CDLT Panel Meeting July 14, 2026: Voting Results

CPT code	Options	Votes
8XX30: Glial fibrillary acidic protein (GFAP)	Activity type	Multiple choice
	Total responses	11
	Unique participants	11
	Response options	Count
	Crosswalk to 83844	2
	Crosswalk to 0548U	9
	Gapfill	0
	Abstain	0
X300U: Neurology (traumatic brain injury), analysis of glial fibrillary acidic protein (GFAP) and ubiquitin carboxy-l terminal hydrolase L1 (UCH-L1), immunoassay	Activity type	Multiple choice
	Total responses	11
	Unique participants	11
	Response options	Count
	Crosswalk to 0570U	11
	Gapfill	0
	Abstain	0
0609U: Oncology (prostate), immunoassay for total prostate-specific antigen (PSA) and free PSA, serum or plasma, combined with clinical features	Activity type	Multiple choice
	Total responses	11
	Unique participants	11
	Response options	Count
	Crosswalk to 81539	1
	Gapfill	10
	Abstain	0
0650U: Drug metabolism (adverse drug reactions and drug response), genotyping of 9 genes	Activity type	Multiple choice
	Total responses	11
	Unique participants	11
	Response options	Count
	Crosswalk to 81418	9
	Crosswalk to 0349U	1

	Gapfill	1
	Abstain	0

0652U: Drug metabolism (adverse drug reactions), DNA analysis of 13 genes by targeted genotyping	Activity type	Multiple choice
	Total responses	11
	Unique participants	11
	Response options	Count
	Crosswalk to 81418	9
	Crosswalk to 0349U	2
	Gapfill	0
	Abstain	0

87638: Infectious agent detection by nucleic acid (DNA or RNA); rubeola (measles) virus	Activity type	Multiple choice
	Total responses	11
	Unique participants	11
	Response options	Count
	Crosswalk to 87635	11
	Gapfill	0
	Abstain	0

87183: Susceptibility studies, antimicrobial agent; carbapenem resistance genes	Activity type	Multiple choice
	Total responses	11
	Unique participants	11
	Response options	Count
	Crosswalk to 87505	11
	Gapfill	0
	Abstain	0

8XX32: Infectious agent detection by nucleic acid (DNA or RNA); Candida species (eg, C. albicans, C. tropicalis, C. parapsilosis,	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0455U	10
	Crosswalk to 87631	2
	Gapfill	0

	Abstain	0

87XX2: Infectious agent detection by nucleic acid (DNA or RNA); Macrolide resistance, 23S rDNA gene mutation(s)	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 87500	12
	Gapfill	0
	Abstain	0

0635U: Autoimmune (atopic dermatitis), mRNA, next-generation sequencing (NGS), gene expression profiling of 487 genes	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0258U	12
	Gapfill	0
	Abstain	0

0605U: Allergy and immunology (hereditary alpha tryptasemia), DNA, analysis of TPSAB1 gene copy number variation using digital PCR	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Gapfill	12
	Abstain	0

0580U: Borrelia burgdorferi, antibody detection of 24 recombinant protein groups, by immunoassay, IgG	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0042U x2	12
	Gapfill	0
	Abstain	0

0615U: Borrelia burgdorferi (Lyme disease), antibody detection of 26 recombinant protein groups, by immunoassay, IgM	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0042U	0
	Crosswalk to 0041U x5	12
	Gapfill	0
	Abstain	0
0636U: Babesia (Babesiosis), antibody detection of 20 recombinant protein groups, by immunoassay, IgG	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0042U x2	12
	Gapfill	0
	Abstain	0
0637U: Babesia (Babesiosis), antibody detection of 20 recombinant protein groups, by immunoassay, IgM	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0041U x4	12
	Gapfill	0
	Abstain	0
0638U: Bartonella (Bartonellosis), antibody detection of 32 recombinant protein groups, by immunoassay, IgG	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0042U x3	12
	Gapfill	0
	Abstain	0

