

# Your health picture, in plain words

Prepared for **Greg Conner** · age 40 · Male · report date September 14, 2026 · DNA from two files (23andMe + AncestryDNA) and a LabCorp panel drawn 2025-09-26

|                 |                                                                                                                                             |
|-----------------|---------------------------------------------------------------------------------------------------------------------------------------------|
| AGE / SEX       | 40 · Male                                                                                                                                   |
| HEIGHT / WEIGHT | 5'7" · 205 lb                                                                                                                               |
| BMI             | 32.1 (calculated)                                                                                                                           |
| ACTIVITY        | 3,000 steps/day · 0 min/week vigorous (self-reported)                                                                                       |
| MEDICINES       | Supplement, Adderall, Buspar, Tylenol, Wegovy, Atenolol, Ambien, Bromelains, tyrosine, Penicillin VK                                        |
| SUPPLEMENTS     | Fish Oil, Vitamin D, Methylene Blue, Whey Protein, Creatine, Multi-Vitamin with Iron, Calcium Supplement, Green Tea, Magnesium, Vitamin B12 |
| LABS            | 62 results, LabCorp, 2025-09-26 (previous 2024-06-17)                                                                                       |
| DNA             | 643,163 positions read; 28 disagreements between files excluded                                                                             |

## HOW TO READ THIS REPORT — EVIDENCE, STRONGEST FIRST

- MEASURED** A lab value from your own blood or urine. The strongest evidence in this report.
- GUIDELINE GENE-DRUG** A gene-medicine relationship with a published CPIC or PharmGKB guideline.
- POPULATION ASSOCIATION** A statistical tendency seen across many people. Usually a small effect; never a diagnosis.
- UNCONFIRMED CALL** A rare variant read at a position this kind of test is unreliable at. Listed for transparency only.
- CRITICAL** A medication-safety item to review promptly with your prescriber or pharmacist. **HIGH-IMPACT** A finding worth a specific test or a conversation with your clinician.

Every action in this report is a question for your own clinician or pharmacist. Do not start, stop, or change any prescription medicine based on this report alone.

## ★ The five things that matter most

Ranked by how current and well-supported each one is: your medication list and measured results first, inherited signals after.

### 1 MAO-inhibiting agent combined with serotonergic medication **CRITICAL**

**WHAT WE FOUND** Involves Methylene Blue, Adderall, Buspar. FDA labeling warns that MAO-inhibiting agents (including methylene blue) taken with serotonergic medicines are associated with serotonin syndrome, and with blood-pressure elevations when stimulants are involved. The exact product, dose, and timing matter — this report cannot see those.

**WHAT TO ASK** Promptly review this combination with your prescriber or pharmacist. Do not stop or change a prescription on your own. Seek urgent care only for symptoms such as agitation, confusion, rapid heart rate, high fever, or muscle rigidity.

**BASIS** FDA prescribing information (methylene blue; serotonergic agents)

### 2 MAO-inhibiting agent combined with a decongestant or pressor amino acid **CRITICAL**

**WHAT WE FOUND** Involves Methylene Blue, tyrosine. Over-the-counter decongestant labels (phenylephrine, pseudoephedrine) tell users not to take them with an MAO inhibitor, or within two weeks of stopping one, because the combination can raise blood pressure sharply. Tyrosine is a building block of the same pressor amines and is listed here for the same review. Product, dose and timing decide the risk — this report cannot see them.

**WHAT TO ASK** Bring this combination to your pharmacist or prescriber promptly, in the same conversation as any other MAO-inhibitor item on this list. Do not stop or change a prescription on your own.

**BASIS** FDA OTC Drug Facts labeling (phenylephrine; pseudoephedrine) — MAOI warning; methylene blue prescribing information

### 3 Stimulant and beta-blocker on the same list **HIGH-IMPACT**

**WHAT WE FOUND** Involves Adderall, Atenolol. These act in opposite directions on heart rate and blood pressure and are sometimes intentionally co-prescribed. This is worth a confirmation, not an alarm.

**WHAT TO ASK** Mention the combination at your next visit and confirm it is intentional; share any palpitations, dizziness, or chest discomfort.

**BASIS** FDA prescribing information (amphetamines; beta-blockers)

4 Alpha-1 antitrypsin carrier variant HIGH-IMPACT LUNG & LIVER

**WHAT WE FOUND** You carry one copy of the rs17580 variant in SERPINA1, while your liver panel shows normal values with AST 30 IU/L and ALT 21 IU/L on September 26, 2025.

**WHAT TO ASK** At your next routine appointment, ask whether checking a direct alpha-1 antitrypsin blood level is appropriate to confirm your baseline.

**BASIS** SERPINA1 rs17580 T/A · September 26, 2025

5 Lipoprotein(a) inherited marker HIGH-IMPACT HEART HEALTH

**WHAT WE FOUND** You carry one copy of the rs10455872 marker in LPA, while your measured LDL cholesterol was 63 mg/dL, down from 107 mg/dL on 2024-06-17.

**WHAT TO ASK** At your next checkup, ask whether a one-time lipoprotein(a) blood test is warranted to complete your cardiovascular assessment.

**BASIS** LPA rs10455872 A/G · September 26, 2025

This report also holds **41 unconfirmed DNA findings** — rare calls that need clinical confirmation before they mean anything. They are deliberately kept out of this list and explained in section 14.

1 What you told us about your health

IN PLAIN WORDS

*This section reflects the personal health history and family background you shared with us. Your personal accounts shaped the emphasis and priority order of this report, but they did not alter any laboratory value or genetic call. Reviewing these details alongside your clinical results provides an integrated view of your current health.*

In your own words

Repeated here so you and your clinician can see it beside everything this report measured. It is your own account, not a clinical record, and nothing in it was verified.

I had gastric sleeve surgery in 2020. My highest weight was 384lbs. I now weigh 205lbs. I don't get enough sleep. I have venous reflux in my lower left leg and have been hospitalized 12 times in the last 11 years, with each stay lasting 4-5 nights because I will get rapid spreading of Cellulitis in my lower left leg. I've been on Penicillin for over a decade. When I go to the hospital, the only thing that reverses the Cellulitis is Anceph. Growing up I was deathly allergic to three types of bees. For about a 20 years, I had chronic athletes foot where the skin between my toes would peel away and bleed. I have a wife and an 8 and 5 year old son who stress me out. I frequently get frustrated with them more than I use too. My mother had breast cancer and is HER2 positive as well as has the BRCA gene.

How your history and your DNA fit together

**What you described.** You shared that your mother had breast cancer and carried a BRCA gene variant. You also reported recurrent lower leg cellulitis associated with venous reflux and long-term penicillin use.

**What this report found.** Your DNA screen for BRCA1 and BRCA2 identified no reportable pathogenic variants in your own sample. In addition, your laboratory results show a normal white blood cell count of 4.1 x10E3/uL, indicating that physical circulatory stasis rather than an inherited systemic immune defect is the primary focus.

Where something you described lines up with a finding here, that is a correlation worth raising with your clinician — not a diagnosis, and not proof that the finding caused it.

2 Medicines — combinations to review

IN PLAIN WORDS

*Your current medication list contains active drug combinations that require a prompt review with your prescribing clinician or pharmacist. Methylene blue acts as a monoamine oxidase inhibitor, creating potential safety interactions when combined with your serotonergic agents or stimulants. Verified clinical guidelines and drug prescribing information outrank general guidance and define how these medicines interact.*

The drug-drug and drug-supplement findings below come from your reported list. Where a genetic marker is also involved, the card says so. This report cannot see doses, timing, or whether items are still taken, so every item is a question for your prescriber or pharmacist, not a conclusion.

1. MAO-inhibiting agent combined with serotonergic medication — shown in full in page 1.
2. MAO-inhibiting agent combined with a decongestant or pressor amino acid — shown in full in page 1.
3. Stimulant and beta-blocker on the same list — shown in full in page 1.

3

Your supplements — what to know

**IN PLAIN WORDS**

*Your supplement routine includes multiple daily products that should be coordinated with your daily prescription medicines. Mineral supplements like iron, calcium, and magnesium can compete for gastrointestinal absorption when taken at the same time. Discussing product timing and selection with your pharmacist ensures your regimen supports your overall therapy safely.*

What you told us you already take

Listed so you and your pharmacist can see the whole picture in one place. This is not an endorsement of any item, and nothing here says you should keep taking something.

| ITEM                    | ACTIVE INGREDIENT                               | WHAT IT IS COMMONLY TAKEN FOR                                                                                                                  |
|-------------------------|-------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------|
| Fish Oil                | Omega-3 fatty acids (EPA and DHA)               | The marine omega-3s studied for triglyceride levels; look at the combined EPA+DHA figure rather than the total fish-oil weight.                |
| Vitamin D               | Cholecalciferol (vitamin D3)                    | Supports calcium absorption and bone maintenance; the common reason people supplement is a measured level below the reference range.           |
| Methylene Blue          | Not recognised — check the label                | This item was not matched to a known ingredient, so no interaction check could be run on it.                                                   |
| Whey Protein            | Whey protein (milk-derived)                     | A convenient way to reach a daily protein target; food sources do the same job.                                                                |
| Creatine                | Creatine monohydrate                            | The most studied sports supplement there is, used to support strength training and muscle retention.                                           |
| Multi-Vitamin with Iron | Mixed vitamins and minerals                     | Broad low-dose cover. Worth checking against your other bottles — overlapping products are the usual route to an unintentionally high dose.    |
| Calcium Supplement      | Calcium (carbonate or citrate salt)             | Bone mineral support. Calcium carbonate is also an antacid, so it is easy to take twice over without noticing.                                 |
| Green Tea               | Green tea extract (EGCG)                        | Concentrated tea polyphenols. High-dose extracts have been linked to liver injury in rare cases, unlike drinking the tea itself.               |
| Magnesium               | Magnesium glycinate (elemental magnesium)       | Involved in muscle and nerve function; the glycinate form is chosen over oxide because it is better absorbed and less likely to loosen stools. |
| Vitamin B12             | Cyanocobalamin or methylcobalamin (vitamin B12) | Needed for red blood cell formation and nerve function; absorption falls with age and with long-term acid-reducing medicines.                  |

Inclusion here is not a medical recommendation and not an endorsement of any brand.

