

Consent Agenda 1:

Motion that the Panel adopt the recommended determinations for the codes listed below as a single motion, any member being free to request that a code be withdrawn for separate consideration (339 codes).

- Original crosswalk maintained (156 codes)
- Original gapfill maintained (107 codes)
- Code with no usable prior basis, to gapfill (76 codes)

Original crosswalk maintained (156 codes)

0007U	0011M	0017M	0017U	0025U	0032U	0036U	0039U
0040U	0051U	0052U	0054U	0061U	0069U	0093U	0096U
0107U	0110U	0111U	0113U	0130U	0154U	0166U	0169U
0176U	0177U	0181U	0182U	0183U	0184U	0185U	0186U
0187U	0188U	0189U	0190U	0191U	0192U	0193U	0194U
0195U	0196U	0197U	0198U	0199U	0200U	0201U	0203U
0205U	0209U	0218U	0227U	0229U	0230U	0231U	0232U
0233U	0234U	0235U	0236U	0237U	0238U	0246U	0259U
0275U	0287U	0289U	0290U	0293U	0294U	0298U	0316U
0321U	0323U	0327U	0342U	0343U	0362U	0371U	0372U
0377U	0385U	0387U	0394U	0405U	0409U	0421U	0424U
0427U	0429U	0437U	0442U	0444U	0452U	0453U	0458U
0469U	0494U	0495U	0497U	0499U	0500U	0502U	0504U
0505U	0514U	0515U	0517U	0518U	0519U	0520U	0521U
0527U	0530U	0535U	0536U	0538U	0545U	0546U	0549U
0557U	0558U	0559U	0563U	0564U	0568U	0570U	0571U
0575U	0576U	0579U	0581U	0584U	0585U	0586U	0588U
0589U	0591U	0592U	0593U	0595U	0599U	81172	81190
81274	81289	81337	81349	81523	87494	87812	P2028

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P2029	P2033	P2038	Q0115				
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Original gapfill maintained (107 codes)

0018M	0019U	0021U	0022U	0055U	0062U	0083U	0102U
0103U	0114U	0121U	0122U	0123U	0133U	0136U	0137U
0153U	0156U	0157U	0158U	0159U	0160U	0161U	0162U
0164U	0165U	0171U	0178U	0179U	0212U	0213U	0214U
0215U	0216U	0217U	0222U	0226U	0228U	0245U	0248U
0253U	0254U	0255U	0262U	0265U	0266U	0268U	0269U
0270U	0271U	0272U	0273U	0274U	0277U	0285U	0291U
0292U	0297U	0301U	0302U	0303U	0304U	0305U	0306U
0307U	0314U	0333U	0341U	0368U	0381U	0383U	0389U
0395U	0399U	0400U	0401U	0408U	0417U	0436U	0439U
0440U	0441U	0463U	0466U	0470U	0478U	0483U	0484U
0496U	0498U	0501U	0526U	0529U	0531U	0534U	0542U
0552U	0569U	0572U	0574U	0590U	0594U	0597U	81493
81524	81560	87182					

Code with no usable prior basis, to gapfill (76 codes)

0004M	0007M	0082U	0116U	0170U	0258U	0260U	0264U
0267U	0296U	0299U	0300U	0317U	0328U	0331U	0335U
0336U	0391U	0413U	0435U	0454U	0465U	0467U	0506U
0511U	0523U	0525U	0553U	0554U	0555U	0560U	0561U
0566U	0567U	0587U	0598U	80190	81195	81354	81504
81535	81536	82143	82286	82387	82415	82485	82965
82979	83045	83633	83661	83662	83775	83857	83987

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84085	84138	84203	84233	84234	84375	84488	84577
87152	88147	88152	88153	88166	88167	88371	88372
89329	G0147	G9143	P2031				

Consent Agenda 2:

Each is recommended for a crosswalk to a target the code has not previously used. The Panel is selecting a comparator, so these are not consent-agenda items, but they share a common posture and may be taken as one motion (75 codes).

