

Preimplantation Genetic Testing and Related Services (for Tennessee Only)

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[Instructions for Use](#)

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Related Policies
<ul style="list-style-type: none"> Cell-Free Fetal DNA Testing (for Tennessee Only) Chromosome Microarray Testing (Non-Oncology Conditions) (for Tennessee Only)
Related Clinical Guideline
<ul style="list-style-type: none"> Fertility Solutions Medical Necessity Clinical Guideline: Infertility

Application

This Medical Policy applies to Medicaid and CoverKids in the state of Tennessee.

Coverage Rationale

[Preimplantation Genetic Testing \(PGT\)](#) for Monogenic/single gene defects (PGT-M) or inherited structural chromosome rearrangements (PGT-SR) is proven and medically necessary using polymerase chain reaction (PCR), next generation sequencing (e.g., Chromosomal Rearrangements), or chromosomal microarray for the following:

- The embryo is at increased risk of a recognized inherited disorder with both of the following:
 - The increased risk of a recognized inherited disorder is due to one of the following:
 - Each of the intended parents are carriers of the same autosomal recessive disease
 - At least one parent is a carrier of an autosomal dominant, sex-linked, or mitochondrial condition
 - At least one parent is a carrier of a structural chromosome rearrangement
 - The medical condition being prevented must result in [Significant Health Problems or Severe Disability](#) and be caused by a single gene (PGT-M) or structural changes of a parents' chromosome (PGT-SR)
- Human leukocyte antigen (HLA) typing on an embryo in order for the future child to provide bone marrow or blood to treat an affected sibling

PGT is unproven and not medically necessary for all other populations and conditions due to insufficient evidence of efficacy. This includes but is not limited to PGT using chromosome microarray, PCR, or next generation sequencing for the following:

- Aneuploidy screening (PGT-A)
- Determining gender when the embryo is not at risk for a sex-linked disorder
- Predicting risk of polygenic disorders (PGT-P) and/or embryo selection based on polygenic scores (ESPS)

Note: PGT must be ordered after genetic counseling.

Definitions

Preimplantation Genetic Testing (PGT): A test performed to analyze the DNA from oocytes or embryos for human leukocyte antigen (HLA)-typing or for determining genetic abnormalities. These include:

- PGT-A: For aneuploidy screening (formerly PGS)
- PGT-M: For monogenic/single gene defects (formerly single-gene PGD)
- PGT-SR: For chromosomal structural rearrangements (formerly chromosomal PGD)

(Zegers-Hochschild et al., 2017)

Significant Health Problems or Severe Disability: A disability or impairment that is physical or mental and substantially limits one or more major life activities. The impairment is expected to last at least 12 months or result in death (Department of Labor; Office of Disability Employment Policy; Federal Government Definition for Social Security Disability Benefits).

Applicable Codes

The following list(s) of procedure and/or diagnosis codes is provided for reference purposes only and may not be all inclusive. Listing of a code in this policy does not imply that the service described by the code is a covered or non-covered health service. Benefit coverage for health services is determined by federal, state, or contractual requirements and applicable laws that may require coverage for a specific service. The inclusion of a code does not imply any right to reimbursement or guarantee claim payment. Other Policies and Guidelines may apply.

Coding Clarification: For preimplantation genetic testing, refer to codes identified below with an asterisk (*).

CPT Code	Description
0254U	Reproductive medicine (preimplantation genetic assessment), analysis of 24 chromosomes using embryonic DNA genomic sequence analysis for aneuploidy, and a mitochondrial DNA score in euploid embryos, results reported as normal (euploidy), monosomy, trisomy, or partial deletion/duplications, mosaicism, and segmental aneuploidy, per embryo tested
0396U	Obstetrics (pre-implantation genetic testing), evaluation of 300000 DNA single-nucleotide polymorphisms (SNPs) by microarray, embryonic tissue, algorithm reported as a probability for single-gene germline conditions
81228	Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number variants, comparative genomic hybridization [CGH] microarray analysis
81229	Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and single nucleotide polymorphism (SNP) variants, comparative genomic hybridization (CGH) microarray analysis
81349	Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and loss-of-heterozygosity variants, low-pass sequencing analysis
81479	Unlisted molecular pathology procedure
*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
Related Services	
*58970	Follicle puncture for oocyte retrieval, any method
*58974	Embryo transfer, intrauterine
*76948	Ultrasonic guidance for aspiration of ova, imaging supervision and interpretation
*89250	Culture of oocyte(s)/embryo(s), less than 4 days

CPT Code	Description
Related Services	
*89251	Culture of oocyte(s)/embryo(s), less than 4 days; with co-culture of oocyte(s)/embryos
*89253	Assisted embryo hatching, microtechniques (any method)
*89254	Oocyte identification from follicular fluid
*89255	Preparation of embryo for transfer (any method)
*89257	Sperm Identification from aspiration (other than seminal fluid)
*89258	Cryopreservation; embryo(s)
*89260	Sperm isolation; simple prep (e.g., sperm wash and swim-up) for insemination or diagnosis with semen analysis
*89261	Sperm isolation; complex prep (e.g., Percoll gradient, albumin gradient) for insemination or diagnosis with semen analysis
*89264	Sperm identification from testis tissue, fresh or cryopreserved
*89268	Insemination of oocytes
*89272	Extended culture of oocyte(s)/embryo(s), 4-7 days
*89280	Assisted oocyte fertilization, microtechnique; less than or equal to 10 oocytes
*89281	Assisted oocyte fertilization, microtechnique; greater than 10 oocytes
*89342	Storage (per year); embryo(s)
*89352	Thawing of cryopreserved; embryo(s)

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HCPCS Code	Description
*S4011	In vitro fertilization; including but not limited to identification and incubation of mature oocytes, fertilization with sperm, incubation of embryo(s), and subsequent visualization for determination of development
*S4015	Complete in vitro fertilization cycle, not otherwise specified, case rate
*S4016	Frozen in vitro fertilization cycle, case rate
*S4022	Assisted oocyte fertilization, case rate
*S4037	Cryopreserved embryo transfer, case rate

Description of Services

Genetic counseling is strongly recommended prior to Preimplantation Genetic Testing (PGT) in order to inform persons being tested about the advantages and limitations of the test as applied to their unique situation.

PGT is an analysis performed on an embryo prior to transfer to screen for aneuploidy (PGT-A), deletions and duplications of genomic material, generally referred to as copy number variations (CNVs) or structural rearrangements (PGT-SR) and analysis of single gene or other inherited disorders in an embryo (PGT-M). Use of this technology is hypothesized to increase the success of infertility treatment, especially in women who have worse outcomes due to advanced maternal age, history of recurrent miscarriage, failed in vitro fertilization (IVF) (CDC, 2017) or a balanced chromosome translocation. In addition, it has been explored as a way to enable single embryo transfer (SET) rather than using multiple embryos to increase the odds of having a successful pregnancy without the risk of a multiple gestation.

Preimplantation Genetic Testing

In a 2021 systematic review and meta-analysis, Hou et al. evaluated the risk of adverse outcomes related to PGT in obstetric and neonatal populations. Enrollees included 785,445 individuals from 19 studies who were separated into an in vitro fertilization (IVF)/intracytoplasmic sperm injection (ICSI) group (n = 731,151) and a PGT group (n = 54,924). Outcomes included mean birth weight, low birth weight (LBW), very low birth weight, mean gestational age at birth, preterm birth, very preterm birth, intrauterine growth retardation (IUGR), birth defects, sex ratio, hypertensive disorders of pregnancy, cesarean section, gestational diabetes, disorders of the placenta and preterm premature rupture of membranes. The analysis showed that PGT pregnancies had reduced rates of LBW (risk ratio [RR] 0.85, 95% confidence interval [CI] 0.75 to 0.98), very low birth rates (RR 0.52, 95% CI 0.33 to 0.81), and very preterm births (RR 0.55, 95% CI 0.42 to 0.70) compared to these rates in the IVF/ICSI pregnancies, but higher rates of hypertensive disorders of pregnancy (RR 1.30, 95% CI 1.08 to 1.57). PGT was not associated with a higher risk of any of the other adverse outcomes. In a subgroup analysis of blastocyte biopsies only, PGT using blastocyte biopsy yielded a lower rate of very low birth weight (RR 0.55, 95% CI 0.31 to 0.95) and was not associated with increased risk of other obstetric/neonatal outcomes. Subgroup analysis was also undertaken for frozen-thawed embryo transfer cycles and indicated that pregnancies with PGT were associated with a lower rate of very low birth weight and cesarean birth but a higher rate of IUGR and preterm birth than in the IVF/ICSI group; no other elevated risk was identified for frozen-thawed embryo transfers. The authors concluded that based on the pooled analysis, PGT did not lead to an increase in the risk of adverse obstetric and neonatal outcomes, however the association between PGT and elevated risk of IUGR will require further investigation. The analysis was limited by differences in the stage of embryo biopsy (cleavage stage vs. blastocyst stage) and lack of studies including obstetric indicators, such as placental disorders. In addition, none of the studies included were randomized controlled trials, reducing the value of the meta-analysis. The researchers suggest ongoing analysis with potential inclusion of spontaneously conceived pregnancies as a control group to help further determine the safety and efficacy of PGT/embryo biopsy. Study by Li et al. (2021), previously discussed in this policy, was included in this systematic review.

