



## Genetic and Molecular Testing Medical Necessity Guideline

Medical Necessity Guideline (MNG) Title: Genetic and Molecular Testing		
MNG #: 002	<input checked="" type="checkbox"/> CCA Senior Care Options (HMO D-SNP) (MA) <input checked="" type="checkbox"/> CCA One Care (FIDE SNP) (MA)	<b>Prior Authorization Needed?</b> <input checked="" type="checkbox"/> <b>Yes (always required)</b> <input type="checkbox"/> Yes (only in certain situations. See this MNG for details) <input type="checkbox"/> No
<b>Benefit Type:</b> <input checked="" type="checkbox"/> Medicare <input checked="" type="checkbox"/> Medicaid	<b>Approval Date:</b> 01/10/2019;	<b>Effective Date:</b> 04/01/2019; 11/09/2023; 01/01/2025; 07/01/2025; 2/12/2026
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### OVERVIEW:

Genetic testing refers to any type of testing that helps to determine the *genotype* of an individual in *germline* or selected *somatic* cells. These tests analyze human chromosomes, deoxyribonucleic acid, ribonucleic acid, *genes*, and other gene products to detect inheritable and/or acquired alterations that cause or are likely to cause a particular disorder or condition. Molecular diagnostic testing is a type of genetic test that examines the changes in one or more genes to determine the order of nucleotides in an individual’s genetic code. Molecular tests use DNA sequencing to detect abnormalities in the gene sequence, to test for histocompatibility antigens, to determine prognosis and/or to predict response to treatment. One particular molecular test, *next generation sequencing (NGS)*, uses parallel sequencing assays to analyze the bulk of an individual’s DNA to detect *variants* in a broad range of rare and complex disorders. It is often used when single gene or panel testing has not provided a diagnosis or when the suspected condition or genetic cause is unclear.

Genetic testing has demonstrated efficacy in predicting outcomes and to be a helpful clinical decision-making tool. It may be used for predictive and pre-symptomatic testing for adult-onset and complex disorders, diagnostic and carrier screening for inherited disorders, and pharmacogenetic testing to guide drug dosage, selection, and response. The likelihood of development of disease depends on the presence of specific genetic variants, *inheritance pattern*, *penetrance*, *expressivity*, the individual’s age, and other contributory genetic and environmental factors. The different methods to identify specific variants include *Sanger sequencing*, *Microarray technologies*, and NGS. Choosing the appropriate test to perform depends on the indication or presenting features, tests available for the suspected condition(s), and the available information regarding the genetic causes of the condition or presenting condition(s).

### DEFINITIONS:

**Expressivity:** The clinical differences in the way a disease is expressed.

**Gene:** Refers to a gene, region of a gene, and/or variants) of a gene that can be assayed serially or in parallel.



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**Genetic test:** Test that involves an analysis of human chromosomes, deoxyribonucleic acid, ribonucleic acid, genes, and gene products (e.g., enzymes, proteins, metabolites) used to detect heritable or somatic variants that are related to disease.

**Genotype:** Refers to the DNA blueprint and is associated with the clinical manifestations of a trait or disease.

**Germline:** Refers to the sex cells (eggs and sperm) that reproducing organisms use to pass on their genomes from one generation to the next.

**High-risk group:** Refers to an individual with a personal or family history of autosomal dominant, autosomal recessive, x-linked recessive, x-linked dominant or a family history of chromosomal abnormality (e.g., chromosomal translocation or inversion).

**Inheritance pattern:** Describe how genetic variants are distributed in families. Certain cancer syndromes or metabolic disorders may be autosomal or sex-linked, and recessive or dominant.

**Microarray technologies:** Genetic testing method that uses an allele-specific oligonucleotide hybridization approach to code for target reference sequence or alternate, disease-associated variant. The purpose of the test is to identify DNA changes at the level of a single nucleotide, larger portions of one or more genes, or larger regions of one or more chromosomes.

**Molecular test:** A type of genetic test that looks for changes in one or more genes. These tests determine the order of nucleotides (DNA building blocks) in an individual's genetic code by DNA sequencing to detect variants in genes and to test for histocompatibility antigens.

**Next generation sequencing (NGS):** Genetic testing method that uses rapid, high-throughput parallel sequencing of multiple small fragments of DNA to determine sequence.

**Penetrance:** Refers to the likelihood that an individual with a disease genotype will actually manifest one or more of the clinical features associated with the disease.

**Sanger sequencing:** Genetic testing method that is used to determine the nucleotides present in a fragment of DNA. It is considered the gold standard in clinical genetic testing for the detection of point mutations and small variants.

**Somatic cells:** Somatic cells are diploid and contain two sets of chromosomes, one set inherited from each parent. Somatic mutations can impact the individual carrying the mutation but cannot be passed on and have no effect on the offspring.

**Variant:** A variation from a reference sequence for clinical testing. Variants are classified into one of five categories: pathogenic, likely pathogenic, variant of uncertain significance, likely benign, or benign.



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### DECISION GUIDELINES:

Commonwealth Care Alliance (CCA) follows applicable Medicare and Medicaid regulations when available to review prior authorization requests for medical necessity. This Medical Necessity Guideline (MNG) Clinical Coverage Criteria applies to genetic and molecular testing unless a more expansive and applicable CMS National Coverage Determinations (NCDs), Local Coverage Determinations (LCDs), or state-specific guidelines for medical necessity determination exists, including, but not limited to the following:

- L3500: Molecular Pathology Procedures
- L37606: Genomic Sequence Analysis Panels in the Treatment of Hematolymphoid Diseases
- L37810: Genomic Sequence Analysis Panels in the Treatment of Solid Organ Neoplasms
- L37851: Biomarker Testing for Neuroendocrine Tumors/Neoplasms
- L38371: Multimarker Serum Tests Related to Ovarian Cancer Testing
- L38968: Thyroid Nodule Molecular Testing
- L39027: Respiratory Pathogen Panel Testing
- L39726: KidneyIntelX and KidneyIntelX.dkd Testing
- NCD 90.2: Next Generation Sequencing (NGS)
- Mass Health Guidelines for Medical Necessity Determination for Gene Expression Profiling Tests for Breast Cancer  
<https://www.mass.gov/guides/masshealth-guidelines-for-medical-necessity-determination-for-genetic-testing-for-hereditary-breast-and-or-ovarian-cancer>
- Mass Health Guidelines for Medical Necessity Determination for Fragile X Carrier Screening
- Mass Health Guidelines for Medical Necessity Determination for Maternal Cell-Free Fetal DNA Testing for Aneuploidy
- MassHealth Provider Manual Series: Independent Clinical Laboratory Manual 6. Service Codes. [download](#)
- CCA Medical Necessity Guideline: Chromosomal Microarray Analysis
- CCA Medical Necessity Guideline: Genetic Testing: BRCA-Related Breast and/or Ovarian Cancer Syndrome
- CCA Medical Necessity Guideline: Experimental & Investigational Services
- CCA Medical Necessity Guideline (MNG) Title: Maternal Cell-Free Fetal DNA Testing

### Clinical Coverage Criteria:

When CMS and/or Mass Health guidelines are not available for requested genetic/molecular test, clinical coverage criteria below will apply:

1. CCA may cover the specific Genetic/Molecular Test if **ALL** of the following criteria are met:



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- a. The member belongs to a high-risk group for a particular disease(s) based on either:
  - i. Personal history, family history, documentation of a genetic variant, and/or ethnic/ancestry; *or*
  - ii. The member displays clinical features of the specific variant in question; *and*
- b. Alternative laboratory or clinical tests to definitively diagnose the disorder/identify the condition are unavailable or do not result in a definitive diagnosis of the suspected disorder; *and*
- c. The test is considered a scientifically proven method for the identification of the specific genetically linked inheritable disease or is a clinically valid test based on published peer reviewed medical literature; *and*
- d. Testing assay(s) are Food and Drug Administration (FDA) approved or cleared for the use in the member's condition; *and*
- e. The test is ordered and furnished by a qualified clinician with expertise in the treatment of the targeted disease OR from a provider with genetic counseling expertise; *and*
- f. The results of the genetic test will directly alter the treatment and/or medical management of the member's diagnosed condition and/or the member's current pregnancy.

