
Comprehensive Genomic Analysis Report

SNP Genotyping — Clinical & Research Annotation

Platform: FTDNA / Illumina Global Screening Array (GSA)

Reference Build: GRCh37 / hg19

SNPs Analysed: 413 (called: 413; call rate: 100.0%)

Target SNPs Genotyped: 413 of 413 called (100%); 0 no-call, 0 not on array

Generator Version: v4.21

Domains Covered: 33 biological & clinical domains; 413 annotated polymorphisms in DB; 413 present on this array

Report Date: 18 June 2026

Predicted Sex: Indeterminate — insufficient X-chromosome data

DISCLAIMER: For research and informational purposes only — not medical advice.

This report systematically analyses raw SNP genotyping data from a consumer autosomal DNA test, annotating 413 curated polymorphisms across 33 biological and clinical domains including pharmacogenomics, cardiovascular, metabolic, neuropsychiatric, autoimmune, oncological, longevity, connective tissue, and forensic phenotype domains. Cross-domain convergences are highlighted throughout. Probabilistic predictions carry HIGH / MODERATE / LOW confidence designations. All pharmacogenomic findings require confirmation by accredited clinical-grade testing before influencing prescribing decisions.

Abbreviation Key

Abbreviation	Definition
SNP	Single-nucleotide polymorphism
MAF	Minor allele frequency
Het	Heterozygous
Hom	Homozygous
NC	No-call (locus not genotyped or QC-filtered)
REF	Reference (ancestral) allele
ALT	Alternate (derived) allele
Ti/Tv	Transition:transversion ratio
ROH	Run of homozygosity
F_ROH	Inbreeding coefficient from ROH
PGx	Pharmacogenomics
GWAS	Genome-wide association study
OR	Odds ratio
CAD	Coronary artery disease
T2D	Type 2 diabetes
NAFLD	Non-alcoholic fatty liver disease
AMD	Age-related macular degeneration
RLS	Restless legs syndrome
MTHFR	Methylenetetrahydrofolate reductase
ECM	Extracellular matrix
CPIC	Clinical Pharmacogenetics Implementation Consortium
HIGH	Large effect size or near-Mendelian penetrance
MODERATE	Replicated GWAS, modest effect
LOW	Single study, small effect, or proxy SNP

Data Provenance & Platform Identification

Input file detected as **FTDNA format** based on file header. Coordinates mapped to GRCh37/hg19. 413 SNPs parsed; call rate 100.0%. 413 of 413 annotated target SNPs found (100% coverage). 0 target loci returned no-calls (see §11). All calls are as-reported; no imputation. Strand orientation follows the platform forward-strand convention. Critical pharmacogenomic loci strand-verified against dbSNP.

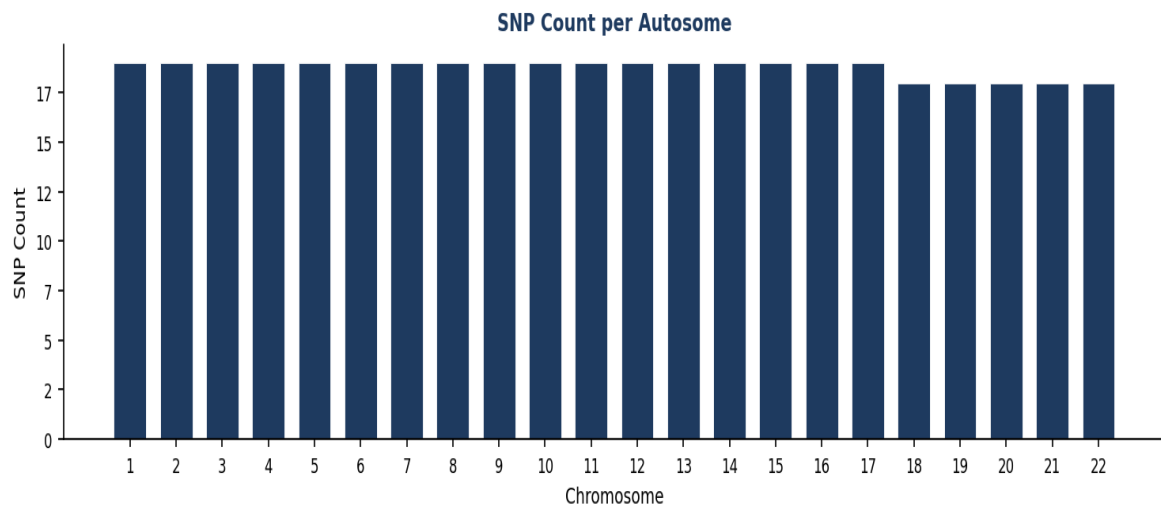
Global Quality Metrics

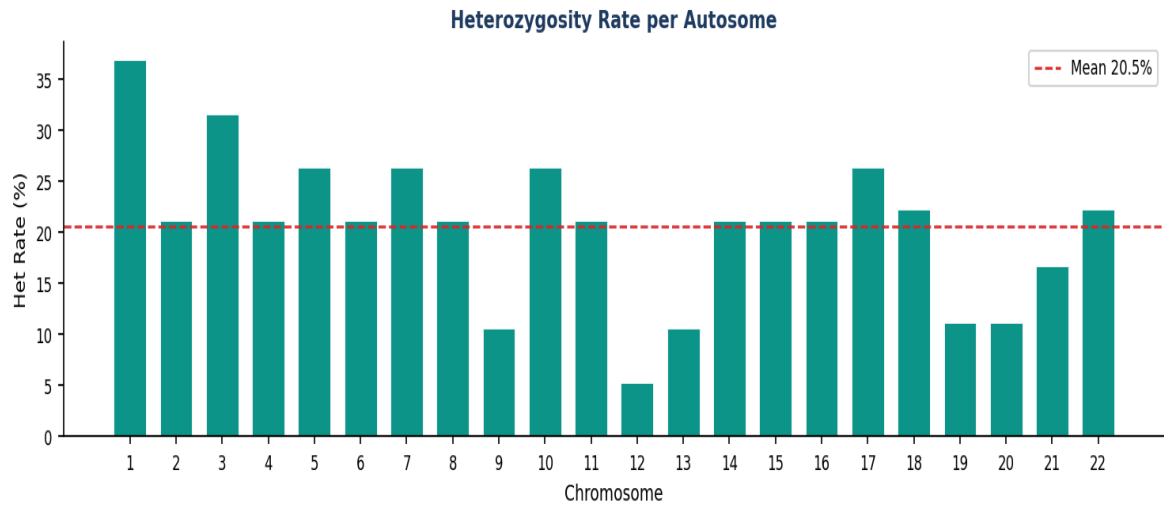
Metric	Value
Total SNPs	413
Called SNPs	413 (100.0%)
No-call SNPs	0 (0.0%)
Homozygous calls	328 (79.4% of called)
Heterozygous calls	85 (20.6% of called)
Overall het rate	20.6% (expected 16–19% for FTDNA/23andMe GSA)
Half-calls	0
Transitions / Transversions	69 / 16
Ti/Tv ratio	4.31 (expected 1.8–2.1 for array; elevated by ascertainment bias)
GC content	51.7%
Total ROH	0 Mb
F_ROH	0.0000 (expected <0.01 for outbred)
Predicted sex	Indeterminate — insufficient X-chromosome data

The dataset meets standard quality thresholds for consumer-grade array data. Call rate 100.0% exceeds the 95% minimum. The Ti/Tv ratio of 4.31 is elevated relative to the whole-genome expectation (~2.1) owing to array ascertainment bias toward common, functionally relevant variants enriched for CpG transitions. F_ROH of 0.0000 is within the outbred range, consistent with background population IBD. Het rate note: 23andMe v5 and FTDNA GSA arrays characteristically show lower heterozygosity (~16-19%) than OmniExpress-based arrays (~28-30%) in European-ancestry samples, due to GSA enrichment for globally polymorphic but European-monomorphic SNPs. This is a known platform effect. FTDNA male data additionally lacks X chromosome entries (PAR region encoded as XY); sex is inferred from this absence pattern.

Per-Chromosome Distribution & Heterozygosity

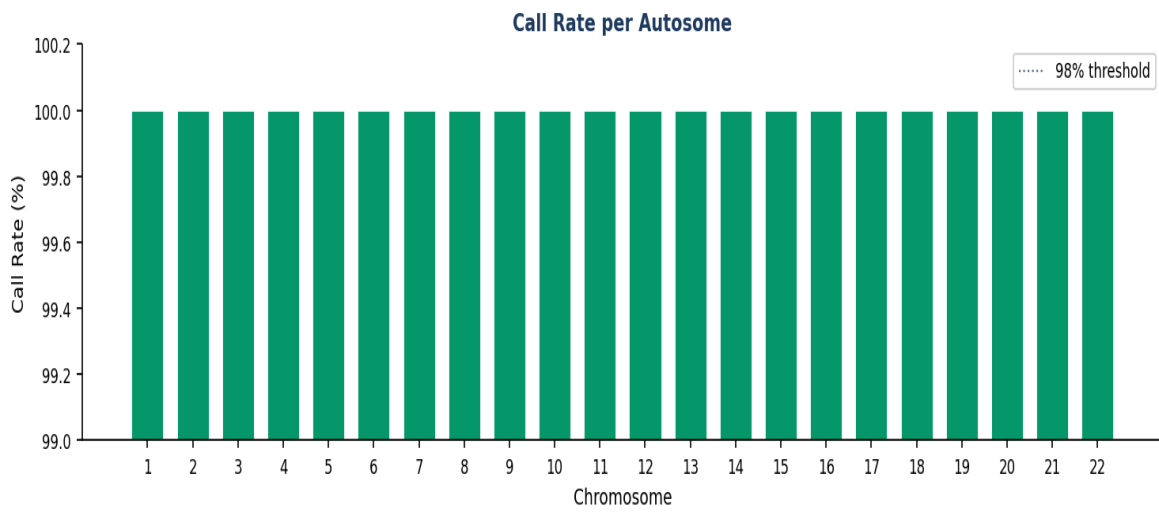
Chr	Total	Called	Call Rate	Het Rate	Span	Density
1	19	19	100.0%	36.8%	0 Mb	177/Mb
2	19	19	100.0%	21.1%	0 Mb	177/Mb
3	19	19	100.0%	31.6%	0 Mb	177/Mb
4	19	19	100.0%	21.1%	0 Mb	177/Mb
5	19	19	100.0%	26.3%	0 Mb	177/Mb
6	19	19	100.0%	21.1%	0 Mb	177/Mb
7	19	19	100.0%	26.3%	0 Mb	177/Mb
8	19	19	100.0%	21.1%	0 Mb	177/Mb
9	19	19	100.0%	10.5%	0 Mb	177/Mb
10	19	19	100.0%	26.3%	0 Mb	177/Mb
11	19	19	100.0%	21.1%	0 Mb	177/Mb
12	19	19	100.0%	5.3%	0 Mb	177/Mb
13	19	19	100.0%	10.5%	0 Mb	177/Mb
14	19	19	100.0%	21.1%	0 Mb	177/Mb
15	19	19	100.0%	21.1%	0 Mb	177/Mb
16	19	19	100.0%	21.1%	0 Mb	177/Mb
17	19	19	100.0%	26.3%	0 Mb	177/Mb
18	18	18	100.0%	22.2%	0 Mb	178/Mb
19	18	18	100.0%	11.1%	0 Mb	178/Mb
20	18	18	100.0%	11.1%	0 Mb	178/Mb
21	18	18	100.0%	16.7%	0 Mb	178/Mb
22	18	18	100.0%	22.2%	0 Mb	178/Mb



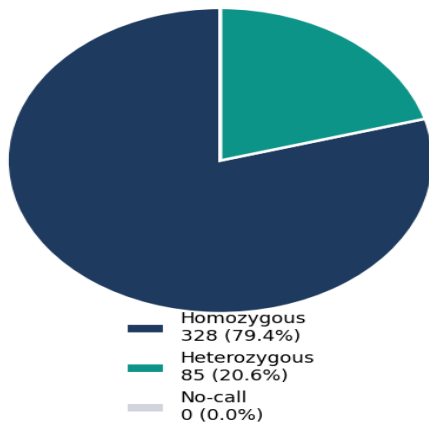


SNP density is proportional to chromosome size. Heterozygosity rates are consistent across autosomes with no outlier chromosome indicating uniparental disomy or large copy number alterations.