4

Your bloodwork — what it says

**IN PLAIN WORDS**

*Your measured blood and urine markers show strong stability, with zero of 62 results falling outside normal reference intervals. Measured laboratory values represent direct physical reality and outrank every genetic prediction in this report. Five results showed clear improvements since your previous tests on 2024-06-17.*

RESULTS

62

6 panels, LabCorp

OUTSIDE RANGE

0

flags: none

AT A BOUNDARY

2

bicarbonate (CO2), alkaline phosphatase

IMPROVED SINCE 2024

5

total cholesterol, triglycerides +3

Collected 2025-09-26, about 11 months before this report — a description of that day, not necessarily of today. Each bar shows the laboratory's reference interval in green and your result as a filled dot; a hollow dot is the 2024-06-17 result. Values are read against the performing laboratory's own reference intervals; changes inside the interval are ordinary variation and are not flagged. The remaining 38 results are listed in section 16.

Cholesterol & triglycerides

| TEST                 | WHERE IT SITS | RESULT    | REFERENCE | PREVIOUS         | STATUS   |
|----------------------|---------------|-----------|-----------|------------------|----------|
| Cholesterol, Total   |               | 142 mg/dL | 100-199   | 194 (2024-06-17) | IN RANGE |
| Triglycerides        |               | 71 mg/dL  | 0-149     | 105 (2024-06-17) | IN RANGE |
| HDL Cholesterol      |               | 65 mg/dL  | >39       | 68 (2024-06-17)  | OPTIMAL  |
| VLDL Cholesterol Cal |               | 14 mg/dL  | 5-40      | 19 (2024-06-17)  | IN RANGE |
| LDL Chol Calc (NIH)  |               | 63 mg/dL  | 0-99      | 107 (2024-06-17) | OPTIMAL  |

Your lipid panel shows marked improvements across multiple markers, with LDL cholesterol at 63 mg/dL, down from 107 mg/dL on 2024-06-17, and total cholesterol at 142 mg/dL, down from 194 mg/dL on 2024-06-17. Triglycerides improved to 71 mg/dL from 105 mg/dL, while HDL cholesterol remains optimal at 65 mg/dL. These measured values demonstrate favorable cardiovascular lipid balance across all five markers.

Blood sugar

| TEST                 | WHERE IT SITS | RESULT   | REFERENCE | PREVIOUS         | STATUS   |
|----------------------|---------------|----------|-----------|------------------|----------|
| Glucose              |               | 74 mg/dL | 70-99     | 92 (2024-06-17)  | IN RANGE |
| Glucose (Urinalysis) |               | Negative | Negative  | —                | IN RANGE |
| Hemoglobin A1c       |               | 4.7 %    | 4.8 - 5.6 | 4.8 (2023-10-13) | OPTIMAL  |

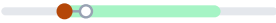
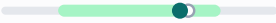
Your fasting glucose measured 74 mg/dL, compared to 92 mg/dL on 2024-06-17, and your hemoglobin A1c sits at 4.7 %, compared to 4.8 % on 2023-10-13. Urine glucose was negative, confirming absence of glucose spillage into the urine. These values reflect optimal blood sugar management within standard clinical targets.

Kidney & electrolytes

| TEST                  | WHERE IT SITS | RESULT          | REFERENCE | PREVIOUS          | STATUS      |
|-----------------------|---------------|-----------------|-----------|-------------------|-------------|
| BUN                   |               | 8 mg/dL         | 6-20      | 14 (2024-06-17)   | IN RANGE    |
| Creatinine            |               | 0.84 mg/dL      | 0.76-1.27 | 0.93 (2024-06-17) | IN RANGE    |
| eGFR                  |               | 114 mL/min/1.73 | >59       | 108 (2024-06-17)  | IN RANGE    |
| BUN/Creatinine Ratio  |               | 10              | 9-20      | 15 (2024-06-17)   | IN RANGE    |
| Sodium                |               | 139 mmol/L      | 134-144   | 140 (2024-06-17)  | IN RANGE    |
| Potassium             |               | 4.5 mmol/L      | 3.5-5.2   | 4.3 (2024-06-17)  | IN RANGE    |
| Chloride              |               | 104 mmol/L      | 96-106    | 104 (2024-06-17)  | IN RANGE    |
| Carbon Dioxide, Total |               | 20 mmol/L       | 20-29     | 21 (2024-06-17)   | AT THE EDGE |
| Calcium               |               | 9.4 mg/dL       | 8.7-10.2  | 9.9 (2024-06-17)  | IN RANGE    |

Total carbon dioxide sits at the lower boundary of normal at 20 mmol/L, compared to 21 mmol/L on 2024-06-17. Meanwhile, your kidney filtration is robust with an eGFR of 114 mL/min/1.73 and creatinine at 0.84 mg/dL. Electrolytes remain stable, with sodium 139 mmol/L, potassium 4.5 mmol/L, and calcium 9.4 mg/dL all within their reference intervals.

Liver

| TEST                 | WHERE IT SITS                                                                     | RESULT    | REFERENCE | PREVIOUS         | STATUS      |
|----------------------|-----------------------------------------------------------------------------------|-----------|-----------|------------------|-------------|
| Protein, Total       |  | 7.0 g/dL  | 6.0-8.5   | 7.2 (2024-06-17) | IN RANGE    |
| Albumin              |  | 4.5 g/dL  | 4.1-5.1   | 4.5 (2024-06-17) | IN RANGE    |
| Globulin, Total      |  | 2.5 g/dL  | 1.5-4.5   | 2.7 (2024-06-17) | IN RANGE    |
| Bilirubin, Total     |  | 0.6 mg/dL | 0.0-1.2   | 1 (2024-06-17)   | IN RANGE    |
| Alkaline Phosphatase |  | 50 IU/L   | 47-123    | 60 (2024-06-17)  | AT THE EDGE |
| AST (SGOT)           |  | 30 IU/L   | 0-40      | 32 (2024-06-17)  | IN RANGE    |
| ALT (SGPT)           |  | 21 IU/L   | 0-44      | 28 (2024-06-17)  | IN RANGE    |

Alkaline phosphatase sits near the lower boundary of normal at 50 IU/L, down from 60 IU/L on 2024-06-17. Your transaminases show healthy hepatic function, with AST at 30 IU/L and ALT at 21 IU/L, while total bilirubin is 0.6 mg/dL and albumin is 4.5 g/dL. Total protein at 7 g/dL confirms stable overall liver synthesis.

Showing 24 of 62 reported analytes, out-of-range results and the panels this report refers to first; the other 38 (including 9 routine urinalysis screens within normal limits) are in section 16 and the uploaded report remains the complete record.

5 Your heart — inherited signals versus measured reality

**IN PLAIN WORDS**  
*Your measured cholesterol and triglyceride levels are in optimal ranges, even though your polygenic score places you in the 90th percentile for coronary artery disease. A measured laboratory result outranks every genetic prediction in this report. Direct blood testing provides the true measure of your cardiovascular health today.*

**The signals.** Your DNA shows one copy of the rs10455872 marker in LPA and both copies of the rs12916 variant in HMGCR. Your polygenic score for coronary artery disease placed in the 90th percentile across 20 markers read of 22 total.

**The reality.** Your measured LDL cholesterol is 63 mg/dL, down from 107 mg/dL on 2024-06-17, and total cholesterol is 142 mg/dL, down from 194 mg/dL on 2024-06-17. A measured result outranks every genetic prediction in this report. Triglycerides measured 71 mg/dL and HDL cholesterol measured 65 mg/dL, confirming optimal lipid balance.

**What it means.** The LPA variant is associated with higher lipoprotein(a) concentrations, a specific particle that routine lipid panels do not detect. At your next visit, ask your clinician whether checking a direct lipoprotein(a) blood test is appropriate.

The polygenic score, on the population scale

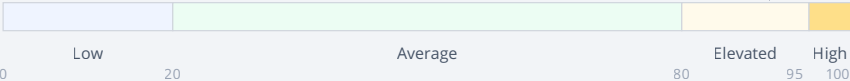
A polygenic score sums many small genetic effects into one number. These are research-grade estimates from published marker panels — they are not diagnoses, they are not calibrated to every ancestry, and they never outrank measured results like your actual lipid panel or blood sugar. The scale shows where your summed score falls among people in the reference model.

Coronary Artery Disease

RESEARCH CONTEXT

ABOVE THE 90TH PERCENTILE

You: about the 90th percentile



Your score is estimated to be **higher than roughly 90% of people** in a population model built from published European-reference allele frequencies. Read this as “association context”: your measured risk factors carry more weight than this score. Your measured lipid and glucose results, where provided, are in section 4.

Marker coverage: 20 of 22 panel markers were readable in your file — a data-quality measure, not a risk level.

Model: Tada et al. 2016 (PGS Catalog PGS000011)

## Your heart-relevant markers

Where computational scores appear, they describe the predicted effect of the DNA change itself. They do not account for how common the variant is, and a common variant can score highly while making little difference to any individual.

| GENE                                                | MARKERS (GENOTYPE)                                                      | ASSOCIATION                                 | WHAT IT MEANS FOR YOU                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|-----------------------------------------------------|-------------------------------------------------------------------------|---------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>ABCC1</b><br>HIGH IMPACT<br>+ HIGH<br>EVIDENCE   | rs45511401 G/T                                                          | Atorvastatin response                       | <p>One of your two copies carries this variant · 4 of 4 computational tools predict this change harms the protein · Top 0.2% of all DNA changes by predicted impact</p> <p>People carrying certain versions of this marker may process the cholesterol medication atorvastatin differently across populations.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| <b>SLCO1B1</b><br>HIGH IMPACT<br>+ HIGH<br>EVIDENCE | rs4149056 T/C                                                           | Statin Metabolism                           | <p>One of your two copies carries this variant · 2 of 4 computational tools predict this change harms the protein · Top 0.3% of all DNA changes by predicted impact · CPIC guidance · PMID 35152405 · Published study · PMID 39414775 (bilirubin levels)</p> <p><b>What the cited study (PMID 39414775) found for rs4149056 T/C:</b> The study linked the C allele to increased blood bilirubin levels, estimating an average effect of 0.19 units per copy. People with the T/C genotype carry one copy of this allele and on average showed higher bilirubin levels than non-carriers. This finding reflects a statistical tendency observed across a group rather than a certain outcome.</p> <p>Differences at this position have been linked to subtle variations in how efficiently the body clears common statin medications.</p> |
| <b>CDKN2B-AS1</b><br>ASSOCIATION                    | rs10757274 G/G ·<br>rs4977574 G/G ·<br>rs1333042 G/G ·<br>rs1333049 C/C | Three Vessel Coronary Disease               | <p>Both copies carry this variant · Published study · PMID 32469254</p> <p><b>What the cited study (PMID 32469254) found for rs10757274 G/G:</b> Individuals with the G/G genotype carry two copies of the G allele linked to higher odds of coronary artery disease. Based on the study model with an odds ratio of 1.22 per copy, people with two copies have the highest statistical odds of the condition among the three genotype groups. Read from the study abstract only.</p> <p>Statistical studies connect this regional variant with a slightly altered population likelihood of developing complex coronary artery disease.</p>                                                                                                                                                                                              |
| <b>HMGR</b><br>ASSOCIATION                          | rs12916 C/C                                                             | Statins, attenuated cholesterol lowering by | <p>Both copies carry this variant · Published study · PMID 34887591</p> <p><b>What the cited study (PMID 34887591) found for rs12916 C/C:</b> People with the C/C genotype carry two copies of the C allele, which the study linked to higher low-density lipoprotein cholesterol levels. Under the additive model, carriers of two copies showed approximately twice the average increase in low-density lipoprotein cholesterol observed in individuals with a single copy. This genotype demonstrated the greatest statistical increase in cholesterol levels among the three groups in the study.</p> <p>Research links this genetic site to modest differences in how the body handles cholesterol-lowering statin therapies.</p>                                                                                                   |
| <b>HS3ST1</b><br>ASSOCIATION                        | rs16881446 T/C                                                          | Arteriosclerosis disorder                   | <p>One of your two copies carries this variant</p> <p>Inherited patterns at this location correlate with a minor shift in the population-wide chances of arterial hardening.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| <b>LPA</b><br>ASSOCIATION                           | rs10455872 A/G                                                          | LIPOPROTEIN(a) POLYMORPHISM                 | <p>One of your two copies carries this variant · Published study · PMID 33115273</p> <p><b>What the cited study (PMID 33115273) found for rs10455872 A/G:</b> People with the A/G genotype carry one copy of the G allele that this study linked to increased lipoprotein(a) levels. Under the study model, having one copy corresponds to an increase in average circulating lipoprotein(a) concentrations. Consequently, these individuals tend to display higher average lipoprotein(a) levels than those carrying no copies of the G allele.</p> <p>Certain inherited changes here are associated with naturally higher or lower circulating blood lipid particle levels in large population cohorts.</p>                                                                                                                            |