- New crosswalk block (75 codes)

Code	Recommended crosswalk
0002U	0256U
0003U	81503
0009U	88271 x 2
0019M	0309U
0030U	81227, 81355
0048U	81455
0050U	81455
0063U	0344U
0092U	0407U
0095U	81500
0105U	0308U
0117U	0344U
0163U	0308U
0174U	0344U
0180U	81405
0221U	81404
0244U	81455
0247U	0256U

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Code	Recommended crosswalk
0249U	0344U
0252U	81265
0263U	0344U
0286U	81306, 81335
0310U	0308U
0319U	0320U
0322U	0344U
0384U	0503U
0388U	81462
0573U	81517
80406	82533 x 2, 84143 x 2
80410	82308 x 3
80412	82533 x 6, 82024 x 6
80416	84244 x 6
80418	82024 x 4, 83002 x 4, 83001 x 4, 84146 x 4, 83003 x 4, 82533 x 4, 84443 x 4
80432	83525, 84681 x 5, 82947 x 5
80434	82533 x 5, 82947 x 5
81313	81315
81341	81262
81346	81227
81427	81417
84379	84378 x 2
84485	82977
85170	85175 x 0.8
85337	83530
85475	86940

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Code	Recommended crosswalk
85536	85044
86155	86344
86408	86769
86409	86769
86590	86406
86732	86612
86771	86625
87003	87250
87164	87166
87267	87260
87271	87273
87283	87279
87320	87808
87391	87390
87472	87487
87475	87540
87495	87531
87525	87520
87526	87521
87527	87522
87528	87531
87534	87520
87537	87520
87552	87542
87557	87542
87562	87542

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Code	Recommended crosswalk
87850	87808
88130	87209
88245	88248
88741	88740
89330	89300

Codes Not Included in the Consent Agenda

FACA Mtg. Order	Block	Code #	Long Code Descriptor	Ballot Options
1	Block 1	0173U	Psychiatry (ie, depression, anxiety), genomic analysis panel, includes variant analysis of 14 genes	1. Abstain 2. Gapfill 3. Crosswalk to 81418
2		0175U	Psychiatry (eg, depression, anxiety), genomic analysis panel, variant analysis of 15 genes	1. Abstain 2. Gapfill 3. Crosswalk to 81418
3		0392U	Drug metabolism (depression, anxiety, attention deficit hyperactivity disorder [adhd]), gene-drug interactions, variant analysis of 16 genes, including deletion/duplication analysis of cyp2d6, reported as impact of gene-drug interaction for each drug	1. Abstain 2. Gapfill 3. Crosswalk to 81418
4		0423U	Psychiatry (eg, depression, anxiety), genomic analysis panel, including variant analysis of 26 genes, buccal swab, report including metabolizer status and risk of drug toxicity by condition	1. Abstain 2. Gapfill 3. Crosswalk to 81418
5		0438U	Drug metabolism (adverse drug reactions and drug response), buccal specimen, gene-drug interactions, variant analysis of 33 genes, including deletion/duplication analysis of cyp2d6, including reported phenotypes and impacted gene-drug interactions	1. Abstain 2. Gapfill 3. Crosswalk to 81418
6		0460U	Oncology, whole blood or buccal, dna single-nucleotide polymorphism (snp) genotyping by real-time pcr of 24 genes, with variant analysis and reported phenotypes	1. Abstain 2. Gapfill 3. Crosswalk to 81418
7		0461U	Oncology, pharmacogenomic analysis of single-nucleotide polymorphism (snp) genotyping by real-time pcr of 24 genes, whole blood or buccal swab, with variant analysis, including impacted gene-drug interactions and reported phenotypes	1. Abstain 2. Gapfill 3. Crosswalk to 81418
8		0476U	Drug metabolism, psychiatry (eg, major depressive disorder, general anxiety disorder, attention deficit hyperactivity disorder [adhd], schizophrenia), whole blood, buccal swab, and pharmacogenomic genotyping of 14 genes and cyp2d6 copy number variant analysis and reported phenotypes	1. Abstain 2. Gapfill 3. Crosswalk to 81418

