

Report Summary

1196

Total Variants

25

Categories

12

Pathway Figures

215

High Risk (+/+)

349

Moderate Risk (+/-)

632

Low Risk (-/-)

Table of Contents

Report Overview 1

Genetic Variants (25 categories) 2

Alzheimers/Cardio/Lipid (86 variants) △ ▢ 2

COMT Activity (121 variants) △ ▢ 5

Cannabinoid Pathway (53 variants) △ ▢ 10

Celiac Disease/Gluten Intolerance (6 variants) △ ▢ 12

Clotting Factors (15 variants) △ ▢ 13

Eye Health (2 variants) ⚡ 14

Glyoxylate Metabolic Process (42 variants) ▲ ▲ 15

HLA (57 variants) ▲ ▲ 17

IgA (22 variants) ▲ ▲ 19

IgE (5 variants) ⚡ 20

IgG (3 variants) ⚡ 21

Iron Uptake & Transport (36 variants) ▲ ▲ 22

Liver Detox - Phase I (80 variants) ▲ ▲ 24

Liver Detox - Phase II (165 variants) ▲ ▲ 27

Methylation & Methionine/Homocysteine Pathways (96 variants) ▲ ▲ 33

Mitochondrial Function (60 variants) ▲ ▲ 37

Molybdenum (37 variants) ▲ ▲ 39

Neurotransmitter Pathway: Glutamate & GABA (8 variants) ▲ ▲ 41

Neurotransmitter Pathway: Serotonin & Dopamine (155 variants) ▲ ▲ 42

Other Immune Factors (15 variants) ▲ ▲ 48

Pentose Phosphate Pathway (43 variants) ▲ ▲ 49

Thiamin/Thiamine Degradation (53 variants) ▲ ▲ 51

Thyroid (5 variants) ⚡ 53

Trans-Sulfuration Pathway (22 variants) ▲ ▲ 54

Yeast/Alcohol Metabolism (9 variants) ▲ ▲ 55

Pathway Figures (12 figures) 56

Figure 1: Liver Detox - Phase II 56

Figure 2: Methylation & Methionine/Homocysteine Pathways 57

Figure 3: Neurotransmitter Pathway: Serotonin & Dopamine 58

Figure 4: COMT Activity 59

Figure 5: Glyoxylate Metabolic Process 60

Figure 6: HLA 61

Figure 7: Yeast/Alcohol Metabolism 62

Figure 8: Trans-Sulfuration Pathway 63

Figure 9: Neurotransmitter Pathway: Glutamate & GABA 64

Figure 10: Pentose Phosphate Pathway 65

Figure 11: Thiamin/Thiamine Degradation 66

Figure 12: Mitochondrial Function 67

Important Disclaimer 68

Quick Navigation: [Overview](#) [Categories](#) [Figures](#) [Disclaimer](#)

Alzheimers/Cardio/Lipid

86 variants found 11 12 63

Risk Summary: 11 high risk variants, 12 moderate risk variants - Consider discussing with healthcare provider

Quick Navigation: [Overview](#) [Categories](#) [Figures](#) [Disclaimer](#)

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs11591147	PCSK9 R46L	T	GG	-/-
rs4970834	CELSR2 -20C7927T	T	CC	-/-
rs6025	F5 Factor V Leiden FVL	T	CC	-/-
rs2227589	SERPINC1 G5301A	T	CC	-/-
rs6656401	CR1 A27577G	A	AG	+/-
rs63750048	PSEN2 Ala85Val	T	CC	-/-
rs63749851	PSEN2 Thr122Pro	C	AA	-/-
rs63750215	PSEN2 Asn141Ile	T	AA	-/-
rs28936379	PSEN2 Met239Val	G	AA	-/-
rs63749884	PSEN2 Met239Ile	A	GG	-/-
rs63750666	PSEN2 Thr429Met	T	CC	-/-
rs63750110	PSEN2 Asp438Ala	C	AA	-/-
rs1523127	NR12 C6709A	A	AC	+/-
rs1049296	TF C34378T	C	CC	+//
rs13146272	CYP4V2 Q259K	C	AC	+/-
rs2036914	F11 T10364C	C	TT	-/-
rs2289252	F11 C25264T	C	CC	+//
rs1801020	F12 T5046C	A	GG	-/-
rs2731672	KNG I598T GP IIIa HPA-1	T	CC	-/-
rs179943	ATXN1 C368404T	A	AG	+/-
rs1799945	HFE H63D	G	CC	-/-

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs1800562	HFE C282Y	A	GG	-/-
rs241448	TAP2 T14863C	A	AG	+/-
rs11754661	MTHFD1L G25264A	G	GG	+/*
rs2069837	IL6 A6262G	G	AA	-/-
rs11136000	CLU A58V	C	CC	+/*
rs7019241	GOLM1 C17857992T	C	CC	+/*
rs10868366	GOLM1 G88700060T	T	GG	-/-
rs4986790	TLR4 D299G	G	AA	-/-
rs1880676	CHAT Asp7Asn	A	AG	+/-
rs3810950	CHAT A120T	A	AG	+/-
rs17571	CTSD A58V	A	GG	-/-
rs11030104	BDNF T64089C	A	AA	+/*
rs5896	F2 C494T	T	CC	-/-
rs10793294	GAB2 G137466T	A	AA	+/*
rs2373115	GAB2 G42719T	G	CC	-/-
rs1792113	SORL1 A146986G	G	AA	-/-
rs669	A2M Ile1000Val	C	TC	+/-
rs12316150	OLR1 T17500A	T	AA	-/-
rs2160525	LRP6 T154522C	A	GG	-/-
rs1012672	LRP6 Cys1270	A	GG	-/-
rs2302685	LRP6 V1062I	C	TT	-/-
rs2248663	RNF219 T79207588C	C	TC	+/-
rs6046	F7 A353G Arg329Gln	A	AG	+/-
rs3211719	F10 113777509 A5397C	A	AA	+/*
rs63749824	PSEN1 Ala75Val	T	CC	-/-
rs63750599	PSEN1 Leu81Pro	C	TT	-/-
rs63750815	PSEN1 Val85Leu	T	GG	-/-
rs63751037	PSEN1 Met135Val	G	AA	-/-
rs63749885	PSEN2 His159Tyr	T	CC	-/-
rs63750590	PSEN1 His159Arg	G	AA	-/-
rs63750577	PSEN1 Ser166Phe	T	CC	-/-
rs63751144	PSEN1 Leu170Met	A	CC	-/-
rs63751068	PSEN1 Gly179Val	T	GG	-/-
rs63750526	PSEN1 Ala242Glu	A	CC	-/-
rs63751163	PSEN1 Leu246Ser	C	TT	-/-
rs63751320	PSEN1 Tyr252Ser	C	AA	-/-
rs63751229	PSEN1 Pro263Ser	T	CC	-/-
rs63750900	PSEN1 Arg265His	A	GG	-/-
rs63750886	PSEN1 Leu267Val	G	CC	-/-
rs63751235	PSEN1 Leu282Val	G	CC	-/-
rs17125721	PSEN1 Glu314Gly	G	AA	-/-
rs63750218	PSEN1 Leu388Pro	C	TT	-/-
rs63751223	PSEN1 Ala422Pro	C	GG	-/-
rs1800775	CETP C4402A	C	CC	+/*
rs5882	CETP I405V	A	AA	+/*

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs5918	ITGB3 P1A2/T196C	C	TT	-/-
rs1800458	TTR Gly26Ser	A	GG	-/-
rs3764650	ABCA7 T1046520G	G	TT	-/-
rs892086	DNM2 G13923A	A	AG	+/-
rs6859	PVRL2 A37642G	A	GG	-/-
rs157580	TOMM40 G45395266A	G	AG	+/-
rs769449	APOE G5964A	A	GG	-/-
rs28931576	APOE A178G	G	AA	-/-
rs769455	APOE C8002T	T	CC	-/-
rs7412	APOE APOE epsilon 2	T	CC	-/-
rs28931579	APOE A8455C	C	AA	-/-
rs1613662	GP6 Pro219Ser	G	AA	-/-
rs1042580	THBD A7681G	C	TT	-/-
rs63749964	APP Val586Gly	C	AA	-/-
rs63750399	APP Ile698Val	C	TT	-/-
rs63750734	APP Val697Met	T	CC	-/-
rs63750973	APP Thr696Ile	A	GG	-/-
rs63750066	APP Ala695Thr	T	CC	-/-
rs63750363	APP Glu647Asp	C	CC	+/*
rs6048	F9 G580A A25386G	G	AA	-/-

COMT Activity

121 variants found 21 38 62

(See Figure 4)

Risk Summary: 21 high risk variants, 38 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs1800440	CYP1B1 N453S	T	TC	+/-
rs1056836	CYP1B1 L432V	C	CG	+/-
rs9828046	DRD3 C44637T	A	GG	-/-
rs9288993	DRD3 T43727C	G	AA	-/-
rs963468	DRD3 C40013T	A	AG	+/-
rs3773678	DRD3 T32822C	G	GG	+//+
rs167771	DRD3 C26625T	A	AA	+//+
rs324029	DRD3 T21277C	A	GG	-/-
rs1486009	DRD3 T14368C	A	AA	+//+
rs6280	DRD3 G25A	T	TT	+//+
rs9825563	DRD3 T2680C	A	AG	+/-
rs1394016	DRD3 G20405035A	G	AG	+/-
rs251937	DRD1 A9244G	C	TT	-/-
rs686	DRD1 C7464T	A	AG	+/-
rs4532	DRD1 G6014A	C	TC	+/-
rs5326	DRD1 G5968A	T	CC	-/-
rs265981	DRD1 T5262C	A	AG	+/-
rs1611114	DBH C3719T	T	TT	+//+
rs1611115	DBH variant	T	CC	-/-
rs3025382	DBH G5837A	A	GG	-/-
rs2007153	DBH T7335C	T	CC	-/-
rs1108580	DBH A486G	A	AG	+/-
rs1108581	DBH A8757G	G	AA	-/-
rs2873804	DBH T9160C	T	TT	+//+
rs5320	DBH G631A	A	GG	-/-
rs1611123	DBH C12599T	T	CC	-/-
rs4531	DBH G952T	T	GG	-/-
rs1541332	DBH G15032A	A	AA	+//+
rs2519154	DBH T15791C	C	TC	+/-
rs2283123	DBH C18813T	T	CC	-/-
rs77905	DBH A1410G	A	AG	+/-

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs2097628	DBH T2145C	A	AG	+/-
rs129882	DBH C27185T	T	TC	+/-
rs11599164	ANK3 C666301A	T	GG	-/-
rs9804190	ANK3 G658454A	C	TC	+/-
rs10761482	ANK3 T62085337C	C	TC	+/-
rs10994336	ANK3 G318473A	T	CC	-/-
rs10994397	ANK3 G219161A	T	CC	-/-
rs3758653	DRD4 T4095C	C	TT	-/-
rs752306	DRD4 C5318T	T	CC	-/-
rs11246226	DRD4 C8887A	A	AA	+/?
rs2070762	TH T1090C	G	AG	+/-
rs28934580	TH G1010A//R337H	T	CC	-/-
rs28934581	TH A733C	G	TT	-/-
rs7483056	TH T7517C	A	AG	+/-
rs6356	TH V112M	T	CC	-/-
rs1800497	ANKK1 E713K	A	GG	-/-
rs10891549	DRD2 A72555G	C	TC	+/-
rs2242592	DRD2 C71572T	G	AG	+/-
rs6275	DRD2 T852C	A	AG	+/-
rs1076560	DRD2 G67314T	A	CC	-/-
rs2734838	DRD2 T64501C	G	GG	+/?
rs1079597	DRD2 G54716A	T	CC	-/-
rs1079596	DRD2 G54383A	T	CC	-/-
rs2471857	DRD2 G52663A	T	CC	-/-
rs4620755	DRD2 C41383T	A	GG	-/-
rs7125415	DRD2 G40321A	T	CC	-/-
rs4648318	DRD2 A37613G	C	TT	-/-
rs17529477	DRD2 C33935T	A	AG	+/-
rs4245146	DRD2 A33029G	C	TC	+/-
rs7131056	DRD2 T21228G	A	AC	+/-
rs4648317	DRD2 C19470T	A	GG	-/-
rs1799978	DRD2 A4651G	T	TT	+/?
rs12364283	DRD2 T4047C	G	AA	-/-
rs1006737	CACNA1C G115699A	A	AA	+/?
rs2159100	CACNA1C C271442T	T	TT	+/?
rs216013	CACNA1C A2729632G	G	AA	-/-
rs2302729	CACNA1C T709021C	T	CC	-/-
rs1801153	PAH G*187A	T	CC	-/-
rs5030861	PAH IVS12+1G>A	T	CC	-/-
rs5030858	PAH R408W	A	GG	-/-
rs5030857	PAH A403V	A	GG	-/-
rs2245360	PAH C81837T	A	AA	+/?
rs5030855	PAH IVS10-11G>A	T	CC	-/-
rs5030853	PAH A300S	A	CC	-/-
rs5030852	PAH IVS7+1G>A	T	CC	-/-

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs5030849	PAH G782A	T	CC	-/-
rs1042503	PAH G735A	T	CC	-/-
rs3817446	PAH A55562G	C	TT	-/-
rs2037639	PAH C45031T	A	GG	-/-
rs1722392	PAH G37636A	T	TT	+/-
rs10860936	PAH A33429G	C	TT	-/-
rs10778209	PAH T32409C	A	AG	+/-
rs62507347	PAH A27743C	C	TT	-/-
rs1522307	PAH T17864C	G	AA	-/-
rs5030841	PAH L48S	G	AA	-/-
rs4767939	ALDH2 A7550G	A	AA	+/-
rs2238151	ALDH2 T12488C	T	TT	+/-
rs4648328	ALDH2 C23443T	T	CC	-/-
rs968529	ALDH2 T35023C	C	CC	+/-
rs4646778	ALDH2 C36438A	A	CC	-/-
rs671	ALDH2 G1369A	A	GG	-/-
rs16941667	ALDH2 C45068T	T	CC	-/-
rs1048943	CYP1A1*2C A4889G	T	TT	+/-
rs1799814	CYP1A1*4 C2453A	T	GG	-/-
rs72547564	ALDH3A2 G641A	A	GG	-/-
rs72547575	ALDH3A2 A1157G	G	AA	-/-
rs876493	PNMT G-184A	A	GG	-/-
rs933271	COMT A2953G	T	TT	+/-
rs1544325	COMT A7406G	A	GG	-/-
rs5993883	COMT T13376G	T	GG	-/-
rs4646312	COMT T24075C	C	TC	+/-
rs165656	COMT G24601C	C	CG	+/-
rs6269	COMT A-1324G	G	AG	+/-
rs4633	COMT H62H	T	TC	+/-
rs2239393	COMT A 26166G	G	AG	+/-
rs4680	COMT V158M	A	AG	+/-
rs769224	COMT -61 P199P	A	GG	-/-
rs4646316	COMT C27870T	T	CC	-/-
rs174699	COMT C30196T	C	TT	-/-
rs9332377	COMT C31430T	T	CC	-/-
rs165599	COMT G*522A	A	AG	+/-
rs5953210	MAOA G3638A	G	AG	+/-
rs5906957	MAOA A36902G	G	GG	+/-
rs909525	MAOA C42794T	C	TC	+/-
rs6323	MAOA R297R/G492T/T941G	G	TG	+/-
rs2235186	MAOA A85020G	A	AG	+/-
rs1137070	MAOA T1011C/1460C	T	TC	+/-
rs1799836	MAOB A118723G	C	CC	+/-
rs10521432	MAOB C112982T	G	AG	+/-
rs6651806	MAOB T57758G	A	AC	+/-

