TenDna

# PERSONALIZED GENETIC REPORT
# BY ANALYZING THE DOWNLOADED DNA DATA

December 05, 2023

## Annotation

The report data is contained in tables. Each table corresponds to research topics - vitamins, microelements, diseases, susceptibility to addiction, effectiveness of diets.

Each table contains SNP (single nucleotide polymorphism) from your raw data file.

Homozygous polymorphisms are marked in red, heterozygous polymorphisms in yellow, normal alleles in white. Homozygous polymorphisms affect both copies of the gene and increase the risk occurrence of the disease; heterozygous polymorphisms affect only one copy of the gene and have less effect on the risk occurrence of the disease.

All report data is based on the latest modern research. The more homozygotes and heterozygotes (red and yellow lines), the higher the risk occurrence of the disease and other problems considered in the studies. At the end of each table you can read a brief explanation of the risk that is associated with polymorphism. There are also direct links to studies that you can read in more detail to better study the topic.

If there is a high risk for a section, it is recommended to check with additional tests and examinations. You can also show the report to your doctor or nutritionist for further testing and treatment if necessary.

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| |
|---|
| **Low-calorie diet** |
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# Vitamins

## Vitamin D

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1544410 | CC | CC |
| rs731236 | AA | AA |
| rs2282679 | TT | TT |
| rs12785878 | TT | GG |
| rs10741657 | AA | GG |
| rs705117 | TT | TT |
| rs1155563 | TT | TT |
| rs222016 | AA | AA |
| rs1491710 | AA | AA |
| rs4588 | GG | CC |
| rs7041 | CC | AA |
| rs3829251 | GG | GG |
| rs2060793 | AA | GG |
| rs2280273 | TA | TT |
| rs11572223 | GG | GG |
| rs11572311 | AG | AA |
| rs61495246 | AA | AA |
| rs7129781 | TT | TT |
| rs75774690 | CG | CC |



Risk level: average

**rs12785878:** Has been associated with serum vitamin D concentrations in several studies. The T risk allele is associated with greater reductions in insulin and HOMA-IR levels in response to a high-protein diet.
[ PMID 23924835 ] [ PMID 22801813 ]

**rs10741657:** Associated with increased 25(OH)D levels in a study of vitamin D levels and multiple sclerosis risk.Also associated with predisposition to type 1 diabetes and vitamin D levels. Increases the risk of gestational diabetes mellitus.

[ PMID 20541252 ]  [ PMID 17607662 ]  [ PMID 22801813 ]

**rs4588:** Associated with lower vitamin D levels and therefore potential vitamin D deficiency. Increases vitamin D deficiency among pregnant women and the likelihood of gestational diabetes.
[ PMID 23505139 ]  [ PMID 32537819 ]  [ PMID 23191998 ]

**rs7041:** Vitamin D binding protein genotype and osteoporosis. Associated with decreased 25-hydroxyvitamin D concentrations. A study of smokers found that vitamin D levels were reduced by 25% with this breakdown and 2 times the risk of chronic obstructive pulmonary disease. Also associated with metabolic syndrome and lower levels of 25-hydroxyvitamin D in polycystic ovary syndrome.
[ PMID 19488670 ]  [ PMID 20363324 ]  [ PMID 21228423 ]  [ PMID 28278285 ]

**rs2060793:** This SNP is part of CYP2R1, which encodes a key C-25 hydroxylase that converts vitamin D3 to the active ligand of the vitamin D receptor.
[ PMID 20418485 ]  [ PMID 21972121 ]

# Vitamin C

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs2681116 | AA | TT |
| rs6596473 | CG | CC |
| rs4257763 | CG | GG |
| rs33972313 | CG | CC |
| rs11950646 | AG | GG |
| rs6053005 | AC | CC |
| rs6133175 | AG | GG |
| rs1279683 | AG | AA |
| rs6139591 | CG | GG |
| rs10063949 | CG | CC |

Risk level: high

**rs2681116:** Polymorphism of a gene for a vitamin C transporter gene from food and decreased blood ascorbic acid levels.
[ PMID 20588054 ] [ PMID 19243932 ]

**rs6596473:** One of two sodium-dependent transporters required for hepatic and renal reabsorption of vitamin C (ascorbic acid) and thus essential for maintaining vitamin C homeostasis in the blood.
[ PMID 6448982 ] [ PMID 24708273 ] [ PMID 20592130 ]

**rs4257763:** The breakage causes a problem with the vitamin C transporter, the absorption of vitamin C from food, and a decrease in blood levels of ascorbic acid.
[ PMID 20588054 ]

**rs33972313:** Causes a decrease in the transport activity of vitamin C. Causes a decrease in vitamin C levels regardless of diet.
[ PMID 20519558 ]

**rs1279683:** Associated with decreased blood levels of vitamin C and risk of glaucoma.
[ PMID 22171153 ]

## Vitamin A

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs12934922 | AA | AA |
| rs7501331 | CC | CC |
| rs6564851 | TT | TT |

Risk level: low

# Vitamin B1 (thiamine)

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs4973216 | CC | CC |
| rs11682956 | TG | GG |
| rs7585481 | TT | CC |
| rs10933203 | CG | CC |
| rs12493802 | TC | CC |
| rs4687718 | GG | GG |
| rs11717712 | CG | CC |
| rs4687717 | CC | CC |
| rs17336718 | CC | CC |
| rs10126322 | CC | CC |
| rs2239466 | AA | AA |
| rs766420 | CC | CC |
| rs10274162 | TA | TT |
| rs7804157 | GG | TT |
| rs2057868 | GG | GG |
| rs4726711 | AG | GG |
| rs371271054 | TT | TT |
| rs13245975 | TT | TT |
| rs4725658 | TA | TT |
| rs228587 | TC | CC |



Risk level: average

**rs7585481:** The breakage results in impairment of the protein's ability to transport thiamine into cells, resulting in decreased absorption of vitamin B1 from food. Thiamine-reactive encephalopathy characterised by seizures responding to high doses of thiamine may develop.
[ PMID 28696212 ] [ PMID 28402605 ] [ PMID 26863430 ]

**rs7804157:** Associated with the occurrence of childhood encephalopathy due to thiaminpyrophosphokinase deficiency. It is a rare treatable neurological disorder caused by mutations in the TPK1 gene.
[ PMID 22152682 ]

**rs11682956:** The breakage results in impaired ability of the protein to transport folate and thiamine into cells, resulting in reduced absorption of vitamin B1 from food. Thiamine-reactive encephalopathy, characterised by seizures responding to high doses of thiamine, may develop.
[ PMID 28696212 ] [ PMID 28402605 ] [ PMID 26863430 ]

**rs12493802:** A breakdown responsible for the production of the enzyme transketolase, which is involved in the regulation of multiple cancer-related events such as cancer cell proliferation, metastasis, invasion, and resistance to chemoradiation therapy. Indications are high doses of thiamine (vitamin B1), which may normalise the enzyme.
[ PMID 30646877 ]

## Vitamin B2 (riboflavin)

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs346822 | CG | CC |
| rs2929859 | TT | TT |
| rs16852179 | TA | TT |
| rs4494951 | GG | GG |
| rs6054605 | CG | GG |
| rs910857 | GG | GG |
| rs3746807 | GG | GG |
| rs3746802 | TT | TT |
| rs3746804 | GG | GG |
| rs34499319 | CG | GG |

Risk level: low

## Vitamin B4 (choline)

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs4244593 | TT | GG |
| rs174548 | GC | CC |
| rs11578532 | TC | TT |
| rs671919 | TT | GG |
| rs4949874 | TT | TT |
| rs6658825 | AC | CC |
| rs10874305 | CC | CC |
| rs1036950 | TA | TT |
| rs12738260 | TT | TT |
| rs649352 | TC | TT |
| rs211699 | GG | GG |
| rs10493565 | AA | AA |
| rs7946 | TT | CC |
| rs4646409 | AA | AA |
| rs750546 | CC | CC |
| rs3760188 | CG | CC |
| rs4646404 | GG | GG |
| rs1051266 | CC | TT |
| rs2236225 | AG | GG |
| rs1880676 | AG | GG |
| rs7520974 | AA | GG |
| rs2289205 | TC | CC |
| rs12325817 | CG | CC |
| rs4646343 | CG | GG |

Risk level: average

**rs7946:** Genetic polymorphisms in methyl group metabolism DNA methylation in peripheral blood. Affect the human need for choline (vitamin B4).
[ PMID 18789905 ] [ PMID 22371529 ] [ PMID 16816108 ]

**rs1051266:** The protein encoded by the gene transports folic acid into the cell and thus plays a role in the intracellular regulation of folate concentration. In this genotype, folate absorption is worse. Folic acid requirement is higher. Alcohol consumption is more critical for the risk of vitamin B9 deficiency.
[ PMID 19172696 ] [ PMID 19650776 ]

**rs174548:** Polymorphisms in this gene are associated with decreased levels of omega-3 fatty acids, increased relative levels of omega-6 fatty acids and increased concentrations of trans-unsaturated fatty acids. In vegetarians, some polymorphisms of this gene may result in an undesirable situation associated with increased inflammation.

**rs2236225:** Possible increased risk of fetal birth defects. A 1.5-fold higher risk for Caucasian mothers to give birth to children with DNT (neural tube defect). The association in children with this mutation with an increased risk of heart defects is greater if their mother did not get enough folic acid during pregnancy. The risk is reduced with adequate levels of folic acid and vitamin B6.
[ PMID 18767138 ] [ PMID 20544798 ] [ PMID 20890936 ]

**rs1880676:** Genetic variability in the choline-O-acetyltransferase gene influences increased risk of depression and Alzheimer's disease.
[ PMID 16223550 ] [ PMID 20147892 ] [ PMID 21507424 ]

**rs2289205:** Choline pathway gene polymorphism increases the risk of intrauterine foetal death.
[ PMID 28509322 ]

## Vitamin B5 (pantothenic acid)

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs4815628 | TC | CC |
| rs41279408 | CG | CC |
| rs12480318 | CC | CC |
| rs71647828 | TA | TT |
| rs11906612 | CG | CC |
| rs4815621 | CA | AA |
| rs6084513 | AC | CC |
| rs6084506 | CC | CC |
| rs6107373 | CG | GG |
| rs6116087 | TA | AA |



Risk level: average

## Vitamin B6 (pyridoxine)

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs17679445 | GG | GG |
| rs11079804 | CC | CC |
| rs2276528 | GG | GG |
| rs8128639 | AC | CC |
| rs1106797 | GG | AA |
| rs13050307 | TA | AA |
| rs4654748 | CC | CC |
| rs1256335 | AG | AA |
| rs2275370 | AA | AA |
| rs3767150 | GG | GG |
| rs3767155 | AC | CC |
| rs1256348 | CG | CC |
| rs2242420 | CC | CC |
| rs885813 | TC | CC |
| rs1772719 | AC | AA |
| rs121964972 | CG | GG |
| rs5742905 | AT | TT |
| rs2236225 | AG | GG |



Risk level: average

**rs1106797:** The gene encodes pyridoxal kinase, which converts inactive vitamin B6 into the active cofactor p-5-p. Breakage can cause polyneuropathy, and high doses of p-5-p are recommended.
[ PMID 33912895 ] [ PMID 31187503 ] [ PMID 32522499 ]

**rs1256335:** Breakage causes a deficiency of the active form of vitamin B6, pyridoxal-5'-phosphate (p-5-p). Supplemental intake of p-5-p is recommended.
[ PMID 25972531 ]

**rs3767155:** Risk of a 1.4-fold decrease in the active form of vitamin B6 in blood and cerebrospinal fluid.
[ PMID 30583557 ]

**rs121964972:** Breakage increases the likelihood of homocystinuria, which is insensitive to vitamin B6.
[ PMID 9156316 ] [ PMID 12686134 ]

**rs5742905:** Responsible for vitamin B6 susceptibility in homocystinuria.

**rs2236225:** Possible increased risk of fetal birth defects. A 1.5-fold higher risk for Caucasian mothers to give birth to children with DNT (neural tube defect). The association in children with this mutation with an increased risk of heart defects is greater if their mother did not get enough folic acid during pregnancy. The risk is reduced with adequate levels of folic acid and vitamin B6.
[ PMID 18767138 ] [ PMID 20544798 ] [ PMID 20890936 ]

## Vitamin B7 (biotin)

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs13073139 | GG | GG |
| rs34885143 | GG | GG |
| rs13078881 | GG | GG |
| rs7640807 | TC | TT |
| rs35034250 | CG | CC |
| rs28934601 | AA | AA |
| rs104893688 | CC | CC |

Risk level: low

## Vitamin B9 (folic acid)

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1801133 | AG | GG |
| rs1801131 | TG | TT |
| rs2236225 | AG | GG |
| rs1805087 | AA | AA |
| rs1801394 | GG | AA |
| rs1051266 | CC | TT |
| rs7925545 | AA | AA |
| rs144637717 | TT | TT |
| rs4973216 | CC | CC |
| rs17349743 | TT | TT |
| rs2295639 | TT | TT |
| rs11754661 | GG | GG |
| rs326124 | GG | GG |
| rs744731 | TT | TT |
| rs10923895 | AT | TT |
| rs6495446 | CC | CC |
| rs942835 | TT | TT |
| rs1076991 | CG | CC |
| rs1031326 | TC | CC |
| rs1532268 | TT | CC |
| rs10064631 | CG | CC |
| rs2287780 | CC | CC |
| rs8011839 | CC | CC |
| rs2281617 | CC | CC |
| rs1979277 | CG | GG |
| rs3828090 | GG | GG |
| rs8004018 | AG | AA |
| rs543703 | AA | AA |
| rs651933 | AG | GG |

| | | |
|---|---|---|
| rs6495449 | GG | GG |
| rs10604 | AG | AA |
| rs162036 | AA | AA |
| rs10498514 | AA | AA |
| rs12512471 | TT | TT |



Risk level: average

**rs1801394:** Polymorphism can lead to elevated homocysteine levels independent of folic acid, vitamin B12 or B6 levels. It is a risk factor for neural tube defects and Down syndrome in the setting of higher homocysteine levels.
[ PMID 10444342 ] [ PMID 10930360 ]

**rs1051266:** The protein encoded by the gene transports folic acid into the cell and thus plays a role in the intracellular regulation of folate concentration. In this genotype, folate absorption is worse. Folic acid requirement is higher. Alcohol consumption is more critical for the risk of vitamin B9 deficiency.
[ PMID 19172696 ] [ PMID 19650776 ]

**rs1801133:** A gene fragment known as MTHFR C677T, which encodes an enzyme involved in folic acid metabolism. A break in this gene fragment results in high levels of homocysteine, low levels of B12 and folic acid. If your tests show high homocysteine levels, your doctor will likely advise you on an appropriate diet and supplementation regime. Taking varieties of the active form of B9 methylfolate (5-MTHF or L-methyltetrahydrofolate), the active form of vitamin B12, methylcobalamin, is recommended to reduce your risks.
[ PMID 8616944 ] [ PMID 1522835 ] [ PMID 7647779 ] [ PMID 8554053 ] [ PMID 8554066 ]

**rs1801131:** Reduces the formation of the active form of folic acid, which is necessary for the remethylation of homocysteine and other DNA molecules. Administration of the active form of folic acid (5-MTHF or L-methyltetrahydrofolate) can significantly improve risk scores for the effects of mutations. Also a factor that moderately increases the need for vitamin B2.
[ PMID 11742092 ] [ PMID 11752418 ] [ PMID 11590551 ] [ PMID 15951337 ] [ PMID 16244782 ]

**rs2236225:** Possible increased risk of fetal birth defects. A 1.5-fold higher risk for Caucasian mothers to give birth to children with DNT (neural tube defect). The association in children with this mutation with an increased risk of heart defects is greater if their mother did not get enough folic acid during pregnancy. The risk is reduced with adequate levels of folic acid and vitamin B6.
[ PMID 18767138 ] [ PMID 20544798 ] [ PMID 20890936 ]

**rs10064631:** Methionine synthase deficiency, impairing the metabolism of folic acid B9 and cobalamin B12.
[ PMID 10484769 ]

**rs1979277:** Polymorphism of enzymes that metabolise folic acid.It is required to obtain sufficient vitamin B6 for optimal gene activity.
[ PMID 22103680 ]

**rs651933:** May mean that folic acid cannot be transported into cells, and may indicate a need for more folic acid
[ PMID 20683905 ]

## Vitamin B12

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs602662 | AG | AA |
| rs1805087 | AA | AA |
| rs1801133 | AG | GG |
| rs601338 | AG | GG |
| rs16982241 | GG | GG |
| rs10925263 | TA | TT |
| rs2283873 | GG | GG |
| rs1801394 | GG | AA |
| rs326124 | GG | GG |
| rs1801239 | TT | TT |
| rs703062 | TT | CC |
| rs5749135 | TT | CC |
| rs557564 | CC | CC |
| rs117699377 | CG | CC |
| rs1532268 | TT | CC |
| rs2287780 | CC | CC |
| rs10064631 | CG | CC |
| rs526934 | AA | AA |
| rs10925257 | AA | AA |
| rs34324219 | CC | CC |
| rs492602 | AG | AA |
| rs9606756 | AA | AA |
| rs7703033 | GG | GG |
| rs162036 | AA | AA |
| rs11254363 | AA | AA |
| rs3760776 | GG | GG |
| rs708686 | CC | CC |

Risk level: average

**rs1801394:** Polymorphism can lead to elevated homocysteine levels independent of folic acid, vitamin B12 or B6 levels. It is a risk factor for neural tube defects and Down syndrome in the setting of higher homocysteine levels.
[ PMID 10444342 ] [ PMID 10930360 ]

**rs602662:** The polymorphism is associated with reduced levels of vitamin B12 in the blood, this effect may be due to reduced absorption of vitamin B12, such people need additional vitamin B12 supplementation in the form of injections.
[ PMID 18776911 ]

**rs1801133:** A gene fragment known as MTHFR C677T, which encodes an enzyme involved in folic acid metabolism. A break in this gene fragment results in high levels of homocysteine, low levels of B12 and folic acid. If your tests show high homocysteine levels, your doctor will likely advise you on an appropriate diet and supplementation regime. Taking varieties of the active form of B9 methylfolate (5-MTHF or L-methyltetrahydrofolate), the active form of vitamin B12, methylcobalamin, is recommended to reduce your risks.
[ PMID 8616944 ] [ PMID 1522835 ] [ PMID 7647779 ] [ PMID 8554053 ] [ PMID 8554066 ]

**rs601338:** FUT2 gene fragment affects serum vitamin B12 concentration via hologaptocorrin. Presumably reduces the amount of vitamin B12 absorption from food and tablets. Administration of B12 in the form of injections is recommended.
[ PMID 29040465 ] [ PMID 18776911 ]

**rs10925263:** Disorders of intracellular metabolism of cobalamin.
[ PMID 34099811 ]

**rs10064631:** Methionine synthase deficiency, impairing the metabolism of folic acid B9 and cobalamin B12.
[ PMID 10484769 ]

**rs492602:** B12 levels are 1.5 times higher in women.
[ PMID 18776911 ]

## Vitamin K

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs17708472 | GG | GG |
| rs9923231 | CC | CC |
| rs7294 | TT | CC |
| rs2359612 | GG | GG |
| rs9934438 | GG | GG |
| rs2884737 | AA | AA |

Risk level: low

**rs7294:** Polymorphism responsible for the level of sensitivity to warfarin (vitamin K antagonist).
[ PMID 15883587 ] [ PMID 16611750 ] [ PMID 17048007 ] [ PMID 20128861 ]

# Vitamin E (tocopherol)

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs12272004 | CC | CC |
| rs11057830 | CG | GG |
| rs6564851 | TT | TT |
| rs1695 | AG | AA |
| rs964184 | CC | CC |

Risk level: low

**rs11057830:** Involved in lipid and vitamin E metabolism. Genotype is a moderate risk factor for reduced vitamin E levels.
[ PMID 21729881 ] [ PMID 24623848 ] [ PMID 26981194 ] [ PMID 31505768 ]

**rs1695:** When vitamin E is consumed, an increase in IL6 production is observed in carriers of this genotype, i.e. a pro-inflammatory effect is observed.
[ PMID 22572643 ]

# Micronutrients

## Magnesium

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs4561213 | TT | TT |
| rs7045949 | TC | TT |
| rs3750425 | CC | CC |
| rs6560408 | N/A | CC |
| rs7859201 | AC | AA |
| rs4072037 | TA | TT |
| rs2592394 | AA | GG |
| rs13146355 | GG | GG |
| rs448378 | GG | AA |
| rs7965584 | AA | AA |
| rs11144134 | CG | CC |
| rs6584273 | CG | CC |
| rs752010 | CG | CC |
| rs7174119 | AG | AA |
| rs35804026 | AA | TT |
| rs1333343 | TT | TT |
| rs2254229 | TT | TT |
| rs11144085 | GG | GG |
| rs2274925 | AA | AA |
| rs3925584 | CC | TT |



Risk level: average

**rs2592394:** Polymorphism affecting serum magnesium, potassium and sodium levels.
[ PMID 20700443 ]

**rs448378:** Polymorphism affecting serum levels of magnesium, potassium and sodium. Also increases the risk of hypertension.
[ PMID 19430479 ] [ PMID 20700443 ] [ PMID 21129164 ]

**rs7045949:** A genetic variant of melastatin, plays a central role in magnesium homeostasis, which is critical for maintaining glucose and insulin metabolism.
[ PMID 19149903 ]

**rs4072037:** Polymorphism affecting serum levels of magnesium, potassium and sodium. Also associated with risk of gastric cancer.
[ PMID 20700443 ] [ PMID 21427165 ] [ PMID 24782603 ] [ PMID 24810688 ] [ PMID 32269683 ] [ PMID 32595997 ]

**rs752010:** Contributes to decreased serum magnesium levels and increased risk of type 2 diabetes.
[ PMID 23300827 ] [ PMID 31361318 ]

## Calcium

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1801725 | GG | GG |
| rs17251221 | AA | AA |
| rs7647446 | CG | GG |
| rs3804592 | GG | GG |
| rs6438715 | CC | CC |
| rs1802757 | CG | CC |
| rs9869969 | AA | AA |
| rs6438707 | TA | AA |
| rs2202127 | AA | AA |
| rs1042636 | AA | AA |
| rs4765913 | TA | TT |
| rs7295250 | TT | TT |
| rs2239101 | TT | TT |
| rs758231 | CG | GG |
| rs1006737 | AA | GG |
| rs17223925 | CG | GG |
| rs16929471 | GG | GG |
| rs4765905 | CC | GG |
| rs111915616 | CG | GG |
| rs2239097 | TT | CC |
| rs2887780 | TC | TT |
| rs116992907 | CG | CC |
| rs2159100 | TT | CC |
| rs2302729 | CC | CC |
| rs16929470 | CC | CC |
| rs2239089 | AG | GG |
| rs16929486 | AA | AA |
| rs1009281 | GG | AA |
| rs4394887 | GG | GG |

| | | |
|---|---|---|
| rs1006564 | GG | GG |
| rs1108385 | AC | CC |
| rs11831085 | AA | AA |
| rs3794288 | AA | AA |
| rs216013 | AA | AA |
| rs2370251 | TT | CC |
| rs886898 | CC | CC |
| rs7972947 | CC | CC |
| rs142704083 | GG | GG |
| rs58173258 | GG | GG |
| rs60734921 | CC | CC |
| rs10848683 | TT | TT |
| rs2238095 | GG | GG |
| rs12298278 | TT | TT |
| rs4765687 | AA | GG |
| rs7312105 | AA | AA |
| rs4926244 | TT | TT |
| rs16019 | TA | TT |
| rs8109003 | TG | GG |
| rs2304094 | CG | GG |
| rs7250783 | AG | GG |
| rs16016 | CC | CC |
| rs11879128 | CC | TT |
| rs10403191 | TC | CC |
| rs2419549 | AG | GG |
| rs1345649 | AG | AA |
| rs17846914 | AA | AA |
| rs35380374 | TA | TT |
| rs10407144 | TT | TT |
| rs75148188 | TA | TT |
| rs4340440 | CG | GG |
| rs12985786 | CG | GG |

| | | |
|---|---|---|
| rs7250857 | TC | TT |
| rs4926293 | TC | CC |
| rs2900964 | AA | AA |
| rs1422257 | TA | TT |
| rs2292035 | TT | TT |
| rs4632265 | TG | TT |
| rs16027 | CC | CC |
| rs4926152 | CG | CC |
| rs10925298 | TT | TT |
| rs2485570 | TG | TT |
| rs722582 | AG | GG |
| rs6683225 | AC | CC |
| rs10925399 | TC | CC |
| rs6683160 | AC | AA |
| rs918241 | CC | CC |
| rs16834780 | AA | AA |