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FACA Mtg. Order	Block	Code #	Long Code Descriptor	Ballot Options
9		0477U	Drug metabolism, psychiatry (eg, major depressive disorder, general anxiety disorder, attention deficit hyperactivity disorder [adhd], schizophrenia), whole blood, buccal swab, and pharmacogenomic genotyping of 14 genes and cyp2d6 copy number variant analysis, including impacted gene-drug interactions and reported phenotypes	1. Abstain 2. Gapfill 3. Crosswalk to 81418
10		0516U	Drug metabolism, whole blood, pharmacogenomic genotyping of 40 genes and cyp2d6 copy number variant analysis, reported as metabolizer status	1. Abstain 2. Gapfill 3. Crosswalk to 81418
11		0533U	Drug metabolism (adverse drug reactions and drug response), genotyping of 16 genes (ie, abcg2, cyp2b6, cyp2c9, cyp2c19, cyp2c, cyp2d6, cyp3a5, cyp4f2, dpyd, g6pd, ggcx, nudt15, slco1b1, tpmt, ugt1a1, vkorc1), reported as metabolizer status and transporter function	1. Abstain 2. Gapfill 3. Crosswalk to 81418
12	Block 2	0220U	Oncology (breast cancer), image analysis with artificial intelligence assessment of 12 histologic and immunohistochemical features, reported as a recurrence score	1. Abstain 2. Gapfill 3. Crosswalk to 0376U
13		0261U	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	1. Abstain 2. Gapfill 3. Crosswalk to 0376U
14		0414U	Oncology (lung), augmentative algorithmic analysis of digitized whole slide imaging for 8 genes (alk, braf, egfr, erbb2, met, ntrk1-3, ret, ros1), and kras g12c and pd-l1, if performed, formalin-fixed paraffin-embedded (ffpe) tissue, reported as positive or negative for each biomarker	1. Abstain 2. Gapfill 3. Crosswalk to 0376U
15		0418U	Oncology (breast), augmentative algorithmic analysis of digitized whole slide imaging of 8 histologic and immunohistochemical features, reported as a recurrence score	1. Abstain 2. Gapfill 3. Crosswalk to 0376U
16		0512U	Oncology (prostate), augmentative algorithmic analysis of digitized whole-slide imaging of histologic features for microsatellite instability (msi) status, formalin-fixed paraffinembedded (ffpe) tissue, reported as increased or decreased probability of msi-high (msi-h)	1. Abstain 2. Gapfill 3. Crosswalk to 0376U

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FACA Mtg. Order	Block	Code #	Long Code Descriptor	Ballot Options
17		0513U	Oncology (prostate), augmentative algorithmic analysis of digitized whole-slide imaging of histologic features for microsatellite instability (msi) and homologous recombination deficiency (hrd) status, formalin-fixed paraffin-embedded (ffpe) tissue, reported as increased or decreased probability of each biomarker	1. Abstain 2. Gapfill 3. Crosswalk to 0376U
18	Block 3	0094U	Genome (eg, unexplained constitutional or heritable disorder or syndrome), rapid sequence analysis	1. Abstain 2. Gapfill 3. Crosswalk to 81425 x 1.5
19		0426U	Genome (eg, unexplained constitutional or heritable disorder or syndrome), ultra-rapid sequence analysis	1. Abstain 2. Gapfill 3. Crosswalk to 81425 x 1.5
20		0532U	Rare diseases (constitutional disease/hereditary disorders), rapid whole genome and mitochondrial dna sequencing for singlenucleotide variants, insertions/deletions, copy number variations, peripheral blood, buffy coat, saliva, buccal or tissue sample, results reported as positive or negative	1. Abstain 2. Gapfill 3. Crosswalk to 81425 x 1.5
21		0582U	Rare diseases (constitutional disease/hereditary disorders), rapid whole genome dna sequencing for singlenucleotide variants, insertions/deletions, copy number variations, blood, saliva, tissue sample, variants reported	1. Abstain 2. Gapfill 3. Crosswalk to 81425 x 1.5
22		0425U	Genome (eg, unexplained constitutional or heritable disorder or syndrome), rapid sequence analysis, each comparator genome (eg, parents, siblings)	1. Abstain 2. Gapfill 3. Crosswalk to 81426 x 1.5
23		0583U	Rare diseases (constitutional disease/hereditary disorders), rapid whole genome comparator dna sequencing for single-nucleotide variants, insertions/deletions, copy number variations, blood, saliva, tissue sample, variants reported with proband results (list separately in addition to code for primary procedure)	1. Abstain 2. Gapfill 3. Crosswalk to 81426 x 1.5

