Rationale
84586, $35.33	The vasoactive intestinal peptide test may be performed by radioimmunoassay and uses similar methodology and resources.

86XX0: Actin Smooth Muscle Antibody (ASMA), each

Public Comment	Rationale
86146, $25.45	Crosswalk is an analyte specific antibody code for antibodies for autoimmune disorders that use an ELISA technique for detection. The methodology is the same and includes similar work and resources.

86X00: Antineutrophil cytoplasmic antibody (ANCA), screen each antibody

Public Comment	Rationale
86146, $25.45	Crosswalk is an analyte specific antibody code for autoimmune disorders. The tests include similar work and resources.

8715X: Culture, typing; identification of blood pathogen and resistance typing, when performed, by nucleic acid (DNA or RNA) probe, multiplexed amplified probe technique including multiplex reverse transcription, when performed, per culture or isolate, 6 or more targets

Public Comment	Rationale
87632, $218.06	Same methodology for detecting multiple pathogen targets simultaneously with targets being 6 or greater.

801XX: Hydroxychloroquine

Public Comment	Rationale
80204, $38.57	Crosswalk to 80204 Methotrexate. Same methodology of LC/MS/MS; the same drug is used in treatment of lupus.

812X0: Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and loss-of-heterozygosity variants, low-pass sequencing analysis

Public Comment	Rationale
81229, $1160	Crosswalk to 81229, molecular cytogenomics for microarray and SNP's. Both are germline assays used for the same indications with similar work and resources.

815X1: Oncology (breast), mRNA, next-generation sequencing gene expression profiling of 70 content genes and 31 housekeeping genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as index related to risk to distant metastasis

Public Comment	Rationale
81521, $3873	Crosswalk to 81521. Gene expression (quantifying levels of mRNA) based on same 70 genes, similar algorithm, same intended use. Use of RNAseq instead of microarray.

835X1: Interleukin-6 (IL-6)

Public Comment	Rationale
83006, $75.60	Crosswalk is an analyte specific code for ST2 (83006); this is a member of the Interleukin-1 receptor family. Similar resources and work for a manual ELISA method.

8352X: Immunoglobulin light chains (ie, kappa, lambda), free, each

Public Comment	Rationale
83520, $17.27	Crosswalk to 83520. The methodology is the same (turbidimetry) and includes similar work and resources.

826X0: Elastase, pancreatic (EL-1), fecal; quantitative

Public Comment	Rationale
82715, $22.97	Crosswalk to 82715. Both use a similar methodology to determine an analyte that is associated with a comparable diagnostic condition. Work and resources are similar.

23. College of American Pathologists (CAP)

Presenter: Michael O. IDOWU, MD, MPH

Codes: 81279, 81338, 81339, 812X0

Centers for Medicare and Medicaid Services (CMS)

Clinical Laboratory Fee Schedule (CLFS) Annual Laboratory Public Meeting

June 24, 2021

Michael O. IDOWU, MD, MPH

Presenter, College of American Pathologists (CAP)

Clinical Laboratory Fee Schedule Recommendations

Reconsideration HCPCS, Level I (CPT) test code:
Molecular Pathology
81279 *JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) targeted sequence analysis (eg, exons 12 and 13)*

Public Comment	Rationale
81272 x1 ($329.51)	Comparable resources are required to complete the targeted sequence analysis of *KIT (v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog)* (eg, gastrointestinal stromal tumor [GIST], acute myeloid leukemia, melanoma) (eg, exons 8, 11, 13, 17, 18)

Clinical Laboratory Fee Schedule Recommendations

Reconsideration HCPCS, Level I (CPT) test code:
Molecular Pathology
81338 *MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; common variants (eg, W515A, W515K, W515L, W515R)*

Public Comment	Rationale
81120 x1 ($193.25)	Comparable resources are required to complete analysis of *IDH1 (isocitrate dehydrogenase 1 [NADP+], soluble*) (eg, glioma), common variants (eg, R132H, R132C)