Risk level: average

**rs1006737:** A polymorphism of the potential-dependent calcium channel gene CACNA1C, is associated with risk of bipolar disorder, schizophrenia and other psychiatric disorders.
[ PMID 18711365 ] [ PMID 19358880 ] [ PMID 20098439 ]

**rs4765913:** CACNA1C gene polymorphism, is associated with risk of bipolar disorder, schizophrenia and other psychiatric disorders.
[ PMID 23025490 ] [ PMID 24339136 ] [ PMID 27271857 ]

## Zinc

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs13266634 | TC | CC |
| rs4908107 | GG | GG |
| rs1505521 | GG | GG |
| rs4646437 | GG | GG |
| rs2072704 | CG | GG |
| rs55901263 | GG | GG |
| rs111811483 | CG | CC |
| rs11558471 | AG | AA |
| rs2466293 | AA | AA |
| rs11781136 | TA | AA |
| rs2047962 | AG | GG |
| rs12522805 | GG | GG |
| rs527392 | TT | TT |
| rs1568569 | GG | GG |
| rs595641 | AG | GG |
| rs17366568 | GG | GG |
| rs7113940 | TT | TT |
| rs3821799 | TT | TT |
| rs185949718 | CG | CC |
| rs7678298 | CC | CC |
| rs17060812 | CG | CC |
| rs896378 | CG | CC |
| rs10488695 | CC | CC |
| rs13427170 | AA | AA |
| rs7833266 | AG | AA |
| rs182052 | GG | GG |
| rs883396 | AG | GG |
| rs10925257 | AA | AA |
| rs1805087 | AA | AA |

| | | |
|---|---|---|
| rs2241767 | TA | AA |
| rs1926740 | TG | GG |
| rs11818989 | TA | TT |
| rs692570 | GG | GG |
| rs2497766 | AG | GG |
| rs12358488 | CG | GG |
| rs2497756 | CG | GG |
| rs6482124 | CC | CC |
| rs2497760 | CG | CC |
| rs7893618 | AG | AA |
| rs573264 | AA | GG |
| rs402311 | TT | TT |
| rs575707 | CC | CC |
| rs848189 | CC | CC |
| rs3781998 | CC | CC |
| rs530532 | GG | AA |
| rs1050631 | AG | GG |
| rs2769264 | TG | TT |



Risk level: average

**rs13266634:** The zinc transporter gene SLC30A8 polymorphism is associated with type 2 diabetes. [ PMID 18162509 ] [ PMID 18210030 ] [ PMID 18400535 ] [ PMID 18628523 ] [ PMID 19590848 ] [ PMID 21810599 ] [ PMID 24757200 ] [ PMID 29093761 ]

**rs11558471:** In this breakdown, zinc intake can cause an increase in fasting glucose levels. [ PMID 21810599 ] [ PMID 23304467 ]

**rs2769264:** Gene variants affecting copper, selenium and zinc content in blood. [ PMID 23720494 ]

## Copper

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs76151636 | GG | GG |
| rs7334118 | TT | TT |
| rs60986317 | GG | GG |
| rs1801249 | AG | GG |
| rs10817465 | CC | CC |
| rs1801248 | CC | CC |
| rs1061472 | TC | CC |
| rs2830051 | TT | TT |
| rs7283136 | TT | TT |
| rs13098532 | TA | TT |
| rs2830008 | TC | TT |
| rs383700 | GG | GG |
| rs7276036 | AG | GG |
| rs2830076 | TC | CC |
| rs3991 | CG | CC |
| rs380417 | CC | TT |
| rs128648 | TC | CC |
| rs13095262 | AA | AA |
| rs462281 | AA | AA |
| rs6516727 | AG | AA |
| rs3008821 | CA | AA |
| rs9689513 | GG | GG |
| rs12515434 | CC | CC |
| rs2984659 | CC | AA |
| rs34259545 | AT | TT |
| rs10147954 | TT | TT |
| rs1955611 | CG | GG |
| rs11623598 | CC | CC |
| rs8020095 | GG | GG |

| | | |
|---|---|---|
| rs3784077 | AA | AA |
| rs10148212 | AA | AA |
| rs11848862 | CC | AA |
| rs7574498 | AA | AA |



Risk level: average

**rs1801249:** Polymorphisms associated with Wilson's disease. Wilson's disease is an inherited disorder in which excess copper is stored in the body.
[ PMID 7626145 ] [ PMID 9887381 ] [ PMID 27398169 ]

## Molybdenum

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs9689513 | GG | GG |
| rs3008821 | CA | AA |
| rs2984659 | CC | AA |
| rs12515434 | CC | CC |
| rs72549324 | TA | TT |
| rs28363581 | TA | TT |
| rs1736557 | GG | GG |
| rs61753344 | GG | GG |
| rs2066532 | CG | GG |
| rs1800822 | CG | CC |
| rs2075992 | TC | CC |
| rs909529 | TC | CC |
| rs10797894 | AA | AA |
| rs2266780 | AA | AA |
| rs1057251 | TT | TT |
| rs491339 | CC | TT |
| rs3744900 | GG | GG |
| rs12454634 | CC | CC |
| rs2848584 | AA | CC |



Risk level: average

**rs72549324:** Mutation in the flavin-containing monooxygenase gene causing fish odour syndrome. [ PMID 10898113 ]

## Iron and ferritin

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1800562 | GG | GG |
| rs9366637 | CC | CC |
| rs855791 | AG | GG |
| rs1799945 | CC | CC |
| rs4880 | AG | AA |
| rs9859260 | TT | TT |
| rs11915082 | AA | GG |
| rs11717368 | CC | CC |
| rs5756506 | GG | GG |
| rs2235321 | GG | GG |
| rs9619658 | CC | CC |
| rs2413450 | TC | CC |
| rs228916 | TT | TT |
| rs2111833 | CC | CC |
| rs5756504 | CC | CC |
| rs2246092 | AA | AA |
| rs4820268 | AG | AA |
| rs4140589 | GG | GG |
| rs62625346 | CG | GG |
| rs7596205 | GG | GG |
| rs1123110 | AG | AA |
| rs1801274 | GG | AA |
| rs1880669 | TC | CC |
| rs8177271 | CG | GG |
| rs3811647 | AG | GG |
| rs2075672 | GG | GG |
| rs1049296 | CC | CC |
| rs1799852 | CC | CC |
| rs17342717 | CC | CC |

| | | |
|---|---|---|
| rs1165196 | GG | AA |
| rs1185567 | AA | GG |
| rs2762353 | AA | GG |
| rs8177191 | GG | GG |
| rs7385804 | AA | AA |
| rs10047462 | TT | TT |
| rs1408272 | TT | TT |
| rs4516970 | GG | GG |
| rs1457451 | GG | GG |
| rs236918 | GG | GG |
| rs2052550 | TA | TT |
| rs13194491 | CC | CC |
| rs973968 | AA | AA |
| rs29880 | AA | AA |
| rs2698530 | AA | AA |
| rs2231164 | TC | CC |
| rs13120400 | TT | TT |
| rs1481012 | AG | GG |
| rs4148155 | AG | AA |
| rs4148152 | TT | TT |
| rs3114018 | CC | AA |
| rs2622604 | CC | TT |
| rs72552713 | GG | GG |
| rs2231142 | TG | GG |
| rs3116448 | TA | AA |
| rs2239484 | AA | AA |
| rs2071594 | GG | GG |
| rs13072552 | TG | GG |
| rs772908 | AG | GG |
| rs960748 | AA | GG |
| rs10455 | AA | GG |
| rs149411 | AA | AA |

| | | |
|---|---|---|
| rs12711924 | AA | GG |
| rs2071302 | TA | TT |



Risk level: average

**rs12711924:** Regulates the interaction between dietary heme iron intake and the risk of developing type 2 diabetes.
[ PMID 23386860 ]

**rs855791:** Variant in transferrin genes as potential risk markers for iron deficiency anaemia. Affects haemoglobin A1(C) levels through glycaemic and non-glycaemic pathways.
[ PMID 19820698 ] [ PMID 19880490 ] [ PMID 20858683 ] [ PMID 21208937 ] [ PMID 21978626 ] [ PMID 22323359 ]

**rs4880:** Polymorphism of antioxidant enzymes as risk factors for complications, leads to increased oxidative stress. Affects the level of selenium in serum.
[ PMID 19074884 ] [ PMID 21052528 ]

**rs2413450:** The gene variant alters hepcidin but not plasma iron in response to oral iron administration in healthy adults. Hepcidin is a peptide hormone, a universal humoral regulator of plasma iron concentration and distribution in tissues.
[ PMID 27332551 ] [ PMID 33850216 ] [ PMID 34790739 ]

**rs4820268:** A common variant of the TFR2 gene involved in the physiological regulation of serum iron levels and with an increased risk of iron deficiency anaemia.
[ PMID 19880490 ] [ PMID 21208937 ] [ PMID 21978626 ] [ PMID 22323359 ] [ PMID 24966834 ]

**rs1123110:** Breakdown affects the association between dietary haem iron intake and risk of developing type 2 diabetes.
[ PMID 23386860 ]

**rs1880669:** Single nucleotide polymorphisms in genes associated with serum iron and ferritin levels.
[ PMID 19673882 ] [ PMID 22761678 ] [ PMID 24121126 ]

**rs3811647:** Genetic determinants of body iron stores and risk of type 2 diabetes.
[ PMID 19820699 ] [ PMID 20095037 ] [ PMID 22815867 ] [ PMID 24391736 ] [ PMID 27255824 ]

## Manganese

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1568569 | GG | GG |
| rs4872479 | CG | GG |
| rs17060812 | CG | CC |
| rs896378 | CG | CC |
| rs7833266 | AG | AA |
| rs13103835 | AT | TT |
| rs2165265 | AT | TT |
| rs151402 | CG | GG |
| rs4588460 | TA | TT |
| rs13126885 | TC | CC |
| rs151392 | CG | CC |
| rs7664683 | CC | CC |
| rs4699012 | AA | AA |
| rs2298752 | CG | GG |
| rs151401 | AG | AA |
| rs7699390 | AA | AA |
| rs6700061 | TC | CC |
| rs4846607 | AG | GG |



Risk level: average

## Potassium

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs2234916 | TA | AA |
| rs12079419 | CG | CC |
| rs10854373 | TC | CC |
| rs16890334 | TT | TT |
| rs2030114 | AG | GG |
| rs10930597 | CC | CC |
| rs11887188 | TC | CC |
| rs9282564 | TT | TT |
| rs55852620 | TA | TT |
| rs2032588 | CG | GG |
| rs3789243 | AA | GG |
| rs10276036 | TT | TT |
| rs4148737 | TT | TT |
| rs1922240 | TT | TT |
| rs12720067 | CG | CC |
| rs3842 | TT | TT |
| rs7787082 | CG | GG |
| rs1128503 | GG | GG |
| rs2235033 | GG | AA |
| rs4148740 | AA | AA |
| rs2032583 | AA | AA |
| rs3213619 | AA | AA |
| rs3747802 | AA | AA |
| rs10808071 | CA | AA |
| rs7218917 | GG | GG |
| rs9894841 | TC | TT |
| rs62070884 | CC | CC |
| rs2247810 | TC | TT |
| rs13050198 | TA | TT |

| | | |
|---|---|---|
| rs2211698 | GG | GG |
| rs727957 | GG | GG |
| rs3453 | CC | TT |
| rs1805127 | CC | CC |
| rs2834485 | AA | AA |
| rs11088283 | AG | AA |
| rs1892593 | GG | GG |



Risk level: average

**rs3453:** Potassium channel regulatory subunit gene associated with risk of hearing loss.
[ PMID 32207011 ]

**rs2234916:** Potassium channel gene polymorphisms and increased risk of heart disease.
[ PMID 12402336 ] [ PMID 14661677 ]

## Selenium

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs12151188 | CC | CC |
| rs2769264 | TG | TT |
| rs4325816 | TT | TT |
| rs11548 | CC | CC |
| rs9637365 | CC | TT |
| rs10412049 | TC | CC |
| rs2769265 | AC | CC |
| rs2264132 | CC | CC |
| rs3733548 | TA | AA |
| rs9420 | CG | GG |
| rs11718498 | AA | GG |
| rs10173522 | AC | CC |
| rs6539137 | TA | TT |
| rs3788317 | GG | GG |
| rs9606186 | CG | GG |
| rs11541479 | GG | GG |
| rs10861192 | CG | CC |
| rs13306278 | CC | CC |
| rs4630362 | CG | CC |
| rs147285094 | CC | CC |
| rs9332314 | CG | CC |
| rs3788314 | AG | AA |
| rs756661 | AG | AA |
| rs4880 | AG | AA |

Risk level: average

**rs9637365:** Selenoprotein gene polymorphism affecting the risk of selenium deficiency.
[ PMID 22615972 ]

**rs2769264:** Gene variants affecting copper, selenium and zinc content in blood.
[ PMID 23720494 ]

**rs4880:** Polymorphism of antioxidant enzymes as risk factors for complications, leads to increased oxidative stress. Affects the level of selenium in serum.
[ PMID 19074884 ] [ PMID 21052528 ]

# Iodine

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs2048722 | CG | GG |
| rs1126799 | TC | CC |
| rs13398180 | TC | CC |
| rs45602038 | CG | CC |
| rs6588678 | GG | GG |
| rs4927608 | TA | AA |
| rs13431646 | CC | CC |
| rs6732480 | CG | CC |
| rs4927606 | CC | CC |
| rs10519477 | CC | CC |
| rs11694726 | CC | CC |
| rs7602332 | CC | CC |
| rs2071403 | AG | GG |
| rs13424221 | CG | GG |
| rs1567919 | CC | CC |



Risk level: average

**rs2048722:** Polymorphism in the thyroid peroxidase gene, is associated with the development of autoimmune thyroid disease and serum levels of thyroid peroxidase antibodies.
[ PMID 28845025 ]

**rs45602038:** Sodium iodide symporter gene polymorphism, increases the likelihood of developing thyroid cancer.
[ PMID 26160439 ]

**rs2071403:** The phosphodiesterase gene is associated with serum TTG levels and thyroid function.
[ PMID 18514160 ] [ PMID 24722205 ] [ PMID 28845025 ]

## Methylation and homocysteine

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1801131 | TG | TT |
| rs2236225 | AG | GG |
| rs1805087 | AA | AA |
| rs1801394 | GG | AA |
| rs1801133 | AG | GG |
| rs567754 | CC | CC |
| rs162036 | AA | AA |
| rs1800779 | AG | AA |
| rs1799983 | CG | GG |
| rs3741049 | AA | GG |
| rs819171 | TA | TT |
| rs651852 | CG | CC |
| rs3733890 | AG | GG |
| rs1051266 | CC | TT |
| rs10380 | CC | CC |
| rs1979277 | CG | GG |
| rs17367504 | AA | AA |
| rs4680 | AG | GG |
| rs4633 | TC | CC |
| rs17349743 | TT | TT |
| rs11754661 | GG | GG |
| rs2287780 | CC | CC |
| rs651933 | AG | GG |
| rs526934 | AA | AA |
| rs6495446 | CC | CC |
| rs9606756 | AA | AA |
| rs234706 | AG | GG |
| rs4244593 | TT | GG |
| rs1476413 | TC | CC |

| | | |
|---|---|---|
| rs1076991 | CG | CC |
| rs2274976 | CC | CC |
| rs502396 | TT | CC |
| rs1131603 | TT | TT |
| rs7946 | TT | CC |
| rs4820889 | GG | GG |
| rs2283873 | GG | GG |
| rs4654748 | CC | CC |
| rs1999594 | AA | AA |
| rs1802059 | AA | GG |



Risk level: average

**rs1801394:** Polymorphism can lead to elevated homocysteine levels independent of folic acid, vitamin B12 or B6 levels. It is a risk factor for neural tube defects and Down syndrome in the setting of higher homocysteine levels.
[ PMID 10444342 ] [ PMID 10930360 ]

**rs3741049:** The gene defect causes 3-ketothiolase deficiency, which causes the growth of intestinal microbes (especially clostridia) and negatively affects methylation.

**rs1051266:** The protein encoded by the gene transports folic acid into the cell and thus plays a role in the intracellular regulation of folate concentration. In this genotype, folate absorption is worse. Folic acid requirement is higher. Alcohol consumption is more critical for the risk of vitamin B9 deficiency.
[ PMID 19172696 ] [ PMID 19650776 ]

**rs7946:** Genetic polymorphisms in methyl group metabolism DNA methylation in peripheral blood. Affect the human need for choline (vitamin B4).
[ PMID 18789905 ] [ PMID 22371529 ] [ PMID 16816108 ]

**rs1801131:** Reduces the formation of the active form of folic acid, which is necessary for the remethylation of homocysteine and other DNA molecules. Administration of the active form of folic acid (5-MTHF or L-methyltetrahydrofolate) can significantly improve risk scores for the effects of mutations. Also a factor that moderately increases the need for vitamin B2.
[ PMID 11742092 ] [ PMID 11752418 ] [ PMID 11590551 ] [ PMID 15951337 ] [ PMID 16244782 ]

**rs2236225:** Possible increased risk of fetal birth defects. A 1.5-fold higher risk for Caucasian mothers to give birth to children with DNT (neural tube defect). The association in children with this mutation with an increased risk of heart defects is greater if their mother did not get enough folic acid during pregnancy. The risk is reduced with adequate levels of folic acid and vitamin B6.
[ PMID 18767138 ] [ PMID 20544798 ] [ PMID 20890936 ]

**rs1801133:** A gene fragment known as MTHFR C677T, which encodes an enzyme involved in folic acid metabolism. A break in this gene fragment results in high levels of homocysteine, low levels of B12 and folic acid. If your tests show high homocysteine levels, your doctor will likely advise you on an appropriate diet and supplementation regime. Taking varieties of the active form of B9 methylfolate (5-MTHF or

L-methyltetrahydrofolate), the active form of vitamin B12, methylcobalamin, is recommended to reduce your risks.
[ PMID 8616944 ] [ PMID 1522835 ] [ PMID 7647779 ] [ PMID 8554053 ] [ PMID 8554066 ]

**rs1800779:** Gene polymorphisms are associated with cardiovascular disease risk markers, impaired methylation.

## Gluten and celiac disease

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs2187668 | CC | CC |
| rs2858331 | GG | AA |
| rs4988889 | CG | GG |
| rs6441961 | CC | TT |
| rs6822844 | TG | GG |
| rs13119723 | AA | AA |
| rs2395182 | TT | TT |
| rs9851967 | TT | CC |
| rs7775228 | TT | TT |
| rs4713586 | AA | AA |
| rs3184504 | TC | CC |
| rs231775 | AA | AA |
| rs1464510 | CG | CC |
| rs1738074 | TC | TT |
| rs2816316 | TA | AA |
| rs45450798 | CG | CC |



Risk level: average

**rs2858331:** Together with the rs4988889 gene breakage, it is a diagnostic criterion for celiac disease.

**rs6441961:** Increased risk of gluten disease.
[ PMID 19693089 ] [ PMID 19542083 ] [ PMID 22087237 ]

**rs9851967:** Genetic risk of celiac disease associated with immune response.
[ PMID 18311140 ]

**rs4988889:** Together with the rs2858331 gene breakage, it is a diagnostic criterion for celiac disease.

**rs6822844:** Combined with the rs13119723 breakage, the study showed the strongest association with celiac disease among Caucasian patients.
[ PMID 17558408 ]

**rs3184504:** A variant of celiac disease genetic risk associated with immune response. Also carrier

associated type 1 diabetes.
[ PMID 18311140 ] [ PMID 18978792 ] [ PMID 19073967 ] [ PMID 20546165 ] [ PMID 20854658 ] [ PMID 21873553 ] [ PMID 24936253 ]

**rs1464510:** Common genetic variant in type 1 diabetes and celiac disease.
[ PMID 18311140 ] [ PMID 19073967 ] [ PMID 20854658 ] [ PMID 22087237 ]

**rs2816316:** Genetic variant risk for type 1 diabetes and gluten disease.
[ PMID 18311140 ] [ PMID 19073967 ] [ PMID 19622889 ] [ PMID 20854658 ] [ PMID 21980299 ] [ PMID 27015091 ]

# Lactose

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs4988235 | AG | AA |
| rs182549 | TC | TT |
| rs2278544 | AA | AA |
| rs2322659 | TC | TT |
| rs2304371 | AG | AA |
| rs145946881 | CC | CC |



Risk level: average

**rs4988235:** Is one of two SNPs linked to the primary haplotype associated with hypolactasia, more commonly known as lactose intolerance in European populations.
[ PMID 11788828 ] [ PMID 15114531 ] [ PMID 25625576 ]

## Omega-3, unsaturated fatty acids

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1535 | AG | AA |
| rs174556 | TC | CC |
| rs174561 | TA | TT |
| rs174575 | GC | CC |
| rs3834458 | TA | TT |
| rs174553 | AA | AA |
| rs99780 | CG | CC |
| rs174583 | TC | CC |
| rs174448 | AG | GG |
| rs174547 | TC | TT |
| rs174546 | TC | CC |
| rs174550 | TC | TT |
| rs174548 | GC | CC |
| rs174602 | TC | TT |
| rs174593 | TC | TT |
| rs174579 | CG | CC |
| rs174570 | CC | CC |
| rs174618 | TC | TT |
| rs2727270 | TC | CC |
| rs498793 | CC | CC |
| rs174577 | AC | CC |
| rs174576 | AC | CC |
| rs2072114 | AG | AA |
| rs2277324 | GG | GG |
| rs16940765 | TT | TT |
| rs17718324 | CG | GG |
| rs953413 | CG | GG |
| rs174537 | TG | GG |
| rs1570069 | AA | AA |

| | | |
|---|---|---|
| rs3798719 | CG | CC |
| rs7744440 | TA | TT |



Risk level: average

**rs1535:** FADS2 polymorphisms affect blood levels of omega-3 and omega-6 polyunsaturated fatty acids during pregnancy, at birth, and at age 7 years.
[ PMID 22194195 ] [ PMID 24643342 ] [ PMID 26950146 ] [ PMID 31991592 ] [ PMID 33509958 ]

**rs174556:** FADS gene polymorphisms increase arachidonic acid levels and risk of Alzheimer's disease.
[ PMID 21599946 ] [ PMID 21818279 ] [ PMID 28929400 ]

**rs174561:** FADS gene polymorphism alters serum glycerophospholipid fatty acid concentrations and their percentage composition in children.
[ PMID 21818279 ]

**rs174575:** Variants in the FADS gene modify the relationship between fish consumption and docosahexaenoic acid content in breast milk. This in turn affects the child's cognitive function and hyperactivity/attention problems.
[ PMID 18936223 ] [ PMID 20335541 ] [ PMID 23737301 ] [ PMID 30541029 ]

**rs3834458:** Single nucleotide polymorphism rs3834458 affects levels of n-3 long-chain polyunsaturated fatty acids.
[ PMID 31487670 ]

**rs174583:** Fatty acid desaturase gene polymorphism increases insulin resistance in association with serum phospholipid polyunsaturated fatty acid composition.
[ PMID 21513558 ]

**rs174448:** The gene polymorphism alters EPA and DHA levels and their effects in brain development and function.
[ PMID 26742060 ] [ PMID 26950146 ]