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FACA Mtg. Order	Block	Code #	Long Code Descriptor	Ballot Options
24	Block 4	0072U	Cyp2d6 (cytochrome p450, family 2, subfamily d, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, cyp2d6-2d7 hybrid gene) (list separately in addition to code for primary procedure)	1. Abstain 2. Gapfill 3. Crosswalk to 81226 (maintain existing) 4. Crosswalk to 81238
25		0073U	Cyp2d6 (cytochrome p450, family 2, subfamily d, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, cyp2d7-2d6 hybrid gene) (list separately in addition to code for primary procedure)	1. Abstain 2. Gapfill 3. Crosswalk to 81226 (maintain existing) 4. Crosswalk to 81238
26		0074U	Cyp2d6 (cytochrome p450, family 2, subfamily d, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, non-duplicated gene when duplication/multiplication is trans) (list separately in addition to code for primary procedure)	1. Abstain 2. Gapfill 3. Crosswalk to 81226 (maintain existing) 4. Crosswalk to 81238
27		0075U	Cyp2d6 (cytochrome p450, family 2, subfamily d, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, 5' gene duplication/multiplication) (list separately in addition to code for primary procedure)	1. Abstain 2. Gapfill 3. Crosswalk to 81226 (maintain existing) 4. Crosswalk to 81238
28		0076U	Cyp2d6 (cytochrome p450, family 2, subfamily d, polypeptide 6) (eg, drug metabolism) gene analysis, targeted sequence analysis (ie, 3' gene duplication/ multiplication) (list separately in addition to code for primary procedure)	1. Abstain 2. Gapfill 3. Crosswalk to 81226 (maintain existing) 4. Crosswalk to 81238
29	Block 5	0365U	Oncology (bladder), 10 protein biomarkers (alat, ang, apoe, ca9, il8, mmp9, mmp10, pai1, sdc1 and vegfa), by immunoassays, urine, diagnostic algorithm, including patient's age, race and gender, reported as a probability of harboring urothelial cancer	1. Abstain 2. Gapfill 3. Crosswalk to 81503 (maintain existing) 4. Crosswalk to 0446U

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FACA Mtg. Order	Block	Code #	Long Code Descriptor	Ballot Options
30		0366U	Oncology (bladder), analysis of 10 protein biomarkers (a1at, ang, apoe, ca9, il8, mmp9, mmp10, pail, sdc1 and vegfa) by immunoassays, urine, algorithm reported as a probability of recurrent bladder cancer	1. Abstain 2. Gapfill 3. Crosswalk to 81503 (maintain existing) 4. Crosswalk to 0446U
31		0367U	Oncology (bladder), analysis of 10 protein biomarkers (a1at, ang, apoe, ca9, il8, mmp9, mmp10, pail, sdc1 and vegfa) by immunoassays, urine, diagnostic algorithm reported as a risk score for probability of rapid recurrence of recurrent or persistent cancer following transurethral resection	1. Abstain 2. Gapfill 3. Crosswalk to 81503 (maintain existing) 4. Crosswalk to 0446U
32	Block 6	0410U	Oncology (pancreatic), dna, whole genome sequencing with 5-hydroxymethylcytosine enrichment, whole blood or plasma, algorithm reported as cancer detected or not detected	1. Abstain 2. Gapfill 3. Crosswalk to 81229
33		0507U	Oncology (ovarian), dna, wholegenome sequencing with 5hydroxymethylcytosine (5hmc) enrichment, using whole blood or plasma, algorithm reported as cancer detected or not detected	1. Abstain 2. Gapfill 3. Crosswalk to 81229
34		0565U	Oncology (hepatocellular carcinoma), next-generation sequencing methylation pattern assay to detect 6626 epigenetic alterations, cell-free dna, plasma, algorithm reported as cancer signal detected or not detected	1. Abstain 2. Gapfill 3. Crosswalk to 81229
35		0010U	Infectious disease (bacterial), strain typing by whole genome sequencing, phylogenetic-based report of strain relatedness, per submitted isolate	1. Abstain 2. Gapfill 3. Crosswalk to 87153 x 3
36		0140U	Infectious disease (fungi), fungal pathogen identification, dna (15 fungal targets), blood culture, amplified probe technique, each target reported as detected or not detected	1. Abstain 2. Gapfill 3. Crosswalk to 87154
37		0224U	Antibody, severe acute respiratory syndrome coronavirus 2 (sars-cov-2) (coronavirus disease [covid-19]), includes titer(s), when performed	1. Abstain 2. Gapfill 3. Crosswalk to 86769