Clinical Laboratory Fee Schedule Recommendations

Reconsideration HCPCS, Level I (CPT) test code:
Molecular Pathology
81339 *MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; sequence analysis, exon 10*

Public Comment	Rationale
81310 x1 ($246.52)	Comparable resources are required to complete the gene analysis of *NPM1 (nucleophosmin)* (eg, acute myeloid leukemia) gene analysis, exon 12 variants

Clinical Laboratory Fee Schedule Recommendations

HCPCS, Level I (CPT) test code:
Molecular Pathology
812X0 *Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and loss-of-heterozygosity variants, low-pass sequencing analysis*

Public Comment	Rationale
81229 x1 ($1160)	Comparable resources are required to complete a cytogenomic constitutional (genome-wide) microarray analysis; interrogation of genomic regions for copy number and single nucleotide polymorphism (SNP) variants for chromosomal abnormalities

Clinical Laboratory Fee Schedule Recommendations

A complete list of CAP CLFS CY2022 recommendations for the CLFS Annual Laboratory Public Meeting has been submitted to the CMS in a supplemental spreadsheet.

Thank you!

24. American Society for Clinical Pathology

Presenter: Lee H. Hilborne

Codes: 86408, 86409, 86413, 87636, 87637, 860XX, 860X1, 860X2, 863X2, 863X3, 862X0, 862XX, 862X1, 863X4, 865X0, 86XX0, 86X00, 86X01, 8715X, 801XX, 812X0, 835X1, 8352X, 826X0

STRONGERTOGETHER

American Society for Clinical Pathology

Comments submitted as written comments only. Questions about these recommendations may be submitted to Lee H. Hilborne, MD, MPH, FASCP, DLM(ASCP)^{CM} or Matthew Schulze, ASCP

Codes: 86408, 86409, 86413, 87636, 87637, 860XX, 860X1, 860X2, 863X2, 863X3, 862X0, 862XX, 862X1, 863X4, 865X0, 86XX0, 86X00, 86X01, 8715X, 801XX, 812X0, 835X1, 8352X, 826X0

Clinical Laboratory Fee Schedule Annual Lab Meeting, June 24, 2021
Centers for Medicare & Medicaid Services

SARS-CoV-2 Immunology

86408 Neutralizing antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]); screen

Public Comment	Rationale
86794 x 2.5 ($42.13)	ASCP recommends crosswalking code 86408 to CPT code 86794 (Zika antibody test) with a multiplier of 2.5. Given the significant additional resources required to perform this test, this proposed crosswalk is appropriate. The Zika antibody test code 86794 represents the methodology required to perform the assay. Both tests detect antibodies for an infectious agent. These tests are technically similar as they both represent qualitative assays used to confirm the presence of an antibody detected against an infectious pathogen. The difference between the two assays is that 86794 measures binding and 86408 relates to neutralization. The SARS-CoV-2 neutralizing antibody screen test uses similar technology and methodology as a Zika antibody test, yet it involves a myriad of additional factors that increase its costs compared to the Zika antibody test and other routine immunology tests. The limited factors that normally are used to establish Medicare reimbursement do not fully account for the increased costs of this service.

SARS-CoV-2 Immunology

86409 Neutralizing antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]); titer

Public Comment	Rationale
86352 ($135.86)	CPT code 86352 (Cellular function assay involving stimulation (e.g., mitogen or antigen) and detection of biomarker (eg, ATP)) represents the best match to the assay method and resources required to perform the new assay. The titer assay involves stimulating the cells with pseudotyped virus, which induces membrane fusion, after which substrate (enduren) is added. It is then read as the biomarker readout (luminescence). Serum samples are serially diluted from 1:80 to 1:2,560, and the additional resources needed to perform the serial dilution series account for the additional costs in performing such testing. Therefore, 86352 represents the resources and materials required for the titer.

