



Louisiana

Genetic Testing for Rett Syndrome

Policy # 00369

Original Effective Date: 11/20/2013

Current Effective Date: 12/20/2017

Applies to all products administered or underwritten by Blue Cross and Blue Shield of Louisiana and its subsidiary, HMO Louisiana, Inc. (collectively referred to as the "Company"), unless otherwise provided in the applicable contract. Medical technology is constantly evolving, and we reserve the right to review and update Medical Policy periodically.

When Services Are Eligible for Coverage

Coverage for eligible medical treatments or procedures, drugs, devices or biological products may be provided only if:

- *Benefits are available in the member's contract/certificate, and*
- *Medical necessity criteria and guidelines are met.*

Based on review of available data, the Company may consider genetic testing for Rett syndrome (RTT) –associated genes (e.g., methyl-CpG-binding protein 2 [*MECP2*], forkhead box G1 [*FOXP1*], or cyclin-dependent kinase-like 5 [*CDKL5*]) to establish a genetic diagnosis of Rett syndrome (RTT) in a child with developmental delay and signs/symptoms of Rett syndrome (RTT), when a definitive diagnosis cannot be made without genetic testing to be **eligible for coverage**.

Based on review of available data, the Company may consider targeted genetic testing for a known familial Rett syndrome (RTT)–associated variant to determine carrier status of a mother or a sister of an individual with Rett syndrome (RTT) to be **eligible for coverage**.

When Services Are Considered Investigational

Coverage is not available for investigational medical treatments or procedures, drugs, devices or biological products.

Based on review of available data, the Company considers all other indications for genetic testing for Rett syndrome (RTT), including carrier testing (preconception or prenatal), and testing of asymptomatic family members to determine future risk of disease, to be **investigational**.*

Background/Overview

RETT SYNDROME

RTT is a severe neurodevelopmental disorder primarily affecting girls, with an incidence of 1:10,000 female births, making it among the most common genetic causes of intellectual disability in girls. RTT is characterized by apparent normal development for the first 6 to 18 months of life, followed by regression of intellectual functioning, acquired fine and gross motor skills, and social skills. Purposeful use of the hands is replaced by repetitive stereotyped hand movements, such as hand-wringing. Other clinical manifestations include seizures, disturbed breathing patterns with hyperventilation and periodic apnea, scoliosis, growth retardation, and gait apraxia.

There is wide variability in the rate of progression and severity of the disease. In addition to the classic form of RTT, there are recognized atypical variants. Variants of RTT may appear with a severe or a milder form. The severe variant has no normal developmental period; individuals with a milder phenotype experience less dramatic regression and milder expression of the characteristics of classical RTT. Diagnostic criteria for

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typical (or classic) RTT and atypical (or variant) RTT have been established. For typical RTT, a period of regression followed by recovery or stabilization and fulfillment of all the main criteria are required to meet the diagnostic criteria for classic RTT. For atypical RTT, a period of regression followed by recovery or stabilization, at least 2 of the 4 main criteria, plus 5 of 11 supportive are required to meet the diagnostic criteria of variant RTT.

Treatment

Currently, there are no specific treatments that halt or reverse disease progression, and there are no known medical interventions that will change the outcome of patients with RTT. Management is mainly symptomatic and individualized, focusing on optimizing each patient's abilities. A multidisciplinary approach is usually applied, with specialist input from dietitians, physical therapists, occupational therapists, speech therapists, and music therapists. Regular monitoring for scoliosis (seen in ≈87% of patients by age 25 years) and possible heart abnormalities, particularly cardiac conduction abnormalities, may be recommended. Spasticity can have a major impact on mobility; physical therapy and hydrotherapy may prolong mobility. Occupational therapy can help children develop communication strategies and skills needed for performing self-directed activities (e.g., dressing, feeding, practicing arts and crafts).

