

UnitedHealthcare® Community Plan [EM1]

Medical Policy

# Carrier Testing Panels for Genetic Diseases (for Louisiana Only)

Policy Number: CS151LA. GH

Effective Date: November 1, 2023 TBD

⇒ Instructions for Use

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# **Application**

This Medical Policy only applies to the state of Louisiana.

## Coverage Rationale

#### State-Specific Criteria

The coverage criteria for genetic counseling contained in this policy represents Louisiana Medicaid Managed Care Organization Manual (LA MCO) coverage policy and is set forth below in accordance with state requirements.

#### Genetic Counseling

Genetic counseling before and after all genetic testing is required. Counseling must consist of at least all of the following and be documented in the medical record:

- Obtaining a structured family genetic history
- Genetic risk assessment; and
- Counseling of the enrollee and family about diagnosis, prognosis, and treatment (LA MCO Genetic Counseling and Testing)

#### Additional Non State Criteria

Ashkenazi Jewish Carrier Screening Reproductive Carrier Screening

Ashkenazi Jewish Reproductive Carrier Screening is panels of up to six genes are proven and medically necessary for evaluating the following:

Individuals who are seeking prenatal care or planning a pregnancy who have not previously had informative Ashkenazi Jewish

- Reproductive Carrier Screening; and
- At least one of the following additional criteria is met:

At least one panels of up to 15 genes are proven and medically necessary when an individual and/or their reproductive partner is meet at least one of the following criteria:

- Ashkenazi Jewish (this ancestry (individual/reproductive partner has at least one Ashkenazi Jewishparent or grandparent); or
- The reproductive partners have a previously affected child with one of the genetic diseases included in the Ashkenazi Jewish Carrier Screening test and the results of this test will inform a currentAshkenazi Jewish descent); or future pregnancy; or
- One or both individuals have a biological First- or Second-Degree Relative who is has been affected and by one or more of the results of this test will inform a current or future pregnancy; or conditions evaluated by the panel
  - o One or both individuals have a First-Degree Relative with an affected offspring and the results of this test will inform a current or future pregnancy; or
  - o One of the reproductive partners is already known to be a carrier for one of the genetic diseases included in the Ashkenazi Jewish carrier screening test and the results of this test will inform a current or future pregnancy

The following are unproven and not medically necessary due to insufficient evidence of efficacy:

- Carrier testing for any additional genetic diseases as part of Ashkenazi
   JewishReproductive Carrier Screening panels comprised of 16 or more genes
- Ashkenazi Jewish Carrier Screening for all other indications

Expanded Note: It is strongly recommended that reproductive Carrier Screening Panel Testing

Expanded Carrier Screening Panel testing is unprovenpanels include screening for cystic fibrosis (CFTR) and not medically necessary for all indications due to insufficient evidence of efficacy. spinal muscular atrophy (SMN1).

#### Definitions

Carrier Screening: Genetic testing that is performed on an individual who does not have any symptoms of a genetic disorder but to determine whether that individual may be at risk to have a genetic variant associated with a certain disorder that could be passed to biological children (American College of Obstetricians and Gynecologists [ACOG], 2017a, reaffirmed 2023).

Expanded Carrier Panel (ECS) Screening: Multiple genetic disorders that are screened for in one test using a single sample without regard to ethnicity or family history (ACOG, 2017a, reaffirmed 2023). For the purpose of this policy, Expanded Carrier Panels for non-Ashkenazi Jewish Carrier Screening analyze 6 or more genes.

First-Degree Relative: First-Degree Relatives include parents, siblings and offspringchildren (National Comprehensive Cancer Network - 2023 [NCCN], 2024).

Panel: A group of laboratory tests that are performed together to assess a body function or disease (Medicare, 2019—and; McGraw Hill, 2002).

Second-Degree Relative: Second-Degree Relatives include half-brothers/sisters\_siblings, aunts/, uncles, grandparents, grandchildren and nieces/nephews affected on the same side of the family (National Comprehensive Cancer Network, 2023(NCCN, 2024).

### **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.

CPT Code	Description
0400U	Obstetrics (expanded carrier screening), 145 genes by next generation sequencing, fragment analysis and multiplex ligation dependent probe amplification, DNA, reported as carrier positive or negative
*81412	Ashkenazi Jewish associated disorders (e.g., 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 (e.g., cystic fibrosis, Ashkenazi Jewish-associated disorders [e.g., Bloom syndrome, Canavan disease, Fanconi anemia type C, mucolipidosis type VI, Gaucher disease, Tay-Sachs disease], beta hemoglobinopathies, phenylketonuria, galactosemia), genomic sequence analysis panel, must include sequencing of at least 15 genes (e.g., ACADM, ARSA, ASPA, ATP7B, BCKDHA, BCKDHB, BLM, CFTR, DHCR7, FANCC, G6PC, GAA, GALT, GBA, GBE1, HBB, HEXA, IKBKAP, MCOLN1, PAH)
81479	Unlisted molecular pathology procedure

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Codes labeled with an asterisk (\*) are not on the State of Louisiana Medicaid Fee Schedule and therefore are not covered by the State of Louisiana Medicaid Program.

# Description of Services

Carrier Screening is performedused to detect genetic mutations that may increase the identify individuals or reproductive partners who are at risk of having a genetic disorder. This testing may impact the reproductive decision-making for parents or prospective parents.

<u>Carrier Screening may be available for child with clinically significant</u> autosomal recessive <u>conditions</u>, <u>autosomal dominant less penetrant conditions</u>, <u>or</u> X-linked conditions, <u>and certain chromosome abnormalities</u>.; <u>screening results may impact reproductive decision-making</u>.

The use of modern technology such as next-generation sequencing (NGS) enables the use of Panel tests which analyze multiple genes at the same time (Gregg, 2021).

In general, Carrier Screening may be performed for conditions that are found in the general population (pan-ethnic), for diseases that are more common in a particular population, (ethnic-based) or based on family history. Current recommendations for general population (pan-ethnic) The American College of Obstetricians and Gynecologists (ACOG) (2022, 2017b, both reaffirmed 2023), recommends screening by ACOG include for cystic fibrosis screening, (CF), spinal muscular atrophy (SMA-screening and hemoglobinopathy screening. For individuals of Ashkenazi Jewish descent (Eastern), and Central European), certain autosomal recessive conditions hemoglobinopathies for all women who are more prevalent. Some of these disorders are lethal in childhood considering pregnancy or are associated with substantial morbidity (ACOG 2022, ACOG 2017b, reaffirmed 2023). currently pregnant

Diagnostic genetic testing of a heritable disease may also be performed using similar methods as Carrier Screening. It may be medically necessary to use genetic testing to establish a molecular diagnosis when an individual has clinical features or is at direct risk of inheriting the mutation in guestion (pre-symptomatic) and the result of the test will directly impact the treatment being delivered.

#### Ashkenazi Jewish Carrier Screening

#### Carrier Screening for Individuals of Ashkenazi Jewish Descent

Certain autosomal recessive conditions are more prevalent in individuals of Ashkenazi Jewish (AJ) descent. Some of these disorders are lethal in childhood or are associated with substantial morbidity. Carrier Screening for individuals of AJ descent is focused on identifying reproductive partners who are at risk of having a child with a disorder that has a higher prevalence in this population. The majority of individuals of Jewish ancestry in North America are of Ashkenazi JewishAJ descent and therefore have an increased risk of having childrena child afflicted with one of these disorders (ACOG, 2017b; reaffirmed 2023).

