AACC 2019 CPT Crosswalk Recommendations

New 2018 CPT Code	New Code Desciption	Test Purpose & Method	AACC Crosswalk Recommendation	Rationale	Proposed NLA - 2019
Reconsider					
81334	RUNX1 (runt related transcription factor 1) (eg, acute myeloid leukemia, familial platelet disorder with associated myeloid malignancy), gene analysis, targeted sequence analysis (eg, exons 3-8).	Purpose: To detect somatic mutations in genes associated with the diagnosis or prognosis of certain heatologic malignancies. Method: PCR amplification followed by a genotyping method (i.e., Sanger sequencing).	**81259** (HBA1/HBA2 (alpha globin 1 and alpha globin 2) (eg, alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; full gene sequence)	The test methods used for sequencing analysis and the amount of DNA sequenced are comparable to that for 81259.	$600.00
81326	PMP22 (peripheral myelin protein 22) (eg, Charcot-Marie-Tooth, hereditary neuropathy with liability to pressure palsies) gene analysis; known familial variant.	Purpose: To detect known familial variants in a patient suspected of being affected by autosomal dominant Charcot-Marie-Tooth or a related neuropathy. Method: For point mutations, PCR amplification and genotyping analysis is used. For del/dup analysis, a multiplex ligation dependent probe amplification (MLPA) is used.	**81215** (BRCA1 (breast cancer 1) (eg, hereditary breast and ovarian cancer) gene analysis; known familial variant)	Similar methodologies and resources are used to detect known variants in BRCA which can be both point mutations or del/dups. Both conditions are autosomal dominant.	$375.25
Tier 1 Molecular Pathology					
8X001	AFF2 (AF4/FMR2 family, member 2 [FMR2]) (eg, fragile X mental retardation 2 [FRAXE]) gene analysis; evaluation to detect abnormal (eg, expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00
8X002	AFF2 (AF4/FMR2 family, member 2 [FMR2]) (eg, fragile X mental retardation 2 [FRAXE]) gene analysis; characterization of alleles (eg, expanded size and methylation status)	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Southern Blot.	**81404** (Molecular pathology procedure, Level 5)	The methodology and amount of work used to characterize the size of the triplet expansion is identical to that described by the Tier 2, level 5 code which is how this procedure was previously coded.	$274.83

8X003	AR (androgen receptor) (eg, spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation) gene analysis; characterization of alleles (eg, expanded size or methylation status)	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00
8X004	AR (androgen receptor) (eg, spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation) gene analysis; full gene sequence	Purpose: To detect variants (eg, SNVs, indels) within the entire gene. Method: Bi-directional sequencing of coding regions as well as exon-intron junctions by sanger sequencing or next generation sequencing.	**81405** (Molecular pathology procedure, Level 6)	The test methods used for sequencing analysis and the amount of DNA sequenced are comparable to that of 81405, which is how this procedure was previously coded. 8X004 is comprised of 5 exons.	$301.35
8X005	AR (androgen receptor) (eg, spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation) gene analysis; known familial variant	Purpose: To detect specific known variant(s) in a gene. Method: PCR amplification followed by a targeted genotyping method (ie, Sanger Sequencing).	**81403** (molecular pathology prodecure level 4)	The test methods used for sequencing analysis and the amount of DNA sequenced are comparable to that of 81403, which is how this procedure was previously coded.	$185.20
8X006	ATN1 (atrophin 1) (eg, dentatorubral-pallidoluysian atrophy) gene analysis, evaluation to detect abnormal (eg, expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00
8X007	ATXN1 (ataxin 1) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00

8X008	ATXN10 (ataxin 10) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00
8X009	ATXN2 (ataxin 2) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00
8X010	ATXN3 (ataxin 3) (eg, spinocerebellar ataxia, Machado-Joseph disease) gene analysis, evaluation to detect abnormal (eg, expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00
8X011	ATXN7 (ataxin 7) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00
8X012	ATXN8OS (ATXN8 opposite strand [non-protein coding]) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00