### LIMITATIONS/EXCLUSIONS:

1. CCA will limit diagnostic genetic testing for a disease to one test per lifetime. **A duplicate genetic test for an inherited condition may be covered if there is uncertainty about the validity of the existing test result or if repeat testing of somatically acquired variant(s) is required to inform appropriate therapeutic decision-making.**
2. For testing panels, including but not limited to, multiple genes or multiple conditions, and in cases where a tiered approach/method is clinically available, testing would be covered ONLY for the number of genes or test that are reasonable and necessary to obtain necessary information for therapeutic decision-making.
3. Medically necessary interpretation and report of the genetic and molecular diagnostic test must be written by a qualified clinician or pathologist eligible to report this service. The report is above and beyond the report of standard laboratory results and may not be reported by non-medical practitioners (e.g., PhD, scientists, etc.).
4. CCA will not cover and does not consider genetic tests that meet **ANY** of the following criteria as medically necessary:
  - a. Testing for the purpose of confirming a suspected diagnosis that can be diagnosed by an alternative laboratory or clinical test.
  - b. Testing for the purpose of informing care of a member's family member.
  - c. Testing that is performed by an out-of-network laboratory when it can be performed by an in-network laboratory.
  - d. Tests that are scientifically unproven and where clinical validity and utility has not been definitively determined due to the paucity of data.
  - e. Tests that have not been approved or cleared by the FDA.
  - f. Tests that are unlikely to impact the treatment, outcome, and/or clinical management in the care of the member.
  - g. Home testing, self-referral testing, and/or direct-to-consumer genetic tests.



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**CODING:**

When applicable, a list(s) of codes requiring prior authorization is provided. This list is for reference purposes only and may not be all inclusive. The inclusion of a code does not imply any right to reimbursement or guarantee claim payment.

**NOTE: Genetic and Molecular diagnostic testing, including Proprietary Laboratory Analyses (PLA), and Multianalyte assays with algorithmic analyses (MAAA) requires prior authorization.**

Coverage of genetic tests will require documentation that supports medical necessity.

CPT/HCPCS CODE	CODE DESCRIPTION
<b>81105</b>	Human Platelet Antigen 1 genotyping (HPA-1), ITGB3 (integrin, beta 3 [platelet glycoprotein IIIa], antigen CD61 [GPIIIa]) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant, HPA-1a/b (L33P)
<b>81106</b>	Human Platelet Antigen 2 genotyping (HPA-2), GP1BA (glycoprotein Ib [platelet], alpha polypeptide [GPIba]) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant, HPA-2a/b (T145M)
<b>81107</b>	Human Platelet Antigen 3 genotyping (HPA-3), ITGA2B (integrin, alpha 2b [platelet glycoprotein IIb of IIb/IIIa complex], antigen CD41 [GPIIb]) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant, HPA-3a/b (I843S)
<b>81108</b>	Human Platelet Antigen 4 genotyping (HPA-4), ITGB3 (integrin, beta 3 [platelet glycoprotein IIIa], antigen CD61 [GPIIIa]) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant, HPA-4a/b (R143Q)
<b>81109</b>	Human Platelet Antigen 5 genotyping (HPA-5), ITGA2 (integrin, alpha 2 [CD49B, alpha 2 subunit of VLA-2 receptor] [GPIa]) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant (eg, HPA-5a/b (K505E))
<b>81110</b>	Human Platelet Antigen 6 genotyping (HPA-6w), ITGB3 (integrin, beta 3 [platelet glycoprotein IIIa, antigen CD61] [GPIIIa]) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant, HPA-6a/b (R489Q)
<b>81111</b>	Human Platelet Antigen 9 genotyping (HPA-9w), ITGA2B (integrin, alpha 2b [platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41] [GPIIb]) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant, HPA-9a/b (V837M)
<b>81112</b>	Human Platelet Antigen 15 genotyping (HPA-15), CD109 (CD109 molecule) (eg, neonatal alloimmune thrombocytopenia [NAIT], post-transfusion purpura), gene analysis, common variant, HPA-15a/b (S682Y)
<b>81120</b>	IDH1 (isocitrate dehydrogenase 1 [NADP+], soluble) (eg, glioma), common variants (eg, R132H, R132C)

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<b>81121</b>	IDH2 (isocitrate dehydrogenase 2 [NADP+], mitochondrial) (eg, glioma), common variants (eg, R140W, R172M)
<b>81161</b>	DMD (dystrophin) (eg, Duchenne/Becker muscular dystrophy) deletion analysis, and duplication analysis, if performed
<b>81168</b>	CCND1/IGH (t(11;14)) (eg, mantle cell lymphoma) translocation analysis, major breakpoint, qualitative and quantitative, if performed
<b>81170</b>	ABL1 (ABL proto-oncogene 1, non-receptor tyrosine kinase) (eg, acquired imatinib tyrosine kinase inhibitor resistance), gene analysis, variants in the kinase domain
<b>81171</b>	AFF2 (ALF transcription elongation factor 2 [FMR2]) (eg, fragile X intellectual disability 2 [FRAXE]) gene analysis; evaluation to detect abnormal (eg, expanded) alleles
<b>81172</b>	AFF2 (ALF transcription elongation factor 2 [FMR2]) (eg, fragile X intellectual disability 2 [FRAXE]) gene analysis; characterization of alleles (eg, expanded size and methylation status)
<b>81173</b>	AR (androgen receptor) (eg, spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation) gene analysis; full gene sequence
<b>81174</b>	AR (androgen receptor) (eg, spinal and bulbar muscular atrophy, Kennedy disease, X chromosome inactivation) gene analysis; known familial variant
<b>81175</b>	ASXL1 (additional sex combs like 1, transcriptional regulator) (eg, myelodysplastic syndrome, myeloproliferative neoplasms, chronic myelomonocytic leukemia), gene analysis; full gene sequence
<b>81176</b>	ASXL1 (additional sex combs like 1, transcriptional regulator) (eg, myelodysplastic syndrome, myeloproliferative neoplasms, chronic myelomonocytic leukemia), gene analysis; targeted sequence analysis (eg, exon 12)
<b>81177</b>	ATN1 (atrophin 1) (eg, dentatorubral-pallidoluysian atrophy) gene analysis, evaluation to detect abnormal (eg, expanded) alleles
<b>81178</b>	ATXN1 (ataxin 1) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles
<b>81179</b>	ATXN2 (ataxin 2) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles
<b>81180</b>	ATXN3 (ataxin 3) (eg, spinocerebellar ataxia, Machado-Joseph disease) gene analysis, evaluation to detect abnormal (eg, expanded) alleles
<b>81181</b>	ATXN7 (ataxin 7) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles
<b>81182</b>	ATXN8OS (ATXN8 opposite strand [non-protein coding]) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles
<b>81183</b>	ATXN10 (ataxin 10) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles
<b>81184</b>	CACNA1A (calcium voltage-gated channel subunit alpha1 A) (eg, spinocerebellar ataxia) gene analysis; evaluation to detect abnormal (eg, expanded) alleles
<b>81185</b>	CACNA1A (calcium voltage-gated channel subunit alpha1 A) (eg, spinocerebellar ataxia) gene analysis; full gene sequence
<b>81186</b>	CACNA1A (calcium voltage-gated channel subunit alpha1 A) (eg, spinocerebellar ataxia) gene analysis; known familial variant

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<b>81187</b>	CNBP (CCHC-type zinc finger nucleic acid binding protein) (eg, myotonic dystrophy type 2) gene analysis, evaluation to detect abnormal (eg, expanded) alleles
<b>81188</b>	CSTB (cystatin B) (eg, Unverricht-Lundborg disease) gene analysis; evaluation to detect abnormal (eg, expanded) alleles
<b>81189</b>	CSTB (cystatin B) (eg, Unverricht-Lundborg disease) gene analysis; full gene sequence
<b>81190</b>	CSTB (cystatin B) (eg, Unverricht-Lundborg disease) gene analysis; known familial variant(s)
<b>81191</b>	NTRK1 (neurotrophic receptor tyrosine kinase 1) (eg, solid tumors) translocation analysis
<b>81192</b>	NTRK2 (neurotrophic receptor tyrosine kinase 2) (eg, solid tumors) translocation analysis
<b>81193</b>	NTRK3 (neurotrophic receptor tyrosine kinase 3) (eg, solid tumors) translocation analysis
<b>81194</b>	NTRK (neurotrophic receptor tyrosine kinase 1, 2, and 3) (eg, solid tumors) translocation analysis
<b>81200</b>	ASPA (aspartoacylase) (eg, Canavan disease) gene analysis, common variants (eg, E285A, Y231X)
<b>81201</b>	APC (adenomatous polyposis coli) (eg, familial adenomatosis polyposis [FAP], attenuated FAP) gene analysis; full gene sequence
<b>81202</b>	APC (adenomatous polyposis coli) (eg, familial adenomatosis polyposis [FAP], attenuated FAP) gene analysis; known familial variants
<b>81203</b>	APC (adenomatous polyposis coli) (eg, familial adenomatosis polyposis [FAP], attenuated FAP) gene analysis; duplication/deletion variants
<b>81204</b>	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)
<b>81205</b>	BCKDHB (branched-chain keto acid dehydrogenase E1, beta polypeptide) (eg, maple syrup urine disease) gene analysis, common variants (eg, R183P, G278S, E422X)
<b>81206</b>	BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis; major breakpoint, qualitative or quantitative
<b>81207</b>	BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis; minor breakpoint, qualitative or quantitative
<b>81208</b>	BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis; other breakpoint, qualitative or quantitative
<b>81209</b>	BLM (Bloom syndrome, RecQ helicase-like) (eg, Bloom syndrome) gene analysis, 2281del6ins7 variant
<b>81210</b>	BRAF (B-Raf proto-oncogene, serine/threonine kinase) (eg, colon cancer, melanoma), gene analysis, V600 variant(s)
<b>81218</b>	CEBPA (CCAAT/enhancer binding protein [C/EBP], alpha) (eg, acute myeloid leukemia), gene analysis, full gene sequence
<b>81219</b>	CALR (calreticulin) (eg, myeloproliferative disorders), gene analysis, common variants in exon 9
<b>81220</b>	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; common variants (eg, ACMG/ACOG guidelines)