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Cannabinoid Pathway

53 variants found 12 14 27

Risk Summary: 12 high risk variants, 14 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs9424398	CNR2 T24221834G	G	TG	+/-
rs4353135	NLRP3 247617036G>T	T	TG	+/-
rs806368	CNR1 T88850100C	T	TT	+/?
rs4707436	CNR1 G88851751A	A	AA	+/?
rs1049353	CNR1 T453T	T	TT	+/?
rs806369	CNR1 T88856178C	T	CC	-/-
rs806374	CNR1 T88857320C	T	TC	+/-
rs806376	CNR1 T88858648C	C	TT	-/-
rs806377	CNR1 T88858723C	T	TT	+/?
rs806378	CNR1 C88859551T	T	CC	-/-
rs6928813	CNR1 A88861698G	G	AA	-/-
rs806381	CNR1 A88865901G	A	AA	+/?
rs12205430	CNR1 T88867925C	C	TT	-/-
rs6454673	CNR1 G88871049A	G	GG	+/?
rs6454674	CNR1 T88872930G	T	TT	+/?
rs1049748	ABP1 P574P	T	TC	+/-
rs3847987	VDR C48238068A	A	CC	-/-
rs1544410	VDR VDR:Bsml	T	TC	+/-
rs7967152	VDR A48244184C	C	AC	+/-
rs2248098	VDR T50459C	G	AG	+/-
rs2239182	VDR T48255411C	C	CC	+/?
rs2107301	VDR C48245T	A	GG	-/-
rs2239181	VDR T47866G	C	AA	-/-
rs1540339	VDR G46489A	T	CC	-/-
rs12721370	VDR G41742T	A	CC	-/-
rs886441	VDR G48262964A	G	AA	-/-
rs2189480	VDR C39987A	T	GG	-/-
rs2239186	VDR T34405C	G	AA	-/-
rs11168275	VDR T48272275C	C	TT	-/-
rs2254210	VDR G48273714A	A	AG	+/-
rs2238136	VDR C48277713T	T	CC	-/-
rs2853564	VDR G48278487A	G	AG	+/-

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs11168287	VDR G48285414A	G	AG	+/-
rs4328262	VDR C18167A	G	TG	+/-
rs4334089	VDR G48286015A	G	AG	+/-
rs4237855	VDR G48287203A	A	AG	+/-
rs3890733	VDR G14442A	T	CC	-/-
rs10875695	VDR C48293037A	A	AC	+/-
rs11168293	VDR G48293716T	G	GG	+/?
rs7136534	VDR G9189A	G	TC	-/-
rs2070586	DAO G8864A	G	GG	+/?
rs2070587	DAO T887G	G	TT	-/-
rs2111902	DAO T9891G	T	TT	+/?
rs3918347	DAO A24464G	G	AA	-/-
rs17221417	NOD2 13533C>G	G	CC	-/-
rs2066843	NOD2 19150C>T	T	CC	-/-
rs2066844	NOD2 Arg675Trp	T	CC	-/-
rs2066845	NOD2 Gly881Arg	C	GG	-/-
rs5743289	NOD2 30725C>T	T	CC	-/-
rs12150220	NLRP1 7466T>A	T	TT	+/?
rs492602	FUT2 A12190G	G	AA	-/-
rs601338	FUT2 G12447A	A	GG	-/-
rs602662	FUT2 G12758A	A	GG	-/-

Celiac Disease/Gluten Intolerance

6 variants found 2 1 3

Risk Summary: 2 high risk variants, 1 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs231775	CTLA4 Thr17Ala	G	AG	+/-
rs6441961	3p21 near CCR3 1184A>G variant	T	CC	-/-
rs9851967	LPP 220966C>T	T	TT	+/?
rs6822844	4q27 Region 123509421G>T	G	GG	+/?
rs2187668	HLA-DQA1 variant	T	CC	-/-
rs2858331	HLA 4126892A>G	G	AA	-/-

Clotting Factors

15 variants found 3 3 9

Risk Summary: 3 high risk variants, 3 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs6025	F5 Factor V Leiden FVL	T	CC	-/-
rs2227589	SERPINC1 G5301A	T	CC	-/-
rs1523127	NR1I2 C6709A	A	AC	+/-
rs13146272	CYP4V2 Q259K	C	AC	+/-
rs2036914	F11 T10364C	C	TT	-/-
rs2289252	F11 C25264T	C	CC	+/ ⁺
rs1801020	F12 T5046C	A	GG	-/-
rs2731672	KNG I598T GP IIIa HPA-1	T	CC	-/-
rs1799963	F2 (Prothrombin 20210A) variant	A	GG	-/-
rs6046	F7 A353G Arg329Gln	A	AG	+/-
rs3211719	F10 113777509 A5397C	A	AA	+/ ⁺
rs1800775	CETP C4402A	C	CC	+/ ⁺
rs5918	ITGB3 P1A2/T196C	C	TT	-/-
rs1613662	GP6 Pro219Ser	G	AA	-/-
rs6048	F9 G580A A25386G	G	AA	-/-

Eye Health

2 variants found 1 1

Risk Summary: 1 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs4889294	BCMO1 36464T>C	C	TT	-/-
rs7501331	BCMO1 A379V Ala379Val	T	TC	+/-

Glyoxylate Metabolic Process

42 variants found 6 22 14

(See Figure 5)

Risk Summary: 6 high risk variants, 22 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs12021720	DBT G384S	T	CC	-/-
rs7079	AGT 17006C>A	T	GG	-/-
rs2478523	AGT 1382T>C	G	AG	+/-
rs2478545	AGT 11216C>T	A	AG	+/-
rs699	AGT M235T/C4072T	G	AG	+/-
rs2004776	AGT 6635G>A	C	CC	+/*
rs2493134	AGT 5978A>G	C	TC	+/-
rs2148582	AGT 5538T>C	G	AG	+/-
rs5051	AGT 5465G>A	C	TC	+/-
rs11568020	AGT 5319G>A	T	CC	-/-
rs34116584	AGXT P11R	T	TC	+/-
rs4426527	AGXT I340M	A	AG	+/-
rs2259073	LIAS A19410C	C	AC	+/-
rs1377210	AGXT2L1 S127P	G	AG	+/-
rs16899974	AGXT2 V498L	A	CC	-/-
rs7717823	AGXT2 C35000795T	C	TT	-/-
rs344156	AGXT2 A35035579G	A	AG	+/-
rs37369	AGXT2 V140I	T	CC	-/-
rs28305	AGXT2 C35044298G	C	GG	-/-
rs40200	AGXT2 A35045745G	G	GG	+/*
rs6931421	BCKDHB T68795G	G	TG	+/-
rs10455370	BCKDHB C229524T	T	TC	+/-
rs2057149	DDO C110717493T	C	TC	+/-
rs10263341	DLD T19214C	T	TC	+/-
rs1049748	ABP1 P574P	T	TC	+/-
rs7848919	GLDC C118216T	G	AA	-/-
rs11789777	GLDC A55715G	T	TC	+/-
rs3740015	DHTKD1 Y272D	T	TG	+/-
rs2297644	HOGA1 T20638C	C	TT	-/-
rs497582	PDHX V271V	T	CC	-/-
rs2070586	DAO G8864A	G	GG	+/*

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs2070587	DAO T887G	G	TT	-/-
rs2111902	DAO T9891G	T	TT	+/?
rs3918347	DAO A24464G	G	AA	-/-
rs732765	DLST A22136G	G	AA	-/-
rs459894	NDUFAB1 A23601488G	G	AA	-/-
rs730168	LDHD C75150275T	C	CC	+/?
rs3810174	BCKDHA C5472T	C	TC	+/-
rs2423322	HAO1 A7873112G	G	AG	+/-
rs16994134	HAO1 T7894092C	T	TT	+/?
rs6118004	HAO1 C7897049T	C	TC	+/-
rs2423334	HAO1 T7905947C	T	TC	+/-

HLA

57 variants found 7 24 26
(See Figure 6)

Risk Summary: 7 high risk variants, 24 moderate risk variants - Consider discussing with healthcare provider

Quick Navigation: [Overview](#) [Categories](#) [Figures](#) [Disclaimer](#)

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs2844846	HLA-F-AS1, MICE 4945T>A	T	TT	+/-
rs1632933	HLA-G 8178C>T	T	TC	+/-
rs3823339	HLA-A 7727C>G	G	GC	+/-
rs1061235	HLA-A 8057A>T	T	TA	+/-
rs3893538	HLA-W 915T>C	T	TT	+/-
rs2517701	HLA-W 2462A>T	T	AA	-/-
rs2001181	HLA-C 7911A>G	C	TT	-/-
rs1058026	HLA-B 8305T>G	C	AA	-/-
rs3819299	HLA-B His363Pro	G	TT	-/-
rs2523608	HLA-B 7431C>T	A	AG	+/-
rs3094228	HLA-X 441A>G	C	TT	-/-
rs3135394	HLA-DRA 5055G>A	G	AA	-/-
rs9268645	HLA-DRA 5085C>G	G	CC	-/-
rs3129878	HLA-DRA 5293C>A	A	AC	+/-
rs3129881	HLA-DRA 6041T>C	T	TC	+/-
rs3129882	HLA-DRA 6087A>G	G	AG	+/-
rs3129883	HLA-DRA 6694C>T	T	TC	+/-
rs9268658	HLA-DRA 7273G>A	A	GG	-/-
rs3135391	HLA-DRA 7544G>A	G	AG	+/-
rs8084	HLA-DRA 7592A>C	C	AA	-/-
rs2239804	HLA-DRA 8080T>C	C	TT	-/-
rs7192	HLA-DRA Leu242Val	T	TT	+/-
rs3129888	HLA-DRA 8283A>G	G	AG	+/-
rs2239803	HLA-DRA 8390C>T	T	CC	-/-
rs2239802	HLA-DRA 8403G>C	C	CG	+/-
rs3177928	HLA-DRA 8958G>A	A	GG	-/-
rs1041885	HLA-DRA 9332A>T	A	AT	+/-
rs9268831	HLA-DRB9 7239C>T	T	CC	-/-
rs660895	HLA-DRB1 variant	G	AA	-/-
rs9271366	HLA variant	G	AG	+/-
rs2858331	HLA 4126892A>G	G	AA	-/-

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs9276431	HLA-DQA2 4158042T>C	T	TT	+/-
rs2239800	HLA-DQA2 4159063A>G	G	AA	-/-
rs7453920	HLA-DQB2 4175809A>G	G	AA	-/-
rs2051549	HLA-DQB2 4175883G>A	G	GG	+/-
rs1573649	HLA-DQB2 Met1Thr	G	GG	+/-
rs11244	HLA-DOB 9102C>T	A	GG	-/-
rs2856997	HLA-DOB 8050G>T	C	AC	+/-
rs2071473	HLA-DOB 7221G>A	C	TC	+/-
rs7383287	HLA-DOB 6740T>C	G	AA	-/-
rs2621326	HLA-DOB 5930C>T	G	AG	+/-
rs2071554	HLA-DOB Arg18Gln	T	CC	-/-
rs2071469	HLA-DOB 5043G>A	C	TC	+/-
rs23544	HLA-DMB 4348055C>T	T	CC	-/-
rs151719	HLA-DMB 4348318T>C	C	TC	+/-
rs3128935	HLA-DOA 9986A>G	T	TT	+/-
rs1044429	HLA-DOA 9748G>A	T	CC	-/-
rs376892	HLA-DOA 9503C>T	G	AA	-/-
rs416622	HLA-DOA 9109A>G	C	TT	-/-
rs9276977	HLA-DOA 8549C>T	A	AG	+/-
rs2581	HLA-DOA 7989C>A	T	TG	+/-
rs399604	HLA-DOA 7376A>G	C	TC	+/-
rs2284191	HLA-DOA 5736C>T	A	AG	+/-
rs86567	HLA-DOA 5631C>A	G	TT	-/-
rs3077	HLA-DPA1 20534T>C	A	AG	+/-
rs2301226	HLA-DPA1 18960C>T	A	GG	-/-
rs9277535	HLA-DPB1 16159A>G	G	AG	+/-

IgA

22 variants found 3 5 14

Risk Summary: 3 high risk variants, 5 moderate risk variants - Consider discussing with healthcare provider

Quick Navigation: [Overview](#) [Categories](#) [Figures](#) [Disclaimer](#)

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs6677604	CFH variant	A	AG	+/-
rs4353135	NLRP3 247617036G>T	T	TG	+/-
rs1990760	IFIH1 (HLA) variant	T	TC	+/-
rs9271366	HLA variant	G	AG	+/-
rs9357155	PSMB8 / TAP1 / TAP2 variant	A	AG	+/-
rs4728142	IRF5 variant	A	GG	-/-
rs3761847	TRAF1 variant	G	AA	-/-
rs2229765	IGF1R variant	G	AA	-/-
rs17221417	NOD2 13533C>G	G	CC	-/-
rs2066843	NOD2 19150C>T	T	CC	-/-
rs2066844	NOD2 Arg675Trp	T	CC	-/-
rs2066845	NOD2 Gly881Arg	C	GG	-/-
rs5743289	NOD2 30725C>T	T	CC	-/-
rs12150220	NLRP1 7466T>A	T	TT	+/+
rs516246	FUT2 11945C>T	T	CC	-/-
rs492602	FUT2 A12190G	G	AA	-/-
rs281377	FUT2 C12376T	T	TT	+/+
rs1047781	FUT2 A12404T	T	AA	-/-
rs601338	FUT2 G12447A	A	GG	-/-
rs602662	FUT2 G12758A	A	GG	-/-
rs485186	FUT2 12979A>G	A	AA	+/+
rs504963	FUT2 14638G>A	A	GG	-/-

IgE

5 variants found 4 1

Risk Summary: 4 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs2814778	DARC 5174T>C	C	TT	-/-
rs2494262	FCER1A / OR10J2P variant	A	AC	+/-
rs2427837	FCER1A variant	A	AG	+/-
rs2251746	FCER1A 15927206T>C	C	TC	+/-
rs2040704	RAD50 85562A>G	A	AG	+/-

IgG

3 variants found 1 2

Risk Summary: 1 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs7483	GSTM3 V224I	T	TC	+/-
rs1801274	FCGR2A variant	A	GG	-/-
rs4792800	TNFRSF13B variant	G	AA	-/-

Iron Uptake & Transport

36 variants found 5 8 23

Risk Summary: 5 high risk variants, 8 moderate risk variants - Consider discussing with healthcare provider

Quick Navigation: [Overview](#) [Categories](#) [Figures](#) [Disclaimer](#)

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs2266917	ATP6V1B1 11708C>T	T	TT	+/+
rs2239484	ATP6V1B1 15411A>G	A	AA	+/+
rs838102	STEAP3 8350G>A	A	AA	+/+
rs960748	CYBRD1 171523426G>A	A	GG	-/-
rs17554	CYBRD1 171546859G>A	A	AG	+/-
rs10455	CYBRD1 Ser208Asn	G	AG	+/-
rs4667287	SLC40A1 190431875C>A	C	AA	-/-
rs1123109	SLC40A1 190444392T>C	C	TC	+/-
rs4428180	TF 6398A>G	G	AA	-/-
rs12493168	TF 6612A>G	G	AA	-/-
rs8177190	TF 7720C>T	T	CC	-/-
rs1799899	TF Gly277Ser	A	GG	-/-
rs3811647	TF 24053G>A	A	GG	-/-
rs1358024	TF 24212C>T	T	CC	-/-
rs1049296	TF Pro589Ser	T	CC	-/-
rs13072552	CP 148913126G>T	T	GG	-/-
rs406271	TFRC 195776976T>C	T	CC	-/-
rs3817672	TFRC Gly142Ser	T	CC	-/-
rs2231164	ABCG2 89015857C>T	T	TC	+/-
rs1481012	ABCG2 89039082A>G	A	AA	+/+
rs2231142	ABCG2 Gln141Lys	T	GG	-/-
rs72552713	ABCG2 Gln126Ter	A	GG	-/-
rs4148155	ABCG2 89060909T>C	C	AA	-/-
rs4148155	ABCG2 89054667A>G	G	AA	-/-
rs2622604	ABCG2 89078924T>C	T	CC	-/-
rs1799945	HFE H63D	G	CC	-/-
rs1800562	HFE C282Y	A	GG	-/-
rs2071594	ATP6V1G2-DDX39B,ATP6V1G2 3093G>C	C	GG	-/-
rs149411	SLC11A2 51380232A>G	G	AG	+/-
rs235756	BMP2 C282Y	G	AG	+/-
rs2071748	HMOX1 5559G>A	A	AG	+/-