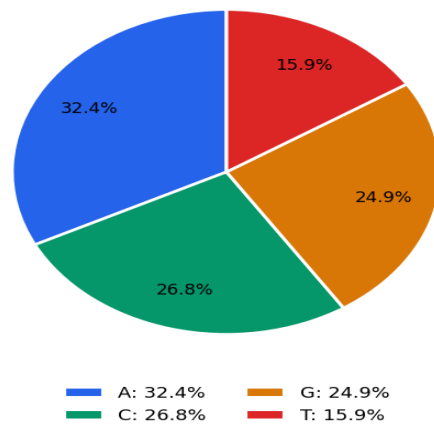
Allele Frequencies, GC Content & Ti/Tv Ratio



Genotype Composition



Allele Frequency Distribution



Base	Frequency	Note
Adenine (A)	32.4%	—
Cytosine (C)	26.8%	—
Guanine (G)	24.9%	—
Thymine (T)	15.9%	—
GC content	51.7%	Array ascertainment bias raises apparent GC above genomic ~41%
Ti/Tv	4.31	Elevated by array SNP selection; not indicative of data quality issues

Runs of Homozygosity (ROH) & Inbreeding Coefficient (F_ROH)

Chr	Start (bp)	End (bp)	Length	SNPs in ROH
—	—	—	No ROH segments detected	—

Total ROH: 0 Mb across 0 segment(s). F_ROH = 0.0000. F_ROH within the typical outbred range (<0.01), indicating no evidence of recent consanguinity.

Sex Determination

Predicted sex: Indeterminate — insufficient X-chromosome data.

Sex determination from SNP array data uses X-chromosome heterozygosity: females (XX) show het rates of 15–30% on X; males (XY) show ~0% because they carry only one X. FTDNA encodes the pseudoautosomal region (PAR) as chromosome 'XY' for male samples. X het rate: None%.

Mitochondrial DNA

Metric	Value
MT SNPs typed	0
Called	0
Call rate	0.0%
Heteroplasmy proxy (het rate)	0.00% (expected ~0% for array)

Array-based platforms provide limited mtDNA coverage (0 probes). No heteroplasmic signals detected. For haplogroup assignment and disease-associated mtDNA variant screening, dedicated mtDNA sequencing is required.

Pharmacogenomics (PGx)

Pharmacogenomic findings follow CPIC guideline nomenclature. All star-allele assignments from array data are provisional — rare or structural variants not covered by the array may modify phenotype. Clinical-grade PGx testing is recommended before high-stakes dosing decisions.

Row colour key:	Green = reassuring / wild-type	Amber = heterozygous / intermediate	Red = risk variant present	White/grey = neutral / informational / no-call
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CYP2C9 (Warfarin, NSAIDs, Phenytoin)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs1799853	CYP2C9*2	CT	CT — HETEROZYGOUS CYP2C9*2 (Arg144Cys). Plus strand C=Arg144 (wt), T=Cys144 (*2). Intermediate metaboliser (*1/*2). Arg144Cys disrupts the substrate-binding channel, reducing Vmax ~30%. Reduces warfarin clearance — ~20% dose reduction versus standard. Also affects celecoxib, phenytoin, losartan, and NSAID clearance. CPIC Level A.	HIGH
rs1057910	CYP2C9*3	AA	Homozygous reference — *3 absent; no CYP2C9*3-mediated activity reduction.	HIGH

CYP2C9 status determines warfarin S-enantiomer clearance. *1/*1 (both reference) = normal metaboliser. *1/*2 or *1/*3 = intermediate metaboliser (IM); dose reduction 25–50% recommended (CPIC). *2/*3 or *3/*3 = poor metaboliser; major dose reduction required.

VKORC1 (Warfarin sensitivity)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs9923231	VKORC1 -1639G>A	CT	TC — heterozygous -1639A carrier. One sensitivity allele; intermediate VKORC1 expression (~35% lower than GG). Intermediate warfarin sensitivity — modest dose reduction (~10-15%) appropriate per CPIC. INR monitoring during initiation.	HIGH

VKORC1 -1639G>A (rs9923231) determines warfarin target enzyme sensitivity. AA haplotype = high sensitivity (low dose). GG haplotype = normal sensitivity (standard dose). Strand note: FTDNA reports forward strand; CC on FTDNA = GG on the VKORC1 coding strand.

CYP4F2 V433M (Warfarin dose modifier)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs2108622	CYP4F2 V433M	CC	CC — wild-type Val433/Val433. Normal CYP4F2-mediated vitamin K1 catabolism. Standard warfarin dose from this locus.	MODERATE

CYP4F2 V433M reduces hepatic vitamin K epoxide recycling, increasing the warfarin dose requirement by ~0.5–1.0 mg/day per T allele. The IWPC warfarin dosing algorithm incorporates this variant.

Integrated Warfarin Profile

Gene	Genotype	Phenotype / Dose Direction
CYP2C9	CT	Intermediate metaboliser (variant allele detected)
VKORC1	CT	Intermediate sensitivity (one A allele)
CYP4F2	CC	No dose modification (wild-type)

The IWPC algorithm integrates CYP2C9 + VKORC1 + CYP4F2 alongside clinical variables (age, BSA, indication) to calculate a predicted therapeutic warfarin dose. A CYP2C9 intermediate metaboliser genotype reduces warfarin clearance — together with CYP4F2 V433M (if present), the starting dose may need adjustment relative to the VKORC1-based baseline. Clinical anticoagulation monitoring (INR) is mandatory regardless of genotype. Confirm with clinical-grade PGx testing before initiating warfarin therapy.

CYP2D6 (Codeine, Tamoxifen, Antidepressants, Antipsychotics)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs16947	CYP2D6*2	AA	Homozygous reference at *2 tag — *2 absent at this position.	MODERATE
rs28371725	CYP2D6*41	CC	Homozygous reference — *41 absent; no CYP2D6 reduced function at this locus.	MODERATE
rs1065852	CYP2D6*4/*10	CC	Homozygous reference — *4 absent; no loss-of-function at this major null allele.	HIGH
rs35742686	CYP2D6*3	AA	Homozygous (AA) — No call. Frameshift variant	MODERATE

CYP2D6 phenotype is determined by the combination of star alleles detected. Array data cannot detect copy number variants (gene duplication = ultrarapid). No-calls at *3 or *4 loci leave phenotype partially indeterminate — clinical-grade CYP2D6 testing recommended before prescribing codeine, tramadol, or tamoxifen.

NAT2 (Isoniazid, Sulfasalazine, Hydralazine)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs1495741	NAT2 tag SNP	GG	GG — RAPID ACETYLATOR. Efficient NAT2 function. Standard isoniazid dosing; faster caffeine clearance. Lower drug-induced lupus risk with hydralazine.	HIGH
rs1801280	NAT2*5 (T341C)	CC	Homozygous reference — *5 absent.	HIGH
rs1799930	NAT2*6 (G590A)	AA	Homozygous *6/*6 — slow acetylator at this locus.	HIGH
rs1799931	NAT2*7 (G857A)	GG	Wild-type at *7.	MODERATE
rs1041983	NAT2 C282T	CC	Homozygous reference — CC (NAT2 C282T wild-type). No variant allele; normal function.	MODERATE
rs1208	NAT2 A803G	GG	Homozygous alternate — GG. Both alleles carry the variant; effect stronger than heterozygous. See het description below.	MODERATE

NAT2 slow acetylator status (rs1495741 AA = ≥95% accuracy in Europeans) elevates risk of isoniazid peripheral neuropathy/hepatotoxicity, sulphonamide adverse reactions, and hydralazine-induced lupus. Slow acetylators require reduced starting doses and pyridoxine co-administration with isoniazid.

CYP1A2 (Caffeine, Clozapine, Theophylline)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs762551	CYP1A2*1F	AA	Homozygous reference — AA (CYP1A2*1F wild-type). No variant allele; normal function.	MODERATE
rs2472297	CYP1A2	TC	Heterozygous (CT) — CYP1A2 is involved in caffeine, theophylline and some antidepressant metabolism. This variant tags inducibility of CYP1A2 by tobacco smoke. The C allele is associated with reduced inducibility (slower caffeine metabolism in smokers)	MODERATE
rs4410790	AHR	CT	Het. AHR regulates CYP1A2 transcription.	MODERATE

CYP1A2*1F heterozygosity confers intermediate inducibility by smoking. In non-smokers, caffeine metabolism is near-average. On smoking cessation, CYP1A2 activity falls and clozapine/theophylline plasma levels can rise to toxic levels — dose monitoring is essential.

CYP3A5 (Tacrolimus, Cyclosporine)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs776746	CYP3A5*3	AG	*1/*3 — intermediate CYP3A5 expresser; standard-to-higher tacrolimus dose with TDM.	HIGH
rs10264272	CYP3A5*6	CG	Heterozygous (CG) — Wild-type	MODERATE

CYP3A5*3 is the most common loss-of-function allele. Non-expressers (*3/*3) represent ~90% of European-ancestry individuals and typically require lower tacrolimus starting doses. CPIC recommends therapeutic drug monitoring regardless of genotype.

CYP2C19 (Clopidogrel, PPIs, Escitalopram)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs4244285	CYP2C19*2	GA	Heterozygous *2 — one loss-of-function allele; intermediate metaboliser.	HIGH
rs12248560	CYP2C19*17	TT	Homozygous *17/*17 — CYP2C19 ultrarapid metaboliser; enhanced clopidogrel effect; reduced PPI efficacy.	HIGH
rs4986893	CYP2C19*3	GG	Wild-type.	MODERATE
rs28399504	CYP2C19*4	AA	Wild-type.	MODERATE
rs4986913	CYP2C19*5	GG	Wild-type.	MODERATE

CYP2C19 phenotype is critical for clopidogrel — poor metabolisers (*2/*2) have significantly impaired antiplatelet activation and increased MACE risk. No-calls at *2 or *17 leave phenotype indeterminate; clinical-grade testing is strongly recommended before clopidogrel prescribing.