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<b>81221</b>	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; known familial variants
<b>81222</b>	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; duplication/deletion variants
<b>81223</b>	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; full gene sequence
<b>81224</b>	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; intron 8 poly-T analysis (eg, male infertility)
<b>81225</b>	CYP2C19 (cytochrome P450, family 2, subfamily C, polypeptide 19) (eg, drug metabolism), gene analysis, common variants (eg, *2, *3, *4, *8, *17)
<b>81226</b>	CYP2D6 (cytochrome P450, family 2, subfamily D, polypeptide 6) (eg, drug metabolism), gene analysis, common variants (eg, *2, *3, *4, *5, *6, *9, *10, *17, *19, *29, *35, *41, *1XN, *2XN, *4XN)
<b>81227</b>	CYP2C9 (cytochrome P450, family 2, subfamily C, polypeptide 9) (eg, drug metabolism), gene analysis, common variants (eg, *2, *3, *5, *6)
<b>81230</b>	CYP3A4 (cytochrome P450 family 3 subfamily A member 4) (eg, drug metabolism), gene analysis, common variant(s) (eg, *2, *22)
<b>81231</b>	CYP3A5 (cytochrome P450 family 3 subfamily A member 5) (eg, drug metabolism), gene analysis, common variants (eg, *2, *3, *4, *5, *6, *7)
<b>81232</b>	DPYD (dihydropyrimidine dehydrogenase) (eg, 5-fluorouracil/5-FU and capecitabine drug metabolism), gene analysis, common variant(s) (eg, *2A, *4, *5, *6)
<b>81233</b>	BTK (Bruton's tyrosine kinase) (eg, chronic lymphocytic leukemia) gene analysis, common variants (eg, C481S, C481R, C481F)
<b>81234</b>	DMPK (DM1 protein kinase) (eg, myotonic dystrophy type 1) gene analysis; evaluation to detect abnormal (expanded) alleles
<b>81235</b>	EGFR (epidermal growth factor receptor) (eg, non-small cell lung cancer) gene analysis, common variants (eg, exon 19 LREA deletion, L858R, T790M, G719A, G719S, L861Q)
<b>81236</b>	EZH2 (enhancer of zeste 2 polycomb repressive complex 2 subunit) (eg, myelodysplastic syndrome, myeloproliferative neoplasms) gene analysis, full gene sequence
<b>81237</b>	EZH2 (enhancer of zeste 2 polycomb repressive complex 2 subunit) (eg, diffuse large B-cell lymphoma) gene analysis, common variant(s) (eg, codon 646)
<b>81238</b>	F9 (coagulation factor IX) (eg, hemophilia B), full gene sequence
<b>81239</b>	DMPK (DM1 protein kinase) (eg, myotonic dystrophy type 1) gene analysis; characterization of alleles (eg, expanded size)
<b>81240</b>	F2 (prothrombin, coagulation factor II) (eg, hereditary hypercoagulability) gene analysis, 20210G>A variant
<b>81241</b>	F5 (coagulation factor V) (eg, hereditary hypercoagulability) gene analysis, Leiden variant
<b>81242</b>	FANCC (Fanconi anemia, complementation group C) (eg, Fanconi anemia, type C) gene analysis, common variant (eg, IVS4+4A>T)

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<b>81243</b>	FMR1 (fragile X messenger ribonucleoprotein 1) (eg, fragile X syndrome, X-linked intellectual disability [XLID]) gene analysis; evaluation to detect abnormal (eg, expanded) alleles
<b>81244</b>	FMR1 (fragile X messenger ribonucleoprotein 1) (eg, fragile X syndrome, X-linked intellectual disability [XLID]) gene analysis; characterization of alleles (eg, expanded size and promoter methylation status)
<b>81245</b>	FLT3 (fms-related tyrosine kinase 3) (eg, acute myeloid leukemia), gene analysis; internal tandem duplication (ITD) variants (ie, exons 14, 15)
<b>81246</b>	FLT3 (fms-related tyrosine kinase 3) (eg, acute myeloid leukemia), gene analysis; tyrosine kinase domain (TKD) variants (eg, D835, I836)
<b>81247</b>	G6PD (glucose-6-phosphate dehydrogenase) (eg, hemolytic anemia, jaundice), gene analysis; common variant(s) (eg, A, A-)
<b>81248</b>	G6PD (glucose-6-phosphate dehydrogenase) (eg, hemolytic anemia, jaundice), gene analysis; known familial variant(s)
<b>81249</b>	G6PD (glucose-6-phosphate dehydrogenase) (eg, hemolytic anemia, jaundice), gene analysis; full gene sequence
<b>81250</b>	G6PC (glucose-6-phosphatase, catalytic subunit) (eg, Glycogen storage disease, type 1a, von Gierke disease) gene analysis, common variants (eg, R83C, Q347X)
<b>81251</b>	GBA (glucosidase, beta, acid) (eg, Gaucher disease) gene analysis, common variants (eg, N370S, 84GG, L444P, IVS2+1G>A)
<b>81252</b>	GJB2 (gap junction protein, beta 2, 26kDa, connexin 26) (eg, nonsyndromic hearing loss) gene analysis; full gene sequence
<b>81253</b>	GJB2 (gap junction protein, beta 2, 26kDa, connexin 26) (eg, nonsyndromic hearing loss) gene analysis; known familial variants
<b>81254</b>	GJB6 (gap junction protein, beta 6, 30kDa, connexin 30) (eg, nonsyndromic hearing loss) gene analysis, common variants (eg, 309kb [del(GJB6-D13S1830)] and 232kb [del(GJB6-D13S1854)])
<b>81255</b>	HEXA (hexosaminidase A [alpha polypeptide]) (eg, Tay-Sachs disease) gene analysis, common variants (eg, 1278insTATC, 1421+1G>C, G269S)
<b>81256</b>	HFE (hemochromatosis) (eg, hereditary hemochromatosis) gene analysis, common variants (eg, C282Y, H63D)
<b>81257</b>	HBA1/HBA2 (alpha globin 1 and alpha globin 2) (eg, alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; common deletions or variant (eg, Southeast Asian, Thai, Filipino, Mediterranean, alpha3.7, alpha4.2, alpha20.5, Constant Spring)
<b>81258</b>	HBA1/HBA2 (alpha globin 1 and alpha globin 2) (eg, alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; known familial variant
<b>81259</b>	HBA1/HBA2 (alpha globin 1 and alpha globin 2) (eg, alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; full gene sequence
<b>81260</b>	IKBKAP (inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein) (eg, familial dysautonomia) gene analysis, common variants (eg, 2507+6T>C, R696P)