Pharmacologic approaches to managing problems associated with RTT include melatonin for sleep disturbances and several agents to control breathing disturbances, seizures, and stereotypic movements. RTT patients have an increased risk of life-threatening arrhythmias associated with a prolonged QT interval, and avoidance of a number of drugs is recommended, including prokinetic agents, antipsychotics, tricyclic antidepressants, antiarrhythmics, anesthetic agents, and certain antibiotics.

In a mouse model of RTT, genetic manipulation of the *MECP2* gene has demonstrated reversibility of the genetic defect.

Genetics

RTT is an X-linked dominant genetic disorder. Pathogenic variants in *MECP2*, which is thought to control expression of several genes, including some involved in brain development, were first reported in 1999. Subsequent screening has shown that over 80% of patients with classic RTT have pathogenic variants in the *MECP2* gene. More than 200 pathogenic variants in *MECP2* have been associated with RTT. However, 8 of the most commonly occurring missense and nonsense variants account for almost 70% of all cases; small C-terminal deletions account for approximately 10%; and large deletions, 8% to 10%. *MECP2* variant type is associated with disease severity. Whole duplications of the *MECP2* gene have been associated with severe X-linked intellectual disability with progressive spasticity, no or poor speech acquisition, and acquired microcephaly. Additionally, the pattern of X-chromosome inactivation (XCI) influences the severity of the clinical disease in females.

Because the spectrum of clinical phenotypes is broad, to facilitate genotype-phenotype correlation analyses, the International Rett Syndrome Association has established a locus-specific *MECP2* variation database (RettBASE) and a phenotype database (InterRett).

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Approximately 99.5% of cases of RTT are sporadic, resulting from a de novo variant, which arise almost exclusively on the paternally derived X chromosome. The remaining 0.5% of cases are familial and usually explained by germline mosaicism or favorably skewed XCI in the carrier mother that results in her being unaffected or only slightly affected (mild intellectual disability). In the case of a carrier mother, the recurrence risk of RTT is 50%. If a variant is not identified in leukocytes of the mother, the risk to a sibling of the proband is below 0.5% (because germline mosaicism in either parent cannot be excluded).

Identification of a variant in *MECP2* does not necessarily equate to a diagnosis of RTT. Rare cases of *MECP2* variants also have been reported in other clinical phenotypes, including individuals with an Angelman-like picture, nonsyndromic X-linked intellectual disability, PPM-X syndrome (an X-linked genetic disorder characterized by psychotic disorders [most commonly bipolar disorder], parkinsonism, and intellectual disability), autism, and neonatal encephalopathy. Recent studies have revealed that different classes of genetic variants in *MECP2* result in variable clinical phenotypes and overlap with other neurodevelopmental disorders.

A proportion of patients with a clinical diagnosis of RTT do not appear to have pathogenic variants in the *MECP2* gene. Two other genes (*CDKL5*, *FOXG1*) have been shown to be associated with atypical variants.

FDA or Other Governmental Regulatory Approval

U.S. Food and Drug Administration (FDA)

Clinical laboratories may develop and validate tests in-house and market them as a laboratory service; laboratory-developed tests (LDTs) must meet the general regulatory standards of the Clinical Laboratory Improvement Amendments (CLIA). Genetic testing for RTT is available under the auspices of CLIA. Laboratories that offer LDTs must be licensed by CLIA for high-complexity testing. To date, the U.S. FDA has chosen not to require any regulatory review of this test.

Centers for Medicare and Medicaid Services (CMS)

There is no national coverage determination (NCD). In the absence of an NCD, coverage decisions are left to the discretion of local Medicare carriers.

Rationale/Source

Validation of the clinical use of any genetic test focuses on 3 main principles: (1) analytic validity, which refers to the technical accuracy of the test in detecting a variant that is present or in excluding a variant that is absent; (2) clinical validity, which refers to the diagnostic performance of the test (sensitivity, specificity, positive and negative predictive values) in detecting clinical disease; and (3) clinical utility (i.e., how the results of the diagnostic test will be used to change management of the patient and whether these changes in management lead to clinically important improvements in health outcomes). Following is a summary of the key literature.

