

Medical Coverage Policy



Effective Date.....12/15/2019
Next Review Date.....12/15/2020
Coverage Policy Number 0514

Genetic Testing for Reproductive Carrier Screening and Prenatal Diagnosis

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Related Coverage Resources

[Genetics](#)
[Genetic Testing Collateral File](#)
[Recurrent Pregnancy Loss: Diagnosis and Treatment](#)
[Infertility Services](#)

INSTRUCTIONS FOR USE

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Overview

This Coverage Policy addresses genetic testing for germline variant reproductive carrier screening and prenatal diagnosis. Germline gene variants occur in the egg and sperm cells; also known as the germ cells. These variants are inherited; that is, passed down in families by blood relatives.

Reproductive carrier screening and prenatal diagnosis refer to testing for the presence of certain germline gene variants that are associated with disease or a risk of disease in an individual's offspring and descendants, before or after pregnancy has occurred. This type of testing allows for reproductive planning.

Coverage Policy

Many benefit plans limit coverage of genetic testing, genetic counseling and infertility services. Please refer to the applicable benefit plan language to determine benefit availability and terms, conditions and limitations of coverage for the services discussed in this Coverage Policy.

For additional information regarding coverage for specific genetic tests please refer to the [Genetic Testing Collateral: Molecular Test and Biomarkers](#).

[Genetic Counseling](#)

Medically Necessary

Pre-and post-test genetic counseling is considered medically necessary for EITHER of the following:

- an individual undergoing genetic testing
- an individual who is a potential candidate for genetic testing

by ANY of the following:

- an independent Board-Certified or Board-Eligible Medical Geneticist
- an American Board of Medical Genetics or American Board of Genetic Counseling-certified Genetic Counselor not employed by a commercial genetic testing laboratory (Genetic counselors are not excluded if they are employed by or contracted with a laboratory that is part of an Integrated Health System which routinely delivers health care services beyond just the laboratory test itself).
- a genetic nurse credentialed as either a Genetic Clinical Nurse (GCN) or an Advanced Practice Nurse in Genetics (APNG) by either the Genetic Nursing Credentialing Commission (GNCC) or the American Nurses Credentialing Center (ANCC) who is not employed by a commercial genetic testing laboratory

(Genetic nurses are not excluded if they are employed by or contracted with a laboratory that is part of an Integrated Health System which routinely delivers health care services beyond just the laboratory test.

Germline Carrier Testing for Familial Disease

Medically Necessary

Preconception or prenatal carrier testing for an individual who has the capacity and intention to reproduce is considered medically necessary when ANY of the following criteria is met:

- There is an identified pathogenic or likely pathogenic variant in a blood relative.
- EITHER of the following criteria is met:
 - an individual's reproductive partner is a known carrier of a disease-causing in a recessively inherited condition
 - a genetic diagnosis has been confirmed in an affected relative, AND the affected relative has not had genetic testing and is unavailable for testing

When ANY of the above criteria is met, preconception or prenatal carrier testing is considered medically necessary for the following indications (list may not be all inclusive):

Nuclear mitochondrial genes	Sickle cell disease
Muscular dystrophies (DMD, BMD, EDMD, DM1, DM2, SM)	Alpha and beta thalassemia
Fragile X syndrome	Gaucher disease
Rett syndrome	Niemann-Pick disease
PTEN-related disorders	Canavan disease
Von Hippel-Lindau disease	Tay-Sachs disease
Long QT syndrome	DFNB1 nonsyndromic hearing loss and deafness
Retinoblastoma	Huntington disease
21-hydroxylase deficiency	Cystic fibrosis

Preconception or prenatal genetic testing of a prospective biologic female parent for Fragile X (i.e., FMR1) gene mutations is considered medically necessary for EITHER of the following indications:

- family history of unexplained intellectual disability or developmental delay, or autism in a blood relative
- personal or family history of premature ovarian insufficiency

Preconception or prenatal carrier testing for spinal muscular atrophy by SMN1 gene variant analysis for the purpose of reproductive screening is considered medically necessary when the individual has the capacity and intention to reproduce and testing has not been previously performed.

Preconception or prenatal carrier testing for cystic fibrosis (CF) with targeted variant analysis of 23 CFTR gene variants (CPT code 81220) as described by the American College of Medical Genetics (ACMG) is considered medically necessary for a prospective biologic parent with the capacity and intention to reproduce and testing has not previously been performed.

Preconception or prenatal carrier testing for common deletions or variants in genes HBB, HBA1, or HBA2 for hemoglobinopathies (i.e., thalassemias, sickle cell disease) is considered medically necessary when ANY of the following criteria are met:

- clinical or laboratory features are suggestive of a hemoglobinopathy

- results of testing by conventional studies (e.g., electrophoresis, liquid chromatography, isoelectric focusing) yield equivocal results
- a definitive diagnosis remains uncertain OR a definitive diagnosis is known but specific mutation identification is necessary and clinical or laboratory features are suggestive of a hemoglobinopathy

Preconception or prenatal carrier testing for a prospective biologic parent of Ashkenazi Jewish (AJ) descent is considered medically necessary for the conditions specified by the American College of Medical Genetics, including but not limited to the following:

- familial dysautonomia (CPT code 81260)
- Tay-Sachs disease (CPT code 81255)
- Canavan disease (CPT code 81200)
- Fanconi anemia group C (CPT code 81242)
- Niemann-Pick disease, type A (CPT code 81330)
- Bloom syndrome (CPT code 81209)
- Mucopolysaccharidosis IV (CPT code 81290)
- Gaucher disease, type 1 (CPT code 81251)
- targeted panel testing for variants found in an individual of AJ descent

Not Medically Necessary

Reproductive carrier screening based on the general population risk, other than conditions noted above, is considered not medically necessary.

Reproductive carrier screening for nonmedical traits (e.g., eye color, hair color) is considered not medically necessary.

Preimplantation Genetic Testing of an Embryo

Medically Necessary

When the specific criteria noted below are met Cigna will cover the embryo biopsy procedure to obtain the cell and genetic testing associated with preimplantation genetic testing (PGT) under the core medical benefits of the plan.

The embryo biopsy procedure, genetic test and pre-and post-test genetic counseling associated with PGT (PGT for monogenic disorders [PGT-M] or PGT for chromosome) structural rearrangements [PGT-SR]) are considered medically necessary when ALL of the following criteria are met:

- for completely penetrant genetic disorders associated with severe disability and limited treatment options
- when the results of the genetic test will impact clinical decision-making and clinical outcome when ANY of the following criteria is met:
 - detection of known familial variants in an embryo when both biologic parents are carriers of a single gene autosomal recessively-inherited disorder
 - detection of a genetic disorder in an embryo when one biologic parent is a known carrier of a single gene autosomal dominantly-inherited disorder or a single x-linked disorder
 - detection of a chromosomal abnormality when one biologic parent is a translocation carrier

When the above criteria are met, PGT is considered medically necessary for the following indications (list may not be all inclusive):

Nuclear mitochondrial genes	Sickle cell disease
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Muscular dystrophies (DMD, BMD, EDMD, DM1, DM2, SM)	Alpha and beta thalassemia
Fragile X syndrome	Gaucher disease
Rett syndrome	Niemann-Pick disease
PTEN-related disorders	Canavan disease
Von Hippel-Lindau disease	Tay-Sachs disease
Long QT syndrome	DFNB1 nonsyndromic hearing loss and deafness
Retinoblastoma	Huntington disease
21-hydroxylase deficiency	Cystic fibrosis

Experimental/Investigational/Unproven

PGT for any other indication, including but not limited to the following, is considered experimental, investigational or unproven:

- human leukocyte antigen (HLA) typing of an embryo to identify a future suitable stem-cell tissue or organ transplantation donor
- testing solely to determine if an embryo is a carrier of an autosomal recessively-inherited disorder
- testing or screening for a condition with incomplete penetrance or significant variability of expression (e.g., Alzheimer's disease, cancer predisposition syndromes which are not fully penetrant)
- testing for a multifactorial condition
- testing for variants of unknown significance

Not Medically Necessary

PGT for testing of an embryo for nonmedical gender selection or nonmedical traits is considered not medically necessary.

Preimplantation Genetic Testing (PGT-A)

Not Medically Necessary

Preimplantation genetic testing for aneuploidy (PGT-AT) by any testing methodology (e.g., comparative genetic hybridization [CGH], fluorescence in situ hybridization [FISH], whole exome sequencing [WES], gene sequencing) for any indication, including but not limited to the following indications is considered not medically necessary:

- advanced maternal age (i.e., \geq age 35 years)
- repeated in vitro fertilization (IVF) failures
- recurrent spontaneous abortions

Prenatal Genetic Screening and Testing of a Fetus

Pre- and post-test genetic counseling is recommended for an individual who is considering genetic screening for fetal aneuploidy.

Sequencing-Based Non-Invasive Prenatal Testing (NIPT)

Medically Necessary

Sequencing-based non-invasive prenatal testing (NIPT) (CPT® codes 81420, 81507) to screen for fetal trisomy 13, 18 and 21 is considered medically necessary in a viable, single gestation pregnancy ≥ 10 weeks gestation.

Experimental/Investigational/Unproven

In-network coverage of sequencing-based NIPT screening tests for fetal trisomy 13, 18 and 21 performed in an out of network laboratory is considered not medically necessary since these are available at an in-network laboratory.

Sequencing-based non-invasive prenatal testing for any other indication, including but not limited to the following, is considered experimental, investigational or unproven:

- multiple gestation
 - screening for a sex-chromosome aneuploidy
 - vanishing twin syndrome
 - screening for trisomy 7, 9, 16 or 22
 - screening for microdeletions
 - single-gene disorders
 - whole genome NIPT
 - when used to determine genetic cause of miscarriage (e.g., missed abortion, incomplete abortion)
 - screening for non-medical traits (e.g., biologic sex)
-

Invasive Prenatal Testing of a Fetus

Medically Necessary

Invasive prenatal testing of a fetus for a familial variant considered medically necessary when the results of genetic testing will impact clinical decision-making and clinical outcome and ANY of the following criteria are met:

- the mother is a carrier of an X-linked condition
- both biologic parents are carriers of an autosomal recessively-inherited disorder OR the mother is a known carrier of an autosomal recessively-inherited disorder and the father's status is unknown and unavailable
- one parent is the carrier of an autosomal dominantly-inherited disorder

Prenatal testing of a fetus is considered medically necessary when abnormal findings have been identified on ultrasound.

Prenatal reproductive comparative genomic hybridization (CGH) testing (chromosomal microarray analysis) (CPT code 81228, 81229) is considered medically necessary for evaluation of a fetus for EITHER of the following indications:

- a woman is undergoing invasive prenatal genetic testing
 - intrauterine fetal loss at ≥20 weeks or stillbirth
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Germline Mutation Reproductive Genetic Testing for Recurrent Pregnancy Loss

Medically Necessary

The following genetic tests are considered medically necessary for the evaluation of recurrent pregnancy loss (i.e., two or more consecutive pregnancy losses):

- peripheral-blood karyotyping of the biologic parents to detect balanced chromosomal abnormalities
- molecular cytogenetic testing, using FISH when there is an inability to perform conventional karyotype testing of the products of conception (e.g., lack of sufficient tissue sample, poor culture growth)
- comparative genomic hybridization testing of products of conception when conventional karyotyping fails

Karyotyping of the products of conception is considered medically necessary for the evaluation of recurrent pregnancy loss when a reproductive couple with two pregnancy losses experiences a subsequent (i.e., third) pregnancy loss.

Not Medically Necessary

EITHER of the following genetic tests for recurrent pregnancy loss is considered not medically necessary:

- molecular testing for highly skewed X-inactivation patterns
- molecular cytogenetic testing using comparative genomic hybridization (CGH) testing for chromosomal analysis (e.g., parental blood)

Genetic testing for coagulation factor V Leiden (i.e., F5 gene mutation 1691G to A nucleotide change or prothrombin (i.e., F2 gene mutation 20210 G to A nucleotide change) for ANY of the following indications is considered not medically necessary (this list may not be all inclusive):

- adverse pregnancy outcomes such as recurrent pregnancy loss (i.e., two or more consecutive pregnancy losses), preeclampsia, intrauterine growth restriction and placental abruption)
- prenatal testing of a fetus or preimplantation genetic diagnosis (PGD)
- general population screening

Single gene mutation analysis, including for ANY of the following genes is considered not medically necessary in the evaluation of recurrent pregnancy loss:

- F2 (coagulation factor II), 1199G to A variant
- F5 (coagulation factor V) HR2 variant
- F7 (coagulation factor VII [serum prothrombin conversion accelerator] R353Q variant)
- F13B (coagulation factor XIII, B polypeptide, V34L variant)
- methylene tetrahydrofolate reductase (MTHFR) gene testing

[Germline Mutation Reproductive Genetic Testing for Infertility](#)

Medically Necessary

The following services are considered medically necessary when performed solely to establish the underlying etiology of infertility:

- genetic testing for cystic fibrosis in males with either congenital bilateral absence of vas deferens or azoospermia or severe oligospermia (i.e., < five million sperm/millimeter) with palpable vas deferens
- karyotyping for chromosomal abnormalities in males with nonobstructive azoospermia or severe oligospermia
- Y-chromosome microdeletion testing in males with nonobstructive azoospermia or severe oligospermia

- Sperm penetration assay (hamster penetration test, zona free hamster oocyte test) for those with male factor infertility, who are considering in vitro fertility (IVF) cycles and intracytoplasmic sperm (ICSI)

Experimental/Investigational/Unproven

In the absence of a diagnosis of infertility, Cigna considers IVF services associated with preimplantation genetic diagnosis to be not medically necessary.

The following tests are considered experimental, investigational or unproven:

- sperm DNA integrity testing (e.g., Sperm Chromatin Structure assay [SCSA], TUNEL assay, Comet assay, Human Sperm Activation Assay [HSAA], Sperm DNA Decondensation™)

General Background

Genetic Counseling

Genetic counseling is defined as the process of helping individuals understand and adapt to the medical, psychological and familial indications of genetic contributions to disease. Genetic counseling services span the life cycle from preconception counseling to infertility evaluation, prenatal genetic screening and diagnosis, and include predisposition evaluation and genetic diagnosis (National Society of Genetic Counselors [NSGC]; Edwards, 2010). Genetic counseling is recommended both pre-and post-genetic test to interpret family and medical histories to assess the chance of disease occurrence and recurrence, educate regarding inheritance, testing, management prevention and resources, and counsel to promote informed choices and adaptation to risk or condition (NSGC). A variety of genetics professionals provide these services: Board-Certified or Board-Eligible Medical Geneticists, an American Board of Medical Genetics or American Board of Genetic Counseling-certified Genetic Counselor, and genetic nurses credentialed as either a Genetic Clinical Nurse (GCN) or an Advanced Practice Nurse in Genetics (APGN) by either the Genetic Nursing Credentialing Commission (GNCC) or the American Nurses Credentialing Center (ANCC). Individuals should not be employed by a commercial genetic testing laboratory, although counseling services by these individuals are not excluded if they are employed by or contracted with a laboratory that is part of an Integrated Health System which routinely delivers health care services beyond just the laboratory test itself.

Germline Genetic Testing

A genetic test is defined as the analysis of human deoxyribonucleic acid (DNA), ribonucleic acid (RNA), chromosomes, proteins, and certain metabolites in order to detect mutations or alterations related to an inherited disorder; that is, one passed down by blood relatives. Genetic tests are often performed for the purpose of reproductive carrier screening and prenatal diagnosis to allow for reproductive planning. These terms refer to a search for certain genotypes that are already associated with disease or predisposition which may lead to disease in an individual's offspring and descendants, or may produce other variations not known to be associated with disease. Genetic testing for reproductive carrier screening and prenatal diagnosis may be appropriate in certain clinical scenarios, including carrier testing for familial disease, ethnic carrier screening, preimplantation genetic diagnostic testing of an embryo, prenatal testing and screening, recurrent pregnancy loss and infertility. Preconception or prenatal testing of a fetus allows for informed reproductive choices.