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38		0016U	Oncology (hematolymphoid neoplasia), rna, bcr/abl1 major and minor breakpoint fusion transcripts, quantitative pcr amplification, blood or bone marrow, report of fusion not detected or detected with quantitation	1. Abstain 2. Gapfill 3. Crosswalk to 81206 (maintain existing) 4. Crosswalk to 81206 + 81207
39		0020M	Oncology (central nervous system), analysis of 30000 dna methylation loci by methylation array, utilizing dna extracted from tumor tissue, diagnostic algorithm reported as probability of matching a reference tumor subclass	1. Abstain 2. Gapfill 3. Crosswalk to 0016M x 0.75
40		0464U	Oncology (colorectal) screening, quantitative real-time target and signal amplification, methylated dna markers, including lass4, lrrc4 and ppp2r5c, a reference marker zdhhc1, and a protein marker (fecal hemoglobin), utilizing stool, algorithm reported as a positive or negative result	1. Abstain 2. Gapfill 3. Crosswalk to 81327 x 3 + 82274 4. Crosswalk to 0433U 5. Crosswalk to 0005U 6. Crosswalk to 0339U 7. Crosswalk to 81528
41		0251U	Hepcidin-25, enzyme-linked immunosorbent assay (elisa), serum or plasma	1. Abstain 2. Gapfill 3. Crosswalk to 83520 (maintain existing) 4. Crosswalk to 84305
42		0390U	Obstetrics (preeclampsia), kinase insert domain receptor (kdr), endoglin (eng), and retinol-binding protein 4 (rbp4), by immunoassay, serum, algorithm reported as a risk score	1. Abstain 2. Gapfill 3. Crosswalk to 0243U (maintain existing) 4. Crosswalk to 81510

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43		0415U	Cardiovascular disease (acute coronary syndrome [acs]), il-16, fas, fasligand, hgf, ctack, eotaxin, and mcp-3 by immunoassay combined with age, sex, family history, and personal history of diabetes, blood, algorithm reported as a 5-year (deleted risk) score for acs	1. Abstain 2. Gapfill 3. Crosswalk to 0309U (maintain existing) 4. Crosswalk to 0375U
44		0445U	B-amyloid (abeta42) and phospho tau (181p) (ptau181), electrochemiluminescent immunoassay (eclia), cerebral spinal fluid, ratio reported as positive or negative for amyloid pathology	1. Abstain 2. Gapfill 3. Crosswalk to 0358U (maintain existing) 4. Crosswalk to 82234 + 84393
45		0459U	B-amyloid (abeta42) and total tau (ttau), electrochemiluminescent immunoassay (eclia), cerebral spinal fluid, ratio reported as positive or negative for amyloid pathology	1. Abstain 2. Gapfill 3. Crosswalk to 0358U (maintain existing) 4. Crosswalk to 82234 + 84394
46		0462U	Melatonin levels test, sleep study, 7 or 9 sample melatonin profile (cortisol optional), enzyme-linked immunosorbent assay (elisa), saliva, screening/preliminary	1. Abstain 2. Gapfill 3. Crosswalk to 83520 (maintain existing) 4. Crosswalk to 82530
47		0471U	Oncology (colorectal cancer), qualitative real-time pcr of 35 variants of kras and nras genes (exons 2, 3, 4), formalinfixxed paraffin-embedded (ffpe), predictive, identification of detected mutations	1. Abstain 2. Gapfill 3. Crosswalk to 0005U (maintain existing) 4. Crosswalk to 81275 + 81276 + 81311

