GENETIC TESTING: EXOME AND GENOME SEQUENCING FOR THE DIAGNOSIS OF GENETIC DISORDERS

OVERVIEW

Exome sequencing (ES) (also known as 'whole exome sequencing (WES)') involves sequencing and often copy number variant (CNV) analysis of the portion of the genome that contains protein-coding DNA, which are termed exons. Together, all of the exons in a genome are known as the exome, which constitutes approximately 1% of the genome and is currently estimated to contain about 85% of heritable disease-causing variants.

Genome sequencing (GS) (also known as 'whole genome sequencing (WGS)') is a comprehensive method that sequences both coding and noncoding regions of the genome. GS has typically been limited to use in the research setting, but is emerging in the clinical setting and has a greater ability to detect large deletions or duplications in protein-coding regions compared with ES. GS requires greater data analysis but less DNA preparation prior to sequencing.

ES and GS have been proposed for use in patients presenting with disorders and anomalies not immediately explained by standard clinical workup. Potential candidates for ES and GS include patients who present with a broad spectrum of suspected genetic conditions.

Rapid exome sequencing (rES) and rapid genome (rGS) sequencing involves sequencing of the exome or genome, respectively, in an accelerated time frame. Preliminary results can typically be returned in less than 7 days, and a final report in less than two weeks. Studies suggest that the use of rES or rGS in acutely-ill infants presenting with complex phenotypes that are likely rare genetic conditions, can identify a genetic diagnosis more quickly, allowing clinicians and family members to change acute medical or surgical management options and end the diagnostic odyssey. Ultra-rapid GS involves sequencing of the genome typically in less than 72 hours and is currently considered investigational.

POLICY REFERENCE TABLE

Below is a list of higher volume tests and the associated laboratories for each coverage criteria section. This list is not all inclusive.

Coverage Criteria Sections	Example Tests (Labs)	Common CPT Codes	Common ICD Codes	Ref
Standard Exome Sequencing	Genomic Unity® Exome Plus Analysis - Proband (Variantyx Inc.)	0214U	F70-F79, F80,0-F89, Q00.0-Q99.9	1, 2, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18
	Genomic Unity® Exome Plus Analysis - Comparator (Variantyx Inc.)	0215U		
	XomeDx (GeneDx)	81415, 81416, 81417		
	Invitae Boosted Exome (Invitae			
	ExomeNext (Ambry Genetics)			
	PGxome (PreventionGenetics)			
	Whole Exome Sequencing (PerkinElmer Genomics)			
	QuestExome (Quest Diagnostics)			
	Whole Exome Sequencing (LabCorp)			
Rapid Exome Sequencing	XomeDxXpress (GeneDx)	81415, 81416, 81417	F70-F79, F80-F89, Q00.0-Q99.9	1, 3, 4, 5, 6, 7, 8, 9, 13, 14, 15, 16
	ExomeNext-Rapid (Ambry)			
	Rapid PGxome (PreventionGenetics)			
	STAT Whole Exome Sequencing (PerkinElmer Genomics)			
Standard Genome Sequencing	Genomic Unity® Whole Genome Analysis - Proband (Variantyx Inc.)	0212U	F70-F79, F80-F89, Q00.0-Q99.9	1, 2, 6, 7, 8, 9, 13, 14, 15, 16
	Genomic Unity® Whole Genome Analysis - Comparator (Variantyx Inc.)	0213U		
	GenomeSeqDx (GeneDx)	81425, 81426, 81427		
	TruGenome Trio (Illumina)			

