CURATIVE HEALTH PLAN

Medical Necessity & Utilization Management Policy

Whole Genome Sequencing for Diagnosis of Constitutional (Germline) Disorders

CPT 81425 and 81426 (with 81427 cross-referenced)

Policy Number	CHP-UM-LAB-WGS-001
Version	1.0
Policy Type	Medical Necessity / Laboratory & Genetic Testing Utilization Management
Lines of Business	Large Group Commercial PPO and EPO
Funding Types	Fully insured, level-funded, and ASO / self-funded (ERISA)
Jurisdictions	Texas, Florida, Georgia, Indiana, District of Columbia, Maryland (members nationwide)
Policy Owner	Chief Medical Officer / Clinical Services — Utilization Management
Effective Date	January 1, 2026
Last Reviewed	June 2026
Review Cycle	Annual, or upon material change in evidence, coding, or applicable law
Determination Authority	Adverse medical-necessity determinations require review by a licensed physician of appropriate specialty (clinical / medical genetics or relevant pediatric subspecialty). Automated systems may approve but may never deny.

This document is a coverage-administration and utilization-management policy. It is not medical advice and does not substitute for the independent clinical judgment of the treating provider. Coverage is always subject to the terms, limitations, and exclusions of the member's benefit plan document, applicable state and federal law, and eligibility at the time of service. Where a conflict exists, the controlling order of precedence in Section 2.4 applies.

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1. Purpose

This policy establishes the medical-necessity criteria, documentation requirements, coverage limitations, and coding and reimbursement conventions that Curative Health Plan (“CHP” or “the Plan”) applies when adjudicating requests for whole genome sequencing (WGS) of a proband (CPT 81425) and any comparator genome(s) (CPT 81426) performed to diagnose an unexplained constitutional (germline) disorder or syndrome. Re-evaluation of a previously obtained genome (CPT 81427) is addressed by cross-reference in Section 8.

The policy is anchored exclusively to publicly available sources, including the American College of Medical Genetics and Genomics (ACMG) evidence-based clinical guideline and policy statements, American Medical Association (AMA) CPT descriptors, professional-society guidance from ACOG/SMFM and the ISPD, and publicly published payer and state-agency clinical criteria. It does not rely on any proprietary criteria set.

2. Scope

2.1 Lines of business and products

This policy applies to large group Commercial Preferred Provider Organization (PPO) and Exclusive Provider Organization (EPO) products administered by CHP.

2.2 Funding types

This policy applies across all funding arrangements administered by the Plan:

- **Fully insured** group plans, which are subject to the insurance laws and benefit mandates of the state in which the group policy is issued;
- **Level-funded** arrangements, which are generally treated as subject to applicable state insurance requirements for the stop-loss/insured component to the extent provided by law; and
- **ASO / self-funded (ERISA)** plans, which are governed by the Employee Retirement Income Security Act and are generally exempt from state benefit-mandate laws. For these plans, the plan sponsor's benefit plan document controls; a sponsor may voluntarily elect to adopt state-mandate-equivalent coverage.

2.3 Jurisdictions

This policy is written to operate uniformly across Texas, Florida, Georgia, Indiana, the District of Columbia, and Maryland, and applies to members residing in any state. Jurisdiction-specific regulatory requirements are consolidated in the State Regulatory Annex (Section 15). Consistent with the Plan's enterprise policy framework, CHP applies a most-restrictive-state superset: where states differ, the most member-protective standard (for example, the most generous coverage trigger, the shortest utilization-review turnaround, or the broadest appeal right) is applied uniformly, except where a benefit-mandate is by its terms inapplicable to a given funding type.

2.4 Order of precedence

Where provisions conflict, the following order of precedence governs:

1. Applicable federal law (including ERISA and the Affordable Care Act) and applicable state law/benefit mandates to the extent not preempted, as determined by funding type;

2. The member's benefit plan document, certificate of coverage, or summary plan description, including its definitions, limitations, and exclusions;
3. Applicable state utilization-review and external-review requirements;
4. This medical-necessity policy and any incorporated clinical criteria; and
5. CHP coding, billing, and reimbursement policies.