SARS-CoV-2 Immunology

86413 Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]) antibody, quantitative

Public Comment	Rationale
86794 x 3.125 ($52.66)	ASCP recommends crosswalking code 86413 to CPT code 86794 (Zika qualitative antibody test) with a multiplier of 3.125. This is appropriate given the additional resources need to perform this test. The quantitative assay code 86413 represents the quantitative detection of antibodies for SARS-CoV-2. There are additional resources needed to perform the quantitative assay, when compared to the qualitative assay. The quantitative assay requires higher complexity laboratory-based testing methods as compared to current qualitative assays. Therefore, we recommend a multiplier of 3.125 that represents the additional work, resources and cost.

SARS-CoV-2 Microbiology

87636 Infectious agent detection by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]) and influenza virus types A and B, multiplex amplified probe technique

Public Comment	Rationale
87631 ($142.63)	CPT code 87631 represents the methodology and resources required to perform the multiplex assay for the detection of respiratory viral targets. The SARS-CoV-2 multiplex assay code 87636 represents the detection of SARS-CoV-2, influenza A and influenza B. The new COVID-19 multiplex CPT code 87636 represents a 3 target multiplex respiratory viral assay specific for the SARS-CoV-2, influenza virus A and influenza virus B targets. A straight crosswalk to code 87631 is most appropriate for the new code 87636. Code 87631 is already priced for 3 to 5 targets and represents a multiplex respiratory viral target assay. Therefore, code 87631 is the most appropriate crosswalk and represents the same methodology and number of targets tested.

SARS-CoV-2 Microbiology

87637 Infectious agent detection by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]), influenza virus types A and B, and respiratory syncytial virus, multiplex amplified probe technique

Public Comment	Rationale
87631 ($142.63)	CPT code 87631 represents the methodology and resources required to perform the multiplex assay for the detection of respiratory viral targets. The SARS-CoV-2 multiplex assay code 87637 represents the detection of SARS-CoV-2, influenza A and influenza B plus respiratory syncytial virus (RSV). The new COVID-19 multiplex CPT code 87637 represents a 4 target multiplex respiratory viral assay specific for the SARS-CoV-2, influenza virus A, influenza virus B and RSV targets. A straight crosswalk to code 87631 is most appropriate for the new code 87637. Code 87631 is already priced for 3 to 5 targets and represents a multiplex respiratory viral target assay. Therefore, code 87631 is the most appropriate crosswalk and represents the same methodology and number of targets tested.

Immunology

860XX Aquaporin-4 (neuromyelitis optica [NMO]) antibody; enzyme-linked immunosorbent immunoassay (ELISA)

Public Comment	Rationale
86146 ($25.45)	Crosswalk to 86146 as it uses the same methodology and similar work/resources.

Immunology

860X1 Aquaporin-4 (neuromyelitis optica [NMO] antibody; cell-based immunofluorescence assay (CBA), each

Public Comment	Rationale
86341 ($23.57)	Crosswalk to 86341. Aquaporin-4 antibody CBA is performed by a cell binding IFA assay. This antibody is found in patients with the autoimmune disease, neuromyelitis optica. Islet cell antibodies are produced in Type 1 diabetes which is an autoimmune disease and is also performed by an IFA assay. ASCP supports crosswalking this code to the islet cell antibody code based on a similar methodology and disease indication.

Immunology

860X2 Aquaporin-4 (neuromyelitis optica [NMO] antibody; flow cytometry (ie, fluorescence-activated cell sorting [FACS]), each

Public Comment	Rationale
86367 ($77.78)	Crosswalk to 86367. NMO antibody, by fluorescence-activated cell sorting (FACS) uses flow cytometry with a single marker to measure the antibody using flow cytometry and a complex algorithm is applied to calculate the ratio of IgG binding or NMO antibody, by fluorescence-activated cell sorting (FACS) uses very similar resources and methods to a total stem cell count. This test has various steps such as isolating the cells, using antibodies to quantify the cells using flow cytometry, and a complex algorithm to determine the ratio of the IgG binding index.