| GENE                 | MARKERS (GENOTYPE) | ASSOCIATION           | WHAT IT MEANS FOR YOU                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|----------------------|--------------------|-----------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| SH2B3<br>ASSOCIATION | rs3184504 T/C      | Primary myelofibrosis | <p>One of your two copies carries this variant · No computational tools predicts this change harms the protein · Top 8% of all DNA changes by predicted impact · Published study · PMID 29455858 (diastolic blood pressure)</p> <p><b>What the cited study (PMID 29455858) found for rs3184504 T/C:</b> For individuals with the T/C genotype, the cited study did not present specific blood pressure outcomes. Without an identified risk allele for this variant, the direction of effect was not established in this study. Read from the study abstract only.</p> <p>Variations in this biological pathway have been statistically connected to red blood cell production patterns in population studies.</p> |

Measured, September 2025

|                                                                                        |                                                                                       |                                                                                       |                                                                                            |
|----------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| <div>LDL CHOLESTEROL</div> <div>63 mg/dL OPTIMAL</div> <div>was 107 (2024-06-17)</div> | <div>HDL CHOLESTEROL</div> <div>65 mg/dL OPTIMAL</div> <div>was 68 (2024-06-17)</div> | <div>TRIGLYCERIDES</div> <div>71 mg/dL IN RANGE</div> <div>was 105 (2024-06-17)</div> | <div>TOTAL CHOLESTEROL</div> <div>142 mg/dL IN RANGE</div> <div>was 194 (2024-06-17)</div> |
|----------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|

6 Metabolism, weight and blood sugar

**IN PLAIN WORDS**

*Given the history of bariatric surgery and substantial weight loss you shared, your metabolic profile shows excellent current stability. Your fasting glucose of 74 mg/dL and hemoglobin A1c of 4.7 % demonstrate optimal blood sugar control, outranking your inherited type 2 diabetes risk markers. Direct laboratory tests reflect your active metabolic state far more accurately than inherited DNA signals.*

**The signals.** Your genotype carries both copies of risk alleles in CDKAL1 and IGF2BP2, alongside single-copy variants in FTO and TCF7L2. These population markers reflect statistical tendencies toward elevated blood sugar and higher body mass index in demographic studies.

**The reality.** Your fasting glucose measured 74 mg/dL, down from 92 mg/dL on 2024-06-17, and your hemoglobin A1c was 4.7 %, compared to 4.8 % on 2023-10-13. A measured result outranks every genetic prediction in this report.

**What it means.** Your actual laboratory values demonstrate excellent glycemic control that supersedes your inherited susceptibility markers. Ask your doctor how your current nutritional habits continue to support this healthy metabolic baseline.

Your metabolic markers

Where computational scores appear, they describe the predicted effect of the DNA change itself. They do not account for how common the variant is, and a common variant can score highly while making little difference to any individual.

| GENE                   | MARKERS (GENOTYPE) | ASSOCIATION | WHAT IT MEANS FOR YOU                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|------------------------|--------------------|-------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| BCDIN3D<br>ASSOCIATION | rs7138803 G/A      | Obesity     | <p>One of your two copies carries this variant · Published study · PMID 36581621 (body mass index)</p> <p><b>What the cited study (PMID 36581621) found for rs7138803 G/A:</b> People carrying the G/A genotype have one copy of the G allele, which this study linked to a decrease in body mass index. Under the study's additive model, carrying one copy corresponds to an intermediate statistical tendency toward lower body mass index, with an estimated decrease of 0.0271 units. This places individuals with this genotype between those with zero and two copies of the allele.</p> <p>Carrying specific alleles here is associated with a tiny, population-level shift in long-term body weight tendencies.</p> |

| GENE                               | MARKERS (GENOTYPE)                            | ASSOCIATION                                                   | WHAT IT MEANS FOR YOU                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|------------------------------------|-----------------------------------------------|---------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>CDKAL1</b><br>ASSOCIATION       | rs7754840 C/C                                 | Obesity                                                       | <p>Both copies carry this variant · Published study · PMID 28869590 (type 2 diabetes)</p> <p><b>What the cited study (PMID 28869590) found for rs7754840 C/C:</b> People with the C/C genotype carry two copies of the C allele linked to an increased risk of type 2 diabetes. Based on the study's additive model, individuals with two copies showed the highest statistical increase in risk among the tested genotypes. These findings describe an average trend across large populations rather than an inevitable health condition.</p> <p>This genomic site shows a mild correlation with average body mass index across broad demographic groups.</p>                                                                                                 |
| <b>EPO</b><br>ASSOCIATION          | rs1617640 A/A                                 | Microvascular complications of diabetes, susceptibility to, 2 | <p>Both copies carry this variant · Published study · PMID 39024449 (hematocrit)</p> <p>Population studies observe a minor relationship between this genetic area and the likelihood of small blood vessel damage in diabetic contexts.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| <b>FTO</b><br>ASSOCIATION          | rs1421085 T/C · rs8050136 C/A · rs9939609 T/A | Obesity (BMIQ14), susceptibility to; FTO-associated variant   | <p>One of your two copies carries this variant · Published study · PMID 39024449</p> <p><b>What the cited study (PMID 39024449) found for rs1421085 T/C:</b> Individuals carrying one copy of the T allele showed an intermediate decrease in type 2 diabetes risk under an additive model. This placed their expected risk reduction between those with two copies and those with none. These results represent statistical averages observed across a study population.</p> <p>Minor variations here correlate with slight, widespread differences in appetite regulation and general body mass trends.</p>                                                                                                                                                  |
| <b>GNPDA2</b><br>ASSOCIATION       | rs10938397 A/G                                | GNPDA2, GABRG1-associated variant                             | <p>One of your two copies carries this variant · Published study · PMID 36581621 (body mass index)</p> <p><b>What the cited study (PMID 36581621) found for rs10938397 A/G:</b> People with the A/G genotype carry one copy of the G allele, which the study linked to an increase in body mass index. Under the study model, carrying one copy corresponds to an intermediate average increase in body mass index, with an estimated effect size of 0.031. Across large populations, individuals with this genotype show a modest statistical tendency toward higher body mass index compared to non-carriers.</p> <p>Genetic diversity at this location has been tied to subtle differences in energy balance and metabolic traits across large cohorts.</p> |
| <b>IGF2BP2</b><br>ASSOCIATION      | rs4402960 T/T                                 | Diabetes mellitus type 2, susceptibility to                   | <p>Both copies carry this variant · Published study · PMID 22885922</p> <p><b>What the cited study (PMID 22885922) found for rs4402960 T/T:</b> People with the T/T genotype carry two copies of the T allele that the study linked to increased odds of type 2 diabetes. Based on an additive model with an odds ratio of 1.13 per copy of the T allele, individuals with two copies were expected to show the greatest increase in odds compared to non-carriers.</p> <p>Individuals carrying certain forms of this marker show a modest statistical association with blood sugar regulation and type 2 diabetes.</p>                                                                                                                                        |
| <b>KCNJ11</b><br>ASSOCIATION       | rs5219 T/C                                    | KCNJ11 — type 2 diabetes susceptibility (common variant)      | <p>One of your two copies carries this variant · 1 of 3 computational tools predicts this change harms the protein · Top 0.9% of all DNA changes by predicted impact · Published study · PMID 32541925</p> <p>A common susceptibility polymorphism; it does not indicate neonatal or MODY-type diabetes.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| <b>LOC105373352</b><br>ASSOCIATION | rs6548238 C/C                                 | Obesity                                                       | <p>Both copies carry this variant · Published study · PMID 36581621 (body mass index)</p> <p>Broad demographic studies identify this locus as having a small statistical influence on average body weight.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| <b>PMAIP1</b><br>ASSOCIATION       | rs17782313 T/C                                | MC4R-region variant — common weight-regulation association    | <p>One of your two copies carries this variant · Published study · PMID 19079261 (body mass index)</p> <p>Associated with a small average difference in body weight; informational only.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |

| GENE                          | MARKERS<br>(GENOTYPE)                                 | ASSOCIATION                                                   | WHAT IT MEANS FOR YOU                                                                                                                                                                                                                                                                                                            |
|-------------------------------|-------------------------------------------------------|---------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>SLC2A9</b><br>ASSOCIATION  | rs6449213 C/T                                         | Uric acid concentration, serum, quantitative trait locus 2    | One of your two copies carries this variant · Published study · PMID 23703922<br>This variant contributes to slight differences in how the body filters and retains circulating uric acid in large populations.                                                                                                                  |
| <b>SLC30A8</b><br>ASSOCIATION | rs13266634 C/T                                        | Diabetes mellitus type 2, susceptibility to                   | One of your two copies carries this variant · 1 of 4 computational tools predicts this change harms the protein · Top 4% of all DNA changes by predicted impact · Published study · PMID 38374256<br>Changes at this point in the genome show a small statistical link with pancreatic cellular function and glucose processing. |
| <b>SOD2</b><br>ASSOCIATION    | rs4880 A/G                                            | Microvascular complications of diabetes, susceptibility to, 6 | One of your two copies carries this variant · No computational tools predicts this change harms the protein · Top 6% of all DNA changes by predicted impact<br>1 notable marker in this gene region.                                                                                                                             |
| <b>TCF7L2</b><br>ASSOCIATION  | rs7903146 C/T ·<br>rs11196205 G/C ·<br>rs12255372 G/T | Diabetes mellitus type 2, susceptibility to                   | One of your two copies carries this variant · Published study · PMID 38374256<br>Epidemiological data connects this site to small statistical variations in how well the pancreas releases insulin and balances blood sugar.                                                                                                     |

Type 2 Diabetes polygenic score: not scored — 11 of 21 panel markers were readable in your file, below the coverage this report requires before showing a percentile.