3. Definitions

Term	Definition
Whole genome sequencing (WGS / GS)	Use of DNA-enrichment methods and massively parallel (next-generation) sequencing to analyze coding and non-coding regions across the human genome to identify disease-associated variants, including single-nucleotide variants, small insertions/deletions, and certain copy-number and structural variants.
Constitutional / germline testing	Analysis of an individual's inherited (constitutional) DNA to identify variants underlying a heritable disorder or syndrome. CPT 81425/81426 describe constitutional genome analysis. This is distinct from somatic / tumor (“biomarker”) testing, which analyzes acquired alterations in diseased tissue to guide treatment.
Proband	The affected individual who is the index patient for whom genome analysis is first performed (CPT 81425).
Comparator genome / trio	Genome analysis of a biological relative (most often each parent, and/or a sibling) performed to aid interpretation of the proband's variants (CPT 81426, reported per comparator). A “trio” is the proband plus both biological parents.
Chromosomal microarray analysis (CMA)	A first-tier cytogenomic test detecting copy-number variants; reported with codes such as 81228/81229 and not part of CPT 81425.
Multigene (targeted) panel	Sequencing limited to a defined, clinically relevant set of genes for a suspected condition.
Rapid WGS (rWGS)	Expedited genome sequencing performed for an acutely ill inpatient (typically a neonate or infant) where a rapid molecular diagnosis is expected to change acute management.
Secondary / incidental findings	Pathogenic or likely-pathogenic variants identified in genes unrelated to the indication for testing, reportable in accordance with the current ACMG Secondary Findings (SF) list.
Variant classification	Standard five-tier classification: pathogenic (P), likely pathogenic (LP), variant of uncertain significance (VUS), likely benign, and benign.
Qualified laboratory	A laboratory that is CLIA-certified for high-complexity testing and is a participating or otherwise approved provider of the service under CHP policy.

4. Codes Addressed

The CPT descriptors below are reproduced for identification only and remain the property of the American Medical Association.

CPT	Descriptor	Role in this policy
81425	Genome (e.g., unexplained constitutional or heritable disorder or syndrome); sequence analysis	Proband WGS — primary code (Sec. 6)
81426	Genome (e.g., unexplained constitutional or heritable disorder or syndrome); sequence analysis, each comparator genome (e.g., parents, siblings) (List separately in addition to code for primary procedure)	Comparator / trio add-on (Sec. 7)
81427	Genome (e.g., unexplained constitutional or heritable disorder or syndrome); re-evaluation of previously obtained genome sequence (e.g., updated knowledge or unrelated condition/syndrome)	Reanalysis — cross-referenced (Sec. 8)

Codes not addressed by this policy. Whole exome sequencing (81415/81416/81417), chromosomal microarray (81228/81229), and condition-specific genomic panels are governed by their own criteria. Proprietary Laboratory Analyses (PLA) codes describing branded whole-genome assays are adjudicated under the medical-necessity criteria of this policy by analogy to the corresponding CPT family.

5. Clinical Background and Evidence Basis

Genome sequencing analyzes both coding (exonic) and non-coding (intronic) regions and can detect variant classes that targeted approaches may miss, including certain structural and copy-number variants. Its principal diagnostic role is in individuals with a complex or heterogeneous phenotype suggestive of a rare genetic condition that cannot be resolved by standard clinical work-up or by a single targeted test.

In 2021 the ACMG published its first evidence-based clinical guideline addressing exome and genome sequencing (ES/GS) in pediatric patients. Applying a GRADE evidence-to-decision framework, the guideline made a strong recommendation that ES/GS be considered a first- or second-tier test for patients with one or more congenital anomalies with onset before one year of age, or with developmental delay or intellectual disability with onset before 18 years of age, finding higher diagnostic yield, favorable effects on clinical and reproductive management, relatively few harms, and potential cost-effectiveness when ordered early in the diagnostic evaluation. The guideline reaffirms that patients whose presentation strongly suggests a specific diagnosis should undergo targeted testing first.