Ashkenazi JewishAJ Carrier Screening panels may commonly include testing for some or all of the genetic diseases outlined by ACOC: below:

- Tay Sachs disease
- Canavan disease
   Cystic fibrosis (CF)
- Spinal muscular atrophy (SMA)
- Familial dysautonomia
- Bloom syndrome

- Fanconi anemia
- Niemann-Pick disease
- Gaucher disease
  - Mucolipidosis IV
  - Maple Syrup Urine
     Usher 1F and 111III Disease
  - Joubert syndrome

- Glycogen storage disease 1A
- Familial hyperinsulinism

#### ExpandedPan-Ethnic Carrier Screening (ECS) Panels

For Carrier Screening, technologies such as next generation seguencing technology or chromosomal microarray have created the ability to screen for genetic mutations using genetic Panels instead of single genes. For the purpose of this policy, Expanded Panels analyze 6 or more genes for non-Ashkenazi Jewish Carrier Screening, which is beyond what is recommended by ACOC for DNA-based screening. For Ashkenazi Jewish disorders, ECS Panels are those that go beyond the diseases listed above, hemoglobinopathy screening, and spinal muscular atrophy screening. Expanded Panels are able to analyze many genes simultaneously, however there is a lack of evidence to establish the clinical utility of gene test panels that include genes that are not associated with a specific inherited

disorder (ACOG 2022, ACOG, 2017a, reaffirmed 2023). Furthermore, there is a lack of standardization in the genetic Panel composition, thus Panels for similar conditions may evaluate different sets of genes.

Historically, Carrier Screening has focused on specific ethnic populations that are known to be at elevated risk of certain clinically significant disorders (e.g., individuals of AJ descent). However, it has become progressively more difficult to classify an individual's true ancestry in today's multi-racial society. As such, the likelihood of being a carrier for a certain disorder may be inconsistent with previous assumptions regarding disease prevalence in the ethnic or racial group with which an individual identifies; this has led to consideration of pan-ethnic screening. Pan-ethnic screening offers Panel testing for certain disorders to all individuals who are pregnant or considering pregnancy, irrespective of ethnicity (ACOG, 2017a, reaffirmed 2023).

Carrier Screening Panels have the capacity to analyze large numbers of genes simultaneously, but there is currently a lack of standardization in conditions screened and Carrier Screening Panel composition. Thus, marketed Panels may include many more genes than would be recommended on an individual basis. Additionally, for every disorder, the gene/mutation/mutation frequency should be known in the population being tested so that negative test results can be translated into an expected residual risk of the disorder (Grody et al., 2013). Unfortunately, many laboratories are unable to calculate the residual risk as they lack the knowledge of the carrier frequency within the testing population and the proportion of disease-causing mutations on the assay platform. ACOG suggests panels targeting conditions with a carrier frequency of at least 1/100, which correlates with a disease incidence of 1/40,000 (ACOG, 2017a, reaffirmed 2023). The American College of Medical Genetics and Genomics (ACMG)'s 2021 practice resource (Gregg et al.) recommends the adoption of a tier-based system built on carrier frequency, with Tier 3 carrier screening that includes conditions with carrier frequencies of  $\geq 1/200$ , plus CF, SMA, and risk-based screening, offered to all individuals who are pregnant or planning a pregnancy.

Leung et al. (2021) developed a method of calculating disease prevalence, ethnic carrier frequency, detection rate (DR) and recurrence risks (RR) metrics across four autosomal ive gene conditions (ABCC8, ASPA, GAA and MMUT) using cystic fibrosis (CF) as proof of concept. A step by step approach for calculating DR and RR was based on the sum of disease allele frequencies of pathogenic variants found in literature. Following CF quidelines, carrier frequencies for five ethnicities were gathered from published studies and public databases. If no specific carrier frequency was available, they were derived om the Hardy Weinberg equation. If neither were available, a default carrier frequency in 500 was used. The disease allele frequencies of the four genes were compared among three laboratories and possible reasons of discrepancy were explored. The study revealed that multiple laboratories testing the same genes demonstrate a wide range of DR and RR. Possible explanations for this discrepancy include difference in calculation method for DR, difference in definitions for DR or laboratories calculate DR that is more consistent with the definition of analytical sensitivity which may increase RR, known technical challenges of NGS may limit detection of variants, timing of publications may also lead to frequency reporting discrepancies. The authors emphasized that assurate DR and RR statistics are critical for reproductive decision making and stated that there is a need for professional societies to offer official recommendations to avoid laboratories using disparate criteria in setting their preferred lowest DR.

Genetic counseling is strongly recommended prior to these tests in order Carrier Screening to inform persons being tested about the advantages and limitations of the test testing as applied to a unique person. For information regarding noninvasive prenatal

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screeningtesting (NIPT) for fetal aneuploidy, ), refer to the Medical Policy titled Cell-Free Fetal DNA Testing (for Louisiana Only).

#### Clinical Evidence

# <u>Carrier Screening for Individuals of Ashkenazi Jewish Carrier Screening</u>Descent

Shi et al. (2017) genotyped over 3,0003000 individuals of self-reported Ashkenazi Jewish (AJ) ancestry to analyze the carrier frequency of 29 recessive genetic diseases to determine if additional disorders should be considered as part of routine carrier screening. The team reviewed the literature and the internal database at their lab to identify the genes that should be screened, and utilized pre-existing, de-identified samples from research participants. There were  $\frac{2,2522252}{2}$  AJ individuals tested for 29 recessive disorders, and an additional  $\frac{1,3901390}{4}$  AJ and  $\frac{6,8136813}{4}$  non-AJ individuals were screened for a subset of 18 recessive disorders. The authors identified seven disorders with a carrier frequency of greater than 1 in 100, nine with a carrier frequency between 1 in 100 and 1 in 200, and four between 1 in 200 and 1 in 500. Nine conditions had a carrier frequency of less than 1 in 500 or were not found. Of the 20 diseases with a carrier frequency higher than 1 in 500, two were eye diseases that the authors felt were not appropriate to be included for reproductive related carrier screening. Of the remaining 18 disorders, the team calculated that the cumulative chance for an individual to be a carrier of one of the 18 diseases was 1 in 6. However, the chance that an AJ couple would be carriers of the same disease and be at risk for an affected pregnancy is 1 in 441.

Arjunan et al. (2016) at the Center for Jewish Genetics explored the difference between targeted mutation analysis for Tay Sachs disease, plus enzyme analysis, with next generation sequencing (NGS). Blood or saliva samples were collected on 506 individuals who underwent NGS for 84 recessive conditions and targeted genotyping. Two hundred and eighty-eight individuals were carriers of at least one condition, represented by 434 pathogenic variants, and eight couples were carriers for the same disorder. When NGS was compared to traditional screening for the diseases routinely screened for in the AJ population, NGS did not find any additional mutations beyond what would have been found by targeted genotyping. However, NGS and the broader panel identified two carrier at risk couples, and 115 (26%) pathogenic variants that would not be found by routine AJ screening.

#### ExpandedPan-Ethnic Carrier Screening (ECS)

There is limited evidence to support the use of ECS testing for any indication. Existing guidelines note the risks of ECS, including identifying variations of uncertain significance and inclusion of disorders that can be characterized by a wide range of phenotypical expression or incomplete penetrance (when not all carriers are symptomatic). ECS may also cause undo anxiety or stress in individuals undergoing testing, and a need for further follow up and counseling.

A 2024 Hayes Precision Medicine Insight found minimal support for the use of expanded carrier screening (ECS) in healthy populations to guide reproductive decision-making. Per Hayes, ECS involves testing parents for variants in many genes that can be associated with a variety of recessive disorders. The Hayes conclusion was based on a review of six abstracts of publications addressing the clinical utility of ECS for informing clinical or reproductive decisions. Four professional guidelines addressing ECS were also

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identified; these guidelines did not show distinct agreement regarding which genes should be included in ECS but generally recommend limiting testing to genes with known clinical impact in terms of reproductive planning. In addition, risks related to ECS, including identification of variants of unknown significance (VUS) and diseases that have a wide range of phenotypic expression, reduced penetrance, or adult onset were identified. Of the four guidelines reviewed, only one was based on a formal evidence review process.