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<b>81261</b>	<u>IGH@ (Immunoglobulin heavy chain locus) (eg, leukemias and lymphomas, B-cell), gene rearrangement analysis to detect abnormal clonal population(s); amplified methodology (eg, polymerase chain reaction)</u>
<b>81262</b>	<u>IGH@ (Immunoglobulin heavy chain locus) (eg, leukemias and lymphomas, B-cell), gene rearrangement analysis to detect abnormal clonal population(s); direct probe methodology (eg, Southern blot)</u>
<b>81263</b>	<u>IGH@ (Immunoglobulin heavy chain locus) (eg, leukemia and lymphoma, B-cell), variable region somatic mutation analysis</u>
<b>81264</b>	<u>IGK@ (Immunoglobulin kappa light chain locus) (eg, leukemia and lymphoma, B-cell), gene rearrangement analysis, evaluation to detect abnormal clonal population(s)</u>
<b>81265</b>	Comparative analysis using Short Tandem Repeat (STR) markers; patient and comparative specimen (eg, pre-transplant recipient and donor germline testing, post-transplant non-hematopoietic recipient germline [eg, buccal swab or other germline tissue sample] and donor testing, twin zygosity testing, or maternal cell contamination of fetal cells)
<b>81266</b>	Comparative analysis using Short Tandem Repeat (STR) markers; each additional specimen (eg, additional cord blood donor, additional fetal samples from different cultures, or additional zygosity in multiple birth pregnancies) (List separately in addition to code for primary procedure)
<b>81267</b>	Chimerism (engraftment) analysis, post transplantation specimen (eg, hematopoietic stem cell), includes comparison to previously performed baseline analyses; without cell selection
<b>81268</b>	Chimerism (engraftment) analysis, post transplantation specimen (eg, hematopoietic stem cell), includes comparison to previously performed baseline analyses; with cell selection (eg, CD3, CD33), each cell type
<b>81269</b>	HBA1/HBA2 (alpha globin 1 and alpha globin 2) (eg, alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; duplication/deletion variants
<b>81270</b>	JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) gene analysis, p.Val617Phe (V617F) variant
<b>81271</b>	HTT (huntingtin) (eg, Huntington disease) gene analysis; evaluation to detect abnormal (eg, expanded) alleles
<b>81272</b>	KIT (v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog) (eg, gastrointestinal stromal tumor [GIST], acute myeloid leukemia, melanoma), gene analysis, targeted sequence analysis (eg, exons 8, 11, 13, 17, 18)
<b>81273</b>	KIT (v-kit Hardy-Zuckerman 4 feline <u>sarcoma</u> viral oncogene homolog) (eg, <u>mastocytosis</u> ), gene analysis, D816 variant(s)
<b>81274</b>	HTT (huntingtin) (eg, Huntington disease) gene analysis; characterization of alleles (eg, expanded size)
<b>81275</b>	KRAS (Kirsten rat sarcoma viral oncogene homolog) (eg, carcinoma) gene analysis; variants in exon 2 (eg, codons 12 and 13)
<b>81276</b>	KRAS (Kirsten rat <u>sarcoma</u> viral oncogene homolog) (eg, <u>carcinoma</u> ) gene analysis; additional variant(s) (eg, codon 61, codon 146)

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<b>81277</b>	Cytogenomic neoplasia (genome-wide) microarray analysis, interrogation of genomic regions for copy number and loss-of-heterozygosity variants for chromosomal abnormalities
<b>81278</b>	<u>IGH@/BCL2 (t(14;18)) (eg, follicular lymphoma) translocation analysis, major breakpoint region (MBR) and minor cluster region (mcr) breakpoints, qualitative or quantitative</u>
<b>81279</b>	<u>JAK2 (Janus kinase 2) (eg, myeloproliferative disorder) targeted sequence analysis (eg, exons 12 and 13)</u>
<b>81283</b>	FNL3 (interferon, lambda 3) (eg, drug response), gene analysis, rs12979860 variant
<b>81284</b>	FXN (frataxin) (eg, Friedreich ataxia) gene analysis; evaluation to detect abnormal (expanded) alleles
<b>81285</b>	FXN (frataxin) (eg, Friedreich ataxia) gene analysis; characterization of alleles (eg, expanded size)
<b>81286</b>	FXN (frataxin) (eg, Friedreich ataxia) gene analysis; full gene sequence
<b>81287</b>	MGMT (O-6-methylguanine-DNA methyltransferase) (eg, glioblastoma multiforme) promoter methylation analysis
<b>81288</b>	MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; promoter methylation analysis
<b>81289</b>	FXN (frataxin) (eg, Friedreich ataxia) gene analysis; known familial variant(s)
<b>81290</b>	MCOLN1 (mucolipin 1) (eg, Mucopolipidosis, type IV) gene analysis, common variants (eg, IVS3-2A>G, del6.4kb)
<b>81291</b>	MTHFR (5,10-methylenetetrahydrofolate reductase) (eg, hereditary hypercoagulability) gene analysis, common variants (eg, 677T, 1298C)
<b>81292</b>	MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis
<b>81293</b>	MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; known familial variants
<b>81294</b>	MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants
<b>81295</b>	MSH2 (mutS homolog 2, <u>colon cancer, nonpolyposis type 1</u> ) (eg, hereditary non-polyposis colorectal cancer, <u>Lynch syndrome</u> ) <u>gene analysis; full sequence analysis</u>
<b>81296</b>	MSH2 (mutS homolog 2, colon cancer, nonpolyposis type 1) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; known familial variants
<b>81297</b>	MSH2 (mutS homolog 2, colon cancer, nonpolyposis type 1) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants
<b>81298</b>	MSH6 (mutS homolog 6 [E. coli]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis
<b>81299</b>	MSH6 (mutS homolog 6 [E. coli]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; known familial variants

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<b>81300</b>	MSH6 (mutS homolog 6 [E. coli]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants
<b>81301</b>	Microsatellite instability analysis (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) of markers for mismatch repair deficiency (eg, BAT25, BAT26), includes comparison of neoplastic and normal tissue, if performed
<b>81302</b>	MECP2 (methyl CpG binding protein 2) (eg, Rett syndrome) gene analysis; full sequence analysis
<b>81303</b>	MECP2 (methyl CpG binding protein 2) (eg, Rett syndrome) gene analysis; known familial variant
<b>81304</b>	MECP2 (methyl CpG binding protein 2) (eg, Rett syndrome) gene analysis; duplication/deletion variants
<b>81305</b>	MYD88 (myeloid differentiation primary response 88) (eg, Waldenstrom's macroglobulinemia, lymphoplasmacytic leukemia) gene analysis, p.Leu265Pro (L265P) variant
<b>81306</b>	NUDT15 (nudix hydrolase 15) (eg, drug metabolism) gene analysis, common variant(s) (eg, *2, *3, *4, *5, *6)
<b>81307</b>	PALB2 (partner and localizer of BRCA2) (eg, breast and pancreatic cancer) gene analysis; full gene sequence
<b>81308</b>	PALB2 (partner and localizer of BRCA2) (eg, breast and pancreatic cancer) gene analysis; known familial variant
<b>81309</b>	PIK3CA (phosphatidylinositol-4, 5-biphosphate 3-kinase, catalytic subunit alpha) (eg, colorectal and breast cancer) gene analysis, targeted sequence analysis (eg, exons 7, 9, 20)
<b>81310</b>	NPM1 (nucleophosmin) (eg, acute myeloid leukemia) gene analysis, exon 12 variants
<b>81311</b>	NRAS (neuroblastoma RAS viral [v-ras] oncogene homolog) (eg, colorectal carcinoma), gene analysis, variants in exon 2 (eg, codons 12 and 13) and exon 3 (eg, codon 61)
<b>81312</b>	PABPN1 (poly[A] binding protein nuclear 1) (eg, oculopharyngeal muscular dystrophy) gene analysis, evaluation to detect abnormal (eg, expanded) alleles
<b>81313</b>	PCA3/KLK3 (prostate cancer antigen 3 [non-protein coding]/kallikrein-related peptidase 3 [prostate specific antigen]) ratio (eg, prostate cancer)
<b>81314</b>	PDGFRA (platelet-derived growth factor receptor, alpha polypeptide) (eg, gastrointestinal stromal tumor [GIST]), gene analysis, targeted sequence analysis (eg, exons 12, 18)
<b>81315</b>	PML/RARalpha, (t(15;17)), (promyelocytic leukemia/retinoic acid receptor alpha) (eg, promyelocytic leukemia) translocation analysis; common breakpoints (eg, intron 3 and intron 6), qualitative or quantitative
<b>81316</b>	PML/RARalpha, (t(15;17)), (promyelocytic leukemia/retinoic acid receptor alpha) (eg, promyelocytic leukemia) translocation analysis; single breakpoint (eg, intron 3, intron 6 or exon 6), qualitative or quantitative
<b>81317</b>	PMS2 (postmeiotic segregation increased 2 [S. cerevisiae]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis

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<b>81318</b>	PMS2 (postmeiotic segregation increased 2 [ <i>S. cerevisiae</i> ]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; known familial variants
<b>81319</b>	PMS2 (postmeiotic segregation increased 2 [ <i>S. cerevisiae</i> ]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants
<b>81320</b>	PLCG2 (phospholipase C gamma 2) (eg, chronic lymphocytic leukemia) gene analysis, common variants (eg, R665W, S707F, L845F)
<b>81321</b>	PTEN (phosphatase and tensin homolog) (eg, Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; full sequence analysis
<b>81322</b>	PTEN (phosphatase and tensin homolog) (eg, Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; known familial variant
<b>81323</b>	PTEN (phosphatase and tensin homolog) (eg, Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; duplication/deletion variant
<b>81324</b>	PMP22 (peripheral myelin protein 22) (eg, Charcot-Marie-Tooth, hereditary neuropathy with liability to pressure palsies) gene analysis; duplication/deletion analysis
<b>81325</b>	PMP22 (peripheral myelin protein 22) (eg, Charcot-Marie-Tooth, hereditary neuropathy with liability to pressure palsies) gene analysis; full sequence analysis
<b>81326</b>	PMP22 (peripheral myelin protein 22) (eg, Charcot-Marie-Tooth, hereditary neuropathy with liability to pressure palsies) gene analysis; known familial variant
<b>81327</b>	SEPT9 (Septin9) (eg, colorectal cancer) promoter methylation analysis
<b>81328</b>	SLCO1B1 (solute carrier organic anion transporter family, member 1B1) (eg, adverse drug reaction), gene analysis, common variant(s) (eg, *5)
<b>81329</b>	SMN1 (survival of motor neuron 1, telomeric) (eg, spinal muscular atrophy) gene analysis; dosage/deletion analysis (eg, carrier testing), includes SMN2 (survival of motor neuron 2, centromeric) analysis, if performed
<b>81330</b>	SMPD1(sphingomyelin phosphodiesterase 1, acid lysosomal) (eg, Niemann-Pick disease, Type A) gene analysis, common variants (eg, R496L, L302P, fsP330)
<b>81331</b>	SNRPN/UBE3A (small nuclear ribonucleoprotein polypeptide N and ubiquitin protein ligase E3A) (eg, Prader-Willi syndrome and/or Angelman syndrome), methylation analysis
<b>81332</b>	SERPINA1 (serpin peptidase inhibitor, clade A, alpha-1 antiproteinase, antitrypsin, member 1) (eg, alpha-1-antitrypsin deficiency), gene analysis, common variants (eg, *S and *Z)
<b>81333</b>	TGFBI (transforming growth factor beta-induced) (eg, corneal dystrophy) gene analysis, common variants (eg, R124H, R124C, R124L, R555W, R555Q)
<b>81334</b>	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)
<b>81335</b>	TPMT (thiopurine S-methyltransferase) (eg, drug metabolism), gene analysis, common variants (eg, *2, *3)
<b>81336</b>	SMN1 (survival of motor neuron 1, telomeric) (eg, spinal muscular atrophy) gene analysis; full gene sequence

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<b>81337</b>	SMN1 (survival of motor neuron 1, telomeric) (eg, spinal muscular atrophy) gene analysis; known familial sequence variant(s)
<b>81338</b>	MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; common variants (eg, W515A, W515K, W515L, W515R)
<b>81339</b>	MPL (MPL proto-oncogene, thrombopoietin receptor) (eg, myeloproliferative disorder) gene analysis; sequence analysis, exon 10
<b>81340</b>	<u>TRB@ (T cell antigen receptor, beta) (eg, leukemia and lymphoma), gene rearrangement analysis to detect abnormal clonal population(s); using amplification methodology (eg, polymerase chain reaction)</u>
<b>81341</b>	<u>TRB@ (T cell antigen receptor, beta) (eg, leukemia and lymphoma), gene rearrangement analysis to detect abnormal clonal population(s); using direct probe methodology (eg, Southern blot)</u>
<b>81342</b>	<u>TRG@ (T cell antigen receptor, gamma) (eg, leukemia and lymphoma), gene rearrangement analysis, evaluation to detect abnormal clonal population(s)</u>
<b>81343</b>	PPP2R2B (protein phosphatase 2 regulatory subunit Bbeta) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles
<b>81344</b>	TBP (TATA box binding protein) (eg, spinocerebellar ataxia) gene analysis, evaluation to detect abnormal (eg, expanded) alleles
<b>81345</b>	TERT (telomerase reverse transcriptase) (eg, thyroid carcinoma, glioblastoma multiforme) gene analysis, targeted sequence analysis (eg, promoter region)
<b>81346</b>	TYMS (thymidylate synthetase) (eg, 5-fluorouracil/5-FU drug metabolism), gene analysis, common variant(s) (eg, tandem repeat variant)
<b>81347</b>	SF3B1 (splicing factor [3b] subunit B1) (eg, myelodysplastic syndrome/acute myeloid leukemia) gene analysis, common variants (eg, A672T, E622D, L833F, R625C, R625L)
<b>81348</b>	SRSF2 (serine and arginine-rich splicing factor 2) (eg, myelodysplastic syndrome, acute myeloid leukemia) gene analysis, common variants (eg, P95H, P95L)
<b>81349</b>	Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and loss-of-heterozygosity variants, low-pass sequencing analysis
<b>81350</b>	UGT1A1 (UDP glucuronosyltransferase 1 family, polypeptide A1) (eg, drug metabolism, hereditary unconjugated hyperbilirubinemia [Gilbert syndrome]) gene analysis, common variants (eg, *28, *36, *37)
<b>81351</b>	TP53 (tumor protein 53) (eg, Li-Fraumeni syndrome) gene analysis; full gene sequence
<b>81352</b>	TP53 (tumor protein 53) (eg, Li-Fraumeni syndrome) gene analysis; targeted sequence analysis (eg, 4 oncology)
<b>81353</b>	TP53 (tumor protein 53) (eg, Li-Fraumeni syndrome) gene analysis; known familial variant
<b>81355</b>	VKORC1 (vitamin K epoxide reductase complex, subunit 1) (eg, warfarin metabolism), gene analysis, common variant(s) (eg, -1639G>A, c.173+1000C>T)
<b>81357</b>	U2AF1 (U2 small nuclear RNA auxiliary factor 1) (eg, myelodysplastic syndrome, acute myeloid leukemia) gene analysis, common variants (eg, S34F, S34Y, Q157R, Q157P)

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<b>81360</b>	ZRSR2 (zinc finger CCCH-type, RNA binding motif and serine/arginine-rich 2) (eg, myelodysplastic syndrome, acute myeloid leukemia) gene analysis, common variant(s) (eg, E65fs, E122fs, R448fs)
<b>81361</b>	HBB (hemoglobin, subunit beta) (eg, sickle cell anemia, beta thalassemia, hemoglobinopathy); common variant(s) (eg, HbS, HbC, HbE)
<b>81362</b>	HBB (hemoglobin, subunit beta) (eg, sickle cell anemia, beta thalassemia, hemoglobinopathy); known familial variant(s)
<b>81363</b>	HBB (hemoglobin, subunit beta) (eg, sickle cell anemia, beta thalassemia, hemoglobinopathy); duplication/deletion variant(s)
<b>81364</b>	HBB (hemoglobin, subunit beta) (eg, sickle cell anemia, beta thalassemia, hemoglobinopathy); full gene sequence
<b>81370</b>	HLA Class I and II typing, low resolution (eg, antigen equivalents); HLA-A, -B, -C, -DRB1/3/4/5, and -DQB1
<b>81371</b>	HLA Class I and II typing, low resolution (eg, antigen equivalents); HLA-A, -B, and -DRB1 (eg, verification typing)
<b>81372</b>	HLA Class I typing, low resolution (eg, antigen equivalents); complete (ie, HLA-A, -B, and -C)
<b>81373</b>	HLA Class I typing, low resolution (eg, antigen equivalents); one locus (eg, HLA-A, -B, or -C), each
<b>81374</b>	HLA Class I typing, low resolution (eg, antigen equivalents); one antigen equivalent (eg, B*27), each
<b>81375</b>	HLA Class II typing, low resolution (eg, antigen equivalents); HLA-DRB1/3/4/5 and -DQB1
<b>81376</b>	HLA Class II typing, low resolution (eg, antigen equivalents); one locus (eg, HLA-DRB1, -DRB3/4/5, -DQB1, -DQA1, -DPB1, or -DPA1), each
<b>81377</b>	HLA Class II typing, low resolution (eg, antigen equivalents); one antigen equivalent, each
<b>81378</b>	HLA Class I and II typing, high resolution (ie, alleles or allele groups), HLA-A, -B, -C, and -DRB1
<b>81379</b>	HLA Class I typing, high resolution (ie, alleles or allele groups); complete (ie, HLA-A, -B, and -C)
<b>81380</b>	HLA Class I typing, high resolution (ie, alleles or allele groups); one locus (eg, HLA-A, -B, or -C), each
<b>81381</b>	HLA Class I typing, high resolution (ie, alleles or allele groups); one allele or allele group (eg, B*57:01P), each
<b>81382</b>	HLA Class II typing, high resolution (ie, alleles or allele groups); one locus (eg, HLA-DRB1, -DRB3/4/5, -DQB1, -DQA1, -DPB1, or -DPA1), each
<b>81383</b>	HLA Class II typing, high resolution (ie, alleles or allele groups); one allele or allele group (eg, HLA-DQB1*06:02P), each
<b>81400</b>	Molecular pathology procedure, Level 1 (eg, identification of single germline variant [eg, SNP] by techniques such as restriction enzyme digestion or melt curve analysis)