Carrier Testing for Familial Disease

Certain principles apply to genetic testing to determine the presence of gene mutations known to cause heritable disease within a blood-related family. It is generally appropriate to utilize a stepwise process for preconception and prenatal carrier testing unless timing of the testing will limit reproductive choice because of gestational age. Published consensus guidelines from the American College of Medical Genetics (AMCG, 2006) and the American Congress of Obstetricians and Gynecologists (2017) support carrier testing for familial disease. Carrier

testing, including testing for a known familial mutation, targeted mutation analysis, gene sequencing, duplication/deletion testing or gene dose analysis methods, is established as a means to improve health outcomes in selected individuals with risk of a familial disease. Such testing allows prospective parents to make informed reproductive choices.

Disorders for which preconception carrier testing may be appropriate include, but are not limited to the following:

Nuclear mitochondrial genes	21-hydroxylase deficiency
Muscular dystrophies (DMB, BMD, EDMD, DM1, DM2, SM)	Sickle cell disease
Fragile X	Alpha and beta Thalassemia
Rett syndrome	Gaucher disease
PTEN-related disorders	Niemann-Pick disease
Von Hippel-Lindau disease	Canavan disease
Long QT syndrome	Tay-Sachs disease
Retinoblastoma	DFNB1 nonsyndromic hearing loss and deafness
Huntington disease	Cystic fibrosis
Spinal Muscular Atrophy (SMA)	

Genetic testing for non-medical traits such as hair and eye color does not result in improved health outcomes and such testing is not considered to have clinical utility for these indications.

Certain disorders are known to occur with greater frequency in defined ethnic populations compared to frequency in the general population. The ACMG (2008) and ACOG (2017) published guidelines to support preconception and prenatal carrier screening for these indications. Genetic testing using targeted mutation panels is considered the standard of care for the following disorders:

- familial dysautonomia (CPT code 81260)
- Tay-Sachs disease (CPT code 81255)
- Canavan disease (CPT code 81200)
- Fanconi anemia group C (CPT code 81242)
- Niemann-Pick disease, type A (CPT code 81330)
- Bloom syndrome (CPT code 81209)
- Mucopolysaccharidosis IV (CPT code 81290)
- Gaucher disease, type 1 (CPT code 81251)

Such testing is considered standard of care in clinical practice for certain defined germline disorders; however, in the absence of clinical features which would suggest one of these disorders, the clinical utility of gene sequencing as a testing approach has not been established.

ACMG (2019) published consensus guidelines to support targeted mutation analysis of 23 CFTR mutations for testing of individuals for whom the risk of cystic fibrosis is a concern. In an effort to standardize the laboratory approach to screening, the Subcommittee on Cystic Fibrosis Screening, the American College of Medical Genetics (ACMG) recommends the use of a pan-ethnic panel that includes all mutations with an allele frequency $\geq 0.1\%$ in the general United States (U.S.) population. Initially, 25 mutations were included in the standard core mutation analysis of the CFTR gene; however, a 2004 update to the ACMG cystic fibrosis carrier screening statement recommended no additions and two deletions (I148T, 1078delT). The ACMG mutation panel is considered the standard test for population-based carrier testing and is performed in Clinical Laboratory Improvement Amendments (CLIA)-certified laboratories.

Targeted mutation analysis for common deletion or gene variants (i.e., HBB, HBA1, HBA2) is supported for thalassemia, and sickle cell disease. Gene sequencing and deletion/duplication studies may be appropriate to identify mutations if results of targeted mutation studies are negative or use of a stepwise approach limits reproductive options due to gestational age.

Consensus support for screening for all heritable conditions in the general population is lacking. According to the ACMG (2019), the approach to genetic counseling and testing for the different phenotypes has not yet been addressed on a population screening level. Except where identified as clinically useful elsewhere in this Coverage Policy, carrier screening in the general population in the absence of definitive clinical features does not impact clinical decision-making or improve health outcomes. Therefore, clinical utility for this indication has not been established.

Professional Societies/Organizations

For a summary of professional society recommendations/guidelines regarding germline genetic testing for familial disease please click [here](#).

Preimplantation Genetic Testing of an Embryo

Preimplantation genetic diagnosis (PGD), now referred to as preimplantation genetic testing (PGT) is clinically useful when a genetic disorder is completely penetrant. Complete penetrance means the gene or genes for a trait are expressed in all the population who have the genes (Genetics Home Reference [GHR], 2019). PGD may also be useful when the disorder is associated with severe disability and both reproductive partners are carriers of a single gene autosomal recessively-inherited disorder or one partner is a known carrier of an autosomal dominant or x-linked heritable disorder and the results will impact clinical decision-making. PGD may be appropriate for the following indications (this list may not be all-inclusive):

Nuclear mitochondrial genes	Sickle cell disease
Muscular dystrophies (DMD, BMD, EDMD, DM1, DM2, SM)	Alpha and beta thalassemia
Fragile X syndrome	Gaucher disease
Rett syndrome	Niemann-Pick disease
PTEN-related disorders	Canavan disease
Von Hippel-Lindau disease	Tay-Sachs disease
Long QT syndrome	DFNB1 nonsyndromic hearing loss and deafness
Retinoblastoma	Huntington disease
21-hydroxylase deficiency	Cystic fibrosis

Prenatal diagnosis or screening for conditions with incomplete penetrance or significant variability of expression (e.g., Alzheimer's disease, cancer predisposition) is possible; however, genetic testing is not helpful in predicting age of onset, severity, type of symptoms, or rate of progression in asymptomatic individuals. Likewise, use of PGD in multifactorial conditions and for testing for variants of unknown significance does not result in improved health outcomes. The clinical utility of PGD has not been established for these indications.

PGD used solely to determine if an embryo is a carrier of an autosomal recessively inherited disorder is not supported in published professional society/organization guidelines. PGD used solely to identify potential suitable stem-cell tissue or solid organ transplantation donor is not considered standard of care for this indication. PGD has also been proposed as a means to detect chromosomal rearrangements (e.g., translocations) in order to decrease the rate of spontaneous abortions. However, at this time there are insufficient data to support preimplantation genetic screening for unexplained recurrent miscarriage.

Although testing for a known familial mutation is an accepted testing strategy for PGD, the role of gene sequencing has not been established in the published peer reviewed scientific literature. Testing of an embryo for nonmedical gender selection or nonmedical traits, such as hair and eye color does not result in improved health outcomes and clinical utility for this indication has not been established.

Professional Societies/Organizations

For a summary of professional society recommendations/guidelines regarding preimplantation genetic diagnostic testing of an embryo please click [here](#).

Preimplantation Genetic Screening for Common Aneuploidy

PGD has been used for the screening of embryos for common aneuploidies in couples undergoing IVF procedures for infertility with a history of recurrent pregnancy loss, repeated IVF failures and/or advanced maternal age. When PGD is performed for any of these indications, it has been referred to as PGD-AS, or as preimplantation genetic screening (PGS). Outcome measures used in PGD-AS include pregnancy rates (e.g., for recurrent pregnancy loss, and live birth rates). The error rate of aneuploidy detection has been reported to be as high as 15%. This use of PGD is a screening procedure to detect those aneuploidies most commonly observed after birth or in miscarriages (e.g., involving detection of chromosomes X, Y, 13, 16, 18, 21, and 22). Together, these chromosomes account for 95% of all chromosomal abnormalities.

Additional well-designed, multicenter studies are needed before the role of preimplantation genetic screening (PGS) for aneuploidy can be established. There is insufficient evidence and professional guidance in the published, peer-reviewed scientific literature to support PGD for: human leukocyte antigen (HLA) - matching, screening of common aneuploidy or chromosomal translocations as a method to improve live birth rates, to reduce the risk of pregnancy loss in women of advanced maternal age, or for late-onset disorders. The clinical treatment utility of PGD for late-onset conditions has not been clearly delineated. Published consensus guidelines from ACOG (2009) do not support PGS as a genetic screening test for common aneuploidy. The clinical utility for this indication has not been established.

Literature Review

Studies evaluating the effectiveness of PGS include prospective nonrandomized and randomized controlled trials. In general study results have suggested that PGS does not improve pregnancy outcomes for young women with recurrent implantation failure or those of advanced maternal age (Rubio, et al., 2013; DeBrock, et al., 2010; Meyer, et al., 2009; Yakin, et al., 2008; Hardarson, et al., 2008; Mastenbroek, et al., 2007; Staessen, et al., 2004).

Professional Societies/Organizations

For a summary of professional society recommendations/guidelines regarding preimplantation genetic screening for common aneuploidy please click [here](#).

Prenatal Genetic Screening and Testing

Discussion of prenatal genetic screening and testing in this Coverage Policy refers to sequencing-based noninvasive prenatal tests (NIPT) (i.e., cell-free deoxyribonucleic acid [DNA] screening) and invasive prenatal tests such as chorionic villus sampling [CVS] and amniocentesis. These tests are performed in early pregnancy and used to test for germline mutation genetic disorders.

[Sequencing-Based Non-Invasive Prenatal Testing \(NIPT\)](#)

Sequencing-based genomic testing, a type of NIPT has been proposed for use as an advanced screening test to assess whether a pregnant woman is at increased risk of having a fetus affected by a genetic disorder (American College of Obstetricians and Gynecologists [ACOG], 2016). One benefit of such screening is the potential decrease in the number of invasive procedures, and therefore, the decrease in the potential for miscarriage as a complication of invasive testing. As a screening test for genetic disorders, sequencing-based NIPT may also allow for reproductive options.

Sequencing-based testing evaluates short segments of relies on the presence of circulating fetal or cell-free deoxyribonucleic acid (DNA) in the maternal plasma during pregnancy. The clinical utility of sequencing-based NIPT has been established as a means to detect fetal trisomy 13, 18 and 22 in the published, peer-reviewed scientific literature for a woman at ≥ 10 weeks gestation with a viable, singleton pregnancy. No specific test has been established to be significantly different than the others for this purpose.

The sensitivity and specificity of cell-free DNA screening has been reported to be uniformly high, ranging from 99.1%-100% and 99.7%-100%, respectively, primarily for trisomy 21. Negative predictive values have been reported to be near, or at 100%, with positive predictive values of 83% and 55% for high- and average-risk populations, respectively. Laboratories variably report screening results as positive, negative or 'no call', a

category to describe indeterminate or uninterpretable results. No-call results comprise approximately 4–8% of screened pregnancies and may occur secondary to assay failure, high assay variance or low fetal fraction. Low fetal fraction, defined as below 4%, confers significantly higher risk for fetal aneuploidy. Counseling before screening should include the possibility of results in this category (Dasche, 2016). Confirmatory CVS or amniocentesis is still needed in pregnancies with a positive result. According to the American College of Obstetricians and Gynecologists and the Society for Maternal-Fetal Medicine (2016), women with a positive screening test result should be counseled regarding their higher risk of aneuploidy and offered the option of diagnostic testing. Those who have a negative test result should be counseled regarding their lower adjusted and residual risk. Women with a negative screening result should not be offered additional screening tests for aneuploidy because this will increase their potential for a false-positive test result.

A number of sequencing-based NIPTs have been developed that utilize cell free DNA to detect fetal aneuploidy. Trisomies 13, 18 and 21 are detected with high accuracy. Many tests offer detection of one or more other syndromes, but detection of other aneuploidies has not have been determined to be clinically beneficial.

Depending on the testing methodology used for each individual test, sequencing-based NIPTs may also detect various other fetal genetic disorders, including trisomy 7, 9, 16 and 22, sex-chromosome aneuploidy (e.g., Klinefelter syndrome, Turner syndrome, Jacob syndrome), vanishing twin syndrome, fetal sex, and microdeletions. However, data are very limited in the published, peer-reviewed scientific literature regarding the predictive value of any of these tests to detect these additional fetal abnormalities, and whether maternal outcomes are improved if further invasive testing is required is unknown. Professional society support for these indications in the form of published consensus guidelines is also lacking.

The clinical utility of sequencing-based NIPT to detect trisomies 7, 9, 16 and 22 is also unknown; there is insufficient evidence in the published peer-reviewed scientific literature to establish whether pregnancy outcomes are improved by detection of these additional chromosomal abnormalities. Validation data regarding the predictive value of any NIPT to detect these trisomies are lacking in the published, peer-reviewed scientific literature.

Several laboratory methods allow for detection of microdeletions; however, data are lacking regarding the predictive value of NIPT for this indication and the impact on pregnancy outcomes is unknown. Such testing is not supported in the form of recommendations by ACMG (2013), the European Society of Human Genetics/American Society of Human Genetics and the Society for Maternal-Fetal Medicine. Validation data are limited regarding the role of NIPT for use as a screening tool in average-risk pregnancies or in a woman with a multiple gestation pregnancy and professional society support is lacking. At present, the role of NIPT for these indications has not been established. The clinical utility for NIPT to detect fetal sex is lacking in the scientific literature; professional society consensus guideline support is also lacking for this indication.

There are limited data in the published peer-reviewed scientific literature regarding the use of next generation sequencing performed via NIPT to identify single gene (monogenetic) disorders (Verhoef 2016, Chitty 2015, Dan 2016). However, unanswered questions about mosaicism and false positives raise concerns for harm and whether such testing requires confirmatory testing by invasive methods is not yet known (Jenkins, 2017). The clinical utility of NIPT to identify single gene disorders is currently unknown given the limited published peer reviewed scientific evidence. Published professional society support in the form of consensus guidelines is also lacking.

Literature Review

Trisomies 13, 18, 21: The role of sequencing-based cell-free DNA testing to detect trisomy 13, 18 and 21 has been investigated in a number of prospective clinical trials, systematic reviews and technology assessments to determine if there are improved clinical outcomes as a result of such testing (Gil, 2015; Zhang, 2015; Walsh, 2012; Norton, 2012).

Zhang et al. (2015) reported results of the clinical performance of massively parallel sequencing-based NIPT in detecting trisomies 21, 18 and 13 in 147,314 clinical samples in low-risk and high-risk pregnancies in a prospective, multicenter observational study. Eligibility for NIPT included participants of at least 18 years old with a singleton or twin pregnancy at nine weeks' gestation or beyond. Individuals were considered high-risk for

aneuploidy for any of the following: advanced maternal age (>35 years), a positive conventional Down syndrome screening test, abnormal sonographic markers, family history of aneuploidy or a previous pregnancy with a trisomic fetus. Individuals with none of the high-risk factors were defined as low risk for aneuploidy. NIPT performance in the detection of trisomy 21 in these two groups was compared using karyotyping or follow-up results as gold standard. There were a small number of cases positive for trisomies 18 and 13 in the low-risk group and NIPT performance for these two trisomies was not compared between risk groups. Results were obtained in 146,958 samples and outcome data were available in 112,669 (76.7%). Repeat sampling was required in 3,213 cases; 145 had test failure. Overall sensitivity of NIPT was 99.17%, 98.24% and 100% for trisomies 21, 18 and 13, respectively. Specificity was 99.95%, 99.95% and 99.96% for trisomies 21, 18 and 13, respectively. There was no significant difference in test performance between high-risk and low-risk subjects (sensitivity, 99.21% vs 98.97% ($p=0.82$); specificity, 99.95% vs 99.95% ($p=0.98$)). Data suggest that sequencing-based NIPT to detect trisomy 21 has high sensitivity and specificity in high and low-risk populations.