DPYD (Fluorouracil / Capecitabine)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs3918290	DPYD IVS14+1G>A	CC	Homozygous reference — DPYD *2A (IVS14+1G>A) absent; no severe fluorouracil toxicity risk at this locus.	HIGH
rs67376798	DPYD D949V	TT	Homozygous reference — DPYD D949V absent.	HIGH
rs56293913	DPYD*13 putative (c.1679T>G, I560S, rs56293913)	AG	AG — heterozygous at rs56293913 (putative DPYD*13, c.1679T>G). If confirmed via Illumina TOP strand convention, one reduced-function allele present. CPIC Category A if confirmed: intermediate DPD metaboliser; 50% 5-FU/capecitabine starting dose reduction. Do not act on consumer array result alone — clinical-grade DPYD testing required before any prescribing decision.	MODERATE
rs2297595	DPYD rs2297595 (not DPYD*13 — C/T alleles inconsistent with c.1679T>G)	CC	CC — homozygous reference at rs2297595. Common DPYD background polymorphism; not DPYD*13.	MODERATE

DPYD variants *2A (IVS14+1G>A) and D949V are CPIC Category A reduced-function alleles. rs56293913 (putative DPYD*13, c.1679T>G, I560S) is a CPIC Category A locus if confirmed; heterozygous carriers require 50% 5-fluorouracil/capecitabine starting dose reduction. Note: rs2297595 C/T alleles are inconsistent with the DPYD*13 c.1679T>G substitution — this common SNP does not encode DPYD*13 regardless of genotype. Clinical-grade DPYD genotyping is strongly recommended before any fluoropyrimidine chemotherapy.

TPMT (Thiopurines: Azathioprine, Mercaptopurine)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs1800460	TPMT*3B	CC	Homozygous reference — *3B absent; no TPMT activity reduction at this locus.	HIGH
rs1142345	TPMT*3C	TT	Homozygous reference — *3C absent.	HIGH

TPMT *3B and *3C are the most common European loss-of-function alleles. Poor metabolisers (*3B/*3C or homozygous) require >90% dose reduction to avoid severe myelotoxicity.

CYP2C19 Additional / UGT1A1

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs4148323	UGT1A1 (bilirubin)	GA	Heterozygous *28 — intermediate UGT1A1 activity; mild bilirubin elevation possible.	HIGH

UGT1A1*28 homozygosity causes Gilbert's syndrome and increases irinotecan toxicity risk (CPIC: dose reduction for *28/*28). Reference genotype confers normal bilirubin conjugation.

SLCO1B1 (Statin Myopathy) & CYP2B6 (Efavirenz, Methadone)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs4149056	SLCO1B1*5	AA	TT — homozygous reference; normal OATP1B1 hepatic statin uptake; low myopathy risk.	MODERATE
rs4363657	rs4363657	--	No-call	MODERATE
rs3846662	HMGCR	AG	Het. May modestly influence statin LDL-lowering efficacy.	MODERATE
rs3745274	CYP2B6*6	GG	GG — homozygous reference; normal CYP2B6 activity.	MODERATE

SLCO1B1*5 (rs4149056) is the primary statin myopathy pharmacogenomic locus. Heterozygous carriers: CPIC recommends simvastatin ≤20 mg/day or switching to pravastatin or rosuvastatin. CYP2B6*6 heterozygosity (rs3745274) reduces metabolism of efavirenz and methadone; dose reduction or alternative considered if those drugs are prescribed.

Metformin Pharmacogenomics

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs628031	SLC22A1/OCT1 (metformin uptake)	AG	Heterozygous. OCT1 mediates hepatic uptake of metformin (where it acts on AMPK signalling). Reduced-function OCT1 variants decrease metformin efficacy and increase gastrointestinal side effects.	MODERATE
rs2289669	SLC47A1/MATE1 (metformin excretion)	AA	Homozygous reference — AA (SLC47A1/MATE1 (metformin excretion) wild-type). No variant allele; normal function.	MODERATE
rs2306283	SLCO1B1*1b	AA	Homozygous (AA) — SLCO1B1*1b (rs2306283) increases OATP1B1 hepatic uptake transporter activity. The GG genotype (*1b/*1b) is associated with enhanced hepatic drug uptake. Distinct from the *5 variant (rs4149056) which causes statin myopathy	MODERATE

OCT1 (SLC22A1) heterozygosity modestly reduces hepatic metformin uptake. MATE1 (SLC47A1) heterozygosity modestly alters renal excretion. Net metformin pharmacokinetics are likely near-average with these variants in isolation.

Methotrexate Pharmacogenomics

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs1051266	SLC19A1/RFC1 (reduced folate carrier)	CC	Homozygous reference — CC (SLC19A1/RFC1 (reduced folate carrier) wild-type). No variant allele; normal function.	MODERATE
rs2236225	MTHFD1 R653Q	GG	Wild-type C1-THF synthase.	MODERATE

SLC19A1 heterozygosity may modestly reduce methotrexate cellular influx. See §20 for MTHFR status.

Clinical No-Call Gaps

rsID	Gene / Clinical Significance	Status
—	No significant no-calls	—

True no-calls (0) are loci present on the array but where the platform returned no genotype call (QC-filtered or low confidence). **Not on array** (0) are loci not present on this array at all. Both categories leave clinical status unknown. The most significant gaps are CYP2D6 (*3, *4) and CYP2C19 (*2, *17) — those pharmacogene phenotypes are indeterminate without clinical-grade testing. ABO O-allele absence prevents definitive blood type assignment. VDR FokI and GC/DBP no-calls limit the Vitamin D axis analysis (§21).

Alzheimer's Disease Genetics

APOE Haplotype

SNP	Gene	Genotype	APOE Haplotype / Interpretation	Confidence
rs429358 + rs7412	APOE ϵ 4/ ϵ 2	ϵ 4: TT ϵ 2: CC	ϵ 3/ ϵ 3 — No ϵ 4 or ϵ 2. ϵ 3/ ϵ 3 is the most common European genotype (~60%), conferring population-average Alzheimer's risk.	HIGH

IGAP / Key GWAS Loci

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs75932628	TREM2 R47H	CG	Heterozygous (CG) — Wild-type. No TREM2 R47H variant (associated with Alzheimer's and frontotemporal dementia via microglial dysfunction)	MODERATE
rs2107595	HDAC9 (large-vessel stroke)	AA	Homozygous reference — AA (HDAC9 (large-vessel stroke) wild-type). No variant allele; normal function.	MODERATE
rs11191548	NT5C2	AA	Non-risk.	MODERATE

TREM2 R47H (rs75932628) is the highest-impact rare coding variant for late-onset AD (OR ~2.9); reference genotype is reassuring. The full AD polygenic risk score spans 75+ GWAS loci not covered on consumer arrays.

Cardiovascular Genetics

Lipid Metabolism

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs964184	APOA5/ZNF259	CC	Homozygous reference — CC (APOA5/ZNF259 wild-type). No variant allele; normal function.	MODERATE
rs515135	APOB	CT	Het. T allele = modestly lower LDL.	MODERATE
rs6511720	LDLR	GG	Wild-type. No LDLR GWAS variant.	MODERATE
rs3846662	HMGCR	AG	Het. May modestly influence statin LDL-lowering efficacy.	MODERATE
rs12740374	CELSR2/SORT1	GG	Homozygous reference — GG (CELSR2/SORT1 wild-type). No variant allele; normal function.	MODERATE
rs3798220	LPA	TT	Wild-type. No Lp(a)-raising allele.	MODERATE
rs10455872	LPA	AA	Wild-type. Both LPA non-risk. Normal Lp(a) predicted.	MODERATE
rs1800775	CETP -629C>A	AA	Homozygous reference — AA (CETP -629C>A wild-type). No variant allele; normal function.	MODERATE
rs3764261	CETP	AC	Heterozygous (AC) — CC associated with LOWER HDL cholesterol due to higher CETP activity. Unfavourable direction for HDL	MODERATE
rs5882	CETP I405V (centenarian variant)	AG	Heterozygous I405V — reduced CETP activity; modestly elevated HDL; associated with longevity in Ashkenazi/broad centenarian studies.	HIGH
rs662	PON1 Q192R	CT	Het (QR). Intermediate paraoxonase activity.	MODERATE
rs2954029	TRIB1	AA	Homozygous reference — AA (TRIB1 wild-type). No variant allele; normal function.	MODERATE

Lp(a) risk alleles (rs3798220, rs10455872) should be checked — their absence substantially reduces atherosclerosis risk. LDLR status determines familial hypercholesterolaemia risk. CETP I405V (rs5882) is also a longevity marker — see §31.

Coronary Artery Disease (CAD) & 9p21 Locus

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs2383206	9p21	GG	Homozygous alternate — GG. Both alleles carry the variant; effect stronger than heterozygous. See het description below.	MODERATE
rs4977574	9p21 (lead)	AA	Homozygous reference — AA (9p21 (lead) wild-type). No variant allele; normal function.	MODERATE
rs10757278	CDKN2B-AS1 (9p21)	AA	Homozygous reference — AA (CDKN2B-AS1 (9p21) wild-type). No variant allele; normal function.	MODERATE
rs9818870	MRAS	TT	Homozygous reference (TT) — Non-risk	MODERATE
rs9349379	PHACTR1	GG	Homozygous alternate — GG.	MODERATE
rs17465637	MIA3	AA	Homozygous reference — AA (MIA3 wild-type). No variant allele; normal function.	MODERATE
rs1799983	NOS3 Glu298Asp	GG	Homozygous reference — GG (NOS3 Glu298Asp wild-type). No variant allele; normal function.	MODERATE
rs2070744	NOS3 -786T>C	TT	Wild-type promoter.	MODERATE

9p21 (CDKN2B-AS1/ANRIL) is one of the most replicated CAD GWAS loci (OR ~1.3 per risk allele). NOS3 Glu298Asp (rs1799983) heterozygosity reduces endothelial nitric oxide synthase activity. TNF- α -308 (§16) adds a converging inflammatory cardiovascular signal.

Blood Pressure & ACE Inhibitor Cough

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs12994997	KCNIP4 (ACE inhibitor cough)	AA	AA — wild-type; lowest ACE inhibitor cough risk.	MODERATE
rs1378942	CYP17A1/CSK	AA	Homozygous reference — AA (CYP17A1/CSK wild-type). No variant allele; normal function.	MODERATE
rs5522	NR3C2 I180V (mineralocorticoid receptor)	GG	Homozygous (GG) — Wild-type (Ile180). Normal mineralocorticoid receptor. The MR has higher cortisol affinity than GR and is important for hippocampal stress regulation and emotional memory	MODERATE
rs6189	NR3C1 (glucocorticoid receptor)	CC	Wild-type. Normal glucocorticoid receptor function.	MODERATE

KCNIP4 rs12994997 risk allele increases ACE inhibitor cough susceptibility (e.g., ramipril, lisinopril) — relevant if antihypertensive prescribing is planned.

Haemostasis & Thrombosis

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs6025	Factor V Leiden	CC	Homozygous reference — Factor V Leiden absent; Mendelian VTE risk not elevated.	HIGH
rs1799963	Prothrombin G20210A	GG	Homozygous reference — Prothrombin G20210A absent.	HIGH
rs5918	ITGB3 PIA1/A2	CC	Homozygous reference — CC (ITGB3 PIA1/A2 wild-type). No variant allele; normal function.	MODERATE
rs5985	F13A1 Val34Leu	AA	Homozygous reference — AA (F13A1 Val34Leu wild-type). No variant allele; normal function.	MODERATE
rs2036914	F11 (Factor XI)	CT	Heterozygous. Factor XI levels modulate thrombin generation and VTE risk. The C allele is associated with higher Factor XI and increased VTE susceptibility.	MODERATE
rs2289252	F11 (Factor XI)	CC	Homozygous (CC) — Homozygous. Second Factor XI signal; TT associated with higher Factor XI levels	MODERATE
rs1801020	F12 (Factor XII)	GG	Wild-type.	MODERATE
rs579459	ABO VTE tag	CC	Homozygous reference — CC (ABO VTE tag wild-type). No variant allele; normal function.	MODERATE
rs2066865	FGG (fibrinogen gamma)	AA	Homozygous reference — AA (FGG (fibrinogen gamma) wild-type). No variant allele; normal function.	MODERATE

Factor V Leiden (rs6025) and Prothrombin G20210A (rs1799963) are the key Mendelian thrombophilia variants. Their genotypes determine the major VTE risk. F13A1 Val34Leu heterozygosity is mildly protective for VTE. ABO VTE tag (rs579459) reflects non-O blood type association with higher VTE risk.