Measured, September 2025

FASTING GLUCOSE  
**74** mg/dL IN RANGE  
was 92 (2024-06-17)

A1C  
**4.7** % OPTIMAL  
was 4.8 (2023-10-13)

BMI  
**32.1**  
5'7", 205 lb

ACTIVITY  
**3,000** steps/day  
0 min/week vigorous, self-reported

7 Lungs, liver and iron handling

IN PLAIN WORDS

Your liver enzymes and protein levels are completely normal, showing healthy active organ function despite an inherited alpha-1 antitrypsin carrier marker. A measured result outranks every genetic prediction in this report, confirming that your liver is operating within standard parameters. A direct blood measurement can clarify whether your carrier status has any functional effect.

**The signals.** You carry one copy of the rs17580 variant in SERPINA1, a gene that encodes the alpha-1 antitrypsin protein protecting the lungs and liver. Carrying a single copy defines carrier status rather than clinical deficiency.

**The reality.** AST 30, ALT 21, bilirubin 0.6 and albumin 4.5 are a normal liver panel. A measured result outranks every genetic prediction in this report, confirming that your liver tissue shows no signs of active cellular stress.

**What it means.** A direct alpha-1 antitrypsin blood protein test can establish your functional circulating levels. Ask your clinician if a one-time direct blood test is appropriate to document your baseline.

Your liver, lung and iron markers

Where computational scores appear, they describe the predicted effect of the DNA change itself. They do not account for how common the variant is, and a common variant can score highly while making little difference to any individual.

| GENE                                              | MARKERS<br>(GENOTYPE) | ASSOCIATION                                                 | WHAT IT MEANS FOR YOU                                                                                                                                                                                                                                                                                                       |
|---------------------------------------------------|-----------------------|-------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>SERPINA1</b><br>HIGH IMPACT +<br>HIGH EVIDENCE | rs17580 T/A           | Alpha-1 Antitrypsin Deficiency — susceptibility association | One of your two copies carries this variant · 4 of 4 computational tools predict this change harms the protein · Top 0.06% of all DNA changes by predicted impact · Published study · PMID 34648354<br>Having certain alleles here relates to altered production of a protective protein that guards lung and liver tissue. |

Measured, September 2025

|                                                                                      |                                                                                      |                                                                                                      |                                                                                             |
|--------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------|
| <div>AST</div> <div>30 IU/L</div> <div>IN RANGE</div> <div>was 32 (2024-06-17)</div> | <div>ALT</div> <div>21 IU/L</div> <div>IN RANGE</div> <div>was 28 (2024-06-17)</div> | <div>ALK. PHOSPHATASE</div> <div>50 IU/L</div> <div>AT THE EDGE</div> <div>was 60 (2024-06-17)</div> | <div>BILIRUBIN</div> <div>0.6 mg/dL</div> <div>IN RANGE</div> <div>was 1 (2024-06-17)</div> |
|--------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------|

## 8 B-vitamins, folate and homocysteine

### IN PLAIN WORDS

Your genetic profile shows variants in enzymes responsible for processing folate and B-vitamins, including two copies of the MTHFR C677T variant. Because this report contains no direct blood measurements for folate, vitamin B12, or homocysteine, your functional vitamin status remains unmeasured. Clinical guidelines suggest discussing whether direct biomarker testing is needed before altering your supplement intake.

- The signals.** You carry both copies of the C677T variant in MTHFR, alongside one copy of the rs1801394 variant in MTRR. These genes direct enzymes involved in cellular folate activation and homocysteine recycling.
- The reality.** This report includes no direct laboratory measurements for serum folate, vitamin B12, or homocysteine. Standard clinical guidelines from PharmGKB indicate that carrying MTHFR variants does not require altering folate intake in the absence of documented deficiency.
- What it means.** Direct blood measurements outrank genetic models when determining functional vitamin adequacy. Ask your clinician whether checking a routine serum B12 and homocysteine panel is appropriate before adjusting your vitamin supplementation.

### Your folate-pathway markers

Where computational scores appear, they describe the predicted effect of the DNA change itself. They do not account for how common the variant is, and a common variant can score highly while making little difference to any individual.

| GENE                                                    | MARKERS (GENOTYPE)          | ASSOCIATION                                                                  | WHAT IT MEANS FOR YOU                                                                                                                                                                                                                                                                                                                                                                               |
|---------------------------------------------------------|-----------------------------|------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <div>MTHFR</div> <div>HIGH IMPACT + HIGH EVIDENCE</div> | rs1801133 A/A               | Folate Metabolism                                                            | <div>Both copies carry this variant · 3 of 4 computational tools predict this change harms the protein · Top 0.2% of all DNA changes by predicted impact · PharmGKB guidance · PMID 25919709 · Published study · PMID 23754956</div> <div>Cellular studies show that this marker corresponds to modest differences in the efficiency of everyday folate processing across large study groups.</div> |
| <div>FUT2</div> <div>ASSOCIATION</div>                  | rs601338 G/A · rs602662 G/A | FUT2 secretor-status variant                                                 | <div>One of your two copies carries this variant · No computational tool predicts this change harms the protein · Top 0.00% of all DNA changes by predicted impact · Published study · PMID 23754956 (vitamin b12 levels)</div> <div>Secretor status is a common trait studied in B12 absorption and infection-resistance research — an association, not a disease finding.</div>                   |
| <div>MTRR</div> <div>ASSOCIATION</div>                  | rs1801394 A/G               | Disorders of Intracellular Cobalamin Metabolism — susceptibility association | <div>One of your two copies carries this variant · 1 of 3 computational tools predicts this change harms the protein · Top 0.5% of all DNA changes by predicted impact</div> <div>Inherited differences at this site are linked to small shifts in how the body recycles essential B vitamins and homocysteine.</div>                                                                               |

Folate, B12 and homocysteine were not on your panel. None is required; a homocysteine level is the measurement that reflects this pathway.

9

# Brain chemistry, mood, sleep and habits

IN PLAIN WORDS

*You described persistent sleep loss and rising daily family stress, which directly influence neurochemical and emotional balance. Your DNA profile carries common variations linked to neurotransmitter signaling and habit regulation, but genetics cannot diagnose mood or sleep patterns. Direct lifestyle adjustments and clinical conversations remain the most effective tools for managing central nervous system demands.*

**The signals.** You carry both copies of regulatory markers in COMT, one copy of the Taq1A marker in ANKK1, and one copy of the rs6265 marker in BDNF. These genes produce enzymes, receptors, and neurotrophic factors that participate in central nervous system neurotransmitter signaling.

**The reality.** These common genetic markers describe broad population tendencies rather than clinical conditions or fixed personality traits. Measured daily sleep duration, stress exposure, and recovery patterns exert far greater influence on cognitive function than these inherited variants.

**What it means.** Nothing changes today based on these inherited brain-chemistry markers. At your next visit, ask your healthcare provider how targeted sleep and stress management strategies can support your day-to-day focus.

## Your brain-chemistry markers

Where computational scores appear, they describe the predicted effect of the DNA change itself. They do not account for how common the variant is, and a common variant can score highly while making little difference to any individual.

| GENE                         | MARKERS (GENOTYPE) | ASSOCIATION                                                          | WHAT IT MEANS FOR YOU                                                                                                                                                                                                                                                                                                                                                 |
|------------------------------|--------------------|----------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>ADH1B</b><br>ASSOCIATION  | rs1229984 C/C      | ADH1B-associated variant                                             | Both copies carry this variant · No computational tools predicts this change harms the protein · Top 5% of all DNA changes by predicted impact · Published study · PMID 30643251 (alcohol consumption)<br>Scientific research correlates this specific location with how rapidly the human body metabolizes alcohol into breakdown products.                          |
| <b>ADH1C</b><br>ASSOCIATION  | rs698 T/C          | Alcohol dependence                                                   | One of your two copies carries this variant · No computational tool predicts this change harms the protein · Top 3% of all DNA changes by predicted impact<br>Observational studies tie this genetic site to subtle differences in alcohol processing speed and population-level patterns of drinking behavior.                                                       |
| <b>ANKK1</b><br>ASSOCIATION  | rs1800497 G/A      | Schizophrenia                                                        | One of your two copies carries this variant · No computational tools predicts this change harms the protein · Top 33% of all DNA changes by predicted impact<br>Evidence links this variant to slight statistical differences in brain reward pathways and dopamine signaling across diverse study cohorts.                                                           |
| <b>BDNF</b><br>ASSOCIATION   | rs6265 C/T         | Memory impairment, susceptibility to                                 | One of your two copies carries this variant · 2 of 4 computational tools predict this change harms the protein · Top 2% of all DNA changes by predicted impact · Published study · PMID 40436827 (body mass index)<br>Neurological research associates this site with minor differences in brain neuroplasticity and cognitive recall performance across populations. |
| <b>CHRNA3</b><br>ASSOCIATION | rs1051730 G/A      | Smoking as a quantitative trait locus 3 — susceptibility association | One of your two copies carries this variant · Published study · PMID 20418890<br>Large-scale studies link this location to mild correlations with nicotine dependence patterns and statistical lung cancer susceptibility.                                                                                                                                            |
| <b>CHRNA5</b><br>ASSOCIATION | rs16969968 G/A     | Nicotine response — susceptibility association                       | One of your two copies carries this variant · No computational tools predicts this change harms the protein · Top 1% of all DNA changes by predicted impact · Published study · PMID 31294817<br>Molecular findings indicate this site influences cellular receptor sensitivity to nicotine, subtly affecting physical responses to tobacco exposure across groups.   |

| GENE                         | MARKERS (GENOTYPE)                               | ASSOCIATION                   | WHAT IT MEANS FOR YOU                                                                                                                                                                        |
|------------------------------|--------------------------------------------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>COMT</b><br>ASSOCIATION   | rs165599 A/A ·<br>rs165728 T/T                   | Catecholamine Metabolism      | <b>Both copies carry this variant</b><br>Enzyme activity at this genomic position relates to the relative speed at which the body breaks down neurotransmitters like dopamine.               |
| <b>GABRA2</b><br>ASSOCIATION | rs279871 T/C ·<br>rs279845 T/A ·<br>rs279836 T/A | Alcoholism, susceptibility to | <b>One of your two copies carries this variant</b><br>Survey data associates this variant with small variations in central nervous system excitability and susceptibility to alcohol misuse. |

## 10 Worth measuring directly

When a direct laboratory measurement answers a health question better than a consumer DNA marker can, the measured phenotype takes priority. These are conversation starters for a routine visit — your clinician decides what is appropriate.