Gil et al. (2015) updated results of a previously published meta-analysis to include 37 studies published up to January 4, 2015. The inclusion criteria were prospective and retrospective peer-reviewed studies reporting clinical validation or implementation of maternal cell-free DNA (cfDNA) testing in screening for aneuploidies, in which data on pregnancy outcome were provided for more than 85% of the study population. Twenty-four studies reported on the performance of screening by cfDNA analysis for trisomy 21. Pooled weighted DNA testing and detection rates (DR) 99.2% and 0.09%, respectively. Twenty-one studies reported on the performance of screening by cfDNA analysis for trisomy 18. Pooled weighted DR and FPR were 96.3% and 0.13%, respectively. A total of 18 studies reported on the performance of screening by cfDNA analysis for trisomy 13. Pooled weighted DR and FPR were 91.0% and 0.13%, respectively. The performance of cfDNA analysis of maternal blood in the identification of singleton pregnancies with trisomy 18 or 13, with respective DRs of 96% and 91%, and a combined FPR of 0.26%, is worse than is the performance of screening for trisomy 21. DR and FPR for monosomy X were 90.3% and 0.23%, respectively, and 93.0% and 0.14%, respectively for sex chromosome aneuploidies other than monosomy X. For twin pregnancies, the DR for trisomy 21 was 93.7% and the FPR was 0.23. The authors note there are no advocates of screening for fetal trisomies 18 and 13 independently from screening for trisomy 21. Data from this systematic review and metaanalysis suggest a high detection rate and low false positive rate when testing for fetal trisomy 21.

There is sufficient evidence in the published, peer-reviewed scientific literature to establish the clinical validity of NIPT as a method to screen for these indications. Further, such testing is supported by published professional society consensus guidelines.

Norton et al. (2015) reported results of a prospective, multicenter trial comparing standard screening (i.e., measurement of nuchal translucency and biochemical analysis) and cell-free DNA (cfDNA) testing in pregnant women >18 years presenting for aneuploidy screening at 10-14 weeks of gestation. Study participants underwent both standard screening and cfDNA testing. Patients were ineligible if they were outside the gestational-age window, had no standard screening result, had known maternal aneuploidy or cancer, had conceived with the use of donor oocytes, or had a twin pregnancy or an empty gestational sac that was identified on ultrasonography. The primary outcome was the area under the receiver-operating-characteristic curve (AUC) for trisomy 21. The risk of trisomy 18 and 13 was also assessed. Lab personnel performing cfDNA analysis were blinded to all other clinical data, including results of ultrasonographic and standard screening. Using the maternal age of enrolled participants mid-trial, the estimate of the prevalence of trisomy 21 was adjusted to 1 in 500, and the required sample size reduced to 18,700. Of 18,955 women who were enrolled, results from 15,841 were available for analysis, with 1489 lost to follow-up.

Sixty-eight chromosomal abnormalities were identified (1 in 236 pregnancies). Of these, 38 were trisomy 21. The AUC for trisomy 21 was 0.999 for cfDNA testing and 0.958 for standard screening ($p=0.001$). Sensitivity to detect Trisomy 21 was 100% and 78.9% in the cfDNA and standard screening groups, respectively ($p=0.008$). False positive rates were 0.06% and 5.4% in the cfDNA and standard screening group, respectively ($p<0.001$). The positive predictive value for cfDNA testing was 80.9% compared with 3.4% for standard screening ($P<0.001$). Approximately 3% of cfDNA tests did not yield a result because of assay variation or a low fetal fraction.

Limitations noted by the authors include that the study only made a comparison between cfDNA testing and standard first-trimester screening and that the study was powered to compare only the detection of trisomy 21 in

the two study groups. The authors also note the rate of detection for trisomy 21 using standard screening methods was lower than the 82%-87% seen in other studies.

Whether results of this test impacted clinical management or improved pregnancy outcomes is unknown. While cfDNA has been validated as a method to detect trisomy 21, maternal serum and nuchal translucency screening can identify the risk for a broad array of abnormalities that are not detectable on cfDNA testing. The role of this test in screening for aneuploidy in woman without increased risk remains uncertain; and clinical utility has not been established.

Sex-Chromosome Aneuploidy: Data are also limited in the published peer-reviewed scientific literature regarding the ability of NIPTs to detect sex-chromosome aneuploidies. In a validation study by Mazloom et al. (2013), massively parallel sequencing was performed on cfDNA isolated from the plasma of 1564 pregnant women with known fetal karyotype. Another study of 411 maternal samples from women with blinded-to-laboratory fetal karyotypes was then performed to determine the accuracy of the classification algorithm. The blinded validation yielded a detection rate of 96.2%, a false positive rate of 0.3% and a nonreportable rate of 5%. Although a high detection rate and low false positive rate was reported in this single study there is insufficient evidence to establish the effectiveness of NIPT to detect sex chromosome aneuploidy, and the impact of such results on treatment planning. Further, support for use of NIPT as a method to detect sex-chromosome aneuploidy is lacking in the form of professional society consensus guidelines. At this time the role of NIPT for this indication has not been established.

Microdeletions: Guidelines from the American College of Medical Genetics (2013) and jointly published recommendations from the European Society of Human Genetics/American Society of Human Genetics (2015) as well as the Publications Committee of the Society for Maternal-Fetal Medicine (2015) note that use of NIPT to test for microdeletions is not recommended. Clinical validation studies relative to use of NIPTs to detect microdeletion syndromes are very limited in the published, peer-reviewed scientific literature. Wapner et al. (2015) reported on a test with a primary purpose of estimating the performance of a single-nucleotide polymorphism (SNP)-based noninvasive prenatal test for five microdeletion syndromes in 469 samples (358 plasma samples from pregnant women, 111 artificial plasma mixtures). These were amplified with the use of a massively multiplexed polymerase chain reaction, sequenced, and analyzed for the presence or absence of deletions of 22q11.2, 1p36, distal 5p, and the Prader-Willi/Angelman region. Detection rates were 97.8% for a 22q11.2 deletion, 100% for Prader-Willi, Angelman, 1p36 deletion, and cri-du-chat syndromes (24/24). False-positive rates were 0.76% for 22q11.2 deletion syndrome and 0.24% for cri-du-chat syndrome. No false positives occurred for Prader-Willi, Angelman or 1p36 deletion syndromes. SNP-based noninvasive prenatal microdeletion screening was accurate in this single study; however, additional validation studies are needed before such testing is useful in routine clinical practice.

Srinivasan et al. (2013) published results of a study involving 11 pregnant women. This small study was designed to determine the deep sequencing and analytic conditions needed to detect fetal subchromosome abnormalities across the genome from a maternal blood sample. Seven of seven cases of microdeletions, duplications, translocations, and one trisomy 20 were detected blindly by massively parallel sequencing. Small study numbers limit the ability to translate these results to routine clinical practice.

Professional Societies/Organizations

For a summary of professional society recommendations/guidelines regarding sequencing-based non-invasive prenatal testing please click [here](#).

[Invasive Diagnostic Prenatal Genetic Testing of a Fetus](#)

Other prenatal genetic testing of a fetus for which clinical utility has been established includes testing when the results of testing will impact clinical decision-making and clinical outcome and the mother is a carrier of an X-linked condition, when both biologic parents are carriers of an autosomal recessively-inherited disorder or the mother is a known carrier of an autosomal recessively-inherited disorder and the father's status is unknown and unavailable and when one parent is the carrier of an autosomal dominantly-inherited disorder. Additionally, prenatal testing using targeted mutation analysis (CPT code 81220) for cystic fibrosis when fetal echogenic

bowel has been identified on ultrasound is considered a standard of care based on professional society consensus guidelines. Prenatal reproductive comparative genomic hybridization (CGH) testing (chromosomal microarray analysis) (CPT code 81228, 81297) is also supported by guidelines published by ACOG (when a woman is undergoing invasive prenatal genetic testing or in the case of intrauterine fetal demise or stillbirth).

Literature Review

A number of prospective cohort and case series studies, systematic review and a meta-analysis have reported on the diagnostic accuracy for CGH/CMA compared with conventional karyotyping in greater than 13,000 prenatal samples (Dhillon, 2014; Calloway, 2013; Hillman, 2013, 2013b; Wapner, 2012; Armengol, 2012; Shaffer, 2012a; Lee, 2012; Reddy, 2012, Fiorentino, 2011a). Indications for testing include abnormal ultrasound, advanced maternal age, abnormal maternal serum screening, positive family history, parental anxiety and other or nonspecific. Overall, the data suggest microarray analysis provides significantly improved detection of clinically significant genomic abnormalities compared to those found with conventional karyotyping.

Professional Societies/Organizations

For a summary of professional society recommendations/guidelines regarding invasive diagnostic prenatal genetic testing of a fetus please click [here](#).

[Reproductive Genetic Testing for Recurrent Pregnancy Loss](#)

Chromosomal analysis tests and cytogenetic testing: Published professional society consensus guidelines support the clinical usefulness of chromosomal analysis, such as karyotyping of peripheral blood and products of conception in the case of three subsequent pregnancy losses. There is also consensus support for molecular cytogenetic testing when karyotyping of the products of conception is not possible because of a lack of tissue sample or poor culture growth.

Factor V Leiden (FVL) and Factor 2 G2021A Prothrombin (F2) Thrombophilia Testing

This Coverage Policy discusses preconception and prenatal carrier screening for recurrent pregnancy loss. For additional information regarding confirmatory testing for Factor V Leiden and Factor 2 prothrombin thrombophilia please see Cigna Coverage Policy 0052 Genetic Testing for Hereditary and Multifactorial Conditions.

Confirmatory genetic testing with targeted mutation analysis for factor V Leiden and F2 prothrombin is considered appropriate for certain individuals (i.e., a woman who is pregnant with a personal history of venous thromboembolism associated with a transient risk factor or who has a first-degree relative with factor V Leiden thrombophilia (FVL) or F2 G2021A (prothrombin) (F2) thrombophilia, a non-pregnant individual in which surgery is planned who has a first-degree relative with FVL or F2) based on published consensus guidelines by the American Congress of Obstetricians and Gynecologists ([ACOG], 2018), the American College of Medical Genetics, American College of Chest Physicians (2009) and others. Presence of the mutation only increases the relative risk for thrombophilia and is not predictive of a thrombotic event (GHR, 2018). Routine screening of all pregnant women is not recommended. Decisions on testing and prophylactic treatment for thrombophilic disorders are based on a risk/benefit assessment.

Whether there is an association between inherited thrombophilias and uteroplacental thrombosis that lead to adverse pregnancy outcomes such as fetal loss, preeclampsia, fetal growth restriction, and placental abruption is controversial. This possible association has resulted in increased screening for thrombophilias in pregnancy, although there has been no confirmation of treatment benefits (ACOG, 2018). Testing for inherited thrombophilias for a woman with recurrent fetal loss is not recommended in published consensus guidelines from the American Congress of Obstetricians and Gynecologists ([ACOG], 2018), the National Society of Genetic Counselors ([NSGC], 2005, reaffirmed 2010), the American Society of Reproductive Medicine ([ASRM], 2005; revised 2008; ASRM, 2012) and the Royal College of Obstetricians and Gynaecologists ([RCOG], 2011).

Literature Review

The scientific literature reports inconsistent findings for supporting any association with inherited thrombophilic disorders and recurrent early pregnancy loss, although some studies have shown a relationship with late pregnancy complications. A combination of thrombophilias may further increase the risk for recurrent fetal loss

(Laurino, et al., 2005), and identification of one or more of the more common thrombophilias in a woman with RSA may warrant further investigation for other risk factors. However, the probability of having a successful pregnancy outcome remains high despite the presence of thrombophilic disorders. The published peer-reviewed scientific evidence suggests that antithrombin III deficiency, protein C or S deficiency, factor V Leiden, prothrombin G20210A, and MTHFR (methylene tetrahydrofolate reductase [associated with hyperhomocysteinemia]) are not typically associated with pregnancy loss prior to 10 weeks gestation.

Factor V Leiden and F2 Prothrombin Thrombophilia: Bradley et al. (2012) reported results of a systematic review of the literature in an attempt to determine if testing reproductive age women with recurrent pregnancy loss for F5 c. 1691G to A nucleotide change and F2 c. 20210G to A variants improve pregnancy outcomes or if testing results useful in medical or decision-making. Of 302 articles reviewed 116 met the initial overall and key question-specific inclusion criteria. Summary estimates of analytic sensitivity and specificity were 98.8% and 99.3% for F5 tests, respectively; and 98.3% and 99.6%, for F2 tests, respectively. Included case-control and cohort studies reflected diversity in design and clinical heterogeneity. The data reflected an association between the presence of F5/F2 variants and recurrent pregnancy loss ($p < 0.001$); therefore, the authors rate the data as adequate to establish clinical validity. No studies were identified that directly addressed the balance of benefits and harms related to F5/F2 testing in this clinical scenario or the impact on decision making. Given the lack of benefit, and the potential harms, F5/F2 testing and treatment in women with recurrent pregnancy loss is likely to be associated with a net harm.

Rodgers et al. (2010) reported results of a meta-analysis and systematic review of prospective cohort studies to estimate the association of maternal FVL or prothrombin gene mutation (PGM) carrier status and placenta mediated pregnancy complications. The findings demonstrated that FVL is likely weakly associated with pregnancy loss and that neither FVL nor PGM are associated with preeclampsia or birth of a small for gestational age infant. The authors note further research is required to determine if FVL or PGM are associated with placental abruption and whether PGM is associated with important increases in pregnancy loss. The study demonstrated that the odds of pregnancy loss in women with FVL appear to be 52% higher as compared with women without FVL; however, the absolute event rate for pregnancy loss is low in women with FV Leiden compared with those without the FVL mutation (4.2% versus 3.2%, respectively).

Biron-Andreani et al. (2009) reported results of a systematic review and a meta-analysis of the literature to estimate precisely the association of the FVL mutation with the risk of first, or recurrent, pregnancy-related VTE. The risk of late fetal loss was higher in women who were homozygous compared with those who were non-carriers (13.7% versus 1.4%, respectively, odds ratio 11.41). It was similar in women who were heterozygous and in non-carriers (3.1% versus 1.4%, $p = 0.68$). The percentage of women with early fetal loss was similar in the three groups ($p = 0.81$). The live-birth rate was 80%, 84%, and 85%, respectively, for women who are homozygous, heterozygous, and non-carriers ($p = 0.88$).

Genetic Testing for Other Gene Mutations (i.e., F2 gene mutation 1199G to A nucleotide change, F5 gene mutation HR2, F7 [serum prothrombin conversion accelerator] gene mutation R353Q, and F13B polypeptide gene mutation V34L): Genetic testing has been proposed for these gene variants; however, data are lacking regarding the clinical utility of these tests to inform health outcomes in an individual with an hereditary hypercoagulability disorder.

Literature Review

High quality controlled clinical trial data are lacking regarding the ability of genetic testing to inform improved health outcomes, including the prevention of venous thromboembolic events in individuals with F2 1199G to A variant, F HR@ variant, F7 R353Q variant, and F13B polypeptide V34L variant.

Microarray Analysis: Evidence in the published peer-reviewed scientific literature, including textbook and reproductive health society positions, evaluating the utility of microarray analysis such as CGH and SNP for recurrent pregnancy loss is lacking and strong evidence-based conclusions cannot be made regarding clinical utility, estimated recurrence rates, and impact on patient management and patient clinical outcomes.

In a recent systematic review and meta-analysis involving nine published studies comparing CMA testing on the products of conception with conventional karyotyping, Dhillon et al. (2014) reported that CMA testing resulted in

a higher detection rate of abnormalities compared to karyotyping. The authors reported there was agreement between CMA and karyotyping in 86% of cases, CMA detected an additional 13% abnormalities versus karyotyping, and karyotyping detected 3% over CMA. The incidence of a variant of unknown significance was 2%. Unless uncertain findings were proven to be benign the authors included them as pathogenic. Overall, the authors acknowledged “additional prospective research is needed in this area using a large cohort, with a representative, prospective population undergoing both a recognized reproducible array and karyotyping.”