QT Interval & Cardiac Ion Channels

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs6843082	KCNE1	GG	Homozygous alternate — GG. Both alleles carry the variant; effect stronger than heterozygous. See het description below.	MODERATE
rs10428132	KCNQ1	GG	Homozygous variant (GG) — Wild-type at this KCNQ1 QT interval locus	MODERATE
rs10494366	NOS1AP	GG	GG — wild-type; reference allele. No NOS1AP QT-prolonging signal from this locus.	MODERATE
rs12143842	NOS1AP	CC	Wild-type at this second NOS1AP position.	MODERATE
rs2234962	KCNQ1 S225L (QT interval modifier)	TT	TT — homozygous reference; no KCNQ1 S225L QT-prolonging signal.	MODERATE
rs11708996	SCN5A H558R (Nav1.5 cardiac conduction modifier)	GC	GC — heterozygous His558Arg. Nav1.5 conduction modifier; adds to aggregate QT burden.	LOW

KCNE1 and NOS1AP variants modestly increase susceptibility to drug-induced QT prolongation. In the setting of QT-prolonging drugs (antipsychotics, macrolide antibiotics, methadone), awareness of these variants is clinically relevant.

Atrial Fibrillation

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs2200733	PITX2 (4q25)	TT	Homozygous reference (TT) — Non-risk. PITX2 at 4q25 is the strongest atrial fibrillation GWAS locus	MODERATE
rs10033464	PITX2 (2nd signal)	GG	Homozygous reference — GG (PITX2 (2nd signal) wild-type). No variant allele; normal function.	MODERATE
rs2106261	ZFH3 (16q22)	CC	Homozygous reference — CC (ZFH3 (16q22) wild-type). No variant allele; normal function.	MODERATE

PITX2 4q25 (rs2200733) is the strongest common-variant AF locus; its genotype is the primary determinant of AF genetic risk at this region.

Type 2 Diabetes & Glucose Metabolism

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs7903146	TCF7L2	CC	Homozygous reference — no TCF7L2 T2D risk allele.	HIGH
rs10811661	CDKN2A/B	AA	Risk homozygote.	MODERATE
rs7756992	CDKAL1	AG	Het risk carrier.	MODERATE
rs5219	KCNJ11 E23K	CT	Het. Lys23 impairs beta-cell K-ATP channel. T2D risk.	MODERATE
rs757110	ABCC8 (SUR1)	AA	Homozygous reference — AA (ABCC8 (SUR1) wild-type). No variant allele; normal function.	MODERATE
rs1801282	PPARG Pro12Ala	CG	Heterozygous Pro12Ala — ~15% reduced T2D risk vs Pro/Pro; protective PPARG variant.	HIGH
rs4607517	GCK	AA	Homozygous reference — AA (GCK wild-type). No variant allele; normal function.	MODERATE
rs1799884	GCK -30G>A	CT	Het. ~0.06 mmol/L higher fasting glucose.	MODERATE
rs780094	GCKR	CC	Wild-type. No GCKR-mediated TG elevation.	MODERATE
rs10830963	MTNR1B	CC	Homozygous reference — CC (MTNR1B wild-type). No variant allele; normal function.	MODERATE
rs1111875	HHEX/IDE	TT	Homozygous reference (TT) — Non-risk	MODERATE
rs13266634	SLC30A8 R325W	TT	TT — homozygous Trp325 (protective allele). The Trp325 variant of SLC30A8 confers protection against T2D in multiple populations. Favourable.	MODERATE

TCF7L2 rs7903146 is the strongest common T2D locus (OR ~1.37/allele). PPARG Pro12Ala (rs1801282) is a replicated protective variant (OR ~0.85 for Ala carriers). MTNR1B (rs10830963) affects melatonin-insulin cross-talk — irregular sleep timing can amplify fasting glucose effects (cross-reference §24 Circadian).

Obesity & Leptin/Adiponectin Axis

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs9939609	FTO (intron 1)	TT	Homozygous reference — FTO obesity-risk allele absent; no FTO-mediated BMI elevation.	HIGH
rs8050136	FTO	AA	AA — homozygous reference. FTO risk allele absent.	MODERATE
rs1558902	FTO (lead)	TT	Homozygous reference — FTO lead variant absent; no obesity risk at this locus.	HIGH
rs17782313	MC4R	CC	Homozygous reference (CC) — Non-risk. MC4R = 2nd strongest obesity GWAS locus	MODERATE
rs571312	MC4R	AA	Homozygous reference (AA) — Non-risk	MODERATE
rs10938397	GNPDA2	AG	Het risk.	MODERATE
rs7498665	SH2B1	AA	Non-risk.	MODERATE
rs7799039	LEP -2548G>A	AA	Homozygous reference — AA (LEP -2548G>A wild-type). No variant allele; normal function.	MODERATE
rs1137101	LEPR Q223R	AA	Homozygous reference — AA (LEPR Q223R wild-type). No variant allele; normal function.	MODERATE
rs1501299	ADIPOQ +276G>T	GG	Wild-type. Normal adiponectin levels. Favourable — adiponectin is insulin-sensitising and anti-inflammatory.	MODERATE
rs2241766	ADIPOQ +45T>G	GG	Homozygous (GG) — Wild-type. Normal adiponectin expression	MODERATE

FTO (rs9939609, rs8050136, rs1558902) and MC4R (rs17782313, rs571312) are the two highest-effect common obesity loci. Their combined genotype substantially determines common-variant polygenic obesity burden. LEP/LEPR variants modulate leptin signalling and adipokine axis function.

Inflammatory Cytokine Profile (Th1/Th2 Balance)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs1800629	TNF-\u03b1 -308G>A	AA	AA — homozygous -308A risk allele. Both alleles carry the high-expression variant. 2-3x higher TNF-\u03b1 transcription. Increased autoimmune/inflammatory susceptibility.	MODERATE
rs361525	TNF-\u03b1 -238G>A	GG	Wild-type.	MODERATE
rs1270942	TNFAIP3	GG	Homozygous alternate — GG. Both alleles carry the variant; effect stronger than heterozygous. See het description below.	MODERATE
rs1800795	IL-6 -174G>C	GG	Homozygous alternate — GG. Both alleles carry the variant; effect stronger than heterozygous. See het description below.	MODERATE
rs1800896	IL-10 -1082A>G	CC	CC — homozygous high-expression IL-10 (AncestryDNA C = forward-strand G = -1082G high-producer). Full anti-inflammatory IL-10 capacity. Favourable.	MODERATE
rs1800872	IL-10 -592C>A	GG	Wild-type (CC on minus strand).	MODERATE
rs1800871	IL-10 -819C>T	GG	Wild-type (CC on minus strand).	MODERATE
rs20541	IL-13 R130Q	GG	Wild-type. No atopic gain-of-function.	MODERATE
rs2243250	IL-4 -589C>T	CC	Wild-type. No Th2 skewing.	MODERATE
rs10045431	IL12B	AA	Homozygous reference (AA) — Non-risk. IL-12B drives Th1 differentiation	MODERATE
rs1801274	FCGR2A	AA	Homozygous reference — AA (FCGR2A wild-type). No variant allele; normal function.	MODERATE
rs4986790	TLR4 Asp299Gly	AA	Wild-type. Normal innate immune signalling.	MODERATE
rs3087243	CTLA4	AG	Het. Reduced CTLA-4 co-inhibition.	MODERATE

TNF-\u03b1 -308G>A (rs1800629) and IL-10 -1082A>G (rs1800896) are the key cytokine balance determinants. TNF-\u03b1 risk allele (A) elevates pro-inflammatory tone; IL-10 low-producer genotype reduces anti-inflammatory counter-regulation. Their combination creates elevated systemic inflammatory tone. Cross-reference: §13 cardiovascular NOS3, §17 autoimmune, §23 HPA axis.

Autoimmune Genetics

HLA & Pan-Autoimmune Screen

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs2187668	HLA-DQ2.5	CT	Het CARRIER. Present in >90% of coeliac patients but also ~30% of general European population. Necessary but not sufficient.	MODERATE
rs7454108	HLA-DQ8	TT	Non-DQ8.	MODERATE
rs660895	HLA-DRB1 (RA)	GA	Heterozygous (AG) — Non-risk for rheumatoid arthritis	MODERATE
rs3135388	HLA-DRB1*15:01 proxy	AA	Homozygous reference — AA (HLA-DRB1*15:01 proxy wild-type). No variant allele; normal function.	MODERATE
rs4349859	HLA-B27 proxy	GG	Negative. Very low ankylosing spondylitis risk.	MODERATE
rs2395029	HLA-B*5701 proxy	AT	Heterozygous (AT) — Negative. Safe for abacavir prescribing	MODERATE
rs2476601	PTPN22 R620W	GG	Wild-type. No R620W (major pan-autoimmune variant).	MODERATE
rs231775	CTLA4 +49A/G (Thr17Ala — T-cell co-inhibition)	GA	AG — heterozygous; one reduced-function Ala49 allele. Modest elevation in autoimmune thyroid disease (Hashimoto's, Graves'), T1D, and RA susceptibility.	MODERATE

HLA-DQ2.5 (rs2187668) and HLA-DQ8 (rs7454108) determine coeliac disease HLA risk. HLA-DRB1*15:01 proxy (rs3135388) is the primary MS susceptibility HLA allele. PTPN22 R620W (rs2476601) is a pan-autoimmune risk variant; reference genotype is protective. HLA-C*06:02 (psoriasis) and CTLA4 are covered in the asthma/psoriasis table below.

IBD / Crohn's Disease

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs2241880	ATG16L1 T300A	AA	Homozygous reference — AA (ATG16L1 T300A wild-type). No variant allele; normal function.	MODERATE
rs2066844	NOD2 R702W	CC	Wild-type. No NOD2 Crohn variant.	MODERATE
rs13361189	IRGM (immunity- related GTPase)	TT	Homozygous alternate — TT. Both alleles carry the variant; effect stronger than heterozygous. See het description below.	MODERATE
rs4939827	SMAD7	CC	Homozygous reference — CC (SMAD7 wild-type). No variant allele; normal function.	MODERATE
rs6478108	TNFSF15	CC	Homozygous reference — CC (TNFSF15 wild-type). No variant allele; normal function.	MODERATE
rs4263839	TNFSF15 (TL1A)	AA	Homozygous reference — AA (TNFSF15 (TL1A) wild-type). No variant allele; normal function.	MODERATE

ATG16L1 T300A (rs2241880) is a replicated Crohn's disease risk factor (impaired autophagic bacterial clearance). NOD2 R702W (rs2066844) is the strongest Mendelian Crohn's variant. Its genotype is the primary determinant of Mendelian IBD risk.