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs2071749	HMOX1 11354A>G	A	AG	+/-
rs5755720	HMOX1 14814A>G	A	AA	+/+
rs1028348	HEPH 6731C>T	T	CC	-/-
rs17216603	HEPH Ala598Thr	A	GG	-/-
rs1264216	HEPH 57825T>G	G	TT	-/-

Liver Detox - Phase I

80 variants found 9 13 58

(See Figure 1)

Risk Summary: 9 high risk variants, 13 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs9341266	CYP1B1 C1871T	A	GG	-/-
rs1800440	CYP1B1 N453S	T	TC	+/-
rs1056836	CYP1B1 L432V	C	CG	+/-
rs9282671	CYP1B1 T241A	A	AA	+/*
rs72549389	CYP1B1 T5795C	G	AA	-/-
rs2855262	SOD3 489 C>T	C	CC	+/*
rs1800730	HFE 193A>T	T	AA	-/-
rs662	PON1 Q192R	T	TT	+/*
rs10264272	CYP3A5*6 G624A	T	CC	-/-
rs776746	CYP3A5*3 G237A	A	CC	-/-
rs4646440	CYP3A4 C608T	A	GG	-/-
rs2242480	CYP3A4*_20239G>A G12A	T	CC	-/-
rs4646437	CYP3A4 C202T	A	GG	-/-
rs2246709	CYP3A4 T258C	G	GG	+/*
rs55785340	CYP3A4*2 S222P	G	AA	-/-
rs55901263	CYP3A4*5 P218R	C	GG	-/-
rs12721627	CYP3A4*16 T185S	G	GG	+/*
rs35599367	CYP3A4 C191T	A	GG	-/-
rs55951658	CYP3A4*4 I118V	C	TT	-/-
rs3091339	CYP3A4*_11460A>G(K96E) K96E	C	TT	-/-
rs56324128	CYP3A4*7 G56D	T	CC	-/-
rs2740574	CYP3A4*1B A392G	C	TT	-/-
rs12248560	CYP2C19*17 C806T	T	CC	-/-
rs4986894	CYP2C19 T98C	T	TT	+/*
rs28399504	CYP2C19*4 A5001G	G	AA	-/-
rs17878459	CYP2C19*2B G276A	C	GG	-/-
rs41291556	CYP2C19*8 T358C	C	TT	-/-
rs72552267	CYP2C19*6 G395A	A	GG	-/-
rs4986893	CYP2C19*3 G636A	A	GG	-/-
rs4244285	CYP2C19*2 G681A	A	GG	-/-
rs72558186	CYP2C19*7 T24294A	A	TT	-/-

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs12767583	CYP2C19 C5709T	T	CC	-/-
rs4917623	CYP2C19 T106C	C	CC	+/?
rs56337013	CYP2C19*5 C1297T	T	CC	-/-
rs4918758	CYP2C9 T1188C	C	TC	+/-
rs72558187	CYP2C9*13 269T>C	C	TT	-/-
rs1799853	CYP2C9*2 430C>T	T	TC	+/-
rs4086116	CYP2C9 C334T	T	TC	+/-
rs2256871	CYP2C9*9 752A>G	G	AA	-/-
rs4917639	CYP2C9 A6326C	C	AC	+/-
rs10509680	CYP2C9 G2337T	T	GG	-/-
rs28371685	CYP2C9*11 1003C>T	T	CC	-/-
rs1057910	CYP2C9*3 1075A>C	C	AA	-/-
rs1934967	CYP2C9 T2674C	T	CC	-/-
rs1057911	CYP2C9 50298A>T	T	AA	-/-
rs9332239	CYP2C9*12 1465C>T	T	CC	-/-
rs3813867	CYP2E1_-1295G>C G1295C	C	GG	-/-
rs2031920	CYP2E1_-1055C>T G1055T	T	CC	-/-
rs2070672	CYP2E1*7_-352A>G A352G	G	AA	-/-
rs6413420	CYP2E1*7_-71G>T G71T	T	TG	+/-
rs72559710	CYP2E1*2 R76H	C	GG	-/-
rs8192772	CYP2E1 T8845C	C	TT	-/-
rs6413419	CYP2E1*4 A4768G	A	AG	+/-
rs1048943	CYP1A1*2C A4889G	T	TT	+/?
rs1799814	CYP1A1*4 C2453A	T	GG	-/-
rs2069526	CYP1A2*1K -739T>G	G	TT	-/-
rs762551	CYP1A2*1F C164A	C	AC	+/-
rs56276455	CYP1A2*3 D348N	A	GG	-/-
rs2470890	CYP1A2 1545T>C	C	TC	+/-
rs1801272	CYP2A6*2 A1799T	T	AA	-/-
rs8192709	CYP2B6 R22C	T	CC	-/-
rs35303484	CYP2B6 A136G	G	AA	-/-
rs12721655	CYP2B6 K139E	G	AA	-/-
rs3745274	CYP2B6 Q172H	T	GG	-/-
rs36079186	CYP2B6 T20715C	C	TT	-/-
rs2279345	CYP2B6 T23499C	T	TC	+/-
rs28399499	CYP2B6 I328T	C	TT	-/-
rs34097093	CYP2B6 C1132T	T	CC	-/-
rs8192719	CYP2B6 C26570T	T	CC	-/-
rs7260329	CYP2B6 G29435A	G	AG	+/-
rs1042389	CYP2B6 T1421C	C	TT	-/-
rs1135840	CYP2D6*2 S486T	C	GC	+/-
rs59421388	CYP2D6 V287M	T	CC	-/-
rs28371725	CYP2D6*41 2988G>A	T	CC	-/-
rs5030867	CYP2D6*7 2935A>C	G	TT	-/-
rs5030865	CYP2D6*14 1758G>A	A	CC	-/-

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs61736512	CYP2D6 G1659A	T	CC	-/-
rs28371706	CYP2D6*17 T107I	A	GG	-/-
rs5030862	CYP2D6*12 124G>A	T	CC	-/-
rs1080985	CYP2D6 G3502C	G	GG	+/+

Liver Detox - Phase II

165 variants found 37 46 82

(See Figure 1)

Risk Summary: 37 high risk variants, 46 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs4846048	MTHFR C24909T	G	AA	-/-
rs2274976	MTHFR G1793A (R594Q)	T	CC	-/-
rs1476413	MTHFR G18861A	T	CC	-/-
rs1801131	MTHFR A1298C	G	TT	-/-
rs1801133	MTHFR C677T	A	AA	+/+
rs17037390	MTHFR C10318T	G	GG	+/+
rs17037396	MTHFR C841T	T	CC	-/-
rs17367504	MTHFR A1572G	G	AA	-/-
rs2066470	MTHFR 03 P39P	A	GG	-/-
rs13306561	MTHFR A4598G	A	AA	+/+
rs13306560	MTHFR C-137T	T	CC	-/-
rs3737964	MTHFR A4117C	T	CC	-/-
rs2239892	GSTM1 8869A>G	G	AG	+/-
rs7483	GSTM3 V224I	T	TC	+/-
rs699	AGT M235T/C4072T	A	AG	+/-
rs823162	DISC1 C14853T	C	TT	-/-
rs4353135	NLRP3 247617036G>T	T	TG	+/-
rs2028900	MAT2A C6635T	C	TC	+/-
rs6430764	HNMT C3616T	T	TT	+/+
rs17583889	HNMT C29232A	A	CC	-/-
rs3749034	GAD1 (GAD) G5276A	A	AG	+/-
rs2241165	GAD1 (GAD) C10180T	T	TC	+/-
rs3828275	GAD1 (GAD) C14541T	T	CC	-/-
rs2241164	GAD1 (GAD) C18360T	C	TC	+/-
rs701492	GAD1 (GAD) C34281T	C	TC	+/-
rs3791850	GAD1 (GAD) G39901A	G	AG	+/-
rs769395	GAD1 (GAD) A48604A	A	AG	+/-
rs887829	UGT1A1 C175181T	T	TC	+/-
rs4148323	UGT1A1 G211A	A	GG	-/-
rs72551341	UGT1A1 L175G	A	TT	-/-
rs6742078	UGT1A1 G179250T	T	TG	+/-

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs4148325	UGT1A1 C179920T	T	TC	+/-
rs62625011	UGT1A1 G182349A	A	GG	-/-
rs72551348	UGT1A1 G328A	G	AA	-/-
rs72551351	UGT1A1 G354A	G	AA	-/-
rs6717546	UGT1A1 A188730G	G	AG	+/-
rs901865	HRH1 T-17C	T	TT	+/+
rs346070	HRH1 T*1687C	T	TT	+/+
rs4961	ADD1 G460W	T	GG	-/-
rs27072	SLC6A3 G56022A	T	CC	-/-
rs40184	SLC6A3 G55467A	C	TC	+/-
rs6347	SLC6A3 A39132G	T	TC	+/-
rs27048	SLC6A3 G37899A	T	TC	+/-
rs464049	SLC6A3 T26639C	A	AA	+/+
rs460000	SLC6A3 C17719T	T	GG	-/-
rs403636	SLC6A3 T12190G	A	AC	+/-
rs2617605	SLC6A3 A8023G	C	TT	-/-
rs6350	SLC6A3 C7345T	A	GG	-/-
rs479405	DMGDH G67591T	C	AA	-/-
rs2253262	DMGDH T372G	A	CC	-/-
rs16876512	BHMT C-448T	T	CC	-/-
rs6875201	BHMT A7961G	G	AA	-/-
rs567754	BHMT-02 C13813T	T	TT	+/+
rs3733890	BHMT R239Q	A	GG	-/-
rs617219	BHMT-04 A26991C	C	CC	+/+
rs1650697	DHFR/MSH T-473A	A	GG	-/-
rs8177412	GPX3 129T>C	T	TC	+/-
rs4869089	MAT2B A7755681G	G	AG	+/-
rs2619522	DTNBP1 T14623G	A	AC	+/-
rs2794719	HFE 6382T>G	T	GG	-/-
rs9366637	HFE 6590C>T	T	CC	-/-
rs1799945	HFE H63D	G	CC	-/-
rs2071303	HFE 8828T>C	C	TT	-/-
rs1800562	HFE C282Y	A	GG	-/-
rs11754661	MTHFD1L G25264A	G	GG	+/+
rs17349743	MTHFD1L T31397C	C	TC	+/-
rs803422	MTHFD1L A33780G	A	AA	+/+
rs4986782	NAT1 R187Q	A	GG	-/-
rs1805158	NAT2 R64W	T	CC	-/-
rs1801279	NAT2 G191A	A	GG	-/-
rs1041983	NAT2 C282T	T	TT	+/+
rs1801280	NAT2 I114T	C	TT	-/-
rs1799929	NAT2 C481T	T	CC	-/-
rs1799930	NAT2 R197Q	A	AA	+/+
rs1208	NAT2 K268R	G	AA	-/-
rs1799931	NAT2 G286E	A	GG	-/-

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs2551715	GSR A43851G	C	CC	+/-
rs6994992	NRG1 C3314T	T	TC	+/-
rs7820268	IDO1 C6202T	T	TC	+/-
rs11545078	GGH C17847T	A	AG	+/-
rs3780127	GGH C15472T	A	AG	+/-
rs4617146	GGH G13894A	T	CC	-/-
rs3780126	GGH C6699T	A	GG	-/-
rs1805398	GAD2 (GAD) G26474809T	G	GG	+/-
rs1538311	ADK G509567T	T	TT	+/-
rs1985908	MAT1A T*1297C	G	AA	-/-
rs2993763	MAT1A C1131T	A	GG	-/-
rs72558181	MAT1A G19502A	T	CC	-/-
rs4934028	MAT1A C15656T	A	GG	-/-
rs480575	CAT A12175G	G	AG	+/-
rs2300181	CAT C21068T	T	CC	-/-
rs1695	GSTP1 I105V	A	AA	+/-
rs1138272	GSTP1 A114V	T	CC	-/-
rs7925545	FOLR3 A3771G	G	AA	-/-
rs7926875	FOLR3 C7672A	C	CC	+/-
rs2071010	FOLR1 G-20A	A	GG	-/-
rs651933	FOLR2 G-1316A	G	GG	+/-
rs3741049	ACAT1 G22670A	A	AG	+/-
rs1544410	VDR VDR:Bsml	T	TC	+/-
rs2070586	DAO G8864A	G	GG	+/-
rs2070587	DAO T887G	G	TT	-/-
rs2111902	DAO T9891G	T	TT	+/-
rs3918347	DAO A24464G	G	AA	-/-
rs7134594	MMAB G16110A	C	TC	+/-
rs7997012	HTR2A T64185C	A	GG	-/-
rs2733103	MTHFS - ST20 MTHFS G56057A	T	CC	-/-
rs6495446	MTHFS - ST20 MTHFS G39646A	C	TC	+/-
rs17221417	NOD2 13533C>G	G	CC	-/-
rs2066843	NOD2 19150C>T	T	CC	-/-
rs2066844	NOD2 Arg675Trp	T	CC	-/-
rs2066845	NOD2 Gly881Arg	C	GG	-/-
rs5743289	NOD2 30725C>T	T	CC	-/-
rs168924	SLC6A2 A5003G	G	AG	+/-
rs2242446	SLC6A2 C5884T	T	TT	+/-
rs36020	SLC6A2 C28547T	T	TC	+/-
rs3785152	SLC6A2 T32009C	T	CC	-/-
rs40147	SLC6A2 G32299A	G	GG	+/-
rs3785157	SLC6A2 C45295T	T	TT	+/-
rs5568	SLC6A2 A45583C	C	AA	-/-
rs36009	SLC6A2 C48079T	T	CC	-/-
rs1800887	SLC6A2 T49048C	T	TT	+/-

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs2242447	SLC6A2 C51371T	T	TT	+/+
rs10517	NQO1 C494+	A	AG	+/-
rs1800566	NQO1 C609T	A	GG	-/-
rs689453	NQO1 G13161A	T	CC	-/-
rs689452	NQO1 G13070C	C	CG	+/-
rs1437135	NQO1 T7706C	G	AA	-/-
rs12150220	NLRP1 7466T>A	T	TT	+/+
rs2759	MPO A15191G	C	TT	-/-
rs2071409	MPO A15067C	T	TT	+/+
rs28730837	MPO C7900T	A	AG	+/-
rs4343	ACE G2328A	G	AG	+/-
rs16940765	HRH4 T3537649C	C	TC	+/-
rs11662595	HRH4 A617G	G	AA	-/-
rs1421125	HRH4 G*385T	T	TG	+/-
rs4800573	HRH4 G*2144A	A	GG	-/-
rs17851582	GAMT C9110T	G	GG	+/+
rs4149452	SULT2A1 G17136A	T	CC	-/-
rs2910393	SULT2A1 A13527G	T	TT	+/+
rs4149449	SULT2A1 G9696A	T	TC	+/-
rs2547231	SULT2A1 G9598T	A	AC	+/-
rs492602	FUT2 A12190G	G	AA	-/-
rs281377	FUT2 C12376T	T	TT	+/+
rs1047781	FUT2 A12404T	T	AA	-/-
rs601338	FUT2 G12447A	A	GG	-/-
rs602662	FUT2 G12758A	A	GG	-/-
rs235756	BMP2 C282Y	G	AG	+/-
rs2273684	GSS A18836C	T	TG	+/-
rs28936396	GSS C373T	A	GG	-/-
rs6060124	GSS G11705T	C	CC	+/+