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TESTING INDIVIDUALS WITH SIGNS OR SYMPTOMS OF RETT SYNDROME

Clinical Context and Test Purpose

The purpose of genetic testing of individuals with signs or symptoms of RTT is to determine the underlying pathogenic variant, predict potential disease severity, to initiate surveillance for potential disease complications (e.g., musculoskeletal deformities, autonomic dysfunction), and to direct treatments.

The relevant question addressed in this evidence review is: Does genetic testing for RTT-associated genes in individuals with suspected but not confirmed RTT lead to improved health outcomes?

The following PICOTS were used to select literature to inform this review.

Patients

The relevant population of interest includes individuals with signs or symptoms of RTT.

Interventions

The relevant intervention of interest is genetic testing for RTT-associated genes.

Comparators

The relevant comparator of interest is standard clinical management without genetic testing.

Outcomes

The potential beneficial outcomes of primary interest are establishing a genetic diagnosis for RTT and predicting potential disease severity and course to initiate surveillance and treatments for disease complications. Some genetic variants may be associated with prolonged QT syndrome, which would require periodic screening and avoidance of certain medications.

Potential harmful outcomes are those resulting from a false-positive or false-negative test results. False-positive test results can lead to unnecessary surveillance (e.g., musculoskeletal or autonomic dysfunction) and treatments (e.g., spinal fusion for scoliosis or kyphosis). False-negative test results can lead to lack of appropriate surveillance and treatments.

Timing

The time frame for outcome measures varies from short-term development of a severe neurodevelopmental disorder to long-term complications such as autonomic dysfunction, scoliosis or kyphosis, and growth retardation.

Setting

The primary settings would be in pediatric neurology, developmental pediatrics, or genetics outpatient offices.

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Analytic Validity

Analytic validity is the technical accuracy of the test in detecting a variant that is present or in excluding a variant that is absent.

The test is generally done as full gene sequencing of the *MECP2* gene to diagnose atypical or classic RTT and as multiplex ligation probe amplification (MLPA) for duplication and deletion analysis. Familial variant testing may be done with targeted sequencing. *FOXP1* or *CDKL5* sequencing may be done for atypical RTT.

According to a large reference laboratory, *MECP2* testing for RTT has an analytic sensitivity for sequencing of 99% and for MLPA, 90%; analytic specificity is 99% for sequencing and for MLPA, 98%.

Clinical Validity

Clinical validity is the diagnostic performance of the test (sensitivity, specificity, and positive and negative predictive values) in detecting clinical disease.

Huppke et al (2000) analyzed the *MECP2* gene in 31 female patients diagnosed clinically with RTT. Sequencing revealed variants in 24 (77%) of the 31 patients. Of the 7 patients in whom no variants were found, 5 fulfilled criteria for classic RTT. In this study, 17 different variants were detected, 11 of which had not been previously described. Several females carrying the same variant displayed different phenotypes, suggesting that factors other than the type or position of variants influenced the severity of RTT.

Cheadle et al (2000) analyzed variants in 48 females with classic sporadic RTT, 7 families with possible familial RTT, and 5 sporadic females with features suggestive, but not diagnostic, of RTT. The entire *MECP2* gene was sequenced in all cases. Variants were identified in 44 (80%) of 55 unrelated classic sporadic and familial RTT patients. Only 1 (20%) of 5 sporadic cases with suggestive but nondiagnostic features of RTT had variants identified. Twenty-one different variants were identified (12 missense, 4 nonsense, and 5 frame-shift variants); 14 of the variants identified were novel. Significantly milder disease was noted in patients carrying missense variants compared with those with truncating variants.