Immunology

863X2 Myelin oligodendrocyte glycoprotein (MOG-IgG1) antibody; cell-based immunofluorescence assay (CBA), each

Public Comment	Rationale
86357 ($37.73)	MOG antibody CBA is performed by a cell binding IFA assay. We suggest a crosswalk to CPT 86357 that describes Natural Killer cells. The NK test includes various steps, such as a fluorescent marker to detect the antigen-antibody complex for autoimmune disorders and is similar to the methodology and resources performed in the MOG assay.

Immunology

863X3 Myelin oligodendrocyte glycoprotein (MOG-IgG1) antibody; flow cytometry (ie, fluorescence-activated cell sorting [FACS]), each

Public Comment	Rationale
86367 ($77.78)	Crosswalk to 86367. MOG antibody, by fluorescence-activated cell sorting (FACS) uses flow cytometry with a single marker to measure the antibody using flow cytometry and a complex algorithm is applied to calculate the ratio of IgG binding or NMO antibody, by fluorescence-activated cell sorting (FACS) uses very similar resources and methods to a total stem cell count. This test has various steps such as isolating the cells, using antibodies to quantify the cells using flow cytometry and a complex algorithm to determine the ratio of the IgG binding index.

Immunology

862X0 Endomysial antibody (EMA), each immunoglobulin (Ig) class

Public Comment	Rationale
86038 x 2 ($24.18)	We suggest a crosswalk to 86038, antinuclear antibody, using immunofluorescence antibody, with an x 2 multiplier. The EMA test uses a rhesus monkey esophagus substrate that is overlaid with dilutions of the patient's serum, incubated and then covered with fluorescein-conjugated IgG antiserum, which accounts for the x 2 multiplier to cover the more costly reagents and additional technologist time for the testing. The methodology is the same and includes similar work and resources.

Immunology

862XX Gliadin (deamidated) (DGP) antibody, each immunoglobulin (Ig) class

Public Comment	Rationale
86147 ($25.45)	ASCP suggests a crosswalk to 86147 which is an analyte specific antibody code for antibodies for autoimmune disorders that use an ELISA technique for detection. The methodology is the same and includes similar work and resources.

Immunology

862X1 Tissue transglutaminase, each immunoglobulin (Ig) class

Public Comment	Rationale
86147 ($25.45)	ASCP suggests a crosswalk to 86147 which is an analyte specific antibody code for antibodies for autoimmune disorders that use an ELISA technique for detection. The methodology is the same and includes similar work and resources.

Immunology
863X4 Mitochondrial antibody (eg, M2), each

Public Comment	Rationale
86146 ($25.45)	We suggest a crosswalk to 86146 which is an analyte specific antibody code for antibodies for autoimmune disorders that use an ELISA technique for detection. The methodology is the same and includes similar work and resources.

Immunology

865X0 Voltage-gated calcium channel antibody, each

Public Comment	Rationale
84586 ($35.33)	ASCP recommends a crosswalk to CPT 84586. The vasoactive intestinal peptide test may be performed by radioimmunoassay and uses similar methodology and resources.

Immunology

86XX0 Actin (Smooth Muscle) Antibody (ASMA), each

Public Comment	Rationale
86146 ($25.45)	We suggest a crosswalk to 86146 which is an analyte specific antibody code for antibodies for autoimmune disorders that use an ELISA technique for detection. The methodology is the same and includes similar work and resources.

Immunology

86X00 Antineutrophil cytoplasmic antibody (ANCA); screen, each antibody

Public Comment	Rationale
86146 ($25.45)	We suggest a crosswalk to 86146 which is an analyte specific antibody code for antibodies for autoimmune disorders. The tests include similar work and resources.

