SAMPLE 001 / EDITION 1.2 / 29 OCTOBER 2026

Sample genome report

22 fictional findings. Six workspaces. Evidence and a specific next question for every record.

Every assigned result, quality metric and review event is invented. No person was sequenced. Sources support the explanations, not the sample results or Whole DNA's clinical performance.

SUGGESTED READING ORDER - NOT A MEDICAL PRIORITY SCORE

M01

CYP2C19 *17/*17

If a PPI is relevant, discuss the confirmed result with a prescriber.

H02

A region could not be resolved

Ask whether the no-call affects the original reason for testing.

H01

A variant remains uncertain

Read why the VUS cannot direct a care change by itself.

E01

Caffeine sensitivity signal

Compare the assigned tendency with actual timing, symptoms and sleep.

REPORT INDEX

How to use this report

Read the finding first, inspect the supporting evidence and limitations, then decide which question belongs in a discussion or a current measurement.

Everyday life

E01-E06 / Food, caffeine, sleep, training and measurement limits.

Health follow-up

H01-H04 / Uncertain findings, no-calls, screening scope and withheld scores.

Medicine passport

M01-M02 / A specific gene-drug relationship and the missing clinical context.

Ancestry atlas

A01-A03 / A fictional regional mix, lineage methods and historical limits.

Family planning

F01-F03 / A carrier example, inheritance model and residual risk.

Genome and files

G01-G04 / Illustrative quality, file formats and interpretation changes.

> READING BOUNDARIES
>
> Some records are unresolved or deliberately unassigned. Those are report outputs, not low-risk results. The HTML adds search, evidence views and interactive models; this PDF preserves the complete source records.

EVERYDAY LIFE / FICTIONAL FINDINGS

Caffeine and lactose

Two assigned trait examples, interpreted alongside symptoms and actual experience.

E01 / FOOD / CAFFEINE

Higher sensitivity signal

The fictional profile is assigned a higher caffeine-sensitivity signal. Timing, sleep, symptoms and medicines still matter more than a simple “fast” or “slow” label.

Evidence: Exploratory association

Limit: This is an invented trait assignment, not a validated score or a personal caffeine limit. The FDA source supports general sensitivity context; it does not validate this sample signal.

Your next question
Would moving my last caffeinated drink earlier change my sleep?

FDA · Caffeine guidance

E02 / FOOD / LACTOSE

Persistence-associated pattern

The sample is assigned a lactase-persistence-associated pattern. This concerns one pathway of lactose digestion; it does not diagnose tolerance, allergy or the cause of digestive symptoms.

Evidence: Established association

Limit: Variant interpretation depends on the particular marker and population. This sample provides no genotype or diagnostic result. Secondary lactose intolerance can have other causes.

Your next question
If I have symptoms after dairy, what evaluation would be appropriate?

MedlinePlus Genetics · Lactose intolerance

EVERYDAY LIFE / FICTIONAL FINDINGS

Sleep and vitamin D

A sleep preference is different from a measured nutrient status. The report treats those questions separately.

E03 / SLEEP / DAILY RHYTHM

Later preference signal

The demonstration profile leans toward a later sleep preference. It is a prompt to look at real sleep timing, work demands and daylight exposure.

Evidence: Exploratory association

Limit: No polygenic model was run. This assigned tendency does not determine a bedtime, required sleep duration or a diagnosis. The source supports healthy routines rather than this synthetic prediction.

Your next question
What does a two-week sleep record say about the schedule that works for me?

NHLBI · Healthy sleep habits

E04 / FOOD / MICRONUTRIENTS

Vitamin D status not determined

DNA does not provide a current vitamin D blood level. This sample deliberately leaves nutrient status unassigned rather than turning a genetic tendency into a supplement instruction.

Evidence: Clinical measurement needed

Limit: A blood test measures vitamin D status. Whether testing or supplementation is appropriate depends on clinical context; no dose or laboratory result is supplied here.

Your next question
Is there a clinical reason to assess my vitamin D status?

MedlinePlus · Vitamin D test

EVERYDAY LIFE / FICTIONAL FINDINGS

Training and meal timing

Use actual performance, recovery, clinical context and preferences. No sport or meal schedule is prescribed.