The 2 studies previously discussed were included in a summary of 6 articles by Lotan et al (2006) who attempted to elicit a genotype-phenotype correlation. The authors found that these studies had yielded inconsistent results and that further controlled studies were needed before valid conclusions could be drawn about the effect of variant type on phenotypic expression. Two subsequent studies used the InterRett database to examine genotype and RTT severity. Of 357 girls with epilepsy who had *MECP2* genotype recorded, those with large deletions were more likely than those with 10 other common variants to have active epilepsy (odds ratio [OR], 3.71; 95% confidence interval [CI], 1.13 to 12.17; $p=0.03$) and had the earliest median age at epilepsy onset (3 years 5 months). Among all girls in the database, those with large deletions were more likely to have never walked (OR=0.42; 95% CI, 0.22 to 0.79; $p=0.007$). Of 260 girls with classic RTT enrolled in the multicenter RTT Natural History study (NCT00299312), those with the R133C substitution variant had clinically less severe disease, assessed by the Clinical Severity, Motor

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Behavior Analysis, and Physician Summary scales. Fabio et al (2014) reported similar genotype-phenotype correlations among 144 patients with RTT in Italy.

Halbach et al (2016) analyzed a cohort from a group of 132 female patients between 2 and 43 years of age with well-defined RTT with extended clinical, molecular, and neurophysiological assessments. Genotype-phenotype analyses of clinical features and cardiorespiratory data were performed after grouping variants by the same type and localization or having the same putative biologic effect on the MeCP2 protein, and subsequently on 8 single recurrent pathogenic variants. A less severe phenotype was seen in females with C-terminal segment of *MECP2* (p.R133C and p.R294X variants). Autonomic disturbances were present in all females and not restricted to nor influenced by 1 specific group or any single recurrent pathogenic variant. The objective information from noninvasive neurophysiological evaluation of the disturbed central autonomic control is of great importance organizing the lifelong care for females with RTT. The study concluded that further research is needed to provide insights into the pathogenesis of autonomic dysfunction, and to develop evidence-based management in RTT.

Pidock et al (2016) identified 96 RTT patients with pathogenic variants in the *MECP2* gene. Among 11 pathogenic variant groups, a statistically significant group effect of variant type was observed for self-care, upper-extremity function, and mobility on standardized measures administered by occupational and physical therapists. Patients with R133C and uncommon variants tended to perform best on upper-extremity and self-care items, whereas patients with R133C, R306C, and R294X variants had the highest scores on the mobility items. The worst performers on upper-extremity and self-care items were patients with large deletions (R255X, R168X, and T158M variants). The lowest scores for mobility were found in patients with T158M, R255X, R168X, and R270X variants. On categorical variables as reported by parents at the time of initial evaluation, patients with R133C and R294X variants were most likely to have hand use; those with R133C, R294X, R306C, and small deletions were most likely to be ambulatory; and those with the R133C variant were most likely to be verbal.

Sajan et al (2017) analyzed 22 RTT patients without apparent *MECP2*, *CDKL5*, and *FOXP1* pathogenic variants were subjected to both whole-exome sequencing and single-nucleotide variant array-based copy-number variant analyses. Three patients had *MECP2* variants initially missed by clinical testing. Of the remaining 19, 17 (89.5%) had 29 other likely pathogenic intragenic variants and/or copy number variants (10 patients had ≥ 2). Thirteen patients had variants in a gene/region previously reported in other neurodevelopmental disorders, thereby providing a potential diagnostic yield of 68.4%. The genetic etiology of RTT without *MECP2*, *CDKL5*, and *FOXP1* variants is heterogeneous, overlaps with other neurodevelopmental disorders, and is complicated by a high variant burden. Dysregulation of chromatin structure and abnormal excitatory synaptic signaling may form 2 common pathologic bases of RTT.

Section Summary: Clinical Validity

Evidence from several small studies has indicated that the clinical sensitivity of genetic testing for classic RTT is reasonably high, in the range of 75% to 80%. However, sensitivity may be lower when classic RTT features are absent. Clinical specificity is unknown, but also is likely to be high, because only rare cases of *MECP2* variants have been reported in other clinical phenotypes, including individuals with an Angelman-

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like picture, nonsyndromic X-linked intellectual disability, PPM-X syndrome, autism, and neonatal encephalopathy. Recent studies have indicated that specific classes, types, or burden of pathogenic variants in genes associated with RTT affect severity of disease (e.g., degree of autonomic dysfunction, functional outcomes, degree of neurodevelopmental disorder).