**rs174547:** Genetic variants that affect circulating lipid levels and risk of cardiovascular disease. People with the C gene variant have lower levels of long forms of fatty acids such as AA. Vegetarians and vegans with the C gene variant have lower plasma concentrations of EPA, DHA and AA than omnivores. Vegetarians with the C gene variant have been shown to benefit from omega-3 supplements or omega-3 rich foods such as chia seeds, flax seeds and canola oil.
[ PMID 19750004 ] [ PMID 20864672 ] [ PMID 20972250 ] [ PMID 29858861 ]

## CBD oil (cannabidiol).

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs806368 | CC | TT |
| rs2494732 | CG | CC |
| rs6454674 | TT | TT |
| rs9900808 | GG | GG |
| rs4680 | AG | GG |
| rs1049353 | CC | CC |
| rs806377 | TT | TT |
| rs324420 | CC | CC |
| rs1057910 | AC | AA |
| rs1417205 | AA | AA |



Risk level: average

**rs806368:** A break in the cannabinoid receptor gene CNR1 modulates the risk of addiction. Cannabis dependence may occur when CBD oil is ingested.
[ PMID 17509535 ] [ PMID 19016476 ]

**rs2494732:** The AKT1 genotype affects the risk of developing psychosis in cannabis users. It also increases the risk of schizophrenia in people with a break in this gene.
[ PMID 21041608 ] [ PMID 22831980 ] [ PMID 24904437 ] [ PMID 32536252 ]

**rs4680:** The study showed a 10% increase in total plasma homocysteine (tHcy)
[ PMID 18064318 ]

## Oxidative stress

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs662 | CC | CC |
| rs1800566 | GG | GG |
| rs4880 | AG | AA |
| rs10517 | GG | GG |
| rs6539137 | TA | TT |
| rs4135168 | TC | TT |
| rs2551715 | CC | CC |
| rs2978663 | TT | TT |
| rs3730192 | TA | TT |
| rs17881586 | CG | GG |
| rs17881734 | CG | GG |
| rs10861192 | CG | CC |
| rs1138272 | CC | CC |
| rs4630362 | CG | CC |
| rs769217 | TT | CC |
| rs147285094 | CC | CC |
| rs1041740 | TT | CC |
| rs4135183 | TC | CC |
| rs17881288 | TA | AA |
| rs2551698 | AA | AA |
| rs2978662 | AA | AA |
| rs8190996 | AG | GG |
| rs2001350 | TT | TT |
| rs2297518 | GG | GG |

Risk level: average

**rs1041740:** A break in the gene that is responsible for the effects of oxidative stress in pregnant women on fetal development.
[ PMID 25463281 ]

**rs4880:** Polymorphism of antioxidant enzymes as risk factors for complications, leads to increased oxidative stress. Affects the level of selenium in serum.
[ PMID 19074884 ] [ PMID 21052528 ]

## Carnitine

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs2229738 | CC | CC |
| rs2229291 | TT | TT |
| rs1871748 | CG | CC |
| rs151003641 | CC | CC |
| rs74315298 | CC | CC |
| rs1799821 | AG | GG |
| rs370493 | AG | AA |
| rs1799822 | AA | AA |
| rs2278907 | AA | AA |
| rs28383481 | GG | GG |
| rs72552726 | GG | GG |
| rs274567 | TT | CC |
| rs2631367 | CG | GG |
| rs274551 | CG | CC |
| rs189174414 | TT | TT |
| rs3019593 | TA | TT |
| rs2924689 | TA | TT |
| rs2924685 | AT | TT |
| rs3019578 | CC | CC |
| rs191107774 | CC | CC |
| rs1017640 | CG | CC |
| rs7938117 | AG | GG |
| rs7112615 | AA | AA |
| rs897047 | TA | AA |
| rs11568520 | CC | CC |

Risk level: average

**rs1799821:** Carnitine palmitoyltransferase polymorphism is associated with multiple syndromes of acute encephalopathy in various infectious diseases. Genetic risk factor for common acute encephalopathy.
[ PMID 20934285 ]

**rs2631367:** OCTN carnitine transporter polymorphism is associated with inflammatory bowel disease, Crohn's disease.
[ PMID 23300620 ] [ PMID 15107849 ] [ PMID 18756601 ]

## Neurotransmitters and hormones

## Serotonin

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs7224199 | TA | TT |
| rs28914829 | CG | GG |
| rs11657536 | GG | GG |
| rs140700 | CC | CC |
| rs2066713 | GG | GG |
| rs1042173 | CC | AA |
| rs6314 | GG | GG |
| rs9316232 | GG | GG |
| rs2224721 | GG | GG |
| rs6313 | AA | GG |
| rs1928040 | CG | GG |
| rs7984966 | CC | CC |
| rs9567737 | TT | CC |
| rs9316233 | CG | CC |
| rs7997012 | GG | AA |
| rs9567746 | AA | AA |
| rs6312 | TT | TT |
| rs1805055 | CG | GG |
| rs6305 | CG | GG |
| rs7330636 | TT | CC |
| rs1328674 | CC | CC |
| rs6311 | TT | CC |
| rs12583882 | AA | AA |
| rs3742278 | AA | AA |
| rs2020933 | AA | AA |
| rs11077820 | TC | TT |
| rs56232120 | CG | GG |
| rs35815285 | CG | GG |

| | | |
|---|---|---|
| rs11604247 | CG | CC |
| rs1062613 | TT | CC |
| rs1176713 | AA | AA |
| rs2276302 | GG | AA |
| rs17288723 | TT | TT |
| rs1487278 | TA | TT |
| rs10879346 | CC | CC |
| rs1843809 | TT | TT |
| rs1799913 | TT | GG |
| rs4570625 | GG | GG |
| rs9325202 | GG | GG |
| rs2129785 | TT | TT |
| rs4565946 | TT | CC |
| rs6295 | GG | GG |
| rs1386494 | CG | CC |
| rs11179003 | CC | CC |
| rs11568817 | TA | AA |
| rs10748189 | CG | CC |
| rs17110563 | CC | CC |
| rs6296 | CC | CC |
| rs11867581 | AA | GG |
| rs878567 | CG | GG |
| rs211107 | AA | CC |
| rs1386488 | AA | AA |
| rs17722134 | AA | AA |
| rs201779669 | TA | TT |
| rs147198243 | TT | TT |
| rs145278314 | TA | TT |
| rs34550504 | TA | TT |
| rs200889198 | GG | GG |
| rs61907889 | GG | GG |
| rs79874540 | CG | GG |

| | | |
|---|---|---|
| rs12805047 | GG | GG |
| rs118187155 | AC | CC |
| rs114014601 | CG | CC |
| rs35201864 | CG | CC |
| rs79779791 | CG | CC |
| rs146411553 | CG | CC |
| rs1549339 | AG | AA |
| rs2276307 | AA | AA |
| rs146375175 | AA | AA |
| rs76303657 | TA | AA |
| rs45570136 | AA | AA |
| rs676643 | CG | GG |
| rs130060 | AA | AA |
| rs17706602 | CG | CC |
| rs7725785 | CC | CC |
| rs78932366 | TA | AA |



Risk level: average

**rs1042173:** The serotonin transporter gene SLC6A4 is associated with premenopausal and perimenopausal hot flashes and headache.
[ PMID 21585624 ] [ PMID 25026114 ]

**rs6313:** TPH-2 polymorphisms affect response to treatment with antidepressants and SSRIs.
[ PMID 19184136 ] [ PMID 19197363 ] [ PMID 21172166 ] [ PMID 25108775 ] [ PMID 27091189 ] [ PMID 27445478 ] [ PMID 27521242 ] [ PMID 32819202 ]

**rs7997012:** Associations of the serotonin receptor gene HTR2A with bipolar disorder and major depressive disorder.
[ PMID 19428704 ] [ PMID 24885933 ] [ PMID 30178121 ]

**rs6311:** Genetic factors specific to obsessive-compulsive disorder.
[ PMID 25017045 ] [ PMID 26616111 ] [ PMID 28576508 ] [ PMID 29331882 ] [ PMID 29785111 ]

**rs1062613:** Fear reactivation and symptoms of combat-related PTSD: specificity and preliminary study of the effect of the 5-HT3A receptor gene.
[ PMID 35413654 ]

**rs2276302:** The HTR3B gene is associated with alcoholism with antisocial behaviour.
[ PMID 19185213 ]

**rs1799913:** Variants in the tryptophan hydroxylase gene involved in the development and treatment of opiate, heroin and cocaine addiction.
[ PMID 18181017 ] [ PMID 20201854 ] [ PMID 26227246 ] [ PMID 28590957 ]

**rs7224199:** Association with major depression and response to antidepressants. The polymorphism is associated with selective serotonin and serotonin-norepinephrine reuptake inhibitor response in depressive disorder.
[ PMID 19844206 ] [ PMID 26674707 ]

## Dopamine

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1611115 | CC | CC |
| rs5320 | GG | GG |
| rs2519154 | TC | CC |
| rs2007153 | CC | CC |
| rs1611123 | TC | CC |
| rs5322 | CG | CC |
| rs1108580 | AG | AA |
| rs1541332 | AG | AA |
| rs3025382 | GG | GG |
| rs1108581 | AA | AA |
| rs77905 | AG | GG |
| rs3025399 | AA | AA |
| rs10993949 | AA | AA |
| rs4703822 | GG | GG |
| rs26907 | GG | GG |
| rs17410422 | CG | CC |
| rs1800497 | AG | GG |
| rs1049353 | CC | CC |
| rs6265 | CC | CC |
| rs2295193 | AA | AA |
| rs324420 | CC | CC |
| rs17030795 | AG | AA |
| rs8044769 | TC | CC |
| rs6280 | TT | TT |
| rs4867798 | TA | TT |
| rs1125394 | TA | TT |
| rs4436578 | TA | TT |
| rs1799978 | TT | TT |
| rs4648317 | GG | GG |

| | | |
|---|---|---|
| rs6277 | CG | GG |
| rs3773678 | AG | GG |
| rs4532 | CC | TT |
| rs2440390 | CG | CC |
| rs1079597 | CC | CC |
| rs2283265 | AC | CC |
| rs5326 | CC | CC |
| rs1076560 | CC | CC |
| rs752306 | CC | CC |
| rs265981 | AA | GG |
| rs686 | GG | AA |
| rs1076563 | AA | AA |
| rs1486009 | AA | AA |
| rs9824856 | TA | AA |
| rs167771 | AG | AA |
| rs12364283 | AA | AA |
| rs9288993 | AA | AA |
| rs4460839 | TA | TT |
| rs12363125 | TC | CC |
| rs1800499 | CG | CC |
| rs11214606 | CC | CC |
| rs2734838 | AG | AA |
| rs2734833 | AG | GG |
| rs1079598 | TA | AA |
| rs3776512 | GG | GG |
| rs460000 | GG | GG |
| rs27072 | CC | CC |
| rs6347 | TT | TT |
| rs2617605 | CC | TT |
| rs28363168 | CG | CC |
| rs921451 | TA | TT |
| rs2242446 | TC | TT |

| | | |
|---|---|---|
| rs1006737 | AA | GG |
| rs968529 | CC | CC |
| rs4633 | TC | CC |
| rs10761482 | CC | CC |
| rs2159100 | TT | CC |
| rs3735273 | CG | CC |
| rs10994336 | CC | CC |
| rs3785143 | CG | CC |
| rs2302729 | CC | CC |
| rs165599 | AA | AA |
| rs6269 | AG | AA |
| rs216013 | AA | AA |
| rs7633291 | TA | TT |
| rs324026 | AA | TT |
| rs167770 | AA | AA |
| rs7876027 | TT | TT |
| rs3025422 | TA | TT |



Risk level: average

**rs4532:** Affects dopamine D1 receptors associated with autism spectrum disorders.
[ PMID 18205172 ]

**rs1006737:** A polymorphism of the potential-dependent calcium channel gene CACNA1C, is associated with risk of bipolar disorder, schizophrenia and other psychiatric disorders.
[ PMID 18711365 ] [ PMID 19358880 ] [ PMID 20098439 ]

**rs1611123:** A gene variant that increases nicotine dependence and difficulty quitting smoking.
[ PMID 24667010 ]

**rs1108580:** Dopaminergic pathway gene polymorphism and genetic predisposition to Parkinson's disease and schizophrenia.
[ PMID 20016224 ] [ PMID 20498626 ] [ PMID 28647493 ] [ PMID 31082450 ]

**rs1800497:** TaqIA polymorphisms of the DRD2 dopamine D2 receptor gene are associated with concomitant alcohol use and depressive disorders.
[ PMID 1969501 ] [ PMID 9650634 ] [ PMID 17989061 ] [ PMID 20146828 ] [ PMID 20180986 ] [ PMID 20482509 ] [ PMID 21083670 ] [ PMID 22698582 ] [ PMID 22728571 ] [ PMID 22978509 ]

**rs4867798:** Breakage of the dopamine D1 receptor gene increases the risk of paranoid schizophrenia.

[ PMID 21955727 ]  [ PMID 24790447 ]

**rs1125394:** The DRD2 polymorphism modulates reward and emotion processing, dopamine neurotransmission, and openness to experience.
[ PMID 22424959 ]

**rs4436578:** The dopamine D2 receptor gene is associated with weight gain in schizophrenic patients with long-term treatment with neuroleptics.
[ PMID 20375926 ]  [ PMID 21185230 ]  [ PMID 27853387 ]

# Oxytocin and empathy

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs53576 | GG | GG |
| rs2254298 | CG | GG |
| rs918316 | TT | TT |
| rs2268492 | CG | CC |
| rs2268491 | CC | CC |
| rs8043440 | TA | TT |
| rs981347 | TC | TT |
| rs4906679 | TT | TT |
| rs6265 | CC | CC |
| rs237899 | AG | GG |
| rs8192466 | GG | GG |
| rs3751582 | TC | TT |
| rs925946 | GG | TT |
| rs3212335 | CC | CC |



Risk level: average

**rs2254298:** Oxytocin receptor gene polymorphism interacts with familial risk of psychopathology to predict symptoms of depression and anxiety.
[ PMID 17383819 ] [ PMID 18207134 ] [ PMID 19515497 ] [ PMID 20585395 ] [ PMID 20708845 ] [ PMID 22336563 ] [ PMID 22357335 ]

**rs3751582:** GABRB3 a candidate gene for autism spectrum disorders.
[ PMID 24999380 ]

# Adrenalin

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1801253 | GC | CC |
| rs1042714 | GG | CC |
| rs1800888 | CC | CC |
| rs1042711 | TA | TT |
| rs1042713 | GG | GG |
| rs1801704 | TA | TT |



Risk level: average

**rs1042714:** Studies have shown an increased risk of polymorphism with autism. The odds ratio was 1.33-1.60. The risk was about twice as high among mothers who had clinical markers of pregnancy-related stress. The breakdown also indicated a predisposition to metabolic syndrome, obesity and increased risk of bronchial asthma.
[ PMID 9275150 ] [ PMID 14557466 ] [ PMID 15867853 ] [ PMID 16935688 ] [ PMID 17199132 ] [ PMID 17512307 ]

**rs1801253:** Polymorphism of a conserved beta(1)-adrenergic receptor motif alters cardiac function and is associated with acute coronary syndrome and cardiovascular risk factors.
[ PMID 16844790 ] [ PMID 26602751 ] [ PMID 35099251 ] [ PMID 35199539 ]

**rs1042711:** A polymorphism of the beta-2 adrenergic receptor gene is associated with an increased risk of arterial hypertension.
[ PMID 27103841 ]

**rs1801704:** A break in the ?2-adrenoreceptor gene increases the likelihood of insulin resistance and polycystic ovarian syndrome.
[ PMID 22900502 ]

## Cortisol

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1360780 | CG | CC |
| rs10482633 | TG | TT |
| rs6190 | CC | CC |
| rs6189 | CG | CC |
| rs9324921 | CC | CC |
| rs852977 | AG | AA |
| rs5522 | TT | TT |
| rs1724385 | CG | GG |
| rs1490453 | GG | GG |
| rs17024387 | AG | GG |
| rs3846329 | GG | GG |
| rs1724422 | AA | AA |
| rs2871 | TA | TT |
| rs4635799 | TA | TT |
| rs3846317 | CC | CC |
| rs6836191 | CC | TT |
| rs1876829 | TA | TT |
| rs7698307 | CC | CC |
| rs17484454 | CC | TT |
| rs13184611 | CG | CC |
| rs13116332 | GG | GG |
| rs7757037 | AG | GG |
| rs110402 | AA | AA |
| rs7658048 | AG | GG |
| rs6812904 | GG | AA |
| rs11655764 | AG | GG |
| rs2766535 | AA | GG |
| rs3800373 | AC | AA |
| rs17024708 | AA | AA |

| | | |
|---|---|---|
| rs1617406 | TA | AA |
| rs941601 | CC | CC |



Risk level: average

**rs1360780:** Polymorphisms in the FK506 protein gene are associated with attention deficit hyperactivity disorder and increased daily cortisol levels. It is also associated with an increased risk of depression with an odds ratio of 1.39.
[ PMID 21316860 ] [ PMID 24166410 ] [ PMID 26032970 ]

**rs10482633:** Genetic variation in the HPA axis is associated with cortisol response and cognitive function during acute stress.
[ PMID 29100174 ]

**rs6189:** A genetic variant in the glucocorticoid receptor gene increases the severity of PTSD and depressive disorders.
[ PMID 33019527 ] [ PMID 34466443 ]

**rs3800373:** FKBP5 polymorphisms increase symptoms of PTSD and anxiety.
[ PMID 27078785 ] [ PMID 27448712 ]

## Mitochondrial function

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs11754661 | GG | GG |
| rs999571 | CG | GG |
| rs1801394 | GG | AA |
| rs2297518 | GG | GG |
| rs2238151 | TC | CC |
| rs1076991 | CG | CC |
| rs968529 | CC | CC |
| rs3783637 | TC | CC |
| rs1532268 | TT | CC |
| rs16941667 | CC | CC |
| rs10064631 | CG | CC |
| rs2236225 | AG | GG |
| rs1800779 | AG | AA |
| rs4850 | CG | GG |
| rs4869089 | AA | AA |
| rs162036 | AA | AA |
| rs7703033 | GG | GG |
| rs1985908 | AG | AA |
| rs16941669 | TG | TT |
| rs1051266 | CC | TT |
| rs2778475 | AG | GG |
| rs7254913 | AA | AA |
| rs1244414 | CC | CC |
| rs1104739 | CC | AA |
| rs34095989 | GG | GG |
| rs35859650 | GG | GG |
| rs17602729 | AG | GG |
| rs926938 | AG | GG |
| rs34677591 | GG | GG |

| | | |
|---|---|---|
| rs11214077 | AA | AA |
| rs12985380 | AG | GG |
| rs3786625 | AG | GG |
| rs11203289 | GG | GG |
| rs33927012 | AA | AA |
| rs2307440 | CG | GG |
| rs2307449 | TT | TT |
| rs2307441 | TT | TT |
| rs3087374 | CC | CC |
| rs12873870 | CG | CC |
| rs667226 | AA | TT |
| rs536662 | CG | GG |
| rs3790694 | CG | CC |
| rs2073643 | TT | TT |
| rs25683 | AG | AA |
| rs17349743 | TT | TT |
| rs4880 | AG | AA |
| rs11585941 | AA | AA |
| rs12770829 | CG | CC |
| rs1024611 | AG | AA |
| rs7946 | TT | CC |
| rs4244593 | TT | GG |
| rs671 | GG | GG |



Risk level: average

**rs1801394:** Polymorphism can lead to elevated homocysteine levels independent of folic acid, vitamin B12 or B6 levels. It is a risk factor for neural tube defects and Down syndrome in the setting of higher homocysteine levels.
[ PMID 10444342 ] [ PMID 10930360 ]

**rs1051266:** The protein encoded by the gene transports folic acid into the cell and thus plays a role in the intracellular regulation of folate concentration. In this genotype, folate absorption is worse. Folic acid requirement is higher. Alcohol consumption is more critical for the risk of vitamin B9 deficiency.

[ PMID 19172696 ]  [ PMID 19650776 ]

**rs7946:** Genetic polymorphisms in methyl group metabolism DNA methylation in peripheral blood. Affect the human need for choline (vitamin B4).
[ PMID 18789905 ]  [ PMID 22371529 ]  [ PMID 16816108 ]

**rs10064631:** Methionine synthase deficiency, impairing the metabolism of folic acid B9 and cobalamin B12.
[ PMID 10484769 ]

**rs2236225:** Possible increased risk of fetal birth defects. A 1.5-fold higher risk for Caucasian mothers to give birth to children with DNT (neural tube defect). The association in children with this mutation with an increased risk of heart defects is greater if their mother did not get enough folic acid during pregnancy. The risk is reduced with adequate levels of folic acid and vitamin B6.
[ PMID 18767138 ]  [ PMID 20544798 ]  [ PMID 20890936 ]

**rs1800779:** Gene polymorphisms are associated with cardiovascular disease risk markers, impaired methylation.

**rs17602729:** AMPD1 gene polymorphism, is associated with speed, endurance and strength.
[ PMID 21540342 ]  [ PMID 23681449 ]  [ PMID 35309536 ]

**rs4880:** Polymorphism of antioxidant enzymes as risk factors for complications, leads to increased oxidative stress. Affects the level of selenium in serum.
[ PMID 19074884 ]  [ PMID 21052528 ]

## Memory

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs17070145 | TC | TT |
| rs10884402 | AA | GG |
| rs7078098 | TA | TT |
| rs950809 | AA | AA |
| rs8067235 | AG | GG |
| rs6314 | GG | GG |
| rs6902875 | AA | AA |
| rs9321334 | AA | AA |
| rs1997794 | TC | TT |
| rs2235751 | AG | GG |
| rs7272891 | CG | CC |
| rs12807809 | TT | TT |
| rs2075650 | AA | AA |
| rs157582 | TC | CC |
| rs425724 | TA | TT |
| rs1493445 | CG | GG |
| rs9528369 | CG | CC |
| rs347702 | TA | TT |
| rs3749622 | CG | CC |
| rs447505 | AC | CC |
| rs797311 | CA | AA |
| rs1486844 | AA | AA |
| rs347713 | CG | GG |
| rs9528371 | CG | CC |
| rs1386320 | CG | CC |
| rs9528370 | CG | GG |
| rs9539264 | CG | GG |
| rs446427 | TA | TT |
| rs427203 | TA | TT |

| | | |
|---|---|---|
| rs9528358 | CG | GG |
| rs7319943 | CG | GG |
| rs9528377 | CC | CC |
| rs11148561 | CA | AA |
| rs67017972 | CG | GG |
| rs7164861 | CG | CC |
| rs78096325 | AC | CC |
| rs2900031 | CG | CC |



Risk level: average

**rs17070145:** The KIBRA gene variant is associated with episodic memory in healthy older adults. Carriers of the KIBRA rs17070145 T allele had 24% better performance on random recall 5 minutes after word presentation and 19% better performance on random recall 24 hours after word presentation than non-carriers.
[ PMID 17353070 ] [ PMID 19397951 ] [ PMID 21643791 ] [ PMID 22794909 ] [ PMID 25146696 ] [ PMID 30134813 ] [ PMID 30953258 ]

## Diseases

## Tuberculosis

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs34536443 | GG | GG |
| rs2057178 | GG | GG |
| rs2853694 | TG | TT |
| rs3212227 | TT | TT |
| rs3213094 | CC | CC |
| rs3213102 | CG | CC |
| rs2569254 | TC | CC |
| rs6871626 | AC | CC |
| rs3213119 | CC | CC |
| rs4971014 | CG | GG |
| rs13411512 | CG | CC |
| rs7449177 | TC | CC |
| rs3867218 | TA | TT |
| rs447600 | TA | TT |
| rs181301 | AA | GG |
| rs692544 | TT | TT |
| rs3218255 | GG | GG |
| rs2202157 | TC | CC |
| rs5928363 | AA | AA |
| rs2505675 | CC | CC |
| rs40363 | GG | GG |
| rs6676375 | TT | TT |
| rs1925714 | AG | GG |
| rs17175227 | GG | GG |
| rs1075309 | CG | CC |
| rs1900442 | TT | TT |
| rs17217757 | CG | GG |
| rs586716 | GG | AA |

| | | |
|---|---|---|
| rs12283022 | AA | AA |
| rs1819084 | CC | CC |
| rs6575836 | AG | AA |
| rs451390 | CG | GG |
| rs958617 | AG | AA |
| rs1934954 | TT | TT |
| rs7947821 | TT | TT |
| rs2837857 | TC | CC |
| rs12294076 | TT | TT |
| rs6538140 | AG | AA |