Zheng et al. (2021) published a systematic review and meta-analysis evaluating outcomes of pregnancies in which an embryonic biopsy with PGT was performed in comparison to spontaneously conceived (SC) pregnancies or pregnancies conceived after IVF/ICSI. A total of 15 studies including 3,682 babies born from PGT pregnancies, 127,719 babies born from IVF/ICSI pregnancies and 915,222 babies born from SC pregnancies were analyzed. Primary outcomes for the study included LBW and congenital malformations (CMs). Secondary outcomes included preterm delivery, very preterm delivery, gestational age, birth weight, very low birth weight, neonatal intensive care unit (NICU) admission, hypertensive disorders of pregnancy, gestational diabetes, placenta previa and preterm rupture of membranes. Subgroups undergoing analyses included preimplantation genetic diagnosis (PGD), preimplantation genetic screening (PGS), cleavage stage biopsy in conjunction with fresh embryo transfer and blastocyst biopsy in conjunction with frozen-thawed embryo transfer. Study findings indicated that RR for LBW was higher in PGT pregnancies when compared to SC pregnancies (RR = 3.95, 95% CI: 2.32–6.72), however there was no difference in the risk of CMs. LBW and CM pooled results showed similar risk in PGT and IVF/ICSI pregnancies. For preterm delivery and hypertensive disorders of pregnancy, risks were significantly higher in PGT pregnancies when compared with SC pregnancies (RR = 3.12, 95% CI: 2.67–3.64 and RR = 3.12, 95% CI: 2.18–4.47, respectively). In addition, lower gestational age (mean difference [MD] = -0.76 weeks, 95% CI -1.17 to -0.34) and birthweight (MD = -163.80 g, 95% CI: -299.35 to -28.24) were found for PGT pregnancies vs. SC pregnancies. Compared with IVF/ICSI pregnancies, however, the risk of very preterm delivery and very low birth weight were significantly decreased in PGT pregnancies (41% and 30%, respectively). Lastly, risk of hypertensive disorders of pregnancy were 50% higher in PGT pregnancies when compared with IVF/ICSI pregnancies. The additional subgroup analyses found that both PGD and PGS pregnancies had an association with a higher risk of preterm delivery and a lower gestational age than SC pregnancies. The authors concluded that overall, their meta-analysis indicates that PGT pregnancies may be related to increased risk of LBW, preterm delivery and hypertensive disorders of pregnancy when compared to SC pregnancies. When compared with IVF/ICSI pregnancies, obstetric and neonatal outcomes appear to be favorable, though PGT pregnancy showed an association with higher risk of hypertensive disorders of pregnancy. Limitations include potential for bias related to merging data from randomized controlled trials (RCTs) and non-RCTs, limited available data, and variations in the populations studied. The authors recommend further studies including randomized controlled trials and prospective cohorts to confirm these findings.

A collaborative multi-center study by Kakourou et al. (2018), with the support of the European Society of Human Reproduction and Embryology (ESHRE), focused on the diagnostic and clinical efficacy of PGT for human leukocyte antigen (HLA) potential positive outcomes. A total of 14 centers submitted data through a custom database from 716 HLA-PGD cycles; of these 704

cycles from 364 couples met inclusion criteria. The mean maternal age was 33.5 years and 81.3% of the couples tested had requested HLA-typing without concurrent exclusion of single monogenic disease (58.63% beta-thalassemia). Overall 9,751 oocytes were obtained and 5,532 embryos underwent analysis. Cycles predominantly used fresh oocytes (94.9%) with day three biopsy (85.3%). A diagnosis was made in 4,343 embryos (78.5%); of these 677 were found to be genetically suitable. Subsequently, 56.6% of the 364 couples underwent embryo transfer and 598 total embryos were transferred (382 cycles). Ultimately, HCG-positive pregnancies were obtained in 164 couples and 136 babies were born to 113 couples. Limitations to overall success of the procedure included maternal age, number of oocytes collected per cycle and genetic chance. In 57 cases, hematopoietic stem cell transplantation (HSCT) was reported; 64.9% utilized combined umbilical cord-blood and bone marrow transplantation and 77% of transplants identified no complications. In this study, the diagnostic efficacy (78.5%) was noted to be lower than the data previously reported for general PGD by ESHRE (92.6%). Pregnancy rate was 23.3% compared to the previously reported 25%. However, when embryo transfer was complete, the live birth rate (LBR) and embryo transfer data were comparable between this study (34.3%) and existing ESHRE PGD data (34%). Diagnostic efficacy was also lower in this study than reported in other PGD-HLA sources (78.5% vs. 89.5%-94.1%). The study was limited by the use of retrospective data collection from facilities with varying practices and strategies for assistive reproductive technology (ART) as well as potential reporting bias when using the online database. As the first multi-center study that analyzed the clinical utility of PGD-HLA over 15 years, important parameters for more positive endpoints were brought to light. The authors indicate that the study reinforces the need for high-level collaboration of all specialists involved in ART including PGD/HLA testing and the need for ongoing data collection. They note that published systematic data on methodology, clinical and diagnostic results and the success rates of ART and HSCT remain limited at this time.

In 2016, Chang and colleagues published a review of the outcomes of in vitro fertilization utilizing preimplantation genetic testing (PGT) from 2011-2012 from the United States Assisted Reproductive Technology Surveillance Data. Overall, they included 97,069 non-PGT cycles and 9,833 cycles that used PGT in their analysis. Most were for aneuploidy screening (55.6%), 29% were for "other reasons," and 15% were for preventing genetic disease. In the "other reasons" category, only 2% of clinics provided information on the reason for PGT, and it was primarily for gender selection. In 2011, 98% of clinics reporting doing at least one PGT cycle, and in 2012, 100% of reporting clinics had performed PGT cycles. The clinical characteristics between the three groups differed. The aneuploidy screening group tended to be older (> 37 years) and had a higher rate of prior miscarriages. As a group, they had fewer miscarriages than other age matched groups in the study and had a higher chance of a live birth compared to the age matched non-PGT group. They were more likely to have multiple births compared to the non-PGT group. This group was also more likely to have low birth weight babies. The genetic disease group was younger and did not have a history of prior miscarriages. In this group, in women ages 35-37, the adjusted odds of achieving a pregnancy and live birth were lower than the non-PGT group. In all categories, women using PGT who were < 35 years old and transferred one embryo, the odds of clinical pregnancy and live birth were lower than compared to the non-PGT group. Information was not available on the PGT techniques used by the different clinics, on biopsy type, protocol to select chromosome abnormalities, number of embryos, embryo morphology, and number of embryos discarded. The authors concluded that PGT might improve outcomes in populations at risk of a genetically affected child, including aneuploidy, on the basis of family history, but additional data collection and outcome data is necessary to better understand the overall value and effectiveness of PGT. Prospective, randomized studies are needed.

Preimplantation Genetic Testing for Monogenic/Single Gene Defects (PGT-M)

In a Cochrane systematic review, Vljakovic et al. (2022) sought to investigate the benefits and/or harms of biopsies performed on day three of embryo development compared to those performed on day five in individuals undergoing PGT-M with IVF or ICSI cycles. Only one small RCT was found, including 20 participants and there was risk of bias due to low level of precision and lack of blinding of study personnel. Based on the limited data available, there is uncertainty regarding whether there is a difference in live births and miscarriages, ectopic pregnancies, stillbirths, termination of pregnancy and viable intrauterine pregnancies between embryos biopsied on day three and day five for PGT-M. Further studies are needed to confirm what impacts may exist for biopsies performed on either day three or five of embryo development.

Ben-Nagi et al. (2019) conducted an observational study to determine if LBR is affected by oocyte yield as well as number of blastocysts biopsied, and/or the number of acceptable blastocysts to transfer post PGT-M or PGT-SR. Participants were 175 couples referred to an IVF center from 2014 to 2017 that chose to undergo either PGT-M or PGT-SR. One hundred forty-five (83%) of couples had PGT-M, while 30 (17%) had PGT-SR. Forty-four (25%) couples had second or third cycles of IVF, for a total of 249 oocyte retrievals and 230 frozen embryo transfers (FET); 196 (79%) due to single-gene disorders and 53 (21%) for chromosomal rearrangement. One hundred twenty-two (53%) of the FETs resulted in live birth, 16 (7%) resulted in ongoing pregnancy, 21 (9%) resulted in miscarriage, and 69 (30%) resulted in failed implantation. The authors found that the number of

oocytes collected ($p = 0.007$; OR 1.06), the number of blastocysts biopsied ($p = 0.001$; OR 1.14), and the number of suitable embryos to transfer ($p = 0.00$; OR 1.38) were all significantly positively associated achieving a live birth. The likelihood of live birth increased by 14% per additional blastocyst biopsied and by 38% per suitable embryo to transfer. Stratified analysis determined that the odds of live birth per acceptable embryo for transfer was 1.28 for single-gene disorders and 3.23 for chromosomal rearrangement.

Rechistky and Kuliev (2018) report on the use of PGT to select embryos at risk for inherited cancer syndromes. In their experience through Reproductive Genetics Innovations, cancer was the largest category of PGT-M for conditions with a genetic pre-disposition. In the PGT-M cohort, there were 5037 cycles, resulting in 3669 transfers of 6038 embryos. In the sub-cohort for cancer pre-disposition, there were 24 cancer syndromes reported, which included hereditary breast and ovarian cancer (BRCA1 and BRCA2), Li Fraumeni syndrome (LFD1), and familial adenomatous polyposis (APC). There were 383 at risk couples that underwent 702 PGT cycles. PGT utilized different methodologies depending on the type of mutation and available parental genetic information. Generally, a polar body or embryo biopsy was taken. Mutation testing using direct mutational analysis or linkage with parental haplotyping was performed. Aneuploidy screening using a 24-chromosome single nucleotide polymorphism (SNP) array or next generation sequencing (NGS) was the final step for couples with advanced maternal age. This resulted in 684 embryos in 484 transfer cycles, and 282 pregnancies. Three hundred and sixteen children were born without the cancer predisposition mutations. The authors reported that the inclusion of 24 chromosome aneuploidy screening for advanced maternal age couple increased the pregnancy rate in the PGT-M group from 50% to 70% and reduced the miscarriage rate from 14% to 9%.