A systematic review and meta-analysis performed by Wang et al. (2023) sought to evaluate the clinical utility of reproductive carrier screening (RCS). The assessment included eleven studies which incorporated screening for a minimum of three to a maximum of 176 conditions. Across these studies, RCS led to identification of one to 24 high-risk couples per 1000 individuals screened. Based on pooled estimations, the prenatal diagnosis (PND) rate in pregnant high-risk couples was 0.644 (95% CI = 0.364, 0.9230), the termination rate for affected pregnancies was 0.714 (95% CI = 0.524, 0.904), and the rate of in-vitro fertilization (IVF) with preimplantation genetic testing (PGT) was 0.631 (95% CI = 0.538, 0.725). The data analysis revealed a statistically significant reduction in the rate of individuals undergoing PND and termination as the number of conditions in the screening test increased. In addition, carriers that were found to have conditions with greater clinical severity were more likely to terminate pregnancy or chose IVF with PGT. The authors concluded that while the number of conditions screened and the severity of those conditions appear to impact the reproductive decisions of high-risk couples, additional study is required to more clearly define clinical utility and provide evidence to assist with design of appropriate screening panels. The researchers also highlighted the importance of genetic counseling in conjunction with RCS. Publications by Ghiossi et al. (2018), previously discussed in this policy, and Johansen Taber et al. (2019), discussed below, were included in this systematic review.

In an effort to ascertain a carrier screening panel design which is consistent with existing carrier screening recommendations published by the American College of Obstetricians and Gynecologists (ACOG) (2017b) and the American College of Medical Genetics and Genomics (ACMG) (2021), Johansen TaborTaber et al. (2022, included in the 2024 Hayes report) conducted a study of the carrier screening results of 460,608 individuals who had been tested using an NGS panel that screened for up to 176 conditions. Individuals with family or personal history of disease or reported consanguinity were excluded, and 11 races/ethnicities were represented. Forty conditions had carrier frequencies of  $\geq$  1 in 100 and 75 conditions had carrier frequencies of  $\geq$  1 in 200. A well-defined phenotype was present for 175 of the conditions and at least one severity criterion and onset early in life were met for 165 conditions. Overall, 37 conditions met conservative thresholds (including carrier frequency of  $\geq 1$  in 100) and 74 conditions met more liberal thresholds (including carrier frequency of  $\geq 1$  in 200). In a panel which tests for 37 conditions, all 7 conditions currently recommended by both ACOG and ACMG for screening in at least one race/ethnicity would be included; this panel would detect 63% of carriers and 84.6% of at-risk couples (ARCs) (as compared to a 176condition panel). In a more liberal panel, testing for 74 conditions, 81.4% of carriers and 96.6% of ARCs would be detected. The authors concluded that panels including screening for either the 37 conditions based on the conservative threshold or the 74 conditions based on the more liberal threshold would both be consistent with established guidelines. Noted limitations include the possibility that conditions beyond what was included in this study may meet ACOG or ACMG quideline criteria. In addition, although the researchers took steps to ensure accuracy of carrier frequency data, there is potential for over- or under-estimation. The development of transparent and consistent panel design which aligns with evidence-based guidelines is recommended.

Ramdaney et al. (2022) conducted a systematic evidence review to evaluate the client and provider experiences for ECS. The authors reviewed literature between January 1, 2003, and May 31, 2021, and found 36 articles that fit the inclusion criteria. Sixteen of the articles evaluated test outcomes, ten articles evaluated provider outcomes, and 20 articles evaluated client outcomes. For the evaluation of client outcomes, the authors focused on the uptake rates of ECS, the yield of carrier couples, and the influence on reproduction decision-making. It was noted that the uptake rate in clients in the general population was 39% which was consistent with other studies. The uptake of ECS among partners varied between 42% and 77% and the main impacting factors were presence of the partner at the initial appointment, disease severity, and ease of logistical factors. The vield of carrier couple rates ranged from 0.1% to 16.9%, The yield of carrier couple rates ranged from 0.1% to 16.9%; however, the specific populations, panels used, and conditions/genes/mutations assessed varied widely. When evaluating in silico studies using modeled data for yield of carrier couples, it was noted that screening for only cystic fibrosis (CF) and spinal muscular atrophy (SMA) would have missed at least 881 of 966 at-risk couples (ARCs). The authors noted that decision-making following actual carrier screening results varied largely depending on whether the clients were preconception or already pregnant. With preconception, most clients elected to pursue or indicated interest in PGT to minimize the risk of an affected pregnancy. For those clients who received PGT and did not pursue or take direct action given the results, some clients noted benefit from a planning and preparation standpoint. For those clients that were already pregnant, ARCs were less likely to alter their reproductive plans than those clients who received results during the preconception period. The authors evaluated the provider influence on reproduction decision-making and noted that more than half of the provider groups analyzed did not offer ECS to their clients and many of the studies were conducted before newer guidelines regarding ECS were published. It was also noted that the time required for proper education and follow-up were a concern for genetic counselors. Limitations included significant inconsistency in methodologies and patient population which limited the ability to assess the impact of ECS within the United States. There was a lack of studies documenting outcomes for minimal guideline-based carrier screening compared to ECS. Additionally, most of the studies included were observational and the majority were rated poor/very poor quality or a high risk of bias.

Leung et al. (2021) developed a method of calculating disease prevalence, ethnic carrier frequency, detection rate (DR) and recurrence risks (RR) metrics across four autosomal recessive conditions (ABCC8, ASPA, GAA and MMUT), using CF as proof of concept. A stepby-step approach for calculating DR and RR was based on the sum of disease allele frequencies of pathogenic variants found in literature. Following CF quidelines, carrier frequencies for five ethnicities were gathered from published studies and public databases. If no specific carrier frequency was available, they were derived from the Hardy-Weinberg equation. If neither were available, a default carrier frequency of 1 in 500 was used. The disease allele frequencies of the four genes were compared among three laboratories and possible reasons of discrepancy were explored. The study revealed that multiple laboratories testing the same genes demonstrated a wide range of DR and RR. Possible explanations for this discrepancy include differences in calculation method for DR, differences in definitions for DR or laboratories calculating DR that is more consistent with the definition of analytical sensitivity which may increase RR, known technical challenges of NGS that may limit detection of variants, and timing of publications that may also lead to frequency reporting discrepancies. The authors emphasized that accurate DR and RR statistics are critical for reproductive decisionmaking and stated that there is a need for professional societies to offer official recommendations to avoid laboratories using disparate criteria in setting their preferred lowest DR.

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To address concerns regarding the impact of ECS on health care utilization, Kauffman et al. (2021) conducted a randomized controlled trial examining the effects of disclosing negative (normal) ECS on utilization compared with usual care (UC). The authors assessed differences between women randomized to ECS (v = 127) and UC (177) by evaluating utilization of mental health services including outpatient, inpatient, and medication use; utilization of outpatient primary care, outpatient specialty care, and inpatient and outpatient mental health services in the year following randomization; and utilization of pregnancy-related services in the five years prior to and at any point following randomization with a documented pregnancy. The authors did not find any evidence of harms on health care utilization in women who had a negative ECS. There were no significant differences in outpatient mental health service use between study arms in the period between randomization and results disclosure or in the 12-month follow-up period after results disclosure. Additionally, there were no significant differences in use of primary care and specialty care services in the year following results disclosure and no significant differences in utilization of pregnancy-related services following ECS testing. Of the 304 participants that had data analyzed, there were only 2 cases noted in which ECS-screening led to inappropriate health care utilization: 1 patient misunderstood the carrier result and sought treatment for hemochromatosis and 1 patient who attempted to refuse first trimester prenatal screening because she did not understand how it differed from ECS. Limitations for this study include the possibility of refusals of standard-of-care treatment that were not documented, lack of racial/ethnic and socioeconomic diversity, and exclusion of male partners. The authors note that future studies should continue to evaluate the possibility of harms of screening, specifically for non-White and low-income populations.