Risk level: average

**rs2853694:** Copy number variation in the IL23R gene associated with susceptibility to leprosy and tuberculosis.
[ PMID 23240095 ] [ PMID 26793196 ]

**rs1925714:** A break in the IL2RB gene that increases the risk of susceptibility to tuberculosis.
[ PMID 28384278 ]

**rs451390:** A break in the C2CD2 gene that increases the risk of susceptibility to tuberculosis.
[ PMID 28384278 ]

**rs2837857:** A break in the DSCAM gene that increases the risk of susceptibility to tuberculosis.
[ PMID 28384278 ]

**rs6538140:** A break in the NAV3 gene that increases the risk of susceptibility to tuberculosis.
[ PMID 28384278 ]

# Diabetes

## Type 1 diabetes

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs2040410 | CG | GG |
| rs7454108 | TT | TT |
| rs6679677 | CC | CC |
| rs9272346 | CG | GG |
| rs2476601 | GG | GG |
| rs11171739 | TC | TT |
| rs17696736 | AG | AA |
| rs12708716 | AG | GG |
| rs2639703 | TC | TT |
| rs17388568 | GG | GG |
| rs2544677 | CG | CC |
| rs17166496 | CG | GG |
| rs2104286 | TT | TT |
| rs11052552 | TA | TT |
| rs2542151 | TT | TT |
| rs7574865 | TG | GG |
| rs3087243 | AG | AA |
| rs237025 | AG | GG |
| rs3772534 | CG | GG |
| rs1990760 | TC | CC |
| rs2296336 | CG | GG |
| rs1465788 | TT | CC |
| rs4900384 | AG | AA |
| rs7202877 | TT | TT |
| rs757411 | TT | TT |
| rs425105 | TC | TT |
| rs5753037 | CC | CC |
| rs10517086 | AG | GG |

| | | |
|---|---|---|
| rs7804356 | TT | TT |
| rs9388489 | AA | AA |
| rs4763879 | GG | GG |
| rs2664170 | AG | AA |
| rs3129934 | CC | CC |
| rs3024505 | GG | GG |
| rs4788084 | TT | CC |
| rs3741208 | AG | GG |
| rs725613 | TG | TT |
| rs2290400 | CC | TT |
| rs3746722 | AA | AA |
| rs11594656 | AA | TT |
| rs11755527 | GC | CC |
| rs12722495 | AT | TT |
| rs1464510 | CG | CC |
| rs1738074 | TC | TT |
| rs17810546 | AA | AA |
| rs1893217 | AA | AA |
| rs2069763 | CG | CC |
| rs2292239 | TG | GG |
| rs229541 | GG | AA |
| rs2816316 | TA | AA |
| rs3184504 | TC | CC |
| rs3788013 | AA | CC |
| rs3825932 | TT | TT |
| rs41295061 | CG | CC |
| rs45450798 | CG | CC |
| rs478582 | CC | TT |
| rs6441961 | CC | TT |
| rs6822844 | TG | GG |
| rs689 | TA | AA |
| rs6897932 | CC | CC |

| | | |
|---|---|---|
| rs763361 | TC | CC |
| rs917997 | CG | CC |
| rs947474 | AG | AA |
| rs9811792 | TT | TT |
| rs11571316 | CG | GG |
| rs1701704 | TG | TT |
| rs1004446 | AG | GG |
| rs7528684 | AG | GG |
| rs2069762 | AC | AA |



Risk level: average

**rs1465788:** Increased risk of islet autoimmunity and type 1 diabetes.
[ PMID 21980299 ] [ PMID 22278338 ] [ PMID 24367383 ]

**rs4788084:** Polymorphism of increased risk of adult autoimmune diabetes and diabetic retinopathy.
[ PMID 21441570 ] [ PMID 21829393 ] [ PMID 21873553 ] [ PMID 22278338 ]

**rs2290400:** increased risk of autoimmune diabetes in adults.
[ PMID 21873553 ] [ PMID 21980299 ] [ PMID 22278338 ] [ PMID 30888520 ]

**rs11594656:** IL2RA gene polymorphism increases susceptibility to type I diabetes 1.19-fold for heterozygotes (AT) and 1.38-fold for homozygotes.
[ PMID 17676041 ] [ PMID 18556337 ] [ PMID 19956099 ] [ PMID 22211793 ]

**rs229541:** A predisposition locus for type 1 diabetes and celiac disease.
[ PMID 19073967 ] [ PMID 20854658 ] [ PMID 21980299 ]

**rs3788013:** A risk factor for islet autoimmunity and type 1 diabetes, as well as celiac disease, systemic lupus erythematosus and rheumatoid arthritis.
[ PMID 19073967 ] [ PMID 24367383 ] [ PMID 25843625 ]

**rs6441961:** Increased risk of gluten disease.
[ PMID 19693089 ] [ PMID 19542083 ] [ PMID 22087237 ]

**rs2040410:** One of two polymorphisms (rs2040410 and rs7454108) that determine the highest risk of type 1 diabetes.
[ PMID 18694972 ] [ PMID 19143810 ] [ PMID 19143815 ]

## Type 2 diabetes

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs9465871 | TA | TT |
| rs10811661 | TT | TT |
| rs12255372 | GG | GG |
| rs12970134 | AA | GG |
| rs7923837 | AG | GG |
| rs4812829 | GG | GG |
| rs10229583 | AG | GG |
| rs4402960 | TT | GG |
| rs5219 | CC | CC |
| rs13266634 | TC | CC |
| rs7903146 | GG | CC |
| rs5215 | TT | TT |
| rs7901695 | TT | TT |
| rs1801282 | GG | CC |
| rs1111875 | AC | CC |
| rs2237892 | CC | CC |
| rs9300039 | GG | CC |
| rs8050136 | AC | CC |
| rs5015480 | TC | CC |
| rs17797882 | CC | CC |
| rs2237897 | CG | CC |
| rs4506565 | AA | AA |
| rs11868035 | AG | AA |
| rs4655595 | GG | AA |
| rs4712523 | AA | AA |
| rs10946398 | TT | AA |
| rs7756992 | AA | AA |
| rs1470579 | CC | AA |
| rs3745367 | CC | GG |

| | | |
|---|---|---|
| rs1423096 | CC | CC |
| rs6930576 | AG | GG |
| rs2106294 | TT | TT |
| rs3792615 | AA | TT |
| rs9472138 | TC | CC |
| rs649891 | TT | TT |
| rs391300 | TC | CC |
| rs10440833 | AA | TT |
| rs7578597 | TT | TT |
| rs6769511 | CC | TT |
| rs6712932 | CC | TT |
| rs10461617 | GG | GG |
| rs472265 | AG | AA |
| rs6426514 | CG | GG |
| rs7636 | GG | GG |
| rs7178572 | GG | GG |
| rs10965250 | CC | GG |
| rs7041847 | AA | GG |
| rs7754840 | GG | GG |
| rs9552911 | GG | GG |
| rs7961581 | TC | TT |
| rs4527850 | TC | TT |
| rs7305618 | CC | CC |
| rs16861329 | GG | CC |
| rs7403531 | GG | CC |
| rs6815464 | CC | CC |
| rs896854 | TT | CC |
| rs1387153 | CC | CC |
| rs11165354 | GG | CC |
| rs17053082 | CC | CC |
| rs11642841 | AC | CC |
| rs17584499 | TT | CC |

| | | |
|---|---|---|
| rs4607103 | TC | CC |
| rs8090011 | CG | CC |
| rs7560163 | GG | CC |
| rs4457053 | TT | AA |
| rs791595 | GG | GG |
| rs17036101 | AG | GG |
| rs4760790 | AG | GG |
| rs7172432 | GG | AA |
| rs515071 | GG | GG |
| rs3802177 | AG | GG |
| rs3923113 | AA | AA |
| rs11708067 | AA | AA |
| rs1861612 | GG | AA |
| rs2383208 | AA | AA |
| rs11634397 | AG | AA |
| rs10906115 | GG | AA |
| rs7630877 | GG | GG |
| rs8042680 | CC | AA |
| rs231362 | AG | AA |
| rs163184 | GG | TT |
| rs864745 | CC | TT |
| rs4430796 | TA | AA |
| rs243021 | AA | GG |
| rs10814916 | CC | AA |
| rs7578326 | AG | AA |
| rs2283228 | AA | AA |
| rs2028299 | CC | AA |
| rs9470794 | TC | TT |
| rs10886471 | TT | CC |
| rs972283 | AA | AA |
| rs849134 | GG | AA |
| rs1531343 | CC | GG |

| | | |
|---|---|---|
| rs7593730 | CC | TT |
| rs831571 | CC | CC |
| rs3786897 | GG | AA |
| rs1048886 | AA | AA |
| rs642858 | CG | GG |
| rs6718526 | CC | CC |
| rs358806 | GG | CC |
| rs7659604 | TT | CC |
| rs9326506 | TT | AA |
| rs12304921 | AG | AA |
| rs1495377 | GG | CC |
| rs2930291 | CA | AA |
| rs2903265 | CG | GG |
| rs2236513 | AA | AA |
| rs6502618 | TT | AA |
| rs1889018 | AA | GG |
| rs2297508 | CG | CC |
| rs2289116 | CC | GG |
| rs741301 | TT | TT |
| rs997509 | CC | CC |
| rs2295490 | TT | AA |
| rs7018475 | GG | TT |
| rs9939609 | TT | TT |
| rs1799999 | GG | CC |

Risk level: high

**rs12970134:** A common obesity variant near the MC4R gene is associated with higher intake of total energy and dietary fat, weight change, insulin resistance and risk of type 2 diabetes.
[ PMID 18454146 ] [ PMID 18697794 ] [ PMID 19478790 ] [ PMID 19822564 ] [ PMID 20110568 ] [ PMID 22869321 ] [ PMID 24843659 ] [ PMID 25239271 ] [ PMID 26363598 ]

**rs4402960:** Locus of risk for developing type 2 diabetes as well as increased risk for gestational diabetes.

[ PMID 17463246 ] [ PMID 17463248 ] [ PMID 17827400 ] [ PMID 18430866 ] [ PMID 18461161 ] [ PMID 18544707 ] [ PMID 18782870 ] [ PMID 19323962 ] [ PMID 19460916 ] [ PMID 19602701 ] [ PMID 20862305 ]

**rs7903146:** This is one of two SNPs in the TCF7L2 gene that have been reported to be strongly associated with type 2 diabetes, the other being rs4506565. They have approximately equal power to assess the risk of developing type 2 diabetes , and the results of one test correlate with the other in 92% of cases. Associated with reduced insulin secretion, as measured by the acute response to insulin and increased rate of glucose production in the liver.
[ PMID 16415884 ] [ PMID 16855264 ] [ PMID 16936215 ] [ PMID 16936217 ] [ PMID 17003358 ] [ PMID 17020404 ] [ PMID 17031610 ] [ PMID 17093941 ]

**rs1801282:** Peroxisome proliferator-activated receptor gamma gene variation on the progression of type 2 diabetes and obesity. Also higher risk of cardiovascular disease with a diet high in saturated fat.
[ PMID 17213274 ] [ PMID 18091023 ] [ PMID 18598350 ] [ PMID 18694974 ] [ PMID 19020323 ]

**rs10946398:** A new risk locus for the development of type 2 diabetes.
[ PMID 17463246 ] [ PMID 18461161 ] [ PMID 20161779 ] [ PMID 20862305 ] [ PMID 24653947 ] [ PMID 29372795 ]

**rs3745367:** RETN resistin polymorphism is associated with obesity and increases susceptibility to type 2 diabetes mellitus.
[ PMID 15517149 ] [ PMID 19074981 ] [ PMID 23203410 ]

**rs864745:** A single nucleotide polymorphism in the JAZF1 gene is nominally associated with type 2 diabetes.
[ PMID 18372903 ] [ PMID 18567820 ] [ PMID 22113416 ]

**rs10886471:** The GRK5 variant is associated with the efficacy of repaglinide in patients with type 2 diabetes mellitus.
[ PMID 22961080 ] [ PMID 29663513 ]

## Insulin

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1801278 | CC | CC |
| rs10830963 | CC | CC |
| rs1044498 | AC | AA |
| rs1799999 | GG | CC |
| rs1169288 | TA | AA |
| rs13266634 | TC | CC |
| rs780094 | TC | CC |
| rs2295490 | TT | AA |
| rs1887922 | TA | TT |
| rs7754840 | GG | GG |
| rs689 | TA | AA |
| rs1111875 | AC | CC |
| rs4607103 | TC | CC |
| rs7903146 | GG | CC |
| rs12255372 | GG | GG |
| rs1801282 | GG | CC |
| rs2229765 | AG | GG |
| rs7202877 | TT | TT |
| rs6220 | GG | AA |
| rs7255710 | CG | GG |
| rs7254921 | TC | CC |
| rs2059807 | GG | GG |
| rs891088 | AG | AA |
| rs7254487 | TA | AA |
| rs17619048 | TT | TT |
| rs10744901 | TT | TT |
| rs487894 | CC | TT |
| rs1517204 | TA | TT |
| rs7342408 | TT | TT |

| | | |
|---|---|---|
| rs1400589 | TA | TT |
| rs484659 | TG | GG |
| rs4492895 | GG | AA |
| rs1004361 | GG | GG |
| rs7964607 | GG | GG |
| rs7976621 | AG | GG |
| rs7977174 | TC | TT |
| rs816200 | TC | TT |
| rs1501635 | AT | TT |
| rs10431397 | CG | CC |
| rs4304868 | CC | CC |
| rs634264 | GG | GG |
| rs12425296 | AA | AA |
| rs10774926 | AA | AA |
| rs30360 | TG | TT |
| rs4698790 | TT | GG |
| rs9787485 | TC | CC |
| rs16891077 | AG | GG |



Risk level: average

**rs1799999:** Widespread amino acid polymorphism is associated with insulin resistance and insulin hypersecretion.
[ PMID 7581368 ] [ PMID 26251103 ]

**rs2295490:** Growing role of TRIB3 as a gene affecting human insulin resistance on glucose homeostasis by altering the interaction between insulin sensitivity and secretion.
[ PMID 18984671 ] [ PMID 19139803 ] [ PMID 20393693 ] [ PMID 25447894 ]

**rs7903146:** This is one of two SNPs in the TCF7L2 gene that have been reported to be strongly associated with type 2 diabetes, the other being rs4506565. They have approximately equal power to assess the risk of developing type 2 diabetes , and the results of one test correlate with the other in 92% of cases. Associated with reduced insulin secretion, as measured by the acute response to insulin and increased rate of glucose production in the liver.
[ PMID 16415884 ] [ PMID 16855264 ] [ PMID 16936215 ] [ PMID 16936217 ] [ PMID 17003358 ] [ PMID 17020404 ] [ PMID 17031610 ] [ PMID 17093941 ]

**rs1801282:** Peroxisome proliferator-activated receptor gamma gene variation on the progression of type 2 diabetes and obesity. Also higher risk of cardiovascular disease with a diet high in saturated fat.

[ PMID 17213274 ] [ PMID 18091023 ] [ PMID 18598350 ] [ PMID 18694974 ] [ PMID 19020323 ]

**rs6220:** Genetic polymorphisms involved in the insulin-like growth factor (IGF) pathway regulate mammographic breast density ratio.
[ PMID 18064566 ] [ PMID 20302654 ]

**rs1044498:** A polymorphism (K121Q) of the region encoding human glycoprotein PC-1 is closely associated with insulin resistance.
[ PMID 10480624 ] [ PMID 11739459 ] [ PMID 16865358 ] [ PMID 16968801 ] [ PMID 17704904 ]

**rs1169288:** Variation in the HNF1A gene region affects CRP levels. The association between the common variant of the HNF1A gene p.I27L (rs1169288) and the risk of developing type 2 diabetes mellitus is weight-dependent.
[ PMID 18439552 ] [ PMID 21094359 ] [ PMID 24933231 ]

**rs13266634:** The zinc transporter gene SLC30A8 polymorphism is associated with type 2 diabetes.
[ PMID 18162509 ] [ PMID 18210030 ] [ PMID 18400535 ] [ PMID 18628523 ] [ PMID 19590848 ] [ PMID 21810599 ] [ PMID 24757200 ] [ PMID 29093761 ]

## Glaucoma

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1048661 | CG | GG |
| rs28936694 | CC | CC |
| rs16958445 | GG | GG |
| rs893818 | AA | GG |
| rs2165241 | CC | CC |
| rs10483727 | CC | TT |
| rs7865618 | AG | GG |
| rs17373884 | CC | CC |
| rs4297993 | CC | CC |
| rs150936840 | CC | CC |
| rs113695387 | TA | AA |
| rs284489 | GG | AA |
| rs162562 | TT | TT |
| rs72549382 | CG | CC |
| rs10916 | AA | AA |
| rs235913 | TG | GG |
| rs604864 | TC | CC |
| rs8014087 | CC | TT |
| rs2028377 | TT | CC |
| rs862037 | AA | GG |
| rs17784350 | AA | AA |
| rs11101190 | AA | AA |
| rs2244380 | TT | TT |
| rs10796028 | TT | TT |
| rs7961361 | TG | GG |
| rs17512962 | AG | GG |
| rs1440101 | CG | GG |
| rs4886776 | AA | GG |
| rs735860 | CC | CC |

| | | |
|---|---|---|
| rs2304721 | CC | CC |
| rs3825942 | CG | GG |
| rs8041685 | GG | GG |
| rs4656461 | AA | AA |
| rs893817 | GG | AA |
| rs3213787 | AA | AA |
| rs4977756 | AG | AA |
| rs523096 | AG | AA |
| rs7095146 | CC | CC |
| rs2157719 | TC | TT |
| rs12940030 | TT | TT |
| rs7830 | TG | GG |
| rs59072263 | TG | GG |
| rs2070744 | TC | CC |
| rs1056836 | GG | GG |
| rs3132306 | CC | TT |
| rs7555523 | AA | CC |
| rs1536482 | AA | GG |
| rs7037117 | TA | AA |



Risk level: average

**rs893818:** LOXL1 gene polymorphism, a candidate polymorphism for exfoliative glaucoma, is also associated with the risk of developing primary open-angle glaucoma.
[ PMID 24938310 ] [ PMID 33396423 ] [ PMID 34012228 ] [ PMID 34726854 ]

**rs10483727:** The common variant GRCh38 are associated with increased predisposition to optic nerve degeneration (association with vertical ratio of the calyx to optic disc) in glaucoma.
[ PMID 22570617 ] [ PMID 22584021 ] [ PMID 22605921 ] [ PMID 27707548 ]

**rs284489:** The common variant is associated with increased susceptibility to optic nerve degeneration in glaucoma.
[ PMID 22570617 ] [ PMID 23963167 ] [ PMID 25171643 ] [ PMID 28499933 ]

**rs7555523:** Genetic variant associated with different risks of developing high-tension glaucoma and normal-tension glaucoma.
[ PMID 25711633 ] [ PMID 26690118 ] [ PMID 28721823 ] [ PMID 33396423 ] [ PMID 33726755 ]

**rs1536482:** Breakage related to the thickness of the central cornea of the eye and keratoconus.
[ PMID 22605921 ] [ PMID 23291589 ] [ PMID 28207827 ] [ PMID 29760442 ]

**rs1048661:** The LOXL1 gene variant is associated with primary open-angle and primary closed-angle glaucoma, exfoliative glaucoma, and cataracts.
[ PMID 17690259 ] [ PMID 18254956 ] [ PMID 18334928 ] [ PMID 18385788 ] [ PMID 18552979 ] [ PMID 18958304 ] [ PMID 20142848 ] [ PMID 21150032 ]

**rs7865618:** A common variant on chromosome 9p21 is associated with normal tension glaucoma.
[ PMID 22428042 ] [ PMID 22792221 ] [ PMID 26690118 ] [ PMID 28721823 ] [ PMID 32509935 ]

**rs235913:** Association of the MYOC gene with primary closed-angle glaucoma.
[ PMID 25268471 ] [ PMID 31456923 ]

## Renal failure

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs4293393 | AA | GG |
| rs41273726 | TT | TT |
| rs2467853 | CG | GG |
| rs12917707 | GG | GG |
| rs17319721 | GG | GG |
| rs3814995 | TC | CC |
| rs56071124 | TA | TT |
| rs10948668 | TT | TT |
| rs1321517 | CG | CC |
| rs2182505 | TC | CC |
| rs113633432 | AA | AA |
| rs9296668 | GG | AA |
| rs2973049 | CC | CC |
| rs114812377 | CG | CC |
| rs2216711 | AA | AA |
| rs11084831 | TG | GG |
| rs28939695 | AC | CC |
| rs10409299 | AG | AA |
| rs4927186 | AA | GG |
| rs12472051 | CA | AA |
| rs73017308 | TA | TT |
| rs36025606 | CC | CC |
| rs11961816 | TA | AA |
| rs4977388 | CG | GG |
| rs141052170 | CG | GG |
| rs73206603 | CG | GG |
| rs10404821 | CC | CC |
| rs12647735 | AC | CC |
| rs6997279 | CG | GG |

| | | |
|---|---|---|
| rs117897666 | CC | CC |
| rs76262407 | TA | AA |
| rs61277444 | AA | AA |
| rs7562121 | CG | GG |
| rs6027504 | CC | TT |
| rs1989248 | CG | GG |
| rs72809865 | AC | CC |



Risk level: average

**rs4293393:** A break in the UMOD gene as a major predisposition gene for terminal renal failure. The gene directly affects levels of uromodulin, glomerular filtration rate and increased degree of albuminuria.higher risk of Crohn's disease.
[ PMID 19959715 ] [ PMID 22947327 ] [ PMID 29578190 ] [ PMID 31231424 ]

**rs2467853:** A genetic locus associated with measures of renal function and chronic kidney disease.
[ PMID 19430482 ] [ PMID 20383145 ] [ PMID 23028791 ] [ PMID 26776194 ] [ PMID 29016630 ]

**rs3814995:** The nephrin gene (NPHS1) is associated with congenital steroid-resistant nephrotic syndrome.
[ PMID 9915943 ] [ PMID 15086927 ] [ PMID 20138859 ] [ PMID 23349334 ]

**rs7562121:** Increased risk of diabetic kidney disease.
[ PMID 31231424 ]

## Varicose veins

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs4151657 | CC | TT |
| rs3025058 | CG | CC |
| rs11121615 | TC | CC |
| rs1799750 | CG | CC |
| rs13155212 | TC | TT |
| rs7704267 | CG | CC |
| rs2911463 | AA | AA |
| rs2861819 | CG | CC |
| rs28558138 | CG | GG |
| rs8053350 | GG | GG |
| rs3101725 | AT | TT |
| rs11135046 | CG | GG |
| rs7773004 | AA | AA |
| rs12625547 | TA | TT |
| rs236597 | CG | CC |
| rs7614922 | TA | TT |
| rs73107980 | CG | CC |
| rs7469817 | CG | GG |
| rs2241173 | AA | AA |
| rs816943 | GG | AA |
| rs1061539 | TA | TT |
| rs1549063 | AA | AA |
| rs16828263 | TA | TT |
| rs9719461 | CG | CC |
| rs2263321 | CG | GG |
| rs247749 | TA | TT |
| rs75522736 | TA | AA |
| rs553399706 | CG | GG |
| rs62512472 | AA | GG |

| | | |
|---|---|---|
| rs584768 | CG | GG |
| rs2089657 | CG | CC |
| rs12594708 | CG | CC |
| rs186005582 | CG | CC |
| rs192647746 | TA | AA |
| rs7856039 | TA | TT |
| rs9880192 | GG | GG |
| rs236530 | TC | CC |
| rs2836405 | AG | AA |
| rs1805087 | AA | AA |



Risk level: average

**rs4151657:** Studies suggest a link between the CFB genomic region and the risk of primary varicose veins.
[ PMID 29551506 ]