	Whole Genome Sequencing (PerkinElmer Genomics)			
	MNGenome (MNG Laboratories)			
	MatePair Targeted Rearrangements, Congenital (Mayo Medical Laboratories)	0012U		
	CNGnome (PerkinElmer Genomics)	0209U		
	Praxis Whole Genome Sequencing (Praxis Genomics LLC)	0265U		
	Praxis Combined Whole Genome Sequencing and Optical Genome Mapping (Praxis Genomics LLC)	0267U		
Rapid Genome Sequencing	Rapid Whole Genome Sequencing (Rady Children's Institute for Genomic Medicine)	0094U	F70-F79, F80-F89, Q00.0-Q99.9	1, 2, 6, 7, 8, 9, 13, 14, 15, 16
	Ultra-Rapid Whole Genome Sequencing (Rady Children's Institute for Genomic Medicine)	81425, 81426, 81427		
	STAT Whole Genome Sequencing (PerkinElmer Genomics)			
	MNGenome STAT (MNG)			
	Rapid Whole Genome - For NICU/PICU, (Fulgent Genetics)			

OTHER RELATED POLICIES

This policy document provides coverage criteria for exome and genome sequencing for the diagnosis of genetic disorders in patients with suspected genetic disorders and for population-based screening. Please refer to:

- ***Oncology: Molecular Analysis of Solid Tumors and Hematologic Malignancies*** for coverage criteria related to exome and genome sequencing of solid tumors and hematologic malignancies.

- ***Genetic Testing: Multisystem Inherited Disorders, Intellectual Disability, and Developmental Delay*** for coverage criteria related to diagnostic genetic testing performed after a child has been born.
- ***Genetic Testing: Prenatal and Preconception Carrier Screening*** for coverage criteria related to prenatal carrier screening, preimplantation genetic testing, or preconception carrier screening.
- ***Genetic Testing: Prenatal Diagnosis (via Amniocentesis, CVS, or PUBS) and Pregnancy Loss*** for coverage related to prenatal exome sequencing.
- ***Genetic Testing: General Approach to Genetic Testing*** for coverage criteria related to exome and genome sequencing that is not specifically discussed in this or another non-general policy.

COVERAGE CRITERIA

STANDARD EXOME SEQUENCING

I. Standard exome sequencing (81415, 81416, 81417, 0214U, 0215U), with trio testing when possible, is considered **medically necessary** when:

A. The member meets **ONE** of the following:

1. The member has a diagnosis of one or more congenital anomalies (CA) with onset prior to age 1 year, **OR**

2. The member has apparently nonsyndromic developmental delay or intellectual disability with onset prior to age 18 years, AND

B. The member has been evaluated by at least **ONE** of the following:

1. Board-Certified or Board-Eligible Medical Geneticist, **OR**
2. Certified Genetic Counselor, **OR**
3. Advanced practice practitioner (e.g. APRN or Physician's Assistant) in genetics, **AND**

C. Testing is predicted to have an impact on clinical decision-making or health outcomes through **ONE** of the following:

1. Guiding prognosis or appropriate follow-up care (i.e., treatment, surveillance for later-onset comorbidities, initiation of palliative care, withdrawal of care, etc.), **OR**

2. Avoidance of future testing for screening or diagnostic purposes, including invasive testing, if such testing could be avoided through the results of ES, **OR**

3. Guiding reproductive decisions (i.e., decisions to become pregnant, terminate a pregnancy, use assisted reproductive technologies, use pre-implantation genetic diagnosis, use donor sperm/egg, or undergo previously unplanned additional prenatal testing such as CVS or amniocentesis, etc), **OR**

4. Guiding family-focused clinical management (cascade genetic testing, referral to specialists, or changes in clinical management resulting from the diagnosis of a previously unknown disorder, etc), **AND**

D. Alternative etiologies have been excluded (e.g., environmental exposures, injury, and/or infection), **AND**

E. The member's clinical presentation does not fit a well-described syndrome for which specific testing (e.g. single-gene testing, chromosomal microarray analysis (CMA)) is available, or such testing has been performed and resulted as negative while suspicion remains high for a genetic cause of the member's symptoms, **AND**

F. A genetic etiology is considered the most likely explanation for the phenotype when no prior genetic testing has been carried out or despite previous genetic testing* (e.g., chromosomal microarray analysis and/or targeted single-gene testing), or previous genetic testing failed to yield a diagnosis and the member is faced with invasive procedures (e.g., muscle biopsy) as the next diagnostic step.