Kaseniit et al. (2020) quantitatively examined the efficacy and equity with which ethnicity-based carrier screening captures disease risk for recessive conditions. A 96-gene ECS panel was performed on 93,419 individuals; correspondence was assessed among carrier status, self-reported ethnicity, and a dual component genetic ancestry calculated from sequencing data. The authors reported that substantial and disproportionate risk for

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recessive disorders is not detected when carrier screening is based on ethnicity, which leads to inequitable reproductive care. This conclusion was made after establishing that self-reported ethnicity was an inaccurate predictor of genetic ancestry with 9% of individuals having > 50% genetic ancestry from a lineage inconsistent with self-reported ethnicity. Self-reported ethnicity resulted in missed carriers in at-risk populations; for 10 ECS conditions, patients with intermediate genetic ancestry, backgrounds- who did not self-report the associated ethnicity had significantly elevated carrier risk. For 7/16 conditions included in current screening guidelines, most detected carriers were not from the population that the guideline was aiming to serve. The algorithm from this study can be utilized across laboratories when considering genes for ECS panel inclusion according to the authors.

Arjunan et al. (2020) utilized a published algorithm that stratifies diseases into four classes of severity (mild, moderate, severe and profound) for 176 genes screened by ECS; objective severity classifications were then assigned. Previous reports from ACOG/ACMG have not defined how to interpret severity criteria for genes included in ECS. Severity categories based on disease traits were mapped to four severity-related ECS panel criteria from the American College of Obstetricians and Cynecologists (ACOG).ACOG. Four medical geneticists and eight genetic counselors applied the severity algorithm to subsets of 176 genes. A group consensus was made on how disease traits mapped to ACOG severity criteria. 39% (n = 68) of genes were classified as profound, 40% (n = 71) as severe, 20% (n = 36) as moderate, and 1% (n = 1) as mild.  $\frac{170/\text{Of}}{176}$  176 total genes, 170 (96.6%) met at least one of the four criteria,  $129\frac{176}{176}$  (73.3%) met at least two,  $73\frac{176}{176}$ (41.5%) met at least three, and  $17\frac{17.6}{17.6}$  (9.7%) met all four. The authors notenoted that the MDmedical geneticists and GC reviewersgenetic counselors who reviewed the conditions for this study may not be replicated in practice by clinicians with either similar or different expertise. In addition, the MDmedical geneticist reviewers were not blinded to the GCgenetic counselors' final classifications, so it'sit is possible they were influenced by the GCgenetic counselors' reviews. Lastly, the genes in the study were based on what is available in the current literature, which may skew toward more severe presentation, especially for rare diseases.

ACOG proposed that disorders included in ECS panels should have a carrier frequency of 1/100 or greater, detrimental impact on quality of life and a well-defined phenotype. Balzotti et al. (2020) utilized a ClinGen framework to determine clinical validity of gene-disease relationship for 208 autosomal recessive and X-linked conditions offered atin commercially-available ECS panels by Myriad Women's Health (Foresight) and Baylor Genetics (GeneAware). 100% ofAll conditions met the evidence threshold for supporting a gene-disease association. 98% Ninety-eight percent of conditions (203/208) reached the strongest (definitive) level of gene-disease association; of the remaining 5, 4five, four were classified as having moderate evidence and one was classified as having limited evidence. Twenty-one gene-disease pairs were curated independently by Myriad and Baylor to determine the level of concordance of classification between the two laboratories. The authors surmised that the majority of ECS panel conditions have demonstrable support for gene-disease association which is a crucial component of ECS clinical validity and ACOGrecommended inclusion criteria for ECS panels. Limitations included potential inconsistencies in how conditions were categorized, (potentially skewing results,) (, and the possibility of the emergence of new evidence that may change the classifications used.

Rosenblum et al. (2020) performed a retrospective study to compare the carrier detection rate between a pan-ethnic panel (87 disorders) and an AJ ethnic-specific panel (an 18-

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disorder subset of the pan-ethnic panel) for 2,398 individuals who self-identified as being of AJ descent with no personal or family history of a genetic disorder. The panethnic panel, which assessed 434 targeted, pre-defined variants in 87 genes that cause 87 disorders was tested in 1,1501150 individuals, and the AJ-specific panel assessed, assessing a subset of 147 variants in 18 genes that cause 18 disorders, was tested in 1,2481248 individuals. The pan-ethnic panel identified 431 individuals (37.5%) as carriers of at least one disorder and 87 of these (76%) were carriers of 2 or more disorders. For the AJ panel, 319 (25.6%) individuals were determined to be carriers of at least one disorder and 60 (4.8%) of these individuals arewere carriers for multiple disorders. The researchers also re-analyzed the pan-ethnic data for the 18 genes in the AJ specific panel for those individuals who were found to be a carrier of one of the 87 genes in the pan-ethnic panel. The carrier detection rate would have been 24.3% (280/1,150) and the researchers state that 151 individuals would have been missed for carrier detection. The researchers conclude that this data may contribute to further professional discussion on the clinical utility of expanded earrier screens.ECS.

Westemeyer et al. (2020) performed a retrospective analysis of data from a cohort (n = 381,014) receiving expanded carrier screeningECS of up to 274 genes. The cohort included mostly women (339,739; 89.17%) and various ethnicities: 148,828 (39.06%) Caucasian, 62,626 (16.44%) Hispanic, 52,454 (13.77%) African American, and the remaining 117,106 (30.74%) were either of other races/ethnicities or did not provide information. The majority of individuals (374,911) were tested for CFTRCF and 14,229 (3.8%) were found to have a pathogenic or likely pathogenic variant yielding a 1/26 carrier frequency. For CF, 44.0% (6,260/14,229) of carriers identified had a variant not on the standard genotyping panel. Similarly, 344,407 individuals were screened for SMAspinal muscular atrophy (SMA) and 14,606 (4.24%, 1/24) were found to be carriers or at-risk silent carriers. Out of the 14,606 carriers for SMA,  $\frac{8,763}{8}$ 8763 (2.54%, 1/39) were at risk for being silent carriers which was not detected by standard screening. In addition, for AJ disorders, 81.6% of carriers identified did not disclose AJ ancestry. For the largest gene panel (274 genes), 60,052 individuals were tested and 38,300 (63.78%) were positive for at least one disorder. The researchers also observednoted the carrier rates for this large 274--qene panel compared to those in the literature. Of the 274 genes screened, 117 had a different than expected carrier rate. that differed from what was expected. The researchers concluded that, assuming random pairing across the study population, approximately 1/175 pregnancies would be affected by a disorder in the 274-gene screening panel.

For the majority of expanded carrierECS panels, there is no consensus on what genes should be included that would be relevant for multiple ethnic groups. Guo and Gregg (2019) conducted an analysis of exome sequencing data (n = 123,136) to determine the carrier rates for six major ancestries (African/African American, Hispanic, Ashkenazi JewishAJ, East Asian, non-Finnish European, and South Asian). The study examined 415 genes that are associated with severe recessive conditions and started with determining the variant carrier rates (VCR) to then be able to estimate the gene carrier rates (GCR). Across the ancestries, the highest GCR for a single gene was determined to be for African/African American at 12% for HBB. The carrier rates declined for most ancestries as; only 30 of the genes in the Ashkenazi JewishAJ group had a carrier rate > 1%. Likewise, in the Hispanic population enonly 6 of the genes had a GCR > 1%. Overall, the researchers found that 32.6% (East Asian) to 62.9% (Ashkenazi JewishAJ) of individuals are variant carriers; however, screening all 415 genes would only identify 0.17-2.52% of couples as at risk.