Consistent with the ACMG points-to-consider, genome or exome sequencing is also appropriate when phenotype or family-history data strongly implicate a genetic etiology but the presentation does not match a specific disorder for which a single-gene clinical test is available, or when the differential is broad enough that multiple separate genetic tests would otherwise be required.

Professional-society guidance does not support routine prenatal genome sequencing outside of specific indications and remains cautious regarding its clinical use (ACOG/SMFM; ISPD). These limitations are reflected in Section 10.

6. Medical Necessity Criteria — Proband Whole Genome Sequencing (CPT 81425)

Proband WGS (CPT 81425) is considered medically necessary when ALL of the gatekeeping requirements in 6.1 are met AND at least ONE qualifying clinical indication in 6.2 is present.

6.1 Gatekeeping requirements (ALL must be met)

- The member has not previously had whole exome sequencing or whole genome sequencing for the same indication (reanalysis is addressed in Section 8);
- The member has had an appropriate clinical genetic evaluation and family-history assessment, documented in a clinical summary letter that includes: (a) the differential diagnoses considered; (b) the testing algorithm and prior tests performed with results; (c) the basis for concluding a genetic etiology is the most likely explanation; (d) the rationale that genome sequencing is the most appropriate next test; and (e) the predicted impact on the member's plan of care;
- A genetic etiology is considered the most likely explanation for the phenotype;
- Alternative non-genetic etiologies have been considered and reasonably excluded (e.g., environmental exposure, injury, infection, isolated prematurity);
- The clinical presentation does not fit a well-described syndrome for which first-tier targeted testing (single-gene analysis or chromosomal microarray) is available and appropriate;
- Either multiple targeted gene panels would otherwise be required based on the presentation, or no adequate single-gene/panel test exists for the suspected condition;
- The result is expected to have a direct impact on health outcomes — for example, initiation or selection of specific treatment, avoidance of contraindicated treatment, surveillance for later-onset comorbidities, reproductive/recurrence-risk counseling, initiation of palliative care, or ending an unproductive diagnostic odyssey;
- A diagnosis cannot be established by standard clinical work-up short of invasive procedures (e.g., muscle biopsy);
- Pre-test genetic counseling and documented informed consent have been provided in accordance with Section 11; and
- The rendering laboratory is a qualified laboratory under Section 14.5.

6.2 Qualifying clinical indications (at least ONE)

A genetic etiology is considered the most likely explanation based on one or more of the following, ordinarily in a member under 21 years of age (see 6.3 regarding adults):

- Unexplained epileptic encephalopathy with onset before three years of age, where an epilepsy multigene panel has not already been performed or is not adequate to the differential;
- Global developmental delay — significant delay in at least two major developmental domains (gross/fine motor; speech/language; cognition; social/personal; activities of daily living) in a child under five years — following formal assessment by a developmental pediatrician or neurologist;
- Moderate, severe, or profound intellectual disability (DSM-5 criteria, diagnosed by 18 years of age) following formal assessment by a developmental pediatrician or neurologist;

- Multiple congenital anomalies, defined as either two or more major anomalies affecting different organ systems, or one major plus two or more minor anomalies affecting different organ systems; OR
- TWO or more of the following are present: a major abnormality affecting at least one organ system; a formal diagnosis of autism; symptoms of a complex neurodevelopmental disorder (e.g., epilepsy, self-injurious behavior, reversed sleep-wake cycles, dystonia, ataxia, alternating hemiplegia, neuromuscular disorder); a severe neuropsychiatric condition (e.g., schizophrenia, bipolar disorder, Tourette syndrome); a period of unexplained developmental regression; or laboratory findings suggestive of an inborn error of metabolism.