0639U: Bartonella (Bartonellosis), antibody detection of 32 recombinant protein groups, by immunoassay, IgM

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0041U*5		12
Gapfill		0
Abstain		0

X258U: Comparative analysis using short tandem repeat (STR) markers, patient and comparative specimen, DNA, buccal swab and tissue, reported match or mismatch

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 81265 + (81266*0		11
Gapfill		1
Abstain		0

X274U: Oncology (central nervous system), low-pass whole genome sequence analysis of cerebrospinal fluid, interrogation for chromosome arm-level and focal losses and gains

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 81349		11
Gapfill		0
Abstain		1

0575U: Transplantation medicine (liver allograft rejection), mirna gene expression profiling by rt-pcr of 4 genes (mir-122, mir-885, mir-23a housekeeping, spike-in control), serum, algorithm reported as risk of liver allograft rejection

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	

	Crosswalk to 81595	11
	Gapfill	1
	Abstain	0

X252U: Transplantation medicine (kidney allograft rejection), mRNA, gene-expression profiling by real-time quantitative PCR of 12 genes (11 content and 1 housekeeping), urine, algorithm reported as a rejection risk score

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 81595		11
Gapfill		0
Abstain		1

X257U: Transplantation medicine (kidney allograft failure), RNA expression transcriptome by next-generation sequencing (NGS), profiling of 13 genes, post-transplant peripheral blood, algorithm

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0320U		12
Gapfill		0
Abstain		0

0630U: Oncology (breast), mRNA, gene expression profiling by microarray of 80 genes (80 content and 465 housekeeping), utilizing formalin-fixed paraffin-embedded tissue

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 81521		11
Crosswalk to 81540		0
Gapfill		0
Abstain		1

X282U: Oncology (pancreas), DNA, genome sequence with 5-hydroxymethylcytosine (5hmC) enrichment and	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0410U + 86301	12
	Gapfill	0
	Abstain	0
0634U: Oncology (breast cancer), cell-free DNA (cfDNA), evaluation of 11 ESR1 variants	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0332U	4
	Gapfill	8
	Abstain	0
X251U: Human papillomavirus (HPV), genotypes 18, 31, 33, and 35, cell-free DNA (cfDNA), whole blood, multiplex digital droplet PCR (ddPCR), quantitative	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0470U x 0.5	4
	Gapfill	7
	Abstain	1
X283U: Human papillomavirus (HPV), genotype 16, cell-free DNA (cfDNA), whole blood, digital droplet PCR (ddPCR), quantitative	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0470U x 0.3	3
	Gapfill	8
	Abstain	1

0604U: Allergy and immunology (chronic recurrent angioedema), 4 bradykinin peptides, liquid chromatography and tandem mass spectrometry (LC-MS/ MS), whole blood, quantitative	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Gapfill	12
	Abstain	0
0614U: Inborn error of metabolism (primary mitochondrial disease), mitochondrial analysis of 4 enzyme complexes by stained blue native polyacrylamide gel electrophoresis (	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Gapfill	12
	Abstain	0
0654U: Inborn error of metabolism (primary mitochondrial disease), mitochondrial analysis of 1 enzyme complex	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Gapfill	12
	Abstain	0
0655U: Inborn error of metabolism (primary mitochondrial disease), mitochondrial analysis of 1 enzyme complex by spectrophotometric kinetic assay	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Gapfill	12
	Abstain	0

0656U: Inborn error of metabolism (primary mitochondrial disease), mitochondrial analysis of 1 enzyme complex

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 82658	12
Gapfill	0
Abstain	0

X266U: Inborn error of metabolism (primary mitochondrial disease), determination of fibroblast growth factor 21 (FGF21)

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0251U	12
Gapfill	0
Abstain	0

0647U: Oncology (molecular residual disease), whole genome sequence analysis, cell-free DNA (cfDNA), whole blood,

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0340U	0
Crosswalk to 0307U	12
Gapfill	0
Abstain	0