II. Repeat standard exome sequencing for the above indications may be considered **medically necessary** when:

A. Significant new symptoms develop in the member or the member's family history, **AND**

B. The member has been re-evaluated by a Board-Certified or Board-Eligible Medical Geneticist, a Certified Genetic Counselor, an advanced practice practitioner (e.g. APRN or Physician's Assistant) in genetics, who is not employed by a commercial genetic testing laboratory that recommends repeat exome sequencing, **AND**

C. There have been improvements in technology/chemistry (e.g., new methods for DNA capture and/or sequencing), bioinformatics advancements, or new information regarding the genetic etiology of a condition that could explain the patient's clinical features and would not have been able to be detected by the previous exome sequencing the patient underwent.

III. Repeat standard exome sequencing (81415, 81416, 0214U, 0215U) is considered **not medically necessary** for all other indications.

IV. Standard exome sequencing is considered **investigational** for all other indications, including screening asymptomatic/healthy individuals for genetic disorders.

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RAPID EXOME SEQUENCING

I. Rapid exome sequencing (81415, 81416, 81417) may be considered **medically necessary** when:

A. The member is an acutely-ill infant (≤4 months), **AND**

B. The patient and patient's family history have been evaluated by a Board Certified or Board-Eligible Medical Geneticist, or an Advanced Practice Nurse in Genetics (APGN), **AND**

C. The etiology of the infant's features is not known and a genetic etiology is considered a likely explanation for the phenotype, based on **EITHER** of the following:

1. Multiple congenital abnormalities affecting unrelated organ systems

2. **TWO** of the following criteria are met:

    a) Abnormality significantly affecting (at minimum) a single organ system

    b) Dysmorphic features

    c) Encephalopathy

    d) Symptoms of a complex neurodevelopmental disorder (e.g., dystonia, hemiplegia, spasticity/hypertonia, epilepsy, hypotonia)

    e) Family history strongly suggestive of a genetic etiology, including consanguinity

    f) Clinical or laboratory findings suggestive of an inborn error of metabolism, **AND**

D. Alternate etiologies have been considered and ruled out when possible (e.g., environmental exposure, injury, infection, isolated prematurity), **AND**

E. Clinical presentation does not fit a well-described syndrome for which rapid single-gene or targeted multi-gene panel testing is available, **AND**

F. A diagnosis cannot be made in a timely manner by standard clinical evaluation, excluding invasive procedures such as muscle biopsy, **AND**

G. There is a predicted impact on the health outcome, including impact on medical management during the hospitalization based on the results, **AND**

H. Pre- and post-test counseling by an appropriate provider, such as a Board-Certified Medical Geneticist, a Certified Genetic Counselor, or an Advanced Practice Nurse in Genetics, **AND**

I. The acutely-ill infant does **not** have any of the following diagnoses:

    1. Isolated Transient Neonatal Tachypnea
    2. Isolated unconjugated hyperbilirubinemia
    3. Isolated Hypoxic Ischemic Encephalopathy with clear precipitating event
    4. Isolated meconium aspiration

II. Rapid exome sequencing (81415, 81416, 81417) is considered **investigational** for all other indications.

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STANDARD GENOME SEQUENCING

I. Standard genome sequencing (81425, 81426, 81427, 0012U, 0209U, 0212U, 0213U, 0265U, 0267U) is considered **investigational**.

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RAPID GENOME SEQUENCING

I. Rapid genome sequencing or ultra rapid genome sequencing (81425, 81426, 81427, 0094U) is considered **investigational**.

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NOTES AND DEFINITIONS

Exome Sequencing (ES) is a genomic technique for sequencing all of the protein-coding regions of genes in the genome (also known as the exome).

Genome Sequencing (GS) is a genomic technique for sequencing the complete DNA sequence, which includes protein coding as well as non-coding DNA elements.

Trio Testing includes testing of the child and both parents and increases the chances of finding a definitive diagnosis, while reducing false-positive findings.