Clinical Utility

Direct Evidence

Direct evidence of clinical utility is provided by studies that have compared health outcomes for patients managed with and without the test. No studies were identified that demonstrated direct evidence of clinical utility.

Indirect Evidence

Indirect evidence of clinical utility rests on clinical validity. There is no specific treatment for RTT; however, identification of the pathogenic variant leading to RTT has been found to correlate with disease severity and predict potential complications of disease (e.g., autonomic dysfunction and functional outcomes such as mobility). Increased surveillance for clinical manifestations, such as scoliosis or cardiac arrhythmia, and tailoring of ancillary treatments, such as occupational or physical therapy, may be performed.

Section Summary: Clinical Utility

There are no studies that report direct evidence on the clinical utility of genetic testing for RTT. Thus, the clinical utility of genetic testing for RTT relies on whether a strong chain of evidence exists. For individuals with suspected RTT, identification of a pathogenic variant may alter patient management via increased surveillance of clinical manifestations such as scoliosis, cardiac arrhythmia, or autonomic dysfunction. The class or type of pathogenic may also impact disease severity, allowing for tailoring of ancillary treatments (e.g., occupational therapy) to maintain or improve functional outcomes (e.g., extremity mobility, ambulation).

TARGETED FAMILIAL VARIANT TESTING OF ASYMPTOMATIC SISTERS OF INDIVIDUALS WITH RTT

Clinical Context and Test Purpose

The purpose of targeted familial variant testing of asymptomatic sisters of individuals with RTT is to predict the potential development of symptoms to determine the need for surveillance in young females and to aid in reproductive planning in females of reproductive age.

The relevant question addressed in this evidence review is: Does targeted familial variant testing of asymptomatic sisters of individuals with RTT lead to improved health outcomes, including changes in surveillance, preimplantation genetic testing to determine the likelihood of an affected offspring, or to informing reproductive planning decisions?

The following PICOTS were used to select literature to inform this review.

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Patients

The relevant population of interest includes asymptomatic sisters of individuals with RTT.

Interventions

The relevant intervention of interest is targeted genetic testing for a known familial variant.

Comparators

The relevant comparator of interest is standard management without genetic screening.

Outcomes

The potential beneficial outcomes of primary interest would be confirming or excluding the need for surveillance in young females or changes in reproductive decision making in females of reproductive age. A negative genetic test result would eliminate the need for surveillance to detect development of symptoms and disease. A positive genetic test result has the potential to confirm a need for active surveillance and may inform reproductive decision making in reproductive-age patients.

Potential harmful outcomes are those resulting from a false-positive or false-negative test results. False-positive test results can lead to unnecessary surveillance (e.g., musculoskeletal or autonomic dysfunction) and treatments (e.g., spinal fusion for scoliosis or kyphosis). False-negative test results can lead to lack of appropriate surveillance and inaccurate risk assessment to determine the likelihood of an affected offspring.

Timing

The time frame for outcome measures varies from short-term development of a neurodevelopmental disorder in young females to long-term complications such as autonomic dysfunction, scoliosis or kyphosis, and growth retardation. In women of reproductive age, outcomes vary from short-term identification of subclinical or mild cognitive disorders to long-term birth of an affected offspring.

Setting

The primary setting would be in pediatric neurology or genetics outpatient offices for young female patients and in obstetrics, general practice, or genetics outpatient offices for female patients of reproductive age.

Analytic Validity

See the discussion of analytic validity in the Testing Individuals With Signs or Symptoms of Rett Syndrome section.

Clinical Validity

See the discussion of clinical validity in the Testing Individuals With Signs or Symptoms of Rett Syndrome section.