0642U: Oncology (minimal residual disease [MRD]), tumor DNA, next-generation sequencing (NGS), whole blood, comparison to

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0307U	12
Gapfill	0
Abstain	0

X294U: Oncology (colorectal cancer), analysis of minimal residual disease (MRD) using patient-specific assays

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0340U	1
Crosswalk to 0307U	11
Gapfill	0
Abstain	0

0645U: Oncology (leukemia), minimal residual disease (MRD) detection for rearrangements, based on digital PCR,

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Gapfill	12
Abstain	0

0641U: Oncology (minimal residual disease [MRD]), tumor DNA, next-generation sequencing (NGS), using formalin-fixed paraffin-embedded (FFPE) tissue

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0306U	10
Gapfill	2
Abstain	0

0646U: Oncology (molecular residual disease), whole genome sequence analysis, cell-free DNA, whole blood, and formalin-fixed paraffin-embedded (FFPE)

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0306U	3
Gapfill	9
Abstain	0

X278U: Oncology (colorectal cancer), analysis of minimal residual disease (MRD), next-generation sequencing (NGS), circulating tumor DNA (ctDNA) analysis in whole blood and tumor

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0306U	9
Gapfill	3
Abstain	0

0644U: Oncology (leukemia), minimal residual disease (MRD) detection for rearrangements, blood or bone marrow, personalized assay design and baseline quantification

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Gapfill	12
Abstain	0

X262U: Oncology (head and neck), circulating tumor DNA (ctDNA), tumor-informed next-generation sequencing (NGS) analysis for 699 genes of patient-specific somatic variants

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0306U	11
Crosswalk to 0560U	0
Gapfill	0
Abstain	1

0611U: Oncology (liver), analysis of over 1,000 methylated regions, cell-free DNA from plasma, algorithm reported as a quantitative result

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count

	Crosswalk to 0565U	11
	Gapfill	1
	Abstain	0

0612U: Oncology (liver), analysis of over 1,000 methylated regions, cell-free DNA from plasma, algorithm reported as a quantitative result	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0565U	11
	Gapfill	1
	Abstain	0

X292U: Cardiology (peripheral artery disease [PAD]), analysis of 3 proteins (midkine, angiopoietin-1, and kidney injury molecule-1 [KIM-1]), immunoassay,	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0308U	11
	Gapfill	0
	Abstain	1

0640U: Oncology (leptomeningeal metastases), tumor cell selection, identification, detection and enumeration based on differential	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0338U	12
	Gapfill	0
	Abstain	0

X261U: Tobacco use, DNA analysis of 2 methylation markers (1 content: cg05575921 [AHRR] and 1 normalizing: cg08141395), methylation-sensitive digital PCR, saliva, algorithm reported	Activity type	Multiple choice
	Total responses	12

	Unique participants	12
	Response options	Count
	Crosswalk to 0566U	2
	Gapfill	10
	Abstain	0
X263U: Tobacco use, DNA analysis of 1 methylation marker (cg05575921 [AHRR]), methylation-sensitive digital PCR, whole blood, algorithm reported as	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0566U	2
	Gapfill	10
	Abstain	0
X265U: Alcohol use disorder, DNA analysis of 4 methylation markers (cg02583484, cg04987734, cg09935388, cg04583842)	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0566U	2
	Gapfill	10
	Abstain	0
X273U: Oncology (lung cancer), DNA analysis of 1 methylation marker (cg05575921), methylation-sensitive digital PCR, whole blood, algorithm results reported as the 20-year-hazard ratio for lung cancer	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0566U	2
	Gapfill	10
	Abstain	0

X286U: Oncology (lung cancer), DNA analysis of 2 methylation markers (1 content: cg05575921 and 1 normalizing: cg08141395), methylation-sensitive digital PCR, saliva, algorithm

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0566U		1
Gapfill		11
Abstain		0

X293U: Alcohol use disorder, DNA analysis of 5 methylation markers

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0566U		2
Gapfill		10
Abstain		0