E05 / MOVEMENT / TRAINING

Mixed research markers

The fictional profile contains a mixed set of exercise-trait signals. It receives no “best sport,” injury forecast or training prescription. Current capacity and response remain the useful measures.

Evidence: Limited practical utility

Limit: Sports-genetics associations are not a reliable basis for talent selection or individualized training. This sample uses no real performance model or genetic markers.

Your next question
What do my training history, recovery and goals suggest I should change?

Australian Institute of Sport · Genetics

E06 / FOOD / MEAL TIMING

No genetic eating window assigned

The sample does not turn a chronotype tendency into an exact eating window. Meal timing needs to fit health, medication requirements, activity and daily life.

Evidence: Insufficient for prescription

Limit: No validated meal-timing algorithm is applied. Discuss meaningful dietary changes with a qualified professional; this is not a fasting or nutrition prescription.

Your next question
Would a dietitian see a reason to change my current meal pattern?

FDA · Consumer genetic tests

HEALTH FOLLOW-UP / FICTIONAL FINDINGS

Uncertain finding and no-call

A variant with unknown significance and a region with insufficient data need different explanations.

H01 / INTERPRETATION / SIM-V204

Variant of uncertain significance

Synthetic finding SIM-V204 remains unresolved. Its relevance to health is unknown. It is shown because uncertainty deserves a visible place in a report.

Evidence: Uncertain significance

Limit: SIM-V204 is an invented identifier, not a real variant. A VUS cannot establish a diagnosis. It should not drive a treatment or screening change on its own.

Your next question
Would my symptoms or family history justify a clinical genetics review independently of this VUS?

NHGRI · Variant of uncertain significance

H02 / TECHNICAL / SIM-R12

No-call: insufficient information

The synthetic region SIM-R12 is not confidently resolved. It is explicitly marked as a gap, even though the example genome-wide average depth is 31.8×.

Evidence: Technical limitation

Limit: SIM-R12 is not a genomic coordinate or gene. Average depth can hide uneven coverage; an unobserved or unresolved region is not a negative finding.

Your next question
Is this region relevant to the reason for testing, and would another method be useful?

Illumina · Sequencing coverage

HEALTH FOLLOW-UP / FICTIONAL FINDINGS

Screening scope and risk models

A negative finding has limits. A score that was not applied is not a reassuring result.

H03 / SCREENING / DEFINED SCOPE

No reportable finding in sample scope

The invented screening summary contains no reportable finding within its demonstration scope. This is a limited result, not an “all clear” for future disease.

Evidence: Scope-limited finding

Limit: No actual clinical panel was analyzed. Real negative results depend on what was assessed and what the method can detect; missed or unknown causes remain possible.

Your next question
How should routine care and family-history-based screening continue?

MedlinePlus Genetics · Interpreting results

H04 / RISK MODELS / CALIBRATION

Polygenic score withheld

This sample withholds a disease percentile because no model, population calibration or clinical inputs have been validated for this fictional member.

Evidence: Model not applied

Limit: A polygenic score uses many variants and is only part of risk assessment. The absence of a score here is deliberate, not a low-risk result.

Your next question
Would a specific validated risk model add useful information beyond my clinical risk factors?

NHGRI · Polygenic risk scores

MEDICINE PASSPORT / DISCUSSION BRIEF

CYP2C19 and PPI context

The fictional pharmacogenomic output below demonstrates a handoff format. It is not a prescription, a dose recommendation, or an instruction to change treatment.

M01 / CYP2C19 / PPI CONTEXT

*17/*17 · ultrarapid metabolizer

The simulated diplotype corresponds to an ultrarapid CYP2C19 metabolizer phenotype. CPIC discusses reduced exposure to selected proton pump inhibitors and possible treatment failure.

Evidence: Guideline-supported interpretation

Limit: Fictional call; not clinically confirmed. The PPI recommendation for ultrarapid metabolizers is rated optional in the cited guideline. This does not apply equally to all drugs or PPIs. No dose advice is provided.

Your next question
If a PPI is relevant to my care, would a confirmed result change the choice, monitoring or prescribing plan?