Liver Detox - Phase II (continued)

(See Figure 1)

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs6088659	GSS A5997G	T	CC	-/-
rs11555566	ADA A239G	C	TT	-/-
rs447833	ADA G22021A	T	TC	+/-
rs452159	ADA C14275A	T	TG	+/-
rs737866	COMT/TXNRD2 A4251G	C	CC	+//+
rs737865	COMT/TXNRD2 T4239C	G	GG	+//+
rs5760485	GGT1 T11756C	T	CC	-/-
rs4820599	GGT1/FAM211B A15496G	G	GG	+//+
rs6519519	GGT1 C17146T	T	TT	+//+
rs5751901	GGT1 T17549C	T	CC	-/-
rs72554664	G6PD R493H	T	CC	-/-
rs2230037	G6PD T438T	G	GG	+//+
rs5030868	G6PD S219F	A	GG	-/-
rs1050829	G6PD N156D	C	TT	-/-
rs1050828	G6PD V98M	T	CC	-/-

Methylation & Methionine/Homocysteine Pathways

96 variants found 22 24 50

(See Figure 2)

Risk Summary: 22 high risk variants, 24 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs4846048	MTHFR C24909T	G	AA	-/-
rs2274976	MTHFR G1793A (R594Q)	T	CC	-/-
rs1476413	MTHFR G18861A	T	CC	-/-
rs1801131	MTHFR A1298C	G	TT	-/-
rs1801133	MTHFR C677T	A	AA	+/ ⁺
rs17037390	MTHFR C10318T	G	GG	+/ ⁺
rs17037396	MTHFR C841T	T	CC	-/-
rs17367504	MTHFR A1572G	G	AA	-/-
rs2066470	MTHFR 03 P39P	A	GG	-/-
rs13306561	MTHFR A4598G	A	AA	+/ ⁺
rs13306560	MTHFR C-137T	T	CC	-/-
rs3737964	MTHFR A4117C	T	CC	-/-
rs10889869	CTH G6010A	A	GG	-/-
rs681475	CTH T8763C	C	TC	+/-
rs1145920	CTH A11886G	A	AG	+/-
rs663649	CTH G25229T	T	TG	+/-
rs1021737	CTH S4031I	T	GG	-/-
rs7526063	MTR C18418T	T	CC	-/-
rs2789352	MTR A50417C	A	CC	-/-
rs2275568	MTR C62048T	T	TC	+/-
rs1770449	MTR T84581C	C	TT	-/-
rs10925257	MTR A92580G	G	AG	+/-
rs1805087	MTR A2756G	G	AG	+/-
rs2275565	MTR G95096T	T	TG	+/-
rs3820571	MTR G106853T	G	TT	-/-
rs2853522	MTR A*112C	A	CC	-/-
rs11799670	MTR A*153G	G	AA	-/-
rs2853523	MTR A*1254C	A	CC	-/-
rs1050993	MTR A*1361G	A	GG	-/-
rs2028900	MAT2A C6635T	C	TC	+/-
rs1801394	MTRR A66G	G	AG	+/-

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs3776467	MTRR G12099A	G	AG	+/-
rs1532268	MTRR C524T	T	CC	-/-
rs7703033	MTRR G15734A	A	GG	-/-
rs162031	MTRR T16071C	T	TT	+/*
rs162036	MTRR K350A	G	AA	-/-
rs2287779	MTRR G1155A	A	AG	+/-
rs2287780	MTRR R415T	T	TC	+/-
rs162049	MTRR G28905A	G	GG	+/*
rs3776455	MTRR C32295T	T	CC	-/-
rs10380	MTRR H595Y	T	CC	-/-
rs1802059	MTRR -11 A664A	A	GG	-/-
rs9332	MTRR G*541A	A	GG	-/-
rs479405	DMGDH G67591T	C	AA	-/-
rs2253262	DMGDH T372G	A	CC	-/-
rs16876512	BHMT C-448T	T	CC	-/-
rs6875201	BHMT A7961G	G	AA	-/-
rs567754	BHMT-02 C13813T	T	TT	+/*
rs3733890	BHMT R239Q	A	GG	-/-
rs617219	BHMT-04 A26991C	C	CC	+/*
rs1650697	DHFR/MSH T-473A	A	GG	-/-
rs4869089	MAT2B A7755681G	G	AG	+/-
rs11754661	MTHFD1L G25264A	G	GG	+/*
rs17349743	MTHFD1L T31397C	C	TC	+/-
rs803422	MTHFD1L A33780G	A	AA	+/*
rs1800779	NOS3 G6797A	A	AA	+/*
rs2070744	NOS3 T786C	T	TT	+/*
rs7830	NOS3 G10T	T	TT	+/*
rs1985908	MAT1A T*1297C	G	AA	-/-
rs2993763	MAT1A C1131T	A	GG	-/-
rs72558181	MAT1A G19502A	T	CC	-/-
rs4934028	MAT1A C15656T	A	GG	-/-
rs526934	TCN1 G4939288A	A	AA	+/*
rs7925545	FOLR3 A3771G	G	AA	-/-
rs7926875	FOLR3 C7672A	C	CC	+/*
rs2071010	FOLR1 G-20A	A	GG	-/-
rs651933	FOLR2 G-1316A	G	GG	+/*
rs2272306	CSAD C25411T	A	GG	-/-
rs2293054	NOS1 T2202C	A	GG	-/-
rs2733103	MTHFS - ST20 MTHFS G56057A	T	CC	-/-
rs6495446	MTHFS - ST20 MTHFS G39646A	C	TC	+/-
rs7946	PEMT G634A	T	TT	+/*
rs4244593	PEMT T17023592G	T	TG	+/-
rs9909104	SHMT1 A23836G	T	TC	+/-
rs72547564	ALDH3A2 G641A	A	GG	-/-
rs72547575	ALDH3A2 A1157G	G	AA	-/-

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs2297518	NOS2 C1823T	A	AG	+/-
rs502396	TYMS C6633T	C	CC	+/?
rs17851582	GAMT C9110T	G	GG	+/?
rs4149452	SULT2A1 G17136A	T	CC	-/-
rs2910393	SULT2A1 A13527G	T	TT	+/?
rs4149449	SULT2A1 G9696A	T	TC	+/-
rs2547231	SULT2A1 G9598T	A	AC	+/-
rs2273684	GSS A18836C	T	TG	+/-
rs28936396	GSS C373T	A	GG	-/-
rs6060124	GSS G11705T	C	CC	+/?
rs6088659	GSS A5997G	T	CC	-/-
rs706209	CBS C*351T	A	GG	-/-
rs706208	CBS T*330C	A	AA	+/?
rs12613	CBS G*299A	T	CC	-/-
rs1801181	CBS A360A	A	GG	-/-
rs4920037	CBS C19150T	A	AG	+/-
rs234706	CBS C699T	A	AG	+/-
rs2851391	CBS A13637G	T	TT	+/?
rs9606756	TCN2 A8700G	G	AA	-/-
rs1801198	TCN2 C766G	G	GC	+/-

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Mitochondrial Function

60 variants found 16 19 25

(See Figure 12)

Risk Summary: 16 high risk variants, 19 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs2028900	MAT2A C6635T	C	TC	+/-
rs1801394	MTRR A66G	G	AG	+/-
rs3776467	MTRR G12099A	G	AG	+/-
rs1532268	MTRR C524T	T	CC	-/-
rs7703033	MTRR G15734A	A	GG	-/-
rs162031	MTRR T16071C	T	TT	+/?
rs162036	MTRR K350A	G	AA	-/-
rs2287779	MTRR G1155A	A	AG	+/-
rs2287780	MTRR R415T	T	TC	+/-
rs162049	MTRR G28905A	G	GG	+/?
rs3776455	MTRR C32295T	T	CC	-/-
rs10380	MTRR H595Y	T	CC	-/-
rs1802059	MTRR -11 A664A	A	GG	-/-
rs9332	MTRR G*541A	A	GG	-/-
rs479405	DMGDH G67591T	C	AA	-/-
rs2253262	DMGDH T372G	A	CC	-/-
rs4869089	MAT2B A7755681G	G	AG	+/-
rs11754661	MTHFD1L G25264A	G	GG	+/?
rs17349743	MTHFD1L T31397C	C	TC	+/-
rs803422	MTHFD1L A33780G	A	AA	+/?
rs2758331	SOD2 406+816G>T	A	AA	+/?
rs4880	SOD2 V16A	A	GG	-/-
rs1800779	NOS3 G6797A	A	AA	+/?
rs2070744	NOS3 T786C	T	TT	+/?
rs7830	NOS3 G10T	T	TT	+/?
rs1244422	ATP5c1 variant	C	TC	+/-
rs1985908	MAT1A T*1297C	G	AA	-/-
rs2993763	MAT1A C1131T	A	GG	-/-
rs72558181	MAT1A G19502A	T	CC	-/-
rs4934028	MAT1A C15656T	A	GG	-/-
rs4147776	NDUFS8 variant	C	AA	-/-

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs2075626	NDUFS8 variant	T	TC	+/-
rs4767939	ALDH2 A7550G	A	AA	+/*
rs2238151	ALDH2 T12488C	T	TT	+/*
rs4648328	ALDH2 C23443T	T	CC	-/-
rs968529	ALDH2 T35023C	C	CC	+/*
rs4646778	ALDH2 C36438A	A	CC	-/-
rs671	ALDH2 G1369A	A	GG	-/-
rs16941667	ALDH2 C45068T	T	CC	-/-
rs2293054	NOS1 T2202C	A	GG	-/-
rs10483639	GCH1 G55306457C	C	CG	+/-
rs2878168	GCH1 C53758T	A	AG	+/-
rs3783637	GCH1 G26425A	C	CC	+/*
rs8004018	GCH1 T23847C	G	AA	-/-
rs3783641	GCH1 A14404T	A	AT	+/-
rs3783642	GCH1 A14340G	T	TC	+/-
rs8007267	GCH1 C36378991T	C	TC	+/-
rs6497563	UQCRC2 variant	T	TT	+/*
rs7946	PEMT G634A	T	TT	+/*
rs4244593	PEMT T17023592G	T	TG	+/-
rs72547564	ALDH3A2 G641A	A	GG	-/-
rs72547575	ALDH3A2 A1157G	G	AA	-/-
rs2297518	NOS2 C1823T	A	AG	+/-
rs1142530	NDUFS7 variant	T	TC	+/-
rs11666067	NDUFS7 variant	A	AC	+/-
rs17851582	GAMT C9110T	G	GG	+/*
rs2273684	GSS A18836C	T	TG	+/-
rs28936396	GSS C373T	A	GG	-/-
rs6060124	GSS G11705T	C	CC	+/*
rs6088659	GSS A5997G	T	CC	-/-

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Molybdenum

37 variants found 4 8 25

Risk Summary: 4 high risk variants, 8 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs291593	DYPD 97543752G>A	A	AG	+/-
rs291592	DYPD 97543764C>T	T	TC	+/-
rs1801268	DYPD Val995Phe	A	CC	-/-
rs67376798	DYPD Asp949Val	A	TT	-/-
rs1399291	DYPD 97576922C>T	T	TC	+/-
rs11587873	DYPD 97653070C>T	T	CC	-/-
rs12137711	DYPD 97700589C>T	T	CC	-/-
rs1801160	DYPD Val732Ile	T	CC	-/-
rs7548189	DYPD 97867713C>A	C	AC	+/-
rs3918290	DYPD 97915614C>T	T	CC	-/-
rs17376848	DYPD 97915624A>G	G	AA	-/-
rs55886062	DYPD Ile560Asn	C	AA	-/-
rs1801159	DYPD Ile543Val	C	TT	-/-
rs1801158	DYPD Ser534Asn	T	CC	-/-
rs1801266	DYPD Arg235Trp	A	GG	-/-
rs1801265	DYPD Cys29Arg	A	AG	+/-
rs207444	XDH 31563797A>G	A	GG	-/-
rs1884725	XDH 31571786A>G	A	AG	+/-
rs1429376	XDH 31588561A>C	A	AC	+/-
rs17011368	XDH Ile703Val	C	TT	-/-
rs17323225	XDH Ile646Val	C	TT	-/-
rs185925	XDH 31609993G>A	G	AA	-/-
rs2073316	XDH 31611029G>A	A	AA	+/*
rs206811	XDH 31636915A>G	A	GG	-/-
rs4717865	ELN 16773G>A	A	AA	+/*
rs2071307	ELN Gly422Ser	G	GG	+/*
rs2856728	ELN 33356C>T	T	TT	+/*
rs2528795	ELN 36068T>C	C	TT	-/-
rs41511151	ELN Gly711Asp	A	GG	-/-
rs1049564	PNP Gly51Ser	G	AA	-/-
rs8020095	GPHN 484734G>A	A	GG	-/-
rs723744	TTR 5747G>T	T	GG	-/-

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs1800458	TTR Gly26Ser	A	GG	-/-
rs76992529	TTR Val142Ile	A	GG	-/-
rs7269297	MOCS3 Ser429Ala	G	TT	-/-
rs1801475	KCNQ2 Asn752Thr	T	TG	+/-
rs2297385	KCNQ2 62070966G>A	A	GG	-/-

Neurotransmitter Pathway: Glutamate & GABA

8 variants found 1 6 1

(See Figure 9)

Risk Summary: 1 high risk variants, 6 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs3749034	GAD1 (GAD) G5276A	A	AG	+/-
rs2241165	GAD1 (GAD) C10180T	T	TC	+/-
rs3828275	GAD1 (GAD) C14541T	T	CC	-/-
rs2241164	GAD1 (GAD) C18360T	C	TC	+/-
rs701492	GAD1 (GAD) C34281T	C	TC	+/-
rs3791850	GAD1 (GAD) G39901A	G	AG	+/-
rs769395	GAD1 (GAD) A48604A	A	AG	+/-
rs1805398	GAD2 (GAD) G26474809T	G	GG	++

Neurotransmitter Pathway: Serotonin & Dopamine

155 variants found 32 50 73

(See Figure 3)

Risk Summary: 32 high risk variants, 50 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs9828046	DRD3 C44637T	A	GG	-/-
rs9288993	DRD3 T43727C	G	AA	-/-
rs963468	DRD3 C40013T	A	AG	+/-
rs3773678	DRD3 T32822C	G	GG	+/*
rs167771	DRD3 C26625T	A	AA	+/*
rs324029	DRD3 T21277C	A	GG	-/-
rs1486009	DRD3 T14368C	A	AA	+/*
rs6280	DRD3 G25A	T	TT	+/*
rs9825563	DRD3 T2680C	A	AG	+/-
rs1394016	DRD3 G20405035A	G	AG	+/-
rs27072	SLC6A3 G56022A	T	CC	-/-
rs40184	SLC6A3 G55467A	C	TC	+/-
rs6347	SLC6A3 A39132G	T	TC	+/-
rs27048	SLC6A3 `	T	TC	+/-
rs464049	SLC6A3 T26639C	A	AA	+/*
rs460000	SLC6A3 C17719T	T	GG	-/-
rs403636	SLC6A3 T12190G	A	AC	+/-
rs2617605	SLC6A3 A8023G	C	TT	-/-
rs6350	SLC6A3 C7345T	A	GG	-/-
rs1650697	DHFR/MSH T-473A	A	GG	-/-
rs251937	DRD1 A9244G	C	TT	-/-
rs686	DRD1 C7464T	A	AG	+/-
rs4532	DRD1 G6014A	C	TC	+/-
rs5326	DRD1 G5968A	T	CC	-/-
rs265981	DRD1 T5262C	A	AG	+/-
rs2167364	DDC T155196C	T	TT	+/*
rs1451375	DDC G15443T	A	AC	+/-
rs1800779	NOS3 G6797A	A	AA	+/*
rs2070744	NOS3 T786C	T	TT	+/*
rs7830	NOS3 G10T	T	TT	+/*
rs1611114	DBH C3719T	T	TT	+/*