**rs3025058:** MMP3 matrix metalloproteinase gene polymorphism is more common in patients with varicose veins of the lower extremities.
[ PMID 19508478 ] [ PMID 28944430 ]

**rs11121615:** A polymorphism in a gene involved in inflammation and blood vessel development affects the risk of varicose veins.
[ PMID 29660117 ] [ PMID 31570750 ]

**rs1799750:** MMP1 matrix metalloproteinase gene polymorphism increases the risk of lower extremity varicose veins.
[ PMID 19508478 ] [ PMID 28944430 ]

**rs13155212:** The polymorphic variant rs13155212 of the AGGF1 gene increases the risk of lower extremity varicose veins.
[ PMID 27704351 ]

**rs7704267:** Polymorphic variant rs7704267 of the AGGF1 gene increases the risk of lower extremity varicose veins.
[ PMID 27704351 ]

## Digestive diseases

## Hepatitis

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs8099917 | GG | TT |
| rs11697186 | AA | AA |
| rs9277535 | AA | AA |
| rs12980275 | GG | GG |
| rs7756516 | TT | TT |
| rs9276370 | TT | TT |
| rs1127354 | CC | CC |
| rs3077 | AA | AA |
| rs7453920 | GG | GG |
| rs738409 | CG | CC |
| rs7270101 | AC | AA |
| rs8103142 | TA | TT |
| rs2856718 | TT | CC |
| rs11725957 | CG | GG |
| rs2254135 | TT | TT |
| rs17067123 | CC | CC |
| rs12979860 | TT | CC |
| rs10789491 | GG | GG |
| rs16864968 | TA | AA |
| rs9366816 | TC | TT |
| rs1946518 | GG | GG |
| rs8105790 | TA | TT |
| rs187238 | CG | CC |
| rs7224000 | AA | AA |

Risk level: average

**rs8099917:** The major polymorphism rs8099917 of the IL28B gene predicts treatment outcomes in patients infected with hepatitis C virus. Associated with ineffectiveness of interferon-alpha and ribavirin therapy in chronic hepatitis C. However, at the same time, there are known cases of spontaneous cure from hepatitis C by carriers of this defect.
[ PMID 19749758 ] [ PMID 20708617 ] [ PMID 21346780 ] [ PMID 21354446 ] [ PMID 21613433 ] [ PMID 22387386 ] [ PMID 28224025 ] [ PMID 28703131 ]

**rs2856718:** HLA-DQB1 polymorphisms are associated with susceptibility to chronic hepatitis B.
[ PMID 24976707 ] [ PMID 27123247 ] [ PMID 27795724 ] [ PMID 33334325 ]

**rs12979860:** A variant of the gene encoding interferon-lambda-4 (IFN-lambda-4) predicts virus elimination induced by hepatitis C treatment. It is associated with an approximately twofold change in response to treatment with pegylated interferon-alpha (PEG-IFN-alpha) in combination with ribavirin (RBV).
[ PMID 19684573 ] [ PMID 20176026 ] [ PMID 20389235 ] [ PMID 20637200 ] [ PMID 21447862 ]

**rs738409:** The rs738409 polymorphism in PNPLA3 is associated with the risk of liver damage and the development of non-alcoholic fatty liver disease. It influences the progression of fibrosis and steatosis in chronic hepatitis C.
[ PMID 19224197 ] [ PMID 20546964 ] [ PMID 21236304 ] [ PMID 21488075 ]

**rs7270101:** The ITPA gene variant protects against ribavirin-induced haemolytic anaemia and reduces the need for ribavirin dose reduction in hepatitis C virus treatment.
[ PMID 20547162 ] [ PMID 20637204 ] [ PMID 22118055 ] [ PMID 22584257 ] [ PMID 24659876 ]

**rs8103142:** IL28B genetic variability is associated with spontaneous HCV elimination, response to treatment, and blood levels of IL-28B.
[ PMID 19749757 ] [ PMID 22649509 ] [ PMID 23109451 ] [ PMID 24696021 ]

**rs9366816:** Polymorphisms influence the risk of hepatitis B virus infection.
[ PMID 24940741 ] [ PMID 27795724 ] [ PMID 29404438 ] [ PMID 31475028 ]

## Crohn's disease

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs17234657 | TT | TT |
| rs1004819 | AG | GG |
| rs11209026 | GG | AA |
| rs10758669 | AA | AA |
| rs2066845 | GG | GG |
| rs2066847 | CG | GG |
| rs4958847 | CG | GG |
| rs2542151 | TT | TT |
| rs13361189 | TC | TT |
| rs10181042 | TC | CC |
| rs16967103 | TT | TT |
| rs4409764 | TG | GG |
| rs12521868 | GG | GG |
| rs17309827 | TA | TT |
| rs2284553 | AG | GG |
| rs10486483 | GG | GG |
| rs181359 | GG | GG |
| rs2188962 | CC | CC |
| rs7517810 | TC | CC |
| rs6545946 | TC | CC |
| rs2301436 | CC | CC |
| rs2274910 | CC | CC |
| rs3091338 | CC | CC |
| rs713875 | CC | CC |
| rs5743289 | CC | CC |
| rs2413583 | CC | CC |
| rs10210302 | TC | CC |
| rs11574514 | CC | CC |
| rs1819658 | CC | CC |

| | | |
|---|---|---|
| rs17221417 | GC | CC |
| rs415890 | GG | GG |
| rs9348876 | CC | CC |
| rs10761659 | AA | AA |
| rs13073817 | AG | GG |
| rs9286879 | AG | AA |
| rs2902440 | CG | GG |
| rs744166 | AG | AA |
| rs1373692 | CC | AA |
| rs7554511 | AC | CC |
| rs9469220 | AA | AA |
| rs762421 | AA | AA |
| rs13428812 | AA | AA |
| rs7714584 | AG | AA |
| rs1456896 | TT | TT |
| rs6856616 | TC | TT |
| rs9988642 | TT | TT |
| rs751728 | TC | CC |
| rs12677663 | TT | TT |
| rs11229030 | TC | TT |
| rs10801047 | TT | TT |
| rs4613763 | TT | TT |
| rs11465804 | TT | TT |
| rs736289 | TT | TT |
| rs7765379 | TT | TT |
| rs17582416 | TT | TT |
| rs3897478 | TT | TT |
| rs7517847 | TT | TT |
| rs1343151 | GG | GG |
| rs3197999 | AA | GG |
| rs7746082 | CG | GG |
| rs6738825 | AG | GG |

| | | |
|---|---|---|
| rs9491697 | GG | AA |
| rs504963 | AG | GG |
| rs1551398 | AA | GG |
| rs3091316 | AG | GG |
| rs281379 | AG | GG |
| rs76418789 | GG | GG |
| rs9858542 | CG | GG |
| rs4871611 | AA | GG |
| rs2872507 | AG | GG |
| rs12994997 | AG | GG |
| rs6837335 | AG | GG |
| rs11564258 | GG | GG |
| rs13003464 | AG | AA |
| rs13126505 | GG | GG |
| rs3792109 | AG | GG |
| rs4263839 | GG | GG |
| rs3024505 | GG | GG |
| rs1728918 | AG | GG |
| rs17293632 | CC | CC |
| rs11190140 | TC | CC |
| rs6651252 | TT | TT |
| rs9292777 | TT | CC |
| rs7423615 | CC | CC |
| rs2549794 | TC | TT |
| rs6478106 | CC | CC |
| rs2797685 | CC | CC |
| rs11742570 | CC | TT |
| rs11584383 | TC | TT |
| rs12035082 | CG | CC |
| rs102275 | TC | CC |
| rs11195128 | CC | CC |
| rs9267911 | TC | TT |

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|---|---|---|
| rs2836754 | CC | TT |
| rs10889677 | AC | CC |
| rs359457 | CC | CC |
| rs9258260 | TC | CC |
| rs151181 | CC | TT |
| rs7927997 | TC | CC |
| rs8005161 | CC | CC |
| rs3094188 | CC | AA |
| rs1000113 | TC | CC |
| rs11805303 | TC | CC |
| rs10495903 | CC | CC |
| rs4077515 | TC | CC |
| rs11209002 | CG | CC |
| rs7927894 | CG | CC |
| rs3810936 | TC | CC |
| rs212388 | TC | CC |
| rs12663356 | TC | TT |
| rs10883365 | AG | AA |
| rs4902642 | AG | GG |
| rs6556412 | AG | GG |
| rs740495 | AA | AA |
| rs7076156 | AG | GG |
| rs1869839 | AA | AA |
| rs4809330 | AG | GG |
| rs2058660 | AA | AA |
| rs1847472 | AC | CC |
| rs1250550 | AC | CC |
| rs11167764 | CC | CC |
| rs12720356 | AC | AA |
| rs10045431 | CC | CC |
| rs9891119 | AC | AA |
| rs3764147 | GG | AA |

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|---|---|---|
| rs2241880 | AG | AA |
| rs12242110 | AA | AA |
| rs2838519 | AA | AA |
| rs2076756 | TA | AA |
| rs1893217 | AA | AA |
| rs3828309 | AG | AA |
| rs11747270 | AG | AA |
| rs10734105 | AG | AA |
| rs11465802 | AA | AA |
| rs7329174 | AA | AA |
| rs2945412 | AG | AA |
| rs2201841 | AG | AA |
| rs3091315 | AG | AA |
| rs6568421 | AG | AA |
| rs7702331 | GG | AA |
| rs17695092 | TG | GG |
| rs1736135 | TC | TT |
| rs6908425 | TC | CC |
| rs10995271 | GG | GG |
| rs11175593 | CC | CC |
| rs1487630 | CC | CC |
| rs2024092 | GG | GG |
| rs1736020 | AC | CC |
| rs7705924 | AA | AA |
| rs1998598 | AG | AA |
| rs1456893 | AA | AA |
| rs2066844 | CC | CC |
| rs272869 | AA | GG |
| rs2111234 | AA | AA |
| rs10512734 | AA | AA |
| rs10883371 | CA | AA |
| rs8057341 | GG | GG |

| | | |
|---|---|---|
| rs2066842 | TC | CC |
| rs11647841 | AG | GG |
| rs1398024 | TG | GG |
| rs274551 | CG | CC |
| rs6596075 | CC | GG |
| rs7753394 | TC | TT |
| rs224136 | CC | CC |
| rs1736148 | TC | TT |
| rs11362 | TC | CC |
| rs1793004 | GG | GG |
| rs1992660 | TT | CC |
| rs1992662 | AA | AA |
| rs1128535 | AC | CC |
| rs12567232 | CG | GG |
| rs6669582 | AA | AA |
| rs11894081 | TT | TT |
| rs10789230 | TG | GG |
| rs11209003 | CG | GG |
| rs5743272 | AA | AA |
| rs419291 | TT | CC |



Risk level: average

**rs11209026:** Association of variant rs11209026 of the interleukin-23 receptor gene with Crohn's disease in children.
[ PMID 17618837 ] [ PMID 17894849 ] [ PMID 18470928 ] [ PMID 20192940 ] [ PMID 31728561 ]

**rs1004819:** rs1004819 is the major IL23R variant associated with Crohn's disease with early onset.
[ PMID 17786191 ] [ PMID 18047539 ] [ PMID 20380008 ]

**rs2066847:** A break in the NOD2 gene increases 3 to 35 times the risk of Crohn's disease.
[ PMID 25365249 ]

**rs4958847:** Deletion polymorphism associated with altered IRGM expression and Crohn's disease. 2.6-fold increased risk of Crohn's disease.
[ PMID 18438406 ] [ PMID 19165925 ]

**rs13361189:** The IRGM rs13361189 polymorphism may contribute to Crohn's disease susceptibility.
[ PMID 18580884 ] [ PMID 20106866 ] [ PMID 25009628 ]

**rs3792109:** Disruption of transmission in the Crohn's disease risk gene ATG16L1 results in sex differences in disease association.
[ PMID 21618365 ]

## Pancreatitis

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs111033565 | GG | GG |
| rs17107315 | TT | TT |
| rs111033566 | TA | AA |
| rs193922659 | CG | GG |
| rs12688220 | TC | CC |
| rs11319 | GG | GG |
| rs4705202 | GG | GG |
| rs11548596 | CG | GG |
| rs928302 | CC | CC |
| rs5751901 | TT | TT |
| rs10273639 | CC | TT |
| rs5751902 | TT | CC |
| rs121909293 | CC | CC |
| rs213950 | AG | GG |
| rs225320 | GG | GG |
| rs10436957 | GG | GG |
| rs121909294 | GG | GG |
| rs144422014 | AA | AA |



Risk level: average

**rs10273639:** PRSS1-PRSS2 variants encoding trypsin influence the risk of asparaginase-related pancreatitis.
[ PMID 30467200 ] [ PMID 31163246 ]

**rs111033566:** A novel cationic trypsinogen (PRSS1) cause autosomal dominant hereditary pancreatitis.
[ PMID 11719509 ] [ PMID 11788572 ] [ PMID 22379635 ]

**rs193922659:** Variants of a signalling peptide that disrupts pancreatic secretory trypsin inhibitor (SPINK1) secretion cause hereditary autosomal dominant pancreatitis.
[ PMID ]

**rs12688220:** A common variant of the MORC4 gene accounts for the predisposition to the disease in patients with chronic pancreatitis.

[ PMID 25253127 ]  [ PMID 26820620 ]  [ PMID 31163246 ]

## Thrombosis

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs5361 | TG | TT |
| rs1799963 | GG | GG |
| rs6025 | CC | CC |
| rs268 | AA | AA |
| rs2066865 | AG | GG |
| rs2289252 | CC | CC |
| rs1613662 | AA | AA |
| rs2227589 | CC | CC |
| rs1800595 | TT | TT |
| rs6048 | AA | GG |
| rs2036914 | CC | CC |
| rs13146272 | AC | AA |
| rs12343867 | TA | TT |
| rs4524 | CC | TT |
| rs670659 | CG | CC |
| rs3756008 | AA | AA |
| rs710446 | TC | TT |
| rs201381904 | CG | CC |
| rs657152 | CG | CC |
| rs2288904 | AG | AA |
| rs138925964 | CC | CC |
| rs137852283 | GG | GG |
| rs7080536 | GG | GG |
| rs6427196 | GG | CC |
| rs6046 | GG | GG |
| rs4851770 | TA | TT |
| rs2842700 | CG | CC |
| rs1867312 | AA | AA |
| rs7585314 | TC | CC |

| | | |
|---|---|---|
| rs13084580 | CC | CC |
| rs6795524 | AA | AA |
| rs2066864 | CG | GG |
| rs4253417 | TA | TT |
| rs4253421 | CG | GG |
| rs4869589 | GG | GG |
| rs16867574 | TA | TT |
| rs2074492 | CG | CC |
| rs9373523 | CG | GG |
| rs7739314 | AA | AA |
| rs10087301 | CG | GG |
| rs4734879 | CG | GG |
| rs4541868 | CG | CC |
| rs8176749 | CC | CC |
| rs687289 | CG | GG |
| rs2519093 | CG | CC |
| rs9411377 | N/A | CC |
| rs579459 | TT | TT |
| rs10886430 | AA | AA |
| rs3136516 | AA | AA |
| rs191945075 | CG | GG |
| rs174536 | AC | CC |
| rs216311 | CG | CC |
| rs1558519 | AA | AA |
| rs216296 | TA | AA |
| rs2851436 | AA | TT |
| rs12824685 | AT | TT |
| rs3211752 | AA | AA |
| rs57328376 | TA | AA |
| rs12445050 | CG | CC |
| rs1048483 | CC | CC |
| rs4548995 | AC | CC |

| | | |
|---|---|---|
| rs1671135 | AC | CC |
| rs1654425 | AT | TT |
| rs6083037 | TA | TT |
| rs6088735 | AC | CC |
| rs867186 | AA | AA |
| rs10747514 | GG | GG |
| rs9607928 | CG | CC |
| rs3002417 | CG | CC |
| rs7051718 | CG | CC |
| rs143478537 | CG | CC |



Risk level: average

**rs5361:** The rs5361 Ser128Arg variant in this gene, known as E-selectin, is associated with several thrombotic disorders. Homozygous carriers of rs5361(CC) have a 4-fold higher risk of recurrent venous thromboembolism
[ PMID 19263529 ]

**rs2066865:** Genetic variability in the fibrinogen-gamma FGG gene increases the risk of deep vein thrombosis by reducing plasma fibrinogen-gamma levels.
[ PMID 16144795 ] [ PMID 17445871 ] [ PMID 31484330 ]

**rs12343867:** The JAK2 46/1 haplotype confers a predisposition to essential thrombocythemia.
[ PMID 19847198 ] [ PMID 19922437 ]

**rs201381904:** A 10-fold higher risk of venous thromboembolism among rs201381904(T) carriers despite normal levels of antithrombin and anticoagulant activity.
[ PMID ]

**rs2288904:** The SLC44A2 rs2288904 variant is associated with the risk of recurrent venous thromboembolism.
[ PMID 30634167 ]

## Mental disorders

## Schizophrenia

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs6277 | CG | GG |
| rs1006737 | AA | GG |
| rs6675281 | CC | CC |
| rs6603272 | TA | TT |
| rs2910032 | TC | TT |
| rs11995572 | CG | GG |
| rs833497 | TT | TT |
| rs4687552 | TT | CC |
| rs2949006 | GG | GG |
| rs947267 | TA | TT |
| rs1538774 | CG | CC |
| rs6878284 | TC | TT |
| rs2373000 | CC | CC |
| rs6461049 | TC | CC |
| rs4801131 | TC | CC |
| rs4950928 | CC | CC |
| rs4129585 | AC | CC |
| rs11225703 | TC | CC |
| rs778371 | AG | AA |
| rs7085104 | AG | GG |
| rs3738401 | CG | GG |
| rs171748 | AG | GG |
| rs165599 | AA | AA |
| rs7940866 | AA | AA |
| rs12991836 | AC | AA |
| rs4938445 | AG | GG |
| rs9268895 | AA | AA |
| rs855050 | AA | GG |

| | | |
|---|---|---|
| rs6932590 | TC | CC |
| rs13194053 | TT | CC |
| rs9272219 | TT | TT |
| rs302719 | TT | TT |
| rs16897515 | CC | AA |
| rs10275045 | TC | CC |
| rs1783925 | AA | AA |
| rs36563 | TG | GG |
| rs1411771 | TC | CC |
| rs2812385 | TG | TT |
| rs6541290 | CC | CC |
| rs3738402 | CC | CC |
| rs16854957 | CC | CC |
| rs821722 | GG | AA |
| rs2793093 | GG | GG |
| rs9431714 | AG | GG |
| rs2356606 | AG | AA |
| rs967244 | AG | AA |
| rs1073179 | AG | AA |
| rs9663054 | AA | AA |
| rs1417866 | TA | AA |
| rs7221595 | AT | TT |
| rs114002140 | CG | GG |
| rs1198588 | TA | AA |
| rs10789369 | AG | GG |
| rs17504622 | CC | CC |
| rs14403 | CC | TT |
| rs11532322 | CG | GG |
| rs10790212 | TC | CC |
| rs175174 | AG | AA |
| rs1800532 | CG | GG |
| rs310762 | TC | TT |

| | | |
|---|---|---|
| rs795009 | TA | TT |
| rs751229 | AA | AA |
| rs497768 | CG | GG |
| rs839523 | CC | CC |
| rs7598440 | TC | Đ¡Đ¡ |
| rs707284 | CC | TT |
| rs27388 | AG | GG |
| rs2270641 | TA | TT |
| rs17101921 | GG | GG |
| rs2024513 | CG | GG |
| rs2159100 | TT | CC |
| rs4129148 | GG | GG |
| rs28694718 | CG | CC |
| rs6422441 | TA | TT |
| rs17883192 | CG | GG |
| rs1801028 | GG | GG |
| rs2848745 | CG | GG |
| rs17651507 | TA | AA |
| rs2499846 | CG | GG |
| rs4958803 | CG | CC |
| rs2053149 | TA | TT |
| rs7582658 | AG | AA |
| rs2119783 | TC | TT |
| rs3131296 | CC | AA |
| rs2312147 | CC | TT |
| rs9960767 | AA | AA |
| rs1502844 | TC | TT |
| rs1572299 | TT | GG |
| rs17512836 | TT | TT |
| rs10503253 | CC | CC |
| rs7004633 | AG | GG |
| rs11191580 | TT | CC |

| | | |
|---|---|---|
| rs12966547 | AG | AA |
| rs1625579 | TT | CC |
| rs17662626 | AA | GG |
| rs2905424 | TC | CC |
| rs2437896 | TT | CC |



Risk level: average

**rs1006737:** A polymorphism of the potential-dependent calcium channel gene CACNA1C, is associated with risk of bipolar disorder, schizophrenia and other psychiatric disorders.
[ PMID 18711365 ] [ PMID 19358880 ] [ PMID 20098439 ]

**rs2312147:** Meta-analysis and brain imaging data support the involvement of VRK2 (rs2312147) in susceptibility to schizophrenia.
[ PMID 23102693 ] [ PMID 27382989 ]

**rs1625579:** The risk genotype MIR137HG rs1625579 is associated with corpus callosum volume in schizophrenia
[ PMID 26123324 ] [ PMID 27095331 ] [ PMID 31586698 ]

**rs6277:** Associated with a 1.6-fold increased risk of schizophrenia.
[ PMID 18255274 ] [ PMID 19158809 ] [ PMID 19197363 ] [ PMID 21981786 ]

**rs6603272:** Interleukin-3 receptor polymorphism is associated with schizophrenia, risk ratio 2.74.
[ PMID 18547720 ] [ PMID 19281803 ]

**rs947267:** Genetic variation in the DAOA gene is associated with schizophrenia and bipolar disorder.
[ PMID 18023149 ] [ PMID 19586533 ] [ PMID 28285246 ] [ PMID 30719257 ]

**rs1800532:** The haplotype of the tryptophan hydroxylase gene (TPH1) is associated with an increased risk of schizophrenia and suicidal tendencies.
[ PMID 19911060 ] [ PMID 27037949 ] [ PMID 30789538 ]

**rs2270641:** A break in the vesicular monoamine transporter gene SLC18A1 - 3.7 times higher risk of schizophrenia.
[ PMID 16936705 ] [ PMID 17134514 ]

## Autism

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1858830 | CG | GG |
| rs7794745 | AA | AA |
| rs4307059 | CC | CC |
| rs2710102 | AA | AA |
| rs10513025 | TC | TT |
| rs1804197 | CC | CC |
| rs4532 | CC | TT |
| rs914232 | CC | TT |
| rs3751582 | TC | TT |
| rs53576 | GG | GG |
| rs2254298 | CG | GG |
| rs2268491 | CC | CC |
| rs1487278 | TA | TT |
| rs3746544 | TT | GG |
| rs686 | GG | AA |
| rs265981 | AA | GG |
| rs6766410 | AC | CC |
| rs2217262 | AA | AA |
| rs1143674 | CG | GG |
| rs2745557 | CG | GG |
| rs6807362 | CG | CC |
| rs373126732 | AA | AA |
| rs184718561 | CG | CC |
| rs757972971 | CG | GG |
| rs2056202 | TA | TT |
| rs25531 | TA | TT |
| rs171748 | AG | GG |
| rs11191580 | TT | CC |
| rs211037 | CC | CC |

| | | |
|---|---|---|
| rs28914829 | CG | GG |
| rs6314 | GG | GG |
| rs6313 | AA | GG |
| rs1042714 | GG | CC |
| rs1079597 | CC | CC |
| rs167771 | AG | AA |



Risk level: average

**rs4532:** Affects dopamine D1 receptors associated with autism spectrum disorders.
[ PMID 18205172 ]

**rs914232:** The SLC19A1/RFC1 gene polymorphism is associated with autism spectrum disorders.
[ PMID 27213354 ]

**rs3746544:** Variations in the muscarinic acetylcholine receptor M2 (CHRM2) gene are associated with alcohol dependence and major depressive disorder.
[ PMID 22224195 ] [ PMID 23593184 ] [ PMID 23872233 ]