Clinical Utility

Direct evidence of the clinical utility for targeted genetic testing of a known familial variant in asymptomatic sisters is lacking. However, a chain of evidence can be constructed for targeted genetic testing to determine

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if sisters of affected child are asymptomatic or subclinical carriers of the known familial variant. The variable penetrance of disease due to random X inactivation in females as well as different classes or types of pathogenic variants leading to different disease severity suggest that targeted testing for a familial variant has potential clinical utility. In young sisters of an affected child, targeted testing for the known familial variant has potential clinical utility in identifying subclinical manifestations and eliminating or necessitating the need for surveillance of clinical manifestations of disease. In sisters of reproductive age, targeted testing can guide whether prenatal testing may be indicated and potentially alter reproductive decisions.

TARGETED TESTING OF FEMALES WITH A CHILD WITH RTT CONSIDERING FURTHER CHILDBEARING

Clinical Context and Test Purpose

The purpose of targeted familial variant testing of females with a child with RTT who are considering having additional children is to determine carrier status and to aid in reproductive planning.

The relevant question addressed in this evidence review is: Does targeted familial variant testing of females with a child with RTT who are considering having additional children lead to improved health outcomes, including preimplantation genetic testing to determine likelihood of an affected offspring, or alter reproductive planning decisions?

The following PICOTS were used to select literature to inform this review.

Patients

The relevant population of interest includes female patients with a child with RTT.

Interventions

The relevant intervention of interest is targeted genetic testing for a known familial variant.

Comparators

The relevant comparator of interest is reproductive planning without genetic testing.

Outcomes

The potential beneficial outcomes of primary interest would be to determine carrier status to aid in reproductive decision making. A negative genetic test result would exclude a maternal inheritance of RTT and predict a low likelihood of an affected offspring derived from paternal inheritance. A positive genetic test result would predict a high likelihood of an affected offspring—a 50% chance of an hemizygous affected male or a 50% chance of an heterozygous affected female.

Potential harmful outcomes are those resulting from a false-positive or false-negative test results. False-positive test results can lead to reproductive decisions based on an incorrectly high prediction for an affected offspring. False-negative test results can lead to lack of appropriate preimplantation genetic diagnosis and inaccurate risk assessment to determine likelihood of an affected offspring.

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Timing

The time frame for outcome measures varies from short-term (i.e., months) in the case of identification of seizures or subclinical or mild cognitive disorders, to long-term (i.e., decades), in the case of decision making about childbearing.

Setting

The primary setting would be in obstetrics, genetics, or general practitioners outpatient offices.

Analytic Validity

See the discussion of analytic validity in the Testing Individuals With Signs or Symptoms of Rett Syndrome section.

Clinical Validity

Sheikh et al (2016) analyzed pathogenic variants in hemizygous males. In heterozygous females, the variable phenotypic severity is modulated by nonrandom X inactivation, thus making genotype-phenotype comparisons unreliable. However, genotype-phenotype correlations in males with hemizygous *MECP2* pathogenic variants can provide more accurate insights in to the true biologic effect of specific pathogenic variant. A wide range of phenotypic/clinical severity was observed, ranging from neonatal encephalopathy to mild psychiatric abnormalities, with correlating functional and molecular results. Overall, clinical severity showed a direct correlation with the functional impairment of MeCP2.

Zahorakova et al (2016) analyzed RTT patients with *MECP2* pathogenic variants and XCI. Skewed XCI (ratio, >75%) was found in 19.3% of the girls, but no gross divergence in clinical severity was observed. Findings confirmed a high pathogenic variant frequency in classic RTT (92%) and a correlation between the *MECP2* variant type and clinical severity. Additionally, limitations of XCI in explaining all of the phenotypic differences in RTT were noted.

Section Summary: Clinical Validity

Genotype-phenotype correlations in heterozygous females are confounded by both random XCI and the class or type of pathogenic variant present. In heterozygous females, the clinical sensitivity correlates with variant type and variable effects of skewed XCI. In contrast, for hemizygous males, the phenotypic/clinical severity of a particular pathogenic variant manifest completely.