**Lipoprotein(a) blood test** [ASK ABOUT THIS TEST](#)

Your LPA marker is associated with higher lipoprotein(a), which a standard lipid panel does not measure. Current guidance supports measuring Lp(a) at least once in adulthood — the blood level, not the genotype, is what matters clinically.

**Alpha-1 antitrypsin (AAT) level** [ASK ABOUT THIS TEST](#)

A simple blood level resolves whether an alpha-1 antitrypsin carrier finding has any functional effect. The measured level is the decision-relevant number.

**Iron studies (ferritin, transferrin saturation)** [ASK ABOUT THIS TEST](#)

An iron-handling gene signal appears in this report. Iron studies measure the actual iron status — do not change any supplement first; review the finding and the blood work with your clinician together. Note: the DNA signal behind this suggestion is itself unconfirmed (section 14), which makes the direct blood measurement the more informative next step.

Ask the ordering clinic for the test by name. Laboratory order numbers differ between Labcorp and Quest and between draw sites, so the test name — and the CPT code your clinician uses — is the reliable identifier.

## 11 Medicine-handling genes (pharmacogenomics)

**IN PLAIN WORDS**

*Your genetic results identify single-copy variants in several drug-processing enzymes and transporters that may influence how you metabolize future medications. None of your current daily prescriptions are directly compromised by these specific genetic findings today. Keeping these pharmacogenomic results on file allows your care team to tailor future prescribing decisions.*

How your genetic markers relate to medication handling. A consumer array reads single markers — it cannot assemble the full diplotype (both gene copies) that real prescribing decisions use, so every entry here is a heads-up to confirm with clinical testing, never a result to dose from.

### Relevant to medications you take now [GOOD NEWS](#)

None of your pharmacogenomic markers affect a medication on your current list.

## Keep on file for future prescribing UNCONFIRMED

| GENE           | MARKER(S)                     | MEDICATIONS AFFECTED                                                                                                                                                                                                                                                       | WHAT THIS COULD MEAN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | EVIDENCE           |
|----------------|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------|
| <b>CYP2C19</b> | rs12769205 A/G; rs4244285 G/A | <div>Clopidogrel (blood thinner)</div> <div>Diazepam (anxiety)</div> <div>Proton-pump inhibitors (acid reflux)</div> <div>Antidepressants (depression)</div>                                                                                                               | <p>One *2 (het) allele — catalogued as “no enzyme function” for that single copy. The second copy of this gene is not resolved by this test, so your overall metabolizer status cannot be assigned here; a reduced-function result (for example, an intermediate metabolizer) is possible and a clinical pharmacogenomic test would settle it.</p> <p><i>The CYP2C19 gene provides instructions for a liver enzyme that helps metabolize medications like clopidogrel, diazepam, proton-pump inhibitors, and certain antidepressants. You carry one copy of the *2 allele, which CPIC guidelines catalogue as having no enzyme function for that single copy. Because this test does not resolve your second copy, your overall metabolizer status cannot be determined. Nothing changes today, useful for future prescriptions.</i></p> | CPIC PMID 34216398 |
| <b>CYP2C9</b>  | rs1057910 A/C                 | <div>Glipizide (diabetes)</div> <div>Lesinurad (gout)</div> <div>Flurbiprofen (pain relief)</div> <div>Piroxicam (pain relief)</div> <div>Tolbutamide (diabetes)</div> <div>Phenytoin (seizures)</div> <div>Warfarin (blood thinner)</div> <div>NSAIDs (pain relief)</div> | <p>One *3 (het) allele — catalogued as “no enzyme function” for that single copy. The second copy of this gene is not resolved by this test, so your overall metabolizer status cannot be assigned here; a reduced-function result (for example, an intermediate metabolizer) is possible and a clinical pharmacogenomic test would settle it.</p> <p><i>The CYP2C9 gene produces an enzyme responsible for clearing drugs such as warfarin, phenytoin, glipizide, and nonsteroidal anti-inflammatory agents. You carry one copy of the *3 allele, which is catalogued as providing no enzyme function for that single copy. Your overall metabolizer status is not determined because the second copy was not resolved. Nothing changes today, useful for future prescriptions.</i></p>                                                 | CPIC PMID 28198005 |
| <b>CYP3A5</b>  | rs776746 C/C                  | <div>Tacrolimus (transplant rejection)</div>                                                                                                                                                                                                                               | <p>A variant in CYP3A5 associated with altered handling of the listed medications.</p> <p><i>The CYP3A5 gene codes for an enzyme involved in processing immunosuppressive therapies, most notably tacrolimus. You carry both copies of the rs776746 marker, a variant associated with altered drug clearance according to CPIC guidelines. You are not taking this medicine currently. Nothing changes today, useful for future prescriptions.</i></p>                                                                                                                                                                                                                                                                                                                                                                                   | CPIC PMID 25801146 |

| GENE           | MARKER(S)                                                                             | MEDICATIONS AFFECTED                                                                                                                                                                                                                                                                                              | WHAT THIS COULD MEAN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | EVIDENCE           |
|----------------|---------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------|
| <b>IFNL4</b>   | rs12979860 C/T; rs8099917 T/G                                                         | <div>Peginterferon alfa-2a (hepatitis C)</div> <div>Peginterferon alfa-2b (hepatitis C)</div> <div>Ribavirin (hepatitis C)</div> <div>Telaprevir (hepatitis C)</div> <div>Boceprevir (hepatitis C)</div> <div>Peginterferon alfa-2b and ribavirin (hepatitis C)</div> <div>Peginterferon alfa (hepatitis C)</div> | <p>A variant in IFNL4 associated with altered handling of the listed medications.</p> <p><i>The IFNL4 gene encodes an interferon protein that influences immune-mediated antiviral responses. You carry one copy of the rs12979860 marker and one copy of rs8099917, variants linked to response rates for older hepatitis C regimens like peginterferon and ribavirin. You are not currently prescribed these agents. Nothing changes today, useful for future prescriptions.</i></p>                                                                                                                                                                                                                                                                                   | CPIC PMID 24096968 |
| <b>SLC01B1</b> | rs4149056 T/C                                                                         | <div>Lovastatin (cholesterol)</div> <div>Pitavastatin (cholesterol)</div> <div>Pravastatin (cholesterol)</div> <div>Rosuvastatin (cholesterol)</div> <div>Simvastatin (cholesterol)</div> <div>Atorvastatin (cholesterol)</div> <div>Fluvastatin (cholesterol)</div> <div>Statins (cholesterol)</div>             | <p>One *5 (het) allele — catalogued as “decreased transporter function” for that single copy. The second copy of this gene is not resolved by this test, so your overall metabolizer status cannot be assigned here; a reduced-function result (for example, an intermediate metabolizer) is possible and a clinical pharmacogenomic test would settle it.</p> <p><i>The SLC01B1 gene encodes a liver transporter that moves statin medications from the bloodstream into liver tissue. You carry one copy of the *5 allele, catalogued under CPIC guidelines as having decreased transporter function for that single copy. Because your second copy is unread, your overall status remains unassigned. Nothing changes today, useful for future prescriptions.</i></p> | CPIC PMID 35152405 |
| <b>VKORC1</b>  | rs7294 C/T; rs2359612 A/G; rs8050894 C/G; rs9934438 G/A; rs2884737 A/C; rs9923231 C/T | <div>Warfarin (blood thinner)</div> <div>Phenprocoumon (blood thinner)</div> <div>Acenocoumarol (blood thinner)</div>                                                                                                                                                                                             | <p>One -1639G&gt;A (het) allele — catalogued as “increased warfarin sensitivity” for that single copy. The second copy of this gene is not resolved by this test, so your overall metabolizer status cannot be assigned here; a reduced-function result (for example, an intermediate metabolizer) is possible and a clinical pharmacogenomic test would settle it.</p> <p><i>The VKORC1 gene encodes the enzyme targeted by warfarin and related vitamin K antagonist blood thinners. You carry one copy of the -1639G&gt;A variant, which CPIC guidelines link to increased sensitivity to warfarin dosing. You are not currently taking anticoagulants. Nothing changes today, useful for future prescriptions.</i></p>                                               | CPIC PMID 28198005 |

| GENE          | MARKER(S)                                                                                               | MEDICATIONS AFFECTED                                                        | WHAT THIS COULD MEAN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | EVIDENCE                     |
|---------------|---------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------|
| <b>MTHFR</b>  | rs1801133 A/A                                                                                           | Methotrexate (chemotherapy / arthritis)<br>Folate supplementation (vitamin) | C677T (hom) — reduced enzyme activity. Current public-health guidance does not recommend changing folate intake or medication choices on this variant alone.<br><i>The MTHFR gene produces an enzyme that activates folate for cellular biochemical pathways and homocysteine recycling. You carry both copies of the C677T variant, which is associated with reduced enzyme activity. Current PharmGKB guidance does not recommend changing folate supplementation or medication choices on this finding alone. Nothing changes today, useful for future prescriptions.</i> | PharmGKB<br>PMID<br>25919709 |
| <b>ABCB1</b>  | rs2235046 T/C; rs2032588 G/A; rs10276036 C/T; rs868755 T/G; rs1202168 G/A; rs1211152 C/C; rs2214102 C/C | Tramadol (pain relief) Digoxin (heart rhythm)                               | A variant in ABCB1 associated with altered handling of the listed medications.<br><i>The ABCB1 gene produces P-glycoprotein, a transport pump that moves drugs across intestinal walls and cellular membranes. Your DNA carries variants that research studies associate with altered transport of medicines such as tramadol and digoxin. You are not currently prescribed these medications. Nothing changes today, useful for future prescriptions.</i>                                                                                                                   | Reported                     |
| <b>ABCC1</b>  | rs45511401 G/T                                                                                          | Atorvastatin (cholesterol)                                                  | A variant in ABCC1 associated with altered handling of the listed medications.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Reported                     |
| <b>APOE</b>   | rs405509 G/G; rs769450 A/A; rs439401 C/C                                                                | Warfarin (blood thinner)                                                    | A variant in APOE associated with altered handling of the listed medications.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Reported                     |
| <b>CHRNA5</b> | rs16969968 G/A                                                                                          | Nicotine (smoking)                                                          | A variant in CHRNA5 associated with altered handling of the listed medications.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Reported                     |
| <b>COMT</b>   | rs165599 A/A; rs165728 T/T                                                                              | Tramadol (pain relief)                                                      | A variant in COMT associated with altered handling of the listed medications.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Reported                     |

Star-allele names (\*2, \*3, ...) are catalog labels for specific variants, not severity grades. A full metabolizer phenotype requires both gene copies, copy-number, and phase — a dedicated clinical pharmacogenomic panel provides that.