6.3 Sequencing modality (genome vs. exome) and adult applicability

Where both exome and genome sequencing are clinically reasonable, the modality should be guided by clinical judgment and shared decision-making. Genome sequencing is appropriate as a first-tier test when the differential is broad, and as a second-tier test when prior CMA and/or exome sequencing were non-diagnostic and intronic, regulatory, or structural variants not assessable by exome are clinically suspected. For an adult member, WGS may be medically necessary when the gatekeeping requirements in 6.1 are met and the phenotype or family history strongly implicates a constitutional genetic etiology for which no adequate targeted test exists; pediatric age thresholds in 6.2 are applied as clinical guideposts rather than absolute bars in the adult setting.

7. Medical Necessity Criteria — Comparator Genome / Trio (CPT 81426)

Comparator genome analysis (CPT 81426) is considered medically necessary when the proband meets the criteria for WGS in Section 6 and comparator sequencing is performed concurrently with, or following, the proband's genome analysis to aid variant interpretation.

- Trio analysis (proband plus both biological parents) is preferred where available, as it materially improves interpretation (e.g., de novo determination, phasing);
- A maximum of two units of 81426 are eligible (typically the two parents); a sibling or other relative may be substituted where clinically more informative;
- Comparator analysis is not separately covered where the proband does not meet, or has not met, the criteria in Section 6.

8. Re-evaluation of a Previously Obtained Genome (CPT 81427) — Cross-Reference

CPT 81427 is not the primary subject of this policy but is addressed here for continuity. Re-analysis of a previously obtained, non-diagnostic genome is considered medically necessary when at least one of the following applies:

- New or additional symptoms have broadened the phenotype assessed at the time of the original analysis; or
- The birth or diagnosis of a similarly affected first-degree relative has expanded the clinical picture.

CPT 81427 is not payable as a reflex from a targeted analysis to a full genome, and is reported on a separate date of service from the original analysis. Detailed reanalysis frequency and documentation rules are maintained in the Plan's companion genetic-testing reanalysis criteria.

9. Rapid Whole Genome Sequencing for Acutely Ill Inpatient Infants

Rapid WGS (rWGS) is considered medically necessary for an acutely ill infant 12 months of age or younger who is an inpatient (e.g., NICU/PICU) at the time of testing when ALL of the following are met:

- No prior exome or genome sequencing has been performed;
- Appropriate genetic and family-history evaluation has occurred;
- The etiology of the infant's presentation is unknown and a genetic etiology is a likely explanation, based on EITHER multiple congenital anomalies affecting unrelated organ systems, OR two of the following: an abnormality affecting at least one organ system; encephalopathy; symptoms of a complex neurodevelopmental disorder (e.g., dystonia, hemiplegia, spasticity, epilepsy, hypotonia); a family history strongly suggestive of a genetic etiology, including consanguinity; laboratory findings suggestive of an inborn error of metabolism; or an abnormal response to standard therapy;
- Alternative etiologies have been considered and reasonably excluded (e.g., exposure, injury, infection, isolated prematurity);
- The presentation does not fit a well-described syndrome for which rapid single-gene or targeted panel testing is available;
- A diagnosis cannot be made in a timely manner by standard evaluation short of invasive procedures; and
- A molecular result is expected to have an immediate impact on acute medical management.

rWGS is not considered medically necessary where the infant's presentation is explained by an isolated, self-limited condition with a clear precipitating cause — for example, isolated transient neonatal tachypnea, isolated unconjugated hyperbilirubinemia, isolated hypoxic-ischemic encephalopathy with a clear precipitating event, isolated meconium aspiration, isolated prematurity, or infection/sepsis with a normal response to therapy.