CPIC · CYP2C19 and proton pump inhibitors

M02 / MEDICATION RECORD / RECONCILIATION

Medication list not supplied

The sample has no medication or supplement list. An isolated metabolism result cannot establish whether a current treatment is appropriate.

Evidence: Clinical context missing

Limit: Drug interactions, indication, response and other health factors affect prescribing. Do not start, stop or change medicines using this document.

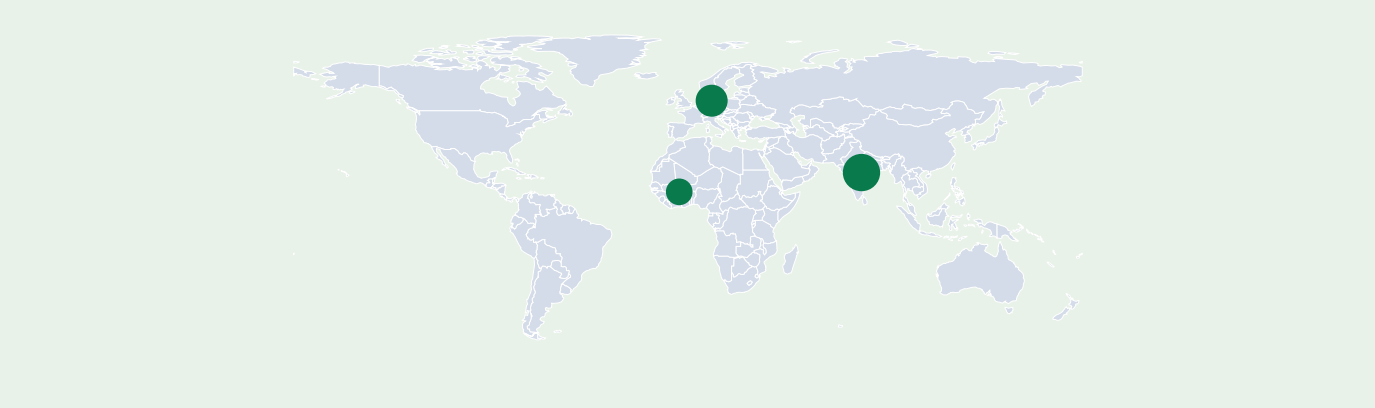
Your next question
Which prescriptions, over-the-counter medicines and supplements should I review with my pharmacist?

NHGRI · Pharmacogenomics

ANCESTRY ATLAS / FICTIONAL ESTIMATES

Reference-region estimates

The regions and percentages in this example are invented. No ancestry calculation was performed, and there is no genetic data behind this map.



NORTHWEST EUROPE

46%

SOUTH ASIA

34%

WEST AFRICA

20%

A01 / REFERENCE AFFINITY / MODEL A

46% / 34% / 20%

The invented mix is Northwest European 46%, South Asian 34% and West African 20%. These numbers exist solely to demonstrate how an ancestry workspace could look.

Evidence: Statistical estimate

Limit: No DNA or reference algorithm was used. Real estimates vary with databases and methods. Percentages are not nationality, identity or proof of a specific ancestor.

Your next question
Which reference populations, model version and confidence ranges would accompany a real estimate?

MedlinePlus Genetics · Genetic ancestry

Natural Earth geography. Approximate reference regions, not a migration route or individual ancestors.

LINEAGE METHODS / FICTIONAL TEACHING ROUTES

Maternal and paternal lineage methods

These DEMO identifiers illustrate two inheritance paths. They are not haplogroups, genetic calls or relatives. Sample 001's lineage status remains not assessed .

A DIRECT MATERNAL PATH

Maternal grandmother DEMO-M0	→	**Mother** DEMO-M1
→		**Teaching subject** DEMO-M2

Mitochondrial DNA is generally inherited through the egg cell. Children can inherit it; transmission onward follows the maternal line. This follows one direct maternal chain, not all of a person's maternal ancestry. The subject's capacity to pass it onward is not inferred here.