Kubikova et al. (2018) reported on the development of a multiplex polymerase chain reaction (PCR) test for PGT-M of the beta-globin gene (*HBB*), responsible for beta-thalassemia and sickle cell anemia. The analysis utilized the amplification of overlapping small *HBB* segments to cover the entire gene, with analysis using next generation sequencing. In addition, 17 closely linked single nucleotide polymorphisms (SNPs) were tested simultaneously to aid in defining haplotypes in combination with *HBB* sequencing. A validation study on five family trios representing 14 different mutations was conducted, and results were consistent with previously obtained genetic results. Three of the families continued on to using this protocol for PGT-M. One couple had a single cell embryo biopsy at an early cleavage stage, and the other two families had about five cells extracted from the trophectoderm from blastocyst stage embryos. A total of 21 embryos were tested and had successful whole genome amplification, and NGS analysis was successful. Typical karyotyping and linkage analysis was performed simultaneously as a comparison for standard PGT methods. All but one embryo had an average read depth of 1000x for *HBB*. The single embryo that failed was found to have nullisomy for chromosome 11 where the *HBB* gene is located. In one couple, there were low call rates and a high allele dropout rate in the standard karyotype method, likely associated with suboptimal amplification after blastocyst biopsy. Results were resolved using linkage analysis of parental SNPs to confirm mutations and haplotypes found in the embryos. The allele drop out was not found in the NGS analysis. The authors concluded that the use of a trophectoderm biopsy with next generation sequencing provided better accuracy than traditional PGT testing. Pregnancy rates, outcomes, and confirmation of PGT results post-natally were not reported in this study.

Current technology allows for PGT-M testing for a multitude of single gene disorders, but the efficacy depends on the performance of gene amplification in a small sample, often a single cell. Volozonoka et al. (2018) examined the difference between multiple displacement amplification (MDA) and Omniplex whole genome amplification when used for comparative genome hybridization (CGH), Sanger sequencing, SNaPshot (single-base extension sequencing) and fragment size analysis. Nine couples at risk for single gene disorders consented to participate in the study. Disease genes involved included *ACTA2*, *HTT*, *KRT14*, *ALOX12B*, *TPP1*, *GLB1*, *MTM1*, and *DMD*. A total of 62 embryos were tested, and 1-8 trophectodermal cells were taken from the outer layer. All embryos survived the extraction. Thirty-nine embryos underwent whole genome amplification using MDA and the remaining went through OmniPlex linear amplification. Amplification detection was determined by capillary electrophoresis. Direct mutation analysis used Sanger sequencing or SNaPshot, and chromosomes were analyzed using CGH. Whole genome amplification, regardless of method, and testing was successful and provided a conclusive result in all embryos. Five unaffected and euploid embryos were transferred, resulting in four clinical pregnancies and the live birth of two healthy children. Key differences were noted, however. The MDA approach to whole genome amplification resulted in heavier DNA strings and resulting electrograms were clearer, and the base error rate was lower compared to other PCR based approaches. MDA had significant amplification bias that caused high CGH noise. The authors concluded that methodology choice should depend on which downstream analysis is most needed, and both amplification techniques could be used if there are enough embryonic cells available.

Sallevelt et al. (2017) reported on the use of PGT-M using a single blastomere for mitochondrial disorders. Mitochondrial diseases are transmitted only from the mother, and the expression of disease is dependent on the mutation load, meaning the number of mitochondria carrying the mutation compared to the number of wildtype mitochondria present. Prenatal diagnosis has a potential problem in that the mutational load across all tissues may not be able to be identified completely, and therefore the future phenotype of the fetus cannot be predicted easily. PGT-M is the preferred choice for female carriers, as only mutation free embryos can be transferred. If no mutation free embryos are available, embryos with a low mutation load can be transferred, which reduces the risk of an affected child, but cannot eliminate it. To date, two blastomeres have been used in PGT-M for mitochondrial disease to better predict the mutation load. This has a negative impact on the LBR. The authors studied the value of using only one blastomere in a cohort of nine women carrying a m.3243A > G mutation that causes mitochondrial encephalopathy with lactic acidosis and stroke-like episodes (MELAS). These women produced 73 embryos that had two or more blastomeres removed from which 294 single blastomeres were analyzed. Only one blastomere was concluded to have a false negative result. This was based on this cell having a mutation load of about 5%, within the range where an embryo transfer might have been considered, but surrounding blastomeres from the same embryo had a higher mutational load of 22-30%. The authors concluded that as the false negative rate was 0.34%, a single blastomere would be sufficient for PGT-M. Pregnancy rates and outcomes were not highlighted by the authors because their goal was to determine first if a single cell would provide the correct diagnosis. Single cells were analyzed but excluded from the data reporting, as well as multi-cells, and used for embryo transfer which they feel would confound the data.

PGT-M was first reported in 1990 for sex selection for an X-linked disorder. The field has evolved since then to encompass many genetic diseases, including early and adult-onset disorders. Testing for tissue typing also occurs, with the hopes that a baby will be born that can provide a blood or bone marrow transplant for an older affected sibling. Testing for adult-onset disorders and tissue typing to rescue an older sibling raises a number of ethical issues. Analysis can be completed with chromosome microarray, polymerase chain reaction (PCR), or next generation sequencing. Technical challenges exist for all methods, such as timing of the biopsy and which cells are biopsied. Collecting too many cells at an early cleavage stage may impact implantation and pregnancy rates, and early-stage biopsies may result in poor DNA amplification. Single cell PCR may also result in allele drop out, which occurs in 10-20% of cases. Alleles drop out can result in misdiagnosis between carrier and affected embryos. Because PGT-M is using only 1-2 cells, there is additional risk of contamination of the sample with DNA from the technician or even sperm sticking on the zona pellucida. Errors can occur from transfer of the wrong embryo, from mislabeling, and from couples having unprotected sex during the cycle that results in pregnancy, versus the transferred embryo. In 2005, the ESHRE reported on the reanalysis of 940 untransferred embryos and noted that 93.7% of embryos were correctly classified, with a sensitivity of 99.2% and a specificity of 80.9%. Recent ESHRE data suggested that the success rate of pregnancy after PGT-M was similar to other assisted reproduction, with a LBR per oocyte retrieved of 24%. Genetic counseling is strongly recommended prior to PGT-M so that couples have a clear understanding of the pros and cons of this approach (Lee et al., 2017).

Preimplantation Genetic Testing for Chromosomal Structural Rearrangements (PGT-SR)

In a 2022 retrospective analysis, Nakano et al. sought to assess the effectiveness of PGT-SR using array comparative genomic hybridization (aCGH) or NGS in the prevention of recurrent miscarriage. The evaluation included 31 couples with balanced translocations who had undergone a total of 68 PGT-SR cycles between 2012 and 2020. In all, 242 blastocysts underwent biopsy for aCGH or NGS and the blastocysts identified as genetically transferrable were transferred in the subsequent frozen-thawed single embryo transfer cycle. The study found a genetically transferable rate of 21.2% with 35 blastocysts transferred to the uterus. Rate of clinical pregnancy was 57.1% and ongoing pregnancy rate was 100%. The authors concluded that their results supported the use of PGT-SR using aCGH or NGS to evaluate chromosomes and ultimately help prevent recurrent miscarriages. In addition, the results may be helpful in genetic counseling for carriers of balanced translocations.

Huang et al. (2019a) performed a retrospective cohort study of 194 reciprocal translocation carrier couples who had experienced two or more adverse pregnancy histories. Two hundred sixty-five PGT-SR cycles were examined to assess the impact of PGT-SR on normal live birth, birth defect, and miscarriage rates in reciprocal translocation carrier couples. Prior to PGT-SR, the reproductive history of the couples consisted of 592 pregnancies — 83.6% resulted in miscarriages, 6.1% live birth with defects, 4.9% were terminated due to unwanted pregnancy, and 2.9% resulted in normal live births. Post PGT-SR, 118 clinical pregnancies resulted in 85.6% normal live births, 11% miscarriage, 3.4% with birth defects. The authors concluded that reciprocal translocation carriers in this study had a low risk of miscarriage and birth defects and a higher frequency of normal live births following PGT-SR.

Next generation sequencing is emerging as an important technique for genetic analysis. Zhou et al. (2018a) examined the validity of using massive parallel sequencing (MPS) on trophectoderm samples for PGT-A for chromosome translocation carriers. Twelve couples with chromosome translocations participated in a study. Nine had balanced translocations, and three were carriers of a numerical chromosome abnormality. A total of 105 embryos were biopsied on day three and had one cell removed. The cells underwent whole genome amplification and were then tested for genomic imbalances using MPS and CGH and confirmed using routine karyotyping. Results were obtained for MPS and CGH for 101 embryos, and there was concordance between MPS and CGH for 19 euploid and 82 unbalanced or aneuploidy embryos. There were four discrepancies, however. In one blastomere, MPS found a deletion of a X chromosome not found by CGH. This might be caused by a low density of SNPs on the CGH platform in that region. In another case, MPS identified a 186 Mbp duplication on chromosome 1, and a 15.6 Mbp duplication on chromosome 5, whereas CGH identified the duplications but of a different size. This could be related to amplification bias impacting CGH that would have been corrected in the MPS bioinformatics process. In the third embryo, karyotyping and MPS identified an unbalanced translocation between chromosome 3 and 6, and CGH only identified the imbalance in chromosome 3. In the final discrepant embryo, karyotype and MPS identified an unbalanced translocation between chromosomes 13 and 22, and CGH only identified the imbalance in chromosome 13. Twelve of the nineteen embryos that were found to be free of genomic imbalances were used for frozen-thaw embryo transfer, resulting in 1 live birth and 5 ongoing pregnancies.