**rs6313:** TPH-2 polymorphisms affect response to treatment with antidepressants and SSRIs.
[ PMID 19184136 ] [ PMID 19197363 ] [ PMID 21172166 ] [ PMID 25108775 ] [ PMID 27091189 ] [ PMID 27445478 ] [ PMID 27521242 ] [ PMID 32819202 ]

**rs1042714:** Studies have shown an increased risk of polymorphism with autism. The odds ratio was 1.33-1.60. The risk was about twice as high among mothers who had clinical markers of pregnancy-related stress. The breakdown also indicated a predisposition to metabolic syndrome, obesity and increased risk of bronchial asthma.
[ PMID 9275150 ] [ PMID 14557466 ] [ PMID 15867853 ] [ PMID 16935688 ] [ PMID 17199132 ] [ PMID 17512307 ]

**rs1858830:** Associated with a 2-fold increase in autism risk based on research. Responsible for impaired cortical MET signalling in autism spectrum disorders.
[ PMID 17053076 ] [ PMID 19681062 ] [ PMID 17696172 ] [ PMID 20615438 ]

**rs10513025:** Based on a linkage mapping study it was found that rs10513025 is associated with autism, and it was observed that expression is reduced in the brains of autistic patients.
[ PMID 22739633 ]

**rs3751582:** GABRB3 a candidate gene for autism spectrum disorders.
[ PMID 24999380 ]

## ADHD (Attention Deficit Hyperactivity Disorder)

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs3746544 | TT | GG |
| rs27072 | CC | CC |
| rs1800544 | TA | TT |
| rs6296 | CC | CC |
| rs6265 | CC | CC |
| rs1843809 | TT | TT |
| rs1412005 | TG | GG |
| rs11074889 | AG | GG |
| rs3785143 | CG | CC |
| rs4747989 | CC | CC |
| rs7224199 | TA | TT |
| rs28914829 | CG | GG |
| rs11657536 | GG | GG |
| rs140700 | CC | CC |
| rs2066713 | GG | GG |
| rs2020933 | AA | AA |
| rs752306 | CC | CC |
| rs7722425 | TT | CC |
| rs11903187 | AG | GG |
| rs1515641 | CG | GG |
| rs4810796 | CG | GG |
| rs10463832 | CG | CC |
| rs12613775 | TC | CC |
| rs12513840 | AA | GG |
| rs910191 | GG | GG |
| rs9512900 | TC | TT |
| rs10229603 | TC | TT |
| rs789560 | TG | TT |
| rs6733379 | TG | TT |

| | | |
|---|---|---|
| rs2764980 | AA | GG |
| rs4533251 | GG | GG |
| rs1521882 | AG | GG |
| rs10492664 | TA | TT |
| rs7236632 | AA | GG |
| rs460000 | GG | GG |
| rs6347 | TT | TT |
| rs2617605 | CC | TT |
| rs28363168 | CG | CC |
| rs6869645 | CC | CC |
| rs2042449 | AG | GG |
| rs11568817 | TA | AA |
| rs130060 | AA | AA |
| rs363043 | TT | CC |
| rs363050 | CG | GG |
| rs363039 | AG | GG |
| rs363020 | AA | AA |
| rs6314 | GG | GG |
| rs1611115 | CC | CC |
| rs6332 | AA | GG |
| rs1801260 | AG | AA |
| rs1125394 | TA | TT |
| rs4436578 | TA | TT |
| rs1799978 | TT | TT |
| rs4460839 | TA | TT |
| rs4648317 | GG | GG |
| rs6277 | CG | GG |
| rs12363125 | TC | CC |
| rs2440390 | CG | CC |
| rs11214606 | CC | CC |
| rs1079597 | CC | CC |
| rs2283265 | AC | CC |

| | | |
|---|---|---|
| rs1800499 | CG | CC |
| rs2734833 | AG | GG |
| rs2734838 | AG | AA |
| rs1076563 | AA | AA |
| rs12364283 | AA | AA |
| rs5569 | GG | GG |
| rs1108580 | AG | AA |
| rs6565113 | CG | GG |
| rs552655 | AT | TT |
| rs550818 | TA | AA |
| rs998424 | CG | GG |
| rs11564750 | CG | GG |
| rs2652511 | CA | AA |
| rs1051312 | TC | TT |
| rs362987 | CC | AA |



Risk level: average

**rs3746544:** Variations in the muscarinic acetylcholine receptor M2 (CHRM2) gene are associated with alcohol dependence and major depressive disorder.
[ PMID 22224195 ] [ PMID 23593184 ] [ PMID 23872233 ]

**rs3785143:** A variant of a rare protective allele in the norepinephrine transporter gene causes risk of attention deficit hyperactivity disorder.
[ PMID 17876324 ] [ PMID 18937296 ] [ PMID 18937309 ] [ PMID 19698724 ] [ PMID 20159345 ]

**rs7224199:** Association with major depression and response to antidepressants. The polymorphism is associated with selective serotonin and serotonin-norepinephrine reuptake inhibitor response in depressive disorder.
[ PMID 19844206 ] [ PMID 26674707 ]

**rs28914829:** A polymorphism in the serotonin transporter locus (SLC6A4) predisposes to autism and compulsive rigid behaviour.
[ PMID 15995945 ]

**rs11568817:** Functional polymorphisms in the serotonin receptor gene HTR1B predict increased anger and hostility.
[ PMID 19350534 ] [ PMID 25658328 ]

**rs1125394:** The DRD2 polymorphism modulates reward and emotion processing, dopamine neurotransmission, and openness to experience.
[ PMID 22424959 ]

**rs4436578:** The dopamine D2 receptor gene is associated with weight gain in schizophrenic patients with long-term treatment with neuroleptics.
[ PMID 20375926 ] [ PMID 21185230 ] [ PMID 27853387 ]

**rs6277:** Associated with a 1.6-fold increased risk of schizophrenia.
[ PMID 18255274 ] [ PMID 19158809 ] [ PMID 19197363 ] [ PMID 21981786 ]

## Dementia

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs5848 | CG | CC |
| rs8070723 | AA | AA |
| rs9268856 | CC | CC |
| rs17125944 | TT | TT |
| rs1476679 | TT | TT |
| rs10498633 | GG | GG |
| rs10792832 | AG | GG |
| rs9969729 | GG | GG |
| rs9331896 | CC | CC |
| rs35349669 | CC | CC |
| rs3865444 | AA | CC |
| rs6733839 | TC | CC |
| rs4676049 | CC | CC |
| rs6859 | AG | AA |
| rs190982 | AG | GG |
| rs4937314 | AA | AA |
| rs6656401 | GG | GG |
| rs983392 | AG | AA |
| rs11983798 | AG | GG |
| rs6468852 | AG | AA |
| rs744373 | AA | AA |
| rs2075650 | AA | AA |
| rs9271192 | AA | AA |
| rs10948363 | AA | AA |
| rs12947764 | TA | TT |
| rs242557 | CG | GG |
| rs3785885 | CG | GG |
| rs4647698 | CG | CC |
| rs1799724 | TC | CC |

| | | |
|---|---|---|
| rs190788828 | TA | AA |
| rs115550680 | AA | AA |



Risk level: average

**rs3865444:** Association of the CD33 rs3865444 polymorphism with Alzheimer's disease pathology and CD33 expression in human cerebral cortex.
[ PMID 23708142 ] [ PMID 25448602 ] [ PMID 26933222 ] [ PMID 35888182 ]

**rs5848:** Common variation in the GRN gene is a major risk factor for TDP43-positive frontal temporal dementia.
[ PMID 18723524 ] [ PMID 19640594 ] [ PMID 20711061 ]

**rs242557:** High levels of cerebrospinal tau are associated with the rs242557 gene variant and a high risk of Parkinson's and Alzheimer's disease.
[ PMID 19308965 ] [ PMID 19912324 ] [ PMID 20951764 ] [ PMID 26303052 ]

**rs1799724:** Polymorphism rs1799724 of the tumour necrosis factor alpha gene in Alzheimer's disease.
[ PMID 11273064 ] [ PMID 33226368 ]

## Obsessive-compulsive disorder (OCD)

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs25532 | AA | AA |
| rs16965628 | CG | GG |
| rs1176713 | AA | AA |
| rs3780412 | TA | TT |
| rs2228622 | AG | GG |
| rs890 | TA | TT |
| rs301443 | GC | GG |
| rs25531 | TA | TT |
| rs1805476 | GG | GG |
| rs3780413 | CG | GG |
| rs4565946 | TT | CC |
| rs6265 | CC | CC |
| rs7997012 | GG | AA |
| rs3737193 | AA | AA |
| rs1232487 | CC | CC |
| rs3177118 | GG | GG |
| rs116567227 | CG | GG |
| rs1805088 | CG | CC |
| rs10835210 | AA | CC |
| rs9652236 | GG | GG |
| rs10974587 | TC | TT |
| rs10974584 | TC | TT |
| rs3776512 | GG | GG |
| rs460000 | GG | GG |
| rs3780415 | TC | TT |
| rs27072 | CC | CC |
| rs7022772 | CC | CC |
| rs28363168 | CG | CC |
| rs7848533 | AC | CC |

| | | |
|---|---|---|
| rs3087879 | CG | GG |
| rs2617605 | CC | TT |
| rs16921385 | AG | AA |
| rs10879346 | CC | CC |
| rs4460839 | TA | TT |
| rs301430 | TC | TT |
| rs7298664 | TT | TT |
| rs1125394 | TA | TT |
| rs737866 | TT | TT |
| rs1843809 | TT | TT |
| rs1799913 | TT | GG |
| rs61888800 | CG | GG |
| rs7224199 | TA | TT |
| rs5993883 | TG | TT |
| rs9325202 | GG | GG |
| rs6277 | CG | GG |
| rs35815285 | CG | GG |
| rs4648317 | GG | GG |
| rs769224 | GG | GG |
| rs2039290 | CG | GG |
| rs6313 | AA | GG |
| rs6314 | GG | GG |
| rs1081003 | CG | GG |
| rs6305 | CG | GG |
| rs56232120 | CG | GG |
| rs28914829 | CG | GG |
| rs3773678 | AG | GG |
| rs4764011 | CG | GG |
| rs9316232 | GG | GG |
| rs4680 | AG | GG |
| rs6267 | GG | GG |
| rs1928040 | CG | GG |

| | | |
|---|---|---|
| rs12579598 | CG | GG |
| rs11657536 | GG | GG |
| rs2160734 | TC | CC |
| rs10814991 | TC | CC |
| rs9567737 | TT | CC |
| rs2268102 | CC | CC |
| rs7124442 | TT | TT |
| rs6296 | CC | CC |
| rs2283265 | AC | CC |
| rs4742007 | CC | CC |
| rs9332377 | CC | CC |
| rs165631 | CG | CC |
| rs10748189 | CG | CC |
| rs9332316 | CC | CC |
| rs17834128 | CG | CC |
| rs1062613 | TT | CC |
| rs11214606 | CC | CC |
| rs1806202 | CG | CC |
| rs2300252 | CC | CC |
| rs17110563 | CC | CC |
| rs6311 | TT | CC |
| rs140700 | CC | CC |
| rs10499905 | AC | CC |
| rs28371725 | CC | CC |
| rs10232398 | AG | AA |
| rs12583882 | AA | AA |
| rs676643 | CG | GG |
| rs220597 | AG | GG |
| rs1805502 | AG | AA |
| rs1568214 | GG | GG |
| rs849876 | AA | AA |
| rs2734838 | AG | AA |

| | | |
|---|---|---|
| rs2066713 | GG | GG |
| rs1019385 | AC | CC |
| rs211107 | AA | CC |
| rs737865 | AA | AA |
| rs7297761 | AA | AA |
| rs167771 | AG | AA |
| rs3742278 | AA | AA |
| rs2150195 | GG | GG |
| rs9824856 | TA | AA |
| rs297941 | GG | GG |
| rs1057519438 | CG | CC |
| rs9499708 | TC | TT |
| rs4570625 | GG | GG |



Risk level: average

**rs7997012:** Associations of the serotonin receptor gene HTR2A with bipolar disorder and major depressive disorder.
[ PMID 19428704 ] [ PMID 24885933 ] [ PMID 30178121 ]

**rs1799913:** Variants in the tryptophan hydroxylase gene involved in the development and treatment of opiate, heroin and cocaine addiction.
[ PMID 18181017 ] [ PMID 20201854 ] [ PMID 26227246 ] [ PMID 28590957 ]

**rs6313:** TPH-2 polymorphisms affect response to treatment with antidepressants and SSRIs.
[ PMID 19184136 ] [ PMID 19197363 ] [ PMID 21172166 ] [ PMID 25108775 ] [ PMID 27091189 ] [ PMID 27445478 ] [ PMID 27521242 ] [ PMID 32819202 ]

**rs1062613:** Fear reactivation and symptoms of combat-related PTSD: specificity and preliminary study of the effect of the 5-HT3A receptor gene.
[ PMID 35413654 ]

**rs6311:** Genetic factors specific to obsessive-compulsive disorder.
[ PMID 25017045 ] [ PMID 26616111 ] [ PMID 28576508 ] [ PMID 29331882 ] [ PMID 29785111 ]

**rs16965628:** A genetic polymorphism of the serotonin transporter gene, SLC6A4 rs16965628, is associated with obsessive-compulsive disorder.
[ PMID 18055562 ] [ PMID 25751280 ]

**rs3780412:** Association of the glutamate transporter gene SLC1A1 with atypical obsessive-compulsive symptoms induced by neuroleptics.
[ PMID 16818867 ] [ PMID 17894418 ] [ PMID 19349310 ] [ PMID 19884611 ] [ PMID 22531293 ] [ PMID 30661718 ] [ PMID 33574671 ]

**rs2228622:** Association between the SLC1A1 gene and early onset of obsessive-compulsive disorder. [ PMID 17894418 ] [ PMID 19884611 ] [ PMID 21990008 ] [ PMID 22531293 ] [ PMID 23411042 ] [ PMID 23564280 ] [ PMID 23660601 ] [ PMID 30315580 ]

## Suicidal tendencies

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs4675690 | CG | CC |
| rs300774 | AC | CC |
| rs7296262 | CG | CC |
| rs320461 | TT | CC |
| rs358592 | TT | TT |
| rs2419374 | TC | CC |
| rs2462021 | TA | TT |
| rs2610025 | CG | GG |
| rs3019286 | GG | GG |
| rs3781878 | AG | GG |
| rs4308128 | TA | AA |
| rs4732812 | CC | CC |
| rs4918918 | TC | CC |
| rs6055685 | GG | GG |
| rs6480463 | TT | TT |
| rs7011192 | GG | GG |
| rs7079041 | CG | GG |
| rs7244261 | CG | CC |
| rs7569963 | AA | AA |
| rs10437629 | AA | AA |
| rs10448044 | TA | TT |
| rs10748045 | AA | AA |
| rs10854398 | CC | TT |
| rs11143230 | AA | AA |
| rs11852984 | AA | AA |
| rs12373805 | AA | GG |
| rs13358904 | AG | AA |
| rs17387100 | AA | AA |

Risk level: average

**rs4675690:** Neurotrophin gene breakdown and antidepressant-enhanced suicidal ideation
[ PMID 20504254 ] [ PMID 21807415 ] [ PMID 24955721 ] [ PMID 27378793 ]

**rs300774:** Replication of rs300774, a genetic biomarker near ACP1 associated with suicide attempts.
[ PMID 21423239 ] [ PMID 27721799 ] [ PMID 28668716 ]

**rs7296262:** A genetic marker associated with suicide attempts: association with cholesterol biosynthesis in the brain.
[ PMID 21423239 ] [ PMID 28668716 ]

**rs2462021:** Increased risk of suicide attempts in patients with mood disorders.
[ PMID 21041247 ]

## Alcohol dependence

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs671 | GG | GG |
| rs2232165 | CG | GG |
| rs1614972 | CC | TT |
| rs17033 | TA | TT |
| rs3762894 | TT | TT |
| rs2238151 | TC | CC |
| rs1159918 | AA | AA |
| rs1042026 | AA | TT |
| rs2075633 | TT | TT |
| rs1353899 | TG | TT |
| rs2827312 | TG | TT |
| rs4770403 | GG | GG |
| rs728115 | GG | GG |
| rs9556711 | GG | AA |
| rs36563 | TG | GG |
| rs8062326 | GG | GG |
| rs4478858 | TT | TT |
| rs11933661 | TA | TT |
| rs933769 | CG | CC |
| rs10253361 | TT | TT |
| rs16985179 | CC | CC |
| rs10893366 | TT | CC |
| rs1793257 | CG | CC |
| rs1789891 | AC | CC |
| rs768048 | TC | TT |
| rs2826659 | AC | CC |
| rs3131513 | AA | AA |
| rs7590720 | AG | AA |
| rs2548145 | AG | AA |

| | | |
|---|---|---|
| rs2810114 | AC | AA |
| rs6701037 | AC | AA |
| rs7144649 | AA | AA |
| rs750338 | GG | AA |
| rs4293630 | AA | GG |
| rs237238 | AA | GG |
| rs27072 | CC | CC |
| rs2948694 | AA | AA |
| rs1799971 | AA | AA |
| rs968529 | CC | CC |
| rs2066701 | CG | GG |
| rs324650 | TA | TT |
| rs2061174 | AA | AA |
| rs1824024 | AC | AA |
| rs27048 | TT | TT |
| rs13273672 | TT | TT |
| rs11640875 | GG | AA |
| rs1229976 | TT | TT |
| rs1344694 | TG | GG |
| rs279858 | CC | TT |



Risk level: average

**rs1614972:** Strong association of the alcohol dehydrogenase 1B (ADH1B) gene with alcohol dependence and alcohol-related medical conditions.
[ PMID 18331377 ] [ PMID 21497796 ]

**rs2232165:** Genetic variation in the ghrelin signalling system is associated with severe alcohol dependence in women.
[ PMID 18828808 ] [ PMID 20586762 ] [ PMID 25278825 ]

**rs17033:** ADH1B Arg47His polymorphism of the alcohol metabolising gene with alcohol dependence.
[ PMID 18331377 ] [ PMID 19298322 ] [ PMID 21083667 ]

**rs1789891:** Alcohol dehydrogenase gene rs1789891 polymorphism with brain grey matter volume, alcohol consumption, alcohol craving and relapse risk.
[ PMID 22004471 ] [ PMID 26013422 ] [ PMID 29058369 ]

**rs7590720:** Genetic predisposition to alcoholism.
[ PMID 20202923 ] [ PMID 21314694 ] [ PMID 21471458 ] [ PMID 21876473 ]

**rs324650:** Variation in the muscarinic acetylcholine receptor M2 (CHRM2) gene is associated with alcohol dependence and major depressive disorder.
[ PMID 15229186 ] [ PMID 18634760 ] [ PMID 21176104 ]

## Tobacco addiction

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs16969968 | AG | GG |
| rs1051730 | AG | GG |
| rs3003609 | TT | CC |
| rs9217 | TC | TT |
| rs12910984 | AA | GG |
| rs12914385 | TC | CC |
| rs1317286 | AG | AA |
| rs3743073 | TA | TT |
| rs3743074 | AG | AA |
| rs3743075 | AC | CC |
| rs3743076 | AA | TT |
| rs3743077 | TC | CC |
| rs3743078 | CG | CC |
| rs4887067 | CG | GG |
| rs6495308 | TT | TT |
| rs6495309 | CC | CC |
| rs660652 | AG | GG |
| rs8023462 | TC | TT |
| rs8040868 | TC | TT |
| rs8042374 | AA | AA |
| rs8192482 | CG | CC |
| rs938682 | AA | GG |
| rs737865 | AA | AA |
| rs279858 | CC | TT |
| rs11200638 | CG | GG |
| rs1800497 | AG | GG |
| rs1049331 | CG | CC |
| rs2672598 | TA | TT |
| rs1938901 | CG | GG |

| | | |
|---|---|---|
| rs996999 | CG | CC |
| rs2229940 | CG | GG |
| rs1044396 | AA | AA |
| rs1044394 | GG | AA |
| rs1044397 | CG | CC |
| rs121909580 | GG | GG |
| rs121912243 | GG | GG |
| rs2236196 | AA | GG |
| rs2273502 | CG | CC |
| rs2273504 | CG | GG |
| rs2273505 | AC | CC |
| rs3787137 | CG | GG |
| rs4522666 | AA | GG |
| rs755204 | CG | GG |
| rs796052317 | AA | AA |
| rs684513 | CC | CC |
| rs588765 | AC | CC |
| rs13277254 | AA | AA |
| rs2072660 | CC | TT |
| rs4953 | CG | GG |
| rs2036527 | AG | GG |
| rs680244 | TC | CC |
| rs4952 | CC | CC |
| rs17487223 | TC | CC |
| rs11637635 | AG | GG |
| rs12898919 | CG | GG |
| rs17408276 | AA | TT |
| rs17486278 | AC | AA |
| rs3829787 | CG | CC |
| rs495956 | AA | TT |
| rs503464 | TA | TT |
| rs555018 | TA | AA |

| | | |
|---|---|---|
| rs55781567 | CG | CC |
| rs55853698 | TG | TT |
| rs569207 | CC | CC |
| rs601079 | TA | TT |
| rs6495306 | TA | AA |
| rs667282 | TT | TT |
| rs951266 | AG | GG |
| rs8034191 | TC | TT |



Risk level: average

**rs3003609:** The (T) rs3003609 allele is associated with heavier smoking and hence nicotine dependence, at least in Caucasians.
[ PMID 18987626 ] [ PMID 27166759 ]

**rs16969968:** The nicotinic acetylcholine receptor risk allele in CHRNA5 causes a higher risk of nicotine dependence, lung cancer, but a lower risk of cocaine dependence.
[ PMID 18227835 ] [ PMID 18385738 ] [ PMID 18519132 ] [ PMID 18519524 ] [ PMID 18957677 ] [ PMID 19010884 ] [ PMID 20581870 ] [ PMID 29993116 ]

**rs1051730:** CHRNA3 single nucleotide polymorphism increases the risk of lung cancer by 1.8 times. It also contributes to a decreased response to alcohol, so there may be an increased risk of alcohol abuse.
[ PMID 19465454 ] [ PMID 19733931 ] [ PMID 23056235 ]

**rs1317286:** Alleles of alpha-5/alpha-3 nicotinic receptor subunits increase the risk of heavy smoking.
[ PMID 18227835 ] [ PMID 20808433 ]

**rs4887067:** CHRNA5-A3-B4 region as a risk factor for age-related nicotine dependence.
[ PMID 18618000 ]

**rs1800497:** TaqIA polymorphisms of the DRD2 dopamine D2 receptor gene are associated with concomitant alcohol use and depressive disorders.
[ PMID 1969501 ] [ PMID 9650634 ] [ PMID 17989061 ] [ PMID 20146828 ] [ PMID 20180986 ] [ PMID 20482509 ] [ PMID 21083670 ] [ PMID 22698582 ] [ PMID 22728571 ] [ PMID 22978509 ]

**rs755204:** Association between CHRN genetic variants and dizziness on first inhalation of cigarette smoke.
[ PMID 24119711 ]

**rs8034191:** A region of chromosome 5p15 associated with the risk of adenocarcinoma.
[ PMID 18385676 ] [ PMID 19641473 ] [ PMID 19836008 ] [ PMID 24254305 ]

## Drug dependence

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1799971 | AA | AA |
| rs5326 | CC | CC |
| rs1799913 | TT | GG |
| rs3778151 | CG | CC |
| rs2236857 | TT | TT |
| rs694066 | CG | GG |
| rs1534891 | TT | CC |
| rs1022563 | CG | CC |
| rs1800497 | AG | GG |
| rs510769 | CG | CC |
| rs6473797 | TA | TT |
| rs2236861 | GG | GG |
| rs3766951 | TT | TT |
| rs3758987 | TT | TT |
| rs737866 | TT | TT |
| rs6882300 | AA | AA |
| rs2952768 | TC | TT |
| rs1045642 | GG | AA |
| rs1128503 | GG | GG |
| rs6275 | AG | AA |
| rs1714984 | CG | GG |
| rs965972 | AA | AA |
| rs1867898 | CG | GG |
| rs5443 | TC | CC |
| rs12364283 | AA | AA |
| rs4648317 | GG | GG |
| rs910079 | AA | AA |
| rs2283265 | AC | CC |
| rs16969968 | AG | GG |

| | | |
|---|---|---|
| rs9387522 | CG | CC |
| rs11503014 | CG | CC |
| rs910080 | AG | AA |
| rs737865 | AA | AA |
| rs1997794 | TC | TT |
| rs2239670 | AG | GG |
| rs12749204 | AA | AA |
| rs72840936 | CG | GG |
| rs111325002 | AA | AA |
| rs4129566 | AA | TT |
| rs11944332 | AA | AA |
| rs75686122 | CG | CC |
| rs11575893 | CC | CC |