A CONDITIONAL PATERNAL PATH

Paternal grandfather DEMO-Y0	→	**Father** DEMO-Y1
→		**Teaching subject** DEMO-Y2

Y-chromosome testing can follow a direct paternal line when suitable Y data exists. This diagram assumes a hypothetical Y dataset; no such data was assessed for Sample 001. A Y lineage represents one paternal chain, not all paternal ancestry. It does not establish the subject's chromosomes, sex, gender or family relationships.

AUTOSOMAL ANCESTRY USES A DIFFERENT METHOD

Autosomal estimates compare signals across many ancestral lines. The fictional 46% / 34% / 20% mix cannot be assigned to these DEMO branches. Geography and dates are not inferred. No geographic origin, ancestral age, haplogroup or migration route is assigned by this teaching tree.

MedlinePlus Genetics · genetic ancestry methods and limits

ANCESTRY ATLAS / SCOPE

Lineages and historical claims

The teaching tree does not assign a haplogroup. A broad regional estimate does not establish a named ancestor, migration date or individual family relationship.

A02 / LINEAGES / MITOCHONDRIAL

Haplogroup not assessed

No mitochondrial or Y-chromosome haplogroup has been assigned in this fictional report. An autosomal mixture cannot substitute for a lineage-specific analysis.

Evidence: Not assessed

Limit: A lineage describes one ancestral path, not the complete family tree. The sample does not infer chromosome complement, sex or family relationships.

Your next question
Would lineage testing answer the genealogical question I actually have?

MedlinePlus Genetics · Genetic ancestry

A03 / HISTORY / MIGRATION

Migration dates withheld

The illustrative map shows reference regions without a migration route or a date. A geographic affinity should not be turned into a precise family story without supporting evidence.

Evidence: Insufficient information

Limit: Historical population movement complicates interpretation. This fictional estimate cannot identify an individual ancestor, a border crossing or a generation.

Your next question
Which records or tested relatives could help investigate our family history?

MedlinePlus Genetics · Genetic ancestry

FAMILY PLANNING / MODEL BASELINE

Carrier result with an untested partner

A simulated carrier example can explain a conversation. It cannot establish reproductive risk when a partner is untested.

ILLUSTRATIVE MEMBER

Aa · carrier model

REPRODUCTIVE PARTNER

Not tested

NO CHILD-RISK PERCENTAGE IS ASSIGNED

This partner is untested in the fictional scenario. Condition-specific, clinically confirmed findings from both reproductive partners and qualified counseling are needed before discussing the relevant inheritance risks.

F01 / CARRIER MODEL / PARENT A

Aa · fictional carrier

Parent A is assigned Aa in a simplified autosomal recessive model. The other reproductive parent is initially untested, so this report does not calculate an affected-child probability.

Evidence: Established inheritance model

Limit: A/a are teaching symbols, not a named gene or real genotype. Recessive inheritance is condition-specific; a carrier result needs appropriate interpretation.

Your next question
Would clinical carrier screening for the same condition be appropriate for both reproductive parents?

ACOG · Carrier screening

FAMILY PLANNING / SCOPE

Partner testing and residual risk

The partner result and screening scope matter as much as the first result. A genetic counselor can put both into the same conversation.

F02 / CARRIER MODEL / PARTNER

Untested · probability withheld

The interactive model only calculates when both genotypes are explicitly selected. Selecting “Untested” clears all percentages rather than assuming the other person is not a carrier.

Evidence: Information incomplete

Limit: The interactive model is a classroom calculation, not a couple’s risk estimate. Each pregnancy is a separate event; the model makes simplified assumptions.

Your next question
What can and cannot be learned from one person’s carrier screen alone?

ACOG · Carrier screening

F03 / SCREENING / RESIDUAL RISK

A negative screen leaves residual risk

Even an informative carrier screen cannot rule out every possible inherited condition or variant. A real result needs test scope, detection limitations and family context.

Evidence: Detection-limited result

Limit: The calculator’s AA option means a known model genotype. It must not be confused with a real negative carrier screen, which can miss variants.

Your next question
What residual risk remains after the particular tests we are considering?