Testing for X-linked Recessive Traits: Genetic mutations such as X-linked recessive traits (e.g., highly skewed X-inactivation patterns) have also been investigated as a cause of RSA; however, data are limited. Some authors have reported that there is no correlation between skewed X-inactivation and RSA (Warburton, et al., 2010; Kaare, et al., 2008; Pasquier, et al., 2007; Hogge, et al., 2007). Moreover, recommendations of the National Society of Genetic Counselors (Laurino, et al., 2005; reaffirmed 2010) indicate that an association between X-inactivation patterns and pregnancy outcome has not been clearly established and further investigation should be conducted. Additionally, according to the ACOG practice bulletin (2001), commercially available testing for this and other related molecular genetic abnormalities is not widely available. At present, testing for highly skewed X-inactivation patterns as a cause of RSA is not well-supported in the literature.

Single Gene Mutation Analysis

Single gene mutation analysis is not indicated in the work-up of recurrent pregnancy loss. There is insufficient evidence in the published, peer-reviewed scientific literature to demonstrate clinical usefulness and it has not been established as a standard of care in clinical practice. To date, professional society support in the form of published consensus guidelines is lacking.

Professional Societies/Organizations

For a summary of professional society recommendations/guidelines regarding reproductive genetic testing for recurrent pregnancy loss please click [here](#).

[Reproductive Genetic Testing for Infertility](#)

Infertility is defined as the failure to achieve pregnancy after 12 months of regular unprotected intercourse (Agency for Healthcare Research and Quality [AHRQ], 2008; American Society of Reproductive Medicine [ASRM], 2013). The etiology of infertility may have a genetic basis such as cystic fibrosis in a male with congenital bilateral absence of vas deferens, azoospermia or severe oligospermia. Genetic testing with targeted mutation analysis of the 23 CFTR mutations as described by the ACMG and ACOG is considered clinically useful. Karyotyping, Y-chromosome microdeletion testing in males with nonobstructive azoospermia or severe oligospermia, and sperm penetration assays may also be considered appropriate. According to the American Urological Association (AUA, 2011), detection of certain genetic causes of male infertility allows couples to be informed about the potential to transmit genetic abnormalities that may affect the health of offspring. Thus, an appropriate male evaluation may allow the couple to better understand the basis of their infertility and to obtain genetic counseling when appropriate.

The clinical utility of sperm DNA integrity testing has not been established in the published, peer-reviewed scientific literature. This test has been proposed to identify a male factor contributing to unexplained infertility or in the treatment of infertility to direct interventions. Several tests for sperm DNA integrity are now available (e.g., Sperm Chromatin Structure Assay [SCSA], TUNEL assay, Comet assay). Another test to assess sperm DNA is the Sperm DNA Decondensation test (e.g., Human Sperm Activation Assay [HSAA], SDD™). The AUA (2011) reported that the assays demonstrate low sensitivity and high specificity; there is insufficient evidence to support the routine use of DNA integrity testing in the evaluation and management of male factor infertility.

Professional Societies/Organizations

For a summary of professional society/organization recommendations/guidelines regarding reproductive genetic testing for infertility please click [here](#).

Appendix A

PROFESSIONAL SOCIETY/ORGANIZATION RECOMMENDATIONS/GUIDELINES

CARRIER TESTING FOR FAMILIAL DISEASE:

American College of Medical Genetics (ACMG): In a policy statement regarding prenatal/preconception expanded carrier screening, ACMG (2013) notes:

- Disorders should be of a nature that most at-risk patients and their partners identified in the screening program would consider having a prenatal diagnosis to facilitate making decisions surrounding reproduction.
- The inclusion of disorders characterized by variable expressivity or incomplete penetrance and those known to be associated with a mild phenotype should be optional and made transparent when using these technologies for screening.
- For each disorder, the causative gene(s), mutations, and mutation frequencies should be known in the population being tested, so that meaningful residual risk in individuals who test negative can be assessed.
- The calculation of residual risk requires knowledge of two factors: one is the carrier frequency within a population, the other is the proportion of disease-causing alleles detected using the specific testing platform. Laboratories using multiplex platforms often have limited knowledge of one or both factors.
- There must be validated clinical association between the mutation(s) detected and the severity of the disorder.

In a policy statement regarding carrier screening for SMA (2008, reaffirmed 2013), ACMG notes:

- A negative screening test for one or both partners reduces but does not eliminate the possibility of an affected offspring, because the test sensitivity is <100% (~90% detection rate).
- Carrier testing should be offered to all couples regardless of race or ethnicity
- Carrier testing should be offered to asymptomatic individuals with a confirmed or suspected family history of SMA.
- A prerequisite for prenatal testing is the previous identification of the homozygous deletion in the proband or positive carrier status in the parents.

Regarding screening for Fragile X, ACMG notes (2004):

- Population carrier screening is not recommended at this time except as part of a well-defined clinical research protocol.
- DNA testing for permutation size alleles should be considered if a woman has ovarian failure before the age of 40, as part of the infertility evaluation and prior to in vitro fertilization.

American College of Medical Genetics (ACMG): ACMG practice guidelines for carrier screening in individuals of Ashkenazi Jewish descent include the following recommendations regarding genetic testing (Gross, et al., 2008, reaffirmed 2013):

- Carrier screening should be offered to all individuals of Ashkenazi Jewish descent who are pregnant or considering pregnancy.
- Carrier screening for these disorders should include testing for the specific mutations related to the conditions, which will result in a carrier detection rate 95% for most disorders.
- The offering of such testing should ideally take place before pregnancy, thereby giving individuals time to make appropriate reproductive decisions based on their own personal choices and cultural backgrounds. Currently, the majority of testing takes place in the primary care obstetrical setting and not in the medical genetic specialty environment. However, regardless of the clinical setting, adequate counseling should be provided to anyone considering testing so that choices are informed.

- If only one member of a couple is of Ashkenazi Jewish background, then testing should still be offered with the individual of Ashkenazi Jewish descent being tested first

Cystic Fibrosis:

In a policy statement regarding laboratory standards and guidelines for population-based cystic fibrosis carrier screening, ACMG (2001) notes the following:

- CF carrier screening should be offered to all individuals regardless of ethnicity
- preconception testing be encouraged whenever possible, although testing will often occur in the prenatal setting
- Couple-based testing is recommended for Caucasian couples of Northern European and Ashkenazi Jewish descent, particularly when concurrently testing for other common genetic disorders in the latter population.
- a pan-ethnic mutation panel that includes all CF-causing mutations with an allele frequency of $\geq 0.1\%$ in the general U.S. population is recommended.

ACMG (2011) states that an extended panel is not recommended for routine carrier screening of reproductive couples. The ACMG (2011) indications for CF genetic testing with the ACMG panel of 23 mutations include:

- carrier testing, partners of individuals with positive family history of CF
- carrier testing, partners of males with CBAVD
- carrier testing, general population of reproductive couples
- carrier testing, premarital population, to assist in selection of mate
- carrier testing, positive family history
- carrier testing, gamete donors
- preimplantation testing
- prenatal diagnostic testing, positive family history or for couples having a CF mutation in both partners
- prenatal diagnostic testing, echogenic bowel fetus during second trimester

American Congress of Obstetricians and Gynecologists (ACOG): A Committee Opinion on carrier screening for genetic conditions included the following recommendations (ACOG, 2017):

- General Recommendations
 - Information about genetic carrier screening should be provided to every pregnant woman. After counseling, a patient may decline any or all screening.
 - Carrier screening and counseling ideally should be performed before pregnancy.
 - If an individual is found to be a carrier for a specific condition, the individual's reproductive partner should be offered testing in order to receive informed genetic counseling about potential reproductive outcomes.
 - Concurrent screening of the patient and her partner is suggested if there are time constraints for decisions about prenatal diagnostic evaluation.
 - Carrier screening for a particular condition generally should be performed only once in a person's lifetime and the results should be documented in the patient's health record. Because of the rapid evolution of genetic testing, additional mutations may be included in newer screening panels. The decision to rescreen a patient should be undertaken only with the guidance of a genetics professional who can best assess the incremental benefit of repeat testing for additional mutations.
- Spinal Muscular Atrophy
 - Screening for spinal muscular atrophy should be offered to all women who are considering pregnancy or are currently pregnant.
 - In patients with a family history of spinal muscular atrophy, molecular testing reports of the affected individual and carrier testing of the related parent should be reviewed, if possible before testing. If reports are not available, SMN1 deletion testing should be recommended for the low-risk partner
- Cystic Fibrosis

- Carrier screening should be offered to all women who are considering pregnancy or are currently pregnant
- Complete analysis of the CFTR gene by DNA sequencing is not appropriate for routine carrier screening
- If a woman's reproductive partner has cystic fibrosis or apparently isolated congenital bilateral absence of the vas deferens, the couple should be provided follow-up genetic counseling by an obstetrician–gynecologist or other health care provider with expertise in genetics for mutation analysis and consultation.
- .Fragile X Syndrome
 - Fragile X premutation carrier screening is recommended for women with a family history of fragile X-related disorders or intellectual disability suggestive of fragile X syndrome and who are considering pregnancy or are currently pregnant.
 - If a woman has unexplained ovarian insufficiency or failure or an elevated follicle-stimulating hormone level before age 40 years, fragile X carrier screening is recommended to determine whether she has an FMR1 premutation.
 - All identified individuals with intermediate results and carriers of a fragile X premutation or full mutation should be provided follow-up genetic counseling to discuss the risk to their offspring of inheriting an expanded full-mutation fragile X allele and to discuss fragile X-associated disorders (premature ovarian insufficiency and fragile X tremor/ataxia syndrome).
 - Prenatal diagnostic testing for fragile X syndrome should be offered to known carriers of the fragile X premutation or full mutation.
 - DNA-based molecular analysis (e.g., Southern blot analysis and polymerase chain reaction) is the preferred method of diagnosis of fragile X syndrome and of determining FMR1 triplet repeat number (e.g., premutations). In rare cases, the size of the triplet repeat and the methylation status do not correlate, which makes it difficult to predict the clinical phenotype. In cases of this discordance, the patient should be referred to a genetics professional.
- Genetic Conditions in Individuals of Eastern and Central European Jewish Descent
 - When only one partner is of Ashkenazi Jewish descent, that individual should be offered screening first. If it is determined that this individual is a carrier, the other partner should be offered screening.
 - Tay–Sachs Disease
 - Screening for Tay–Sachs disease should be offered when considering pregnancy or during pregnancy if either member of a couple is of Ashkenazi Jewish, French–Canadian, or Cajun descent. Those with a family history consistent with Tay–Sachs disease also should be offered screening.
 - When one member of a couple is at high risk (i.e., of Ashkenazi Jewish, French–Canadian, or Cajun descent or has a family history consistent with Tay–Sachs disease) but the other partner is not, the high-risk partner should be offered screening. If the high-risk partner is found to be a carrier, the other partner also should be offered screening.
 - If Tay–Sachs disease screening is performed as part of pan-ethnic expanded carrier screening, it is important to recognize the limitations of the mutations screened in detecting carriers in the general population. In the presence of a family history of Tay–Sachs disease, expanded carrier screening panels are not the best approach to screening unless the familial mutation is included on the panel.
 - Referral to an obstetrician–gynecologist or other health care provider with genetics expertise may be helpful in instances of inconclusive enzyme testing results or in discussion of carrier testing of an individual with non-Ashkenazi Jewish ethnicity whose reproductive partner is a known carrier of Tay–Sachs disease.

Use Outside of the US:

European Cystic Fibrosis Society (2008): Guidelines published by Edenborough note that if a woman is pregnant and her genotype is unknown it is important to genotype her and her partner as soon as practical. If the partner is negative, no further tests are required but if he is a carrier or he is unavailable for testing consideration needs to be given to antenatal diagnosis via chorionic villus biopsy or amniocentesis.

Genetics Committee of the Society of Obstetricians and Gynaecologists of Canada (SOGC) and the Prenatal Diagnosis Committee of the Canadian College of Medical Geneticists (CCMG): Clinical practice guidelines for carrier screening for thalassemia and hemoglobinopathies in Canada include the following recommendations (Langlois, et al., 2008):

- If both partners are found to be carriers of thalassemia or an Hb variant, or of a combination of thalassemia and a hemoglobin variant, they should be referred for genetic counselling- ideally prior to conception, or as early as possible in the pregnancy. Additional molecular studies may be required to clarify the carrier status of the parents and thus the risk to the fetus.
- Prenatal diagnosis should be offered to the pregnant woman/couple at risk for having a fetus affected with a clinically significant thalassemia or hemoglobinopathy

The International Myotonic Dystrophy Consortium (IDMC, 2000): Published his society published genetic testing guidelines for DM1. Regarding reproductive carrier screening the Guidelines note that prenatal testing may be appropriate if:

- a parent has already been diagnosed with DM1, prenatal testing can be used to assess fetal risk
- a parent is at 50% risk and asymptomatic, the best approach is a two-step process by which the at-risk parent is tested first and prenatal testing done subsequently (if still necessary)

PREIMPLANTATION GENETIC DIAGNOSTIC TESTING OF AN EMBRYO:

American Society for Reproductive Medicine and the Society for Assisted Reproductive Technology (2007): Recommendations for PGD include:

- Before PGD is performed, genetic counseling must be provided.
- PGD can reduce the risk for conceiving a child with a genetic abnormality carried by one or both parents if that abnormality can be identified with tests performed on a single cell.
- Prenatal diagnostic testing to confirm the results of PGD is encouraged strongly because PGD has technical limitations that include the possibility of false negatives.

Use Outside of the US

Preimplantation Genetic Diagnosis International Society ([PGDIS], 2007): Guidelines note that PGD is currently performed for single gene disorders, late onset disorders with genetic predisposition, chromosomal disorders, including aneuploidy and structural rearrangements, and HLA typing to improve the access to HLA matched stem cell transplantation. The PGDIS recommends that first and second polar body cells and blastomeres (cleavage stage biopsy) be used in PGD and states that although blastocyst biopsy can be performed, the clinical application of this technique is new and requires large scale validation. In this consensus document, the PGDIS made the following recommendations for the indications in which PGD should be used:

- carriers of Mendelian disorders
- HLA typing for stem cell therapy of an affected sibling
- carriers of translocations or other structural chromosome abnormalities
- idiopathic recurrent pregnancy loss
- to reduce trisomic conceptions and spontaneous abortions in infertile patients

PREIMPLANTATION GENETIC SCREENING FOR COMMON ANEUPLOIDY:

American Society for Reproductive Medicine and the Society for Assisted Reproductive Technology (2007): Recommendations for PGS:

- Before PGS is performed, thorough education and counseling must be performed to ensure the patient understands the limitations of the technique, risk of error, and lack of evidence that PGS improves outcomes.

- Available evidence does not support the use of PGS as currently performed to improve live-birth rates in patients with advanced maternal age.
- Available evidence does not support the use of PGS as currently performed to improve live-birth rates in patients with previous implantation failure.
- Due to the high prevalence of aneuploidy in patients with recurrent implantation failure, decisions concerning future treatments should not be based on the results of PGS in one or more cycles.
- Available evidence does not support the use of PGS as currently performed to improve live-birth rates in patients with recurrent pregnancy loss.
- Available evidence does not support the use of PGS as currently performed to reduce miscarriage rates in patients with recurrent pregnancy loss related to aneuploidy.