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs1611115	DBH variant	T	CC	-/-
rs3025382	DBH G5837A	A	GG	-/-
rs2007153	DBH T7335C	T	CC	-/-
rs1108580	DBH A486G	A	AG	+/-
rs1108581	DBH A8757G	G	AA	-/-
rs2873804	DBH T9160C	T	TT	+/*
rs5320	DBH G631A	A	GG	-/-
rs1611123	DBH C12599T	T	CC	-/-
rs4531	DBH G952T	T	GG	-/-
rs1541332	DBH G15032A	A	AA	+/*
rs2519154	DBH T15791C	C	TC	+/-
rs2283123	DBH C18813T	T	CC	-/-
rs77905	DBH A1410G	A	AG	+/-
rs2097628	DBH T2145C	A	AG	+/-
rs129882	DBH C27185T	T	TC	+/-
rs11599164	ANK3 C666301A	T	GG	-/-
rs9804190	ANK3 G658454A	C	TC	+/-
rs10761482	ANK3 T62085337C	C	TC	+/-
rs10994336	ANK3 G318473A	T	CC	-/-
rs10994397	ANK3 G219161A	T	CC	-/-
rs3758653	DRD4 T4095C	C	TT	-/-
rs752306	DRD4 C5318T	T	CC	-/-
rs11246226	DRD4 C8887A	A	AA	+/*
rs2070762	TH T1090C	G	AG	+/-
rs28934580	TH G1010A//R337H	T	CC	-/-
rs28934581	TH A733C	G	TT	-/-
rs7483056	TH T7517C	A	AG	+/-
rs6356	TH V112M	T	CC	-/-
rs1800497	ANKK1 E713K	A	GG	-/-
rs10891549	DRD2 A72555G	C	TC	+/-
rs2242592	DRD2 C71572T	G	AG	+/-
rs6275	DRD2 T852C	A	AG	+/-
rs1076560	DRD2 G67314T	A	CC	-/-
rs2734838	DRD2 T64501C	G	GG	+/*
rs1079597	DRD2 G54716A	T	CC	-/-
rs1079596	DRD2 G54383A	T	CC	-/-
rs2471857	DRD2 G52663A	T	CC	-/-
rs4620755	DRD2 C41383T	A	GG	-/-
rs7125415	DRD2 G40321A	T	CC	-/-
rs4648318	DRD2 A37613G	C	TT	-/-
rs17529477	DRD2 C33935T	A	AG	+/-
rs4245146	DRD2 A33029G	C	TC	+/-
rs7131056	DRD2 T21228G	A	AC	+/-
rs4648317	DRD2 C19470T	A	GG	-/-
rs1799978	DRD2 A4651G	T	TT	+/*

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs12364283	DRD2 T4047C	G	AA	-/-
rs1006737	CACNA1C G115699A	A	AA	+/?
rs2159100	CACNA1C C271442T	T	TT	+/?
rs216013	CACNA1C A2729632G	G	AA	-/-
rs2302729	CACNA1C T709021C	T	CC	-/-
rs2272306	CSAD C25411T	A	GG	-/-
rs1801153	PAH G*187A	T	CC	-/-
rs5030861	PAH IVS12+1G>A	T	CC	-/-
rs5030858	PAH R408W	A	GG	-/-
rs5030857	PAH A403V	A	GG	-/-
rs2245360	PAH C81837T	A	AA	+/?
rs5030855	PAH IVS10-11G>A	T	CC	-/-
rs5030853	PAH A300S	A	CC	-/-
rs5030852	PAH IVS7+1G>A	T	CC	-/-
rs5030849	PAH G782A	T	CC	-/-
rs1042503	PAH G735A	T	CC	-/-
rs3817446	PAH A55562G	C	TT	-/-
rs2037639	PAH C45031T	A	GG	-/-
rs1722392	PAH G37636A	T	TT	+/?
rs10860936	PAH A33429G	C	TT	-/-
rs10778209	PAH T32409C	A	AG	+/-
rs62507347	PAH A27743C	C	TT	-/-
rs1522307	PAH T17864C	G	AA	-/-
rs5030841	PAH L48S	G	AA	-/-
rs4767939	ALDH2 A7550G	A	AA	+/?
rs2238151	ALDH2 T12488C	T	TT	+/?
rs4648328	ALDH2 C23443T	T	CC	-/-
rs968529	ALDH2 T35023C	C	CC	+/?
rs4646778	ALDH2 C36438A	A	CC	-/-
rs671	ALDH2 G1369A	A	GG	-/-
rs16941667	ALDH2 C45068T	T	CC	-/-
rs2293054	NOS1 T2202C	A	GG	-/-
rs10483639	GCH1 G55306457C	C	CG	+/-
rs2878168	GCH1 C53758T	A	AG	+/-
rs3783637	GCH1 G26425A	C	CC	+/?
rs8004018	GCH1 T23847C	G	AA	-/-
rs3783641	GCH1 A14404T	A	AT	+/-
rs3783642	GCH1 A14340G	T	TC	+/-
rs8007267	GCH1 C36378991T	C	TC	+/-
rs168924	SLC6A2 A5003G	G	AG	+/-
rs2242446	SLC6A2 C5884T	T	TT	+/?
rs36020	SLC6A2 C28547T	T	TC	+/-
rs3785152	SLC6A2 T32009C	T	CC	-/-
rs40147	SLC6A2 G32299A	G	GG	+/?
rs3785157	SLC6A2 C45295T	T	TT	+/?

This report is intended to translate your results into an easier to understand form. It is not intended to diagnose or treat. For diagnosis or treatment, please present this to your doctor (or find a doctor on MTHFRSupportTM website under Find a Practitioner). Additionally, genetic mutations are flags that something **could** be wrong and not a guarantee that you are having all or any of the associated issues. Other factors like environment, ethnic background, diet, age, personal history, etc all have a factor in whether a mutation starts to present itself or not and when. Copyright all rights reserved MTHFR SupportTM

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs5568	SLC6A2 A45583C	C	AA	-/-
rs36009	SLC6A2 C48079T	T	CC	-/-
rs1800887	SLC6A2 T49048C	T	TT	+/+
rs2242447	SLC6A2 C51371T	T	TT	+/+
rs7946	PEMT G634A	T	TT	+/+
rs4244593	PEMT T17023592G	T	TG	+/-
rs72547564	ALDH3A2 G641A	A	GG	-/-
rs72547575	ALDH3A2 A1157G	G	AA	-/-
rs2297518	NOS2 C1823T	A	AG	+/-
rs876493	PNMT G-184A	A	GG	-/-
rs11077820	AANAT C10236T	T	CC	-/-
rs933271	COMT A2953G	T	TT	+/+
rs1544325	COMT A7406G	A	GG	-/-
rs5993883	COMT T13376G	T	GG	-/-
rs4646312	COMT T24075C	C	TC	+/-
rs165656	COMT G24601C	C	CG	+/-
rs6269	COMT A-1324G	G	AG	+/-
rs4633	COMT H62H	T	TC	+/-
rs2239393	COMT A 26166G	G	AG	+/-
rs4680	COMT V158M	A	AG	+/-
rs769224	COMT -61 P199P	A	GG	-/-
rs4646316	COMT C27870T	T	CC	-/-
rs174699	COMT C30196T	C	TT	-/-
rs9332377	COMT C31430T	T	CC	-/-
rs165599	COMT G*522A	A	AG	+/-
rs5953210	MAOA G3638A	G	AG	+/-
rs5906957	MAOA A36902G	G	GG	+/+
rs909525	MAOA C42794T	C	TC	+/-
rs6323	MAOA R297R/G492T/T941G	G	TG	+/-

Neurotransmitter Pathway: Serotonin & Dopamine (continued)

(See Figure 3)

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs2235186	MAOA A85020G	A	AG	+/-
rs1137070	MAOA T1011C/1460C	T	TC	+/-
rs1799836	MAOB A118723G	C	CC	+/*
rs10521432	MAOB C112982T	G	AG	+/-
rs6651806	MAOB T57758G	A	AC	+/-

Other Immune Factors

15 variants found 2 4 9

Risk Summary: 2 high risk variants, 4 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs10210302	ATG16L1 C234158839T	C	TC	+/-
rs6822844	4q27 Region 123509421G>T	G	GG	+/ ⁺
rs479405	DMGDH G67591T	C	AA	-/-
rs2253262	DMGDH T372G	A	CC	-/-
rs2069812	IL5 A131879916G	G	AG	+/-
rs20541	IL-13 variant	A	AG	+/-
rs1800629	TNF -308 variant	A	GG	-/-
rs361525	TNF -238 variant	A	GG	-/-
rs660895	HLA-DRB1 variant	G	AA	-/-
rs28940879	TYR (MeFV) V726A variant	A	GG	-/-
rs28940578	MeFV M694I variant	T	CC	-/-
rs11466023	MeFV P369S variant	A	AG	+/-
rs1801275	IL4R Q576R variant	G	AA	-/-
rs7216389	GSDMB variant	T	CC	-/-
rs17851582	GAMT C9110T	G	GG	+/ ⁺

Pentose Phosphate Pathway

43 variants found 11 12 20

(See Figure 10)

Risk Summary: 11 high risk variants, 12 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs2268169	H6PD G9321241A	A	AA	+/-
rs6688832	H6PD G9323910A	G	GG	+/-
rs9434742	H6PD Y673Y	T	CC	-/-
rs855315	PGM1 A64069612G	G	AA	-/-
rs2269260	PGM1 G64085337A	A	AG	+/-
rs2269241	PGM1 T64108771C	G	TT	-/-
rs4643	PGM1 A64125439C	C	AA	-/-
rs6702820	DDR2 A162603881G	G	AG	+/-
rs10494373	DDR2 A162619362C	C	AA	-/-
rs10799854	DDR2 C162619828T	T	TT	+/-
rs12044481	DDR2 G162635875A	A	GG	-/-
rs7553831	DDR2 T162661011G	G	TG	+/-
rs4559477	DDR2 T162681151G	T	GG	-/-
rs1780007	DDR2 A162748025C	C	CC	+/-
rs4666014	RBKS G28019175A	G	GG	+/-
rs4666020	RBKS G28046028A	A	GG	-/-
rs11130362	TKT C53265766T	T	CC	-/-
rs4687717	TKT T53282188C	T	TC	+/-
rs4687718	TKT A53282303G	A	GG	-/-
rs1650697	DHFR/MSH T-473A	A	GG	-/-
rs7768030	PHACTR1 12822973A>C	A	AA	+/-
rs9369640	PHACTR1 12901441C>A	C	AC	+/-
rs9349379	PHACTR1 12903957A>G	G	AG	+/-
rs4715166	PHACTR1 13216058A>G	G	GG	+/-
rs202072	PHACTR1 13268211A>G	A	GG	-/-
rs11754661	MTHFD1L G25264A	G	GG	+/-
rs17349743	MTHFD1L T31397C	C	TC	+/-
rs803422	MTHFD1L A33780G	A	AA	+/-
rs4129219	FBP1 T97390288C	C	TC	+/-
rs11246300	TALDO1 C749776T	T	CC	-/-
rs2733103	MTHFS - ST20 MTHFS G56057A	T	CC	-/-

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs6495446	MTHFS - ST20 MTHFS G39646A	C	TC	+/-
rs7062536	PRPS2 G12839152A	G	GG	+/?
rs766420	TKTL1 C35378G	G	GC	+/-
rs766419	TKTL1 A35635G	G	AG	+/-
rs2872817	TKTL1 A39392G	G	AG	+/-
rs72554664	G6PD R493H	T	CC	-/-
rs2230037	G6PD T438T	G	GG	+/?
rs5986990	G6PD G153761628A	A	GG	-/-
rs5030868	G6PD S219F	A	GG	-/-
rs1050829	G6PD N156D	C	TT	-/-
rs1050828	G6PD V98M	T	CC	-/-
rs762515	G6PD A16260G	C	TT	-/-

Thiamin/Thiamine Degradation

53 variants found 4 22 27

(See Figure 11)

Risk Summary: 4 high risk variants, 22 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs4646487	CYP4B1 R173W	T	CC	-/-
rs2297810	CYP4B1 M332I	A	GG	-/-
rs2297809	CYP4B1 R376C	T	CC	-/-
rs6656822	SLC19A2 A23663G	T	CC	-/-
rs3749034	GAD1 (GAD) G5276A	A	AG	+/-
rs2241165	GAD1 (GAD) C10180T	T	TC	+/-
rs3828275	GAD1 (GAD) C14541T	T	CC	-/-
rs2241164	GAD1 (GAD) C18360T	C	TC	+/-
rs701492	GAD1 (GAD) C34281T	C	TC	+/-
rs3791850	GAD1 (GAD) G39901A	G	AG	+/-
rs769395	GAD1 (GAD) A48604A	A	AG	+/-
rs11130362	TKT C53265766T	T	CC	-/-
rs4687717	TKT T53282188C	T	TC	+/-
rs4687718	TKT A53282303G	A	GG	-/-
rs2066786	RFC1 P848P	C	TC	+/-
rs6844176	RFC1 T39366590C	C	TC	+/-
rs6851075	RFC1 T39367654C	C	TC	+/-
rs969356	TPK1 C364824T	G	AG	+/-
rs12009	HSPA5 (GRP78) C11364T	A	GG	-/-
rs2236418	GAD2 (GAD) A26505496G	A	AG	+/-
rs8190612	GAD2 (GAD) C26512375T	T	CC	-/-
rs8190646	GAD2 (GAD) A26520507G	G	AA	-/-
rs1330581	GAD2 (GAD) A26528835G	A	AG	+/-
rs1805398	GAD2 (GAD) G26474809T	G	GG	+/*
rs480575	CAT A12175G	G	AG	+/-
rs2300181	CAT C21068T	T	CC	-/-
rs7320729	ATP8A2 (ATP) T7044148C	T	TT	+/*
rs6491066	ATP8A2 (ATP) F561F	T	TC	+/-
rs3117849	ATP8A2 (ATP) G7279179A	A	GG	-/-
rs3783139	ATP8A2 (ATP) T7520642C	C	TT	-/-
rs912514	ATP8A2 (ATP) C7524369T	C	TC	+/-

SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs975508	ATP8A2 (ATP) A7545586G	A	AG	+/-
rs2156310	TFF1 G781047A	A	GG	-/-
rs12613	CBS G*299A	T	CC	-/-
rs1051298	SLC19A1 C32560T	A	AG	+/-
rs1051296	SLC19A1 T32525G	C	AC	+/-
rs3788190	SLC19A1 C30428T	A	GG	-/-
rs2838956	SLC19A1 T22362C	A	AA	+/+
rs4818789	SLC19A1 C18559A	G	TT	-/-
rs12659	SLC19A1 P192P	A	GG	-/-
rs914232	SLC19A1 A14636G	T	CC	-/-
rs1051266	SLC19A1 H27R	T	CC	-/-
rs766420	TKTL1 C35378G	G	GC	+/-
rs766419	TKTL1 A35635G	G	AG	+/-
rs2872817	TKTL1 A39392G	G	AG	+/-
rs72554664	G6PD R493H	T	CC	-/-
rs2230037	G6PD T438T	G	GG	+/+
rs5986990	G6PD G153761628A	A	GG	-/-
rs5030868	G6PD S219F	A	GG	-/-
rs1050829	G6PD N156D	C	TT	-/-
rs1050828	G6PD V98M	T	CC	-/-
rs762515	G6PD A16260G	C	TT	-/-
rs2472394	G6PD G9437T	A	CC	-/-