10. Limitations and Exclusions

The following are considered experimental, investigational, unproven, or otherwise not a covered benefit under this policy, subject to any contrary requirement of the benefit plan document or applicable law as resolved under Section 2.4:

- Prenatal diagnosis by genome sequencing, which is not supported for routine use by current professional-society guidance (ACOG/SMFM; ISPD);
- Genome sequencing used to screen asymptomatic or pre-symptomatic individuals (no state biomarker mandate analyzed in Section 15 requires coverage of screening);
- Genome sequencing combined with optical genome mapping as a single bundled assay, which lacks sufficient evidence of added clinical utility;

- Reporting CPT 81425 for a targeted (non-whole-genome) analysis; the appropriate panel, Tier 1/Tier 2, or unlisted molecular code must be used instead;
- Repeat CPT 81425 beyond once per lifetime, except as re-analysis properly reported under CPT 81427 (Section 8);
- Testing performed by a laboratory that is not a qualified laboratory under Section 14.5, including direct-to-consumer testing; and
- Genome sequencing for a condition for which an adequate, clinically available targeted test should be performed first.

11. Genetic Counseling and Informed Consent

Consistent with ACMG points-to-consider, pre-test counseling by a medical geneticist or affiliated genetic counselor, with documented written informed consent, is expected before genome/exome sequencing. Counseling should address the expected outcomes of testing, the possibility and types of incidental/secondary findings, which results will and will not be returned, policies on databasing and the member's ability to opt out, and policies on re-contact as variant knowledge evolves. Testing of a minor is appropriate for phenotype-driven diagnostic purposes or where early monitoring or intervention is available and effective.

12. Secondary and Incidental Findings

Reporting of secondary findings is governed by the current ACMG Secondary Findings list (SF v3.x). Only pathogenic and likely-pathogenic variants on the applicable list are reported as secondary findings; variants of uncertain significance, likely-benign, and benign variants are not reported as secondary findings. The member's documented election to receive or decline secondary findings is honored as part of the informed-consent process. The performance of secondary-findings analysis does not, by itself, create a separately reimbursable service under this policy.

13. Prior Authorization and Documentation Requirements

Prior authorization is required for CPT 81425, 81426, and 81427 across all lines of business, subject to the member's benefit plan. Requests must include the clinical summary letter described in Section 6.1 and the following:

- Member demographics, ordering and rendering provider, and the rendering laboratory with CLIA certification;
- The specific CPT/PLA code(s) and units requested (including the number of comparator genomes);
- Relevant phenotype documentation, prior genetic test results (CMA, panels, single-gene, prior ES/GS), and the differential diagnosis;
- Documentation that pre-test counseling and informed consent occurred; and
- For rWGS, documentation of inpatient status and the expected immediate impact on acute management.

Utilization-review determinations are made within the timeframes required by the applicable jurisdiction (Section 15). When information is insufficient, the Plan requests the specific missing items before any adverse determination is made.

14. Coding, Billing, and Reimbursement

14.1 Proband (81425)

CPT 81425 is reported once for the proband and only when the entire genome is analyzed rather than a targeted gene set. CPT 81425 is reimbursable once per lifetime; subsequent constitutional re-evaluation is reported under 81427.

14.2 Comparator (81426)

CPT 81426 is an add-on to 81425, reported per comparator genome, with a maximum of two units eligible for reimbursement. A trio (proband plus both parents) is preferred; another relative may be substituted where more informative.

14.3 Reanalysis (81427)

CPT 81427 is reported on a separate date of service and is not payable as a reflex from a targeted analysis to a full genome.

14.4 Bundling and unlisted codes

Genome deletion/duplication analysis (e.g., 81228/81229) is not separately reimbursable when reported with genome sequencing for the same specimen and episode. Targeted analyses reported in error under 81425 are not reimbursable as billed and must be resubmitted with the correct code. A single comprehensive genome assay is expected per diagnostic episode.

14.5 Qualified laboratory

Reimbursement requires that the rendering laboratory hold CLIA high-complexity certification and be a participating or otherwise Plan-approved provider of the service. Claims submitted without the data elements necessary for adjudication (e.g., diagnosis code, place of service, units, laboratory identifiers) may be returned and are subject to post-service medical-record review.