Comparator Exome Sequencing is used only for comparison with the proband (individual undergoing exome sequencing) and is used to inform the pathogenicity of variants. A comparator exome is typically one or both parents to the proband.

Congenital anomalies according to ACMG are multiple anomalies not specific to a well-delineated genetic syndrome. These anomalies are structural or functional abnormalities usually evident at birth, or shortly thereafter, and can be consequential to an individual's life expectancy, health status, physical or social functioning, and typically require medical intervention.

Developmental delay is a slow-to-meet or not reaching milestones in one or more of the areas of development (communication, motor, cognition, social-emotional, or, adaptive skills) in the expected way for a child's age

Intellectual disability (ID) is defined by the DSM V as:

a. Deficits in intellectual functions, such as reasoning, problem solving, planning, abstract thinking, judgment, academic learning, and learning from experience, confirmed by both clinical assessment and individualized, standardized intelligence testing.

b. Deficits in adaptive functioning that result in failure to meet developmental and sociocultural standards for personal independence and social responsibility. Without ongoing support, the adaptive deficits limit functioning in one or more activities of daily life, such as communication, social participation, and independent living, across multiple environments, such as home, school, work, and community.

c. Onset of intellectual and adaptive deficits during the developmental period.

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CLINICAL CONSIDERATIONS

Trio testing is preferred whenever possible. Testing of one available parent is a valid alternative if both are not immediately available and one or both parents can be done later if needed. While trio sequencing is preferred and recommended, an alternative method

referred to as “Patient Plus” by PreventionGenetics may be considered. “Patient Plus” involves sequencing and copy number variant (CNV) analysis of the patient, and then targeted testing for the key variants found in the patient is performed on parental specimens. This approach permits detection of de novo variants and phasing of variants in recessive genes to increase diagnostic yield from a singleton sample in situations where full trio sequencing may not be feasible or preferable.

Exome sequencing or genome sequencing can reveal incidental findings or secondary findings. These findings are defined as results that are not related to the indication for undergoing the sequencing, but may be of medical value or utility. Disclosure of these findings has been a topic of intense debate within the medical genetics community. In 2013, ACMG published recommendations for reporting secondary findings that included a list of conditions to be included. The list currently includes 59 genes that confer highly-penetrant and medically actionable conditions.

Pre-test and post-test genetic counseling that facilitates informed decision-making, the possibility to identify secondary finding with the option to ‘opt out’ of receiving these results, elicits patient preferences regarding secondary and/or incidental findings if possible, and formulates a plan for returning such results before testing occurs is strongly advised.

If a genetic diagnosis is not found by ES or GS, periodic reanalysis of the previously obtained genomic sequence is recommended. Reevaluation can occur on the variant-level or case-level. When appropriate, retesting may be considered (see above). Any variants identified and reported prior to the current ACMG variant classification standards should be reevaluated using the current ACMG standards.

Variant-level reanalysis should be considered in the following circumstances:

- Availability of a new community resource (e.g., gnomAD)
- Publication and/or adoption of a novel/updated methodology for variant assessment
- Publication of evidence supporting new gene–disease relationships and/or mechanisms of disease

Case-level reanalysis should be considered in the following circumstances:

- Significant changes in clinical and family history occur
- Significant improvements have been made to the bioinformatics handling of the data

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BACKGROUND AND RATIONALE

Practice Guidelines and Position Statements

American College of Medical Genetics and Genomics

The American College of Medical Genetics and Genomics (ACMG) (2012) published a position statement on clinical application of exome and genome testing. ACMG recommends considering ES/GS sequencing in the clinical diagnostic assessment of a phenotypically affected individual when:

- "The phenotype or family history data strongly implicate a genetic etiology, but the phenotype does not correspond with a specific disorder for which a genetic test is available."
- "A patient presents with a defined genetic disorder that demonstrates a high degree of genetic heterogeneity, making WES or WGS analysis of multiple genes simultaneously a more practical approach."
- "A patient presents with a likely genetic disorder, but specific genetic tests available for that phenotype have failed to arrive at a diagnosis."
- "A fetus with a likely genetic disorder in which specific genetic tests, including targeted sequencing tests, available for that phenotype have failed to arrive at a diagnosis."