0606U: Hematology (red cell membrane disorders), RBCs, osmotic gradient ektacytometry, whole blood, quantitative

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0305U		11
Gapfill		1
Abstain		0

X259U: Hepatology (metabolic dysfunction-associated steatohepatitis [MASH]), enzyme-linked immunosorbent assay (ELISA) for YKL40 and quantitative reverse transcription polymerase chain reaction (RT-qPCR)

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0468U-(83883+83		11
Gapfill		1
Abstain		0

0616U: Neurology (dementia), DNA methylation analysis of more than 30,000 sites, whole blood, algorithm reported as positive or negative risk

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0020M	2
Crosswalk to 0565U	9
Crosswalk to 0318U	0
Gapfill	0
Abstain	1

0617U: Cardiovascular (atherosclerotic cardiovascular disease [ASCVD]), DNA methylation analysis of more than 20,000 sites, whole blood, algorithm reported as positive or negative risk

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0020M	1
Crosswalk to 0565U	10
Crosswalk to 0318U	0
Gapfill	0
Abstain	1

0618U: Psychiatry (bipolar disorder), DNA methylation analysis of more than 10,000 sites, whole blood, algorithm reported as positive or negative risk

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0020M	0
Crosswalk to 0565U	11
Crosswalk to 0318U	0
Gapfill	0
Abstain	1

0619U: Pulmonary (chronic obstructive pulmonary disease [COPD]), DNA methylation analysis of more than 18,000 sites, whole blood, algorithm reported as positive or negative risk

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0020M	0
Crosswalk to 0565U	11
Crosswalk to 0318U	0
Gapfill	0
Abstain	1

0620U: Oncology (hepatocellular carcinoma), DNA methylation analysis of more than 5,000 sites, whole blood, algorithm reported as positive or negative risk

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0020M	0
Crosswalk to 0565U	11
Crosswalk to 0318U	0
Gapfill	0
Abstain	1

0622U: Psychiatry (major depressive disorder), DNA methylation analysis of more than 20,000 sites, whole blood, algorithm reported as positive or negative risk

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0020M OR 0291U	0
Crosswalk to 0565U	11
Crosswalk to 0318U	0
Gapfill	0
Abstain	1

0623U: Autoimmune (multiple sclerosis), DNA methylation analysis of more than 5,000 sites, whole blood, algorithm reported as positive or negative risk

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0020M	0
Crosswalk to 0565U	11
Crosswalk to 0318U	0
Gapfill	0
Abstain	1

0624U: Hepatology (nonalcoholic steatohepatitis [NASH]), DNA methylation analysis of 5,000 sites, whole blood, algorithm reported as positive or negative risk

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0020M	0
Crosswalk to 0565U	11
Crosswalk to 0318U	0
Gapfill	0
Abstain	1

0625U: Endocrinology (osteoporosis), DNA methylation analysis of more than 5,000 sites, whole blood, algorithm reported as positive or negative risk

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0020M	0
Crosswalk to 0565U	11
Crosswalk to 0318U	0
Gapfill	0
Abstain	1

0626U: Neurology (Parkinson disease), DNA methylation analysis of more than 20,000 sites, whole blood, algorithm reported as positive or negative risk

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0020M	0
Crosswalk to 0565U	11
Crosswalk to 0318U	0
Gapfill	0
Abstain	1

0621U: Infectious disease (Lyme borreliosis), DNA methylation analysis of more than 10,000 sites, whole blood, algorithm reported as positive or negative risk

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0020M	0
Crosswalk to 0565U	11
Gapfill	0
Abstain	1

0627U: Psychiatry (schizophrenia), DNA methylation analysis of more than 15,000 sites, whole blood, algorithm reported as positive or negative risk

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0020M	0
Crosswalk to 0565U	11
Crosswalk to 0318U	0
Gapfill	0
Abstain	1