Use Outside of the US

European Society of Human Reproduction and Embryology (ESHRE) Preimplantation Genetic Diagnosis (PGD) Consortium: The Consortium published best practice guidelines for PGD and PGS which recommend the use of polar body or cleavage stage biopsy but state that experience with and clinical application of blastocyst biopsy is limited at this time. Included in the guidelines were recommendations for inclusion criteria for PGD and PGS as well recommendations for timing of biopsy. The Consortium listed the following inclusion criteria for PGS (Thornhill, et al., 2004):

- recurrent miscarriage (> 2 miscarriages)
- repeated implantation failure (e.g. > 3 embryo transfers with high quality embryos or the transfer of ≥ 10 embryos in multiple transfers) defined as the absence of a gestational sac on ultrasound at ≥ 5 weeks

SEQUENCING-BASED NON-INVASIVE PRENATAL TESTING (NIPT):

American Congress of Obstetricians and Gynecologists (ACOG)/Society for Maternal-Fetal Medicine (SMFM), 2016: Joint guidelines from ACOG/SMFM include the following recommendations regarding screening for fetal aneuploidy:

Based on good and consistent scientific evidence (Level A):

- Women who have a negative test result should not be offered additional screening tests for aneuploidy because this will increase their potential for a false-positive test result.
- Because cell-free DNA is a screening test with the potential for false-positive and false-negative results, such testing should not be used as a substitute for diagnostic testing.
- All women with a positive cell-free DNA test result should have a diagnostic procedure before any irreversible action, such as pregnancy termination, is taken.
- Women whose cell-free DNA screening test results are not reported, are indeterminate, or are uninterpretable (a no call test result) should receive further genetic counseling and be offered comprehensive ultrasound evaluation and diagnostic testing because of an increased risk of aneuploidy.
- Women with a positive screening test result should be offered further detailed counseling and testing.

Based on limited or inconsistent scientific evidence (Level B):

- Cell-free DNA screening tests for microdeletions have not been validated clinically and are not recommended at this time.
- No method of aneuploidy screening is as accurate in twin gestations as it is in singleton pregnancies

Based primarily on consensus and expert opinion (Level C):

- Screening for aneuploidy should be an informed patient choice
- Aneuploidy screening or diagnostic testing should be discussed and offered to all women early in pregnancy, ideally at the first prenatal visit.
- All women should be offered the option of aneuploidy screening or diagnostic testing regardless of age
- Parallel or simultaneously testing with multiple screening methodologies is not cost-effective and should not be performed.

In a Committee Opinion by ACOG/SMFM on microarrays and next-generation sequencing technologies (2016) the Committee notes that cell-free whole genome DNA screening is not recommended.

American College of Medical Genetics ([ACMG], 2013): On behalf of the ACMG Gregg et al. published guidelines regarding noninvasive prenatal screening for aneuploidy. The Guidelines note:

- NIPS is not able to distinguish specific forms of aneuploidy. Identification of the mechanism of aneuploidy is important for recurrence risk counseling and emphasizes the importance of diagnostic testing following NIPS.
- NIPS does not screen for single-gene mutations.
- Uninformative test results due to insufficient isolation of cell-free fetal DNA could lead to a delay in diagnosis or eliminate the availability of information for risk assessment.
- NIPS does not screen for open neural tube defects.
- NIPS does not replace the utility of a first-trimester ultrasound examination
- Limited data are currently available on the use of NIPS in twins and higher-order pregnancies.
- NIPS has no role in predicting late-pregnancy complications.

European Society of Human Genetics (ESHG) and the American Society of Human Genetics (ASHG): On behalf of the ESHG/ASHG, Dondorp et al. (2015) published recommendations regarding NIPTs. The recommendations note the following:

- NIPT offers improved accuracy when testing for common autosomal aneuploidies compared with existing tests such as cFDS. However, a positive NIPT result should not be regarded as a final diagnosis
- Expanding NIPT-based prenatal screening to also report on sex chromosomal abnormalities and microdeletions not only raises ethical concerns related to information and counseling challenges but also risks reversing the important reduction in invasive testing achieved with implementation of NIPT for aneuploidy, and is therefore currently not recommended.

Society for Maternal-Fetal Medicine Publications Committee (2015): In publication #36 the Committee notes the following:

- The presence of a second gestational sac has been associated with false-positive cfDNA results; therefore, this test is not a good option for women with a “vanishing twin” or empty second sac. At this time, the data are too limited to recommend routine cfDNA aneuploidy screening in women with multifetal gestations.
- It is important for providers to recognize that a positive result for any of these aneuploidies confers a chance that the fetus is affected, which is usually far <99%, particularly in lower risk patients.
- When testing for rare conditions (such as aneuploidy in younger women), the positive predictive value is much lower than when testing for more common conditions (such as trisomy 21 in older women). More false-positive results are expected in women who are at low risk or when screening is done for very rare conditions. The PPV for trisomy 21 has been reported as varying from 45% in low-risk patients to ≥96% in the highest risk patients. In one study of diagnostic testing after abnormal cfDNA screens, aneuploidy was confirmed in 93% of trisomy 21 cases, in 64% of trisomy 18 cases, in 44% of trisomy 13 cases, and in 38% of sex chromosomal abnormalities.
- Testing for microdeletions using free cell DNA has not been validated in clinical trials; rather, proof-of-principle studies have included the mixing of normal and abnormal DNA in laboratory samples at ratios thought to represent typical fetal fraction. Even with very high sensitivity and specificity, at such low prevalence, the PPV of such testing is likely very low, and the clinical utility is unclear. At this time, routine screening for microdeletions with cfDNA is not recommended.

INVASIVE DIAGNOSTIC PRENATAL GENETIC TESTING OF A FETUS:

American Congress of Obstetricians and Gynecologists (ACOG)/Maternal and the Society for Maternal-Fetal Medicine (SMFM): In an update of the 2013 committee opinion, ACOG/SMFM published a document

regarding the use of chromosomal microarray analysis in prenatal diagnosis (2016). ACOG made the following recommendations:

- In patients with a fetus with one or more major structural abnormalities identified on ultrasonographic examination and who are undergoing invasive prenatal diagnosis, chromosomal microarray analysis is recommended. This test replaces the need for fetal karyotype.
- In patients with a structurally normal fetus undergoing invasive prenatal diagnostic testing, either fetal karyotyping or a chromosomal microarray analysis can be performed.
- Most genetic mutations identified by chromosomal microarray analysis are not associated with increasing maternal age; therefore, the use of this test for prenatal diagnosis can be considered for all women, regardless of age.
- In cases of intrauterine fetal demise or stillbirth when further cytogenetic analysis is desired, chromosomal microarray analysis on fetal tissue (ie, amniotic fluid, placenta, or products of conception) is recommended because of its increased likelihood of obtaining results and improved detection of causative abnormalities.
- Limited data are available on the clinical utility of chromosomal microarray analysis to evaluate first-trimester and second-trimester pregnancy losses; therefore, this is not recommended at this time.
- Comprehensive patient pretest and posttest genetic counseling from qualified personnel such as a genetic counselor or geneticist regarding the benefits, limitations, and results of chromosomal microarray analysis is essential.

Use Outside of the US

Italian Society of Human Genetics ([SIGU], 2012): Based on a review of the recent literature and the knowledge and experience of the working group, the Society made the following recommendations for prenatal CGH testing:

- never as a substitute for conventional karyotyping;
- for specific diagnostic purposes in selected pregnancies and not for general screening in all pregnancies;
- only in prenatal cases with specific indications, such as:
 - single (apparently isolated) or multiple sonographic fetal abnormalities;
 - de novo chromosomal rearrangements, even if apparently balanced, detected by standard karyotyping, to investigate the possible presence of cryptic imbalance(s) related to the structural chromosome abnormality;
 - supernumerary marker chromosomes in order to characterize their origin and genetic content.

SIGU is recommended using a genome-wide array and parental testing when an uncommon CNV is found.

Genetics Committee of the Society of Obstetricians and Gynaecologists of Canada (SOGC) and the Prenatal Diagnosis Committee of the Canadian College of Medical Geneticists (CCMG): In a technology update (Duncan, et al., 2011), the Committee summarized the current literature and made recommendations for aCGH in the prenatal setting. The recommendations included the following:

- Array genomic hybridization is not recommended in pregnancies at low risk for a structural chromosomal abnormality; for example, advanced maternal age, positive maternal serum screen, previous trisomy, or the presence of soft markers on fetal ultrasound.
- Array genomic hybridization may be an appropriate diagnostic test in cases with fetal structural abnormalities detected on ultrasound or fetal magnetic resonance imaging; it could be done in lieu of a karyotype if rapid aneuploidy screening is negative and an appropriate turnaround time for results is assured.

Any pregnant woman who qualifies for microarray genomic hybridization testing should be seen in consultation by a medical geneticist before testing so that the benefits, limitations, and possible outcomes of the analysis can be

discussed in detail. The difficulties of interpreting some copy number variants should also be discussed. This will allow couples to make an informed decision about whether or not they wish to pursue such prenatal testing.

REPRODUCTIVE GENETIC TESTING FOR RECURRENT PREGNANCY LOSS:

American College of Medical Genetics (ACMG, 2013): On behalf of the ACMG, Hickey et al. published guidelines regarding MTHFR polymorphism testing. The guideline notes that MTHFR polymorphism genotyping should not be ordered as part of the clinical evaluation for thrombophilia or recurrent pregnancy loss.

American Congress of Obstetricians and Gynecologists ([ACOG]: A Practice Bulletin regarding thromboembolism in pregnancy (ACOG, 2016) notes women who have a history of thrombosis who have not had a complete evaluation of underlying etiologies should be tested for antiphospholipid antibodies and inherited thrombophilias.

A Practice Bulletin regarding inherited thrombophilias in pregnancy (ACOG, 2018) notes:

- Screening for inherited thrombophilias is useful only when results will impact management decisions. It is not useful when treatment is indicated for other risk factors.
- Screening is not recommended for women with a history of fetal loss or adverse pregnancy outcomes (e.g., abruption, preeclampsia, fetal growth restriction)
- Screening with MTHFR mutation analysis or fasting homocysteine level is not recommended

ACOG/The Society for Maternal Fetal Medicine: ACOG/SMFM (2016) published a Committee Opinion regarding chromosomal microarray (CMA) and next generation sequencing for prenatal diagnosis. The Committee notes that CMA of fetal tissue (i.e., amniotic fluid, placenta, products of conception) is recommended in the evaluation of intrauterine death or stillbirth when further cytogenetic analysis is desired. The Opinion also noted that whole exome and whole genome sequencing for prenatal diagnosis is not recommended outside the context of clinical trials. Cell-free DNA screening is not recommended.

American Society of Reproductive Medicine ([ASRM], 2012): ASRM published the following recommendations for the evaluation and treatment of recurrent pregnancy loss:

- assessment of RSA focuses on screening for genetic factors and antiphospholipid syndrome, assessment of uterine anomaly, hormonal and metabolic factors, and lifestyle variables. These may include the following genetic tests:
 - peripheral karyotypic analysis of parents
 - karyotypic analysis of products of conception in the setting of ongoing therapy for RSA

ASRM notes if a remediable cause of recurrent pregnancy loss is identified cytogenetic analysis of subsequent losses can be employed to determine whether the event was random and not a treatment failure per se. If a 46 XX karyotype is revealed by cytogenetic analysis, reflex DNA extraction and analysis of maternal serum by microsatellite analysis may permit differentiation between a fetal source versus a maternal source.

National Society for Genetic Counselors ([NSGC], 2005, reaffirmed 2010: on behalf of the NSGC, Laurino, et al. published guidelines noting a referral to a genetics specialist is indicated when prior evaluations for RSA have been normal and when the pregnancy, medical and family history evaluation indicate a possible genetic cause for RSA. Other NSGC genetic evaluation and testing recommendations include the following:

- when possible, chromosomal analysis on fetal tissue
- routine karyotyping of each partner
- testing for factor V Leiden and prothrombin G20210A should be considered
- testing for less common thrombophilias (anticoagulant protein C, protein S, antithrombin III) should be reserved for those women with a personal and/or family history of venous thromboembolism

- testing for thermolabile C677T methylenetetrahydrofolate reductase mutation (MTHFR) is not justified (associated with some hereditary thrombophilia patterns such as hyperhomocysteinemia)
- testing for alpha thalassemia for Southeast Asian and Mediterranean ancestry is recommended (with or without a personal family history of fetal hydrops)
- specialized chromosomal studies such as comparative genome hybridization, subtelomeric studies, interphase studies on sperm, and assays for skewed X-inactivation patterns are not warranted (the clinical utility has yet to be proven)

The NSGC reaffirmed that the use of specialized chromosomal studies such as comparative genome hybridization, subtelomeric studies, interphase studies on sperm and assays for skewed X-inactivation patterns are not warranted at this time, as their clinical utility has yet to be determined

Pregnancy and Thrombosis Working Group: On behalf of this association, Duhl et al. (2007) published a consensus report and recommendations for prevention and treatment of VTE and adverse pregnancy outcome. The authors acknowledged that no clear conclusions can be drawn from the studies they reviewed regarding an association between inherited thrombophilias and adverse pregnancy outcomes—some studies show a positive relationship, and other studies show no relationship. According to Duhl, most of the research demonstrated that FVL is not typically associated with pregnancy loss prior to 10 weeks' gestation. More evidence exists suggesting that a loss after 10 weeks' gestation may be associated with these disorders.

Use Outside of the US:

Royal College of Obstetricians and Gynaecologists (RCOG): The RCOG (2011) guidelines note:

- Cytogenetic analysis should be performed on products of conception of the third and subsequent consecutive miscarriages(s).
- All couples with a history of recurrent miscarriage should have peripheral-blood karyotyping performed where testing of products of conception reports an unbalanced structural chromosomal abnormality.
- Women with second-trimester miscarriage should be screened for inherited thrombophilias including factor V Leiden, factor II (prothrombin) gene mutation and protein S.

REPRODUCTIVE GENETIC TESTING FOR INFERTILITY:

American Society of Reproductive Medicine (2013): The Practice Committee of the ASRM (2013) noted there is insufficient evidence to recommend the routine use of sperm DNA integrity tests in the evaluation and treatment of the infertile couple.

American Urological Association ([AUA], 2011): Regarding genetic etiology for male infertility the AUA notes:

- Men with nonobstructive azoospermia and severe oligospermia should be informed that they might have chromosomal abnormalities or Y- chromosome microdeletions. In addition, men with azoospermia due to CBAVD should be informed that they probably have an abnormality of the cystic fibrosis transmembrane conductance regulator (CFTR) gene. Genetic counseling should be provided whenever a genetic abnormality is detected.
- Men with congenital bilateral absence of the vasa deferentia should be offered genetic counseling and testing for cystic fibrosis transmembrane conductance regulator mutations.
- The female partner should also be offered cystic fibrosis transmembrane conductance regulator mutations testing before proceeding with treatments that utilize the sperm of a man with congenital bilateral absence of the vasa deferentia.

Coding/Billing Information

Note: 1) This list of codes may not be all-inclusive.