Johansen Taber et al. (2019) reported on a-survey of theresults from females from 1,701partners of 391 at risk couples (ARC) who participated in ECS of 176 genetic conditions. The cohort was identified from over 270,000 individuals who underwent screening via the laboratory's ECS panel from September 1, 2015, to December 31, 2017. Females were identified from the database who (1) were found to be carriers of a pathogenic or likely pathogenic variant conferring risk for at least one of 176 autosomal recessive or X-linked conditions currently included in the labelab's ECS panel, (2) were aged 18 years or older, (3) had consented to being contacted about participating in research at the lab, and (4) for those carrying pathogenic or likely pathogenic variants associated with autosomal recessive conditions, had reproductive partners meeting the same eligibility criteria and were confirmed by the lab as being carriers of a pathogenic variant in the same gene. Couples carrying only variants known to cause mild presentations of biotinidase deficiency (D444H), NPHS2-related nephrotic syndrome (R229Q), and 21-OH deficient congenital adrenal hyperplasia (CAH) (CYP21A2 gene duplication) were excluded. The 1,701 ARC1701 ARCs invited to complete the survey were geographically dispersed and comprisedencompassed 15 ethnicities and over 9 religions. The ARCARCs reported being at--risk for 53 different conditions, with 10% indicating they were at risk for 2 conditions, and 1.8% reporting being at risk for 3 conditions. The actions taken by the ARCARCs were broken down into those receiving preconception ECS results and those receiving the results during the prenatal period. ECS was performed on 235 preconception ARC, ARCs; 77% of whichthese couples indicated they planned or pursued pregnancy management options, of which 59% for in vitro fertilization (IVF) with preimplantation genetic diagnosis for monogenic/single gene disorders (PCT-M), 48% prenatal diagnosis, 18% donor gamete, 12% addition and 9% no longer planning to get pregnant.avoid having an affected child. Of the 154 ARCs who received the ECS results while pregnant, 37% pursued invasivereported pursuing prenatal diagnostic testing (PNDx), of which). Of those, 36% had affected pregnancies, and ;40% of thoseaffected pregnancies resulted in termination. Of the 63% of cases that did not have report PNDx, 75% had given resulted in live birth at the time of the survey and 44% of those; postnatal testing was planned or had been pursued postnatal diagnosis in 62% of those. In addition, 2.1% terminated the pregnancy without PNDx. The authors asked about also surveyed the ARCs for actions and outcomes in subsequent pregnancies. Of those who perusedpursued PNDx through Chorionic villus sampling (CVS) or amniocentesis, 29% had affected fetuses, and 75% of those terminated their pregnancies. Limitations of the study included patient's recallaccuracy of participant recollection of actions, possible response bias, and a larger number of ARCs whose current or future pregnancies were at risk for conditions that occur more often in the population, such as **cystic fibrosisCF and fragile** X syndrome. However, the authors tried to decrease these effects by analyzing results in aggregate and by condition severity. Overall, this study represents the largest cohort of ARCs to dateat-risk and diverse couples screened to date. The authors assert that the study's results indicate that ECS directs changes in pregnancy management that can lead to fewer births of children with clinically significant genetic diseases and suggests that there may be clinical value in screening for up to 176 conditions diseases that have not traditionally been assessed for in prenatal/preconception screens.

Peyser et al. (2019) compared the efficiency of ECS to ethnic-based screening to identify carriers. A cohort of 4,232 patients seeking fertility treatment was studied. ECS was performed at one genetic testing laboratory for patients seen between June 2013 and July 2015. Ethnicity was self-reported. Carrier status rates based on ECS was were calculated. Carrier rates were also determined for the ACOG-recommended ECS panel tests (ACOG-based screening) and ethnic-ethnicity-based screening (ACOG and ACMG ethnicity panel recommendations). The ECS utilized test under study was made up of 400 variants of 102 genes associated with 100 genetic conditions. Fragile X CGG repeat size and the number of

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SMN1 exon 7 copy-number status to screen for spinal muscular atrophySMA screening were also included in the ECS panel. Carrier rates were calculated for the overall study population and for each ethnic subpopulation and then compared to determine differences between carrier identification rates by each panel. The ECS panel did not screen for  $\alpha$ thalassemia and maple syrup urine disease 1A (MSUD1A), 2two conditions included in the ACOG-based screening panel. Therefore, the carrier rate for the ACOG-based screening was calculated without including these two conditions. A total of 4,232 patients individuals were tested [2,880 females (68.1%); 1,352 males (31.9%)] for carrier status using ECS. Applying ethnic-based screening recommendations would have resulted in 359 out of 4,232 (8.5%) patients individuals identified as carriers. Upon applying Applying the ACOC ACOG-based screening guidelines, 659 out of 4,232 (15.6%) would have been identified as carriers. With the ECS panel, 1,243 (29.4%) of patients participants were identified as carriers. A large and highly significant difference was found between carrier rates when each panel was applied to the population and then compared to each other. The authors also looked at the data from subpopulations based on self-reported ethnicity. The number of carriers identified increased with the increasing panel size across the total study cohort and in all but 3 three of 14 self-reported ethnicities. In the Southeast Asian and Native American populations, the only increase was seen from ACOG-based screening to ECS resulting in identification of additional carriers. However, the identification of carriers did not change regardless of the panel for the Pacific Islander cohort. Further, looking at the overall population and five subpopulations, carrier rates were statistically different in all 3 three comparisons: Mixed or Other Caucasian, Southern European, Northern European, Unknown/Not Reported, and Ashkenazi Jewish.AJ. In three subpopulations, (Hispanic, South Asian, and Middle Eastern), significant differences were observed in ethnic-based screening versus ECS and ACOG-based ethnic screening versus ECS, but not the ethnic-base based screening versus ACOG-based screening. Ethnic based screening versus ECS only provided statistical differences in the African or African American population. However, in two subethnic populations, East Asian and Southeast Asian, the carrier numbers for each panel were not statistically significant. A total of 1,206 couples were screened using the  $\frac{ESC}{ECS}$  panel $\frac{1}{7}$  15 (1.2%) of which were identified as carrier couples. In revealing the ethnicity of each partner, 8-of-/15 (53%) would have been recognized through ethnic-based screening quidelines. In addition to carrier couples, 73 women were found be carriers of Fragile X, with variation in repeat numbers identified and thus variation in classification of the reproductive risk. In conclusion, the authors present data that ECS is **greater superior** to ethnic-based genetic screening at identifying genetic disease carriers and carrier couples. The authors argue that their study provides additional evidence that ECS provides a larger amount of preconception information for patients. The study did have noted limitations; study participants who were seeking ECS due to family history of a specific disorder were included in the analysis, which could have elevated the rate of carrier couples found in the study. In addition, learning carrier status for diseases with late onset or variable phenotypes could lead to increased anxiety and confusion for those undergoing ECS.

Terhaar et al. examined outcomes for three unique multigene RCS panels in a 2018 retrospective analysis. Panel sizes varied; genes associated with a minimum of three diseases (trio) to a maximum of 218 diseases (global) were analyzed. Data was reviewed for 75,036 individuals referred by a healthcare provider in the United States. Trio screening was applied to 51,584 samples and 7.2% of those yielded a positive result. A 23-gene panel (standard) was used for the assessment of 19,550 samples with a 13.2% positive rate. Finally, 3902 samples were assessed with the global panel; 35.8% were positive. Overall, 127 conditions were identified at least once in this group. The authors noted that those that seeking the global panel were more ethnically diverse when compared to

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the other groups. It was not reported in this study if any at risk couples were identified. The researchers speculate that although receiving more genomic information can be beneficial to patients and providers who want a lot of information to inform medical management, this may also place a burden on clinical care. Most of the disorders identified were inherited in a recessive manner, requiring the clinicians to provide counseling and screening for a reproductive partner. In addition, large panels may identify conditions with mild phenotypes. Common diseases like CF may be familiar to clinicians, but rare diseases may not be. Educational resources for clinicians and patients are needed in order to ensure informed conversations and decision making.