Brunet, et al. (2018) examined the use of next generation sequencing to identify complex chromosome rearrangements in the embryos of chromosomal translocation carriers. Six couples with complex rearrangements underwent PGT-SR. Biopsies were done on day 5 or 6 blastocysts. A total of 84 oocytes were retrieved, resulting in 25 embryos that had trophectoderm biopsy and NGS analysis. Vitrified warm single embryo transfers were done with six euploid embryos resulting in four healthy live births for four couples. One couple chose to confirm the PGT-SR results with prenatal diagnosis, and the other three did not. Two couples did not have any transferable embryos after two cycles.

Segmental mosaicism is a concern for both PGT-A and PGT-SR. Zhou et al. (2018b) examined the frequency of de-novo segmental aneuploidy identified by next generation sequencing (NGS). The study took place over a three-year time period and involved 5,735 blastocysts from 1,854 couples who underwent PGT-A (n = 770) and PGT-SR (n = 1084) on trophectoderm biopsies. Biopsied cells underwent whole genome amplification using GenomePlex amplification, and low coverage massively parallel sequencing (MPS) on the Proton platform. Overall, 581 blastocysts were found to have 782 de novo segmental aneuploidies. Most carried only one, but 115 had two, and 38 had three or more. There was no association with advanced maternal age or a specific chromosome. In 1,377 cycles, 1,686 blastocysts were transferred resulting in clinical pregnancies in 49% of the PGT-SR group and 47% of the PGT-A group. The miscarriage rate was about 9% in both groups. At the time of publication, there were 84 prenatal diagnosis tests and 645 delivered babies that were considered normal and healthy. Forty blastocysts with de novo segmental aneuploidy were donated for further research and were additionally analyzed by FISH as a comparison analysis. Of the donated blastocysts, 39 were successfully analyzed and FISH confirmed the segmental aneuploidy identified by NGS. Because de novo segmental aneuploidy can be caused by either meiosis during gamete formation or during mitosis during embryo development, the trophectoderm and inner cell mass were evaluated for 26 blastocysts. Five showed pure segmental mosaicism in both the trophectoderm and inner cell mass, but fourteen showed different levels of mosaicism between the two tissue types. The authors concluded that this analysis showed that segmental de novo aneuploidy is a real issue and is not an artifact of whole genome amplification. Further studies are needed to understand de novo segmental mosaicism and its impact on embryo development.

Maithripala et al. (2018) reviewed the reproductive choices of 36 couples who experienced recurrent miscarriage as a result of one member of the couple carrying a balanced chromosome translocation. The couples were identified through a retrospective chart review of 2,321 couples seen in a highly specialized reproductive assistance clinic between 2005 and 2013. The pre-diagnosis obstetrical history was obtained, and it was similar for all couples. The date of parental diagnosis was identified for each couple and used in determining the time from diagnosis to live birth as a point of comparison between couples that chose natural conception and those that picked PGD as their reproductive choice. Twenty-three couples chose to pursue natural conception, and thirteen chose PGT-SR. In the natural conception group, there were 24 live births with a live birth incidence of 1 birth per 4.09 years, and 74% of women had at least one live birth in the follow up period. In the PGT-SR group, six live births were recorded, reflecting a live birth incidence of 1 birth per 5.63 years, and 38% of women had at least one live birth in the follow up period. There was no significant difference between the groups in post-parental diagnosis miscarriage or LBRs. It should be noted that in the PGT-SR group, the miscarriage rate did not take into consideration PGT-SR specific variables. There were 8 failed PGT-SR cycles, which included four euploid embryo transfers that did not result in pregnancy. While failed PGT-

SR and miscarriage cannot be equated, the authors felt it was meaningful to report as cycle failure represents a significant effort resulting in a failure to achieve a live birth.

lews et al. (2018) conducted a systematic review of the literature to examine the evidence supporting the use of PGT-SR in couples who have experienced recurrent miscarriage due to an inherited structural chromosome rearrangement. Meta-analysis was not possible because of significant differences between the studies. The authors identified 20 studies after a comprehensive review of the literature. Live birth was the primary outcome that was analyzed, and secondary outcomes reviewed included miscarriage rate and time to successful pregnancy. A pooled total of 847 couples that conceived naturally had a LBR of 25-71%. A pooled total of 562 couples had PGT-SR and had a similar LBR of 26-87%. There were no large comparative or randomized studies found. The studies also had different inclusion criteria and some evaluated patients for additional causes of miscarriage, such as auto-immune disease, whereas others did not. Some studies found a lower miscarriage rate in the PGT-SR group, and others did not. Two studies were identified as the best comparative analysis for examining the miscarriage rate and time to live birth post-parental diagnosis, and the studies had conflicting results. One found a lower miscarriage rate in the PGD group, and the other did not. Both found a similar time to LBR for PGT-SR and natural conception.

The ability of NGS to detect complex chromosome rearrangements as compared with CGH was the focus of a study by Chow et al. (2018). The authors used archived whole genome amplified DNA from 342 embryos at risk of genomic imbalance because of translocation or inversion carrier parents. All embryos had been previously analyzed by CGH. There were 287 blastomere biopsies and 55 trophectoderm biopsies. Overall, the concordance rate on abnormal results was 100% between NGS and CGH, regardless of the biopsy type. The concordance in normal embryos was 98% in the blastomere biopsy group, and 79% on trophectoderm biopsies. NGS detected a de novo segmental aneuploidy and low-level mosaicisms that were not identified by CGH. The authors concluded that NGS was an acceptable technology to use in PGT-SR.

Zhang et al. (2017) examined the utility of using SNP-microarray in families with balanced translocations to accurately identify euploid embryos for transfer. In 68 blastocysts from 11 translocation families, SNP-microarray identified 42 unbalanced or aneuploidy embryos, and 26 balanced or normal chromosomes. Ten families became pregnant on the first cycle; one family was successful on cycle three. Amniocentesis on the resulting pregnancies matched the embryo microarray analysis, resulting in a 100% sensitivity and sensitivity in this cohort, but the authors caution that a larger sample size is needed to further validate sensitivity and sensitivity.

Tobler et al. (2014) conducted a retrospective analysis comparing SNP-array and aCGH in 543 embryos from 63 couples, of which one parent carried a reciprocal translocation. Couples were from 16 different fertility centers with samples being analyzed at one lab. SNP-array was used for molecular karyotyping from 2007 to 2011, and from 2011 to 2014 aCGH was used. No embryo was analyzed by both methods. A cell was obtained from the embryo at day 5 or the blastocyst stage and placed in a stabilizing buffer and frozen for transport. Whole genome amplification (WGA) was accomplished for the SNP-array using a *phi* 29 polymerase protocol, and aCGH WGA was done using a Klenow fragment and a modified random priming protocol. Molecular karyotypes were obtained on 92% (498) of the biopsied embryos. In the 8% (45) samples that failed, WGA failed and was strongly correlated with poor embryo quality. Overall, 45% of embryos were chromosomally normal, and the remaining had translocation errors or aneuploidy. The pregnancy rates were equivalent for SNP (60%) and aCGH (65%). The pregnancy rate was slightly higher if the biopsy was done on blastocysts (65%) vs. cleavage stage embryos (59%). Overall, the authors concluded that SNP or aCGH microarray technologies demonstrate equivalent clinical findings that maximize the pregnancy potential in patients with known parental reciprocal chromosome translocations.

Preimplantation Genetic Testing for Aneuploidy Screening (PGT-A)

There is insufficient evidence to support the use of PGT for aneuploidy screening at this time. Further studies focused on clinical utility and the development of algorithms to identify populations for which this testing may be beneficial are needed.

In a retrospective cohort study, Kucherov et al. (2023) analyzed the impact of PGT-A on cumulative live birth rate (CLBR) when used in IVF cycles. Data from the Society for Assisted Reproductive Technology Clinical Outcome Reporting System (SART CORS), a national registry including over 85% of US programs performing IVF, was used to compare CLBR for individuals using autologous oocytes either with or without PGT-A. Donor oocyte cycles, donor embryo cycles, gestational carrier cycles, cycles where both fresh embryo transfer (ET) and thawed embryo which had previously been frozen (ET plus FET) or cycles using fresh ET after PGT-A were excluded from the study. In all, 133,494 IVF cycles were evaluated. A decrease in CLBR was found in the PGT-A group across age groups with the exception of individuals over 40 years ($p < 0.01$). The researchers performed a

subgroup analysis of only individuals who had undergone FET subsequent to PGT-A (not including those where no embryos were transferrable) and found a very high CLBR (ranging from 71.2% for individuals less than 35 years old to 50.2% for individuals over 42 years old). Of note, rates for preterm birth, early pregnancy loss, multiple gestations, and LBW were greater in the group that had not undergone PGT-A. The study was limited by its retrospective design, impacting its use for demonstration of causal relationships, and had missing and/or outlier data points. The researchers concluded that overall, for individuals 40 years of age or younger with blastocysts available for ET or PGT-A, there was an association between PGT-A and decreased CLBR which was notably higher for individuals under 35 years of age. They further state that PGT-A may show utility for individuals with advanced maternal age and may be associated with lower rates of miscarriage. For the most accurate individual outcome measure, the authors recommend the use of CLBR per cycle vs. first transfer LBR when determining utility of PGT-A. Lastly, the importance of counseling regarding utility of PGT-A based not only on maternal age, but potential miscarriage benefit is stressed.