0600U: Infectious disease (wound infection), identification of 65 organisms and 30 antibiotic resistance genes, wound swab, real-time PCR, reported as positive or negative for each organism	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0593U x2	12
	Gapfill	0
	Abstain	0
X264U: Infectious disease (wound infection), DNA, multiplex real-time PCR, wound swab, detection of 27 microbial targets and 28 antibiotic resistance targets, reported as semiquantitative	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0593U	12
	Gapfill	0
	Abstain	0
X287U: Infectious disease (Bartonella species, Borrelia species, and Babesia species), multiplex digital PCR for detection of DNA at the genus level for each species, blood, qualitative reporting	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0301U × 3	12
	Gapfill	0
	Abstain	0
X255U: Rare diseases (constitutional/heritable disorders), whole exome and mitochondrial DNA sequence analysis, including small sequence changes,	Activity type	Multiple choice

	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0214U + 0215U	12
	Gapfill	0
	Abstain	0

X303U: Rare diseases (constitutional/heritable disorders), whole exome and mitochondrial DNA sequence analysis, including small sequence changes, deletions, duplications,

	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0214U + 2*0215U	11
	Gapfill	1
	Abstain	0

X250U: Rare diseases (constitutional/heritable disorders), whole genome and mitochondrial DNA sequence analysis, including small sequence changes, insertions/deletions, copy number variants, mobile element insertions,

	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0212U + 0213U	12
	Gapfill	0
	Abstain	0

X271U: Rare diseases (constitutional/heritable disorders), whole genome sequence analysis combination of short and long reads for single-nucleotide variants, insertions/deletions and characterized intronic variants, copy number variants,

	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count

Crosswalk to 0212U+0213U		4
Crosswalk to 0212U*2 + 0213U		1
Gapfill		7
Abstain		0

X285U: Rare diseases (constitutional/heritable disorders), whole genome sequence analysis, including small sequence changes, copy number variants, deletions, duplications, mobile element insertions,

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0335U + 0336U		12
Gapfill		0
Abstain		0

X272U: Rare diseases (constitutional/heritable disorders), whole genome and mitochondrial DNA sequence analysis, including small sequence changes, insertions/deletions, copy number variants,

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0212U + 2*0213U		11
Gapfill		1
Abstain		0

X302U: Rare diseases (constitutional/heritable disorders), whole genome sequence analysis combination of short and long reads for single-nucleotide variants

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0212U + 0213U*2		2
Crosswalk to 0212U*2 + 0213U*		3
Gapfill		7
Abstain		0

X291U: Rare diseases (constitutional/heritable disorders), whole genome sequence analysis, including small sequence changes, copy number variants, deletions, duplications, mobile element insertions,

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Cross walk to 0335U+0336U*2		7
Gapfill		5
Abstain		0

0657U: Rare diseases (constitutional/heritable disorders), rapid whole genome sequence analysis of comparator nuclear and mitochondrial DNA by next-generation sequencing (NGS),

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0425U		4
Crosswalk to 0213U		2
Crosswalk to 0583U		3
Gapfill		3
Abstain		0

0658U: Rare diseases (constitutional/heritable disorders), rapid whole genome sequence analysis of nuclear and mitochondrial DNA by next-generation sequencing (NGS)

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0094U		8
Crosswalk to 0212U		1
Crosswalk to 0532U		1
Gapfill		2
Abstain		0

0659U: Rare diseases (constitutional/heritable disorders), ultrarapid whole genome sequence analysis of nuclear and mitochondrial DNA by next-generation sequencing (NGS) for single-nucleotide variants (SNVs),	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 81425 * 1.65	2
	Crosswalk to 0212U	1
	Crosswalk to 0426U	8
	Gapfill	1
	Abstain	0
0607U: Reproductive medicine (endometrial microbiome assessment), real-time PCR analysis for 31 bacterial DNA targets from endometrial biopsy,	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0505U	2
	Gapfill	10
	Abstain	0
0608U: Reproductive medicine (endometrial microbiome assessment), real-time PCR analysis for 10 bacterial DNA targets from endometrial biopsy, reported with quantified levels	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0557U	2
	Gapfill	10
	Abstain	0
0562U: Oncology (solid tumor), targeted genomic sequence analysis, 33 genes, detection of single-nucleotide variants (snvs), insertions and deletions, copy-number amplifications,	Activity type	Multiple choice