- 2) Deleted codes and codes which are not effective at the time the service is rendered may not be eligible for reimbursement

Genetic Counseling

Considered Medically Necessary when criteria in the applicable policy statements listed above are met:

CPT® Codes	Description
96040	Medical genetics and genetic counseling services, each 30 minutes face-to-face with patient/family

HCPCS Codes	Description
S0265	Genetic counseling, under physician supervision, each 15 minutes

Germline Carrier Testing for Familial Disease

Considered Medically Necessary when criteria in the applicable policy statements listed above are met:

CPT® Codes	Description
81161	DMD (dystrophin) (eg, Duchenne/Becker muscular dystrophy) deletion analysis, and duplication analysis, if performed
81187	CNBP (CCHC-type zinc finger nucleic acid binding protein) (eg, myotonic dystrophy type 2) gene analysis, evaluation to detect abnormal (eg, expanded) alleles
81200	ASPA (aspartoacylase) (eg, Canavan disease) gene analysis, common variants (eg, E285A, Y231X)
81205	BCKDHB (branched-chain keto acid dehydrogenase E1, beta polypeptide) (eg, maple syrup urine disease) gene analysis, common variants (eg, R183P, G278S, E422X)
81209	BLM (Bloom syndrome, RecQ helicase-like) (eg, Bloom syndrome) gene analysis, 2281del6ins7 variant
81220	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; common variants (eg, ACMG/ACOG guidelines)
81221	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; known familial variants
81222	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; duplication/deletion variants
81223	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; full gene sequence
81224	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; intron 8 poly-T analysis (eg, male infertility)
81234	DMPK (DM1 protein kinase) (eg, myotonic dystrophy type 1) gene analysis; evaluation to detect abnormal (expanded) alleles
81239	DMPK (DM1 protein kinase) (eg, myotonic dystrophy type 1) gene analysis; characterization of alleles (eg, expanded size)
81242	FANCC (Fanconi anemia, complementation group C) (eg, Fanconi anemia, type C) gene analysis, common variant (eg, IVS4+4A>T)
81243	FMR1 (fragile X mental retardation 1) (eg, fragile X mental retardation) gene analysis; evaluation to detect abnormal (eg, expanded) alleles
81244	FMR1 (fragile X mental retardation 1) (eg, fragile X mental retardation) gene analysis; characterization of alleles (eg, expanded size and methylation status)
81251	GBA (glucosidase, beta, acid) (eg, Gaucher disease) gene analysis, common variants (eg, N370S, 84GG, L444P, IVS2+1G>A)
81252	GJB2 (gap junction protein, beta 2, 26kDa, connexin 26) (eg, nonsyndromic hearing loss) gene analysis; full gene sequence
81253	GJB2 (gap junction protein, beta 2, 26kDa, connexin 26) (eg, nonsyndromic hearing loss) gene analysis; known familial variants

81254	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)])
81255	HEXA (hexosaminidase A [alpha polypeptide]) (eg, Tay-Sachs disease) gene analysis, common variants (eg, 1278insTATC, 1421+1G>C, G269S)
81256	HFE (hemochromatosis) (eg, hereditary hemochromatosis) gene analysis, common variants (eg, C282Y, H63D)
81257	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, and Constant Spring)
81258	HBA1/HBA2 (alpha globin 1 and alpha globin 2) (eg, alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; known familial variant
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
81260	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)
81269	HBA1/HBA2 (alpha globin 1 and alpha globin 2) (eg, alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; duplication/deletion variants
81271	HTT (huntingtin) (eg, Huntington disease) gene analysis; evaluation to detect abnormal (eg, expanded) alleles
81274	HTT (huntingtin) (eg, Huntington disease) gene analysis; characterization of alleles (eg, expanded size)
81290	MCOLN1 (mucolipin 1) (eg, Mucopolipidosis, type IV) gene analysis, common variants (eg, IVS3-2A>G, del6.4kb)
81302	MECP2 (methyl CpG binding protein 2) (eg, Rett Syndrome) gene analysis; full sequence analysis
81303	MECP2 (methyl CpG binding protein 2) (eg, Rett Syndrome) gene analysis; known familial variant
81304	MECP2 (methyl CpG binding protein 2) (eg, Rett Syndrome) gene analysis; duplication/deletion variants
81321	PTEN (phosphatase and tensin homolog) (eg, Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; full sequence analysis
81322	PTEN (phosphatase and tensin homolog) (eg, Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; known familial variant
81323	PTEN (phosphatase and tensin homolog) (eg, Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; duplication/deletion variant
81329	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
81330	SMPD1 (sphingomyelin phosphodiesterase 1, acid lysosomal) (eg, Niemann-Pick disease, Type A) gene analysis, common variants (eg, R496L, L302P, fsP330)
81336	SMN1 (survival of motor neuron 1, telomeric) (eg, spinal muscular atrophy) gene analysis; full gene sequence
81337	SMN1 (survival of motor neuron 1, telomeric) (eg, spinal muscular atrophy) gene analysis; known familial sequence variant(s)
81361	HBB (hemoglobin, subunit beta) (eg, sickle cell anemia, beta thalassemia, hemoglobinopathy); common variant(s) (eg, HbS, HbC, HbE)
81362	HBB (hemoglobin, subunit beta) (eg, sickle cell anemia, beta thalassemia, hemoglobinopathy); known familial variant(s)
81363	HBB (hemoglobin, subunit beta) (eg, sickle cell anemia, beta thalassemia, hemoglobinopathy); duplication/deletion variant(s)
81364	HBB (hemoglobin, subunit beta) (eg, sickle cell anemia, beta thalassemia, hemoglobinopathy); full gene sequence

81400 ^{††}	Molecular pathology procedure, Level 1 (eg, identification of single germline variant [eg, SNP] by techniques such as restriction enzyme digestion or melt curve analysis)
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)
81403 ^{††}	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)
81404	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)
81405 ^{††}	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)
81406 ^{††}	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)
81408	Molecular pathology procedure, Level 9 (eg, analysis of > 50 exons in a single gene by DNA sequence analysis)
81430	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
81431	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
81479 ^{†††}	Unlisted molecular pathology procedure
83080	b-Hexosaminidase, each assay

[†]Note: Considered Not Medically Necessary when used to report:

- F2 (coagulation factor 2) (eg, hereditary hypercoagulability), 1199G>A variant) (81400)
- F5 (coagulation factor V) (eg, hereditary hypercoagulability) (81400)
- F7 (coagulation factor VII [serum prothrombin conversion accelerator] R353Q variant) for recurrent pregnancy loss (81400)
- F13B (coagulation factor XIII, B polypeptide, V34L variant) for recurrent pregnancy loss (81400)

^{††}Note: Considered Experimental/Investigational/Unproven when used to report:

- APOE (apolipoprotein E) (eg, hyperlipoproteinemia type III, cardiovascular disease, Alzheimer disease), common variants (eg, *2, *3, *4) (81401)
- molecular testing for highly skewed X-inactivation patterns for recurrent pregnancy loss (81401)
- RHD (Rh blood group, D antigen) (eg, hemolytic disease of the fetus and newborn, Rh maternal/fetal compatibility), deletion analysis (eg, exons 4, 5, and 7, pseudogene), performed on cell-free fetal DNA in maternal blood (81403)
- PSEN1 (presenilin 1) (eg, Alzheimer's disease), full gene sequence (81405)
- APP (amyloid beta [A4] precursor protein) (eg, Alzheimer's disease), full gene sequence (81406)
- PSEN2 (presenilin 2 [Alzheimer's disease 4]) (eg, Alzheimer's disease), full gene sequence (81406)

^{†††}Note: Considered Medically Necessary when used to report any covered genetic test for germline mutation carrier testing for familial disease that does not have an assigned CPT/HCPCS code when criteria in the applicable policy statements listed above are met

HCPCS Codes	Description
S3841	Genetic testing for retinoblastoma
S3842	Genetic testing for Von Hippel-Lindau disease

S3844	DNA analysis of the connexin 26 gene (GJB2) for susceptibility to congenital, profound deafness
S3845	Genetic testing for alpha-thalassemia
S3846	Genetic testing for hemoglobin E beta-thalassemia
S3849	Genetic testing for Niemann-Pick disease
S3850	Genetic testing for sickle cell anemia
S3853	Genetic testing for myotonic muscular dystrophy

Considered Medically Necessary when performed for preconception or prenatal carrier testing for a biologic parent of Ashkenazi Jewish descent:

CPT®* Codes	Description
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
81443	Genetic testing for severe inherited conditions (eg, cystic fibrosis, Ashkenazi Jewish-associated disorders [eg, Bloom syndrome, Canavan disease, Fanconi anemia type C, mucopolysaccharidosis 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)

ICD-10-CM Diagnosis Codes	Description
Z31.430	Encounter of female for testing for genetic disease carrier status for procreative management
Z31.438	Encounter for other genetic testing of female for procreative management
Z31.440	Encounter of male for testing for genetic disease carrier status for procreative management
Z31.448	Encounter for other genetic testing of male for procreative management
Z3A.01-Z3A.49	Weeks of gestation

Considered Not Medically Necessary:

CPT®* Codes	Description
81440	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

Preimplantation Genetic Testing of an Embryo

Considered Medically Necessary when criteria in the applicable policy statements listed above are met:

CPT®* Codes	Description
81161	DMD (dystrophin) (eg, Duchenne/Becker muscular dystrophy) deletion analysis, and duplication analysis, if performed
81187	CNBP (CCHC-type zinc finger nucleic acid binding protein) (eg, myotonic dystrophy type 2) gene analysis, evaluation to detect abnormal (eg, expanded) alleles
81200	ASPA (aspartoacylase) (eg, Canavan disease) gene analysis, common variants (eg, E285A, Y231X)
81205	BCKDHB (branched-chain keto acid dehydrogenase E1, beta polypeptide) (eg, maple syrup urine disease) gene analysis, common variants (eg, R183P, G278S, E422X)

81220	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; common variants (eg, ACMG/ACOG guidelines)
81221	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; known familial variants
81222	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; duplication/deletion variants
81223	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; full gene sequence
81224	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; intron 8 poly-T analysis (eg, male infertility)
81234	DMPK (DM1 protein kinase) (eg, myotonic dystrophy type 1) gene analysis; evaluation to detect abnormal (expanded) alleles
81239	DMPK (DM1 protein kinase) (eg, myotonic dystrophy type 1) gene analysis; characterization of alleles (eg, expanded size)
81242	FANCC (Fanconi anemia, complementation group C) (eg, Fanconi anemia, type C) gene analysis, common variant (eg, IVS4+4A>T)
81243	FMR1 (fragile X mental retardation 1) (eg, fragile X mental retardation) gene analysis; evaluation to detect abnormal (eg, expanded) alleles
81244	FMR1 (fragile X mental retardation 1) (eg, fragile X mental retardation) gene analysis; characterization of alleles (eg, expanded size and methylation status)
81251	GBA (glucosidase, beta, acid) (eg, Gaucher disease) gene analysis, common variants (eg, N370S, 84GG, L444P, IVS2+1G>A)
81252	GJB2 (gap junction protein, beta 2, 26kDa, connexin 26) (eg, nonsyndromic hearing loss) gene analysis; full gene sequence
81253	GJB2 (gap junction protein, beta 2, 26kDa, connexin 26) (eg, nonsyndromic hearing loss) gene analysis; known familial variants
81254	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)])
81255	HEXA (hexosaminidase A [alpha polypeptide]) (eg, Tay-Sachs disease) gene analysis, common variants (eg, 1278insTATC, 1421+1G>C, G269S)
81256	HFE (hemochromatosis) (eg, hereditary hemochromatosis) gene analysis, common variants (eg, C282Y, H63D)
81257	HBA1/HBA2 (alpha globin 1 and alpha globin 2) (eg, alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease) gene analysis; for common deletions or variant (eg, Southeast Asian, Thai, Filipino, Mediterranean, alpha3.7, alpha4.2, alpha20.5, and Constant Spring)
81258	HBA1/HBA2 (alpha globin 1 and alpha globin 2) (eg, alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; known familial variant
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
81269	HBA1/HBA2 (alpha globin 1 and alpha globin 2) (eg, alpha thalassemia, Hb Bart hydrops fetalis syndrome, HbH disease), gene analysis; duplication/deletion variants
81271	HTT (huntingtin) (eg, Huntington disease) gene analysis; evaluation to detect abnormal (eg, expanded) alleles
81274	HTT (huntingtin) (eg, Huntington disease) gene analysis; characterization of alleles (eg, expanded size)
81290	MCOLN1 (mucolipin 1) (eg, Mucopolipidosis, type IV) gene analysis, common variants (eg, IVS3-2A>G, del6.4kb)
81302	MECP2 (methyl CpG binding protein 2) (eg, Rett Syndrome) gene analysis; full sequence analysis
81303	MECP2 (methyl CpG binding protein 2) (eg, Rett Syndrome) gene analysis; known familial variant
81304	MECP2 (methyl CpG binding protein 2) (eg, Rett Syndrome) gene analysis; duplication/deletion variants

81321	PTEN (phosphatase and tensin homolog) (eg, Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; full sequence analysis
81322	PTEN (phosphatase and tensin homolog) (eg, Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; known familial variant
81323	PTEN (phosphatase and tensin homolog) (eg, Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; duplication/deletion variant
81329	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
81330	SMPD1 (sphingomyelin phosphodiesterase 1, acid lysosomal) (eg, Niemann-Pick disease, Type A) gene analysis, common variants (eg, R496L, L302P, fsP330)
81336	SMN1 (survival of motor neuron 1, telomeric) (eg, spinal muscular atrophy) gene analysis; full gene sequence
81337	SMN1 (survival of motor neuron 1, telomeric) (eg, spinal muscular atrophy) gene analysis; known familial sequence variant(s)
81361	HBB (hemoglobin, subunit beta) (eg, sickle cell anemia, beta thalassemia, hemoglobinopathy); common variant(s) (eg, HbS, HbC, HbE)
81362	HBB (hemoglobin, subunit beta) (eg, sickle cell anemia, beta thalassemia, hemoglobinopathy); variant(s)
81363	HBB (hemoglobin, subunit beta) (eg, sickle cell anemia, beta thalassemia, hemoglobinopathy); duplication/deletion variant(s)
81364	HBB (hemoglobin, subunit beta) (eg, sickle cell anemia, beta thalassemia, hemoglobinopathy); full gene sequence
81400 [†]	Molecular pathology procedure, Level 1 (eg, identification of single germline variant [eg, SNP] by techniques such as restriction enzyme digestion or melt curve analysis)
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)
81403 ^{††}	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)
81404	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)
81405 ^{††}	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)
81406 ^{††}	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)
81408	Molecular pathology procedure, Level 9 (eg, analysis of > 50 exons in a single gene by DNA sequence analysis)
81430	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
81431	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
81479 ^{†††}	Unlisted molecular pathology procedure
83080	b-Hexosaminidase, each assay
89290	Biopsy, oocyte polar body or embryo blastomere, microtechnique (for pre-implantation genetic diagnosis); less than or equal to 5 embryos
89291	Biopsy, oocyte polar body or embryo blastomere, microtechnique (for pre-implantation genetic diagnosis); greater than 5 embryos

†Note: Considered Not Medically Necessary when used to report:

- F2 (coagulation factor 2) (eg, hereditary hypercoagulability), 1199G>A variant) (81400)
- F5 (coagulation factor V) (eg, hereditary hypercoagulability) (81400)
- F7 (coagulation factor VII [serum prothrombin conversion accelerator] R353Q variant) for recurrent pregnancy loss (81400)
- F13B (coagulation factor XIII, B polypeptide, V34L variant) for recurrent pregnancy loss (81400)

††Note: Considered Experimental/Investigational/Unproven when used to report:

- APOE (apolipoprotein E) (eg, hyperlipoproteinemia type III, cardiovascular disease, Alzheimer disease), common variants (eg, *2, *3, *4) (81401)
- RHD (Rh blood group, D antigen) (eg, hemolytic disease of the fetus and newborn, Rh maternal/fetal compatibility), deletion analysis (eg, exons 4, 5, and 7, pseudogene), performed on cell-free fetal DNA in maternal blood (81403)
- PSEN1 (presenilin 1) (eg, Alzheimer's disease), full gene sequence (81405)
- APP (amyloid beta [A4] precursor protein) (eg, Alzheimer's disease), full gene sequence (81406)
- PSEN2 (presenilin 2[Alzheimer's disease 4]) (eg, Alzheimer's disease), full gene sequence (81406)

†††Note: Considered Medically Necessary when used to report any covered genetic test for preimplantation diagnostic testing of an embryo that does not have an assigned CPT/HCPCS code when criteria in the applicable policy statements listed above are met