In a 2022 systematic review and meta-analysis (Cheng et al.), pregnancy outcomes of individuals undergoing IVF either with or without PGT-A were compared. Nine RCTs including 3,334 individual participants were included in the review. The analysis found that PGT-A was not related to an increase in LBR overall (RR 1.13, 95% CI 0.96–1.34, $I^2 = 79\%$), but it was associated with an increase in the LBR for those with advanced maternal age (RR 1.34, 95% CI 1.02–1.77, $I^2 = 50\%$). In addition, PGT-A was related to a decreased miscarriage rate (RR 0.53, 95% CI 0.35–0.81; $I^2 = 50\%$). The primary limitation of the study is the high level of heterogeneity of the studies included ($p < .001$, $I^2 = 79\%$). Subgroup analysis identified age as the main factor leading to the high heterogeneity. Based on the study results, the authors posit that PGT-A increases LBR for individuals of advanced maternal age. Studies by Yan (2021) and Verpoest (2018), previously discussed in evidence, were included in this systematic review.

The use of PGT-A in individuals with recurrent pregnancy loss (RPL) was the focus of a retrospective study performed by Bhatt et al. (2021) using data from SART CORS. The researchers aimed to discern whether PGT-A was associated with improved LBRs in couples with RPL who were undergoing IVF with frozen embryo transfer (IVF-FET). RPL was defined as a history of at least 3 pregnancy losses. In total, 12,631 FET cycles for 10,060 couples were analyzed, including 4,287 cycles in couples with history of a tubal disease, who formed a control group. Couples with RPL undergoing FET either with or without PGT-A made up the experimental group. The primary outcome of this study was LBR. Rates of clinical pregnancy, spontaneous abortion and biochemical pregnancy loss were secondary outcomes. Results indicated that in this large study, PGT-A was associated with an increase in LBR and clinical pregnancy for individuals with RPL. The greatest difference was seen in individuals older than 42 years. However, because this retrospective study included only individuals with RPL undergoing FET, the results may not be generalizable to all those with RPL. In addition, the data regarding clinical evaluation and treatments received for RPL for the individuals included in the study was not obtainable. The authors encourage counseling on all options for management of RPL which may include IVF with PGT-A for embryo selection to increase the chance of live birth, especially for those individuals with advanced maternal age.

Simopoulou et al. (2021) published a systematic review and meta-analysis of RCTs focusing on identification of age group(s) that may benefit from PGT-A and the best day to perform biopsy for the testing. A systematic literature search identified 11 RCTs using PGT-A with comprehensive chromosomal screening (CCS) on either day three or day five that met eligibility criteria. After analysis, the researchers found that PGT-A was not related to improved LBRs per individual in the overall population (RR:1.11; 95%CI:0.87-1.42; $n = 1513$; $I^2 = 75\%$), but it was associated with lower miscarriage rates (RR:0.45; 95%CI:0.25-0.80; $n = 912$; $I^2 = 49\%$). Notably, however, PGT-A was associated with improved cumulative LBR per individual (RR:1.36; 95%CI:1.13-1.64; $n = 580$; $I^2 = 12\%$). In subgroup analysis, PGT-A was associated with a higher LBR for individuals older than 35 years (RR:1.29; 95%CI:1.05-1.60; $n = 692$; $I^2 = 0\%$) but did not have this association for younger individuals (RR:0.92; 95%CI:0.62-1.39; $n = 666$; $I^2 = 75\%$). In terms of timing, day five biopsies showed an improved LBR per ET (RR: 1.37; 95% CI: 1.03-1.82; $I^2 = 72\%$). The authors concluded that while PGT-A did not appear to improve outcomes for the overall population, it was associated with improved LBRs when performed on blastocyst stage embryos in individuals over the age of 35 years. However, the number of studies included in the meta-analysis was relatively small and the ages of most of the individuals included were not necessarily representative of individuals who commonly undergo PGT-A testing. The researchers encourage further study to evaluate characteristics of individuals that may benefit from PGT-A and focus on developing an algorithm to assist with decision making regarding the appropriate population for PGT-A use.

In a 2021 publication, Tiegs et al. reported the outcome of their prospective, multi-center, blinded, nonselection study to evaluate the value of a diagnosis of aneuploidy (made via targeted next-generation sequencing preimplantation genetic testing [PGT-A]) in predicting failure of a successful delivery. A secondary outcome measured was the impact of trophectoderm biopsy

on lasting implantation. A total of 402 individuals with infertility received 484 single, frozen blastocyst transfers. Unblinded PGT-A results performed using NextSeq 500/550 NGS-based PGT-A were compared to clinical outcomes of embryo transfers and a calculation of predictive values was made. Significant difference in outcome by PGT-A diagnosis was found: 64.7% (202/312) of euploid embryos progressed to either sustained implantation or delivery while none of the 102 embryos diagnosed as whole chromosome aneuploid progressed to either sustained implantation or delivery. Thus, the clinical error rate in aneuploid diagnoses was 0%. There was no difference in sustained implantation between the control group, which was aged matched and had not undergone biopsy, and the PGT-A testing group. The authors assert that the PGT-A assay evaluated was found to be prognostic of failure to deliver when such testing revealed an aneuploid result and did not result in the discard of embryos that have significant reproductive potential. They do, however, note limitations, including the inability to analyze predictive values associated with segmental PGT-A or whole chromosome mosaic diagnoses due to the low incidence of those results. Additionally, the retrospective identification of a control group to evaluate impact of cell biopsy on sustained implantation limits the study's strength. Lastly, about half of the study subjects were less than 35 years of age; however, the false positive rates of aneuploidy are typically higher in this group compared with older subjects, so this may have further challenged the accuracy of the assay used in this study. The researchers recommend non-selection studies be performed for every new PGT-A assay as additional technologies emerge.

Konstantinidis et al. (2020) studied the incidence and patterns of trisomies and recombination separately and in conjunction with each other at the blastocyst stage by single nucleotide polymorphism (SNP) testing with aCGH. Interesting findings regarding recombination and aneuploidy origin were revealed. SNP microarrays were performed on 1,442 blastocyst embryos from 268 couples who underwent PGT for known single gene disorders; 24-chromosome aneuploidy screening by aCGH was done concurrently. One hundred percent of meiotic trisomies were maternal in origin and incidence increased significantly with maternal age ($p < 0.0001$). Meiosis I trisomies and meiosis II trisomies were 55.8% and 44.2%, respectively. Recombination studies were performed for 11, 476 chromosomes and 17,763 recombination events were reported. The average number of recombination sites was 24.0 ± 0.3 for male meiosis and 41.2 ± 0.6 for autosomal female meiosis. One hundred ninety euploid embryos and 69 embryos with maternal meiotic trisomies were compared which revealed similar recombination rates ($p = 0.425$) and non-recombinant chromatid rates ($p = 0.435$). Although the study provided unique data regarding recombination and aneuploidies in embryos, further research and data is needed to establish clinical validity and clinical utility.

The effectiveness and safety of PGT-A was evaluated by Cornelisse et al. (2020) who performed a systematic review of six databases and two trial registries in September 2019. Thirteen randomized controlled trials involving 2,794 women reporting data on clinical outcomes in patients who underwent IVF with PGT-A versus IVF without PGT-A were included. The quality of evidence ranged from low to moderate. Cumulative live birth (CLBR) was the primary outcome; LBR after first embryo transfer, miscarriage rate, ongoing pregnancy rate, clinical pregnancy rate, multiple pregnancy rate, proportion of women obtaining an embryo transfer and mean number of embryo transfers represented the secondary outcomes. The author's reported results were as follows: One trial used polar body biopsy with aCGH. It is uncertain whether the addition of PGT-A by polar body biopsy increases the CLBR compared to IVF without PGT-A (odds ratio (OR) 1.05, 95% confidence interval (CI) 0.66 to 1.66, 1 RCT, $n = 396$, low-quality evidence). The evidence suggests that for the observed CLBR of 24% in the control group, the chance of live birth following the results of one IVF cycle with PGT-A is between 17% and 34%. It is uncertain whether the LBR after the first embryo transfer improves with PGT-A by polar body biopsy (OR 1.10, 95% CI 0.68 to 1.79, 1 RCT, $n = 396$, low-quality evidence). PGT-A with polar body biopsy may reduce miscarriage rate (OR 0.45, 95% CI 0.23 to 0.88, 1 RCT, $n = 396$, low-quality evidence). No data on ongoing pregnancy rate were available. The effect of PGT-A by polar body biopsy on improving clinical pregnancy rate is uncertain (OR 0.77, 95% CI 0.50 to 1.16, 1 RCT, $n = 396$, low-quality evidence). Another trial used blastocyst stage biopsy with next-generation sequencing. It is uncertain whether IVF with the addition of PGT-A by blastocyst stage biopsy increases CLBR compared to IVF without PGT-A, since no data were available. It is uncertain if LBR after the first embryo transfer improves with PGT-A with blastocyst stage biopsy (OR 0.93, 95% CI 0.69 to 1.27, 1 RCT, $n = 661$, low-quality evidence). It is uncertain whether PGT-A with blastocyst stage biopsy reduces miscarriage rate (OR 0.89, 95% CI 0.52 to 1.54, 1 RCT, $n = 661$, low-quality evidence). No data on ongoing pregnancy rate or clinical pregnancy rate were available. IVF with PGT-A versus IVF without PGT-A with the use of FISH for the genetic analysis; eleven trials were included in this comparison. It is uncertain whether IVF with addition of PGT-A increases CLBR (OR 0.59, 95% CI 0.35 to 1.01, 1 RCT, $n = 408$, low-quality evidence). The evidence suggests that for the observed average CLBR of 29% in the control group, the chance of live birth following the results of one IVF cycle with PGT-A is between 12% and 29%. PGT-A performed with FISH probably reduces live births after the first transfer compared to the control group (OR 0.62, 95% CI 0.43 to 0.91, 10 RCTs, $n = 1680$, $I^2 = 54\%$, moderate-quality evidence). The evidence suggests that for the observed average LBR per first transfer of 31% in the control group, the chance of live birth after the first embryo transfer with PGT-A is between 16% and 29%. There is probably little or no difference in miscarriage rate between PGT-A and the control group (OR 1.03, 95% CI 0.75 to 1.41; 10 RCTs, $n = 1680$, $I^2 =$

16%; moderate-quality evidence). The addition of PGT-A may reduce ongoing pregnancy rate (OR 0.68, 95% CI 0.51 to 0.90, 5 RCTs, $n = 1121$, $I^2 = 60\%$, low-quality evidence) and probably reduces clinical pregnancies (OR 0.60, 95% CI 0.45 to 0.81, 5 RCTs, $n = 1131$; $I^2 = 0\%$, moderate-quality evidence). The authors concluded that due to the poor quality of evidence regarding CLBR, LBR after transfer or miscarriage rate between IVF with and IVF without PGT-A, routine clinical practice of PGT-A is not supported.