Thyroid

5 variants found 3 2

Risk Summary: 3 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs231775	CTLA4 Thr17Ala	G	AG	+/-
rs10984009	FOXE1 8124G>A	A	AG	+/-
rs4889294	BCMO1 36464T>C	C	TT	-/-
rs7501331	BCMO1 A379V Ala379Val	T	TC	+/-
rs1800458	TTR Gly26Ser	A	GG	-/-

Trans-Sulfuration Pathway

22 variants found 4 9 9

(See Figure 8)

Risk Summary: 4 high risk variants, 9 moderate risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs10889869	CTH G6010A	A	GG	-/-
rs681475	CTH T8763C	C	TC	+/-
rs1145920	CTH A11886G	A	AG	+/-
rs663649	CTH G25229T	T	TG	+/-
rs1021737	CTH S4031I	T	GG	-/-
rs2272306	CSAD C25411T	A	GG	-/-
rs2733103	MTHFS - ST20 MTHFS G56057A	T	CC	-/-
rs6495446	MTHFS - ST20 MTHFS G39646A	C	TC	+/-
rs4149452	SULT2A1 G17136A	T	CC	-/-
rs2910393	SULT2A1 A13527G	T	TT	+/?
rs4149449	SULT2A1 G9696A	T	TC	+/-
rs2547231	SULT2A1 G9598T	A	AC	+/-
rs2273684	GSS A18836C	T	TG	+/-
rs28936396	GSS C373T	A	GG	-/-
rs6060124	GSS G11705T	C	CC	+/?
rs6088659	GSS A5997G	T	CC	-/-
rs706209	CBS C*351T	A	GG	-/-
rs706208	CBS T*330C	A	AA	+/?
rs1801181	CBS A360A	A	GG	-/-
rs4920037	CBS C19150T	A	AG	+/-
rs234706	CBS C699T	A	AG	+/-
rs2851391	CBS A13637G	T	TT	+/?

Yeast/Alcohol Metabolism

9 variants found 3 6
(See Figure 7)

Risk Summary: 3 high risk variants - Consider discussing with healthcare provider

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SNP ID	SNP Name	Risk Allele	Your Allele	Result
rs4767939	ALDH2 A7550G	A	AA	+/-
rs2238151	ALDH2 T12488C	T	TT	+/-
rs4648328	ALDH2 C23443T	T	CC	-/-
rs968529	ALDH2 T35023C	C	CC	+/-
rs4646778	ALDH2 C36438A	A	CC	-/-
rs671	ALDH2 G1369A	A	GG	-/-
rs16941667	ALDH2 C45068T	T	CC	-/-
rs72547564	ALDH3A2 G641A	A	GG	-/-
rs72547575	ALDH3A2 A1157G	G	AA	-/-

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Figure 1: Liver Detox - Phase II

Phase I & II Liver Detox

*Phase I (Cytochrome P450)

Fat Soluble Metabolite
(e.g., hormones, toxins)



Intermediate Metabolites

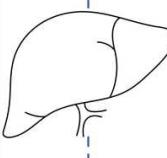


*Phase II (Conjugation Pathways)

Water Soluble Excretory Derivative

Serum to Kidneys
to Urine
or
Bile to Stool

- CYP19A1
- CYP1A1
- CYP1A2
- CYP1B1 (reproductive tissue, eye)
- CYP21A1
- CYP2481
- CYP26A1
- CYP27B1
- CYP2A13
- CYP2A6
- CYP2B6
- CYP2C19
- CYP2C9
- CYP2D6
- CYP3A4



Reactive Oxygen
Intermediaries
(Anti-oxidants
quench)

Acetylation - NAT1, NAT2, etc.

Glucuronidation - UGT1A1, UGT2A1, etc.

Glutathione Conjugation - GGT1, GPX3,
GSR, GSTM, GSTP, etc.

Peptide Conjugation - Glycine, Taurine

Methylation - MTHFR, MTR, MTRR,
COMT, etc.

Sulfation - SULT1A1, SULT1A2, etc.

*Enzyme CoFactors:

- Vitamins: B2, B3, B6, B9 (folate)
- Other: Glutathione, Leucine, Isoleucine, Valine, Flavonoids, Phospholipids

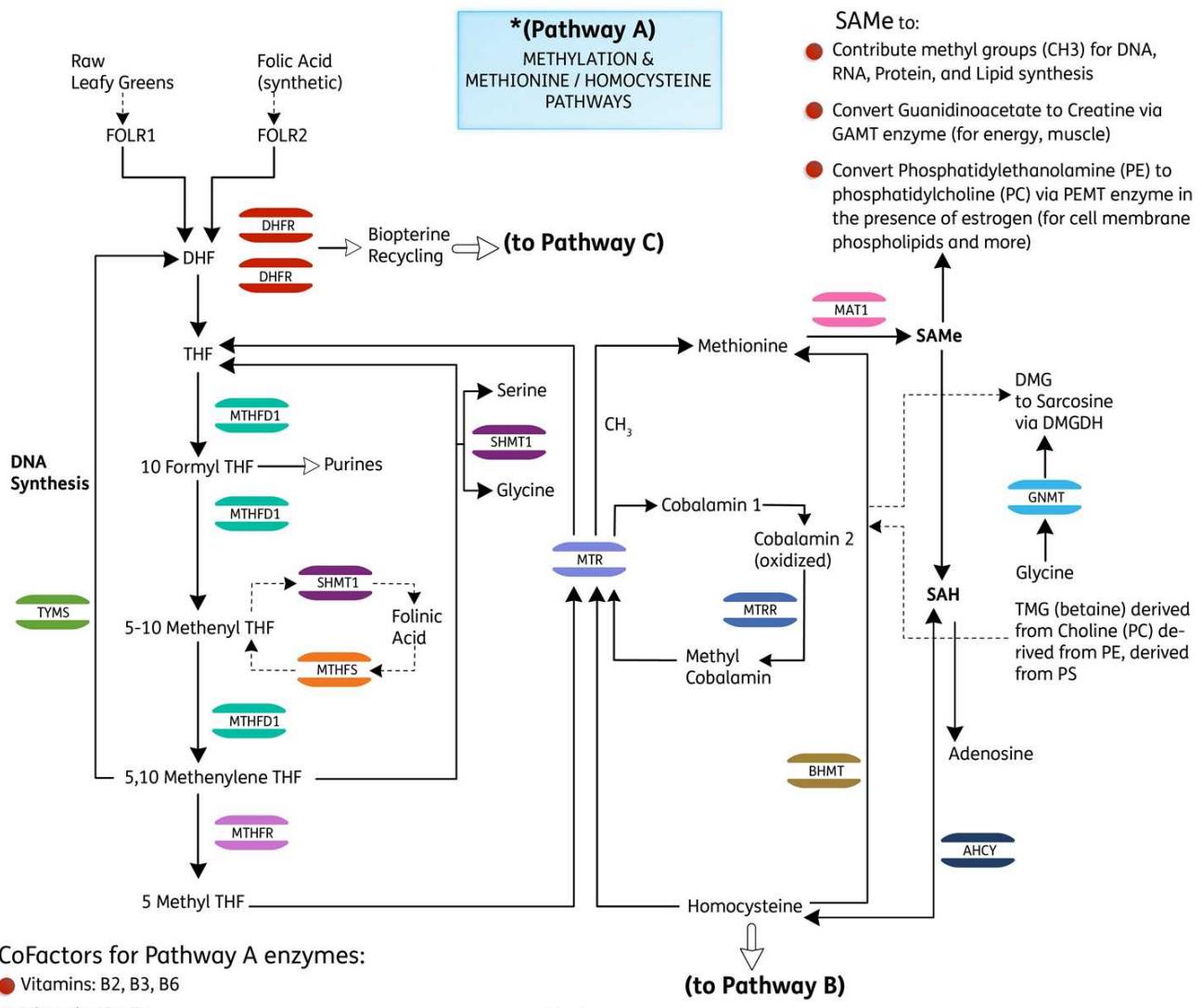
*Enzyme CoFactors:

- Glycine
- Taurine
- Glutamine
- N-acetylcysteine
- Cysteine
- Methionine

Note: Slow Phase II Conjugation (e.g., COMT SNPs) wrt to Phase I, contributes to disease as Reactive Oxygen Intermediaries can cause free radical damage to tissue.

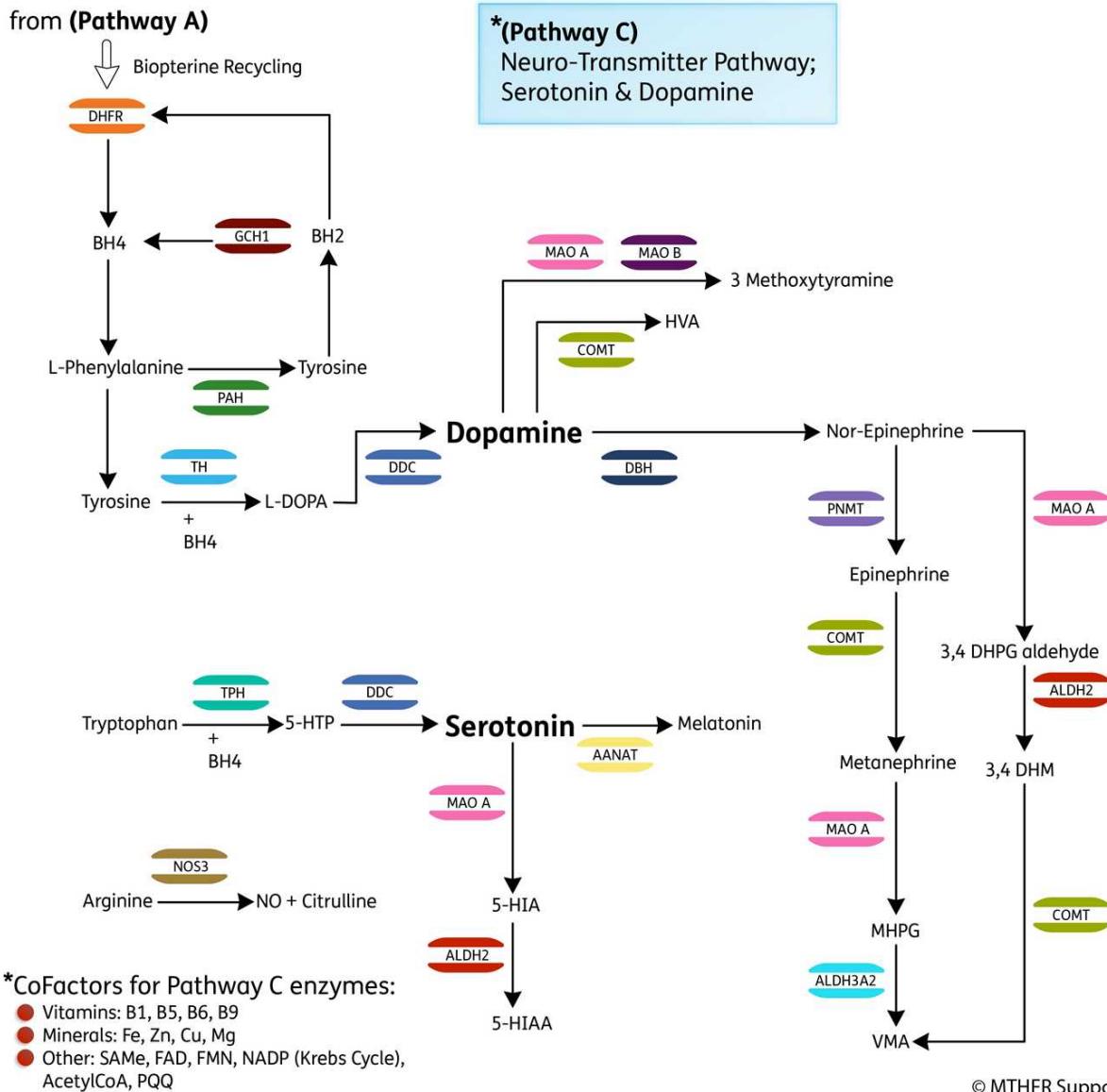
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Pathway diagram illustrating genetic variants and their interactions in the Liver Detox - Phase II category. Refer to your specific variant results in the corresponding category section.

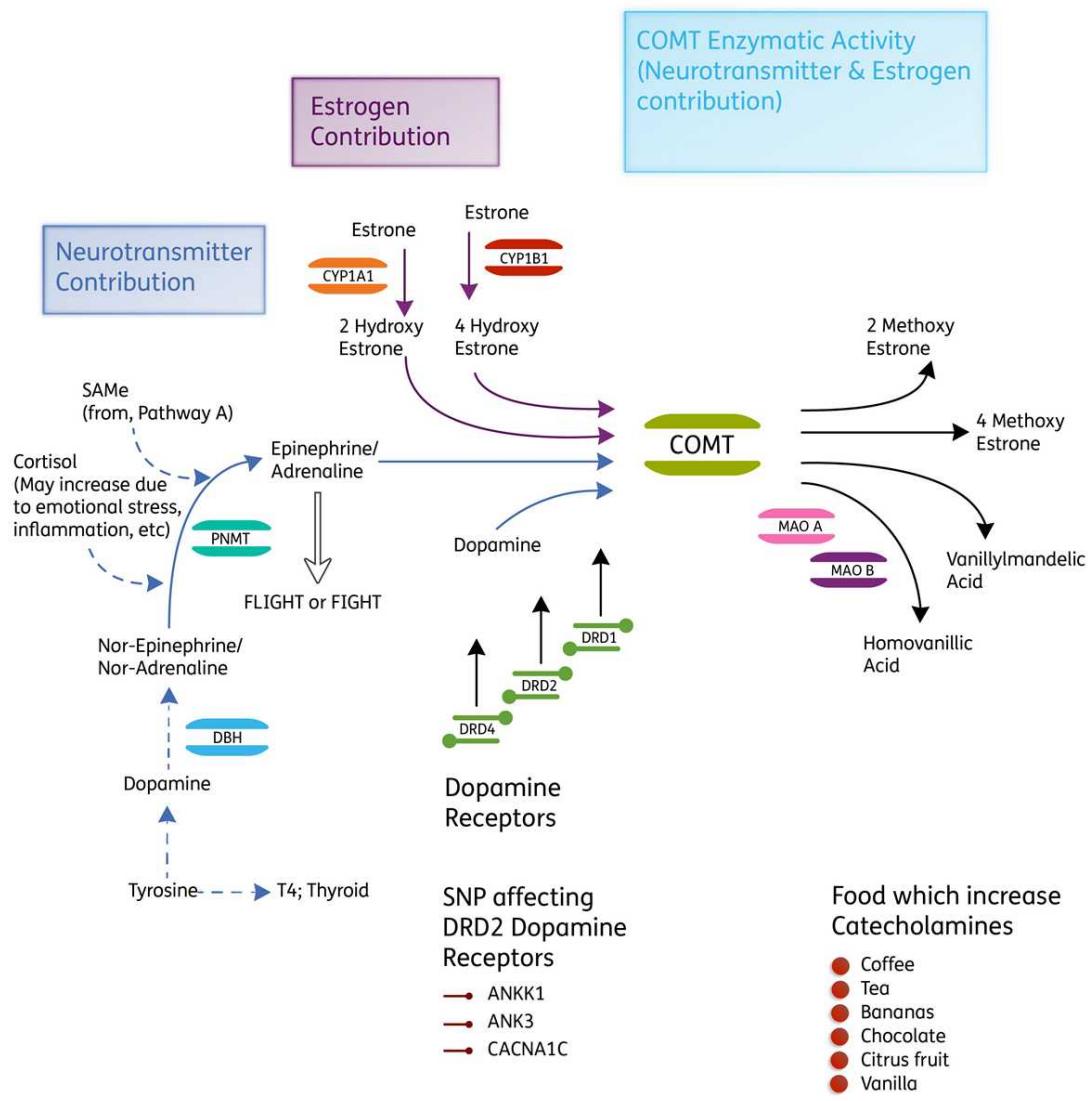
Figure 2: Methylation & Methionine/Homocysteine Pathways


Pathway diagram illustrating genetic variants and their interactions in the Methylation & Methionine/Homocysteine Pathways category. Refer to your specific variant results in the corresponding category section.