Wilfond et al. (2018) reported on lessons learned from the NextGen study, a prospective study designed to explore the best approaches to genomics-based RCS. The study enrolled women interested in carrier screening, randomizing them to either receive genomic sequencing (n=133) or receive usual care (no additional screening) (n = 180). If a woman was positive, her male partner was offered genome sequencing to determine the risk of having an affected pregnancy. In the genome sequencing arm, the team chose to report on 728 conditions categorizing the conditions into five classes that participants could opt to learn about. The classes included diseases resulting in a shortened life span, serious conditions, mild conditions, conditions with unpredictable outcomes, adult-onset conditions, and medically actionable conditions related to the individual's personal health (secondary to carrier screening). Overall, 15 at-risk couples were identified; most were at-risk for adult-onset conditions. Eight were carriers for hereditary hemochromatosis, two were carriers for alpha-1-antitrypsin deficiency, one was a carrier for non-syndromic hearing loss, one was a carrier for Factor V Leiden homozygosity, and the remaining were carriers for X-linked disorders. These included spondyloepiphyseal dysplasia, G6PD deficiency, and hemophilia A. Overall, 78% of participants had at least one finding. This leads to concerns about implementation of this approach into clinical workflows. The median time needed by a genetic counselor to prepare for a follow up visit for positive results was 64 minutes. In this study, 26% of women became pregnant before disclosure, adding additional time sensitivity to developing a genomic sequencing-based screening program. The authors noted that their study design and size did not allow for a complete analysis of clinical utility, but they highlighted some anecdotal evidence that was collected. It was reported that women receiving genomic sequencing-based screening did not seek out more mental health or other services compared to those receiving usual care. They also did not report more anxiety or depression. One participant declined amniocentesis for chromosome abnormalities because she believed the ECS assessed that; this misconception was later corrected. The participants identified as a carrier of hemophilia A did undergo an amniocentesis; the fetus was male and found to carry the pathogenic variant, which altered the birth plan and allowed the neonatal team to intervene early. Finally, the authors noted that their study was small and on an older, more educated population. In conclusion, the researchers noted that genomics-based carrier screening could have significant impact on clinical workflow and resources, but the optimal gene targets need to be identified. Additionally, this testing may not be accessible to low-income patients. Additional research is needed to address these issues.

Shraga et al. (20182017) reported on reliability of self-reported ethnicity verses genetic ancestry for clinical decision-making in the context of genetic carrier screening. The total of 9,138 participants were referred by a variety of healthcare providers such as fertility specialists, obstetricians/gynecologists, and genetic counselors from the United States and Spain. The carrier screening test offered consisted of 311 autosomal recessive and X-linked conditions. Ethnicity information was gathered two times, first at the time the test was ordered, and second when self-recorded on the

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test requisition form. The couples were asked to choose all applicable ethnicities from the following list of options: African, East Asian, European, French Canadian, Jewish, Latin American, Mediterranean, Middle Eastern, Native American, South Asian, Southeast Asian, and/or Other. For the option "Other", individuals could write in the selfidentified ethnicity. All "Other" responses were mapped to appropriate categories when applicable,  $\frac{1}{2}$  (e.g., Caucasian/White mapped to European.). The second self-report was obtained during the post-test appointment with a genetic counselor. During the family history portion of the consultation, individuals were asked to identify their race/ethnicity or where their family originated from. For situations where patients did not participate in counseling or were unreachable, a "family history" ethnicity was not generated, and the patients were not considered in that part of the analysis. However, they were still included in the comparison between "requisition form" ethnicity and genetic ancestry. A set of single nucleotide polymorphisms (SNPs) was selected that could accurately determine continental genetic ancestry in the patient population. SNP frequencies were obtained from the ALFRED database, and through a repetitive process, a set of SNPs that could separate the continental groups was selected. Six of the eight continental groups were determined to be well separated. The Middle Eastern and Central Asian groups are closely related to the European and South Asian groups, respectively, and require an extra set of markers to properly estimate population separations. For this reason, it was decided not to use these two groups as separate ancestral populations and they were removed them from the ultimate estimation. The authors also validated the genetic ancestry model by applying a set of 2,504 samples with known origin from the 10001,000 Genomes project. This test showed the set of 1,142 SNPs was able to correctly estimate continental ancestry in the included populations. The results also validatevalidated the approach of using pre-commuted population allele frequencies. A comparison of the self-reports in the two situations was then performed. First, the ethnicity reported on the requisition form was compared to that provided during the genetic counseling session. For each ethic group, counts were generated for: 1) each patient who selected it on the requisition form, 2) each patient who identified it during consults, and 3) each patient who did both. PatientPatients who selected "Other" on the requisition form were excluded. Consistent patterns were seen in self-reported identification in both situations. For example, 97.7% of patients that participants who selected East Asian on the requisition form identified as have East Asian during the genetic counseling session, while 99.2% of patients who identified as having East Asian ancestry during the consult also selected East Asian on the requisition form. However, for ethnicities such as Mediterranean, Native American, and Southeast Asian, the responses between the two sources of self-report were different. Another observed difference was between self-reported ethnicity on the requisition form and genetic ancestry in South Asians and Southeast Asians. However, these differences were diminished when obtaining ethnicity during the genetic counseling session. The differences indicate that there is confusion about the meaning of different labels, indicating that selfreporting of ethnicity cannot be relied upon. When calculating genetic reproductive risk, inaccurate reporting of ethnicity results in inaccurate calculation of risk. Admixed populations were also looked at, and results indicate that carrier rates and residual risks are dependent on genetic ancestry in these populations. For example, in the carrier rate for cystic fibrosis CF varies from 1.6% to 3.67% in the Latin American population, depending on the percent of European ancestry, and the carrier rate for sickle cell anemia varies from 1.3% to 4.6% depending on the amount of African ancestry. Thus, it cannot be assumed that the genetic risk to admixed populations occurs in a consistent manner. The source of ethnic background can have an impact on estimating carrier and recurrence risk and providing appropriate testing, and  $\frac{can}{can}$  impact decision making.  $\frac{Thus}{r}$ the The authors suggest that in order to mitigate these risks and ensure serious genetic disorders are not missed; expanded earrier screening, ECS panels should be utilized.

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Despite the disadvantages of expanded carrier panelsECS, given that self-reporting of ethnicity is unreliable and can lead to providing the provision of an uncompleteincomplete picture of risks to couples, the expanded carrier screens provideECS provides a comprehensive approach. The authors also concluded that genetic ancestry should be determined by appropriate clinical testing rather than self-report reporting in order to provide accurate carrier rates, detection rates and residual risks based on self-reported ethnicity. The retrospective nature of this study is one of its limitations. Another is that self-reported ethnicity could have been incorrectly entered in the database or modified. A third limitation is that the ancestry model used is based on allele **frequencies frequency** estimates from **a** small sample size and assumes that assembling people by continent provides meaningful estimates of origin. Additional studies with larger cohorts are needed to improve the ancestry model and to measure the relationship between carrier rates and genetic ancestry for more diseases. Additional work is needed to understand the factors leading to self-identified ethnicity. In conclusion, self-reported ethnicity is shown to be unreliable, leading to the possibility of inaccurate calculation of carrier rates and residual risk. To decrease the risk of ordering the incorrect testing panel, the authors recommend the use of expanded panethnic carrier screeningECS panels. In addition, in order to accurately estimate carrier rates and residual risks, they recommend the use of a genetic ancestry model in clinical genetic testing.

Terhaar et al. (2018) retrospectively report on their experience as a commercial laboratory with reproductive carrier screening comparing three panels; 3 genes, 23 genes, or 218 genes. Data was assessed on 75,036 individuals referred by a healthcare provider in the United States. Three genes were assessed in 51,584 samples, and 7.2% had a positive result. The 23 gene panel was assessed for 19.550 samples, and 13.2% were positive. Finally, 3,902 samples were assessed for 218 genes, and 36% were positive. Overall, 127 conditions came up positive at least once in this group. The authors noted that those that seeking the 218 gene panel were more ethnically diverse when compared to the other groups. It was not reported in this study if any at risk couples were identified. In addition, it was noted that while receiving more genomic information can be beneficial to patients and providers who want a lot of information to inform medical management, this may also place a burden on clinical care. Most of the disorders identified were inherited in a recessive manner, requiring the clinicians to provide counseling and screening for a reproductive partner. Large panels may identify conditions with mild phenotypes. Common diseases like cystic fibrosis may be familiar to clinicians, but rare diseases may not. Educational resources for clinicians and patients are needed order to ensure informed conversations and decision making.