Trophectoderm (TE) biopsy, a technique to assess aneuploidy for PGT, can result in false positive and false negative test results because the chromosome number in TE cells is not always concordant with the chromosome number of the inner cell mass, which develops into the fetus. Huang et al. (2019b) conducted an investigational study to determine the effectiveness of noninvasive preimplantation genetic testing for aneuploidy (niPGT-A) as compared to the standard TE biopsy method. Fifty-two frozen donated blastocysts were analyzed by next-generation sequencing to serve as a gold standard. TE biopsy PGT-A and niPGT-A results were generated for all samples and compared with sequencing results from corresponding embryos. The false negative rate for niPGT-A was zero. The positive predictive value and specificity were higher for niPGT-A than for TE biopsy PGT-A. In addition, the authors stated that the concordance rates for embryo ploidy and chromosome copy number were also higher for niPGT-A than seen in TE biopsy PGT-A. Based on this study, the authors concluded that niPGT-A by DNA sequencing of DNA released in culture media from both trophectoderm and ICM provides a non-invasive method which is less prone to errors linked to embryo mosaicism, though future studies with larger sample sizes are necessary.

Simon et al. (2018) conducted a retrospective study examining IVF outcomes using single nucleotide polymorphism (SNP) based PGT-A. Outcome data was collected on procedures performed at two U.S. fertility centers from 2010-2013. Women 18-55 years of age who underwent IVF treatment were eligible for inclusion; those who did not elect 24 chromosome SNP-based PGT-A were excluded from analysis. During the study timeframe, 974 women (20-46 years of age) underwent 1,884 IVF cycles (1,621 non-donor, 262 donor) and elected to use SNP-based PGT-A. An implantation rate of 69.9%, clinical pregnancy rate per transfer of 70.6%, and LBR per transfer of 64.5% were observed in the non-donor cycles. Data were stratified by maternal age for analysis, with no significant difference observed in outcome rates per transfer, even for women > 40 years of age. No difference in pregnancy outcome was seen in single embryo transfers (SET) compared with double embryo transfers which supported the authors' recommendation for the utilization of SET when SNP-based PGT-A is used. Larger, prospective studies are recommended to further assess the impact of SNP-based PGT-A on pregnancy outcomes.

Zore et al. (2018) compared the outcomes of frozen single embryo transfer between euploid embryos and those with segmental mosaicism. Three hundred and twenty-seven women had 377 frozen embryo transfers. All embryos underwent biopsy at the blastocyst stage where two or more cells were taken from the trophectoderm. CGH was used to determine if embryos were euploid or had segmental mosaicism. Three hundred and fifty-seven were euploid, and 20 had segmental mosaicism. The spontaneous miscarriage rate was 18.2% in euploid embryos, compared to 40% in segmental mosaic embryos. Furthermore, the LBR for euploid embryos was 53.8%, whereas for segmental mosaics the LBR was 30%. The authors concluded that reporting segmental mosaicism was important to help with selection of embryos for transfer, and noted that although reduced, segmental mosaics still had the potential to result in a live birth.

Munné (2018) reported on the outcomes of the 2018 Preimplantation Genetic Diagnosis International Society (PGDIS) conference regarding PGT-A. Studies and data were reviewed at the conference that demonstrated improved pregnancy rates per transfer in experience centers and in women over the age of 35 who utilize PGT-A, but not in younger women. Studies using cell-free embryo DNA in spent media were promising, showing 80-90% concordance with biopsy. Mosaicism in the trophectoderm was a topic of debate, the outcome of which was PGDIS agreeing to update their guidelines. However, the guidelines will still recommend transferring euploid embryos favorably over mosaic embryos.

Friedenthal et al. (2018) evaluated the difference in pregnancy outcomes using NGS compared to CGH in single frozen thawed transferred embryos (STEET) in a retrospective review. A total of 916 STEET cycles from 2014 to 2016 were reviewed, and included 548 NGS cases, and 368 cases using CGH. The outcomes analyzed included implantation rate, LBR, and miscarriage rate. The NGS group had a higher implantation rate (72% vs. 65%) than CGH, and a higher LBR compared to CGH (62% vs 54%). The miscarriage rate was similar between the two groups. The authors concluded that NGS was better at detecting reduced viability embryos caused by mosaicism and using NGS may result in better pregnancy outcomes when compared to using CGH.

Gleicher and Orvieto (2017) conducted a comprehensive literature review through January 2017 on research related to current PGS methodologies and outcomes using comparative chromosome screening on 5-6-day TE biopsies, which they call PGS

2.0. This includes aCGH and SNP-based array technologies. Overall, they noted that the literature has a skewed view of clinical utility and uses embryo transfer as the starting point for measuring success, whereas generally IVF literature uses the initiated IVF cycles as the starting point. When using initiated cycles as a starting point, non-PGS cycles result in a higher LBR over PGS cycles. In addition, they report from their analysis that TE mosaicism may be present in at least half of all embryos, and mathematical models suggest that the likelihood of false negative and positive results is too high to safely determine which embryos should be transferred or not. Their overall conclusion is that PGS 2.0 does not have clinical utility and may in fact reduce LBRs.

Barad et al. (2017) conducted a retrospective analysis of the impact of PGT-A on pregnancy outcomes in donor oocyte-recipient cycles. The authors utilized the data obtained between 2005 and 2013 from the Society for Assisted Reproductive Technology Clinic Outcome Reporting System. This database relies on voluntary reporting, and 90% of the US IVF centers participate. In this cohort, first embryo transfers with day 5/6 embryos were reviewed, for a total of 20,616 control cycles and 392 PGT-A cycles. The data showed that the pregnancy and LBRs were lower in the PGT-A group by 35% when compared to the control group. The authors concluded that PGT-A was not associated with improved odds of pregnancy, live birth, or miscarriage rate.

Gleicher et al. (2017) addressed the issue of trophoctoderm mosaicism in a collaboration between The Center for Human Reproduction in New York City and the Center for Studies in Physics and Biology and the Brivanlou Laboratory of Stem Cell Biology and Molecular Embryology using mathematical modeling. As molecular methodologies improve, it has become more apparent that the trophoctoderm has more mosaicism than previously appreciated. Recent studies have shown that over a third of embryos considered to be aneuploid were actually mostly euploid-normal on follow up studies. This has raised concerns about the impact on PGT-A results and whether or not mosaic embryos can be transferred. The authors developed two models to assess the likelihood of false positive and false negative results on an average six cell biopsy from a 300 cell trophoctoderm, with the understanding that trophoctoderm biopsies often include only one cell. The models assumed that mosaicism was distributed evenly throughout the trophoctoderm, even though in reality it is often clonal. In their first model that examined the probability of a false negative with results from one or more euploid cells, they determined that there is a high probability of selecting a euploid cell, even when the ratio of euploid cells is low. In the second model, the probability of a false positive from an aneuploid result was examined. The authors found that even with 1-2 cells being aneuploidy, the embryo could theoretically still be mostly euploid. When three cells were found to be aneuploid, it is mathematically more likely consistent with embryo aneuploidy. The author's goal was to examine through mathematical modeling the likely reliability of being able to choose or discard an embryo based on ploidy results of a single cell trophoctoderm biopsy. They concluded that mathematically, one cannot use the results of a single cell to determine the ploidy of an embryo, and therefore cannot reliably predict which embryos should be used or discarded.

Capalbo et al. (2015) compared SNP based microarray screening, aCGH, and qPCR techniques for screening embryos. The authors conducted a prospective double-blind observational study from Oct. 2012-Dec. 2013. TE biopsies were done on day 5-6. Forty-five patients were included who had indications of advanced maternal age, recurrent miscarriage, or parental carrier of a balanced translocation. A total of 124 blastocysts underwent aCGH. Of these, 122 survived warming and re-expansion and underwent TE biopsy and qPCR analysis. Two samples failed qPCR and were excluded. Eighty-two percent of embryos showed the same diagnosis between aCGH and qPCR and 18% were discordant for at least one chromosome. Discordant blastocysts were warmed, and TE was biopsied again on 21 embryos that survived another rewarming and underwent a blinded SNP array analysis. A conclusive result was obtained in 18 of the 21. In four of these, the qPCR, aCGH, and SNP array did not match and were considered mosaic aneuploid. Overall, when the data is viewed per chromosome, the aCGH and qPCR results were consistent in 99.9% of cases where both methods were performed on TE biopsy from the same embryo. The SNP based reanalysis, however, showed a higher discordant rate between aCGH and qPCR. The authors concluded that TE biopsies can be a highly reliable and effective approach for PGS, and that until aCGH is studied for their clinical negative predictive value, this comparative study can only demonstrate that aCGH results in a higher aneuploidy rate than other contemporary and better validated methods of chromosome screening.