Immunology

86X01 Antineutrophil cytoplasmic antibody (ANCA); titer, each antibody

Public Comment	Rationale
86146 ($25.45)	We suggest a crosswalk to 86146 which is an analyte specific antibody code for antibodies for autoimmune disorders. The tests include similar work and resources.

Microbiology

8715X Culture, typing; identification of blood pathogen and resistance typing, when performed, by nucleic acid (DNA or RNA) probe, multiplexed amplified probe technique including multiplex reverse transcription, when performed, per culture or isolate, 6 or more targets

Public Comment	Rationale
87632 ($218.06)	Crosswalk to 87632. Both use same methodology for detecting multiple pathogen targets simultaneously with targets being 6 or greater.

Therapeutic Drug Assays

801XX Hydroxychloroquine

Public Comment	Rationale
80204 ($38.57)	Crosswalk to 80204 Methotrexate. Same methodology of LC/MS/MS and is also used in treatment of lupus. Code 80299, which is currently used, is a not elsewhere specified code, and doesn't represent the similarity in method, resources and use of the therapeutic drug.

Molecular Pathology

812X0 Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and loss-of-heterozygosity variants, low-pass sequencing analysis

Public Comment	Rationale
81229 ($1,160)	Code 81277 for tumor cytogenomics was a new code for the 2021 CLFS. The CMS final determination for 81277 was to crosswalk this code to 81229, molecular cytogenomics for microarray and SNP's. Code 81229 is also a good crosswalk for the new code 812X0, molecular cytogenomics using next generation sequencing. These are both germline assays used for the same indications with similar work and resources.

Chemistry

835X1 Interleukin-6 (IL-6)

Public Comment	Rationale
83006 ($75.60)	Crosswalk to 83006 which is an analyte specific code for ST2. This is a member of the IL-1 receptor family. Resources and work would be similar and also is an ELISA method.

Chemistry

8352X Immunoglobulin light chains (ie, kappa, lambda), free, each

Public Comment	Rationale
83520 ($17.27)	Suggested crosswalk to 83520. The methodology is immunoturbidimetry which measures the absorbance of light by the sample. The level of analyte is determined by comparison of known concentration.

Chemistry

826X0 Elastase, pancreatic (EL-1), fecal; quantitative

Public Comment	Rationale
82715 ($22.97)	Crosswalk to 82715. Both use similar methodology to determine an analyte that is associated with a comparable diagnostic condition. Work and resources are similar.

25. PerkinElmer Genetics

Placenta Growth Factor pre-eclampsia screen (PlGF)

- Presenter: Mike O'Shea

- 0243U Obstetrics (preeclampsia), biochemical assay of placental-growth factor, time-resolved fluorescence immunoassay, maternal serum, predictive algorithm reported as a risk score for pre-eclampsia

PerkinElmer, Inc. (NYSE PKI) Corporate Overview

- PerkinElmer, Inc. is the global leader in prenatal screening and detecting fetal anomalies during pregnancy for over 30 years
- PerkinElmer, Inc. is a global leader in newborn screening for metabolic, endocrine and inborn error of metabolism both in US and globally
- PerkinElmer, Inc. assays and platforms are used in more than 120 countries to perform some +10 million prenatal risk assessments per year- including pre-eclampsia testing
- PerkinElmer, Inc. is an American global corporation focused in the business areas of diagnostics, life science research, food, environmental and industrial testing. Its capabilities include detection, imaging, informatics, and service