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48		0539U	Oncology (solid tumor), cellfree circulating tumor dna (ctdna), 152 genes, nextgeneration sequencing, interrogation for singlenucleotide variants, insertions/deletions, gene rearrangements, copy number alterations, and microsatellite instability, using whole-blood samples, mutations with clinical actionability reported as actionable variant	1. Abstain 2. Gapfill 3. Crosswalk to 81464 (maintain existing) 4. Crosswalk to 0326U
49		0547U	Neurofilament light chain (nfl), chemiluminescent enzyme immunoassay, plasma, quantitative	1. Abstain 2. Gapfill 3. Crosswalk to 0361U (maintain existing) 4. Crosswalk to 0443U
50		0548U	Glial fibrillary acidic protein (gfap), chemiluminescent enzyme immunoassay, using plasma	1. Abstain 2. Gapfill 3. Crosswalk to 0361U (maintain existing) 4. Crosswalk to 83884
51		0556U	Infectious disease (bacterial or viral respiratory tract infection), pathogen-specific dna and rna by real-time pcr, 12 targets, nasopharyngeal or oropharyngeal swab, including multiplex reverse transcription for rna targets, each analyte reported as detected or not detected	1. Abstain 2. Gapfill 3. Crosswalk to 81513 (maintain existing) 4. Crosswalk to 87633
52		0580U	Borrelia burgdorferi (lyme disease), antibody detection of 31 recombinant protein groups, by immunoassay, igg	1. Abstain 2. Gapfill 3. Crosswalk to 0042U (maintain existing) 4. Crosswalk to 0042U x 2
53		0562U	Oncology (solid tumor), targeted genomic sequence analysis, 33 genes, detection of single-nucleotide variants (snvs), insertions and deletions, copy-number amplifications, and translocations in human genomic circulating cell-free dna, plasma, reported as presence of actionable variants	1. Abstain 2. Gapfill 3. Crosswalk to 81445 (maintain existing) 4. Crosswalk to 81462

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54		0578U	Oncology (cutaneous melanoma), rna, gene expression profiling by realtime qpcr of 10 genes (8 content and 2 housekeeping), utilizing formalin-fixed paraffin-embedded (ffpe) tissue, algorithm reports a binary result, either low-risk or high-risk for sentinel lymph node metastasis and recurrence	1. Abstain 2. Gapfill 3. Crosswalk to 81519
55		0596U	Neurology (alzheimer disease), plasma, 3 distinct isoform-specific peptides (apoe2, apoe3, and apoe4) by liquid chromatography with tandem mass spectrometry (lcms/ms), reported as an apoe prototype	1. Abstain 2. Gapfill 3. Crosswalk to 81401
56		81188	Cstb (cystatin b) (eg, unverricht-lundborg disease) gene analysis; evaluation to detect abnormal (eg, expanded) alleles	1. Abstain 2. Gapfill 3. Crosswalk to 81178 4. Crosswalk to 81404
57		87183	Sc std carbapenem resist gen	1. Abstain 2. Gapfill 3. Crosswalk to 87150 (maintain existing) 4. Crosswalk to 87150 x 5
58		87627	Jt spc pthgn&rx resist gen26+	1. Abstain 2. Gapfill 3. Crosswalk to 0528U (maintain existing) 4. Crosswalk to 87507 + 87506 5. Crosswalk to 87633