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<b>81401</b>	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)
<b>81402</b>	Molecular pathology procedure, Level 3 (eg, >10 SNPs, 2-10 methylated variants, or 2-10 somatic variants [typically using non-sequencing target variant analysis], immunoglobulin and T-cell receptor gene rearrangements, duplication/deletion variants of 1 exon, loss of heterozygosity [LOH], uniparental disomy [UPD])
<b>81403</b>	Molecular pathology procedure, Level 4 (eg, analysis of single exon by DNA sequence analysis, analysis of >10 amplicons using multiplex PCR in 2 or more independent reactions, mutation scanning or duplication/deletion variants of 2-5 exons)
<b>81404</b>	Molecular pathology procedure, Level 5 (eg, analysis of 2-5 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of 6-10 exons, or characterization of a dynamic mutation disorder/triplet repeat by Southern blot analysis)
<b>81405</b>	Molecular pathology procedure, Level 6 (eg, analysis of 6-10 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of 11-25 exons, regionally targeted cytogenomic array analysis)
<b>81406</b>	Molecular pathology procedure, Level 7 (eg, analysis of 11-25 exons by DNA sequence analysis, mutation scanning or duplication/deletion variants of 26-50 exons)
<b>81407</b>	Molecular <u>pathology procedure</u> , Level 8 (eg, <u>analysis</u> of 26-50 exons by DNA sequence <u>analysis</u> , <u>mutation scanning</u> or duplication/deletion variants of >50 exons, <u>sequence analysis</u> of multiple genes on one platform)
<b>81408</b>	Molecular pathology procedure, Level 9 (eg, analysis of >50 exons in a single gene by DNA sequence analysis)
<b>81410</b>	Aortic dysfunction or dilation (eg, 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
<b>81411</b>	Aortic dysfunction or dilation (eg, Marfan syndrome, Loeys Dietz syndrome, Ehler Danlos syndrome type IV, arterial tortuosity syndrome); duplication/deletion analysis panel, must include analyses for TGFBR1, TGFBR2, MYH11, and COL3A1
<b>81412</b>	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
<b>81413</b>	Cardiac ion channelopathies (eg, Brugada syndrome, long QT syndrome, short QT syndrome, catecholaminergic polymorphic ventricular tachycardia); genomic sequence analysis panel, must include sequencing of at least 10 genes, including ANK2, CASQ2, CAV3, KCNE1, KCNE2, KCNH2, KCNJ2, KCNQ1, RYR2, and SCN5A
<b>81414</b>	Cardiac ion channelopathies (eg, Brugada syndrome, long QT syndrome, short QT syndrome, catecholaminergic polymorphic ventricular tachycardia);

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	duplication/deletion gene analysis panel, must include analysis of at least 2 genes, including KCNH2 and KCNQ1
<b>81415</b>	Exome (eg, unexplained constitutional or heritable disorder or syndrome); sequence analysis
<b>81416</b>	Exome (eg, unexplained constitutional or heritable disorder or syndrome); sequence analysis, each comparator exome (eg, parents, siblings) (List separately in addition to code for primary procedure)
<b>81417</b>	Exome (eg, unexplained constitutional or heritable disorder or syndrome); re-evaluation of previously obtained exome sequence (eg, updated knowledge or unrelated condition/syndrome)
<b>81418</b>	Drug metabolism (eg, pharmacogenomics) genomic sequence analysis panel, must include testing of at least 6 genes, including CYP2C19, CYP2D6, and CYP2D6 duplication/deletion analysis
<b>81419</b>	Epilepsy genomic sequence analysis panel, must include analyses for ALDH7A1, CACNA1A, CDKL5, CHD2, GABRG2, GRIN2A, KCNQ2, MECP2, PCDH19, POLG, PRRT2, SCN1A, SCN1B, SCN2A, SCN8A, SLC2A1, SLC9A6, STXB1, SYNGAP1, TCF4, TPP1, TSC1, TSC2, and ZEB2
<b>81422</b>	Fetal chromosomal microdeletion(s) genomic sequence analysis (eg, DiGeorge syndrome, Cri-du-chat syndrome), circulating cell-free fetal DNA in maternal blood
<b>81425</b>	Genome (eg, unexplained constitutional or heritable disorder or syndrome); sequence analysis
<b>81426</b>	Genome (eg, unexplained constitutional or heritable disorder or syndrome); sequence analysis, each comparator genome (eg, parents, siblings) (List separately in addition to code for primary procedure)
<b>81427</b>	Genome (eg, unexplained constitutional or heritable disorder or syndrome); re-evaluation of previously obtained genome sequence (eg, updated knowledge or unrelated condition/syndrome)
<b>81430</b>	Hearing loss (eg, 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
<b>81431</b>	Hearing loss (eg, nonsyndromic hearing loss, Usher syndrome, Pendred syndrome); duplication/deletion analysis panel, must include copy number analyses for STRC and DFNB1 deletions in GJB2 and GJB6 genes
<b>81432</b>	Hereditary breast cancer-related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer); genomic sequence analysis panel, must include sequencing of at least 10 genes, always including BRCA1, BRCA2, CDH1, MLH1, MSH2, MSH6, PALB2, PTEN, STK11, and TP53
<b>81433</b>	Hereditary breast cancer-related disorders (eg, hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer); duplication/deletion analysis panel, must include analyses for BRCA1, BRCA2, MLH1, MSH2, and STK11
<b>81434</b>	Hereditary retinal disorders (eg, retinitis pigmentosa, Leber congenital amaurosis, cone-rod dystrophy), genomic sequence analysis panel, must include sequencing of

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	at least 15 genes, including ABCA4, CNGA1, CRB1, EYS, PDE6A, PDE6B, PRPF31, PRPH2, RDH12, RHO, RP1, RP2, RPE65, RPGR, and USH2A
<b>81435</b>	Hereditary colon cancer disorders (eg, Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis); genomic sequence analysis panel, must include sequencing of at least 10 genes, including APC, BMPR1A, CDH1, MLH1, MSH2, MSH6, MUTYH, PTEN, SMAD4, and STK11
<b>81437</b>	Hereditary neuroendocrine tumor disorders (eg, medullary thyroid carcinoma, parathyroid carcinoma, malignant pheochromocytoma or paraganglioma); genomic sequence analysis panel, must include sequencing of at least 6 genes, including MAX, SDHB, SDHC, SDHD, TMEM127, and VHL
<b>81439</b>	Hereditary cardiomyopathy (eg, hypertrophic cardiomyopathy, dilated cardiomyopathy, arrhythmogenic right ventricular cardiomyopathy), genomic sequence analysis panel, must include sequencing of at least 5 cardiomyopathy-related genes (eg, DSG2, MYBPC3, MYH7, PKP2, TTN)
<b>81440</b>	Nuclear encoded mitochondrial genes (eg, neurologic or myopathic phenotypes), genomic sequence panel, must include analysis of at least 100 genes, including BCS1L, C10orf2, COQ2, COX10, DGUOK, MPV17, OPA1, PDSS2, POLG, POLG2, RRM2B, SCO1, SCO2, SLC25A4, SUCLA2, SUCLG1, TAZ, TK2, and TYMP
<b>81441</b>	Inherited bone marrow failure syndromes (IBMFS) (eg, Fanconi anemia, dyskeratosis congenita, Diamond-Blackfan anemia, Shwachman-Diamond syndrome, GATA2 deficiency syndrome, congenital amegakaryocytic thrombocytopenia) sequence analysis panel, must include sequencing of at least 30 genes, including BRCA2, BRIP1, DKC1, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, GATA1, GATA2, MPL, NHP2, NOP10, PALB2, RAD51C, RPL11, RPL35A, RPL5, RPS10, RPS19, RPS24, RPS26, RPS7, SBDS, TERT, and TINF2
<b>81442</b>	Noonan spectrum disorders (eg, Noonan syndrome, cardio-facio-cutaneous syndrome, Costello syndrome, LEOPARD syndrome, Noonan-like syndrome), genomic sequence analysis panel, must include sequencing of at least 12 genes, including BRAF, CBL, HRAS, KRAS, MAP2K1, MAP2K2, NRAS, PTPN11, RAF1, RIT1, SHOC2, and SOS1
<b>81445</b>	Solid organ neoplasm, genomic sequence analysis panel, 5-50 genes, interrogation for sequence variants and copy number variants or rearrangements, if performed; DNA analysis or combined DNA and RNA analysis
<b>81448</b>	Hereditary peripheral neuropathies (eg, Charcot-Marie-Tooth, spastic paraplegia), genomic sequence analysis panel, must include sequencing of at least 5 peripheral neuropathy-related genes (eg, BSCL2, GJB1, MFN2, MPZ, REEP1, SPAST, SPG11, SPTLC1)
<b>81449</b>	Solid organ neoplasm, genomic sequence analysis panel, 5-50 genes, interrogation for sequence variants and copy number variants or rearrangements, if performed; RNA analysis
<b>81450</b>	Hematolymphoid neoplasm or disorder, genomic sequence analysis panel, 5-50 genes, interrogation for sequence variants, and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; DNA analysis or combined DNA and RNA analysis