Pre-eclampsia (PE) disease

- Pre-eclampsia affects 2-8% of pregnant women and is one of the leading causes of maternal and perinatal morbidity and mortality. Worldwide, 76,000 women and 500,000 babies die yearly from this disorder (1)
- Preterm birth (PTB) effects 8-11% of the US population. Preeclampsia is the cause of PTB in 15-18% of these births. (20)
- PE develops as a result of abnormal placental growth and blood flow, resulting in fetal growth-restriction or pre-term birth. When left untreated, PE leads to eclampsia - a serious multi system condition that can endanger and harm both the newborn and mother's life (2)
- Mothers who have had PE increased their risk for future cardiovascular disease and diabetes (3,4). Babies who experience a preeclamptic birth are at increased risk of cerebral palsy as a result of fetal growth restriction and premature birth (5)
- PE is defined as failure of the placenta to support normal fetal growth. PE screening including PlGF diagnostic test (at 11-13 weeks gestation) is a life-saving tool, validated by numerous clinical studies that support early identification and treatment to expectant mothers that may be at risk for complications (6)

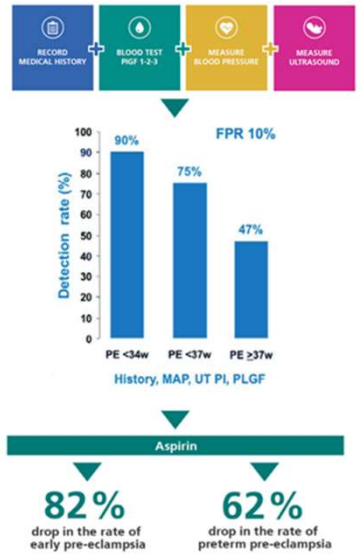
PlGF test by PerkinElmer

- PlGF test is a lab developed test (LDT) performed in Pittsburgh, PA clinical lab, meeting all federal and state regulatory, quality, CAP and CLIA criteria
- PlGF is a biochemical assay detecting placental growth factor in a maternal serum via a collected blood sample. The serum sample is tested by sandwich based, time resolved fluorescence immunoassay for PlGF, it compares value on weekly gestational median. (7, 8, 9).
- This model with PIGF is confirmed via multiple studies to early detect PE or maternal history alone (1,6,11,12)
- The lab technician measures the PlGF concentration. The lab accessioning group records maternal history ultrasound and Bp measurements provided by the OBGYN. The test report is a clinical tool to aid in the prediction of risk to develop PE in a pregnancy, and provides actionable information for OBGYN clinically, in order to manage patients, and to ensure a healthy pregnancy for the mother and newborn

PlGF improves PE detection and treatment

- PlGF test improves prediction of early onset pre-eclampsia (1,6,12) so appropriate treatment (aspirin) with the correct dose can be administered
  - 150 mg of aspirin per day, from 11-14 weeks gestation until 36 weeks gestation = 62% reduction in rate of pre-term pre-eclampsia (1,6) and a 68% reduction in length of stay in NICU (13). Dose and administration matter (1)
  - Increases physician surveillance of "at risk" patients, resulting in increased patient compliance with aspirin prescribed (12)

- Supports current guidelines and builds on them via clinically validated studies that demonstrate adding PlGF test with validated FMF approach increases risk detection (1,6,15)
  - Improves screening to increase risk detection (1,3,6,12)
  - Maternal history alone (such as NICE and ACOG approach) result in poor PE detection and in missed opportunities to intervene on behalf of the mother and her unborn child



PlGF Test Benefits

- Patient Benefits
  - Provides reassurance that their risk for pre-eclampsia has been thoroughly assessed
  - Improves compliance with prescribed medication (12)
  - Improves clinical and quality outcomes by identifying risk and prompting correct intervention and treatment (1,6)
  - Reduces society, family, economic and cost burden of pre-eclampsia with early detection (13)

- Physician Benefits
  - Enables physician to access patient with most sensitive/specific test available in medical literature, reducing unnecessary need to treat (NTT) (1,6,16)
  - Allows for appropriate targeted intervention that improves clinical outcomes, reduces risk and complications for mother and child (16)