81X78	BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis	Purpose: To detect variants (SNVs and small indels) within one or both BRCA genes in their entirety. Method: Full gene sequencing: Bi-directional sequencing of coding regions as well as exon-introl junctions by Sanger sequencing or next generation sequencing. Del/Dup analysis: Generally Muliplexed Ligation-dependent Probe Amplification (MLPA).	**81408** DMD (dystrophin) (eg, Duchenne/Becker muscular dystrophy), full gene sequence; Molecular Pathology Procedure, Level 9	The methodology and amount of DNA sequenced is comparable to the sequencing of the large gene DMD.	$2,000.00
81X79	BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full duplication/deletion analysis (ie, detection of large gene rearrangements)	Generally Multiplexed Ligation-dependent Probe Amplification (MLPA)	**81213** BRCA 1, BRCA 2 (breast cancer 1 and 2) (eg, hereditary breast and ovarian cancer) gene analysis; uncommon duplication/deletion variants	The methodology used for detection of Dup/Dels is the same as the previously used code for BRCA1/2 Dup/del uncommon analysis.	$553.00
81X81	BRCA1 (BRCA1, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis	Purpose: To detect variants (SNVs and small indels) within one or both BRCA genes in their entirety. Method: Full gene sequencing: Bi-directional sequencing of coding regions as well as exon-introl junctions by Sanger sequencing or next generation sequencing. Del/Dup analysis: Generally Muliplexed Ligation-dependent Probe Amplification (MLPA).	**81408 x 0.5**	The methodology and amount of DNA sequenced is comparable to half that of the sequencing of the large gene DMD.	$1,000.00

81X82	BRCA1 (BRCA1, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full duplication/deletion analysis (ie, detection of large gene rearrangements)	Generally Multiplexed Ligation-dependent Probe Amplification (MLPA)	**81213 x 0.5**	The methodology used for detection of Dup/Dels is the same as the previously used code for BRCA1/2 Dup/del uncommon analysis.	$276.50
81X83	BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full duplication/deletion analysis (ie, detection of large gene rearrangements)	Generally Multiplexed Ligation-dependent Probe Amplification (MLPA)	**81213 x 0.5**	The methodology used for detection of Dup/Dels is the same as the previously used code for BRCA1/2 Dup/del uncommon analysis.	$276.50
81X09	BTK (Bruton's tyrosine kinase) (eg, chronic lymphocytic leukemia) gene analysis, common variants (eg, C481S, C481R, C481F)	Purpose: To detect common variant(s) in a gene or gene promoter region. Method: PCR amplification followed by a targeted genotyping method (i.e., Sanger Sequencing).	**81210** (BRAF (B-Raf proto-oncogene, serine/threonine kinase) (eg, colon cancer, melanoma), gene analysis, V600 variant(s)	Assessment of a single codon, hotspot variant. Similar methodologies are employed to detect variants at V600 in BRAF.	$175.40
81X10	PLCG2 (phospholipase C gamma 2) (eg, chronic lymphocytic leukemia) gene analysis, common variants (eg, R665W, S707F and L845F)	Purpose: To detect common variant(s) in a gene or gene promoter region. Method: PCR amplification followed by a targeted genotyping method (i.e., Sanger Sequencing).	**81225** CYP2C19 (cytochrome P450, family 2, subfamily C, polypeptide 19) (eg, drug metabolism), gene analysis, common variants (eg, *2, *3, *4, *8, *17)	Similar methodologies and reasources are used in the assessment of 3 distant codons compared to 5 common variants in 81225.	$291.36

8X013	CACNA1A (calcium voltage-gated channel subunit alpha1 A) (eg, spinocerebellar ataxia) gene analysis; evaluation to detect abnormal (eg, expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code which is how this procedure was previously coded.	$137.00
8X014	CACNA1A (calcium voltage-gated channel subunit alpha1 A) (eg, spinocerebellar ataxia) gene analysis; full gene sequence	Purpose: To detect variants (eg, SNVs, indels) within the entire gene. Method: Bi-directional sequencing of coding regions as well as exon-intron junctions by sanger sequencing or next generation sequencing.	**81407** (Molecular pathology procedure, Level 8)	The test methods used for sequencing analysis and the amount of DNA sequenced are comparable to that of 81407, which is how this procedure was previously coded. 8X014 is comprised of 47 exons.	$846.27
8X015	CACNA1A (calcium voltage-gated channel subunit alpha1 A) (eg, spinocerebellar ataxia) gene analysis; known familial variant	Purpose: To detect specific known variant(s) in a gene. Method: PCR amplification followed by a targeted genotyping method (ie, Sanger Sequencing).	**81403** (molecular pathology prodecure level 4)	The test methods used for sequencing analysis and the amount of DNA sequenced are comparable to that of 81403, which is how this procedure was previously coded.	$185.20
8X016	CNBP (CCHC-type zinc finger nucleic acid binding protein) (eg, myotonic dystrophy type 2) gene analysis, evaluation to detect abnormal (eg, expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00
8X017	CSTB (cystatin B) (eg, Unverricht-Lundborg disease) gene analysis; evaluation to detect abnormal (eg, expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00