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<b>81451</b>	Hematolymphoid neoplasm or disorder, genomic sequence analysis panel, 5-50 genes, interrogation for sequence variants, and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; RNA analysis
<b>81455</b>	Solid organ or hematolymphoid neoplasm or disorder, 51 or greater genes, genomic sequence analysis panel, interrogation for sequence variants and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; DNA analysis or combined DNA and RNA analysis
<b>81456</b>	Solid organ or hematolymphoid neoplasm or disorder, 51 or greater genes, genomic sequence analysis panel, interrogation for sequence variants and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; RNA analysis
<b>81457</b>	Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis, microsatellite instability
<b>81458</b>	Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis, copy number variants and microsatellite instability
<b>81459</b>	Solid organ neoplasm, genomic sequence analysis panel, interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants, microsatellite instability, tumor mutation burden, and rearrangements
<b>81460</b>	Whole mitochondrial genome (eg, Leigh syndrome, mitochondrial encephalomyopathy, lactic acidosis, and stroke-like episodes [MELAS], myoclonic epilepsy with ragged-red fibers [MERFF], neuropathy, ataxia, and retinitis pigmentosa [NARP], Leber hereditary optic neuropathy [LHON]), genomic sequence, must include sequence analysis of entire mitochondrial genome with heteroplasmy detection
<b>81462</b>	Solid organ neoplasm, genomic sequence analysis panel, cell-free nucleic acid (eg, plasma), interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants and rearrangements
<b>81463</b>	Solid organ <u>neoplasm</u> , genomic sequence <u>analysis</u> panel, <u>cell-free nucleic acid</u> (eg, <u>plasma</u> ), interrogation for sequence variants; <u>DNA analysis</u> , <u>copy number variants</u> , and microsatellite instability
<b>81464</b>	Solid organ neoplasm, genomic sequence analysis panel, cell-free nucleic acid (eg, plasma), interrogation for sequence variants; DNA analysis or combined DNA and RNA analysis, copy number variants, microsatellite instability, tumor mutation burden, and rearrangements
<b>81465</b>	Whole mitochondrial genome large deletion analysis panel (eg, Kearns-Sayre syndrome, chronic progressive external ophthalmoplegia), including heteroplasmy detection, if performed
<b>81470</b>	X-linked intellectual disability (XLID) (eg, syndromic and non-syndromic XLID); genomic sequence analysis panel, must include sequencing of at least 60 genes, including ARX, ATRX, CDKL5, FGD1, FMR1, HUWE1, IL1RAPL, KDM5C, L1CAM, MECP2, MED12, MID1, OCRL, RPS6KA3, and SLC16A2

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<b>81471</b>	X-linked intellectual disability (XLID) (eg, syndromic and non-syndromic XLID); duplication/deletion gene analysis, must include analysis of at least 60 genes, including ARX, ATRX, CDKL5, FGD1, FMR1, HUWE1, IL1RAPL, KDM5C, L1CAM, MECP2, MED12, MID1, OCRL, RPS6KA3, and SLC16A2
<b>81479</b>	Unlisted molecular pathology procedure
<b>81490</b>	Autoimmune (rheumatoid arthritis), analysis of 12 biomarkers using immunoassays, utilizing serum, prognostic algorithm reported as a disease activity score
<b>81493</b>	Coronary artery disease, mRNA, gene expression profiling by real-time RT-PCR of 23 genes, utilizing whole peripheral blood, algorithm reported as a risk score
<b>81500</b>	Oncology (ovarian), biochemical assays of two proteins (CA-125 and HE4), utilizing serum, with menopausal status, algorithm reported as a risk score
<b>81503</b>	Oncology (ovarian), biochemical assays of five proteins (CA-125, apolipoprotein A1, beta-2 microglobulin, transferrin, and pre-albumin), utilizing serum, algorithm reported as a risk score
<b>81504</b>	Oncology (tissue of origin), microarray gene expression profiling of > 2000 genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as tissue similarity scores
<b>81506</b>	Endocrinology (type 2 diabetes), biochemical assays of seven analytes (glucose, HbA1c, insulin, hs-CRP, adiponectin, ferritin, interleukin 2-receptor alpha), utilizing serum or plasma, algorithm reporting a risk score
<b>81517</b>	Liver disease, analysis of 3 biomarkers (hyaluronic acid [HA], procollagen III amino terminal peptide [PIIINP], tissue inhibitor of metalloproteinase 1 [TIMP-1]), using immunoassays, utilizing serum, prognostic algorithm reported as a risk score and risk of liver fibrosis and liver-related clinical events within 5 years
<b>81518</b>	Oncology (breast), mRNA, gene expression profiling by real-time RT-PCR of 11 genes (7 content and 4 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithms reported as percentage risk for metastatic recurrence and likelihood of benefit from extended endocrine therapy
<b>81519</b>	Oncology (breast), mRNA, gene expression profiling by real-time RT-PCR of 21 genes, utilizing formalin-fixed paraffin embedded tissue, algorithm reported as recurrence score
<b>81520</b>	Oncology (breast), mRNA gene expression profiling by hybrid capture of 58 genes (50 content and 8 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a recurrence risk score
<b>81521</b>	Oncology (breast), mRNA, microarray gene expression profiling of 70 content genes and 465 housekeeping genes, utilizing fresh frozen or formalin-fixed paraffin-embedded tissue, algorithm reported as index related to risk of distant metastasis
<b>81522</b>	Oncology (breast), mRNA, gene expression profiling by RT-PCR of 12 genes (8 content and 4 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as recurrence risk score
<b>81523</b>	Oncology (breast), mRNA, next-generation sequencing gene expression profiling of 70 content genes and 31 housekeeping genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as index related to risk to distant metastasis



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<b>81525</b>	Oncology (colon), mRNA, gene expression profiling by real-time RT-PCR of 12 genes (7 content and 5 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a recurrence score
<b>81529</b>	Oncology (cutaneous melanoma), mRNA, gene expression profiling by real-time RT-PCR of 31 genes (28 content and 3 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as recurrence risk, including likelihood of sentinel lymph node metastasis
<b>81535</b>	Oncology (gynecologic), live tumor cell culture and chemotherapeutic response by DAPI stain and morphology, predictive algorithm reported as a drug response score; first single drug or drug combination
<b>81536</b>	Oncology (gynecologic), live tumor cell culture and chemotherapeutic response by DAPI stain and morphology, predictive algorithm reported as a drug response score; each additional single drug or drug combination (List separately in addition to code for primary procedure)
<b>81538</b>	Oncology (lung), mass spectrometric 8-protein signature, including amyloid A, utilizing serum, prognostic and predictive algorithm reported as good versus poor overall survival
<b>81540</b>	Oncology (tumor of unknown origin), mRNA, gene expression profiling by real-time RT-PCR of 92 genes (87 content and 5 housekeeping) to classify tumor into main cancer type and subtype, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a probability of a predicted main cancer type and subtype
<b>81541</b>	Oncology (prostate), mRNA gene expression profiling by real-time RT-PCR of 46 genes (31 content and 15 housekeeping), utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as a disease-specific mortality risk score
<b>81542</b>	Oncology (prostate), mRNA, microarray gene expression profiling of 22 content genes, utilizing formalin-fixed paraffin-embedded tissue, algorithm reported as metastasis risk score
<b>81546</b>	Oncology (thyroid), mRNA, gene expression analysis of 10,196 genes, utilizing fine needle aspirate, algorithm reported as a categorical result (eg, benign or suspicious)
<b>81552</b>	Oncology (uveal melanoma), mRNA, gene expression profiling by real-time RT-PCR of 15 genes (12 content and 3 housekeeping), utilizing fine needle aspirate or formalin-fixed paraffin-embedded tissue, algorithm reported as risk of metastasis
<b>81554</b>	Pulmonary disease (idiopathic pulmonary fibrosis [IPF]), mRNA, gene expression analysis of 190 genes, utilizing transbronchial biopsies, diagnostic algorithm reported as categorical result (eg, positive or negative for high probability of usual interstitial pneumonia [UIP])
<b>81595</b>	Cardiology (heart transplant), mRNA, gene expression profiling by real-time quantitative PCR of 20 genes (11 content and 9 housekeeping), utilizing subfraction of peripheral blood, algorithm reported as a rejection risk score
<b>81596</b>	Infectious disease, chronic hepatitis C virus (HCV) infection, six biochemical assays (ALT, A2-macroglobulin, apolipoprotein A-1, total bilirubin, GGT, and haptoglobin) utilizing serum, prognostic algorithm reported as scores for fibrosis and necroinflammatory activity in liver
<b>81599</b>	Unlisted multianalyte assay with algorithmic analysis