Kurahashi et al. (2015) conducted a comprehensive review of the literature regarding the analytical validity of CMA for PGS. The authors reported that while oligonucleotide arrays (CMA) are the standard for clinical analysis of individuals with developmental delay and congenital anomalies, the need to use a single cell and then perform WGA when using CMA for PGS may introduce amplification bias. Uneven amplification can occur of various regions of the DNA sampled from the embryo and lead to inaccuracy in the test results. Newer technologies including bacterial artificial chromosome (BAC) and a multiple displacement method are being explored as ways to mitigate amplification bias. Mosaicism in the embryo is also reported by the authors as a

factor to overcome in using CMA for PGS. It has been demonstrated in the oocyte and blastomere that the spindle assembly process that regulates chromosome segregation is transiently deficient, which leads to a high rate of mosaicism during this stage and raises the question of whether or not a single cell biopsied during this stage is representative of the whole embryo. In addition, self-correction of the mosaicism to a euploid embryo has been demonstrated, so low-level mosaicism may not be a concern. Studies have shown that CMA can identify mosaicism in only 25% of embryos and so may miss low levels of mosaicism. This review further describes issues of cell cycle replication as a confounding factor for CMA. DNA replication begins at more than 10,000 sites in a genome, and during S phase, some parts of the genome have finished replicating and have two copies while other regions have not completed replicating and have a single copy of DNA. This variation in copy number could be incorrectly interpreted as abnormal or as high background noise. The risk of cell cycle issues may be mitigated by performing cell sampling just after cell division, or by trophectoderm biopsy in the blastocyst state. Finally, CMA is not optimal for identifying polyploidy which is a significant limitation because triploidy is one of the most common chromosome abnormalities found in miscarriages. Microarrays that are SNP based can be used for detection of polyploidy, but at the time of publication, SNP arrays have not been optimized for WGA. Overall, the authors conclude that CMA for PGS is slowly becoming a clinical standard, but states that the procedure needs to be optimized on an individual basis and tailored protocols are required.

Novik et al. (2014) published a comparison of fluorescence in situ hybridization (FISH) methods used to evaluate chromosomal mosaicism in IVF embryos with CMA to determine the limits of mosaicism detection, accuracy, and mosaicism prevalence. Chromosomal mosaicism is higher in IVF created embryos than in other prenatal specimens and may be found in 71-73% of human embryos. Low levels of mosaicism in prenatal specimens suggest selective pressure against mosaic embryos for ongoing pregnancy. Mosaicism has been reported in embryos evaluated by CMA using trophectoderm (TE) biopsies, but the effect of TE mosaicism on development, implantation and pregnancy outcome is unknown. To determine the limits of mosaicism detection, the authors mixed different ratios of amplified DNA from aneuploid and euploid cells, as well as tested clinical samples. Overall, they were able to identify the limit of mosaicism detection with CMA at 25-37% for gains of DNA, and 37-50% for losses. They used the CMA technique developed to CMA was used to determine if an embryo was euploid, non-mosaic aneuploidy, or mosaic aneuploid. The diagnostic accuracy of the CMA test was assessed by FISH analysis on non-transferred embryos. In 47 embryos, 26 were considered to be non-mosaic aneuploid by CMA, and 100% were confirmed by FISH. In the mosaic category, 95% were confirmed by FISH. The single embryo not confirmed by FISH did have a discordant result with 7% of nuclei with an aneuploid FISH signal that was below the threshold to call the embryo abnormal. Embryos predicted to be euploid by CMA were not tested by FISH. The authors concluded that CMA testing can identify mosaicism in day 5/6 blastocysts and that FISH confirms that the mosaicism is real and not likely a technical artifact.

Preimplantation Genetic Testing for Polygenic Disorders (PGT-P)

PGT-P is genetic testing that screens for disorders that involve multiple genes. Evidence for the utility of PGT-P for the selection of embryos is currently lacking and ethical concerns exist related to use of this technology.

In a recent systematic review of guidelines for PGT-M, Siermann et al. (2022) sought to leverage PGT-M guidelines to better understand current issues and practice on the ethical acceptability of PGT-M and make comparisons with PGT-P. A total of 38 documents were reviewed including national, European and global guidelines. The researchers identified two main themes, including 1) what PGT is considered appropriate for and 2) who should make decisions regarding the use of PGT. They felt that many topics addressed in the PGT-M documents may apply to PGT-P as well, however, PGT-P screens for risks involving multiple polygenic conditions which compounds the ethical challenges for this type of testing. There is a lack of regulatory guidance, guidelines or position papers that address the ethical use of PGT-P. Ultimately, the authors concluded that based on the PGT-M documents reviewed, the ethical acceptability for PGT-P is limited at this time.

In a 2022 Precision Medicine Insight, Hayes addressed the use of PGT-P for selection of embryos for implantation. Evidence was limited and focused mostly on models for validation of polygenic risk scoring that could be used for embryo screening. No studies that could inform utility of PGT-P for embryo selection were identified. Per Hayes, professional guidelines addressing the use of PGT-P for embryo selection were also limited and provided weak support against using PGT-P in this manner.

Clinical Practice Guidelines

American College of Medical Genetics and Genomics (ACMG)

In a 2021 position statement, the ACMG addressed direct-to-consumer prenatal testing for multigenic or polygenic disorders indicating that issues surrounding testing for such disorders are very complex. These disorders have been shown to be

controlled, at least in part, by multiple genetic loci and the potential influence of unknown environmental factors. The ACMG ultimately recommends that prenatal testing for diseases or disorders that exhibit polygenic or multigenic heritability is not appropriate for clinical use at this time and should not be offered direct-to-consumer.

American College of Obstetricians and Gynecologists (ACOG)

Committee Opinion Number 799 (ACOG, 2020) indicates that the clinical utility of PGT-M and PGT-SR is firmly established, but the utility of PGT-A has not yet been fully determined. ACOG further recommends:

- Confirmation of PGT-M results by chorionic villus sampling (CVS) or amniocentesis should be offered to all patients.
- Confirmation of PGT-SR results by CVS or amniocentesis should be offered to all patients.
- Traditional diagnostic testing or screening for aneuploidy should be offered to all patients who have had PGT-A, in accordance with recommendations for all pregnant patients.

In Committee Opinion Number 410 (2008, reaffirmed 2020) ACOG addressed ethical issues related to genetic testing for pregnant individuals and those considering pregnancy. ACOG urges providers to maximize their knowledge of available genetic tests along with the limitations of those tests and recognize the potential consequences to individuals who have undergone such testing if/when a genetic diagnosis is uncovered. The importance of integrating geneticists and genetic counselors into the care of individuals for whom genetic testing is being considered is also stressed. ACOG encourages clinicians to discuss with their patients the importance of sharing pertinent genetic information with potentially impacted family members as well. Lastly, because it may be possible for genetic information to lead to discrimination (e.g., in the workplace, related to insurability), ACOG encourages clinicians to work to prevent such consequences when possible and advocate against genetic discrimination.

American Society for Reproductive Medicine (ASRM)

In 2022, the ASRM Ethics Committee addressed the use of reproductive technology for the selection of sex for nonmedical reasons in an Ethics Committee Opinion. The opinion indicates that the use of PGT-A with IVF for sex selection only, with no medical indications, is ethically controversial and should not be encouraged. Discussion of knowledge of embryo sex at the time of transfer and the impact this may have on embryo selection should take place at the time of informed consent for PGT-A, as PGT-A may be performed for indications unrelated to sex selection with fetal sex as an incidental finding. The opinion asserts that providers that offer assisted reproduction services are not ethically obligated to either provide, or refuse to provide, methods of sex selection that are not medically indicated.

The ASRM Practice Committee released an opinion report on clinical management of mosaic results from PGT-A of blastocysts in 2020. The report states that there is not yet data to suggest that PGT-A is appropriate for all cases of IVF. Data on outcomes related to pregnancies and children resulting from mosaic embryos is only beginning to emerge. The authors emphasized the importance of comprehensive genetic counseling, based on the most recent empirical studies, for patients undergoing or considering IVF; this counseling is critically important in the case of a mosaic embryo. The Practice Committee recommends that clinicians inform patients that there is no evidence-based method which can determine which mosaic embryos have the best chance of resulting in successful pregnancy and concludes that while PGT-A is a technique which may have a role among technologies that can be offered to patients looking to ensure they have healthy children, there is not enough data to endorse its universal application (Practice Committee and Genetic Counseling Professional Group (GCPG) of ASRM, 2020).

An opinion regarding the disclosure of fetal sex when incidentally revealed as part of preimplantation genetic testing was published by the ASRM in 2018. The committee recommends that clinics should have policies in place regarding the determination and disclosure of fetal sex when performing PGT. Patients should give consent as to whether they wish to know available information on sex of embryo(s). Nondiscrimination policies should be developed by clinics performing PGT and patients should be made aware of such policies. In addition, clinics should have policies for using randomized selection of embryos in cases where more embryos are available than can be transferred. Finally, clinics should also develop policies that prohibit consideration of sex of embryo as a factor for transfer and prioritize embryo quality for selection instead (Ethics Committee of the ASRM, 2018).

The Ethics committee of ASRM published a comprehensive review of the use of PGT-M for adult-onset conditions in 2018. The committee concluded that PGT-M for monogenic adult-onset conditions is ethical when the condition is serious and no safe, effective interventions are available. Genetic counselors experienced with PGT-M should provide comprehensive counseling to couples considering PGT-M for adult-onset diseases.