## 12 Everyday traits and lifestyle

**What you are already doing.** Completing a detailed health and genetics review, and keeping an accurate medication and supplement list, are the two things that make every other decision in this report better. The goal from here is to make sure what you are doing is evidence-based, safe in combination, and aimed at measurements that matter.

### DAILY MOVEMENT

**~3,000 steps/day**

Self-reported average. Increasing this gradually — for example by 500 to 1,000 steps a day over several weeks — is a practical way to raise total activity. There is no single step count that is medically required.

AEROBIC ACTIVITY

**0 min/week vigorous**

You reported no vigorous exercise. You do not necessarily need vigorous exercise specifically, but this is an opportunity to add purposeful aerobic activity. A commonly used adult target is about 150 minutes of moderate activity or 75 minutes of vigorous activity per week, or an equivalent mix, plus muscle-strengthening on at least two days.

BODY MASS INDEX

**32.1**

At age 40, your BMI is one useful but imperfect measure of cardiometabolic risk. It is best read alongside blood pressure, waist circumference, glucose or A1c, lipids, fitness, and your weight trend over time — several of which appear in section 4.

Used well, the items in this report can help you and your healthcare team find modifiable areas worth measuring, discussing, and improving over time. Nothing here promises a particular health outcome.

Traits & wellness markers (non-clinical)

APOE-based traits are not shown: a defining APOE marker disagreed between your two DNA files (see section 15).

Population associations for everyday traits, strongest reported effect first. These are statistical tendencies, usually small, and none of them is medical guidance.

| GENE  | MARKER        | TRAIT                           | WHAT THE RESEARCH SAYS                                                                                                                                                                                                             |
|-------|---------------|---------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| HTR2A | rs6311 CC     | Sexual dysfunction risk on SSRI | Associated in some studies with a higher likelihood of sexual side-effects on SSRI antidepressants. The evidence is mixed, and current prescribing guidelines do not use this marker to choose or change antidepressants.          |
| COMT  | rs4680 GG     | Dopamine/Stress (Val158Met)     | Higher-activity COMT variant — faster dopamine clearance. Population studies associate it with small differences in stress response and pain threshold; effects are modest and not predictive for any individual.                  |
| CETP  | rs708272 CT   | HDL Cholesterol Levels (TaqIB)  | Common CETP variant associated with modestly different HDL cholesterol levels in population studies. Your measured lipid panel is the direct source of truth for your own levels.                                                  |
| ALDH2 | rs671 GG      | Alcohol Flush ('Asian Flush')   | Two typical-function copies of ALDH2: you clear acetaldehyde (an alcohol breakdown product) at the usual rate and are unlikely to experience alcohol-related facial flushing. This says nothing about alcohol-related health risk. |
| MC4R  | rs10871777 AG | Weight Regulation #2            | Associated with a very small average difference in adult BMI (about 0.2 units) — informational only.                                                                                                                               |

13 The long tail — other population associations

IN PLAIN WORDS

*The population associations listed here represent statistical research patterns rather than medical diagnoses or deterministic health risks. Every finding reflects statistical tendencies observed across large study cohorts, not personal certainty for your health. Verified laboratory measurements and direct clinical evaluations always outrank these background research markers.*

These are population-level statistical associations, not diagnoses, and only associations meeting this report’s evidence threshold are shown. Markers are grouped by gene region so linked markers read as one finding instead of several. “Susceptibility” means a statistical population signal — not a condition you have. Coordinates are hg38.

Where computational scores appear, they describe the predicted effect of the DNA change itself. They do not account for how common the variant is, and a common variant can score highly while making little difference to any individual.

Immune system & inflammation

| GENE      | MARKERS (GENOTYPE) | ASSOCIATION                                             | WHAT IT MEANS FOR YOU                                                                                                                                                                         |
|-----------|--------------------|---------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| AP4B1-AS1 | rs2488457 G/C      | Diabetes mellitus, insulin-dependent, susceptibility to | One of your two copies carries this variant<br>Statistical associations connect this specific chromosomal region to minor, population-level fluctuations in long-term diabetes vulnerability. |

| GENE                           | MARKERS (GENOTYPE) | ASSOCIATION                                             | WHAT IT MEANS FOR YOU                                                                                                                                                                                                                                       |
|--------------------------------|--------------------|---------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>CD209</b><br>ASSOCIATION    | rs735239 A/G       | Mycobacterium tuberculosis, susceptibility to           | <b>One of your two copies carries this variant</b><br>Specific forms of this marker correlate with slight shifts in how immune cells recognize and respond to tuberculosis bacteria.                                                                        |
| <b>CD244</b><br>ASSOCIATION    | rs3766379 T/C      | Rheumatoid arthritis                                    | <b>One of your two copies carries this variant</b><br>Immunological studies show this variant has a small statistical association with autoimmune regulation and population likelihood of joint inflammation.                                               |
| <b>CHI3L1</b><br>ASSOCIATION   | rs4950928 G/C      | Asthma-related traits, susceptibility to, 7             | <b>One of your two copies carries this variant</b><br>Respiratory studies connect differences here with circulating inflammatory protein levels and a minor shift in population-wide airway reactivity traits.                                              |
| <b>CRP</b><br>ASSOCIATION      | rs1205 T/T         | Inflammation                                            | <b>Both copies carry this variant · Published study · PMID 33339817 (c-reactive protein levels)</b><br>Genetic variation at this position is associated with subtle baseline differences in systemic inflammatory protein levels across demographic groups. |
| <b>IL1B</b><br>ASSOCIATION     | rs1143627 G/A      | Gastric cancer susceptibility after h. pylori infection | <b>One of your two copies carries this variant</b><br>Stomach research links variants here to subtle differences in inflammatory responses following common bacterial infections in large populations.                                                      |
| <b>IL6-AS1</b><br>ASSOCIATION  | rs1800795 C/G      | Diabetes mellitus, type 1, susceptibility to            | <b>One of your two copies carries this variant</b><br>Cohort data reveals a minor statistical correlation between this site and long-term susceptibility to bile duct inflammatory conditions.                                                              |
| <b>IRF5</b><br>ASSOCIATION     | rs10954213 G/A     | Systemic lupus erythematosus, susceptibility to, 10     | <b>One of your two copies carries this variant · Published study · PMID 24097067 (sjögren's syndrome)</b><br>Genome-wide studies link this variant to small variations in immune signaling pathways tied to systemic autoimmune reactions.                  |
| <b>MAPKAPK3</b><br>ASSOCIATION | rs414171 T/T       | Bacteremia, susceptibility to, 2                        | <b>Both copies carry this variant</b><br>1 notable marker in this gene region.                                                                                                                                                                              |
| <b>NPSR1</b><br>ASSOCIATION    | rs324981 A/T       | Asthma-related traits, susceptibility to, 2             | <b>One of your two copies carries this variant · No computational tools predicts this change harms the protein · Top 2% of all DNA changes by predicted impact</b><br>1 notable marker in this gene region.                                                 |
| <b>PHF20L1</b><br>ASSOCIATION  | rs180195 G/G       | Autoimmune thyroid disease, susceptibility to, 3        | <b>Both copies carry this variant</b><br>1 notable marker in this gene region.                                                                                                                                                                              |
| <b>PTGDR</b><br>ASSOCIATION    | rs708494 A/A       | Asthma, aspirin-induced, susceptibility to              | <b>Both copies carry this variant</b><br>1 notable marker in this gene region.                                                                                                                                                                              |

## Cancer-risk association markers (population level)

| GENE                         | MARKERS (GENOTYPE) | ASSOCIATION       | WHAT IT MEANS FOR YOU                                                                                                                                                                                             |
|------------------------------|--------------------|-------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>GABRG2</b><br>ASSOCIATION | rs7711080 G/G      | Colorectal cancer | <b>Both copies carry this variant · Published study · PMID 37890997</b><br>Oncology studies link this marker to a small statistical difference in lifetime susceptibility to colon tissue changes in populations. |
| <b>KCNB2</b><br>ASSOCIATION  | rs2919408 A/A      | Colorectal cancer | <b>Both copies carry this variant · Published study · PMID 37890997</b><br>1 notable marker in this gene region.                                                                                                  |

## Medicine-response research markers

| GENE                                             | MARKERS (GENOTYPE)                               | ASSOCIATION            | WHAT IT MEANS FOR YOU                                                                                                                                                                                                                                                                     |
|--------------------------------------------------|--------------------------------------------------|------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>SLC29A3</b><br>HIGH IMPACT +<br>HIGH EVIDENCE | rs780668 T/T                                     | Gemcitabine response   | Both copies carry this variant · 1 of 4 computational tools predicts this change harms the protein · Top 0.4% of all DNA changes by predicted impact<br>Biomedical research has examined this locus for its minor role in cellular nucleoside transport and related metabolic phenotypes. |
| <b>DIO1</b><br>ASSOCIATION                       | rs2235544 C/A                                    | Levothyroxine response | One of your two copies carries this variant · Published study · PMID 41238958 (thyroxine levels)<br>Clinical research connects this site to how the body naturally converts and processes the thyroid medication levothyroxine.                                                           |
| <b>HELLS</b><br>ASSOCIATION                      | rs12777823 G/A                                   | Warfarin response      | One of your two copies carries this variant · Published study · PMID 23755828<br>Studies show that this genetic location correlates with how efficiently the body clears and metabolizes the blood-thinning medicine warfarin.                                                            |
| <b>IPCEF1</b><br>ASSOCIATION                     | rs7759388 G/A                                    | Tramadol response      | One of your two copies carries this variant<br>Pharmacological findings indicate this marker relates to subtle individual differences in how cellular receptors interact with the pain medicine tramadol.                                                                                 |
| <b>LOC101929829</b><br>ASSOCIATION               | rs1081004 C/T                                    | Tramadol response      | One of your two copies carries this variant<br>1 notable marker in this gene region.                                                                                                                                                                                                      |
| <b>MIR4713HG</b><br>ASSOCIATION                  | rs727479 C/A                                     | Letrozole response     | One of your two copies carries this variant · Published study · PMID 29325096 (estradiol levels)<br>1 notable marker in this gene region.                                                                                                                                                 |
| <b>OPRM1</b><br>ASSOCIATION                      | rs675026 G/G ·<br>rs562859 T/T ·<br>rs650245 G/G | Tramadol response      | Both copies carry this variant · Published study · PMID 40436827 (high-density lipoprotein levels)<br>3 notable markers in this gene region.                                                                                                                                              |