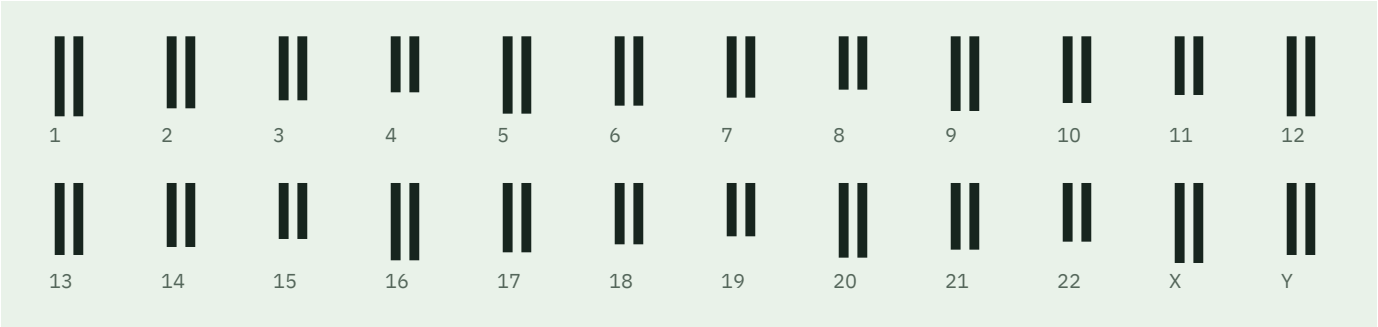
ACOG · Carrier screening

No compatibility ranking. Genetics cannot choose a romantic partner or grade a future child. Carrier information supports condition-specific conversations; the decisions remain personal.

GENOME AND FILES / SYNTHETIC ATLAS

Illustrative coverage and no-call

An atlas connects a location with its coverage, interpretation and source. The chromosome bands below are purely synthetic interface illustrations.



G01 / SEQUENCING / ILLUSTRATIVE QUALITY

31.8× average depth

The example manifest records 31.8× average depth. This is an invented laboratory-style metric, not evidence of a completed sequence or the quality of the proposed service.

Evidence: Synthetic quality metric

Limit: Depth is an average, not uniform completeness or a guarantee of variant detection. The proposed service targets 30× average; no real sample QC exists in this preview.

Your next question
What breadth of coverage and region-specific limitations would the laboratory provide?

Illumina · Sequencing coverage

A NO-CALL IS VISIBLE

The chromosome interface starts with synthetic region SIM-R12. Its no-call status means insufficient information. It is not a negative result and should not disappear behind an empty marker.

GENOME AND FILES / MANIFEST

File formats and analysis context

These filenames describe the proposed handover, not files embedded in this sample. No raw genome data or working genomic downloads are included.

FASTQ / PROPOSED DATA FORMAT

sample001.reads.fastq.gz

Sequence reads and quality scores.

CRAM / PROPOSED DATA FORMAT

sample001.aligned.cram

Reads aligned to a reference genome.

VCF / PROPOSED DATA FORMAT

sample001.variants.vcf.gz

Called variants and metadata.

G02 / DATA / SYNTHETIC MANIFEST

FASTQ · CRAM · VCF catalogue

The manifest names the kinds of files a genomic handover might include. Filenames are invented; file sizes and checksums are omitted. No raw genome files exist behind these rows.

Evidence: Format guide

Limit: FASTQ holds reads and quality scores; aligned reads and called variants are processed products. Formats and analysis metadata matter when considering reanalysis.

Your next question
Which deliverables, reference build and pipeline versions are included in the live service?

Illumina · Sequence file formats

Genomic files can identify a person and reveal family information. This fictional sample contains none. Store and share real files deliberately.

GENOME AND FILES / VERSION HISTORY

Uncertain to likely benign

G03 / RECORD / INTERPRETATION VERSIONS

v1.1 to v1.2

The fictional report preserves a previous interpretation beside a newer edition. The underlying sequence stays the same in this example; the meaning assigned to one finding changes.

Evidence: Illustrative change log

Limit: These editions and review events are invented. No monitoring, expert review or notification service has taken place for this sample.

Your next question
Will a real update show the reason, evidence date and practical implications of a change?

MedlinePlus Genetics · Variant classifications

G04 / RECLASSIFICATION / SIM-V102

Uncertain to likely benign

Synthetic finding SIM-V102 moves from uncertain significance in v1.1 to likely benign in v1.2. The sample illustrates an update that reduces concern instead of adding another warning.