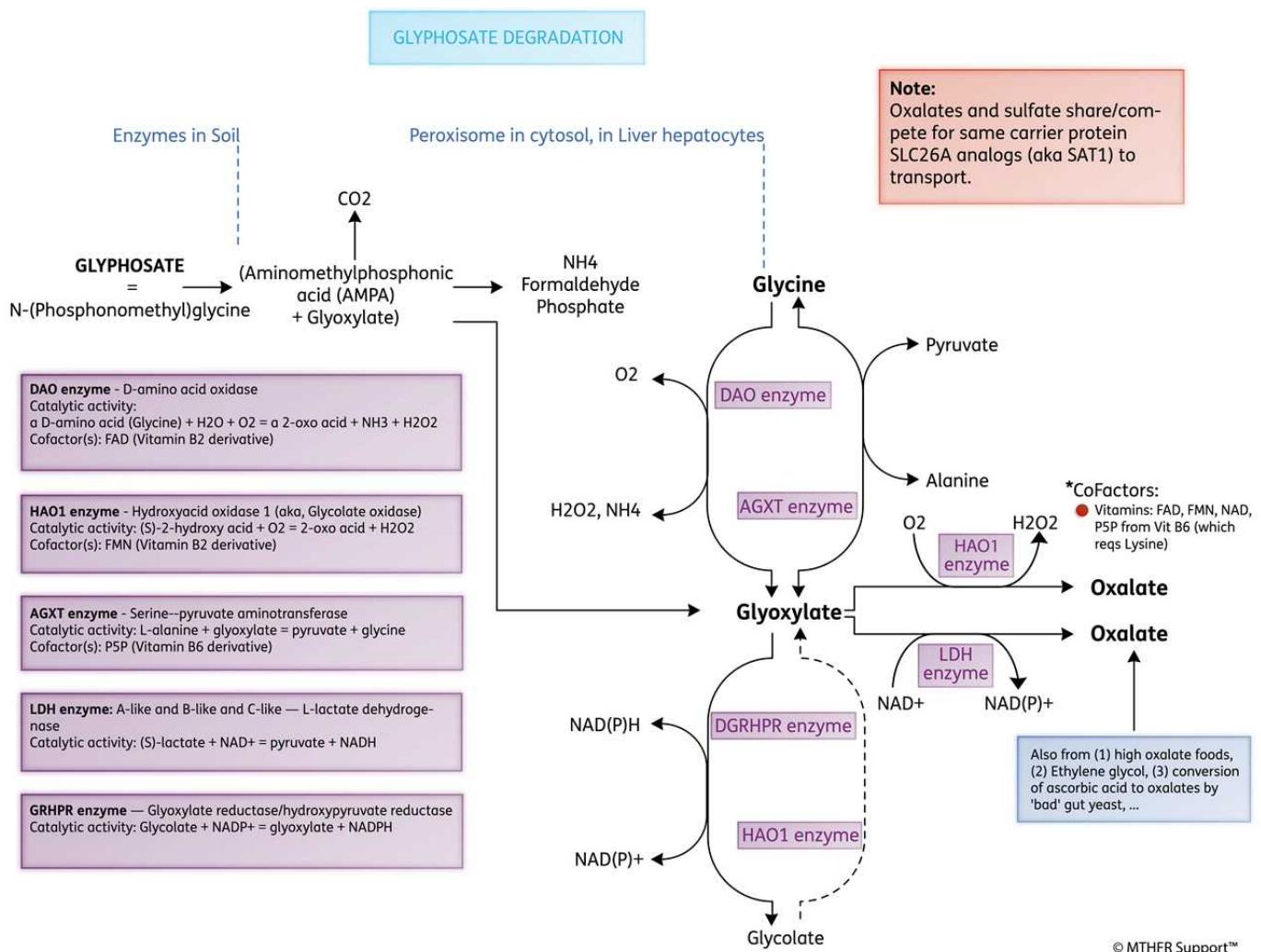
Figure 3: Neurotransmitter Pathway: Serotonin & Dopamine



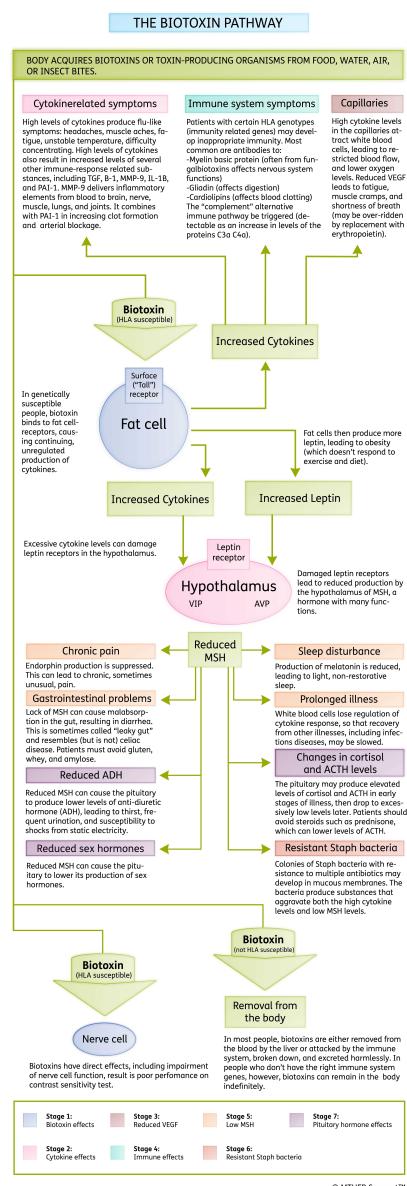
Pathway diagram illustrating genetic variants and their interactions in the Neurotransmitter Pathway: Serotonin & Dopamine category. Refer to your specific variant results in the corresponding category section.

Figure 4: COMT Activity


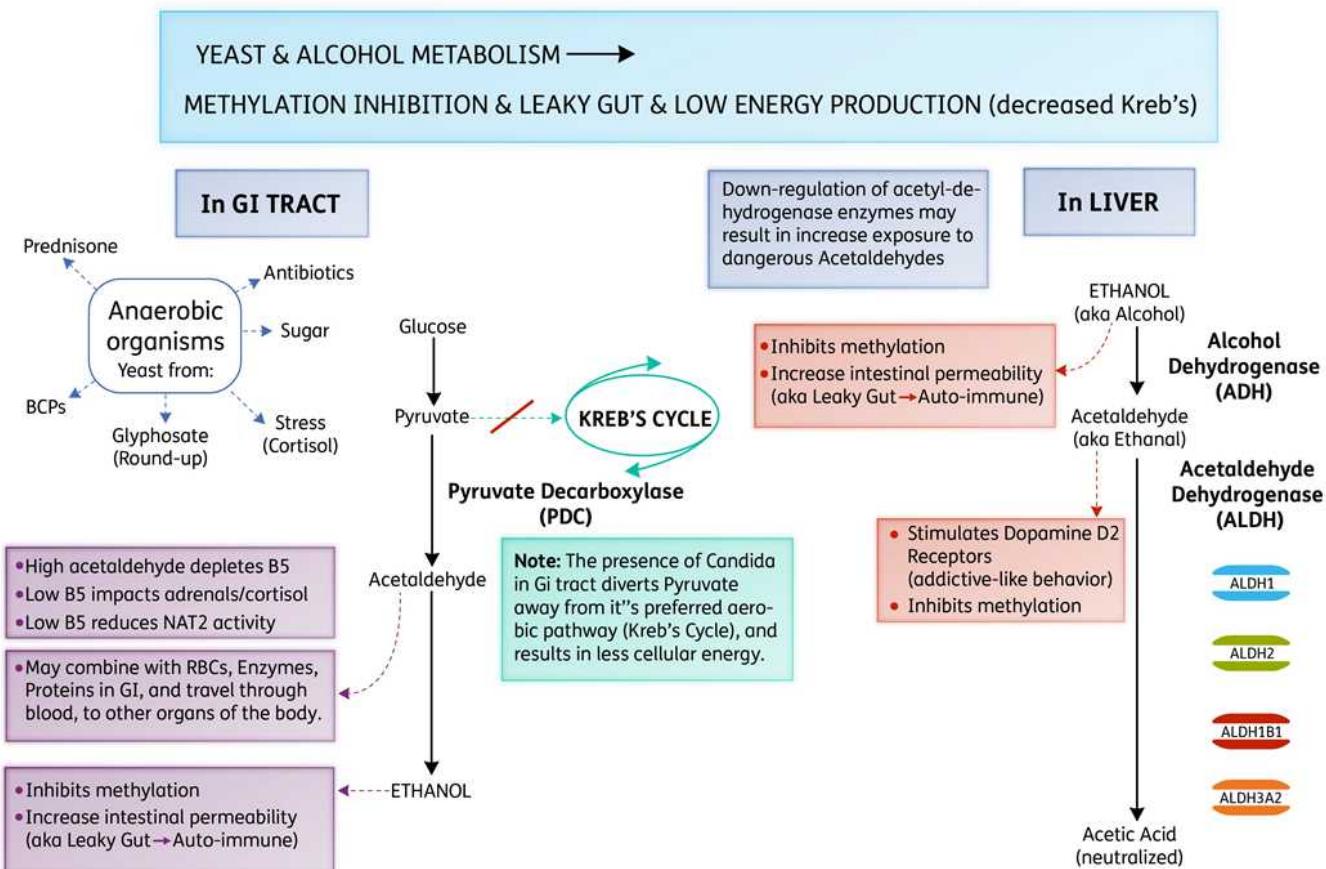
Pathway diagram illustrating genetic variants and their interactions in the COMT Activity category. Refer to your specific variant results in the corresponding category section.

Figure 5: Glyoxylate Metabolic Process


Pathway diagram illustrating genetic variants and their interactions in the Glyoxylate Metabolic Process category. Refer to your specific variant results in the corresponding category section.

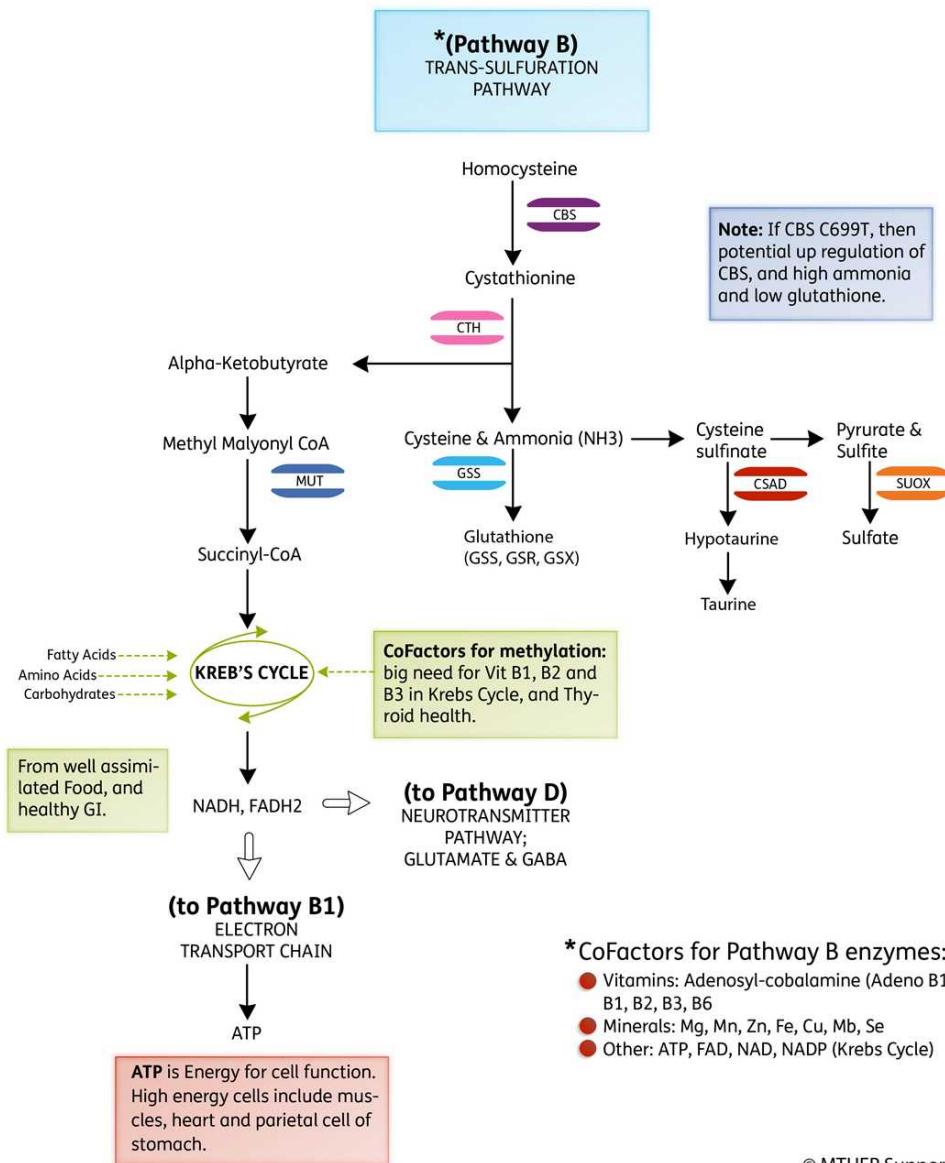
Figure 6: HLA


Pathway diagram illustrating genetic variants and their interactions in the HLA category. Refer to your specific variant results in the corresponding category section.

Figure 7: Yeast/Alcohol Metabolism


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Pathway diagram illustrating genetic variants and their interactions in the Yeast/Alcohol Metabolism category. Refer to your specific variant results in the corresponding category section.