Risk level: average

**rs1799913:** Variants in the tryptophan hydroxylase gene involved in the development and treatment of opiate, heroin and cocaine addiction.
[ PMID 18181017 ] [ PMID 20201854 ] [ PMID 26227246 ] [ PMID 28590957 ]

**rs1534891:** Csnk1e is a genetic regulator of sensitivity to psychostimulants and opioids.
[ PMID 22089318 ]

**rs1022563:** Polymorphisms of the prodynorphin (PDYN) gene are associated with heroin and cocaine dependence.
[ PMID 19298317 ] [ PMID 22443215 ] [ PMID 32597371 ]

**rs1800497:** TaqIA polymorphisms of the DRD2 dopamine D2 receptor gene are associated with concomitant alcohol use and depressive disorders.
[ PMID 1969501 ] [ PMID 9650634 ] [ PMID 17989061 ] [ PMID 20146828 ] [ PMID 20180986 ] [ PMID 20482509 ] [ PMID 21083670 ] [ PMID 22698582 ] [ PMID 22728571 ] [ PMID 22978509 ]

**rs2283265:** Functional variants of the dopamine receptor gene are a potential factor in neuropsychiatric disorders.
[ PMID 21438146 ] [ PMID 24495967 ] [ PMID 33529975 ]

**rs16969968:** The nicotinic acetylcholine receptor risk allele in CHRNA5 causes a higher risk of nicotine dependence, lung cancer, but a lower risk of cocaine dependence.
[ PMID 18227835 ] [ PMID 18385738 ] [ PMID 18519132 ] [ PMID 18519524 ] [ PMID 18957677 ] [ PMID 19010884 ] [ PMID 20581870 ] [ PMID 29993116 ]

## Depression

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1360780 | CG | CC |
| rs7174755 | TC | TT |
| rs12054895 | GG | GG |
| rs6305 | CG | GG |
| rs6314 | GG | GG |
| rs6313 | AA | GG |
| rs4570625 | GG | GG |
| rs1006737 | AA | GG |
| rs5443 | TC | CC |
| rs7412 | CC | CC |
| rs1805054 | CC | CC |
| rs6537837 | CC | CC |
| rs6311 | TT | CC |
| rs1386494 | CG | CC |
| rs242941 | CG | CC |
| rs6265 | CC | CC |
| rs11568817 | TA | AA |
| rs110402 | AA | AA |
| rs7997012 | GG | AA |
| rs310501 | GG | AA |
| rs1545843 | CG | GG |
| rs2522833 | AA | AA |
| rs10065906 | AA | AA |
| rs17144465 | AA | AA |
| rs7647854 | AA | AA |
| rs7713917 | GG | AA |
| rs324650 | TA | TT |
| rs1799913 | TT | GG |
| rs1824024 | AC | AA |

| | | |
|---|---|---|
| rs2061174 | AA | AA |
| rs737865 | AA | AA |
| rs7757037 | AG | GG |
| rs2766535 | AA | GG |
| rs3800373 | AC | AA |
| rs264272 | GG | TT |
| rs10174573 | CG | CC |
| rs2462686 | AA | TT |
| rs10520045 | GG | GG |
| rs7742824 | GG | GG |
| rs12210761 | GG | GG |
| rs166040 | GG | AA |
| rs9943849 | CC | CC |
| rs606149 | TC | CC |
| rs9601248 | TT | TT |
| rs912988 | TC | CC |
| rs6534441 | TC | TT |
| rs2721937 | CC | CC |
| rs1780436 | AG | GG |
| rs974379 | AA | AA |
| rs4625554 | AA | AA |
| rs4238010 | AA | AA |
| rs9805786 | TG | TT |
| rs3827730 | TT | TT |
| rs17750015 | TT | TT |
| rs237899 | AG | GG |
| rs729861 | N/A | AA |
| rs3770018 | TA | AA |
| rs7933505 | AA | GG |
| rs1031681 | CC | CC |
| rs1549870 | CG | GG |
| rs1880916 | CG | GG |

| | | |
|---|---|---|
| rs1954787 | TC | TT |
| rs10514299 | CC | CC |
| rs2179744 | CG | GG |
| rs454214 | CG | CC |
| rs301806 | CC | CC |
| rs1475120 | AA | AA |
| rs10786831 | CA | AA |
| rs12552 | GG | GG |
| rs6476606 | TA | AA |
| rs8025231 | CA | AA |
| rs12065553 | GG | AA |
| rs1656369 | AA | AA |
| rs4543289 | CG | GG |
| rs2125716 | GG | AA |
| rs2422321 | CA | AA |
| rs7044150 | CG | CC |



Risk level: average

**rs6313:** TPH-2 polymorphisms affect response to treatment with antidepressants and SSRIs.
[ PMID 19184136 ] [ PMID 19197363 ] [ PMID 21172166 ] [ PMID 25108775 ] [ PMID 27091189 ] [ PMID 27445478 ] [ PMID 27521242 ] [ PMID 32819202 ]

**rs1006737:** A polymorphism of the potential-dependent calcium channel gene CACNA1C, is associated with risk of bipolar disorder, schizophrenia and other psychiatric disorders.
[ PMID 18711365 ] [ PMID 19358880 ] [ PMID 20098439 ]

**rs6311:** Genetic factors specific to obsessive-compulsive disorder.
[ PMID 25017045 ] [ PMID 26616111 ] [ PMID 28576508 ] [ PMID 29331882 ] [ PMID 29785111 ]

**rs7997012:** Associations of the serotonin receptor gene HTR2A with bipolar disorder and major depressive disorder.
[ PMID 19428704 ] [ PMID 24885933 ] [ PMID 30178121 ]

**rs1799913:** Variants in the tryptophan hydroxylase gene involved in the development and treatment of opiate, heroin and cocaine addiction.
[ PMID 18181017 ] [ PMID 20201854 ] [ PMID 26227246 ] [ PMID 28590957 ]

**rs1360780:** Polymorphisms in the FK506 protein gene are associated with attention deficit hyperactivity disorder and increased daily cortisol levels. It is also associated with an increased risk of depression with an odds ratio of 1.39.

[ PMID 21316860 ] [ PMID 24166410 ] [ PMID 26032970 ]

**rs6305:** Serotonin transporter and serotonin receptor gene polymorphisms are associated with susceptibility to substance abuse.
[ PMID 22933845 ]

**rs1386494:** TPH2 gene polymorphism increases the risk and magnitude of depressive disorder.
[ PMID 19590397 ] [ PMID 22693556 ] [ PMID 29314569 ]

## Diseases of the nervous system

## Multiple sclerosis

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs4149584 | TC | CC |
| rs6680578 | TA | TT |
| rs4728142 | AA | GG |
| rs3135391 | GG | GG |
| rs1321172 | CG | CC |
| rs9282860 | CG | CC |
| rs8702 | CG | CC |
| rs926103 | TC | GG |
| rs17445836 | CG | GG |
| rs929230 | GG | GG |
| rs12722561 | CC | CC |
| rs3807306 | TT | GG |
| rs7775228 | TT | TT |
| rs2155219 | TT | TT |
| rs2858331 | GG | AA |
| rs9275572 | GG | GG |
| rs6897932 | CC | CC |
| rs3194051 | GG | AA |
| rs9271366 | AA | AA |
| rs2734583 | AA | AA |
| rs660895 | AA | AA |
| rs35445101 | CA | AA |
| rs2303759 | TT | TT |
| rs4613763 | TT | TT |
| rs6984045 | TT | TT |
| rs1800693 | TC | TT |
| rs2243123 | TC | TT |
| rs2019960 | TT | TT |

| | | |
|---|---|---|
| rs6604026 | TT | TT |
| rs2104286 | TT | TT |
| rs1077667 | TC | CC |
| rs2283792 | GG | GG |
| rs1841770 | TG | TT |
| rs7238078 | TT | TT |
| rs13192841 | GG | GG |
| rs10411936 | CG | GG |
| rs3135388 | GG | GG |
| rs3761959 | TC | CC |
| rs2425752 | TC | CC |
| rs4410871 | TC | CC |
| rs170934 | CC | CC |
| rs8070463 | TC | CC |
| rs9292777 | TT | CC |
| rs882300 | TC | CC |
| rs7595037 | TC | TT |
| rs3135338 | TT | TT |
| rs2300603 | TC | TT |
| rs2293152 | CG | CC |
| rs4939490 | CC | CC |
| rs17824933 | CC | CC |
| rs11154801 | AA | CC |
| rs7255066 | TC | CC |
| rs17174870 | CC | CC |
| rs806321 | TC | CC |
| rs13333054 | TT | CC |
| rs6952809 | TT | CC |
| rs12048904 | TC | TT |
| rs10492972 | TT | TT |
| rs630923 | CC | CC |
| rs11810217 | CC | CC |

| | | |
|---|---|---|
| rs12722489 | CC | CC |
| rs650258 | TC | CC |
| rs2248359 | TC | CC |
| rs2523393 | AA | AA |
| rs2293370 | GG | GG |
| rs6498169 | AG | AA |
| rs7592330 | AG | AA |
| rs7789940 | AA | AA |
| rs17066096 | AA | AA |
| rs744166 | AG | AA |
| rs354033 | AG | GG |
| rs180515 | AG | AA |
| rs10984447 | AG | AA |
| rs2546890 | AG | GG |
| rs228614 | AA | AA |
| rs233100 | AA | GG |
| rs874628 | AG | AA |
| rs12212193 | GG | AA |
| rs12368653 | GG | GG |
| rs6718520 | AG | GG |
| rs669607 | AA | AA |
| rs6896969 | CC | AA |
| rs9891119 | AC | AA |
| rs12466022 | AC | CC |
| rs2119704 | CC | CC |
| rs4285028 | CC | AA |
| rs4648356 | AC | CC |
| rs908821 | CA | AA |
| rs3780792 | AA | AA |
| rs2300747 | TA | AA |
| rs2040406 | TA | AA |
| rs1335532 | AA | AA |

| | | |
|---|---|---|
| rs11581062 | AA | AA |
| rs11962089 | AA | AA |
| rs3129889 | AA | AA |
| rs290986 | AA | AA |
| rs10466829 | AA | AA |
| rs2744148 | AA | AA |
| rs12487066 | TT | TT |
| rs7577363 | CG | GG |
| rs7536563 | GG | GG |
| rs12044852 | CC | CC |
| rs11164838 | TT | CC |
| rs10735781 | CG | CC |
| rs4763655 | AA | GG |
| rs10975200 | AA | AA |
| rs4959039 | AA | AA |
| rs9657904 | TT | TT |
| rs10201872 | CC | CC |
| rs1386330 | TT | TT |
| rs1557351 | TT | TT |
| rs17157903 | CC | CC |
| rs12047808 | AA | AA |
| rs2842483 | GG | AA |
| rs3129934 | CC | CC |
| rs3913163 | TT | TT |
| rs77360604 | TA | TT |
| rs13115869 | TA | TT |
| rs2200997 | TT | TT |
| rs10519631 | GG | GG |
| rs1364920 | GG | GG |
| rs2636670 | GG | GG |
| rs2636683 | TC | CC |
| rs336408 | CC | CC |

| | | |
|---|---|---|
| rs2172023 | CG | CC |
| rs79442729 | CG | CC |
| rs1992418 | GG | GG |
| rs12504681 | AA | AA |
| rs7295402 | TT | TT |
| rs2216228 | TC | TT |
| rs10841979 | TC | CC |
| rs2268858 | TG | TT |
| rs2300726 | TC | CC |
| rs10459079 | TC | CC |
| rs2418058 | GG | GG |
| rs12817074 | AG | GG |
| rs2728827 | AG | AA |
| rs2268861 | GG | GG |
| rs4762899 | CG | CC |
| rs2300731 | CC | CC |
| rs7964012 | AG | AA |
| rs704219 | CG | GG |
| rs6993386 | AG | AA |
| rs9282641 | GG | GG |
| rs11117432 | GG | GG |
| rs3130058 | CC | CC |
| rs2239709 | CG | CC |
| rs2920001 | TT | TT |
| rs7923837 | AG | GG |
| rs771767 | AG | GG |
| rs17090640 | GG | GG |
| rs703842 | GG | GG |
| rs1821625 | GG | GG |
| rs12513380 | AG | GG |
| rs2069763 | CG | CC |
| rs140915863 | CG | CC |

| | | |
|---|---|---|
| rs201921967 | TA | AA |
| rs765866317 | CG | GG |
| rs870849 | TC | CC |
| rs12708716 | AG | GG |
| rs2041670 | AG | GG |
| rs3853601 | CC | CC |
| rs3093976 | GG | GG |
| rs3093948 | GG | GG |
| rs2516393 | CC | CC |



Risk level: average

**rs4728142:** Validation of IRF5 as a multiple sclerosis risk gene: putative role in human herpes virus-6 infection.
[ PMID 18285424 ] [ PMID 20861862 ]

**rs926103:** SH2D2A gene breakage may contribute to susceptibility to multiple sclerosis.
[ PMID 18554728 ]

**rs2858331:** Together with the rs4988889 gene breakage, it is a diagnostic criterion for celiac disease.

**rs3194051:** Alteration of the interleukin 7 receptor (IL7R) alpha chain influences the risk of multiple sclerosis.
[ PMID 15674389 ] [ PMID 17660816 ] [ PMID 19221116 ] [ PMID 28446795 ]

**rs4149584:** Genetic association of TNFRSF1A variant with multiple sclerosis, odds ratio is 1.6
[ PMID 19525953 ] [ PMID 20362272 ] [ PMID 20430450 ] [ PMID 23624563 ] [ PMID 28927886 ] [ PMID 35963536 ]

**rs6680578:** A variant of the ecotropic viral integration 5 (EVI5) gene is associated with multiple sclerosis.
[ PMID 19865102 ] [ PMID 20087403 ] [ PMID 26433934 ] [ PMID 29141798 ] [ PMID 32152937 ]

**rs1321172:** Slightly higher (1.08 times) risk of multiple sclerosis.
[ PMID 32760600 ]

**rs9282860:** Liver B1 kinase kinase polymorphism increases 2-fold risk of multiple sclerosis.
[ PMID 34371271 ]

## Parkinson's disease

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs112176450 | GG | GG |
| rs34778348 | GG | GG |
| rs34637584 | CG | GG |
| rs11931074 | GG | GG |
| rs4998386 | CC | CC |
| rs356219 | AG | AA |
| rs33939927 | CC | CC |
| rs2736990 | AG | AA |
| rs12456492 | AG | AA |
| rs421016 | TA | AA |
| rs287235 | CG | GG |
| rs11176013 | AG | AA |
| rs34410987 | CC | CC |
| rs34995376 | GG | GG |
| rs35870237 | TT | TT |
| rs356220 | TC | CC |
| rs11248060 | TC | CC |
| rs6812193 | TT | CC |
| rs838552 | AA | AA |
| rs283413 | CC | CC |
| rs1559085 | AA | AA |
| rs10513789 | TT | TT |
| rs11564148 | AT | TT |
| rs281865052 | AA | AA |
| rs281865054 | GG | GG |
| rs33949390 | GG | GG |
| rs34594498 | CC | CC |
| rs34805604 | AA | AA |
| rs35801418 | AA | AA |

| | | |
|---|---|---|
| rs35808389 | AA | AA |
| rs3761863 | TC | AA |
| rs7133914 | GG | GG |
| rs7308720 | CC | CC |
| rs74163686 | AA | AA |
| rs78365431 | GG | GG |
| rs1442190 | GG | GG |
| rs3129882 | GG | AA |
| rs17577094 | AA | AA |
| rs7971935 | CG | GG |
| rs393152 | AA | GG |
| rs1866995 | AA | AA |
| rs2846468 | AG | AA |
| rs12174214 | TT | TT |
| rs2849518 | TC | CC |
| rs7454474 | CC | AA |
| rs10918270 | CG | GG |
| rs1941184 | AA | AA |
| rs1994090 | GG | TT |
| rs2395163 | TT | TT |
| rs2102808 | CG | GG |
| rs9917256 | GG | GG |
| rs12726330 | GG | GG |
| rs6599389 | GG | GG |
| rs7617877 | AG | GG |
| rs6430538 | TC | TT |
| rs12063142 | TC | CC |
| rs199515 | CC | CC |
| rs6532194 | CC | CC |
| rs12431733 | CC | CC |
| rs11248051 | TC | CC |
| rs34372695 | CC | CC |

| | | |
|---|---|---|
| rs12185268 | AA | AA |
| rs199533 | GG | GG |
| rs823156 | AA | AA |
| rs947211 | GG | GG |
| rs8070723 | AA | AA |
| rs4698412 | AG | GG |
| rs11711441 | GG | GG |
| rs183211 | GG | GG |
| rs10464059 | GG | GG |
| rs6532197 | AA | AA |
| rs2242330 | AA | AA |
| rs4538475 | AG | AA |
| rs10519131 | AA | AA |
| rs823128 | AA | AA |
| rs2723264 | TC | CC |
| rs11564187 | TA | AA |
| rs4912537 | CG | CC |
| rs117499775 | AT | TT |
| rs2435203 | TA | TT |
| rs12947764 | TA | TT |
| rs242557 | CG | GG |
| rs11868035 | AG | AA |
| rs3775442 | CC | CC |
| rs66737902 | TA | TT |
| rs1630500 | GG | GG |
| rs3889917 | TT | TT |
| rs2619369 | AA | AA |
| rs2275336 | GG | GG |
| rs11026412 | CG | GG |
| rs35095275 | CG | GG |
| rs775129424 | CG | GG |

Risk level: low

**rs6812193:** SCARB2 gene expression as an essential genetic component for Parkinson's disease.
[ PMID 21738488 ] [ PMID 23473716 ] [ PMID 25929833 ] [ PMID 26793951 ]

**rs3761863:** Missense LRRK2 variant is a risk factor for Parkinson's disease.
[ PMID 16960813 ] [ PMID 17614198 ] [ PMID 18952485 ] [ PMID 20301387 ] [ PMID 20669299 ] [ PMID 21885347 ]

**rs3129882:** The HLA-DRB1 allele variant is associated with susceptibility to sporadic Parkinson's disease.
[ PMID 20711177 ] [ PMID 21425343 ] [ PMID 21482477 ] [ PMID 22096524 ] [ PMID 23083294 ] [ PMID 23139797 ] [ PMID 25319953 ] [ PMID 32253955 ]

**rs393152:** Genetic risk underlying Parkinson's disease.
[ PMID 18985386 ] [ PMID 19915575 ] [ PMID 20070850 ] [ PMID 21412835 ] [ PMID 21898123 ] [ PMID 24868370 ] [ PMID 25687773 ]

**rs1994090:** The SLC2A13 polymorphism is a significant genetic component for Parkinson's disease.
[ PMID 21044948 ] [ PMID 21738487 ] [ PMID 26687033 ] [ PMID 28927418 ]

**rs34637584:** A frequent mutation of the LRRK2 gene associated with autosomal dominant Parkinson's disease.
[ PMID 15680455 ] [ PMID 15680456 ] [ PMID 15680457 ] [ PMID 15811455 ] [ PMID 15929036 ] [ PMID 16145815 ] [ PMID 16311269 ] [ PMID 16436781 ] [ PMID 16436782 ] [ PMID 17353388 ]

**rs356219:** Alpha-synuclein gene polymorphism is associated with an increased risk (1.3-fold) of Parkinson's disease.
[ PMID 17683088 ] [ PMID 18485051 ] [ PMID 18606870 ] [ PMID 18985386 ] [ PMID 19063963 ] [ PMID 21060011 ] [ PMID 21159074 ] [ PMID 22349157 ] [ PMID 25111979 ]

**rs2736990:** SNCA rs2736990 variants are associated with a twofold increased likelihood of Parkinson's disease.
[ PMID 19915575 ] [ PMID 20961626 ] [ PMID 21046180 ] [ PMID 21060011 ] [ PMID 21425343 ] [ PMID 21953863 ] [ PMID 24868370 ] [ PMID 25129240 ]

## Alzheimer's disease

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs429358 | TA | TT |
| rs744373 | AA | AA |
| rs2075650 | AA | AA |
| rs17125944 | TT | TT |
| rs28834970 | CC | TT |
| rs7274581 | TT | TT |
| rs74615166 | TT | TT |
| rs1476679 | TT | TT |
| rs10498633 | GG | GG |
| rs10792832 | AG | GG |
| rs7561528 | GG | GG |
| rs9349407 | CG | GG |
| rs7920721 | CA | AA |
| rs10838725 | TT | TT |
| rs9331896 | CC | CC |
| rs35349669 | CC | CC |
| rs72807343 | CG | CC |
| rs3865444 | AA | CC |
| rs12989701 | CC | CC |
| rs6733839 | TC | CC |
| rs9381040 | TC | CC |
| rs4676049 | CC | CC |
| rs6859 | AG | AA |
| rs190982 | AG | GG |
| rs6656401 | GG | GG |
| rs983392 | AG | AA |
| rs2373115 | CC | CC |
| rs4420638 | AA | AA |
| rs11771145 | AG | GG |

| | | |
|---|---|---|
| rs9271192 | AA | AA |
| rs10948363 | AA | AA |
| rs561655 | AG | AA |
| rs2718058 | AG | AA |
| rs10972300 | CG | CC |
| rs12947764 | TA | TT |
| rs242557 | CG | GG |
| rs3785883 | GG | GG |
| rs1864325 | CC | CC |
| rs8070723 | AA | AA |
| rs1981997 | GG | GG |
| rs1467967 | TA | AA |
| rs1800750 | GG | GG |
| rs1799724 | TC | CC |
| rs7412 | CC | CC |
| rs9390537 | TT | TT |
| rs2061333 | TT | TT |
| rs2446581 | GG | GG |
| rs11782819 | TT | CC |
| rs17314229 | CG | CC |
| rs75932628 | CC | CC |
| rs157580 | AA | AA |
| rs7081208 | AG | GG |
| rs73660619 | TC | TT |
| rs74006954 | AG | GG |
| rs11023139 | GG | GG |
| rs340635 | GG | GG |
| rs4794202 | GG | GG |
| rs11154851 | CC | CC |
| rs538867 | CC | CC |
| rs4700060 | CC | CC |
| rs117964204 | CG | CC |

| | | |
|---|---|---|
| rs7009219 | CG | CC |
| rs112724034 | CC | CC |
| rs148763909 | CC | CC |
| rs77636885 | CC | CC |
| rs17393344 | GG | GG |
| rs75617873 | AA | AA |
| rs34972666 | AG | AA |
| rs2421847 | AA | AA |
| rs58370486 | AA | AA |
| rs61144803 | AA | AA |
| rs115102486 | AA | AA |
| rs6738962 | AA | AA |
| rs72832584 | AA | AA |
| rs11218343 | TT | TT |
| rs4938933 | TC | TT |
| rs514716 | TC | TT |
| rs7039300 | TG | TT |
| rs2121433 | CC | TT |
| rs6922617 | GG | GG |
| rs610932 | TG | GG |
| rs536841 | TC | TT |
| rs249153 | TT | TT |
| rs3764650 | TT | TT |
| rs569214 | TG | GG |
| rs2279590 | TT | CC |
| rs1923775 | TT | TT |
| rs727153 | CC | CC |
| rs11136000 | TT | CC |
| rs1532278 | TT | CC |
| rs4746003 | CC | CC |
| rs11610206 | TT | TT |
| rs3851179 | TC | CC |

| | | |
|---|---|---|
| rs6509701 | TT | TT |
| rs1562990 | AC | AA |
| rs753129 | AA | AA |
| rs3818361 | GG | GG |
| rs10273775 | GG | GG |
| rs690705 | AG | AA |
| rs12044355 | AA | AA |
| rs63750066 | CC | CC |
| rs2227564 | CC | CC |
| rs1160985 | TT | TT |
| rs59007384 | TG | GG |
| rs157581 | TA | TT |
| rs157582 | TC | CC |
| rs3781838 | TA | TT |
| rs7946599 | CG | GG |
| rs2298813 | GG | GG |
| rs12364988 | TA | TT |
| rs676759 | TT | TT |
| rs3862605 | CC | TT |
| rs726601 | CG | CC |
| rs3781836 | GG | GG |
| rs10892752 | GG | AA |
| rs4420280 | AC | AA |
| rs11218325 | CC | AA |
| rs1784931 | CG | CC |
| rs3781834 | AA | AA |
| rs17125523 | AA | AA |
| rs1422438 | TG | GG |
| rs56131196 | GG | GG |
| rs509208 | CC | CC |
| rs9877502 | GG | GG |
| rs1801277 | TA | TT |

| | | |
|---|---|---|
| rs10205233 | CG | CC |
| rs17268434 | CG | GG |
| rs16822607 | TA | AA |
| rs11754661 | GG | GG |
| rs9969729 | GG | GG |
| rs4937314 | AA | AA |
| rs11983798 | AG | GG |
| rs6468852 | AG | AA |
| rs3785885 | CG | GG |
| rs4647698 | CG | CC |
| rs190788828 | TA | AA |
| rs115550680 | AA | AA |