In 2013, ACMG published the following recommendations for reporting of incidental findings in clinical exome and genome sequencing:

1. "Constitutional mutations found in the genes on the minimum list (Table 1) should be reported by the laboratory to the ordering clinician, regardless of the indication for which the clinical sequencing was ordered.
    - Additional genes may be analyzed for incidental variants, as deemed appropriate by the laboratory.
    - Incidental variants should be reported regardless of the age of the patient.
    - Incidental variants should be reported for any clinical sequencing conducted on a constitutional (but not tumor) tissue. This includes the normal sample of a tumor-normal sequenced dyad and unaffected members of a family trio."
2. "The Working Group recommends that laboratories seek and report only the types of variants within these genes that we have delineated (Table 1).

- For most genes, only variants that have been previously reported and are a recognized cause of the disorder or variants that are previously unreported but are of the type that is expected to cause the disorder, as defined by prior ACMG guidelines, 20 should be reported.
- For some genes, predicted loss-of-function variants are not relevant (e.g., COL3A1 and most hypertrophic cardiomyopathy genes).
- For some genes (e.g., APOB), laboratories should only report variants for certain associated conditions."

3. "It is the responsibility of the ordering clinician/team to provide comprehensive pre and posttest counseling to the patient.
    - Clinicians should be familiar with the basic attributes and limitations of clinical sequencing.
    - Clinicians should alert patients to the possibility that clinical sequencing may generate incidental findings that could require further evaluation.
    - Given the complexity of genomic information, the clinical geneticist should be consulted at the appropriate time, which may include ordering, interpreting, and communicating genomic testing. "
4. "These recommendations reflect limitations of current technology and are therefore focused on disorders that are caused by point mutations and small insertions and deletions, not those primarily caused by structural variants, repeat expansions, or copy-number variations."
5. "The Working Group recommends that the ACMG, together with content experts and other professional organizations, refine and update this list at least annually."

In 2016, ACMG updated its recommendations on reporting secondary findings in WGS and WES testing. ACMG determined that reporting some secondary findings would likely have medical benefit for the patients and families of patients undergoing clinical sequencing, recommending that, when a report is issued for clinically indicated exome and genome sequencing, a minimum list of conditions, genes, and variants should be routinely evaluated and reported to the ordering clinician. The 2016 update added 4 genes and removed 1 gene resulting in an updated secondary findings minimum list including 59 medically actionable genes recommended for return in clinical genomic sequencing.

In 2018, ACMG published points to consider encouraging engagement of older children and adolescents being considered for exome and/or genome sequencing, and that:

- "The purpose of the engagement process is to ensure that the mature older child is actively involved in conversation to understand the goals and implications of

genomic testing and potential findings and to consider its personal benefits and limitations while having the opportunity to express their feelings and opinions".
- "It is critical to engage the child as much as possible in this process, which includes the assent of the child whenever reasonable."
- "Children as young as 8 years of age should be part of an active engagement process to the extent that they are considered by the clinician and parent to be psychologically and cognitively capable."

In 2019, ACMG published points to consider around exome or genome reanalysis and retesting (discussed in Clinical Considerations). These considerations include points to consider for variant-level reanalysis, case-level reanalysis, and retesting for laboratories and clinicians.

In 2021, ACMG published ACMG SF v3.0, an updated list of genes included in the secondary findings, which added an additional 14 genes bringing the total up to 73 genes. ACMG also published a policy statement regarding updated recommendations for reporting of secondary findings in clinical exome and genome sequencing which clarified that ACMG supports the continued research and discussion around population screening for the genes included in the secondary findings list, however "ACMG has made it clear that the ACMG SF is not validated for general population screening".