8X018	CSTB (cystatin B) (eg, Unverricht-Lundborg disease) gene analysis; full gene sequence	Purpose: To detect variants (eg, SNVs, indels) within the entire gene. Method: Bi-directional sequencing of coding regions as well as exon-intron junctions by sanger sequencing or next generation sequencing.	**81404** (Molecular pathology procedure, Level 5)	The test methods used for sequencing analysis and the amount of DNA sequenced are comparable to that of 81404, which is how this procedure was previously coded. 8X018 is comprised of 3 exons.	$274.83
8X019	CSTB (cystatin B) (eg, Unverricht-Lundborg disease) gene analysis; known familial variant(s)	Purpose: To detect specific known variant(s) in a gene. Method: PCR amplification followed by a targeted genotyping method (ie, Sanger Sequencing).	**81403** (molecular pathology prodecure level 4)	The test methods used for sequencing analysis and the amount of DNA sequenced are comparable to that of 81403, which is how this procedure was previously coded.	$185.20
8X020	DMPK (DM1 protein kinase) (eg, myotonic dystrophy type 1) gene analysis; evaluation to detect abnormal (expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00
8X021	DMPK (DM1 protein kinase) (eg, myotonic dystrophy type 1) gene analysis; characterization of alleles (eg, expanded size)	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Southern Blot.	**81404** (Molecular pathology procedure, Level 5)	The methodology and amount of work used to characterize the size of the triplet expansion is identical to that described by the Tier 2, level 5 code which is how this procedure was previously coded.	$274.83
81X07	EZH2 (enhancer of zeste 2 polycomb repressive complex 2 subunit) (eg, myelodysplastic syndrome, myeloproliferative neoplasms) gene analysis, full gene sequence	Purpose: To detect variants (SNV and small indels) in the entire EZH2 gene in cancer or precancer. Method: PCR amplification follow by sanger sequencing or next generation sequencing.	**81175** (ASXL1 (additional sex combs like 1, transcriptional regulator) (eg, myelodysplastic syndrome, myeloproliferative neoplasms, chronic myelomonocytic leukemia), gene analysis; full gene sequence)	The methodology and amount of DNA sequenced is comparable to the sequencing of AXL1, which is also relevant in hematologic malignancy.	$707.02

81X08	EZH2 (enhancer of zeste 2 polycomb repressive complex 2 subunit) (eg, diffuse large B-cell lymphoma) gene analysis, common variant(s) (eg, codon 646)	Purpose: To detect common variant(s) in a gene or gene promoter region. Method: PCR amplification followed by a targeted genotyping method (i.e., Sanger Sequencing).	**81210** (BRAF (B-Raf proto-oncogene, serine/threonine kinase) (eg, colon cancer, melanoma), gene analysis, V600 variant(s)	Assessment of a single codon, hotspot variant. Similar methodolgies are employed to detect variants at V600 in BRAF (81210).	$175.40
8X022	FXN (frataxin) (eg, Friedreich ataxia) gene analysis; evaluation to detect abnormal (expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code which is how this procedure was previously coded.	$137.00
8X023	FXN (frataxin) (eg, Friedreich ataxia) gene analysis; characterization of alleles (eg, expanded size)	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Southern Blot.	**81404** (Molecular pathology procedure, Level 5)	The methodology and amount of work used to characterize the size of the triplet expansion is identical to that described by the Tier 2, level 5 code which is how this procedure was previously coded.	$274.83
8X024	FXN (frataxin) (eg, Friedreich ataxia) gene analysis; full gene sequence	Purpose: To detect variants (eg, SNVs, indels) within the entire gene. Method: Bi-directional sequencing of coding regions as well as exon-intron junctions by sanger sequencing or next generation sequencing.	**81404** (Molecular pathology procedure, Level 5)	The test methods used for sequencing analysis and the amount of DNA sequenced are comparable to that of 81404, which is how this procedure was previously coded. 8X024 is comprised of 5 exons.	$274.83
8X025	FXN (frataxin) (eg, Friedreich ataxia) gene analysis; known familial variant(s)	Purpose: To detect specific known variant(s) in a gene. Method: PCR amplification followed by a targeted genotyping method (ie, Sanger Sequencing).	**81403** (molecular pathology prodecure level 4)	The test methods used for sequencing analysis and the amount of DNA sequenced are comparable to that of 81403, which is how this procedure was previously coded.	$185.20