Evidence: Illustrative reclassification

Limit: SIM-V102 is not a real variant. Reclassification can occur as evidence develops; an actual update must be tied to a particular laboratory finding and current clinical context.

Your next question
What evidence changed, and does the new classification affect any previous clinical discussion?

NCI · Genetic testing fact sheet

Service scope: Proposed updates are for the lifetime of the Whole DNA service, within its supported scope. New sequencing, laboratory assays and clinical appointments are separate. Final cadence, retention and exit arrangements remain to be confirmed before ordering opens.

DISCUSSION CHECKLIST

Questions to take to a professional

These are prompts drawn from the sample outputs. A real report would travel with the actual laboratory documents and the context your care team needs.

01 / EVERYDAY

Would moving my last caffeinated drink earlier change my sleep?

02 / HEALTH

Would my symptoms or family history justify a clinical genetics review independently of this VUS?

03 / MEDICINE

If a PPI is relevant to my care, would a confirmed result change the choice, monitoring or prescribing plan?

04 / FAMILY

Would clinical carrier screening for the same condition be appropriate for both reproductive parents?

05 / GENOME

What breadth of coverage and region-specific limitations would the laboratory provide?

> BEFORE ANY MEDICAL DECISION
>
> Confirm relevant findings in an appropriate clinical setting. Take your symptoms, family history, medicines and goals into the discussion. This sample cannot diagnose, exclude disease, choose a romantic partner, prescribe a lifestyle or establish your reproductive risk.

SOURCE CONTEXT / 1

Sources and method context

These resources support the educational context in the HTML sample. They do not endorse Whole DNA, establish the simulated outputs, or validate a proposed service.

01 / FDA · Caffeine guidance

www.fda.gov/consumers/consumer-updates/spilling-beans-how-much-caffeine-too-much

02 / MedlinePlus Genetics · Lactose intolerance

medlineplus.gov/genetics/condition/lactose-intolerance/

03 / NHLBI · Healthy sleep habits

www.nhlbi.nih.gov/health/sleep-deprivation/healthy-sleep-habits

04 / MedlinePlus · Vitamin D test

medlineplus.gov/lab-tests/vitamin-d-test/

05 / Australian Institute of Sport · Genetics

www.ausport.gov.au/ais/position_statements/genetics

06 / FDA · Consumer genetic tests

www.fda.gov/medical-devices/in-vitro-diagnostics/direct-consumer-tests

07 / NHGRI · Variant of uncertain significance

www.genome.gov/genetics-glossary/Variant-of-Uncertain-Significance-VUS

08 / Illumina · Sequencing coverage

www.illumina.com/science/technology/next-generation-sequencing/plan-experiments/coverage.html

09 / MedlinePlus Genetics · Interpreting results

medlineplus.gov/genetics/understanding/testing/interpretingresults/

SOURCE CONTEXT / 2

Sources and method context

These resources support the educational context in the HTML sample. They do not endorse Whole DNA, establish the simulated outputs, or validate a proposed service.

10 / NHGRI · Polygenic risk scores

www.genome.gov/genetics-glossary/Polygenic-Risk-Score-PRS

11 / CPIC · CYP2C19 and proton pump inhibitors

pmc.ncbi.nlm.nih.gov/articles/PMC7868475/

12 / NHGRI · Pharmacogenomics

www.genome.gov/about-genomics/educational-resources/fact-sheets/pharmacogenomics

13 / MedlinePlus Genetics · Genetic ancestry

medlineplus.gov/genetics/understanding/dtcgenetictesting/ancestrytesting/

14 / ACOG · Carrier screening

www.acog.org/womens-health/faqs/carrier-screening

15 / Illumina · Sequence file formats

www.illumina.com/informatics/sequencing-data-analysis/sequence-file-formats.html

16 / MedlinePlus Genetics · Variant classifications

medlineplus.gov/genetics/understanding/mutationsanddisorders/neutralmutations/

17 / NCI · Genetic testing fact sheet

www.cancer.gov/about-cancer/causes-prevention/genetics/genetic-testing-fact-sheet