15. State Regulatory Annex

15.1 Governing principles

There is no federal or state benefit mandate that specifically requires coverage of constitutional whole genome sequencing as such. The most relevant body of state law is the recent wave of biomarker-testing coverage mandates. Three principles govern how those mandates interact with this policy:

6. **Funding-type applicability.** State biomarker mandates apply to state-regulated, fully insured (and, to the extent provided by law, level-funded) plans. They do not apply to ASO / self-funded ERISA plans, although a plan sponsor may elect to adopt equivalent coverage.
7. **Evidence-pegged coverage.** These mandates generally tie required coverage to FDA labeling, Medicare national/local coverage determinations, and nationally recognized clinical practice guidelines, and they uniformly exclude screening. Because the medical-necessity criteria in Sections 6–10 are anchored to ACMG and other recognized guidance and exclude screening, a diagnostic WGS request that satisfies this policy also satisfies the evidentiary standard these mandates impose.
8. **Germline vs. somatic scope.** Biomarker mandates are oriented chiefly toward somatic/tumor (precision-oncology) testing that guides treatment, whereas CPT 81425/81426 describe constitutional (germline) analysis. Statutory “biomarker” definitions are nonetheless broad (a biological molecule in blood, fluids, or tissue indicating a process, condition, or disease). Where a fully insured member in a mandate state presents a non-screening, diagnostic indication that meets this policy's criteria, CHP applies the mandate's evidence standard and covers accordingly; screening WGS remains excluded everywhere.

15.2 Biomarker-mandate applicability matrix

The following summarizes the Plan's working analysis. It is an operational summary and not a legal opinion; statutory citations and effective dates are to be confirmed by Compliance/Legal (Section 15.4).

State	Biomarker coverage mandate (working analysis)	Reaches commercial fully insured?	Effect on WGS under this policy
Texas	Biomarker coverage law enacted 2023 (SB 989, 88th Leg.). Evidence-pegged; screening excluded.	Yes — state-regulated fully insured and level-funded; not ERISA self-funded.	Diagnostic WGS meeting Sec. 6–10 is covered; apply mandate evidence standard. Screening excluded.
Florida	HB 885 (2024) requires biomarker coverage for Florida Medicaid and the state-employee (State Group Insurance) program only; screening excluded.	No — the mandate does not reach private commercial group plans.	No commercial biomarker mandate applies; WGS governed by Sec. 6–10 and the benefit plan.
Georgia	Biomarker coverage law enacted 2023. Evidence-pegged; screening excluded.	Yes — state-regulated fully insured and level-funded; not ERISA self-funded.	Diagnostic WGS meeting Sec. 6–10 is covered; apply mandate evidence standard. Screening excluded.

State	Biomarker coverage mandate (working analysis)	Reaches commercial fully insured?	Effect on WGS under this policy
Indiana	SEA 273 (2024), Ind. Code 27-8-14.3, effective July 1, 2024. Coverage for diagnosis, treatment, management, and monitoring; references nationally recognized clinical practice guidelines; screening excluded.	Yes — applies to commercial accident-and-sickness policies; not ERISA self-funded.	Diagnostic WGS meeting Sec. 6–10 is covered; apply mandate evidence standard. Screening excluded.
District of Columbia	No biomarker-specific coverage mandate identified as of the effective date.	N/A — no specific mandate.	WGS governed by Sec. 6–10, the benefit plan, and DC utilization-review/external-review law.
Maryland	Biomarker coverage law enacted 2023 (effective 2024); evidence-pegged; screening excluded. Maryland Medicaid has separately published WGS clinical criteria.	Yes — state-regulated fully insured and level-funded; not ERISA self-funded.	Diagnostic WGS meeting Sec. 6–10 is covered; apply mandate evidence standard. Screening excluded.

Superset operating rule. To preserve a single uniform clinical standard, CHP applies the most member-protective coverage trigger across the mandate states (TX, GA, IN, MD) to all fully insured and level-funded business in those states, and offers the same clinical criteria to Florida and DC fully insured business and to self-funded plans as the default, recognizing that the latter are not legally bound by the mandates.