Considered Experimental/Investigational/Unproven when used to report:

- CHEK2 genetic testing with full sequence analysis or deletion/duplication analysis
- SDHAF2 gene testing
- PALB2 deletion/duplication analysis
- FANCA gene mutation testing

HCPCS Codes	Description
S3841	Genetic testing for retinoblastoma
S3842	Genetic testing for Von Hippel-Lindau disease
S3844	DNA analysis of the connexin 26 gene (GJB2) for susceptibility to congenital, profound deafness
S3845	Genetic testing for alpha-thalassemia
S3846	Genetic testing for hemoglobin E beta-thalassemia
S3849	Genetic testing for Niemann-Pick disease
S3850	Genetic testing for sickle cell anemia
S3853	Genetic testing for myotonic muscular dystrophy

Considered Not Medically Necessary:

CPT® Codes	Description
81291	MTHFR (5,10-methylenetetrahydrofolate reductase) (eg, hereditary hypercoagulability) gene analysis, common variants (eg, 677T, 1298C)
81440	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

Considered Experimental/Investigational/Unproven:

CPT® Codes	Description
81162	BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis and full duplication/deletion analysis (ie, detection of large gene rearrangements)

81163	BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis
81164	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)
81165	BRCA1 (BRCA1, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis
81166	BRCA1 (BRCA1, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full duplication/deletion analysis (ie, detection of large gene rearrangements)
81167	BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full duplication/deletion analysis (ie, detection of large gene rearrangements)
81201	APC (adenomatous polyposis coli) (eg, familial adenomatosis polyposis [FAP], attenuated FAP) gene analysis; full gene sequence
81202	APC (adenomatous polyposis coli) (eg, familial adenomatosis polyposis [FAP], attenuated FAP) gene analysis; known familial variants
81203	APC (adenomatous polyposis coli) (eg, familial adenomatosis polyposis [FAP], attenuated FAP) gene analysis; duplication/deletion variants
81206	BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis; major breakpoint, qualitative or quantitative
81207	BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis; minor breakpoint, qualitative or quantitative
81208	BCR/ABL1 (t(9;22)) (eg, chronic myelogenous leukemia) translocation analysis; other breakpoint, qualitative or quantitative
81210	BRAF (B-Raf proto-oncogene, serine/threonine kinase) (eg, colon cancer, melanoma), gene analysis, V600 variant(s)
81211	BRCA1, BRCA2 (breast cancer 1 and 2) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis and common duplication/deletion variants in BRCA1 (ie, exon 13 del 3.835kb, exon 13 dup 6kb, exon 14-20 del 26kb, exon 22 del 510bp, exon 8-9 del 7.1kb) (Code deleted 12/31/2018)
81212	BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; 185delAG, 5385insC, 6174delT variants
81213	BRCA1, BRCA2 (breast cancer 1 and 2) (eg, hereditary breast and ovarian cancer) gene analysis; uncommon duplication/deletion variants (Code deleted 12/31/2018)
81214	BRCA1 (breast cancer 1) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis and common duplication/deletion variants (ie, exon 13 del 3.835kb, exon 13 dup 6kb, exon 14-20 del 26kb, exon 22 del 510bp, exon 8-9 del 7.1kb) (Code deleted 12/31/2018)
81215	BRCA1 (BRCA1, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; known familial variant
81216	BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; full sequence analysis
81217	BRCA2 (BRCA2, DNA repair associated) (eg, hereditary breast and ovarian cancer) gene analysis; known familial variant
81240†	F2 (prothrombin, coagulation factor II) (eg, hereditary hypercoagulability) gene analysis, 20210G>A variant
81241†	F5 (coagulation factor V) (eg, hereditary hypercoagulability) gene analysis, Leiden variant
81265	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)
81266	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)

81275	KRAS (Kirsten rat sarcoma viral oncogene homolog) (eg, carcinoma) gene analysis; variants in exon 2 (eg, codons 12 and 13)
81288	MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; promoter methylation analysis
81292	MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis
81293	MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; known familial variants
81294	MLH1 (mutL homolog 1, colon cancer, nonpolyposis type 2) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants
81295	MSH2 (mutS homolog 2, colon cancer, nonpolyposis type 1) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis
81296	MSH2 (mutS homolog 2, colon cancer, nonpolyposis type 1) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; known familial variants
81297	MSH2 (mutS homolog 2, colon cancer, nonpolyposis type 1) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants
81298	MSH6 (mutS homolog 6 [E. coli]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis
81299	MSH6 (mutS homolog 6 [E. coli]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; known familial variants
81300	MSH6 (mutS homolog 6 [E. coli]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants
81301	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
81317	PMS2 (postmeiotic segregation increased 2 [S. cerevisiae]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis
81318	PMS2 (postmeiotic segregation increased 2 [S. cerevisiae]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; known familial variants
81319	PMS2 (postmeiotic segregation increased 2 [S. cerevisiae]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants
81321	PTEN (phosphatase and tensin homolog) (eg, Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; full sequence analysis
81322	PTEN (phosphatase and tensin homolog) (eg, Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; known familial variant
81323	PTEN (phosphatase and tensin homolog) (eg, Cowden syndrome, PTEN hamartoma tumor syndrome) gene analysis; duplication/deletion variant
81370	HLA Class I and II typing, low resolution (eg, antigen equivalents); HLA-A, -B, -C, -DRB1/3/4/5, and -DQB1
81371	HLA Class I and II typing, low resolution (eg, antigen equivalents); HLA-A, -B, and -DRB1 (eg, verification typing)
81372	HLA Class I typing, low resolution (eg, antigen equivalents); complete (ie, HLA-A, -B, and -C)
81373	HLA Class I typing, low resolution (eg, antigen equivalents); one locus (eg, HLA-A, -B, or -C), each
81374	HLA Class I typing, low resolution (eg, antigen equivalents); one antigen equivalent (eg, B*27), each
81375	HLA Class II typing, low resolution (eg, antigen equivalents); HLA-DRB1/3/4/5 and -DQB1
81376	HLA Class II typing, low resolution (eg, antigen equivalents); one locus (eg, HLA-DRB1, -DRB3/4/5, -DQB1, -DQA1, -DPB1, or -DPA1), each
81377	HLA Class II typing, low resolution (eg, antigen equivalents); one antigen equivalent, each
81378	HLA Class I and II typing, high resolution (ie, alleles or allele groups), HLA-A, -B, -C, and -DRB1
81379	HLA Class I typing, high resolution (ie, alleles or allele groups); complete (ie, HLA-A, -B, and -C)

81380	HLA Class I typing, high resolution (ie, alleles or allele groups); one locus (eg, HLA-A, -B, or -C), each
81381	HLA Class I typing, high resolution (ie, alleles or allele groups); one allele or allele group (eg, B*57:01P), each
81382	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
81383	HLA Class II typing, high resolution (ie, alleles or allele groups); one allele or allele group (eg, HLA-DQB1*06:02P), each
81403	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)
81404	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)
81405	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)
81406	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)
81408	Molecular pathology procedure, Level 9 (eg, analysis of >50 exons in a single gene by DNA sequence analysis)
81435	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
81436	Hereditary colon disorders (eg, Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis); duplication/deletion analysis panel, must include analysis of at least 5 genes, including MLH1, MSH2, EPCAM, SMAD4, and STK11
81437	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
81438	Hereditary neuroendocrine tumor disorders (eg, medullary thyroid carcinoma, parathyroid carcinoma, malignant pheochromocytoma or paraganglioma); duplication/deletion analysis panel, must include analyses for SDHB, SDHC, SDHD, and VHL

†Note: Considered Not Medically Necessary when used to report evaluation of recurrent pregnancy loss

HCPCS Codes	Description
S3840	DNA analysis for germline mutations of the RET proto-oncogene for susceptibility to multiple endocrine neoplasia type 2
S3852	DNA analysis for APOE epsilon 4 allele for susceptibility to Alzheimer's disease

Preimplantation Genetic Testing for Aneuploidy (PGT-A)

Considered Not Medically Necessary:

CPT®* Codes	Description
81415	Exome (eg, unexplained constitutional or heritable disorder or syndrome); sequence analysis
81416	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)
81417	Exome (eg, unexplained constitutional or heritable disorder or syndrome); re-evaluation of previously obtained exome sequence (eg, updated knowledge or unrelated condition/syndrome)

81425	Genome (eg, unexplained constitutional or heritable disorder or syndrome); sequence analysis
81426	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)
81427	Genome (eg, unexplained constitutional or heritable disorder or syndrome); re-evaluation of previously obtained genome sequence (eg, updated knowledge or unrelated condition/syndrome)
88271	Molecular cytogenetics; DNA probe, each (eg, FISH)
88272	Molecular cytogenetics; chromosomal in situ hybridization, analyze 3-5 cells (eg, for derivatives and markers)
88273	Molecular cytogenetics; chromosomal in situ hybridization, analyze 10-30 cells (eg, for microdeletions)
88274	Molecular cytogenetics; interphase in situ hybridization, analyze 25-99 cells
88275	Molecular cytogenetics; interphase in situ hybridization, analyze 100-300 cells

Sequencing-Based Non-Invasive Prenatal Testing

Considered Medically Necessary when criteria in the applicable policy statements listed above are met except when used to report Experimental/Investigational/Unproven microdeletion testing:

CPT®* Codes	Description
81420	Fetal chromosomal aneuploidy (eg, trisomy 21, monosomy X) genomic sequence analysis panel, circulating cell-free fetal DNA in maternal blood, must include analysis of chromosomes 13, 18, and 21
81507	Fetal aneuploidy (trisomy 21, 18, and 13) DNA sequence analysis of selected regions using maternal plasma, algorithm reported as a risk score for each trisomy
0009M	Fetal aneuploidy (trisomy 21, and 18) DNA sequence analysis of selected regions using maternal plasma, algorithm reported as a risk score for each trisomy (Code deleted 12/31/2019)

ICD-10-CM Diagnosis Codes	Description
O09.01-O09.03	Supervision of pregnancy with history of infertility
O09.11-O09.13	Supervision of pregnancy with history of ectopic pregnancy,
O09.A1-O09.A3	Supervision of pregnancy with history of molar pregnancy
O09.211-O09.213	Supervision of pregnancy with history of pre-term labor
O09.291-O09.293	Supervision of pregnancy with other poor reproductive or obstetric history
O09.31-O09.33	Supervision of pregnancy with insufficient antenatal care
O09.41-O09.43	Supervision of pregnancy with grand multiparity
O09.511-O09.513	Supervision of elderly primigravida
O09.521-O09.523	Supervision of elderly multigravida
O09.611-O09.613	Supervision of young primigravida
O09.621-O09.623	Supervision of young multigravida

O09.71- O09.73	Supervision of high risk pregnancy due to social problems
O09.811- O09.813	Supervision of pregnancy resulting from assisted reproductive technology
O09.821- O09.823	Supervision of pregnancy with history of in utero procedure during previous pregnancy
O09.891- O09.893	Supervision of other high risk pregnancies
O09.91- O09.93	Supervision of high risk pregnancy, unspecified
O10.011- O10.013	Pre-existing essential hypertension complicating pregnancy
O10.111- O10.113	Pre-existing hypertensive heart disease complicating pregnancy
O10.211- O10.213	Pre-existing hypertensive chronic kidney disease complicating pregnancy
O10.311- O10.313	Pre-existing hypertensive heart and chronic kidney disease complicating pregnancy
O10.411- O10.413	Pre-existing secondary hypertension complicating pregnancy
O10.911- O10.913	Unspecified pre-existing hypertension complicating pregnancy
O11.1-O11.3	Pre-existing hypertension with pre-eclampsia
O12.01- O12.03	Gestational edema
O12.11- O12.13	Gestational proteinuria
O12.21- O12.23	Gestational edema with proteinuria
O13.1-O13.3	Gestational [pregnancy-induced] hypertension without significant proteinuria
O14.02	Mild to moderate pre-eclampsia, second trimester
O14.03	Mild to moderate pre-eclampsia, third trimester
O14.12	Severe pre-eclampsia, second trimester
O14.13	Severe pre-eclampsia, third trimester
O14.22	HELLP syndrome (HELLP), second trimester
O14.23	HELLP syndrome (HELLP), third trimester
O14.92	Unspecified pre-eclampsia, second trimester
O14.93	Unspecified pre-eclampsia, third trimester
O15.02	Eclampsia complicating pregnancy, second trimester
O15.03	Eclampsia complicating pregnancy, third trimester
O16.1-O16.3	Unspecified maternal hypertension
O21.0-O21.9	Excessive vomiting in pregnancy
O22.01- O22.03	Varicose veins of lower extremity in pregnancy
O22.11- O22.13	Genital varices in pregnancy
O22.21-O22.23	Superficial thrombophlebitis in pregnancy
O22.31-O22.33	Deep phlebothrombosis in pregnancy
O22.41-O22.43	Hemorrhoids in pregnancy
O22.51-O22.53	Cerebral venous thrombosis in pregnancy
O22.8X1- O22.8X3	Other venous complications in pregnancy
O22.91-O22.93	Venous complication in pregnancy, unspecified
O23.01-O23.03	Infections of kidney in pregnancy

O23.11-O23.13	Infections of bladder in pregnancy
O23.21-O23.23	Infections of urethra in pregnancy
O23.31-O23.33	Infections of other parts of urinary tract in pregnancy
O23.41-O23.43	Unspecified infection of urinary tract in pregnancy
O23.511- O23.513	Infections of cervix in pregnancy
O23.521- O23.523	Salpingo-oophoritis in pregnancy
O23.591- O23.593	Infection of other part of genital tract in pregnancy
O23.91-O23.93	Unspecified genitourinary tract infection in pregnancy
O24.011- O24.013	Pre-existing diabetes mellitus, type 1, in pregnancy
O24.111- O24.113	Pre-existing diabetes mellitus, type 2, in pregnancy
O24.311- O24.313	Unspecified pre-existing diabetes mellitus in pregnancy
O24.410- O24.419	Gestational diabetes mellitus in pregnancy
O24.811- O24.813	Other pre-existing diabetes mellitus in pregnancy
O24.911- O24.913	Unspecified diabetes mellitus in pregnancy
O25.11-O25.13	Malnutrition in pregnancy
O26.01-O26.03	Excessive weight gain in pregnancy
O26.11-O26.13	Low weight gain in pregnancy
O26.21-O26.23	Pregnancy care for patient with recurrent pregnancy loss
O26.31-O26.33	Retained intrauterine contraceptive device in pregnancy
O26.41-O26.43	Herpes gestationis
O26.51-O26.53	Maternal hypotension syndrome
O26.611- O26.613	Liver and biliary tract disorders in pregnancy
O26.711- O26.713	Subluxation of symphysis (pubis) in pregnancy
O26.821- O26.823	Pregnancy related peripheral neuritis
O26.831- O26.833	Pregnancy related renal disease
O26.841- O26.843	Uterine size-date discrepancy
O26.851- O26.853	Spotting complicating pregnancy
O26.891- O26.893	Other specified pregnancy related conditions
O26.91-O26.93	Pregnancy related conditions, unspecified
O28.0-O28.9	Abnormal findings on antenatal screening of mother
O31.11X0	Continuing pregnancy after spontaneous abortion of one fetus or more, first trimester, not applicable or unspecified
O31.12X0	Continuing pregnancy after spontaneous abortion of one fetus or more, second trimester, not applicable or unspecified
O31.13X0	Continuing pregnancy after spontaneous abortion of one fetus or more, third trimester, not applicable or unspecified
O31.21X0	Continuing pregnancy after intrauterine death of one fetus or more, first trimester, not applicable or unspecified