	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0388U	0
	Crosswalk to 81462	12
	Gapfill	0
	Abstain	0

0648U: Oncology (solid tumor), targeted genomic sequencing analysis, to detect deletions, insertions, and substitutions in 42 genes, copy number amplifications in 10 genes,

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0022U	9
Gapfill	2
Abstain	1

X295U: Oncology (solid organ), targeted genomic sequence analysis, formalin-fixed paraffin-embedded (FFPE) tumor tissue, RNA analysis, 350 or more genes for RNA alterations (eg, gene rearrangements and splice isoforms)

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 81456	12
Gapfill	0
Abstain	0

0601U: Infectious disease (periprosthetic joint infection), analysis of 11 biomarkers (alpha defensins 1–3, C-reactive protein, microbial antigens for Staphylococcus [SPA, SPB], Enterococcus, Candida, and C. acnes, total nucleated cell count,

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0342U	2

	Gapfill	10
	Abstain	0

0610U: Infectious disease (antimicrobial susceptibility), phenotypic antimicrobial susceptibility testing of positive blood culture using microfluidic sensor technology to quantify bacterial growth	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Gapfill	12
	Abstain	0

0629U: Infectious disease (tuberculosis), DNA, analysis of 1 target by PCR with clustered regularly interspaced short palindromic repeat (CRISPR)-based probe detection, plasma or serum, qualitative report as detected or not detected	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Gapfill	12
	Abstain	0

X269U: Oncology (monoclonal gammopathy), immunoprecipitation and matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry, identification of intact monoclonal	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Gapfill	12
	Abstain	0

0628U: Nephrology (kidney disease-related genetic conditions), genomic analysis, renal disease panel, saliva, DNA, next-generation sequencing of 449 genes,

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 81455	1
Crosswalk to 81432	10
Gapfill	1
Abstain	0

0651U: Oncology (hereditary cancer), genomic DNA, 55 hereditary cancer pre-dispositioned genes, next-generation sequencing (NGS) and digital multiplex ligation-dependent probe amplification for variants,

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0474U	0
Crosswalk to 81432	12
Gapfill	0
Abstain	0

0653U: Nephrology (inherited kidney disorders), DNA, analysis of approximately 700 genes associated with inherited kidney diseases by exome sequencing,

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 81455	0
Crosswalk to 0474U	0
Crosswalk to 81432	12
Gapfill	0
Abstain	0

8XX19: Alport syndrome, genomic sequence analysis panel, must include COL4A3, COL4A4, and COL4A5,interrogation for sequence

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to (81407 + (81408 x		0
Crosswalk to 81407		0
Crosswalk to 81432		11
Gapfill		0
Abstain		1

X254U: Oncology (hereditary hematologic cancer), genomic DNA, whole genome sequence (single-nucleotide variants, deletions/insertions, and characterized intronic variants), copy number variants,

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0218U+88233+814		2
Crosswalk to 81432		3
Gapfill		7
Abstain		0

X280U: Oncology (hereditary cancer), genome sequence for 117 genes (single-nucleotide variants, deletions/insertions, and characterized intronic variants), copy number variants,

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0218U + 81435		2
Crosswalk to 0218U + 81432		0
Crosswalk to 81432		1
Crosswalk to 81435		2
Gapfill		7
Abstain		0

8XX17: Genetic testing for heritable immune conditions (eg, combined immunodeficiency/severe combined immunodeficiency, antibody deficiencies, autoinflammatory disorders, phagocytic disorders,

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 81443		0
Crosswalk to 81432		12
Gapfill		0
Abstain		0

8XX22: Genetic testing for heritable complement-mediated thrombotic microangiopathy (CM-TMA) (eg, atypical hemolytic uremic syndrome [aHUS], C3 glomerulopathy [C3G]), genomic sequence