## Development, pregnancy & other

| GENE                       | MARKERS (GENOTYPE) | ASSOCIATION         | WHAT IT MEANS FOR YOU                                                                                                                                                                                                 |
|----------------------------|--------------------|---------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>BMP2</b><br>ASSOCIATION | rs1884302 T/C      | Craniosynostosis 7  | One of your two copies carries this variant · Published study · PMID 23160099<br>Developmental research associates this genetic marker with subtle alterations in biological pathways that guide cranial bone fusion. |
| <b>MCM6</b><br>ASSOCIATION | rs4988235 G/A      | Lactase persistence | One of your two copies carries this variant · Published study · PMID 34648354<br>1 notable marker in this gene region.                                                                                                |

## Other

| GENE                       | MARKERS (GENOTYPE)                            | ASSOCIATION                    | WHAT IT MEANS FOR YOU                                                                                                                                                                                          |
|----------------------------|-----------------------------------------------|--------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>APOE</b><br>ASSOCIATION | rs405509 G/G ·<br>rs769450 A/A · rs439401 C/C | Late-Onset Alzheimer's Disease | Both copies carry this variant · Published study · PMID 34122051<br>Variations in this regulatory region show a modest population-level statistical correlation with the odds of late-onset cognitive decline. |

Showing the 24 highest-evidence gene regions of 34 in this section.

24 gene regions here plus 38 discussed under the health themes account for all 72 regions that passed the threshold.

## 14 Unconfirmed rare calls — for transparency, not action

**Read this first.** Consumer DNA arrays are designed for common variants. At rare positions a call like these is **more often a reading error than a real finding**. This analysis produced 22 such calls; the entries below are the ones with a supporting citation or computational evidence to report. Each carries a “pathogenic” label in a public database but was read at a position this kind of test is unreliable at. They are listed for completeness and transparency, deliberately separated from the action items. None is a diagnosis and none should change any treatment. **Confirmation, if pursued, is a clinical-grade test ordered by your clinician — not another consumer test.** These are not being labelled artifacts: some rare calls do prove real, which is exactly why confirmation rather than dismissal is the right next step.

### Possible carrier findings — relevant mainly for family planning, and only if clinically confirmed

| GENE          | DATABASE LABEL                                     | MARKER / GENOTYPE     | WHY IT IS LISTED                                                                                                                                                                                                                                                                                                                                                                                                                 |
|---------------|----------------------------------------------------|-----------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>CHRNA</b>  | Autosomal recessive multiple pterygium syndrome    | rs267606725 C/T (Het) | <b>This label describes a severe congenital syndrome affecting fetal joint movement, making an unconfirmed single-copy finding in an adult an expected carrier state or technical reading artefact rather than active disease.</b> If this call were confirmed, the predicted effect of the change would be: 1 of 1 computational tool predicts this change harms the protein; Top 0.04% of all DNA changes by predicted impact. |
| <b>MPDZ</b>   | Hydrocephalus, nonsyndromic, autosomal recessive 2 | rs192227753 C/T (Het) | If this call were confirmed, the predicted effect of the change would be: 3 of 4 computational tools predict this change harms the protein; Top 0.2% of all DNA changes by predicted impact.                                                                                                                                                                                                                                     |
| <b>MYO6</b>   | Autosomal recessive nonsyndromic hearing loss 37   | rs41269323 G/A (Het)  | If this call were confirmed, the predicted effect of the change would be: 4 of 4 computational tools predict this change harms the protein; Top 0.1% of all DNA changes by predicted impact.                                                                                                                                                                                                                                     |
| <b>TCIRG1</b> | Autosomal recessive osteopetrosis 1                | rs139617644 G/A (Het) | If this call were confirmed, the predicted effect of the change would be: 1 of 1 computational tool predicts this change harms the protein; Top 0.04% of all DNA changes by predicted impact.                                                                                                                                                                                                                                    |

### Single-copy calls at rare positions

| GENE          | DATABASE LABEL                                    | MARKER / GENOTYPE     | WHY IT IS LISTED                                                                                                                                                                                                                                                                                                                                                                     |
|---------------|---------------------------------------------------|-----------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>AGXT</b>   | Primary hyperoxaluria, type I                     | rs180177297 G/T (Het) | <b>This disorder causes severe early-onset kidney stones and renal failure, making an unconfirmed call unlikely given your normal eGFR of 114 mL/min/1.73 and healthy renal panel.</b> If this call were confirmed, the predicted effect of the change would be: 1 of 1 computational tool predicts this change harms the protein; Top 0.05% of all DNA changes by predicted impact. |
| <b>APOA2</b>  | APOA2 variant — diet-interaction association      | rs5082 G/A (Het)      | Studied in saturated-fat/weight interaction research; not familial hypercholesterolemia.                                                                                                                                                                                                                                                                                             |
| <b>ASL</b>    | Argininosuccinate lyase deficiency                | rs28940585 C/T (Het)  | <b>This metabolic urea cycle disorder typically presents in the newborn period with acute ammonia buildup, making an unconfirmed adult call a probable technical artefact.</b> If this call were confirmed, the predicted effect of the change would be: 4 of 4 computational tools predict this change harms the protein; Top 0.2% of all DNA changes by predicted impact.          |
| <b>DNAH11</b> | Primary ciliary dyskinesia 7                      | rs35865357 G/A (Het)  | If this call were confirmed, the predicted effect of the change would be: 2 of 3 computational tools predict this change harms the protein; Top 0.3% of all DNA changes by predicted impact.                                                                                                                                                                                         |
| <b>FREM1</b>  | Congenital diaphragmatic hernia                   | rs41298151 C/G (Het)  | If this call were confirmed, the predicted effect of the change would be: 3 of 4 computational tools predict this change harms the protein; Top 0.3% of all DNA changes by predicted impact.                                                                                                                                                                                         |
| <b>HBG1</b>   | HBG1 — hereditary persistence of fetal hemoglobin | rs7482144 G/A (Het)   | A benign, often protective blood trait that raises fetal hemoglobin levels.                                                                                                                                                                                                                                                                                                          |

| GENE     | DATABASE LABEL                                                                         | MARKER / GENOTYPE        | WHY IT IS LISTED                                                                                                                                                                                                                                                                                                                                                                    |
|----------|----------------------------------------------------------------------------------------|--------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| HGSNAT   | Mucopolysaccharidosis, MPS-III-C                                                       | rs112029032<br>G/A (Het) | If this call were confirmed, the predicted effect of the change would be: 2 of 3 computational tools predict this change harms the protein; Top 0.5% of all DNA changes by predicted impact.                                                                                                                                                                                        |
| HYKK     | 15q25 locus (HYKK/CHRNA5) — smoking-related susceptibility                             | rs8034191<br>T/C (Het)   | A susceptibility association from smoking-behavior and lung studies; not a diagnosis of COPD.                                                                                                                                                                                                                                                                                       |
| LARGE1   | Muscular dystrophy-dystroglycanopathy type B6                                          | rs121908675<br>C/T (Het) | If this call were confirmed, the predicted effect of the change would be: 3 of 4 computational tools predict this change harms the protein; Top 0.2% of all DNA changes by predicted impact.                                                                                                                                                                                        |
| LIPT1    | Lipoyl transferase 1 deficiency                                                        | rs137891647<br>C/G (Het) | If this call were confirmed, the predicted effect of the change would be: 1 of 1 computational tool predicts this change harms the protein; Top 0.03% of all DNA changes by predicted impact.                                                                                                                                                                                       |
| MCM4     | Primary immunodeficiency with natural-killer cell deficiency and adrenal insufficiency | rs117063344<br>G/C (Het) | If this call were confirmed, the predicted effect of the change would be: 3 of 4 computational tools predict this change harms the protein; Top 0.3% of all DNA changes by predicted impact.                                                                                                                                                                                        |
| MMAB     | Methylmalonic aciduria, cblB type                                                      | rs869320654<br>A/C (Het) | If this call were confirmed, the predicted effect of the change would be: 4 of 4 computational tools predict this change harms the protein; Top 0.2% of all DNA changes by predicted impact.                                                                                                                                                                                        |
| NECTIN4  | Ectodermal dysplasia-syndactyly syndrome 1                                             | rs1537044<br>G/A (Het)   | If this call were confirmed, the predicted effect of the change would be: 3 of 4 computational tools predict this change harms the protein; Top 0.1% of all DNA changes by predicted impact.                                                                                                                                                                                        |
| PTF1A    | Permanent neonatal diabetes mellitus                                                   | rs7918487<br>T/C (Het)   | <b>This condition causes severe insulin-dependent diabetes at birth, an outcome that is completely incompatible with your adult onset and normal measured hemoglobin A1c of 4.7 %.</b> If this call were confirmed, the predicted effect of the change would be: 2 of 4 computational tools predict this change harms the protein; Top 0.8% of all DNA changes by predicted impact. |
| RAPSN    | Congenital myasthenic syndrome 11                                                      | rs104894301<br>G/T (Het) | If this call were confirmed, the predicted effect of the change would be: 1 of 1 computational tool predicts this change harms the protein; Top 0.03% of all DNA changes by predicted impact.                                                                                                                                                                                       |
| SLC26A10 | SLC26A10-associated variant                                                            | rs113207856<br>G/A (Het) | If this call were confirmed, the predicted effect of the change would be: 1 of 1 computational tool predicts this change harms the protein; Top 0.01% of all DNA changes by predicted impact.                                                                                                                                                                                       |

Of the remainder, 2 further calls are not shown for length. None is actionable without clinical confirmation, and customer service can provide the full list of positions on request.