Economic Benefit of PlGF test

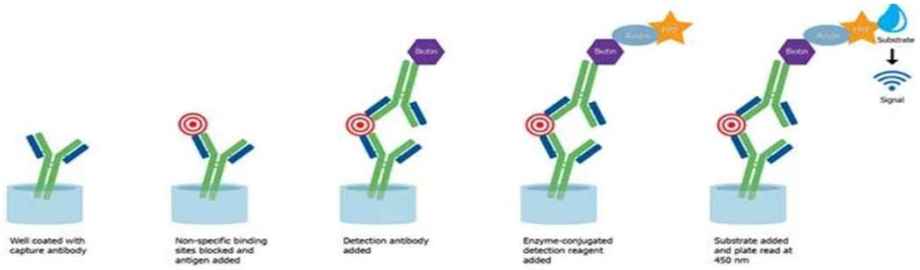
Model for Preeclampsia screening (CA cost)	N	Cost
Number of Births	10000	
Estimated PTB Deliveries Weeks 28-37	**980**	**$60,975,600**
Estimates preeclampsia	**147**	**$9,146,340**
PE population after screening and treatment	**83**	**$5,164,260**
Reduction in NICU cost		**$3,982,080**
Cost of Screening		**$650,000**
Saving on Preeclampsia screening		**$3,332,080**

Variables		Reference
NICU Cost (2008) US	$3,500	18
NICU Cost (2009-2011) CA	**$4,148**	17
PTB in population.	**9.8%**	20
Ave #r of NICU days for PE <37W, w/o aspirin	**15**	17
Preeclampsia Contribution to PTB	**15%**	20
Detection rate of Screening	**70%**	6
Percentage that responds to treatment	**62%**	6
Cost to Screen patient/population	**$65**	
Preeclampsia in population	2-8%	20

- Pre-eclampsia is costly. Early identification and treatment saves on NICU days for the child and mother hospitalization (15)
  - Reducing the rate of pre-eclampsia, reduces the rate of preterm birth, preterm birth = primary cost in NICU (13)
  - Preventing pre-eclampsia will bring substantial improvements to our US healthcare system (5, 14)
- Model
  - NICU LOS average cost in the US 2008 was $3500.00 per day (18)
  - NICU LOS CA average cost was $ 4148.00 per day 2009-2011 data (17)
- Above model does not factor in maternal complications cost, and long-term spending for families with children born with pre-eclampsia (2,5). Above model is conservative at 1.5% preeclampsia rate.

Rationale for cross walk fFN to PlGF

- Fetal Fibronectin (fFN) utilized to predict risk, negative predictive value (NPV) via immunoassay test
- If fFN is negative = pregnant mother may avoid hospitalization overnight cost $2607.000 is US average cost per day (19) Kaiser Family Foundation July 2020
- PlGF concentration in mother's serum is measured via sandwich immunoassay, patients at low risk do not need aspirin. High Risk patient with aspirin treatment can minimize NICU admission $4148.00 per day (17)
- Both fFN and PlGF use immunoassay techniques to perform the test
    - Elisa (EIMA) assay/ DELFIA (FIMA)assay, both are monoclonal protein capture sandwich immunoassay's



0243U Obstetrics (pre-eclampsia), biochemical assay of placental-growth factor, time-resolved fluorescence immunoassay, maternal serum, predictive algorithm reported as a risk score for pre-eclampsia

Public Comment	Rationale
Cross walk to 82731: Fetal fibronectin (fFN), cervicovaginal secretions, semi-quantitative ($64.41)	Similar methodology (sandwich immunoassays) • Both are reproductive hormones • Similar instrumentation • Similar resources • Reduction in unnecessary NICU stay

CMS Annual Lab Meeting, June 24, 2021

Perkin Elmer Genetics, Name of Presenter (O'Shea Mike)

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Final Remarks

MEETING COMPLETE
THANK YOU!

-Lunch Break-

Speakers/Presenters check back in at 12:45 p.m. E.S.T.

Session continues at 1:00 p.m. E.S.T.