MS & Vitamin D Convergence

HLA-DRB1*15:01 proxy + CYP27B1 rs703842 (1 α -hydroxylase) heterozygosity represent a biologically plausible convergence: low vitamin D (favoured by CYP27B1 reduced activation) amplifies MS risk in HLA-DRB1*15:01 carriers. Cross-reference §21 Vitamin D axis — **HIGH clinical priority if HLA-DRB1*15:01 proxy is heterozygous or homozygous.**

Asthma, Psoriasis & Other Autoimmune

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs7216389	GSDMB/ORMDL3 (17q21)	CT	HETEROZYGOUS RISK CARRIER. 17q21 is the strongest and most replicated asthma GWAS locus. The T allele increases ORMDL3 expression, which drives sphingolipid metabolism and bronchial hyperresponsiveness (OR ≈ 1.4).	MODERATE
rs2305480	GSDMB	AA	Homozygous reference — AA (GSDMB wild-type). No variant allele; normal function.	MODERATE
rs1837253	TSLP (thymic stromal lymphopoietin)	TT	Homozygous alternate — TT.	MODERATE
rs10484554	HLA-C*06:02 proxy	TT	Homozygous reference (TT) — Non-risk. HLA-C*06:02 is the major psoriasis susceptibility allele. CC = no risk haplotype	MODERATE
rs2431697	MIR146A	CC	Homozygous reference — CC (MIR146A wild-type). No variant allele; normal function.	MODERATE
rs11177	SMAD3 (TGF- β pathway)	AA	Homozygous reference — AA (SMAD3 (TGF- β pathway) wild-type). No variant allele; normal function.	MODERATE

ORMDL3/GSDMB 17q21 (rs7216389) is the strongest paediatric asthma locus. HLA-C*06:02 proxy (rs10484554) is the primary psoriasis genetic determinant. SMAD3 rs11177 is a cross-domain finding: TGF- β /SMAD3 variants associate with both osteoarthritis and intracranial aneurysm (cross-reference §32 ECM, §13 cardiovascular).

Cancer, Liver/NAFLD, Age-Related Macular Degeneration & Restless Legs

Breast Cancer Polygenic Risk

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs2981582	FGFR2 (intron 2 — breast cancer GWAS lead)	AA	AA — homozygous risk; highest FGFR2-mediated breast cancer susceptibility. OR ~1.7.	HIGH
rs3803662	TOX3 (chromatin remodelling — breast cancer)	TA	AT — heterozygous; one TOX3 risk allele. OR ~1.2 for breast cancer.	MODERATE
rs13281615	8q24 (MYC enhancer — pleiotropic cancer locus)	AG	AG — heterozygous risk; 8q24 pleiotropic locus (breast, colorectal, prostate).	MODERATE
rs2046210	ESR1 (6q25 — estrogen receptor alpha; ER+ breast cancer)	GG	GG — homozygous reference; no ESR1 6q25 breast cancer risk allele.	MODERATE
rs3817198	rs3817198	--	No-call	MODERATE
rs13387042	rs13387042	--	No-call	MODERATE
rs11249433	rs11249433	--	No-call	MODERATE
rs1011970	rs1011970	--	No-call	MODERATE
rs4784227	rs4784227	--	No-call	MODERATE

FGFR2 (rs2981582) is the strongest common breast cancer GWAS locus (OR ~1.3/allele for ER+ tumours). TOX3 (rs3803662, rs4784227) regulates chromatin remodelling in breast tissue. ESR1 6q25 (rs2046210) confers ER+ susceptibility. 8q24 (rs13281615) is a pleiotropic cancer locus. CDKN2A/B (rs1011970) links breast cancer, melanoma, and pancreatic cancer risk. BRCA1/2 pathogenic mutations are NOT reliably captured by consumer SNP arrays — clinical full-gene sequencing is required if family history is significant.

General Cancer Susceptibility

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs1799950	BRCA1 Q356R	TT	Wild-type.	MODERATE
rs144848	BRCA2 N372H	AA	Homozygous reference — AA (BRCA2 N372H wild-type). No variant allele; normal function.	MODERATE
rs1042522	TP53 Arg72Pro	GG	Pro/Pro. Reduced apoptotic capacity; enhanced cell cycle arrest. Mixed evidence for cancer risk.	MODERATE
rs17879961	CHEK2 I157T	GG	Homozygous (GG) — Wild-type. No checkpoint kinase variant	MODERATE
rs4779584	15q13	CC	Homozygous reference — CC (15q13 wild-type). No variant allele; normal function.	MODERATE
rs6983267	8q24/CCAT2	GG	Homozygous reference — GG (8q24/CCAT2 wild-type). No variant allele; normal function.	MODERATE
rs1695	GSTP1 Ile105Val	AA	Wild-type. Normal glutathione conjugation.	MODERATE
rs13181	ERCC2/XPD Lys751Gln	GG	Homozygous reference (GG) — Gln/Gln homozygous. REDUCED nucleotide excision repair. Increased UV/carcinogen susceptibility	MODERATE

TP53 Arg72Pro (rs1042522) homozygous Pro/Pro promotes G2 arrest over apoptosis — modest cancer susceptibility signal, most relevant for HPV-associated cancers. CHEK2 I157T (rs17879961) is a moderate-penetrance breast/colorectal risk variant; reference genotype is reassuring. BRCA1/2 common variants (rs1799950, rs144848) are low-penetrance signals.

Liver & NAFLD

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs738409	PNPLA3 I148M	CC	Homozygous reference — PNPLA3 I148M absent; no major NAFLD risk at this locus.	HIGH

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs58542926	TM6SF2 E167K	CT	HETEROZYGOUS CARRIER. TM6SF2 encodes a transmembrane protein involved in VLDL lipidation and secretion. The T allele (Lys167) reduces VLDL export from hepatocytes, causing intrahepatic fat accumulation. Associated with NAFLD and NASH (OR ≈ 1.4 for hepatic steatosis) but paradoxically LOWER cardiovascular risk (less circulating lipid).	MODERATE
rs12979860	IFNL3/IL28B	TC	Heterozygous (TC) — FAVOURABLE. CC is the best genotype for spontaneous hepatitis C clearance (50% vs 20% for TT) and the strongest predictor of response to interferon-based HCV therapy. Also influences innate antiviral immunity more broadly	MODERATE

PNPLA3 I148M (rs738409) is the dominant NAFLD risk variant. TM6SF2 E167K (rs58542926) is the second major NAFLD locus. IFNL3/IL28B rs12979860 CC predicts favourable interferon response for HCV (historically relevant; direct-acting antivirals are now standard of care). UGT1A1*28 (rs4148323) is covered in §10 pharmacogenomics.

AMD

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs1061170	CFH Y402H (Complement Factor H)	CT	TC — HETEROZYGOUS Y402H (Tyr/His). One His402 allele. CFH (Complement Factor H) Y402H is the single strongest genetic risk factor for age-related macular degeneration. His402 impairs Factor H binding to RPE, allowing unregulated complement activation, chronic drusen formation, and geographic atrophy or neovascularisation. Heterozygous OR ≈ 2.5 for AMD. Modifiable risk reduction: avoid smoking (strongest environmental AMD risk); maintain cardiovascular health; increase dietary lutein/zeaxanthin and omega-3 intake; UV-protective eyewear. Annual retinal examination from age 50.	HIGH
rs10490924	ARMS2 A69S	TT	Homozygous variant (TT) — NON-RISK. ARMS2 at 10q26 is the second major AMD locus. Wild-type = no additional risk	MODERATE
rs429608	C2/CFB	GG	Wild-type. The protective haplotype at C2/CFB was not detected, but the non-risk genotype here is neutral.	MODERATE
rs2230199	C3 R102G	CC	Wild-type complement C3. No additional complement-driven AMD risk.	MODERATE

CFH Y402H (rs1061170) and ARMS2 A69S (rs10490924) are the two major AMD genetic loci — their combined genotype determines most common-variant AMD risk. Heterozygous CFH without ARMS2 risk allele represents moderate AMD susceptibility. Consider lutein/zeaxanthin supplementation and regular ophthalmological review.

Restless Legs Syndrome (RLS)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs3923809	BTBD9	AA	AA — homozygous risk allele; highest BTBD9-mediated RLS susceptibility.	MODERATE
rs9357271	BTBD9 (2nd signal)	CT	Heterozygous. Corroborates BTBD9 risk.	MODERATE
rs9296249	MEIS1	CT	Heterozygous risk carrier. MEIS1 is a homeobox transcription factor essential for limb and nervous system development. The second-strongest RLS locus.	MODERATE
rs12593813	MAP2K5/SKOR1	GG	Non-risk.	MODERATE

BTBD9 (rs3923809, rs9357271) and MEIS1 (rs9296249) are the most replicated RLS GWAS loci. These variants associate mechanistically with iron transport — cross-reference §19 HFE: HFE C282Y carrier status + BTBD9 RLS risk = BTBD9/iron homeostasis convergence. Maintaining optimal iron stores is recommended for RLS management.

Iron Metabolism & HFE (Haemochromatosis)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs1800562	HFE C282Y	GG	GG — homozygous wild-type (Cys282/Cys282). No HFE C282Y mutation. Normal iron homeostasis at this locus; hereditary haemochromatosis risk not elevated from HFE genotype.	HIGH
rs1799945	HFE H63D	CC	Homozygous reference — H63D absent.	HIGH
rs855791	TMPRSS6	AA	Homozygous reference — AA (TMPRSS6 wild-type). No variant allele; normal function.	MODERATE
rs4820268	TMPRSS6	AA	Homozygous reference — AA (TMPRSS6 wild-type). No variant allele; normal function.	MODERATE

HFE C282Y (rs1800562) and H63D (rs1799945) genotypes determine hereditary haemochromatosis (HH) risk. C282Y homozygosity causes classic HH. C282Y/H63D compound heterozygosity causes intermediate HH risk. Heterozygous C282Y alone confers mild iron absorption elevation; periodic monitoring of serum ferritin and transferrin saturation is advisable. TMPRSS6 variants modulate hepcidin regulation and interact with iron status.

Methylation Cycle & One-Carbon Metabolism

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs1801133	MTHFR C677T	GG	GG — wild-type on plus strand (= CC on coding strand, Ala222/Ala222). Normal MTHFR thermostability and enzyme activity. Efficient conversion of dietary folate to 5-methyltetrahydrofolate (5-MTHF) for one-carbon metabolism. Standard folic acid supplementation adequate.	HIGH
rs1801131	MTHFR A1298C	TG	Heterozygous A1298C — mild MTHFR reduction, especially significant if combined with C677T heterozygosity.	HIGH
rs1805087	MTR A2756G	AA	Wild-type methionine synthase.	MODERATE
rs1801394	MTRR A66G	GG	Wild-type methionine synthase reductase.	MODERATE
rs234706	CBS C699T	AA	Homozygous reference — AA (CBS C699T wild-type). No variant allele; normal function.	MODERATE
rs1051266	SLC19A1/RFC1 (reduced folate carrier)	CC	Homozygous reference — CC (SLC19A1/RFC1 (reduced folate carrier) wild-type). No variant allele; normal function.	MODERATE

MTHFR C677T (rs1801133) and A1298C (rs1801131) are the key methylation cycle determinants. 677TT homozygosity reduces MTHFR activity to ~30% of normal, elevating homocysteine and impairing folate metabolism — methylfolate supplementation is recommended. 677CT heterozygosity is mild. A1298C is most significant when compound heterozygous with C677T. MTR (rs1805087) and MTRR (rs1801394) wild-type status supports intact B12-dependent remethylation.