Additionally, the following policy recommendations were made regarding consenting and reporting practices:

- "The SF list is intended as a "minimum list" of actionable secondary findings."
- "Providing the opportunity for an informed decision and opt out, if desired, at the time of consent should continue to be the standard for secondary findings."
- "The option to receive SFs should be offered regardless of the age of the patient. The best interest of the child should still be prioritized when disclosing risk for adult-onset conditions in minors."
- "The option to opt out of SFs should also be presented to the individual in the context of prenatal ES/GS."
- "The consent process should include discussion of the categories of reportable gene–phenotype pairs related to the ACMG SF list."
- "Thoughtful consideration of the context of a positive SF result during results disclosure, and when making related medical management recommendations, is necessary."
- "If laboratories report apparent somatic mosaicism, the consent process should address this."

- "Pre-test and post-test genetic counseling should be provided to any person receiving SF results in order to discuss the types of possible results, limitations of testing, and medical implications of any results."

In 2021, The American College of Medical Genetics and Genomics (ACMG) published an evidence-based clinical practice guideline on exome and genome sequencing for pediatric patients with congenital anomalies or intellectual disability. ACMG recommends using exome or genome sequencing be used as a first or second tier test for patients diagnosed with one or more congenital anomalies before the age of 1, or with intellectual disability/developmental delay before the age of 18. In previous guidelines, ACMG has recommended the use of such testing for clinical management of the proband. In this 2021 guideline, ACMG recommends exome or genome sequencing for active and long-term clinical management of the program, as well as for implications on family-focused and reproductive outcomes.

National Society for Genetic Counselors

The National Society for Genetic Counselors (NSGC) released a position statement (2013, updated 2020) stating the following in regard to secondary and incidental findings in genetic testing:

> "The National Society of Genetic Counselors strongly advises pre-test counseling that facilitates informed decision-making, elicits patient preferences regarding secondary and/or incidental findings if possible, and formulates a plan for returning such results before testing occurs.
>
> Germline and somatic genetic testing, in both clinical and research contexts, may identify secondary findings and incidental findings as a part of the test performed. Secondary findings are purposely analyzed as part of the test, but unrelated to the primary testing indication. Incidental findings are detected unexpectedly during the analysis, and also unrelated to the primary testing indication. Both of these types of variants may be disclosed as a part of the return-of-results process.
>
> The pre-test counseling process should establish clear expectations for what categories of results will and will not be returned. Healthcare practitioners conducting the informed consent and return-of-results processes for broad genomic testing and screening should ensure that their patients have access to practitioners with genetic expertise, such as genetic counselors."

UpToDate

Intellectual disability in children: Evaluation for a cause

"Whole exome sequencing — WES should be considered for patients with moderate to severe ID in whom other standard tests (including CMA) have failed to identify the cause. The diagnostic yield of WES in this setting is approximately 16 to 33 percent. The diagnostic yield is likely lower in patients with mild ID without additional findings and the role of WES testing in this population is not defined. WES testing should be performed with consultation of a clinical geneticist and should include appropriate pretest counseling to discuss the risk of incidental findings unrelated to the child's ID that may be medically actionable (eg, BRCA1 or BRCA2 mutation). Incidental findings can be minimized if a focused analysis is conducted. Due to the falling costs of sequencing and its high diagnostic yield, WES is rapidly becoming a clinical tool for the evaluation of ID, especially at specialty centers. Adoption of WES testing into the diagnostic process will depend on its cost, availability, access to expert interpretation, and the allocation of resources within each health care setting."

Kingsmore SF, Cakici JA, Clark MM et al.

This report is from the NSIGHT2 study, a prospective, randomized, controlled, blinded trial (RCT) in acutely ill infants, primarily from the NICU, PICU, and CVICU at Rady Children's Hospital, San Diego (RCHSD) to compare the effectiveness and outcomes between rWGS and rWES, with analysis as singleton probands and familial trios. The inclusion criteria for the 1,248 ill infants defined the maximum age as four months.

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