Figure 8: Trans-Sulfuration Pathway


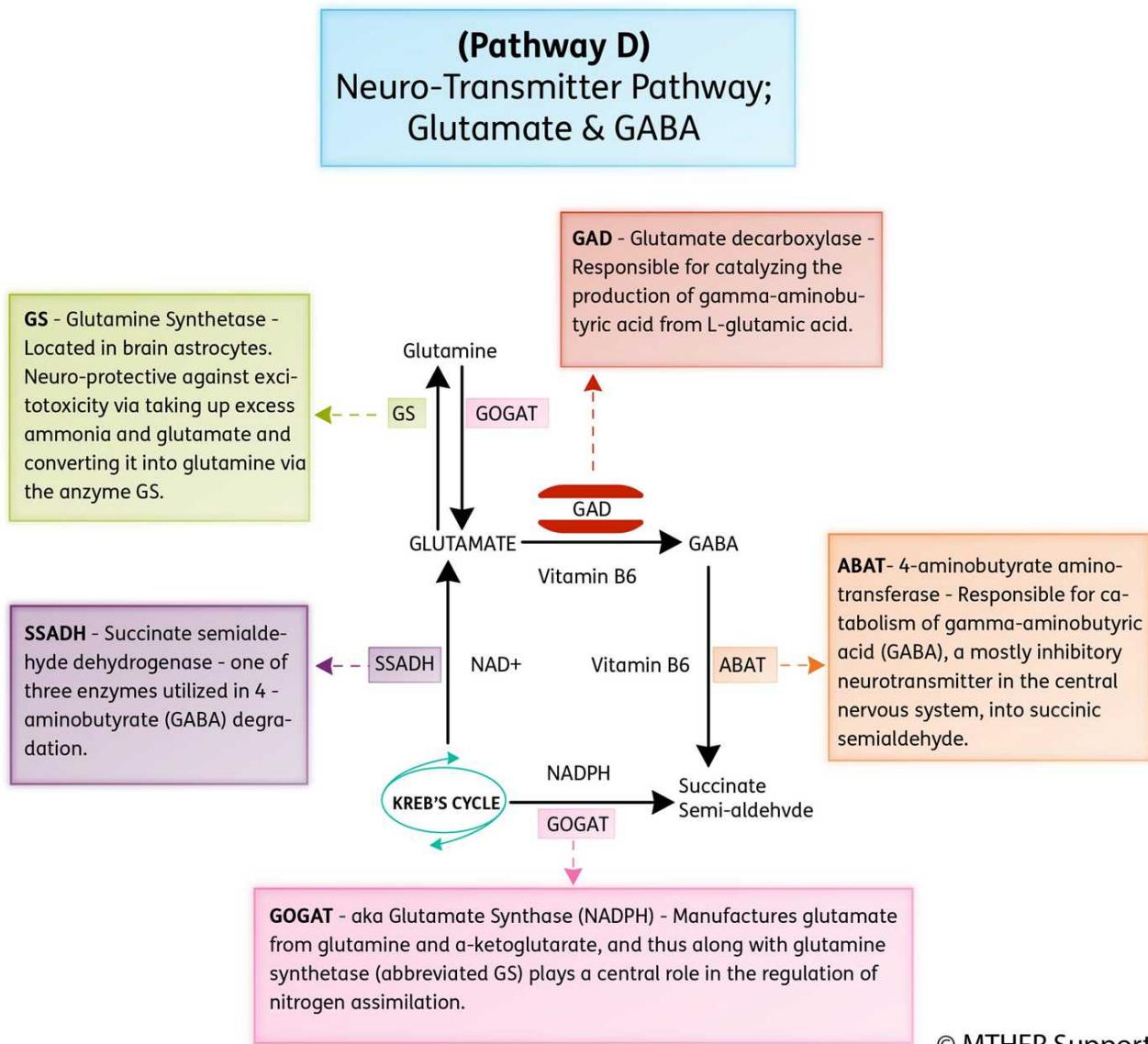
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Pathway diagram illustrating genetic variants and their interactions in the Trans-Sulfuration Pathway category. Refer to your specific variant results in the corresponding category section.

***CoFactors for Pathway B enzymes:**

- Vitamins: Adenosyl-cobalamin (Adeno B12), B1, B2, B3, B6
- Minerals: Mg, Mn, Zn, Fe, Cu, Mb, Se
- Other: ATP, FAD, NAD, NADP (Krebs Cycle)

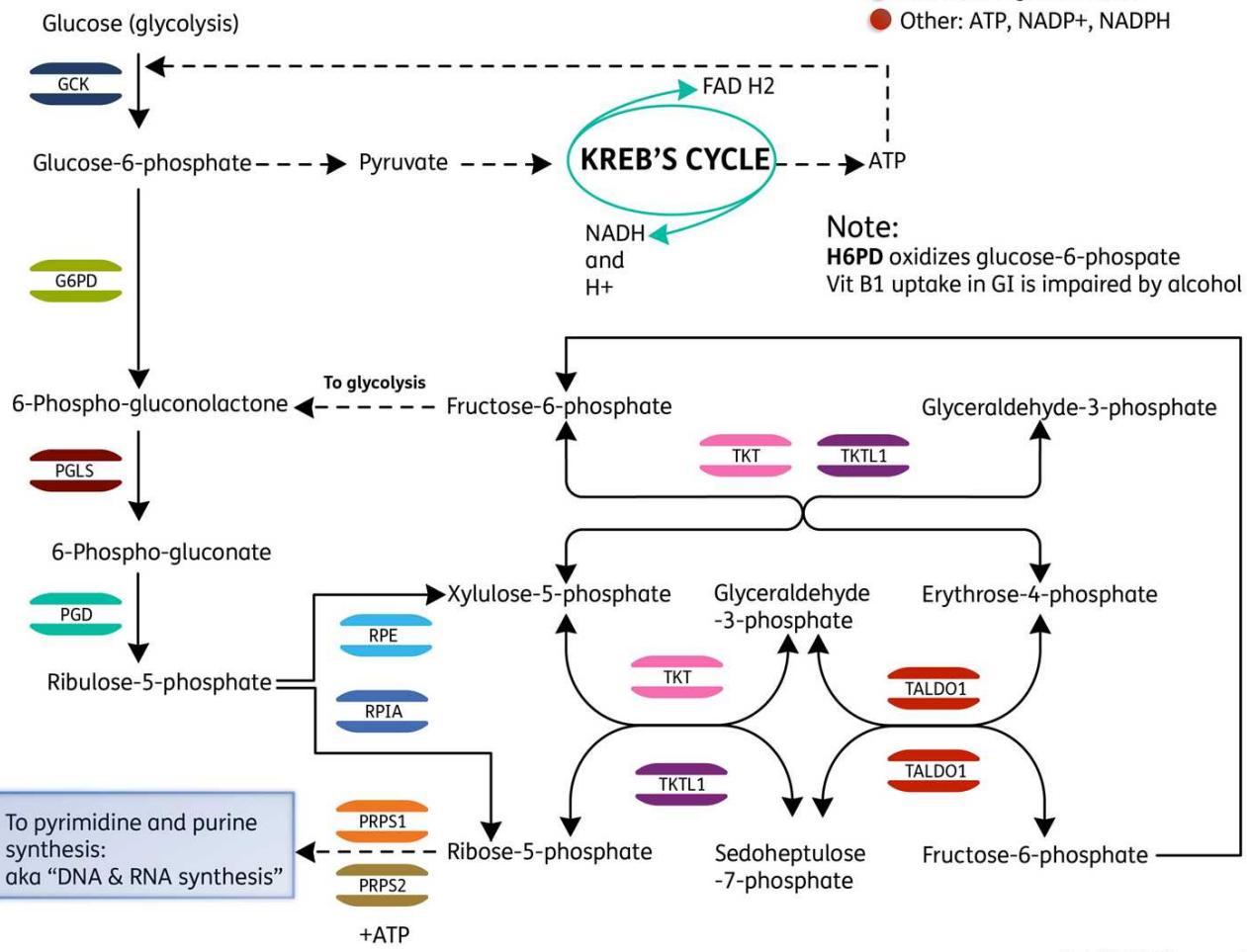
Figure 9: Neurotransmitter Pathway: Glutamate & GABA



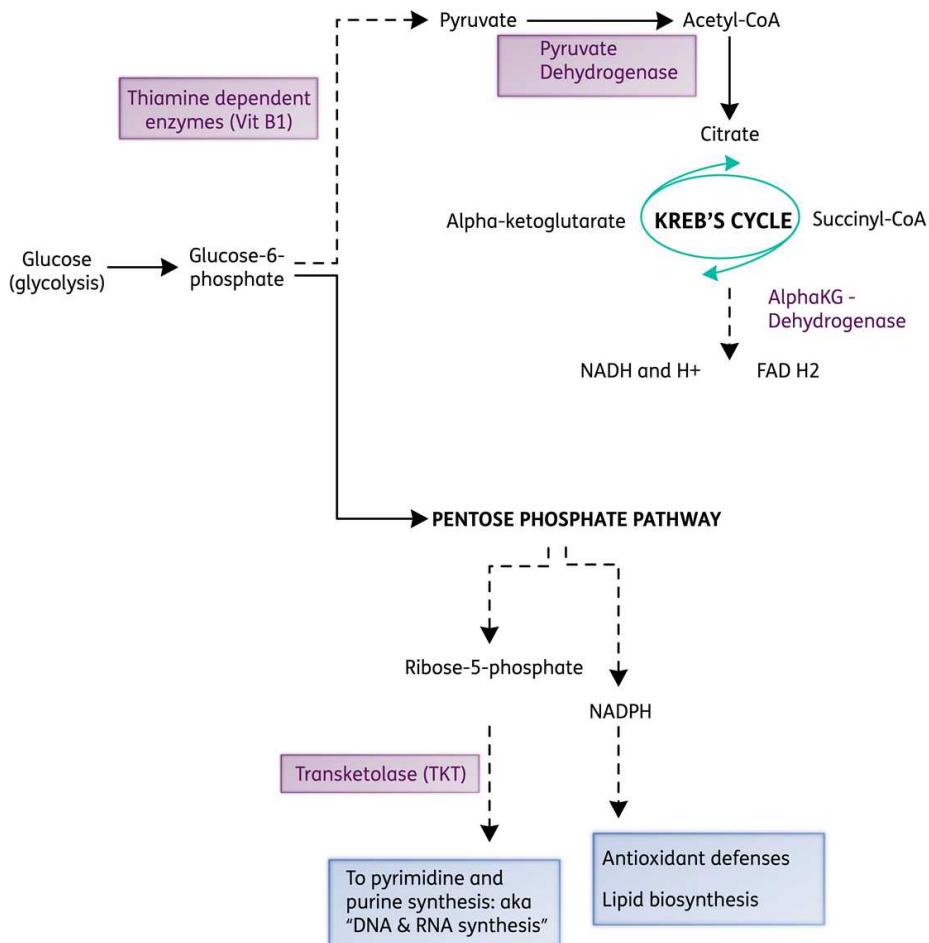
Pathway diagram illustrating genetic variants and their interactions in the Neurotransmitter Pathway: Glutamate & GABA category. Refer to your specific variant results in the corresponding category section.

Figure 10: Pentose Phosphate Pathway

*Pentose phosphate pathway

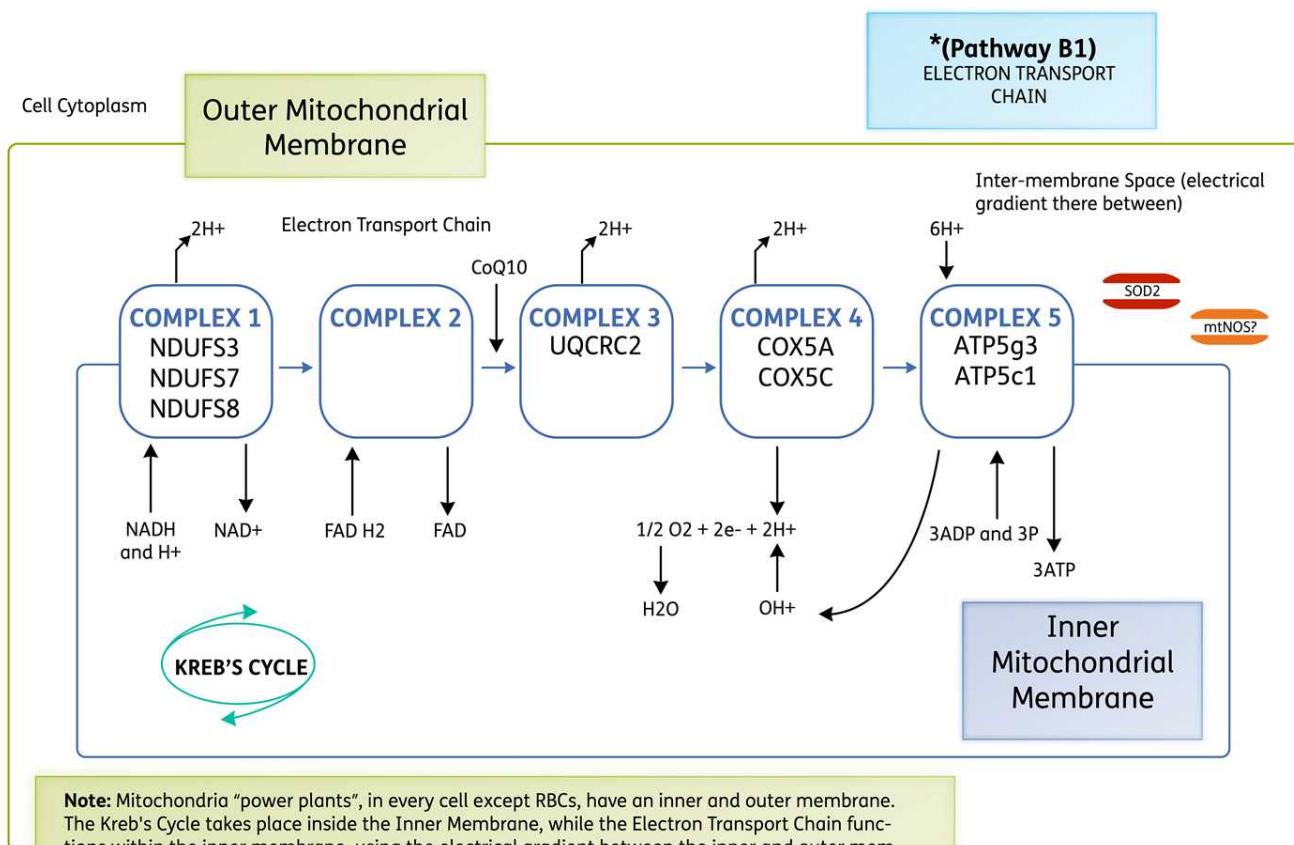


Pathway diagram illustrating genetic variants and their interactions in the Pentose Phosphate Pathway category. Refer to your specific variant results in the corresponding category section.

Figure 11: Thiamin/Thiamine Degradation
OVERVIEW CONNECTION BETWEEN: GLYCOLYSIS & PENTOSE PHOSPHATE PATHWAY & KREBS CYCLE & THIAMINE


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Pathway diagram illustrating genetic variants and their interactions in the Thiamin/Thiamine Degradation category. Refer to your specific variant results in the corresponding category section.

Figure 12: Mitochondrial Function


Note: Mitochondria “power plants”, in every cell except RBCs, have an inner and outer membrane. The Krebs Cycle takes place inside the Inner Membrane, while the Electron Transport Chain functions within the inner membrane, using the electrical gradient between the inner and outer membrane. Healthy membranes are key, as are good assimilation of fats, carbs and proteins (e.g., healthy GI function) which drive the Krebs cycle, along with Vitamins B1, B2 and B3.

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Pathway diagram illustrating genetic variants and their interactions in the Mitochondrial Function category. Refer to your specific variant results in the corresponding category section.

⚠ Important Disclaimer

Medical Disclaimer: This report is intended to translate your results into an easier to understand form. It is **not intended to diagnose or treat** any medical condition.

Professional Consultation: For diagnosis or treatment, please present this report to your qualified healthcare provider or find a practitioner on the MTHFRSupport™ website under "Find a Practitioner".

Genetic Interpretation: Genetic mutations are indicators that something *could* be affected, but they are **not a guarantee** that you are experiencing all or any of the associated issues.

Contributing Factors: Many factors influence whether genetic variants manifest as health issues, including:

- Environmental factors
- Ethnic background
- Diet and lifestyle
- Age and personal history
- Other genetic interactions

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