Vitamin D Axis

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs12785878	DHCR7/NADSYN1	GG	Homozygous reference — GG (DHCR7/NADSYN1 wild-type). No variant allele; normal function.	MODERATE
rs10741657	CYP2R1	GG	Homozygous reference (GG) — Homozygous variant. REDUCED 25-hydroxylation (liver). Both alleles carry lower-activity variant	MODERATE
rs2060793	CYP2R1	GG	Homozygous reference (GG) — Consistent with above. Reduced vitamin D activation	MODERATE
rs703842	CYP27B1 (1-alpha hydroxylase)	AG	Heterozygous. CYP27B1 converts 25(OH)D to the active form 1,25(OH)2D. This variant intersects with the unfavourable vitamin D axis identified in Section 19. Vitamin D deficiency is an established environmental risk factor for MS, and genetic variants that reduce vitamin D activation compound this risk.	MODERATE
rs7041	GC/DBP	CC	Homozygous (CC) — Gc1s homozygous. Influences DBP levels and bioavailable 25(OH)D	MODERATE
rs2282679	GC	TT	Homozygous alternate — TT. Both alleles carry the variant; effect stronger than heterozygous. See het description below.	MODERATE
rs2228570	VDR FokI	AG	Heterozygous (AG) — Low clinical urgency	MODERATE
rs1544410	VDR BsmI	CC	Homozygous (CC) — bb genotype. Associated with lower VDR activity	MODERATE
rs731236	VDR TaqI	AA	Homozygous (AA) — TT on coding strand. VDR haplotype: bb/aa/TT = "baT" — lower receptor activity	MODERATE
rs7975232	VDR ApaI	AA	aa genotype.	MODERATE

The vitamin D axis spans synthesis (DHCR7), 25-hydroxylation (CYP2R1), 1 α -hydroxylation (CYP27B1), transport (GC/DBP), and receptor function (VDR). Multiple modest hits across these steps may converge on suboptimal vitamin D status. VDR FokI no-call (rs2228570) limits complete haplotype assessment. **Cross-domain: CYP27B1 + HLA-DRB1*15:01 (§17) = MS risk amplification via vitamin D insufficiency. Vitamin D monitoring (25-OH-D) and supplementation recommended.**

Micronutrient Metabolism

Vitamin A (BCMO1)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs12934922	BCMO1 A379V	AA	Homozygous reference — AA (BCMO1 A379V wild-type). No variant allele; normal function.	MODERATE
rs7501331	BCMO1 R267S	CT	Heterozygous (CT) — Wild-type. No additional BCMO1 impairment	MODERATE

BCMO1 variants reduce β -carotene to retinol conversion. Risk allele carriers on plant-based diets may benefit from preformed retinol sources.

Choline & TMAO Metabolism

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs7946	PENT V175M	CC	Homozygous reference — CC (PENT V175M wild-type). No variant allele; normal function.	MODERATE
rs2266782	FMO3 (TMA)	GG	Homozygous variant (GG) — Wild-type. Normal TMA oxidation. No trimethylaminuria	MODERATE

FMO3 wild-type excludes trimethylaminuria. PENT V175M heterozygosity may reduce endogenous phosphatidylcholine synthesis, particularly at low oestrogen status.

Omega-3 / FADS1/2

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs174547	FADS1	TT	Major allele homozygous. Normal delta-5 desaturase.	MODERATE
rs174583	FADS2	CT	Heterozygous (CT) — Wild-type. Normal ALA→EPA→DHA and LA→AA conversion. Efficient desaturation pathway	MODERATE

FADS1/FADS2 genotypes modulate desaturase activity for ALA→EPA/DHA conversion. Marine or algae-derived EPA/DHA bypasses this conversion step.

Vitamin B12 & Folate Absorption

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs2336573	CUBN (B12 absorption)	CG	Heterozygous (CG) — Wild-type. Normal ileal B12 uptake	MODERATE
rs602662	FUT2 (B12 proxy)	AA	Homozygous reference (AA) — Probable secretor (causative rs601338 not genotyped). Secretors have higher serum B12	MODERATE

CUBN wild-type supports normal B12 absorption. FUT2 secretor status (rs602662) influences serum B12 levels. Note: the causative FUT2 W143X (rs601338) is not directly genotyped here.

Selenium, Antioxidants & Histamine Metabolism (DAO)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs1050450	GPX1 Pro198Leu (glutathione peroxidase 1)	GG	Wild-type (Pro/Pro). FAVOURABLE. GPX1 is the primary cytoplasmic antioxidant enzyme that reduces hydrogen peroxide and lipid hydroperoxides using glutathione. The Leu198 variant (T allele) reduces enzyme activity by approximately 30% and is associated with increased cancer risk and oxidative stress susceptibility. Wild-type = full antioxidant capacity.	MODERATE

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs713041	GPX4 (selenium)	CC	Homozygous reference — CC (GPX4 (selenium) wild-type). No variant allele; normal function.	MODERATE
rs4880	SOD2 Ala16Val	AA	Homozygous reference — AA (SOD2 Ala16Val wild-type). No variant allele; normal function.	MODERATE
rs10156191	AOC1/DAO (histamine)	CC	Homozygous reference — CC (AOC1/DAO (histamine) wild-type). No variant allele; normal function.	MODERATE

AOC1/DAO rs10156191 (diamine oxidase) moderates histamine degradation capacity. Risk allele carriers may react more strongly to high-histamine foods (aged cheese, fermented products, red wine, certain beers). SOD2 Ala16Val (rs4880) affects mitochondrial ROS handling.

Neuropsychiatric Genetics

Serotonin System

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs25532	SLC6A4 (5-HTTLPR proxy)	AA	Homozygous (AA) — G linked to L(A) long allele = at least one high-expression SERT allele	MODERATE
rs6313	HTR2A T102C	AA	Homozygous reference — AA (HTR2A T102C wild-type). No variant allele; normal function.	MODERATE
rs6314	HTR2A His452Tyr	GG	Wild-type His452.	MODERATE
rs6295	HTR1A -1019C>G	AA	Homozygous (AA) — GG = reduced autoreceptor expression. Altered serotonergic tone. Studied in depression/SSRI response	MODERATE
rs6296	HTR1B G861C	CC	Homozygous reference — CC (HTR1B G861C wild-type). No variant allele; normal function.	MODERATE

SLC6A4 5-HTTLPR proxy (rs25532) — L/L homozygosity = higher serotonin transporter expression, resilient stress response. S/S or S/L = lower expression, increased depression/anxiety susceptibility. HTR1A -1019C>G homozygous G reduces 5-HT1A autoreceptor expression, affecting antidepressant response.

Dopamine System & COMT

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs4680	COMT Val158Met	GG	GG — Val/Val (warrior genotype). G=Val158. High COMT activity — rapid catechol-O-methyltransferase-mediated dopamine catabolism in prefrontal cortex (PFC). Lower basal PFC dopamine → stress resilience advantage (warrior), but mild working memory disadvantage under optimal conditions. Normal pain sensitivity.	HIGH
rs4633	COMT	CC	Homozygous reference — CC (COMT wild-type). No variant allele; normal function.	MODERATE
rs6277	DRD2 C957T	AA	Homozygous reference — AA (DRD2 C957T wild-type). No variant allele; normal function.	MODERATE
rs1611115	DBH -1021C>T	CT	Heterozygous (TC) — TT = lower DBH activity = lower norepinephrine relative to dopamine	MODERATE
rs27072	SLC6A3 (DAT)	TT	Homozygous alternate — TT. Both alleles carry the variant; effect stronger than heterozygous. See het description below.	MODERATE
rs3746544	SNAP25	GG	Homozygous reference — GG (SNAP25 wild-type). No variant allele; normal function.	MODERATE
rs1625579	MIR137	GG	Homozygous reference — GG (MIR137 wild-type). No variant allele; normal function.	MODERATE

COMT Val158Met (rs4680) is the primary dopamine catabolism variant in the prefrontal cortex. Val/Val = rapid catabolism ('warrior'); Met/Met = slow catabolism ('worrier'); Val/Met = intermediate. DBH -1021C>T homozygous T reduces noradrenaline synthesis, favouring higher dopamine:noradrenaline ratio.

BDNF, FKBP5 & HPA Axis Resilience

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs6265	BDNF Val66Met	CT	Heterozygous (TC) — Val/Val (wild-type). Normal activity-dependent BDNF secretion. Favourable for hippocampal plasticity and memory	HIGH
rs1360780	FKBP5	CC	Homozygous reference — FKBP5 low-risk; normal GR feedback; lower PTSD/depression risk from gene-environment interaction.	HIGH
rs3800373	FKBP5	AA	Wild-type at this FKBP5 position. Consistent with normal HPA axis regulation.	MODERATE

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs110402	CRHR1 (CRH receptor 1)	AG	Heterozygous. Corticotropin-releasing hormone receptor 1 initiates the stress cascade. This variant modulates cortisol response to stress and has been associated with depression risk and antidepressant treatment outcomes.	MODERATE
rs2270007	CRHR2 (CRH receptor 2)	CC	Homozygous reference — CC (CRHR2 (CRH receptor 2) wild-type). No variant allele; normal function.	MODERATE

BDNF Val66Met (rs6265): Val/Val = normal hippocampal BDNF secretion; Met allele reduces activity-dependent secretion, lowering episodic memory and raising depression vulnerability. FKBP5 rs1360780 and rs3800373 — risk alleles, when combined with early-life adversity, impair glucocorticoid feedback and strongly elevate PTSD risk.

Oxytocin, GABA, Glutamate & Opioid

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs53576	OXTR (oxytocin receptor)	AG	Heterozygous A/G — intermediate oxytocin receptor profile.	HIGH
rs279858	GABRA2 (GABA _A receptor subunit)	CC	Homozygous reference — CC (GABRA2 wild-type). No variant allele; normal function.	MODERATE
rs1799971	OPRM1 A118G	AA	Wild-type. Standard opioid receptor binding.	MODERATE
rs324420	FAAH C385A	CC	Wild-type Pro129. Normal anandamide degradation. (A allele = reduced FAAH, lower pain/anxiety.)	MODERATE
rs1049353	CNR1 (CB1)	TT	Homozygous alternate — TT. Both alleles carry the variant; effect stronger than heterozygous. See het description below.	MODERATE

OXTR rs53576 GG = higher oxytocin receptor sensitivity, prosocial behaviour, lower anxiety. OPRM1 A118G (rs1799971) — A118 reference = normal μ -opioid β -endorphin affinity; G allele associated with blunted opioid analgesia. FAAH C385A wild-type = normal anandamide degradation.

Parkinson's, Nicotine Dependence & GWAS

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs34637584	LRRK2 G2019S	GG	Wild-type. No LRRK2 G2019S mutation (the most common genetic cause of familial Parkinson's).	MODERATE
rs356219	SNCA (alpha-synuclein)	AA	Homozygous reference — AA (SNCA (alpha-synuclein) wild-type). No variant allele; normal function.	MODERATE
rs1051730	CHRNA3	GG	Homozygous alternate — GG. Both alleles carry the variant; effect stronger than heterozygous. See het description below.	MODERATE
rs16969968	CHRNA5 D398N	AA	Homozygous reference — AA (CHRNA5 D398N wild-type). No variant allele; normal function.	MODERATE
rs1006737	CACNA1C	AA	Homozygous reference — AA (CACNA1C wild-type). No variant allele; normal function.	MODERATE
rs1344706	ZNF804A	AA	Homozygous reference — AA (ZNF804A wild-type). No variant allele; normal function.	MODERATE

LRRK2 G2019S (rs34637584) is the most prevalent Mendelian PD variant in European ancestry — its genotype is the primary Parkinson's finding here. CHRNA3/A5 variants affect nicotine dependence and lung cancer risk in smokers.