O31.22X0	Continuing pregnancy after intrauterine death of one fetus or more, second trimester, not applicable or unspecified
O31.23X0	Continuing pregnancy after intrauterine death of one fetus or more, third trimester, not applicable or unspecified
O31.31X0	Continuing pregnancy after elective fetal reduction of one fetus or more, first trimester, not applicable or unspecified
O31.32X0	Continuing pregnancy after elective fetal reduction of one fetus or more, second trimester, not applicable or unspecified
O31.33X0	Continuing pregnancy after elective fetal reduction of one fetus or more, third trimester, not applicable or unspecified
O34.01-O34.03	Maternal care for unspecified congenital malformation of uterus
O34.11-O34.13	Maternal care for benign tumor of corpus uteri
O34.211-O34.29	Maternal care due to uterine scar from previous cesarean delivery
O34.31-O34.33	Maternal care for cervical incompetence
O34.41-O34.43	Maternal care for other abnormalities of cervix
O34.511-O34.513	Maternal care for incarceration of gravid uterus
O34.521-O34.523	Maternal care for prolapse of gravid uterus
O34.531-O34.533	Maternal care for retroversion of gravid uterus
O34.591-O34.593	Maternal care for other abnormalities of gravid uterus
O34.61-O34.63	Maternal care for abnormality of vagina
O34.71-O34.73	Maternal care for abnormality of vulva and perineum
O34.81-O34.83	Maternal care for other abnormalities of pelvic organs
O34.91-O34.93	Maternal care for abnormality of pelvic organ, unspecified
O35.0XX0	Maternal care for (suspected) central nervous system malformation in fetus, not applicable or unspecified
O35.1XX0	Maternal care for (suspected) chromosomal abnormality in fetus, not applicable or unspecified
O35.2XX0	Maternal care for (suspected) hereditary disease in fetus, not applicable or unspecified
O35.3XX0	Maternal care for (suspected) damage to fetus from viral disease in mother, not applicable or unspecified
O35.4XX0	Maternal care for (suspected) damage to fetus from alcohol, not applicable or unspecified
O35.5XX0	Maternal care for (suspected) damage to fetus by drugs, not applicable or unspecified
O35.6XX0	Maternal care for (suspected) damage to fetus by radiation, not applicable or unspecified
O35.7XX0	Maternal care for (suspected) damage to fetus by other medical procedures, not applicable or unspecified
O35.8XX0	Maternal care for other (suspected) fetal abnormality and damage, not applicable or unspecified
O35.9XX0	Maternal care for (suspected) fetal abnormality and damage, unspecified, not applicable or unspecified
O36.21X0	Maternal care for hydrops fetalis, first trimester, not applicable or unspecified
O36.22X0	Maternal care for hydrops fetalis, second trimester, not applicable or unspecified
O36.23X0	Maternal care for hydrops fetalis, third trimester, not applicable or unspecified
O36.5110	Maternal care for known or suspected placental insufficiency, first trimester, not applicable or unspecified
O36.5120	Maternal care for known or suspected placental insufficiency, second trimester, not applicable or unspecified
O36.5130	Maternal care for known or suspected placental insufficiency, third trimester, not applicable or unspecified

O36.5910	Maternal care for other known or suspected poor fetal growth, first trimester, not applicable or unspecified
O36.5920	Maternal care for other known or suspected poor fetal growth, second trimester, not applicable or unspecified
O36.5930	Maternal care for other known or suspected poor fetal growth, third trimester, not applicable or unspecified
O36.61X0	Maternal care for excessive fetal growth, first trimester, not applicable or unspecified
O36.62X0	Maternal care for excessive fetal growth, second trimester, not applicable or unspecified
O36.63X0	Maternal care for excessive fetal growth, third trimester, not applicable or unspecified
O36.71X0	Maternal care for viable fetus in abdominal pregnancy, first trimester, not applicable or unspecified
O36.72X0	Maternal care for viable fetus in abdominal pregnancy, second trimester, not applicable or unspecified
O36.73X0	Maternal care for viable fetus in abdominal pregnancy, third trimester, not applicable or unspecified
O36.8120	Decreased fetal movements, second trimester, not applicable or unspecified
O36.8130	Decreased fetal movements, third trimester, not applicable or unspecified
O36.8310	Maternal care for abnormalities of the fetal heart rate or rhythm, first trimester, not applicable or unspecified
O36.8320	Maternal care for abnormalities of the fetal heart rate or rhythm, second trimester, not applicable or unspecified
O36.8330	Maternal care for abnormalities of the fetal heart rate or rhythm, third trimester, not applicable or unspecified
O36.8910	Maternal care for other specified fetal problems, first trimester, not applicable or unspecified
O36.8920	Maternal care for other specified fetal problems, second trimester, not applicable or unspecified
O36.8930	Maternal care for other specified fetal problems, third trimester, not applicable or unspecified
O36.91X0	Maternal care for fetal problem, unspecified, first trimester, not applicable or unspecified
O36.92X0	Maternal care for fetal problem, unspecified, second trimester, not applicable or unspecified
O36.93X0	Maternal care for fetal problem, unspecified, third trimester, not applicable or unspecified
O40.1XX0	Polyhydramnios, first trimester, not applicable or unspecified
O40.2XX0	Polyhydramnios, second trimester, not applicable or unspecified
O40.3XX0	Polyhydramnios, third trimester, not applicable or unspecified
O41.01X0	Oligohydramnios, first trimester, not applicable or unspecified
O41.02X0	Oligohydramnios, second trimester, not applicable or unspecified
O41.03X0	Oligohydramnios, third trimester, not applicable or unspecified
O41.1010	Infection of amniotic sac and membranes, unspecified, first trimester, not applicable or unspecified
O41.1020	Infection of amniotic sac and membranes, unspecified, second trimester, not applicable or unspecified
O41.1030	Infection of amniotic sac and membranes, unspecified, third trimester, not applicable or unspecified
O41.1210	Chorioamnionitis, first trimester, not applicable or unspecified
O41.1220	Chorioamnionitis, second trimester, not applicable or unspecified
O41.1230	Chorioamnionitis, third trimester, not applicable or unspecified
O41.1410	Placentitis, first trimester, not applicable or unspecified
O41.1420	Placentitis, second trimester, not applicable or unspecified
O41.1430	Placentitis, third trimester, not applicable or unspecified
O41.8X10	Other specified disorders of amniotic fluid and membranes, first trimester, not applicable or unspecified

O41.8X20	Other specified disorders of amniotic fluid and membranes, second trimester, not applicable or unspecified
O41.8X30	Other specified disorders of amniotic fluid and membranes, third trimester, not applicable or unspecified
O41.91X0	Disorder of amniotic fluid and membranes, unspecified, first trimester, not applicable or unspecified
O41.92X0	Disorder of amniotic fluid and membranes, unspecified, second trimester, not applicable or unspecified
O41.93X0	Disorder of amniotic fluid and membranes, unspecified, third trimester, not applicable or unspecified
O43.011- O43.013	Fetomaternal placental transfusion syndrome
O43.101- O43.103	Malformation of placenta, unspecified
O43.111- O43.113	Circumvallate placenta
O43.121- O43.123	Velamentous insertion of umbilical cord
O43.191- O43.193	Other malformation of placenta
O43.211- O43.213	Placenta accreta
O43.221- O43.223	Placenta increta
O43.231- O43.233	Placenta percreta
O43.811- O43.813	Placental infarction
O43.891- O43.893	Other placental disorders
O43.91- O43.93	Unspecified placental disorder
O44.01-O44.03	Complete placenta previa NOS or without hemorrhage
O44.11-O44.13	Complete placenta previa with hemorrhage
O44.21-O44.23	Partial placenta previa NOS or without hemorrhage
O44.31-O44.33	Partial placenta previa with hemorrhage
O44.41-O44.43	Low lying placenta NOS or without hemorrhage
O44.51-O44.53	Low lying placenta with hemorrhage
O45.001- O45.003	Premature separation of placenta with coagulation defect
O45.011- O45.013	Premature separation of placenta with afibrinogenemia
O45.021- O45.023	Premature separation of placenta with disseminated intravascular coagulation
O45.091- O45.093	Premature separation of placenta with other coagulation defect
O45.8X1- O45.8X3	Other premature separation of placenta
O45.91-O45.93	Premature separation of placenta, unspecified
O46.001- O46.003	Antepartum hemorrhage with coagulation defect, unspecified
O46.011- O46.013	Antepartum hemorrhage with afibrinogenemia

O46.021- O46.023	Antepartum hemorrhage with disseminated intravascular coagulation
O46.091- O46.093	Antepartum hemorrhage with other coagulation defect
O46.8X1- O46.8X3	Other antepartum hemorrhage
O46.91-O46.93	Antepartum hemorrhage, unspecified
O47.02	False labor before 37 completed weeks of gestation, second trimester
O47.03	False labor before 37 completed weeks of gestation, third trimester
O47.1	False labor at or after 37 completed weeks of gestation
O47.9	False labor, unspecified
O48.0	Post-term pregnancy
O48.1	Prolonged pregnancy
O60.02	Preterm labor without delivery, second trimester
O60.03	Preterm labor without delivery, third trimester
O98.011- O98.013	Tuberculosis complicating pregnancy
O98.111- O98.113	Syphilis complicating pregnancy
O98.211- O98.213	Gonorrhea complicating pregnancy
O98.311- O98.313	Other infections with a predominantly sexual mode of transmission complicating pregnancy
O98.411- O98.413	Viral hepatitis complicating pregnancy
O98.511- O98.513	Other viral diseases complicating pregnancy
O98.611- O98.613	Protozoal diseases complicating pregnancy
O98.711- O98.713	Human immunodeficiency virus [HIV] disease complicating pregnancy
O98.811- O98.813	Other maternal infectious and parasitic diseases complicating pregnancy
O98.911- O98.913	Unspecified maternal infectious and parasitic disease complicating pregnancy
O99.011- O99.013	Anemia complicating pregnancy
O99.111- O99.113	Other diseases of the blood and blood-forming organs and certain disorders involving the immune mechanism complicating pregnancy
O99.211- O99.213	Obesity complicating pregnancy
O99.281- O99.283	Endocrine, nutritional and metabolic diseases complicating pregnancy
O99.311- O99.313	Alcohol use complicating pregnancy
O99.321- O99.323	Drug use complicating pregnancy
O99.331- O99.333	Smoking (tobacco) complicating pregnancy
O99.341- O99.343	Other mental disorders complicating pregnancy
O99.351- O99.353	Diseases of the nervous system complicating pregnancy

O99.411- O99.413	Diseases of the circulatory system complicating pregnancy
O99.511- O99.513	Diseases of the respiratory system complicating pregnancy
O99.611- O99.613	Diseases of the digestive system complicating pregnancy
O99.711- O99.713	Diseases of the skin and subcutaneous tissue complicating pregnancy
O99.810	Abnormal glucose complicating pregnancy
O99.820	Streptococcus B carrier state complicating pregnancy
O99.830	Other infection carrier state complicating pregnancy
O99.841- O99.843	Bariatric surgery status complicating pregnancy
O9A.111- O9A.113	Malignant neoplasm complicating pregnancy
O9A.211- O9A.213	Injury, poisoning and certain other consequences of external causes complicating pregnancy
O9A.311- O9A.313	Physical abuse complicating pregnancy
O9A.411- O9A.413	Sexual abuse complicating pregnancy
O9A.511- O9A.513	Psychological abuse complicating pregnancy
Z34.01- Z34.03	Encounter for supervision of normal first pregnancy
Z34.81- Z34.83	Encounter for supervision of other normal pregnancy
Z34.91- Z34.93	Encounter for supervision of normal pregnancy, unspecified
Z36.0- Z36.9	Encounter for antenatal screening of mother
Z3A.10- Z3A.19	Weeks of gestation of pregnancy, weeks 10-19
Z3A.20- Z3A.29	Weeks of gestation of pregnancy, weeks 20-29
Z3A.30- Z3A.39	Weeks of gestation of pregnancy, weeks 30-39
Z3A.40- Z3A.49	Weeks of gestation of pregnancy, weeks 40 or greater

Considered Experimental/Investigational/Unproven:

CPT®* Codes	Description
81422	Fetal chromosomal microdeletion(s) genomic sequence analysis (eg, DiGeorge syndrome, Cri-du-chat syndrome), circulating cell-free fetal DNA in maternal blood

Invasive Prenatal Testing

Considered Medically Necessary when criteria in the applicable policy statements listed above are met:

CPT®* Codes	Description
81220	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; common variants (eg, ACMG/ACOG guidelines)
81221	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; known familial variants
81222	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; duplication/deletion variants
81223	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; full gene sequence

81224	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; intron 8 poly-T analysis (eg, male infertility)
81228†	Cytogenomic constitutional (genome-wide) microarray analysis; interrogation of genomic regions for copy number variants (eg, bacterial artificial chromosome [BAC] or oligo-based comparative genomic hybridization [CGH] microarray analysis)
81229†	Cytogenomic constitutional (genome-wide) microarray analysis; interrogation of genomic regions for copy number and single nucleotide polymorphism (SNP) variants for chromosomal abnormalities
81255	HEXA (hexosaminidase A [alpha polypeptide]) (eg, Tay-Sachs disease) gene analysis, common variants (eg, 1278insTATC, 1421+1G>C, G269S)
81406	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)

†Note: Considered Experimental/Investigational/Unproven when used to report genetic mutation reproductive genetic testing for recurrent pregnancy loss.

Considered Not Medically Necessary when used to report preimplantation genetic screening for common aneuploidy

Germline Mutation Reproductive Genetic Testing for Recurrent Pregnancy Loss

Considered Medically Necessary when criteria in the applicable policy statements listed above are met:

CPT®* Codes	Description
81228	Cytogenomic constitutional (genome-wide) microarray analysis; interrogation of genomic regions for copy number variants (eg, bacterial artificial chromosome [BAC] or oligo-based comparative genomic hybridization [CGH] microarray analysis)
81229	Cytogenomic constitutional (genome-wide) microarray analysis; interrogation of genomic regions for copy number and single nucleotide polymorphism (SNP) variants for chromosomal abnormalities
88262	Chromosome analysis; count 15-20 cells, 2 karyotypes, with banding
88271	Molecular cytogenetics; DNA probe, each (eg, FISH)
88272	Molecular cytogenetics; chromosomal in situ hybridization, analyze 3-5 cells (eg, for derivatives and markers)
88273	Molecular cytogenetics; chromosomal in situ hybridization, analyze 10-30 cells (eg, for microdeletions)
88274	Molecular cytogenetics; interphase in situ hybridization, analyze 25-99 cells
88275	Molecular cytogenetics; interphase in situ hybridization, analyze 100-300 cells

Considered Not Medically Necessary:

CPT®* Codes	Description
81291	MTHFR (5,10-methylenetetrahydrofolate reductase) (eg, hereditary hypercoagulability) gene analysis, common variants (eg, 677T, 1298C)

Germline Mutation Reproductive Genetic Testing for Infertility

Considered Medically Necessary when criteria in the applicable policy statements listed above are met:

CPT®* Codes	Description
81220	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; common variants (eg, ACMG/ACOG guidelines)
81221	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; known familial variants
81222	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; duplication/deletion variants

81223	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; full gene sequence
81224	CFTR (cystic fibrosis transmembrane conductance regulator) (eg, cystic fibrosis) gene analysis; intron 8 poly-T analysis (eg, male infertility)
81403	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)
88280	Chromosome analysis; additional karyotypes, each study
89329	Sperm evaluation; hamster penetration test

Considered Experimental/Investigational/Unproven when used to report sperm DNA integrity testing:

CPT®* Codes	Description
88182	Flow cytometry, cell cycle or DNA analysis

*Current Procedural Terminology (CPT®) ©2019 American Medical Association: Chicago, IL.

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