Wilfond et al. (2019) reported on lessons learned from the NextGen study, a prospective study designed to explore the best approaches to genomic based reproductive carrier screening. The study randomized women who saw a genetic counselor in person who desired carrier screening and randomized them to those that received genomic sequencing (n = 133) and those who received usual care-meaning no additional screening (n = 180). If a woman was positive, her male partner was offered genome sequencing to determine the risk of having an affected pregnancy. In the genome sequencing arm, the team chose to report on 728 conditions, and categorized the conditions into five classes that participants could choose to learn about or not. The classes included diseases with a shortened life span, serious conditions, mild conditions, conditions with unpredictable outcomes, adult-onset conditions, and medically actionable conditions related to the individual's personal health (secondary to carrier screening.) Overall, 15 at risk couples were identified, and most were for adult-onset conditions. Eight were at risk for hereditary hemochromatosis, two for alpha-1-antitrypsin deficiency; one for non-syndromic hearing loss, one for

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Factor V Leiden homozygous offspring, and the remaining were for X-linked disorders. These included spondyloepiphyseal dysplasia, G6PD deficiency, and hemophilia A. Overall, however, 78% of participants had at least one finding. This leads to concerns about implementation of this approach into clinic workflows. The median time needed to prepare for a follow up visit for positive results disclosure by a genetic counselor was 64 minutes. In this study, 26% of women became pregnant before disclosure, adding additional time sensitivity to developing a genomic based screening program. The authors noted that their study design and size did not allow for a complete analysis of clinical utility, but they highlighted some anesdotal evidence that was collected. It was reported that women did not seek out more mental health or other services compared to those receiving usual care. They did not report more anxiety or depression. One participant declined amniocentesis for chromosome abnormalities because she believed the expanded carrier screening covered that, and this misconception was later corrected. The woman identified as a carrier of hemophilia A did undergo an amniocentesis, and the fetus was male and found to carry the pathogenic variant. This altered the birth plan and allowed the neonatal team to intervene early. The baby did experience a rare subgaleal hemorrhage after birth, which was immediately treated. Finally, the authors noted that their study was small and on an older, more educated population. When asked about what they might pay out of pocket for genome sequencing, participants were willing to pay a little more than a copay, but the amount varied based on income. In conclusion, the authors noted that genomic sequencing as an approach to routine carrier screening could have significant impact on clinical workflow and resources, the optimal gene targets need to be identified, and may not be accessible to low-income patients. Additional research

Chiossi et al. (2018) studied the decision making of 537 couples who were identified to be carriers of the same genetic disease after undergoing expanded carrier screening for 110 genes through their commercial lab. These couples represented 1% of 51,775 couples screened between August 2014 and August 2015. The diseases included in the study were classified to be profound, severe, or moderate in terms of clinical impact. All couples were invited to participate in a survey about reproductive decision making, and 64 completed the survey. Of these, 45 couples had sought screening prior to pregnancy, and 62% reported that they planned to use preimplantation genetic diagnosis or prenatal diagnosis in a future pregnancy. Twenty-nine percent did not plan to alter reproductive decision making and the remaining four survey responses were unclear. Of the 19 pregnant couples, 10 elected to have prenatal diagnosis but two miscarried before testing could occur. Of those that had testing, five pregnancies were unaffected, and three were affected. Two affected pregnancies were terminated. The remaining couples did not think the condition they were at risk for was significant enough to undergo invasive testing. Perceived severity of the disorder appeared to impact decision making, as 76% of couples who were at risk for a profound or severe disorder reported altering reproductive decision making as a result, compared to only 22% of those at risk for moderate conditions. The authors also compared the choices made by the couples by diseases in professional society screening quidelines (20 couples) and diseases not currently in quidelines (22 couples) and found no significant difference in decision making. The authors noted that limitations of the study included the low response rate, lack of random sampling, and possible response bias.

Haque et al. (2016) created a model of fetal risk based on a commercial laboratories experience with expanded carrier screening. ECS. From January 2012 to July 2015, the laboratory screened 346,790 individuals that were referred for testing by their healthcare provider. The expanded carrier screening ECS panel test offered was for analyzed 110 genes, including 94 conditions categorized as severe or profound. Two platforms were

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utilized. The first was a targeted genotyping platform for 417 known pathogenic variants, and the second was next generation sequencingNGS for all genes. Healthcare providers could select the testing platform and genes desired for their patient, so not all patients were screened for all conditions. Targeted genotyping was performed on 308,668 patients, and 47,590 carriers were identified, and f which 279 individuals were homozygous or compound heterozygotes. Next generation sequencingheterozygous. NGS was completed on 38,122 individuals, and; of these, 11,088 peopleindividuals were carriers, and 124 were identified as homozygous or compound heterozygous. Results were reviewed in the context of the participant gender and self-reported race/ethnicity. The largest racial mix in the study was "mixed or other Caucasian." The smallest group included in the analysis was SE Southeast Asian, although; Finnish was the smallest overall and was excluded from the final analysis due to small numbers. The authors utilized used the results of both platforms to estimate the carrier frequency by ethnic group, and then modeled the carrier frequency, carrier couple frequency for couples of the same ethnicity, and resulting fetal risk. Based on the model, the authors then compared the detection rate of potential at--risk couples for diseases included in current professional society carrier screening guidelines against the detection rate of all profound and severe diseases in the expanded carrier screening ECS panel. When hemoglobinopathy genes are excluded from analysis, African Americans were noted to have 18% risk of profound or severe recessive diseases covered by guidelines, and 82% wererisk outside of guidelines, with a calculated cumulative risk of 1 one in 1,741 to have a fetus affected by any profound/severe condition in the study. The Ashkenazi Jewish AJ group had 45% risk within guidelines, and 55% risk outside of guidelines with a modeled fetal risk on lof one in 255. Mixed or other Caucasian had 32% risk within guidelines, and 68% risk outside of quidelines with a modeled fetal risk on lof one in 649. The authors conclude that current quidelines do not perform equally well between selfreported ethnic groups, and currently target diseases prevalent in European populations. Expanded carrier screeningECS may identify couples at risk for other conditions that are important in a diverse population. Limitations identified for the study include the use of an artificial construct to calculate disease frequencies and fetal resultingresults from random mating within an ethnic group. Disease frequencies in the general population might vary when compared to the population referred for genetic testing by a healthcare provider. The model does not fully address the racial/ethnic admixture possible in the study population or in real world reproductive pairing. Prospective studies comparing current standard of care with expanded carrier screeningECS are needed before expanded carrier screening ECS is fully adopted.

#### Clinical Practice Guidelines

#### American College of Obstetricians and Gynecologists (ACOG)

In a 2022 (reaffirmed 2023) Practice Advisory, ACOG updated their recommendations on hemoglobinopathies in pregnancy, noting that previouslyprevious, recommendations for testing were based on race/ethnicity. This strategy is no longer recommended because self-reported race/ethnicity is not always accurate in terms of genetic ancestry. Since about 1 in 66 individuals in the United States have a trait related to hemoglobinopathy, ACOG recommends offering hemoglobinopathy testing (which may be performed using hemoglobin electrophoresis or molecular genetic testing) to all individuals planning a pregnancy or at the first prenatal visit if no prior testing for hemoglobinopathies has been performed. Following this model, individuals who are at-risk can receive important counseling regarding their genetic risk, explore potential options, and make informed decisions.