15.3 Utilization review, adverse determinations, and external review

Each jurisdiction's utilization-review timeframes, notice content, peer-to-peer, internal-appeal, and independent external-review requirements apply to determinations under this policy. Consistent with the superset principle, where the six jurisdictions differ, CHP applies the shortest decision timeframe and the broadest appeal/external-review right uniformly. For ERISA self-funded plans, ERISA claims-procedure and federal external-review requirements apply in place of state external review unless the plan sponsor elects otherwise.

15.4 Legal verification

Flagged for Compliance/Legal: the exact statutory citations, bill numbers, effective dates, and the precise reach of each biomarker mandate to germline (versus somatic) testing and to level-funded arrangements should be confirmed by Compliance counsel before this annex is relied upon for adverse determinations. This section is a coverage-operations summary, not legal advice.

16. Human Review and Governance

Automated and algorithmic tools may be used to identify requests that clearly meet criteria and to issue approvals; they may never issue an adverse medical-necessity determination. Any denial, partial denial, or modification on medical-necessity grounds requires review and sign-off by a licensed physician of appropriate specialty (clinical/medical genetics or a relevant pediatric or neurology subspecialty). The ordering provider is offered a peer-to-peer discussion prior to or following an adverse determination as required by applicable law. Determinations are documented in

an event-sourced audit record, and the clinical criteria in this policy are maintained as a versioned, governed configuration asset reviewed at least annually by the Plan's clinical governance committee.

17. References (Public Sources)

9. Manickam K, McClain MR, Demmer LA, et al. Exome and genome sequencing for pediatric patients with congenital anomalies or intellectual disability: an evidence-based clinical guideline of the ACMG. Genet Med. 2021;23(11):2029-2037.
10. ACMG Board of Directors. Points to consider for informed consent for genome/exome sequencing. Genet Med. 2013;15(9):748-749.
11. Miller DT, Lee K, Abul-Husn NS, et al. ACMG SF v3.2 list for reporting of secondary findings in clinical exome and genome sequencing. Genet Med. 2023;25(8):100866.
12. Rehm HL, Bale SJ, Bayrak-Toydemir P, et al. ACMG clinical laboratory standards for next-generation sequencing. Genet Med. 2013;15(9):733-747.
13. American College of Obstetricians and Gynecologists / Society for Maternal-Fetal Medicine. Committee guidance on microarrays and next-generation sequencing in obstetrics and gynecology (2016; reaffirmed 2023).
14. International Society for Prenatal Diagnosis. Updated position statement on the use of genome-wide sequencing for prenatal diagnosis. Prenat Diagn. 2022;42(6):796-803.
15. American Medical Association. Current Procedural Terminology (CPT) descriptors for 81425, 81426, 81427.
16. Maryland Department of Health. Whole Genome Sequencing clinical criteria (Medicaid), 2021/2022.
17. Indiana Code 27-8-14.3, Coverage for Biomarker Testing (SEA 273, 2024); Indiana Health Coverage Programs bulletins on biomarker testing.
18. Florida CS/CS/HB 885 (2024), Coverage for Biomarker Testing; s. 409.906, Florida Statutes.
19. Texas SB 989 (88th Legislature, 2023), biomarker testing coverage.
20. Published commercial payer and lab-management clinical criteria for genome sequencing (e.g., UnitedHealthcare commercial medical policy; EviCore/Carelon lab-management guidelines), used for criteria modeling only.

18. Document History

Version	Date	Summary of change
1.0	Jun 2026	Initial issuance. Medical-necessity criteria for CPT 81425/81426 (with 81427 cross-reference), rWGS provisions, exclusions, counseling and secondary-findings requirements, coding/reimbursement conventions, and six-jurisdiction regulatory annex (TX/FL/GA/IN/DC/MD).

Disclaimer. *This policy supports consistent coverage administration and does not direct the practice of medicine. It does not guarantee member eligibility or payment, which are determined at adjudication under the applicable benefit plan and law. Nothing herein is legal advice.*