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 81412		1
Crosswalk to 81432		11
Gapfill		0
Abstain		0

X279U: Carrier screening (cystic fibrosis, spinal muscular atrophy, beta hemoglobinopathies [including sickle cell disease], alpha thalassemia, and Duchenne muscular dystrophy),

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0449U		11
Gapfill		0
Abstain		1

X253U: Transplantation medicine (allograft rejection), quantification of donor-derived cell-free DNA (cfDNA) using digital PCR analysis of 45 single-nucleotide polymorphisms, plasma

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0493U		10
Crosswalk to 0055U		1
Gapfill		1
Abstain		0

0643U: Oncology (genitourinary cancer), cell-free circulating tumor DNA (ctDNA), 200 genes, next-generation sequencing (NGS), interrogation for single-nucleotide variants (SNVs),

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Crosswalk to 0539U		1
Crosswalk to 81464		9
Gapfill		1
Abstain		0
Crosswalk to 0539U * 1.3		1

0602U: Endocrinology (diabetes), insulin (INS) gene methylation using digital droplet PCR, insulin, and C-peptide immunoassay, serum, Hemoglobin A1c immunoassay, whole blood

Activity type	Multiple choice	
Total responses		12
Unique participants		12
Response options	Count	
Gapfill		12
Abstain		0

0649U: Neurology (Alzheimer disease), DNA, targeted next-generation sequencing (NGS) of AD-1 and AD-2 target regions, whole blood, prognostic algorithmic analysis, reported as categorization of cognitive status

Activity type	Multiple choice

	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0506U	0
	Gapfill	12
	Abstain	0

X268U: Oncology (prostate), mRNA, next-generation sequencing (NGS) gene expression profiling of 22 genes, formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reported as risk score

	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 81542	12
	Gapfill	0
	Abstain	0

X298U: Obesity, DNA genotyping, analysis of up to 41 genes, buccal swab or blood specimen, patient biometrics, risk-score algorithm to identify a predisposition to up to 4 phenotypes, reported as likelihood to benefit from therapeutics

	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0349U	0
	Crosswalk to 0466U	12
	Gapfill	0
	Abstain	0

0603U: Drug assay, presumptive, 77 drugs or metabolites, urine, liquid chromatography with tandem mass spectrometry (LC-MS/MS), results reported as positive or negative

	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 80307	11

	Gapfill	1
	Abstain	0

0613U: Oncology (urothelial carcinoma), DNA methylation and mutation analysis of 6 biomarkers (TWIST1, OTX1, ONECUT2, FGFR3, HRAS, TERT promoter region),	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0420U	12
	Gapfill	0
	Abstain	0

0632U: Red blood cell antigen (fetal RhD gene analysis), multiplex polymerase chain reaction (PCR) and next-generation sequencing (NGS) of circulating cell-free DNA (cfDNA), plasma	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0488U	10
	Gapfill	1
	Abstain	1

0633U: Obstetrics (single-gene noninvasive prenatal test), cell-free DNA (cfDNA), next-generation sequencing (NGS) analysis of 1 or more targets (eg, CFTR, SMN1, HBB, HBA1,	Activity type	Multiple choice
	Total responses	12
	Unique participants	12
	Response options	Count
	Crosswalk to 0489U	10
	Gapfill	0
	Abstain	2

X256U: Obstetrics (fetal platelet antigen noninvasive prenatal test [NIPT]), cell-free DNA (cfDNA) sequence analysis for detection of fetal presence or absence of 1 human

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 0488U	11
Gapfill	0
Abstain	1

0631U: Oncology (solid tumor), DNA, sequence analysis of 15 genes including BRCA1 and BRCA2 for identification of clonal

Activity type	Multiple choice
Total responses	12
Unique participants	12
Response options	Count
Crosswalk to 81162	0
Crosswalk to 81443	0
Crosswalk to 81462	0
Gapfill	11
Abstain	1