15

About your data — and what this test cannot do

IN PLAIN WORDS

*This report was built from two consumer DNA files, one laboratory panel. Here is exactly what was read, what was excluded, and what this kind of test cannot do.*

|                                                                                             |                                                                                   |                                                                                                        |                                                                                               |
|---------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------|
| <div>POSITIONS READ</div> <div>643,163</div> <div>97.0% called successfully</div>           | <div>FILES MERGED</div> <div>2</div> <div>two files (23andMe + AncestryDNA)</div> | <div>READ BY BOTH</div> <div>159,782</div> <div>99.98% agreement</div>                                 | <div>EXCLUDED</div> <div>28</div> <div>positions where the files disagreed</div>              |
| <div>HEALTH-RELEVANT VARIANTS</div> <div>192</div> <div>after the significance filter</div> | <div>CONFIRMED-QUALITY</div> <div>101</div> <div>in 72 gene regions</div>         | <div>UNCONFIRMED RARE CALLS</div> <div>41</div> <div>listed separately, never among the findings</div> | <div>POLYGENIC PANELS</div> <div>1 of 2</div> <div>a panel below coverage is not scored</div> |

510,882 positions were added by the second file.

**28 markers disagreed between your two files and were excluded from every section of this report.** A disagreement between two arrays is an unreliable read; reporting either side would present a coin-flip as a finding. Agreement between two consumer arrays is technical corroboration — it is not clinical confirmation. Nothing is deleted from your data; these markers are simply not used here.

**APOE status is not reported.** A defining APOE marker (rs7412) disagreed between your two files, so any APOE result from this data would be a guess. A targeted clinical test can resolve it if APOE testing is relevant to your care.

What this analysis screened for

Consumer arrays cover only some markers in each gene, so “none found” means none found *among the covered markers* — it never rules a condition out and is not a substitute for guideline-recommended screening.

- SCREENED

**Breast & ovarian cancer risk (BRCA):** no notable variant among the covered markers. Not excluded — unassayed variants remain possible.
- FINDING

**Heart health / familial cholesterol:** a finding in this report — detail in section 5.
- SCREENED

**Iron overload (hemochromatosis):** no notable variant among the covered markers. Not excluded — unassayed variants remain possible.
- NOT REPORTED

**Memory & brain aging (APOE):** APOE status is not reported for this order — see section 15.
- SCREENED

**Celiac / gluten sensitivity:** no notable variant among the covered markers. Not excluded — unassayed variants remain possible.
- FINDING

**B-vitamin processing (MTHFR):** a finding in this report — detail in section 8.
- UNCONFIRMED

**Hereditary colon cancer:** an unconfirmed signal only — see section 14.
- SCREENED

**Blood clot risk (Factor V Leiden & prothrombin):** no notable variant among the covered markers. Not excluded — unassayed variants remain possible.
- FINDING

**Alpha-1 antitrypsin (lung & liver):** a finding in this report — detail in section 7.

What this kind of test cannot do

- **Reads positions, not genes.** A consumer array checks a fixed list of positions. It cannot find variants it was not designed to read, so “nothing found” never rules a condition out.
  - **Unreliable at rare positions.** Accuracy is high for common variants and poor for rare ones. That is why 41 rare “pathogenic” calls sit in section 14, not in the findings.
  - **One marker at a time.** It cannot tell which parent a variant came from, count gene copies, or assemble the two-copy picture that drug-dosing decisions use.
  - **Ancestry matters.** Polygenic scores and many associations were built mostly on European-ancestry data and transfer imperfectly to others.
  - **A snapshot.** Labs describe the day they were drawn; DNA never changes, but what science knows about it does.
- How this report was made: your raw files were aligned to the hg38 reference; variants were annotated against public clinical-variant and computational-prediction resources and tiered by evidence; medicine-handling markers were checked against CPIC and PharmGKB guidance; the laboratory PDF was read into structured values; and every sentence drafted by a language model passed a rule check — no advice, no invented statistics, no unconfirmed gene — before printing. Rare pathogenic-labelled calls at positions consumer arrays read unreliably were set apart before any sentence was written.

16

Appendix — remaining laboratory results

The 38 results not shown in section 4, as extracted from the LabCorp report collected 2025-09-26. Previous values are the ones the laboratory printed beside each result. The uploaded PDF remains the complete record.

| TEST                   | RESULT               | REFERENCE   | PREVIOUS | TREND  | STATUS   |
|------------------------|----------------------|-------------|----------|--------|----------|
| Bilirubin (Urinalysis) | <b>Negative</b>      | Negative    | —        | Stable | IN RANGE |
| TSH                    | <b>0.736</b> uIU/mL  | 0.450-4.500 | 2.44     | Stable | IN RANGE |
| WBC                    | <b>4.1</b> x10E3/uL  | 3.4-10.8    | 5.6      | Stable | IN RANGE |
| RBC                    | <b>4.87</b> x10E6/uL | 4.14-5.80   | 5        | Stable | IN RANGE |
| Hemoglobin             | <b>14.9</b> g/dL     | 13.0-17.7   | 16.3     | Stable | IN RANGE |

| TEST                         | RESULT                | REFERENCE      | PREVIOUS | TREND    | STATUS   |
|------------------------------|-----------------------|----------------|----------|----------|----------|
| Hematocrit                   | <b>44.5</b> %         | 37.5-51.0      | 46.8     | Stable   | IN RANGE |
| MCV                          | <b>91</b> fL          | 79-97          | 94       | Stable   | IN RANGE |
| MCH                          | <b>30.6</b> pg        | 26.6-33.0      | 32.6     | Stable   | IN RANGE |
| MCHC                         | <b>33.5</b> g/dL      | 31.5-35.7      | 34.8     | Stable   | IN RANGE |
| RDW                          | <b>12.5</b> %         | 11.6-15.4      | 12.2     | Stable   | IN RANGE |
| Platelets                    | <b>236</b> x10E3/uL   | 150-450        | 226      | Stable   | IN RANGE |
| Neutrophils                  | <b>52</b> %           | Not Estab.     | 62       | Stable   | IN RANGE |
| Lymphs                       | <b>35</b> %           | Not Estab.     | 27       | Stable   | IN RANGE |
| Monocytes                    | <b>8</b> %            | Not Estab.     | 8        | Stable   | IN RANGE |
| Eos                          | <b>4</b> %            | Not Estab.     | 3        | Stable   | IN RANGE |
| Basos                        | <b>1</b> %            | Not Estab.     | 0        | Stable   | IN RANGE |
| Neutrophils (Absolute)       | <b>2.2</b> x10E3/uL   | 1.4-7.0        | 3.5      | Stable   | IN RANGE |
| Lymphs (Absolute)            | <b>1.5</b> x10E3/uL   | 0.7-3.1        | 1.5      | Stable   | IN RANGE |
| Monocytes (Absolute)         | <b>0.3</b> x10E3/uL   | 0.1-0.9        | 0.5      | Stable   | IN RANGE |
| Eos (Absolute)               | <b>0.2</b> x10E3/uL   | 0.0-0.4        | 0.1      | Stable   | IN RANGE |
| Baso (Absolute)              | <b>0.0</b> x10E3/uL   | 0.0-0.2        | 0        | Stable   | IN RANGE |
| Immature Granulocytes        | <b>0</b> %            | Not Estab.     | 0        | Stable   | IN RANGE |
| Immature Grans (Abs)         | <b>0.0</b> x10E3/uL   | 0.0-0.1        | 0        | Stable   | IN RANGE |
| Specific Gravity             | <b>1.023</b>          | 1.005-1.030    | 1.023    | Stable   | IN RANGE |
| Urine-Color                  | <b>Yellow</b>         | Yellow         | —        | Stable   | IN RANGE |
| WBC Esterase                 | <b>Negative</b>       | Negative       | —        | Stable   | IN RANGE |
| Ketones                      | <b>Negative</b>       | Negative       | —        | Stable   | IN RANGE |
| Occult Blood                 | <b>Negative</b>       | Negative       | —        | Stable   | IN RANGE |
| Urobilinogen, Semi-Qn        | <b>0.2</b> mg/dL      | 0.2-1.0        | 0.2      | Stable   | IN RANGE |
| Nitrite, Urine               | <b>Negative</b>       | Negative       | —        | Stable   | IN RANGE |
| WBC (Microscopic)            | <b>None seen</b> /hpf | 0-5            | —        | Stable   | IN RANGE |
| RBC (Microscopic)            | <b>None seen</b> /hpf | 0-2            | —        | Improved | IN RANGE |
| Epithelial Cells (non renal) | <b>None seen</b> /hpf | 0-10           | —        | Stable   | IN RANGE |
| Casts                        | <b>None seen</b> /lpf | None seen      | —        | Stable   | IN RANGE |
| Bacteria                     | <b>None seen</b>      | None seen/Few  | —        | Stable   | IN RANGE |
| pH                           | <b>5.5</b>            | 5.0-7.5        | 6.5      | Stable   | IN RANGE |
| Appearance                   | <b>Clear</b>          | Clear          | —        | Stable   | IN RANGE |
| Protein (Urinalysis)         | <b>Negative</b>       | Negative/Trace | —        | Stable   | IN RANGE |

## 17 Glossary

|                               |                                                                                                                                                                        |
|-------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>One copy / both copies</b> | You inherit one copy of every gene from each parent. “One copy” (heterozygous) means the variant was read on one of the two; “both copies” (homozygous) means on both. |
| <b>Variant</b>                | A position in DNA where your letter differs from the reference sequence. Most variants are common and harmless.                                                        |
| <b>Association</b>            | A statistical link seen across a population. It shifts the odds slightly for a group; it does not say what will happen to one person.                                  |
| <b>Susceptibility</b>         | Used for association markers: a small tilt toward a condition, not the condition itself.                                                                               |
| <b>Polygenic score</b>        | Many small genetic effects added into one number and compared with a reference population. Research-grade; not calibrated for every ancestry.                          |
| <b>Percentile</b>             | Where your score sits among 100 people in the reference model. The 90th percentile means higher than about 90 of them.                                                 |

|                             |                                                                                                                                                          |
|-----------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Star allele (*3, *5)</b> | A catalogue name for a specific variant in a drug-processing gene. It is a label, not a severity grade.                                                  |
| <b>Metabolizer status</b>   | How quickly a person processes a medicine, which needs both gene copies. A consumer array reads one marker, so status is never assigned here.            |
| <b>Reference range</b>      | The interval a laboratory expects for healthy people. Values just outside it are common and rarely meaningful alone.                                     |
| <b>Unconfirmed call</b>     | A rare variant read at a position consumer arrays are unreliable at. More often a reading error than a real finding; only a clinical test can settle it. |

This report is educational and is not a medical diagnosis, prescription, or treatment plan. It applies publicly established gene-drug and gene-health relationships to your data and is not a validated clinical diagnostic. Do not start, stop, or change any medication based on this report; any pharmacogenomic implication requires confirmatory clinical testing ordered by your provider. Always talk with a qualified healthcare provider before making decisions about your health. Questions about this report? Email [CustomerService@MarkerView.com](mailto:CustomerService@MarkerView.com).