Clinical Utility

Direct evidence of clinical utility for targeted genetic testing of a known familial variant in females with a child with RTT is lacking. However, a chain of evidence can be constructed for targeted genetic testing of a known familial variant to determine carrier status. The variable penetrance of disease due to random XCI in females as well as different classes or types of pathogenic variants leads to unpredictable disease severity. Although the majority of cases of RTT are due to de novo pathogenic variants in RTT-associated genes, determination of carrier status in a female with a child with RTT eliminates or necessitates prenatal testing and informs reproductive decision making. If a female tests negative for a known familial variant, future offspring are not at increased risk for RTT. In the rare situation where the mother carries a pathogenic

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variant, all future offspring have a 50% chance of being affected, with males typically presenting with more severe disease.

SUMMARY OF EVIDENCE

For individuals who have signs and/or symptoms of RTT who receive genetic testing for RTT-associated genes, the evidence includes case series and prospective cohort studies. Relevant outcomes are test accuracy and validity, other test performance measures, symptoms, health status measures, and quality of life. *MECP2* variants are found in most patients with RTT, particularly in those who present with classic clinical features of RTT. The diagnostic accuracy of genetic testing for RTT cannot be determined with absolute certainty given variable clinical presentations of typical versus atypical RTT, but testing appears to have high sensitivity and specificity. Genetic testing has clinical utility when signs and symptoms of RTT are present to establish a specific genetic diagnosis. Identification of a specific class or type of pathogenic variant may alter some aspects of management and may eliminate or necessitate surveillance for different clinical manifestations of disease. The evidence is sufficient to determine that the technology results in a meaningful improvement in the net health outcome.

For individuals who are asymptomatic sisters of an individual with RTT who receive targeted genetic testing for a known familial RTT-associated variant, the evidence includes case series and prospective cohort studies. Relevant outcomes are test accuracy and validity, other test performance measures, changes in reproductive decision making, symptoms, and symptoms. Targeted familial variant testing of asymptomatic sisters can eliminate or necessitate surveillance given the variability of clinical presentation in girls due to XCI and clinical severity based on the type of pathogenic variant present. In sisters of reproductive age, determination of carrier status can eliminate or necessitate prenatal testing and inform reproductive decision making. The evidence is sufficient to determine that the technology results in a meaningful improvement in the net health outcome.³

For individuals who are females with a child with RTT who are considering future childbearing who receive targeted genetic testing for a known familial RTT-associated variant, the evidence includes cases series and prospective cohort studies. Relevant outcomes are test accuracy and validity, other test performance measures, and changes in reproductive decision making. Targeted familial variant testing of a woman with a child with RTT to determine carrier status may inform prenatal testing and reproductive decision making. In the rare situation where the mother carries a pathogenic variant, all future offspring have a 50% of being affected, with males typically presenting with more severe disease. The evidence is sufficient to determine that the technology results in a meaningful improvement in the net health outcome.

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Louisiana

Genetic Testing for Rett Syndrome

Policy # 00369
 Original Effective Date: 11/20/2013
 Current Effective Date: 12/20/2017

Policy History

Original Effective Date:	11/20/2013
Current Effective Date:	12/20/2017
11/07/2013	Medical Policy Committee review
11/20/2013	Medical Policy Implementation Committee approval. New policy.
12/04/2014	Medical Policy Committee review
12/17/2014	Medical Policy Implementation Committee approval. Coverage eligibility unchanged.
08/03/2015	Coding update: ICD10 Diagnosis code section added; ICD9 Procedure code section removed.
12/03/2015	Medical Policy Committee review
12/16/2015	Medical Policy Implementation Committee approval. Coverage eligibility unchanged.
12/01/2016	Medical Policy Committee review
12/21/2016	Medical Policy Implementation Committee approval. Coverage eligibility unchanged.
01/01/2017	Coding update: Removing ICD-9 Diagnosis Codes
12/07/2017	Medical Policy Committee review
12/20/2017	Medical Policy Implementation Committee approval. The policy is revised with updated genetics nomenclature. "Mutations" changed to "variants" in policy statements. Policy rewritten with new PICOs for indications 2 and 3 to limit populations to sisters of child with Rett syndrome (indication 2) or females with a child with Rett syndrome (indication 3) with the intervention revised to "targeted genetic testing for a known familial variant." Policy statements updated to define "genetic testing for Rett syndrome- associated genes (e.g., <i>MECP2</i> , <i>FOXG1</i> , or <i>CDKL5</i>)"; Removed "female" requirement of child for testing; Added 2 new medical necessity statements for "targeted genetic testing for a known familial variant" in a sister of a child with Rett syndrome or a female with a child with Rett syndrome.