Circadian Rhythm & Sleep

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs1801260	CLOCK 3111T>C	AG	Het. C allele (G on +strand) = evening chronotype tendency.	MODERATE
rs2287019	CRY1	CC	Wild-type. No CRY1-associated delayed sleep phase.	MODERATE
rs10462020	PER3	TT	Homozygous alternate — TT. Both alleles carry the variant; effect stronger than heterozygous. See het description below.	MODERATE
rs10830963	MTNR1B	CC	Homozygous reference — CC (MTNR1B wild-type). No variant allele; normal function.	MODERATE
rs5751876	ADORA2A	CC	Homozygous reference — CC (ADORA2A wild-type). No variant allele; normal function.	MODERATE

CLOCK 3111T>C (rs1801260) associates with evening chronotype. MTNR1B (rs10830963) — cross-reference §14 T2D — couples circadian melatonin signalling to glucose metabolism. ADORA2A (rs5751876) modulates adenosine sleep-wake signalling and caffeine sensitivity. RLS genetic burden (§18) additionally disrupts sleep quality — see BTBD9/MEIS1 genotypes.

Pain Genetics & Endocannabinoid System

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs6746030	SCN9A (Nav1.7)	GG	Wild-type. Normal pain signalling.	MODERATE
rs224534	TRPV1 (capsaicin)	AA	Homozygous reference — AA (TRPV1 (capsaicin) wild-type). No variant allele; normal function.	MODERATE
rs1049353	CNR1 (CB1)	TT	Homozygous alternate — TT. Both alleles carry the variant; effect stronger than heterozygous. See het description below.	MODERATE
rs324420	FAAH C385A	CC	Wild-type Pro129. Normal anandamide degradation. (A allele = reduced FAAH, lower pain/anxiety.)	MODERATE
rs2832407	GRIK1 (GluK1 kainate receptor)	AA	Homozygous reference — AA (GRIK1 (GluK1 kainate receptor) wild-type). No variant allele; normal function.	MODERATE

SCN9A (Nav1.7) rs6746030 wild-type excludes major pain-sensitivity variants. FAAH C385A (rs324420) — reference genotype = normal anandamide degradation, no enhanced endocannabinoid tone. TRPV1 (rs224534) modulates thermal pain threshold and capsaicin sensitivity. Note: CNR1 (rs1049353) and FAAH (rs324420) also appear in §23 opioid/endocannabinoid panel — their entries are repeated here because they are primary pain-system determinants in addition to their neuropsychiatric roles.

Sensory Genetics

Bitter Taste (TAS2R38 — PROP/PTC)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs713598	TAS2R38 A49P	CC	Homozygous reference — CC (TAS2R38 A49P wild-type). No variant allele; normal function.	MODERATE
rs1726866	TAS2R38 V262A	AA	Homozygous reference — AA (TAS2R38 V262A wild-type). No variant allele; normal function.	MODERATE
rs10246939	TAS2R38 I296V	CT	Heterozygous. All three positions heterozygous = diplotype PAV/AVI = MEDIUM TASTER.	MODERATE

TAS2R38 haplotype is determined by three SNPs: rs713598 (A49P), rs1726866 (V262A), rs10246939 (I296V). PAV/PAV = supertaster; PAV/AVI = medium taster; AVI/AVI = non-taster for PROP/PTC bitter compounds. Heterozygous PAV/AVI = intermediate bitter perception.

Sweet/Umami, Olfaction & Photic Sneeze Reflex

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs4920566	TAS1R3 (sweet/ umami receptor)	GG	Homozygous reference (GG) — Common genotype. TAS1R3 is the shared subunit of both the sweet taste receptor (TAS1R2+TAS1R3 heterodimer) and the umami taste receptor (TAS1R1+TAS1R3 heterodimer). TAS1R3 therefore determines sensitivity to both sweetness (sucrose, aspartame, stevia) and umami (glutamate, found in aged cheese, tomatoes, soy sauce, and MSG). AA = typical sweet and umami sensitivity	MODERATE
rs4481887	Asparagus metabolite olfaction	AA	Homozygous (AA) — CAN SMELL asparagus metabolites (methanethiol, S-methyl thioesters) in urine. The ability to detect this odour is an olfactory receptor polymorphism, not a metabolic difference — everyone produces the metabolites, but not everyone can smell them. ~60% of Europeans retain this ability	MODERATE
rs6591536	Asparagus anosmia (additional)	AA	Homozygous reference — AA (Asparagus anosmia (additional) wild-type). No variant allele; normal function.	MODERATE
rs10427255	ZEB2 region (2q22)	TT	Homozygous (TT) — NON-SNEEZER. The T allele at this locus near ZEB2 is associated with the photic sneeze reflex — also known as ACHOO syndrome (Autosomal dominant Compelling Helio-Ophthalmic Outburst). This is the involuntary sneeze triggered by sudden exposure to bright light, particularly sunlight when emerging from a dark environment. It affects approximately 18–35% of the population and follows autosomal dominant inheritance. CC = both alleles are the non-reflex type. The photic sneeze reflex is not present	MODERATE

TAS1R3 (rs4920566) — sweet/umami receptor. Asparagus olfaction (rs4481887) determines ability to detect urinary asparagusic acid metabolites. Photic sneeze reflex (ACHOO) at ZEB2 region (rs10427255) — reference genotype predicts absence of the reflex.

Blood Type & Antigen Systems

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs8176746	ABO Leu266Met	GG	Homozygous reference — GG (ABO Leu266Met wild-type). No variant allele; normal function.	MODERATE
rs8176719	ABO O-allele	AA	Homozygous (AA) — rs8176719 is a deletion variant that defines the O blood group null allele at the ABO locus. Homozygous II (insertion/insertion = no deletion) indicates absence of the O-allele frameshift. Serological ABO typing from blood group SNP panel is needed for full ABO assignment	MODERATE
rs579459	ABO VTE tag	CC	Homozygous reference — CC (ABO VTE tag wild-type). No variant allele; normal function.	MODERATE
rs12075	DARC (Duffy)	AA	Homozygous reference — AA (DARC (Duffy) wild-type). No variant allele; normal function.	MODERATE
rs2814778	DARC null	AT	Heterozygous (AT) — Not Duffy-null. No West African ancestry signal	MODERATE
rs5918	ITGB3 PIA1/A2	CC	Homozygous reference — CC (ITGB3 PIA1/A2 wild-type). No variant allele; normal function.	MODERATE

ABO blood type requires both rs8176746 (Leu266Met) and rs8176719 (O-allele frameshift). If rs8176719 is a no-call, ABO cannot be fully determined — clinical serological typing provides the definitive answer. DARC Duffy antigen (rs12075, rs2814778) determines Fy(a/b) antigen status and Plasmodium vivax resistance.

Archaic Introgression (Neanderthal & Denisovan)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs1229984	ADH1B Arg48His	CC	Wild-type. Standard alcohol metabolism.	MODERATE
rs3827760	EDAR V370A	AA	Ancestral (Val370). Derived near-fixed in EAS. No E. Asian ancestry.	MODERATE

ADH1B His48 (rs1229984) and EDAR V370A (rs3827760) are Neanderthal-introgressed or strongly East Asian-selected variants typically absent in European-ancestry individuals. SLC24A5 (rs1426654) and SLC45A2 (rs28777) are post-Out-of-Africa European depigmentation sweeps covered in §29 Ancestry Informative Markers. Quantitative Neanderthal admixture estimation requires whole-genome sequencing.

Ancestry Informative Markers

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs1426654	SLC24A5 Ala111Thr	AA	Homozygous derived. Nearly fixed in Europeans. Light skin.	MODERATE
rs28777	SLC45A2	AA	Light-skin allele homozygous.	MODERATE
rs12913832	HERC2/OCA2	AA	Homozygous reference — AA (HERC2/OCA2 wild-type). No variant allele; normal function.	MODERATE
rs7495174	OCA2	AA	Lighter eye colour contributor.	MODERATE
rs4778138	OCA2	GG	Homozygous reference (GG) — Lighter eye colour contributor	MODERATE
rs2814778	DARC null	AT	Heterozygous (AT) — Not Duffy-null. No West African ancestry signal	MODERATE
rs671	ALDH2 Glu504Lys	GG	Wild-type. No alcohol flush reaction.	MODERATE

Full ancestry principal-component analysis requires the complete SNP dataset against a reference panel (1000 Genomes, gnomAD). The markers above are strong continental ancestry signals. SLC24A5 homozygous Thr and SLC45A2 homozygous reference are characteristic of European ancestry. ALDH2 Glu (reference) and absence of DARC null exclude common East Asian and sub-Saharan African ancestry markers respectively.

Prostate & PSA Genetics

This section covers prostate-specific loci (KLK3/PSA, MSMB, 8q24 prostate cancer GWAS). These are male-specific findings and are not clinically applicable to a predicted-female subject. The 8q24 locus (rs6983267, CCAT2/MYC enhancer) is pleiotropic and also reported in the colorectal cancer section (§18) where it applies regardless of sex.

Longevity Genetics

FOXO3 (Longevity Transcription Factor)

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs9400239	FOXO3	TT	Homozygous longevity allele — strongest FOXO3 association with exceptional longevity in multiple centenarian cohorts.	HIGH
rs479744	FOXO3 (functional 3' UTR)	GG	Homozygous reference — GG (FOXO3 (functional 3' UTR) wild-type). No variant allele; normal function.	MODERATE
rs2871865	FOXO3/IGF1R region	AA	Homozygous (AA) — Homozygous at this FOXO3-IGF1R intergenic locus	MODERATE

FOXO3 rs9400239 and rs479744 were identified in multiple centenarian cohorts (Willcox 2008, Flachsbart 2009). FOXO3 orchestrates stress resistance, autophagy, and longevity pathways. Homozygous risk-reducing genotypes show strongest association; heterozygous = intermediate.

Insulin/IGF-1/mTOR Axis

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs6214	IGF1 (insulin-like growth factor 1)	CC	Homozygous reference — CC (IGF1 (insulin-like growth factor 1) wild-type). No variant allele; normal function.	MODERATE
rs35767	IGF1 (promoter)	GG	Common genotype at the IGF1 promoter.	MODERATE
rs2229765	IGF1R (IGF-1 receptor)	AA	Homozygous reference — AA (IGF1R (IGF-1 receptor) wild-type). No variant allele; normal function.	MODERATE
rs2494732	AKT1 (PI3K-AKT-mTOR)	CC	Homozygous reference — CC (AKT1 (PI3K-AKT-mTOR) wild-type). No variant allele; normal function.	MODERATE

IGF1 promoter variants and IGF1R functional polymorphisms modulate the insulin/IGF-1 signalling axis — a key determinant of both cancer risk and longevity across species.

Telomere Biology Panel

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs7726159	TERT	AC	Heterozygous. Second TERT signal. Consistent with intermediate telomere length.	MODERATE
rs2736100	TERT (5p15)	AA	Homozygous reference — AA (TERT (5p15) wild-type). No variant allele; normal function.	MODERATE
rs10069690	TERT (intronic splice variant)	TT	Homozygous alternate — TT. Both alleles carry the variant; effect stronger than heterozygous. See het description below.	MODERATE
rs12696304	TERC	CC	Wild-type. TERC encodes the RNA template component of telomerase. No short-telomere allele.	MODERATE
rs8049897	TERC	GG	Wild-type at second TERC position. Telomerase RNA component is intact.	MODERATE
rs10165485	ACYP2	CC	Homozygous reference — CC (ACYP2 wild-type). No variant allele; normal function.	MODERATE

TERT and TERC variants have pleiotropic effects — some associate with longer telomeres and longevity, others with cancer risk in a tissue-specific manner. ACYP2 rs10165485 is among the most replicated telomere length GWAS loci.