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<b>S3840</b>	DNA analysis for germline mutations of the RET proto-oncogene for susceptibility to multiple endocrine neoplasia type 2
<b>S3841</b>	Genetic testing for retinoblastoma
<b>S3842</b>	Genetic testing for Von Hippel-Lindau disease
<b>S3845</b>	Genetic testing for alpha-thalassemia
<b>S3846</b>	Genetic testing for hemoglobin E beta-thalassemia
<b>S3849</b>	Genetic testing for Niemann-Pick disease
<b>S3850</b>	Genetic testing for sickle cell anemia
<b>S3853</b>	Genetic testing for myotonic muscular dystrophy
<b>S3854</b>	Gene expression profiling panel for use in the management of breast cancer treatment
<b>S3861</b>	Genetic testing, sodium channel, voltage-gated, type V, alpha subunit (SCN5A) and variants for suspected Brugada Syndrome
<b>S3865</b>	Comprehensive gene sequence analysis for hypertrophic cardiomyopathy
<b>S3866</b>	Genetic analysis for a specific gene mutation for hypertrophic cardiomyopathy (HCM) in an individual with a known HCM mutation in the family
<b>S3870</b>	Comparative genomic hybridization (CGH) microarray testing for developmental delay, autism spectrum disorder and/or intellectual disability



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### REGULATORY NOTES:

Medical Necessity Guidelines are published to provide a better understanding of the basis upon which coverage decisions are made. CCA makes coverage decisions on a case-by-case basis by considering the individual member's health care needs. If at any time an applicable CMS LCD or NCD or state-specific MNG is more expansive than the criteria set forth herein, the NCD, LCD, or state-specific MNG criteria shall supersede these criteria.

This MNG references the specific regulations, coverage, limitations, service conditions, and/or prior authorization requirements in the following:

Medicare Benefit Policy Manual, Publication 100-02, Chapter 15, Section 80.1

Medicare National Coverage Determinations, Publication 100-03, Chapter 1, Part 2, Section 90.2

Medicare, Local Coverage Determination (L35000)

Medicare, Local Coverage Determination (L37606)

Medicare, Local Coverage Determination (L37810)

Medicare, Local Coverage Determination (L38371)

Medicare, Local Coverage Determination (L38968)

MassHealth, 130 CMR 433.000: Physician Services

MassHealth, 130 CMR 401.000, Independent Clinical Laboratory Manual, Subchapter 6

### DISCLAIMER:

Commonwealth Care Alliance (CCA) follows applicable Medicare and Medicaid regulations and uses evidence based InterQual® criteria, when available, to review prior authorization requests for medical necessity. This Medical Necessity Guideline (MNG) applies to all CCA Products unless a more expansive and applicable CMS National Coverage Determinations (NCDs), Local Coverage Determinations (LCDs), or state-specific medical necessity guideline exists. Medical Necessity Guidelines are published to provide a better understanding of the basis upon which coverage decisions are made. CCA makes coverage decisions on a case-by-case basis by considering the individual member's health care needs. If at any time an applicable CMS LCD or NCD or state-specific MNG is more expansive than the criteria set forth herein, the NCD, LCD, or state-specific MNG criteria shall supersede these criteria.

Benefit coverage for health services is determined by the member specific benefit plan document and applicable laws that may require coverage for a specific service. This Medical Necessity Guideline is subject to all applicable Plan Policies and Guidelines, including requirements for prior authorization and other requirements in Provider's agreement with the Plan (including complying with Plan's Provider Manual specifications).

This Medical Necessity Guideline is not a rigid rule. As with all CCA's criteria, the fact that a member does not meet these criteria does not, in and of itself, indicate that no coverage can be issued for these services. Providers are advised, however, that if they request services for any member who they know does not meet our criteria, the request should be accompanied by clear and convincing documentation of medical necessity. The preferred type of documentation is the letter of medical necessity, indicating that a request should be covered either because there is supporting science indicating medical necessity (supporting literature (full text preferred) should be attached to the request), or describing



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the member's unique clinical circumstances, and describing why this service or supply will be more effective and/or less costly than another service which would otherwise be covered. Note that both supporting scientific evidence and a description of the member's unique clinical circumstances will generally be required.

### RELATED REFERENCES:

1. Genetic Testing. UpToDate.com/login [via subscription only]. Published July 22, 2024. Accessed July 30, 2024. [https://www.uptodate.com/contents/genetic-testing?search=genetic&source=search\\_result&selectedTitle=6%7E150&usage\\_type=default&display\\_rank=6](https://www.uptodate.com/contents/genetic-testing?search=genetic&source=search_result&selectedTitle=6%7E150&usage_type=default&display_rank=6)
2. Next-generation DNA sequencing (NGS): Principles and clinical applications. UpToDate.com/login [via subscription only]. Published February 7, 2024. Accessed August 1, 2024. [https://www.uptodate.com/contents/next-generation-dna-sequencing-ngs-principles-and-clinical-applications?search=MOLECULAR%20TEST&source=search\\_result&selectedTitle=1%7E150&usage\\_type=default&display\\_rank=1](https://www.uptodate.com/contents/next-generation-dna-sequencing-ngs-principles-and-clinical-applications?search=MOLECULAR%20TEST&source=search_result&selectedTitle=1%7E150&usage_type=default&display_rank=1)
3. Overview of Pharmacogenomics. UpToDate.com/login [via subscription only]. Published July 5, 2024. Accessed July 23, 2024. [https://www.uptodate.com/contents/overview-of-pharmacogenomics?search=genetic&source=search\\_result&selectedTitle=10%7E150&usage\\_type=default&display\\_rank=10](https://www.uptodate.com/contents/overview-of-pharmacogenomics?search=genetic&source=search_result&selectedTitle=10%7E150&usage_type=default&display_rank=10)
4. October 3, 2023. Accessed July 30, 2024. [https://www.uptodate.com/contents/tools-for-genetics-and-genomics-gene-expression-profiling?search=MOLECULAR%20TEST&source=search\\_result&selectedTitle=2%7E150&usage\\_type=default&display\\_rank=2](https://www.uptodate.com/contents/tools-for-genetics-and-genomics-gene-expression-profiling?search=MOLECULAR%20TEST&source=search_result&selectedTitle=2%7E150&usage_type=default&display_rank=2)

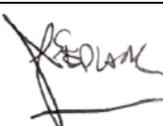


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**REVISION LOG:**

REVISION	DESCRIPTION
2/12/26	Removed deleted codes 81433, 81436, 81438.
2/13/25	Effective July 1, 2025, CPT 81490, 81506, 81517, 81596 are covered with prior authorization; CPT 81539, 81551 do not require prior authorization.
1/1/25	Template and CCA product update. Code updates: CPT 81508-81514, 81528 no longer require prior authorization. CPT 81535, 81536, 81538, 81539 covered with prior authorization.
8/8/24	Language clarification regarding use of applicable CMS/Mass Health guidelines. MNG refers to applicable LCD/NCD and MassHealth guidelines Current CPT code table replaced by updated CPT code list and no longer includes ICD 10 codes. Clinical coverage criteria are applicable when no CMS or MassHealth guidance.
12/31/23	Utilization Management Committee approval
11/9/23	CPT 81432 removed from Table 2 Noncovered codes, added to Table 1 covered codes. CPT codes removed, 81162, 81163, 81164, 81165, 81166, 81167, 81212, 81215, 81216, 81217; refer to Genetic Testing: BRCA-Related Breast and/or Ovarian Cancer Syndrome MNG.
9/26/22	Format of CPT codes changed. References to other internally developed genetic test MNGs added.
9/20/22	Noncovered CPT codes added.
6/2/22	Template update. Background information added to the overview and definitions section. Clinical eligibility and limitations updated to reflect CMS local coverage determination (L35000) and article (A56199). CPT codes added.

**APPROVALS:**

Jeffrey Sedlack	Senior Medical Director Utilization Review and Medical Policy
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	2/12/2026
<b>Signature</b>	<b>Date</b>
<b>CCA Senior Operational Lead</b>	<b>Title</b>
<b>Signature</b>	<b>Date</b>
<b>CCA CMO or Designee</b>	<b>Title</b>