8X026	HTT (huntingtin) (eg, Huntington disease) gene analysis; evaluation to detect abnormal (eg, expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00
8X027	HTT (huntingtin) (eg, Huntington disease) gene analysis; characterization of alleles (eg, expanded size)	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Southern Blot.	**81404** (Molecular pathology procedure, Level 5)	The methodology and amount of work used to characterize the size of the triplet expansion is identical to that described by the Tier 2, level 5 code which is how this procedure was previously coded.	$274.83
81X11	MYD88 (myeloid differentiation primary response 88) (eg, Waldenstrom's macroglobulinemia, lymphoplasmacytic leukemia) gene analysis, p.Leu265Pro (L265P) variant	To detect common variant(s) in a gene or gene promoter region Method: PCR amplification followed by a targeted genotyping method (ie Sanger Sequencing)	**81210** (BRAF (B-Raf proto-oncogene, serine/threonine kinase) (eg, colon cancer, melanoma), gene analysis, V600 variant(s)	Assessment of a single codon, hotspot variant. Similar methodologies are employed to detect variants at V600 in BRAF (81210).	$175.40
8X000	NUDT15 (nudix hydrolase 15) (eg, drug metabolism) gene analysis, common variant(s) (eg, *2, *3, *4, *5, *6)	Purpose: To detect specific known variant(s) in a gene. Method: PCR amplification followed by a targeted genotyping method (ie, Sanger Sequencing).	**81225** CYP2C19 (cytochrome P450, family 2, subfamily C, polypeptide 19) (eg, drug metabolism), gene analysis, common variants (eg, *2, *3, *4, *8, *17)	Similar methodologies and resources are used to detect a comparable number of known variants in 81225.	$291.36
8X028	PABPN1 (poly[A] binding protein nuclear 1) (eg, oculopharyngeal muscular dystrophy) gene analysis, evaluation to detect abnormal (eg, expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00

8X035	PPP2R2B (protein phosphatase 2 regulatory subunit Bbeta) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00
8X032	SMN1 (survival of motor neuron 1, telomeric) (eg, spinal muscular atrophy) gene analysis; dosage/deletion analysis, includes SMN2 (survival of motor neuron 2, centromeric) analysis, if performed	Purpose: To detect specific known variant(s) in a gene. Method: PCR amplification followed by a targeted genotyping method (ie, Sanger Sequencing).	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code which is how this procedure was previously coded.	$137.00
8X033	SMN1 (survival of motor neuron 1, telomeric) (eg, spinal muscular atrophy) gene analysis; full gene sequence	Purpose: To detect variants (eg, SNVs, indels) within the entire gene. Method: Bi-directional sequencing of coding regions as well as exon-intron junctions by sanger sequencing or next generation sequencing.	**81317** (PMS2 (postmeiotic segregation increased 2 [S. cerevisiae]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis)	Similar methodologies and resources are used in the full sequencing of SMN1 and PMS2. SMN1 is comprised of 9 exons but extra work is required to distinquish between highly homologous genes.	$707.02
8X034	SMN1 (survival of motor neuron 1, telomeric) (eg, spinal muscular atrophy) gene analysis; known familial sequence variant(s)	Purpose: To detect specific known variant(s) in a gene. Method: PCR amplification followed by a targeted genotyping method (ie, Sanger Sequencing).	**81403** (molecular pathology prodecure level 4)	The test methods used for sequencing analysis and the amount of DNA sequenced are comparable to that of 81403, which is how this procedure was previously coded.	$185.20
8X036	TBP (TATA box binding protein) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles	Purpose: To aid in the diagnosis of a triplet repeat disorder. Method: Repeat primed PCR with capillary electrophoresis.	**81401** (Molecular pathology procedure, Level 2 (eg, 2-10 SNPs, 1 methylated variant, or 1 somatic variant [typically using nonsequencing target variant analysis], or detection of a dynamic mutation disorder/triplet repeat)	The methodology and amount of work used to detect this triplet repeat expansion disorder is identical to that described by the Tier 2, level 2 code (81401) which is how this procedure was previously coded.	$137.00

