Association for Molecular Pathology and College of American Pathologists Comments on New Code Crosswalks

2015 Advisory Panel on Clinical Diagnostic Laboratory Tests

August 26, 2015

AMP Association for Molecular Pathology

College of American Pathologists

Association for Molecular Pathology

- Professional scientific society that advances the clinical practice, science, and excellence of molecular and genomic laboratory medicine through education, innovation, and advocacy to enable highest quality health care.
- AMP represents more than 2,300 physicians, scientists, technologists and students who perform molecular diagnostic procedures.

AMP Association for Molecular Pathology

AMP Closely Involved with the AMA to Develop CPT Codes for Molecular Pathology Procedures

AMP responsible for:

- Submitting the initial proposal to the AMA CPT Editorial panel for development of the Genomic Sequencing Procedure (GSP) CPT codes.
- Submitting the framework for the Molecular Pathology Tier 1 and Tier 2 CPT code structure.
- Participating in the AMA advisory group and submitting additional code change proposals for new molecular pathology and GSPs procedures as new diagnostic methods evolve.

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College of American Pathologists

- Representing more than 18,000 physicians who practice anatomic and/or clinical pathology, CAP is the largest national pathology professional organization composed exclusively of pathologists.
- College members practice their specialty in clinical laboratories, academic medical centers, research laboratories, community hospitals and federal and state health facilities.

COLLEGE of AMERICAN PATHOLOGISTS

Genomic Sequencing Procedures Rationale for Crosswalk Recommendation

Crosswalk =

(single gene sequencing code times a multiplier)

Plus

(bioinformatic-based code times a multiplier)

1. Based on relativity of resources to 81292 for the MLH1 gene
   - has representative number of exons (21) and coding sequence (2271 base pairs) for a gene.
   - **genomic sequencing procedures are approximately one-fifth or 20% of the cost compared to equivalently sized traditional Sanger sequencing methods.**

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2. Bioinformatic Component

- Based on relativity of resources to 87900 HIV Infectious agent drug susceptibility phenotype prediction using regularly updated genotypic bioinformatics
  - Consists of the analysis of two HIV genes or approximate 1620 nucleotides similar to the amount of coverage in 81292.
  - The method and resources of analyzing the nucleotide sequence to understand the alterations and predict the impact overlaps very closely with the activity and resources involved in the bioinformatic analysis for genomic sequencing procedures and is relative to the amount of data being generated in the particular procedure.

Genomic Sequencing Procedures Rationale for Crosswalk Recommendation

Crosswalk =

(81292 code times a multiplier)

Plus

(87900 times a multiplier)

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3. Multiplier

Is based on the amount of genetic material sequenced times 20%

Example: 81410

Code	CPT Descriptor
81410	Aortic dysfunction or dilation (e.g., Marfan syndrome, Loeys Dietz syndrome, Ehler Danlos syndrome type IV, arterial tortuosity syndrome); genomic sequence analysis panel, must include sequencing of at least 9 genes, including FBN1, TGFBR1, TGFBR2, COL3A1, MYH11, ACTA2, SLC2A10, SMAD3, and MYLK

- the minimum required genes for 81410 is 9 and totals 240 exons.
- 20% of 240 is 48 exons.
- This is approximately 2 times the number of exons for the *MLH1* gene in 81292 and the genetic material for 87900.
- Thus the multiplier is 2 for both: (81292 times 2) plus (87900 times 2)

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4. Economies of Scale

- In calculating the minimum required exons per genomic sequencing procedure and applying the 80% reduction to determine the crosswalk, we identified that the natural log of the number of minimum genes was almost identical
  - In the above example the natural log (ln) of 9 genes is 2.198 similar to the multiplier we had determined.
- Furthermore, the resources for genomic sequencing procedures do not increase linearly with greater numbers of gene targets.
- Applying the natural logarithm to the number of genes per procedure scales the resource with increasing numbers of genes.

Example: Recommendation for Hearing Loss Genomic Sequence Analysis (81430)

GSP recommendation = (81292* multiplier) + (87900 * multiplier)
Multiplier= ln(Min # of genes)

For code 81430, a minimum of 60 genes is required.
Multiplier for 81430 = ln(60) = 4.09
Crosswalk recommendation for GSP code 81430 = (81292*4) + (87900*4)

Code	CPT Descriptor	Rationale	Recommendation
81430	Hearing loss (e.g., nonsyndromic hearing loss, Usher syndrome, Pendred syndrome); genomic sequence analysis panel, must include sequencing of at least 60 genes, including CDH23, CLRN1, GJB2, GPR98, MTRNR1, MYO7A, MYO15A, PCDH15, OTOF, SLC26A4, TMC1, TMPRSS3, USH1C, USH1G, USH2A, and WFS1	Min of 60 genes ln(60) = 4	Crosswalk to 81292 x 4 plus 87900 x 4

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