In Committee Opinion 690 (2017a, reaffirmed 2023), ACOG states that if an expandedall individuals who are pregnant or considering pregnancy should be offered carrier screening testfor cystic fibrosis (CF), spinal muscular atrophy (SMA) and complete blood count and screening for thalassemias and hemoglobinopathies. If ECS is to be considered, several of the following consensus—driven criteria should be met:

- The disorder should have a carrier frequency greater than 1 in 100
- The condition should have a well-defined phenotype, a detrimental effect on quality of life, cause physical or cognitive impairment, and have onset early in life
- Diagnosis can be made prenatally to provide opportunities for antenatal intervention to improve perinatal outcomes such as changes in delivery management, and to educate parents about special needs after birth
- Carrier screening panels should not include adult-onset conditions.

ACOG advises that not all individuals who are at risk of the conditions screened will be identified through carrier screening and stresses the importance of genetic counseling for all individuals undergoing testingcarrier screening.

In ACOG Committee Opinion No. 691 (2017b, reaffirmed in 2023), carrier screening for the four diseases below was recommended for individuals of Ashkenazi Jewish (AJ) descent:

- Canavan disease  $(\frac{1/6,400;}{carrier frequency})$  1/40)
- Cystic fibrosis (1/2,500-3,000; carrier frequency 1/29)
- Familial Dysautonomia (<del>1/3,600;</del>carrier frequency 1/32)
- Tay-Sachs disease (disease incidence 1/3000; carrier frequency 1/30)

The Committee Opinion points out that more comprehensive screening panels for individuals of Ashkenazi JewishAJ descent have been promoted by some experts, to include less-common diseases with carrier rates from 1/15 to 1/168. These include:

- Bloom syndrome
- Familial hyperinsulinism
- Fanconi anemia
- Gaucher disease
- Glycogen storage disease
- Joubert syndrome
- Maple syrup urine disease
- Mucolipidosis type IV
- Niemann-Pick disease
- Usher syndrome

When only one partner is of Ashkenazi JewishAJ descent, that individual should be offered screening first, and if found to be a carrier, the other partner should then be offered screening. Of note; carrier frequency and detection rate in non-Jewish individuals are unknown for the majority of disorders discussed above, so accuracy in predicting risk is likely reduced.

#### American College of Medical Genetics and Genomics (ACMG)

An ACMG Practice Resource (Gregg, et al. 2021) identifies and recommends adoption of a tiered approach to carrier screening.

- Tier 1- Cystic Fibrosis (CF) + Spinal Muscular Atrophy (SMA) + Risk Based Screening
- Tier  $2- \ge 1/100$  carrier frequency (includes Tier 1)

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- Tier  $3- \ge 1/200$  carrier frequency (includes Tier 2) includes and X-linked conditions)
- Tier 4- < 1/200 carrier frequency (includes Tier 3)

In addition, the ACMG resource includes the following recommendations:

- The term "carrier screening" should replace the term "expanded carrier screening"
- Promotion of paradigms for carrier screening that are ethnic and population neutral
- Tier 3 carrier screening for autosomal recessive and X-linked conditions should be offered to all pregnant patients and those planning a pregnancy
- Tier 3 carrier screening for autosomal recessive conditions may be offered to reproductive partners of pregnant individuals or those planning pregnancy when screening is performed simultaneously with their partner
- Tier 4 screening should only be considered if a pregnancy stems from a known or possible consanguineous relationship (second cousins or closer) or when a family or personal medical history warrants such testing

An ACMG Position Statement states that although some commercial laboratories offer expanded carrier screening panels, there is little consensus on which disease genes and mutations to include in these panels (Grody et al., 2013; Edwards et al., 2015). Panels for that include multiple carrier screening tests may be useful if they include the diseases that are present with increased frequency in a specific population (i.e., Ashkenazi Jewish Carrier Screening), but do not have clinical utility when they include a larger number of genetic diseases for which the individual does not have an increased risk of being a carrier.

#### National Society of Genetic Counselors

The National Society of Genetic Counselors (Sagaser et al.) published an evidence-based practice guideline in 2023, recommending that ECS be offered to all individuals considering reproduction, pregnant individuals and their partners and those who might otherwise contribute biologically to the pregnancy. They assert that the final decision regarding carrier screening should take place after shared decision-making, considering the specific features of individuals and their personal values and preferences. Use of ECS provides an alternative to ethnicity-based screening and would potentially identify more carriers of autosomal recessive and X-linked conditions without dependence on race. The authors note that this recommendation is conditional and is "based on the balance of benefits and harms of ECS, and low and moderate certainty in the evidence. There are no specific clinical criteria or set of conditions associated with the conditional recommendation for ECS." Efforts to focus on addressing barriers to ECS, including insurance coverage, access to genetics professionals and educational needs of impacted individuals, are recommended.

# 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.

Laboratories that perform genetic tests are regulated under the Clinical Laboratory Improvement Amendments (CLIA) Act of 1988. More information is available at: <a href="https://www.fda.gov/medicaldevices/deviceregulationandguidance/ivdregulatoryassistance/ucm124105.htm">https://www.fda.gov/medicaldevices/deviceregulationandguidance/ivdregulatoryassistance/ucm124105.htm</a>.

(Accessed June 14, 2023April 24, 2024)

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# Policy History/Revision Information

Coverage Rationale  Additional Non-State Criteria  Removed content addressing expanded carrier screening panel testing Reproductive Carrier Screening  Revised language to indicate:  Revised language to indicate:  Reproductive Carrier Screening Panels of up to six genes are proven and medically necessary  Reproductive Carrier Screening Panels of up to 15 genes are proven and medically necessary when an individual and/or their reproductive partner meet at least one of the following criteria:  Ashkenazi Jewish ancestry (individual/reproductive partner has at least one parent or grandparent of Ashkenazi Jewish descent)  A biological First- or Second-Degree Relative has been affected by one or more of the conditions evaluated by the Panel  The following are unproven and not medically necessary due to insufficient evidence of efficacy:  Reproductive Carrier Screening Panels comprised of 16 or more genes  Carrier Screening for all other indications  It is strongly recommended that reproductive Carrier Screening Panels include screening for cystic fibrosis (CFTR) and spinal muscular atrophy (SMNI)  Definitions  Removed definition of "Expanded Carrier Panel Screening (ECS)"  Removed definition of:  Carrier Screening  First-Degree Relative	Date	Summary of Changes
Removed content addressing expanded carrier screening panel testing Reproductive Carrier Screening Revised language to indicate:  O Reproductive Carrier Screening Panels of up to six genes are proven and medically necessary Reproductive Carrier Screening Panels of up to 15 genes are proven and medically necessary when an individual and/or their reproductive partner meet at least one of the following criteria:  Ashkenazi Jewish ancestry (individual/reproductive partner has at least one parent or grandparent of Ashkenazi Jewish descent) Abiological First- or Second-Degree Relative has been affected by one or more of the conditions evaluated by the Panel The following are unproven and not medically necessary due to insufficient evidence of efficacy: Reproductive Carrier Screening Panels comprised of 16 or more genes Carrier Screening for all other indications It is strongly recommended that reproductive Carrier Screening Panels include screening for cystic fibrosis (CFTR) and spinal muscular atrophy (SMN1)  Definitions Removed definition of "Expanded Carrier Panel Screening (ECS)" Updated definition of: Carrier Screening	TBD	Coverage Rationale
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Supporting Information		
• Updated Description of Services, Clinical Evidence, and References		
sections to reflect the most current information		
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#### **Instructions for Use**

This Medical Policy provides assistance in interpreting UnitedHealthcare standard benefit plans. When deciding coverage, the federal, state or contractual requirements for benefit plan coverage must be referenced as the terms of the federal, state or contractual requirements for benefit plan coverage may differ from the standard benefit plan. In the event of a conflict, the federal, state or contractual requirements for benefit plan coverage govern. Before using this policy, please check the federal, state or contractual requirements for benefit plan coverage. UnitedHealthcare reserves the right to modify its

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