80X00	TERT (telomerase reverse transcriptase) (eg, thyroid carcinoma, glioblastoma multiforme) gene analysis, targeted sequence analysis (eg, promoter region)	Purpose: To detect common variant(s) in a gene or gene promoter region. Method: PCR amplification followed by a targeted genotyping method (i.e., Sanger Sequencing).	**81121** (IDH2 (isocitrate dehydrogenase 2 [NADP+], mitochondrial) (eg, glioma), common variants (eg, R140W, R172M))	Similar methodologies and resources are used to determine the genotype at two distant codons in IDH2.	$295.79
813X0	TGFBI (transforming growth factor beta-induced) (eg, corneal dystrophy) gene analysis, common variants (eg, R124H, R124C, R124L, R555W, R555Q)	Purpose: To detect specific known variant(s) in a gene. Method: PCR amplification followed by a targeted genotyping method (ie, Sanger Sequencing).	**81230** CYP3A4 (cytochrome P450 family 3 subfamily A member 4) (eg, drug metabolism), gene analysis, common variant(s) (eg, *2, *22)	Similar methodologies and resources are used to detect a comparable number of known variants in 81230.	$174.81
Genomic Sequencing Procedures (GSP)					
81X43	Genetic testing for severe inherited conditions (eg, cystic fibrosis, Ashkenazi Jewish disorders [eg, Bloom syndrome, Canavan disease, Fanconi anemia type C, mucolipidosis type VI, Gaucher disease, Tay-Sachs disease], beta hemoglobinopathies, phenylketonuria, galactosemia), genomic sequence analysis panel, must include sequencing of at least 15 genes (eg, ACADM, ARSA, ASPA, ATP7B, BCKDHA, BCKDHB, BLM, CFTR, DHCR7, FANCC, G6PC, GAA, GALT, GBA, GBE1, HBB, HEXA, IKBKAP, MCOLN1, PAH)	Purpose: To detect carrier status in diseases relevant to severe inherited disease. Method: Next generation sequencing.	**81412** (Ashkenazi Jewish associated disorders (eg, Bloom syndrome, Canavan disease, cystic fibrosis, familial dysautonomia, Fanconi anemia group C, Gaucher disease, Tay-Sachs disease), genomic sequence analysis panel, must include sequencing of at least 9 genes, including ASPA, BLM, CFTR, FANCC, GBA, HEXA, IKBKAP, MCOLN1, and SMPD1)	The methodologies and amount of resources are similar for these clinically similar codes.	$2,448.56
Chemistry					
80X01	Dihydrotestosterone (DHT)	Purpose: Determine levels of Dihydrotestosterone (DHT)in blood or urine. Method: Unspecified.	**82634** 11-Deoxycortisol	In 2014, the CPT was 82651 with an NLA of $35.22. We are recommending a price structure comparable to 82651. CPT 82634, Dexoycortisol, 11- provides a comparable NLA of $36.14.	$36.14
8372X	Lipoprotein, direct measurement; small dense LDL cholesterol	Purpose: Determine small dense LDL cholesterol in the blood as a cardiovascular risk marker. Method: Unspecified.	**83704** Lipoprotein, blood; quantitation of lipoprotein particle number(s) (eg, by nuclear magnetic resonance spectroscopy), includes lipoprotein particle subclass(es), when performed	Crosswalking to 83704, Lipoprotein, blood; quantitation of lipoprotein particle number(s) (eg, by NMR) includes lipoprotein particle subclass(es) , when performed.	$38.95