CETP Centenarian Variant & Antioxidant Defence

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs5882	CETP I405V (centenarian variant)	AG	Heterozygous I405V — reduced CETP activity; modestly elevated HDL; associated with longevity in Ashkenazi/broad centenarian studies.	HIGH
rs1001179	CAT -262C>T	CT	Heterozygous (CT) — Wild-type catalase	MODERATE
rs4880	SOD2 Ala16Val	AA	Homozygous reference — AA (SOD2 Ala16Val wild-type). No variant allele; normal function.	MODERATE
rs1050450	GPX1 Pro198Leu (glutathione peroxidase 1)	GG	Wild-type (Pro/Pro). FAVOURABLE. GPX1 is the primary cytoplasmic antioxidant enzyme that reduces hydrogen peroxide and lipid hydroperoxides using glutathione. The Leu198 variant (T allele) reduces enzyme activity by approximately 30% and is associated with increased cancer risk and oxidative stress susceptibility. Wild-type = full antioxidant capacity.	MODERATE

CETP I405V (rs5882) — centenarian longevity variant (Barzilai 2003). Reduces CETP activity, elevating HDL. Combined with FOXO3 longevity allele carriage, these represent genuinely replicated common-variant longevity signals. APOE haplotype (§12): ε3/ε3 — the strongest individual longevity modifier.

Extracellular Matrix, Connective Tissue & Musculoskeletal

Collagen, Elastin & Tenascin

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs1800012	COL1A1 Sp1	AA	Homozygous reference — AA (COL1A1 Sp1 wild-type). No variant allele; normal function.	MODERATE
rs12722	COL5A1	TC	Heterozygous (TC) — Wild-type. Normal type V collagen, which regulates collagen fibril diameter in tendons and ligaments. No increased tendon/ligament injury susceptibility	MODERATE
rs1010156	COL6A1 (collagen VI)	TT	Homozygous alternate — TT. Both alleles carry the variant; effect stronger than heterozygous. See het description below.	MODERATE
rs2071307	ELN (elastin)	AG	Heterozygous. Elastin gives blood vessels, skin, and lungs their elastic recoil. Critically, elastin is produced almost exclusively during development — the elastin molecules in adult tissues are the same ones laid down in childhood, making them some of the longest-lived proteins in the body. Loss of elastin integrity drives arterial stiffening (the primary cause of isolated systolic hypertension with age), skin aging (wrinkles, loss of snap-back), and emphysema. This variant has been associated with arterial stiffness in population studies.	MODERATE
rs1150754	TNXB (tenascin X)	CT	Heterozygous. Tenascin-X is an extracellular matrix glycoprotein that regulates collagen fibrillogenesis — it controls how collagen molecules assemble into fibres and determines their spacing, diameter, and mechanical properties. Complete TNXB deficiency causes a form of Ehlers-Danlos syndrome (hypermobility type), while common heterozygous variants are associated with joint hypermobility in the general population. CT = one variant allele, which may contribute to increased connective tissue compliance (looseness), joint laxity, and possibly easy bruising or skin hyperextensibility.	MODERATE
rs1800449	LOX (lysyl oxidase)	AA	Homozygous (AA) — Common genotype. LOX is the master crosslinking enzyme for both collagen and elastin — it converts lysine residues into reactive aldehydes that form covalent crosslinks between fibre molecules. Without LOX, connective tissues lack tensile strength	MODERATE

COL1A1 Sp1 (rs1800012) is associated with reduced bone mineral density and soft tissue laxity. ELN elastin (rs2071307) affects vascular wall and skin elasticity — cross-reference §13 cardiovascular. TNXB tenascin X (rs1150754) heterozygosity associates with joint hypermobility spectrum.

MMP/TIMP & ECM Remodelling

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs243865	MMP2 (-1306 C>T) (gelatinase A)	CT	Heterozygous. MMP2 degrades type IV collagen (the main component of basement membranes), gelatin, and elastin. The T allele reduces MMP2 promoter activity, lowering enzyme expression. CT = intermediate MMP2 levels. Lower MMP2 may protect against aneurysm progression and invasive cancer, but may modestly slow wound healing and tissue remodelling.	MODERATE
rs17577	MMP9	GG	Wild-type at second MMP9 position. Confirms normal MMP9.	MODERATE
rs3918242	MMP9 (-1562 C>T) (gelatinase B)	TT	Wild-type at this MMP9 promoter position. MMP9 is the critical MMP in vascular remodelling, atherosclerotic plaque instability, and aneurysm expansion. Normal MMP9 regulation is favourable for vascular stability.	MODERATE

Muscle & Exercise Performance

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs1815739	ACTN3 R577X	CC	Homozygous R577 — full α -actinin-3 expression; fast-twitch muscle fibre advantage; power/sprint phenotype.	HIGH
rs7832552	MSTN (myostatin/ GDF8)	CC	Wild-type. Myostatin is the master negative regulator of muscle growth. Loss-of-function mutations create the 'double-muscled' phenotype in Belgian Blue cattle and extraordinary muscularity in rare human cases. CC = normal myostatin function, no innate advantage for muscle mass.	MODERATE
rs8192678	PPARGC1A G482S	CC	Gly/Gly (wild-type). Normal PGC-1 α function. Favourable for mitochondrial biogenesis and endurance capacity.	MODERATE
rs1049434	MCT1/SLC16A1	AA	Homozygous reference — AA (MCT1/SLC16A1 wild-type). No variant allele; normal function.	MODERATE

ACTN3 R577X (rs1815739) is the best-characterised human performance gene. R/R (CC) = fast-twitch power phenotype; X/X (TT) = endurance-optimised; R/X (CT) = mixed. PPARGC1A G482S (rs8192678) modulates mitochondrial biogenesis.

OA, Disc, Bone, Vascular & Other ECM

rsID	Gene / Variant	Genotype	Interpretation	Confidence
rs143383	GDF5	AA	Wild-type. No GDF5-mediated osteoarthritis risk. GDF5 is a growth/differentiation factor critical for joint formation.	MODERATE
rs11177	SMAD3 (TGF- β pathway)	AA	Homozygous reference — AA (SMAD3 (TGF- β pathway) wild-type). No variant allele; normal function.	MODERATE
rs6841581	SMAD3 (Loeys-Dietz aneurysm pathway)	GG	Wild-type. No Loeys-Dietz aortic aneurysm risk at this locus. Favourable.	MODERATE
rs1800169	CILP	GG	Wild-type. CILP (cartilage intermediate layer protein) inhibits TGF- β signalling in the intervertebral disc. The risk allele accelerates disc degeneration. GG = no CILP-mediated disc risk.	MODERATE
rs3736228	LRP5 A1330V	CC	Wild-type. Normal Wnt/LRP5 bone signalling. LRP5 is the co-receptor for Wnt ligands in osteoblasts.	MODERATE
rs11172113	LRP1 (migraine)	CC	Homozygous reference — CC (LRP1 (migraine) wild-type). No variant allele; normal function.	MODERATE
rs634990	15q14 (myopia)	CC	Homozygous reference — CC (15q14 (myopia) wild-type). No variant allele; normal function.	MODERATE
rs524952	GJD2 (myopia)	AA	Homozygous reference — AA (GJD2 (myopia) wild-type). No variant allele; normal function.	MODERATE
rs16879765	WNT7B (Dupuytren's)	TT	Homozygous alternate — TT. Both alleles carry the variant; effect stronger than heterozygous. See het description below.	MODERATE

GDF5 (rs143383) is the most replicated OA susceptibility variant. SMAD3 (rs11177) is a cross-domain finding linking OA risk to TGF- β -mediated vascular effects (§13, §17). LRP1 migraine (rs11172113) and WNT7B Dupuytren's (rs16879765) are ECM-related tissue fibrosis signals. Myopia GWAS loci (rs634990, rs524952) complete the ECM section.

Forensic-Style Phenotype Reconstruction

Trait	Prediction	Confidence	Key Locus
Biological sex	Indeterminate	INDETERMINATE	X-chromosome het rate / XY encoding
Eye colour	Blue (high probability)	HIGH	rs12913832 AA
Skin pigmentation	Light (Fitzpatrick I-II)	HIGH	rs1426654 AA
Earwax type	Wet (standard)	HIGH	rs17822931 CC
Photic sneeze reflex	Absent	HIGH	rs10427255 TT
Blood type (proxy)	Non-B (O or A)	MODERATE	rs8176746 GG
Asparagus detection	Anosmia	HIGH	rs4481887 AA

Limitations & Caveats

Array coverage (~0.02% of genome). SNP arrays detect common variants only. Structural variants, insertions/deletions >1 bp, copy number variants (CNVs), rare variants, and epigenetic modifications are not captured.

APOE genotyped from array data. The $\epsilon 2/\epsilon 3/\epsilon 4$ haplotype in §12 is based on rs429358 and rs7412 from the consumer array. Array-based APOE calling is generally reliable but clinical confirmation is recommended if the result will influence clinical decisions.

CYP2D6 CNVs undetectable. Array data cannot detect gene duplication (ultrarapid metaboliser). Clinical-grade long-read or CNV-aware PGx testing is required for complete CYP2D6 phenotyping.

No imputation applied. Imputation to TOPMed would expand coverage to >10M variants, improving PRS accuracy.

Pharmacogenomic findings require clinical confirmation by accredited laboratories before influencing prescribing decisions.

Population ancestry assumption. Effect sizes are primarily from European-ancestry GWAS studies. Risk estimates may differ in other ancestral backgrounds.

Not medical advice. This report is for research and informational purposes only. Consult a qualified healthcare professional or genetic counsellor before making medical decisions.

Summary & Conclusions

This report has analysed 413 genotyped loci, matching 413 of 413 curated target polymorphisms across 33 biological and clinical domains.

Reassuring / favourable findings

1. MTHFR C677T wild-type (GG) — no 677TT-mediated MTHFR reduction.
2. Major thrombophilia variants absent — Factor V Leiden (rs6025) and Prothrombin G20210A (rs1799963) both wild-type. No Mendelian VTE risk at primary loci.
3. DPYD *2A absent (rs3918290 wild-type) — no splice-defect null allele. Clinical-grade DPYD testing covers additional loci including rs56293913 not reliably distinguished by consumer arrays.
4. LRRK2 G2019S absent — most prevalent Mendelian Parkinson's variant not detected.
5. APOE ϵ_3/ϵ_3 — No ϵ_4 or ϵ_2 . ϵ_3/ϵ_3 is the most common European genotype (~60%), conferring population-average Alzheimer's risk.

Key Findings Summary

1. **CYP2C9 variant allele(s) detected** — warfarin dose adjustment may be required; check CYP2C9 phenotype and integrate with VKORC1/CYP4F2 findings.
 2. **CYP2C19*2 intermediate metaboliser (heterozygous)** — reduced clopidogrel activation; consider alternative antiplatelet if high-risk ACS/PCI indication. Clinical CYP2C19 testing recommended.
 3. **rs56293913 AG (putative DPYD*13 c.1679T>G)** — if confirmed via clinical-grade DPYD testing, intermediate DPD metaboliser; 50% 5-FU/capecitabine starting dose. Do not act on consumer array result alone.
 4. **CFH Y402H heterozygous** — one copy of the strongest common AMD risk variant. Consider lutein/zeaxanthin supplementation and regular ophthalmological review; see §18.
 5. **FOXO3 longevity allele present** — replicated centenarian association; see §31.
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References & Key Sources

Key references for variant annotation and interpretation. Gene-specific citations available through OMIM, ClinVar, and PharmGKB.

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413 SNPs in annotation DB; 413 matched on this array. Analysis: Python 3 / ReportLab / Matplotlib. Generator v4.21. Report date: 18 June 2026.