Next Scheduled Review Date: 12/2018

Coding

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Codes used to identify services associated with this policy may include (but may not be limited to) the following:

Code Type	Code
CPT	81302, 81303, 81304, 81404, 81406, 81470, 81471
HCPCS	No codes
ICD-10 Diagnosis	F84.2, G31.81, G31.82

*Investigational – A medical treatment, procedure, drug, device, or biological product is Investigational if the effectiveness has not been clearly tested and it has not been incorporated into standard medical practice. Any determination we make that a medical treatment, procedure, drug, device, or biological product is Investigational will be based on a consideration of the following:

- A. Whether the medical treatment, procedure, drug, device, or biological product can be lawfully marketed without approval of the U.S. Food and Drug Administration (FDA) and whether such approval has been granted at the time the medical treatment, procedure, drug, device, or biological product is sought to be furnished; or
- B. Whether the medical treatment, procedure, drug, device, or biological product requires further studies or clinical trials to determine its maximum tolerated dose, toxicity, safety, effectiveness, or effectiveness as compared with the standard means of treatment or diagnosis, must improve health outcomes, according to the consensus of opinion among experts as shown by reliable evidence, including:
 - 1. Consultation with the Blue Cross and Blue Shield Association technology assessment program (TEC) or other nonaffiliated technology evaluation center(s);
 - 2. Credible scientific evidence published in peer-reviewed medical literature generally recognized by the relevant medical community; or
 - 3. Reference to federal regulations.

**Medically Necessary (or “Medical Necessity”) - Health care services, treatment, procedures, equipment, drugs, devices, items or supplies that a Provider, exercising prudent clinical judgment, would provide to a patient for the purpose of preventing, evaluating, diagnosing or treating an illness, injury, disease or its symptoms, and that are:

- A. In accordance with nationally accepted standards of medical practice;
- B. Clinically appropriate, in terms of type, frequency, extent, level of care, site and duration, and considered effective for the patient’s illness, injury or disease; and
- C. Not primarily for the personal comfort or convenience of the patient, physician or other health care provider, and not more costly than an alternative service or sequence of services at least as likely to produce equivalent therapeutic or diagnostic results as to the diagnosis or treatment of that patient’s illness, injury or disease.

For these purposes, “nationally accepted standards of medical practice” means standards that are based on credible scientific evidence published in peer-reviewed medical literature generally recognized by the relevant medical community, Physician Specialty Society recommendations and the views of Physicians practicing in relevant clinical areas and any other relevant factors.

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APPENDIX

Appendix Table 1. Categories of Genetic Testing

Category	Addressed
1. Testing of an affected individual’s germline to benefit the individual	
1a. Diagnostic	X
1b. Prognostic	
1c. Therapeutic	
2. Testing cancer cells from an affected individual to benefit the individual	

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2a. Diagnostic	
2b. Prognostic	
2c. Therapeutic	
3. Testing an asymptomatic individual to determine future risk of disease	X
4. Testing of an affected individual's germline to benefit family members	
5. Reproductive testing	
5a. Carrier testing: preconception	X
5b. Carrier testing: prenatal	X
5c. In utero testing: aneuploidy	
5d. In utero testing: familial variants	
5e. In utero testing: other	
5f. Preimplantation testing with in vitro fertilization	

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