American Society for Reproductive Medicine (ASRM)/Society for Assisted Reproductive Technology (SART)

In this joint Practice Committee Opinion from 2018, ASRM and SART state that while some studies have demonstrated higher birth rates after the use of PGT-A and single-embryo transfer, the studies have important limitations. They conclude that the value of PGT-A as a screening test for in vitro fertilization patients has yet to be determined. Large, prospective studies evaluating a variety of approaches to embryo selection are needed to determine the safety and risks of various technologies.

European Society for Human Reproduction and Embryology (ESHRE)

A 2022 position statement from ESHRE supports the ESHG position regarding PRS in PGT, acknowledging that PRSs can yield helpful data for populations by identifying at-risk groups, but asserting that making predictions for individuals is not reliable. In addition, ESHRE agrees with ESHG that significant ethical and scientific concerns exist around this technology. In summary, ESHRE states that the clinical utility of PRS is low to absent for selection of embryos and does not support its use in clinical practice.

In 2020, ESHRE published a series of four papers promoting best practices in PGT; however, the authors note that the papers should not be interpreted as standard of care or inclusive/exclusive of other methods of care. ESHRE recommends that PGT should only be applied when the reliability of the diagnosis is high and potential contraindications (such as age, ability to retrieve gametes, signs/symptoms of autosomal dominant or x-linked disorder which could cause medical complications during the IVF/pregnancy process) have been considered. Physical and psychological problems should be addressed as well. PGT testing is inappropriate in case of uncertain genetic diagnosis (for example genetic/molecular heterogeneity), or in case of uncertain mode of inheritance. For identifying chromosome structural rearrangements, PGT-SR is a routine procedure in most IVF/PGT centers for patients unable to achieve a pregnancy or at high risk of pregnancy loss and/or abnormal live born births resulting from inheritance of unbalanced products of the rearrangement. However, PGT-SR is only recommended if the technique applied can detect all expected unbalanced forms of the chromosomal rearrangement. PGT-M testing is carried out to confirm pathogenic germline genetic variant(s) that may have serious health effects potentially manifesting at birth, in childhood or in adulthood. Exclusion or non-disclosure testing may be appropriate for late-onset disease, such as Huntington's disease, to avoid pre-symptomatic testing of the individual with a family history of the disease. Exclusion testing is preferred over PGT with non-disclosure of test results to the couple. Cited indications for PGT-A have included advanced maternal age, recurrent implantation failure, severe male factor (SMF) and recurrent miscarriage in couples with normal karyotypes, however the value of PGT-A for all or a subset of individuals undergoing IVF remains heavily debated and is the subject of ongoing discussions and research.

European Society of Human Genetics (ESHG)

In a 2022 publication, Forzano et al. (on behalf of the Executive Committee and the Public and Professional Policy Committee of the ESHG) states the utility for embryo selection using polygenic risk score (PRS) analysis is "severely limited" with no clinical research assessing its diagnostic effectiveness in embryos performed to date. The ESHG recommends education regarding the use of PRS and its limitations and indicates that societal debate focused on what could be considered acceptable regarding individual trait selection must take place before any further implementation of this technology.

European Society of Human Genetics (ESHG) and the European Society for Human Reproduction and Embryology (ESHRE)

In a 2017 consensus paper, ESHG and ESHRE (Harper et al., 2017) reviewed the pros and cons of PGT-M and PGT-A. The authors noted that RCTs for PGT-A are lacking, and that what constitutes success in the literature has been defined differently by different authors, creating a situation where it is not possible to conduct a meta-analysis of available literature. The data to date suggests that PGT-A may improve the clinical outcome for patients with normal ovarian reserve, but more data is needed to determine the validity of PGT-A in other patient populations and at which stage of embryo biopsy.

Preimplantation Genetic Diagnosis International Society (PGDIS)

The PGDIS recently updated their position statement regarding the transfer of mosaic embryos to include new evidence. The position statement indicates that embryos with higher-level mosaicism appear to be associated with less favorable outcomes when compared to lower-level mosaicism, and relative percentage of mosaicism seems to better predict outcome than the involvement of specific chromosomes. As such, relative percentage of mosaicism should be included in patient discussions and in reporting. The PGDIS further states that decision to transfer a mosaic embryo can be prioritized based either on the level

or type of mosaicism, and if there is a choice between similar levels of mosaicism, preference may be considered based on morphology of embryo or the nature of the variation. Comprehensive patient education and support regarding potential mosaic embryos and prioritization of euploid blastocysts continue to be part of the recommendations for clinicians (PGDIS, 2021).

In a 2019 position statement (Cram et al.), the PGDIS states that “chromosome testing strategies, such as PGT-A, improve initial IVF outcomes by avoiding unwitting transfer of aneuploid embryos in morphology-based selection practices.” The statement goes on to address the transfer of mosaic embryos stating that transfer of an euploid embryo is preferred, but if that is not feasible, priority for transfer of a mosaic embryo should be based on the level of mosaicism over the specific chromosome involved, with preference given to embryos with a mosaicism of less than forty percent. In the event where there must be a choice between the transfer of two unequivocal mosaic embryos, mosaicism involving uniparental disomy, intra-uterine growth retardation, or live-born syndromes should be given lower priority. Patients should be educated on the risks associated with the transfer of mosaic embryos, and it is recommended that an additional cycle of PGT-A be considered to increase the likelihood of obtaining an euploid embryo for transfer.

The PGDIS position statement on chromosome mosaicism and preimplantation aneuploidy at the blastocyst state states that only a validated next generation sequencing (NGS) platform that can quantitatively measure copy number should be used, and can accurately measure 20% of mosaicism in a known sample (PGDIS, 2016).

U.S. Food and Drug Administration (FDA)

This section is to be used for informational purposes only. FDA approval alone is not a basis for coverage.

A search of the FDA website identified an approval (K042279) for the Affymetrix Genechip Microarray Instrumentation System on December 23, 2004. Refer to the following website for more information:

http://www.accessdata.fda.gov/cdrh_docs/pdf4/K042279.pdf. (Accessed January 25, 2023)

Additional Products

180K Oligo Array and SNP+CGH Array (Ambry Genetics Corp.); Cytogenomic SNP Microarray (2003414), Cytogenomic SNP Microarray, Prenatal (2002366), and Cytogenomic SNP Microarray, Products of Conception (2005633) (ARUP Laboratories); Chromosomal Microarray Analysis – HR (Test #8655), Chromosomal Microarray Analysis HR+SNP Screen (Test #8665), Chromosomal Microarray Analysis – CytoScan HD SNP Array – Non-Tumor (Test #8650), Targeted Chromosomal Microarray Analysis – Prenatal (Test #8656 [Amniocentesis] or #8657 [CVS]), and Expanded Chromosomal Microarray Analysis – Prenatal (Test #8670 [Amniocentesis] or #8671 [CVS]) (Baylor College of Medicine Medical Genetics Laboratories); Whole-Genome Chromosomal Microarray (GenomeDx), Whole-Genome Chromosomal Microarray, Prenatal, and Whole-Genome Chromosomal Microarray, Products of Conception (GeneDx Inc.); Reveal SNP Microarray- Pediatric; Reveal SNP Microarray – Prenatal, and Reveal SNP Microarray – POC (Integrated Genetics); Chromosomal Microarray, Postnatal, Clarisure Oligo-SNP (Test 16478), Chromosomal Microarray, Prenatal, Clarisure Oligo-SNP (Test 90927), and Chromosomal Microarray, POC, Clarisure Oligo-SNP (Test 90929) (Quest Diagnostics Inc.); Signature ChipOS, Signature ChipOS+SNP, Signature PrenatalChipOS, Signature PrenatalChipOS+SNP, Signature PrenatalChipTE, and Signature PrenatalChipTE+SNP (Signature Genomic Laboratories LLC), HumanKaryomap-12 DNA Analysis Kit (Illumina), IdentifySGD (Progenity, Inc.), Spectrum PGS (Natera, Inc.), Spectrum-PGD+PGS (Natera, Inc.), NexCCS (Foundation for Embryonic Competence).

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Policy History/Revision Information

Date	Summary of Changes
08/01/2023	<p data-bbox="337 220 548 247">Related Policies</p> <ul data-bbox="337 256 1481 283" style="list-style-type: none"><li data-bbox="337 256 1481 283">● Added reference link to the Medical Policy titled <i>Cell-Free Fetal DNA Testing (for Tennessee Only)</i> <p data-bbox="337 294 592 321">Coverage Rationale</p> <ul data-bbox="337 329 1510 556" style="list-style-type: none"><li data-bbox="337 329 1510 424">● Revised coverage criteria for Preimplantation Genetic Testing (PGT) for monogenic/single gene defects (PGT-M) or inherited structural chromosome rearrangements (PGT-SR) when the embryo is at increased risk of a recognized inherited disorder; replaced criterion requiring:<ul data-bbox="386 432 1510 556" style="list-style-type: none"><li data-bbox="386 432 1510 489">○ “The parents are carriers of <i>an</i> autosomal recessive disease” with “<i>each of the intended</i> parents are carriers of <i>the same</i> autosomal recessive disease”<li data-bbox="386 497 1510 556">○ “At least one parent is a carrier of a <i>balanced</i> structural chromosome rearrangement” with “at least one parent is a carrier of a structural chromosome rearrangement” <p data-bbox="337 567 641 594">Supporting Information</p> <ul data-bbox="337 602 1399 659" style="list-style-type: none"><li data-bbox="337 602 1399 630">● Updated <i>Clinical Evidence</i> and <i>References</i> sections to reflect the most current information<li data-bbox="337 638 889 659">● Archived previous policy version CS160TN.G

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