Risk level: average

**rs28834970:** The common PTK2B variant is associated with late-onset Alzheimer's disease.
[ PMID 25188341 ] [ PMID 26680604 ] [ PMID 27080426 ]

**rs3865444:** Association of the CD33 rs3865444 polymorphism with Alzheimer's disease pathology and CD33 expression in human cerebral cortex.
[ PMID 23708142 ] [ PMID 25448602 ] [ PMID 26933222 ] [ PMID 35888182 ]

**rs2279590:** The CLU rs2279590 polymorphism contributes to susceptibility to Alzheimer's disease in Caucasian and Asian populations.
[ PMID 20570404 ] [ PMID 20599866 ] [ PMID 24947876 ] [ PMID 28973302 ]

**rs429358:** The APOE-E4 allele has a strong influence on the risk of developing Alzheimer's disease. One meta-analysis estimated the odds ratio for individuals homozygous for rs429358 to be 12 times higher for late-onset Alzheimer's disease and 61 times higher for early-onset disease. People with APOE4-4 allele C genotype should avoid eating animals raised on plants/grains that have higher levels of omega-6 compared to omega-3. It is advisable to practice vegetarianism to avoid all animal fats and measure the ratio of omega-3 to omega-6 in these people. Also, people with APOE 4 may do better on unmethylated forms of B12.
[ PMID 21263195 ] [ PMID 30665447 ]

**rs9349407:** Analysis of 54,936 samples confirms an association between the CD2AP rs9349407 polymorphism and susceptibility to Alzheimer's disease.
[ PMID 21460841 ] [ PMID 25092125 ]

**rs11771145:** Genetic variation in EPHA1 affects cerebrospinal fluid and neuroimaging biomarkers in people with Alzheimer's disease.
[ PMID 21460840 ] [ PMID 25182741 ] [ PMID 31659653 ]

**rs2718058:** The NME8 rs2718058 polymorphism increases the risk of developing Alzheimer's disease.
[ PMID 27144521 ]

**rs242557:** High levels of cerebrospinal tau are associated with the rs242557 gene variant and a high risk of Parkinson's and Alzheimer's disease.
[ PMID 19308965 ] [ PMID 19912324 ] [ PMID 20951764 ] [ PMID 26303052 ]

## Migraine

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs10504861 | TC | CC |
| rs6741751 | AG | GG |
| rs4379368 | TC | CC |
| rs11172113 | TC | CC |
| rs10849061 | TC | CC |
| rs11759769 | GG | GG |
| rs6478241 | GG | GG |
| rs9349379 | AG | AA |
| rs3094117 | AA | AA |
| rs10166942 | TC | CC |
| rs2651899 | TC | TT |
| rs6951030 | TT | TT |
| rs2653349 | GG | AA |
| rs566529 | CG | GG |
| rs1835740 | CC | CC |
| rs1042838 | CG | CC |
| rs11624776 | AA | CC |
| rs2076054 | TC | TT |
| rs17051917 | CG | CC |
| rs4345220 | AA | AA |
| rs3790455 | TC | TT |
| rs2274316 | AC | AA |
| rs3781719 | AA | AA |



Risk level: average

**rs10504861:** rs10504861 is a SNP located on chromosome 8q21 that has been found to be associated with an increased incidence of migraine without aura in whole-genome association studies.
[ PMID 24852292 ] [ PMID 26231841 ] [ PMID 28079315 ]

**rs4379368:** The rs4379368 polymorphism may be a genetic marker for migraine patients.
[ PMID 26231841 ] [ PMID 31505242 ]

**rs2651899:** The PRDM16 rs2651899 polymorphism is a risk factor for patients with common migraine.
[ PMID 24021092 ] [ PMID 30635810 ] [ PMID 31557325 ]

## Polyneuropathy

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs200945460 | AA | AA |
| rs28931574 | CG | CC |
| rs28933979 | CG | GG |
| rs104894080 | CC | CC |
| rs1132787 | TC | CC |
| rs137852737 | GG | GG |
| rs3826795 | GG | GG |
| rs502716 | GG | GG |
| rs4722585 | AA | GG |
| rs886039872 | CG | GG |
| rs267606624 | GG | GG |
| rs587777602 | GG | CC |
| rs587777604 | CG | CC |
| rs587777603 | CC | CC |
| rs172378 | AG | AA |
| rs2275697 | GG | GG |
| rs41264871 | CA | AA |
| rs7294354 | TT | GG |
| rs147738081 | CG | CC |
| rs522521 | CG | CC |
| rs4369876 | CC | CC |
| rs12478318 | TA | TT |
| rs73969684 | CC | CC |
| rs80356586 | AA | AA |
| rs182650126 | TT | TT |
| rs281865138 | TA | TT |
| rs137852739 | CG | GG |
| rs104894160 | CC | CC |
| rs755919784 | TT | TT |

| | | |
|---|---|---|
| rs11189867 | TA | TT |



Risk level: average

**rs28931574:** Apolipoprotein AI mutation is associated with familial amyloidotic polyneuropathy.
[ PMID 2123470 ]

**rs28933979:** Val30Met transthyretin gene breakage is associated with motor-dominant sensorimotor polyneuropathy and unusual pathological changes of the calf nerve.
[ PMID 1520326 ] [ PMID 11709003 ]

**rs1132787:** Variation associated with polyneuropathy as a consequence of complications of type 2 diabetes.
[ PMID 33430853 ]

**rs41264871:** Single nucleotide polymorphism of transient axonal glycoprotein-1 increases the risk of chronic inflammatory demyelinating polyneuropathy.
[ PMID ]

**rs12478318:** SCN9A gene mutation associated with risk of idiopathic small fibre neuropathy.
[ PMID 21698661 ]

**rs281865138:** Increased risk of congenital hypomyelinating neuropathy.
[ PMID 9537424 ]

**rs137852739:** Mutation in FAM134B, encoding Golgi protein, cause severe sensory and autonomic neuropathy.
[ PMID 19838196 ]

# Myasthenia

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs4553808 | TA | AA |
| rs16862847 | TA | TT |
| rs743777 | AA | AA |
| rs3087243 | AG | AA |
| rs733618 | TT | TT |
| rs2476601 | GG | GG |
| rs6477872 | TA | TT |
| rs772025588 | TA | AA |
| rs764497513 | CG | GG |
| rs794727516 | CC | CC |
| rs7169523 | AG | AA |
| rs6850606 | CG | GG |
| rs118203994 | GG | GG |
| rs118203995 | CC | CC |
| rs121912815 | CC | CC |
| rs121912816 | GG | GG |
| rs121912817 | GG | GG |
| rs121912818 | AA | AA |

Risk level: low

**rs4553808:** CTLA4 variants contribute to genetic predisposition to myasthenia gravis.
[ PMID 25003519 ] [ PMID 30009380 ]

**rs3087243:** The CTLA4 allelic variant alters T cell phosphorylation patterns and causes an increased risk of autoimmune diseases.
[ PMID 17554260 ] [ PMID 17606874 ] [ PMID 18940880 ] [ PMID 21121051 ]

## Stroke

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs556621 | TT | GG |
| rs16851055 | AG | GG |
| rs879324 | GG | GG |
| rs2107595 | CG | GG |
| rs2238151 | TC | CC |
| rs11984041 | TC | CC |
| rs13407662 | CC | CC |
| rs12425791 | GG | GG |
| rs6843082 | AA | AA |
| rs11672433 | AG | GG |
| rs4076317 | CG | CC |
| rs225132 | TT | TT |
| rs7937106 | TT | TT |
| rs1842681 | CG | GG |
| rs2236406 | AA | TT |
| rs13299556 | AA | TT |
| rs114947355 | AC | CC |
| rs142655108 | CG | CC |
| rs115670077 | CG | GG |
| rs72976591 | CG | CC |
| rs184221467 | CG | GG |
| rs138134155 | CG | GG |
| rs77460585 | CG | GG |
| rs114527838 | CG | GG |
| rs6967981 | CG | GG |
| rs112455974 | CG | CC |
| rs565295967 | CG | CC |
| rs140164788 | CG | CC |
| rs115825287 | CG | CC |

| | | |
|---|---|---|
| rs192977447 | TA | TT |
| rs55931441 | CG | GG |
| rs113949028 | CG | GG |
| rs181095590 | CG | GG |
| rs73923591 | CG | GG |
| rs12646447 | TT | TT |
| rs6797312 | TA | TT |
| rs4792143 | CC | CC |
| rs2200733 | CC | CC |
| rs2084898 | CG | GG |
| rs1401296 | AA | TT |
| rs1364044 | TC | CC |
| rs469568 | AA | CC |
| rs173686 | AA | AA |
| rs161802 | GG | GG |
| rs6025 | CC | CC |
| rs5443 | TC | CC |
| rs3783799 | CG | CC |
| rs2230500 | CG | GG |
| rs74475935 | CC | CC |
| rs635634 | CC | CC |
| rs505922 | TA | TT |
| rs579459 | TT | TT |
| rs12438353 | CC | CC |
| rs2219939 | CG | GG |
| rs899997 | TT | GG |
| rs783396 | CC | CC |
| rs4471613 | GG | GG |
| rs10744777 | TC | CC |
| rs34311906 | AA | TT |
| rs9351814 | CC | AA |
| rs880315 | TC | TT |

| | | |
|---|---|---|
| rs42039 | CC | CC |
| rs1333040 | TC | CC |
| rs2383207 | AG | GG |
| rs1333047 | TA | AA |
| rs1333049 | GC | GG |
| rs10757272 | TC | CC |
| rs9899375 | CC | CC |
| rs7859727 | TA | TT |
| rs7283054 | CG | GG |
| rs12413409 | GG | AA |
| rs17612742 | TA | TT |
| rs6841581 | GG | GG |
| rs6842241 | CC | CC |
| rs1937787 | CC | CC |
| rs6825454 | TA | TT |
| rs10400694 | CG | GG |
| rs4959130 | CG | GG |
| rs12204590 | TT | TT |
| rs4932370 | CG | GG |
| rs28688791 | TA | TT |
| rs7771564 | AA | AA |
| rs1804689 | CG | GG |
| rs5752326 | CC | CC |
| rs11681884 | CG | CC |
| rs2229383 | TA | TT |
| rs7156510 | CG | GG |
| rs1564060 | AG | GG |
| rs768606 | TT | TT |
| rs12476527 | CG | GG |
| rs10820405 | CG | GG |
| rs2822388 | TA | AA |
| rs11957829 | AA | AA |

| | | |
|---|---|---|
| rs12291066 | CG | GG |
| rs1800801 | TC | CC |
| rs2005108 | CG | CC |
| rs34166160 | CG | CC |
| rs11833579 | CG | GG |
| rs4867766 | CG | GG |
| rs6891174 | CG | GG |
| rs7304841 | CA | AA |
| rs2634071 | CG | CC |
| rs2634074 | AA | AA |
| rs13143308 | CG | GG |
| rs6817105 | TT | TT |
| rs1052053 | AG | AA |
| rs2984613 | TA | TT |
| rs4714955 | TC | CC |
| rs17114036 | TA | AA |
| rs11867415 | AA | AA |
| rs704341 | CG | GG |
| rs12449964 | TC | CC |
| rs12936587 | AG | GG |
| rs146390073 | CG | CC |
| rs248812 | CG | CC |
| rs2295786 | TA | AA |
| rs10455872 | AA | AA |
| rs72794386 | TA | AA |
| rs16896398 | TA | AA |
| rs8103309 | TA | TT |
| rs1122608 | GG | GG |
| rs599839 | AG | GG |
| rs781542 | GG | GG |
| rs7705819 | CG | CC |
| rs35436 | CC | CC |

| | | |
|---|---|---|
| rs12190287 | CG | CC |
| rs13168506 | CG | GG |
| rs7610618 | CG | CC |
| rs2084637 | CC | CC |
| rs9345396 | CC | CC |
| rs12124533 | CG | CC |
| rs12122341 | CC | CC |
| rs17771318 | AG | GG |
| rs7582720 | TC | TT |
| rs12037987 | TA | TT |
| rs11556924 | TC | CC |
| rs12445022 | GG | GG |
| rs7193343 | CC | CC |
| rs12932445 | AT | TT |
| rs72184 | AA | AA |
| rs10507391 | CA | AA |



Risk level: average

**rs556621:** The rs556621 variant on chromosome 6p21.1 is associated with large artery atherosclerotic stroke and ischaemic stroke.
[ PMID ]

**rs2107595:** HDAC9 Rs2107595 variant alters susceptibility to coronary heart disease and severity of coronary atherosclerosis.
[ PMID 26093197 ] [ PMID 27494404 ] [ PMID 29695241 ]

**rs11984041:** HDAC9 variant associated with large vessel ischaemic stroke contributes to carotid atherosclerosis.
[ PMID 22306652 ] [ PMID 23449258 ] [ PMID 27025970 ] [ PMID 27642596 ]

**rs6797312:** Twice the risk of stroke is higher in Caucasian women.
[ PMID ]

**rs2230500:** SNP 1425G/A in PRKCH is associated with ischaemic stroke and cerebral haemorrhage.
[ PMID 19520989 ] [ PMID 24534126 ] [ PMID 27796860 ]

**rs505922:** There is a 1.2-fold increased risk of pancreatic cancer.
[ PMID ]

**rs1800801:** Gla rs1800801 matrix protein polymorphism is associated with ischaemic stroke recurrence.

[ PMID 28821877 ]  [ PMID 32584873 ]

**rs11833579:** NINJ2 promoter polymorphism predicts risk of large artery atherosclerotic stroke.
[ PMID 21722921 ]  [ PMID 22297388 ]  [ PMID 22795341 ]  [ PMID 25096477 ]  [ PMID 26687183 ]

## Epilepsy

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs211037 | CC | CC |
| rs11890028 | GG | GG |
| rs580041 | CC | CC |
| rs6432860 | AA | GG |
| rs7587026 | CC | CC |
| rs200945460 | AA | AA |
| rs4426541 | GG | GG |
| rs6735544 | AA | AA |
| rs17679445 | GG | GG |
| rs747283 | TA | TT |
| rs3769955 | AC | CC |
| rs684513 | CC | CC |
| rs2304016 | TA | AA |
| rs121912707 | CC | CC |
| rs16019 | TA | TT |
| rs2290732 | AA | AA |
| rs3804505 | GG | GG |
| rs39861 | AA | AA |
| rs28940576 | GG | GG |
| rs147484110 | CC | CC |
| rs148382729 | CG | CC |
| rs964112 | CG | CC |
| rs11031434 | CG | GG |
| rs986527 | GG | GG |
| rs2273697 | GG | GG |
| rs121909580 | GG | GG |

Risk level: low

**rs2304016:** SCN2A gene polymorphism affects response to antiepileptic drugs in the treatment of epilepsy.
[ PMID 28144265 ] [ PMID 30693367 ] [ PMID 31297029 ] [ PMID 33096315 ] [ PMID 33519675 ]

## Blood clotting disorders

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1799963 | GG | GG |
| rs2289252 | CC | CC |
| rs267606981 | TT | TT |
| rs2731672 | CC | CC |
| rs2036914 | CC | CC |
| rs1801020 | GG | GG |
| rs1613662 | AA | AA |
| rs13146272 | AC | AA |
| rs9923231 | CC | CC |
| rs699664 | CC | CC |
| rs7294 | TT | CC |
| rs9934438 | GG | GG |
| rs17708472 | GG | GG |
| rs2359612 | GG | GG |
| rs2884737 | AA | AA |
| rs12340895 | AC | CC |
| rs769900251 | CG | CC |
| rs774572099 | CG | CC |
| rs121918145 | CC | CC |
| rs121918481 | TT | TT |
| rs121918476 | GG | GG |
| rs5918 | TT | TT |
| rs1800775 | AC | AA |

Risk level: low

**rs7294:** Polymorphism responsible for the level of sensitivity to warfarin (vitamin K antagonist).
[ PMID 15883587 ] [ PMID 16611750 ] [ PMID 17048007 ] [ PMID 20128861 ]

**rs769900251:** Partial protein C deficiency - increased risk of blood clotting problems.
[ PMID ]

## Heart and vascular diseases

## Myocardial infarction

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs10757274 | AG | AA |
| rs1333042 | AG | AA |
| rs17465637 | CC | AA |
| rs4804611 | CA | AA |
| rs3798220 | TC | TT |
| rs646776 | TC | TT |
| rs886126 | CC | CC |
| rs17672135 | TT | TT |
| rs11066280 | TT | TT |
| rs2505083 | TC | TT |
| rs6725887 | TC | TT |
| rs7808424 | TT | TT |
| rs1842896 | TG | TT |
| rs12740374 | TG | TT |
| rs12413409 | GG | AA |
| rs11671653 | CG | GG |
| rs2259816 | GG | GG |
| rs7203193 | AG | GG |
| rs6504218 | AA | GG |
| rs11669133 | GG | GG |
| rs12200560 | AA | AA |
| rs9546711 | AA | GG |
| rs1994016 | TC | TT |
| rs3729639 | CC | CC |
| rs2895811 | TC | TT |
| rs3127599 | CG | CC |
| rs7767084 | TA | TT |
| rs2048327 | TC | TT |

| | | |
|---|---|---|
| rs11924705 | AT | TT |
| rs1746048 | CC | TT |
| rs1412444 | CG | CC |
| rs9818870 | CC | CC |
| rs12526453 | CG | GG |
| rs6601299 | CC | CC |
| rs7801190 | CC | CC |
| rs7569328 | CC | CC |
| rs974819 | CC | CC |
| rs46522 | TT | CC |
| rs11650066 | AA | GG |
| rs9268402 | AG | AA |
| rs4773144 | AA | AA |
| rs1231206 | AG | GG |
| rs12936587 | AG | GG |
| rs7697839 | AA | AA |
| rs2515629 | TA | TT |
| rs514659 | N/A | AA |
| rs10933436 | CC | CC |
| rs17114046 | AG | AA |
| rs6905288 | AG | AA |
| rs1333040 | TC | CC |
| rs10811661 | TT | TT |
| rs10757278 | AG | AA |
| rs2383207 | AG | GG |
| rs7025486 | AG | GG |
| rs4977574 | AG | AA |
| rs1333049 | GC | GG |
| rs1041981 | CC | CC |
| rs909253 | AA | AA |
| rs5918 | TT | TT |
| rs1048990 | GC | CC |

| | | |
|---|---|---|
| rs2383206 | AG | AA |
| rs11206510 | TC | CC |
| rs619203 | CG | GG |



Risk level: average

**rs17465637:** SNP of the MIA3 gene associated with increased risk of myocardial infarction with odds ratios of 1.17 (CI: 1.04-1.32) and 1.37 (CI: 1.08-1.74) for carriers.
[ PMID 21463265 ] [ PMID 24125424 ] [ PMID 28400043 ]

**rs46522:** The rs46522 polymorphism of the E2Z ubiquitin-conjugating enzyme gene is associated with abnormal metabolic parameters in patients with myocardial infarction.
[ PMID ]

**rs10757274:** A genetic variant on chromosome 9p21 is the strongest genetic predictor of early myocardial infarction (heart attack) found so far. SNPs in this region are also associated with an increased risk of stroke, abdominal aortic aneurysm (AAA) and intracranial aneurysm.
[ PMID 18066490 ] [ PMID 19956784 ] [ PMID 21385355 ] [ PMID 26772723 ] [ PMID 31055994 ]

**rs1333042:** Intronic polymorphisms in the CDKN2B-AS1 gene are strongly associated with the risk of myocardial infarction and coronary heart disease.
[ PMID 26999117 ] [ PMID 27096864 ]

**rs3798220:** rs3798220, also known as I4399M or Ile4399Met, is a SNP in the apolipoprotein (A) LPA gene , which has been reported to be associated with elevated plasma lipoprotein levels and increased cardiovascular risk, well-tolerated by low-dose aspirin.
[ PMID 17975119 ] [ PMID 18775538 ] [ PMID 23278389 ]

**rs646776:** A new locus of coronary atherosclerosis and associations with myocardial infarction in coronary atherosclerosis.
[ PMID 21242481 ]

**rs2505083:** Increased risk of sudden myocardial infarction and coronary heart disease.
[ PMID 26950853 ]

**rs2895811:** HHIPL-1 gene polymorphism (rs2895811) is associated with cardiovascular risk factors and cardiometabolic parameters in patients with myocardial infarction.
[ PMID 29655894 ]

## Hypertension

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs4961 | TG | GG |
| rs5186 | AC | AA |
| rs1529927 | CG | GG |
| rs16890334 | TT | TT |
| rs2030114 | AG | GG |
| rs10930597 | CC | CC |
| rs11887188 | TC | CC |
| rs4963 | CG | CC |
| rs4149601 | AG | GG |
| rs2820037 | AA | AA |
| rs6997709 | GG | TT |
| rs2304483 | TC | TT |
| rs2846680 | AC | AA |
| rs675482 | GG | AA |
| rs11825181 | CG | GG |
| rs11823543 | GG | GG |
| rs2954033 | GG | GG |
| rs2266788 | AA | AA |
| rs2288774 | TT | TT |
| rs3865418 | CG | CC |
| rs7961152 | CG | CC |
| rs1937506 | AG | GG |
| rs2398162 | GG | GG |
| rs4684847 | TC | CC |
| rs3755351 | GG | GG |
| rs3794260 | CG | GG |
| rs9739493 | TC | TT |
| rs1805762 | CG | GG |
| rs3754777 | CG | CC |

| | | |
|---|---|---|
| rs6749447 | TT | TT |
| rs1126742 | CG | CC |
| rs3781719 | AA | AA |
| rs1799983 | CG | GG |
| rs1801253 | GC | CC |



Risk level: average

**rs4961:** The ADD1 gene variant is associated with the progression of blood pressure and the occurrence of hypertension. The risk of arterial hypertension is increased by 1.8 times. Increased sensitivity of blood pressure to salt, good response to salt-restricted diet.
[ PMID 9149697 ] [ PMID 27480094 ]

**rs5186:** A polymorphism known as A1166C, one of the most studied genes, is associated with an increased risk of essential hypertension with an odds ratio of 7.3 (CC homozygote).
[ PMID 8021009 ] [ PMID 9084931 ] [ PMID 20486282 ] [ PMID 21799445 ]

**rs1529927:** A polymorphism with an increased risk of hypertension treatable with hydrochlorothiazide as first-line therapy, without a beta-blocker and without a vasodilator.
[ PMID ]

**rs4963:** Phosphorylation-related variant ADD1 rs4963 affects blood pressure sensitivity to salt.
[ PMID 19574959 ] [ PMID 21058046 ] [ PMID 25816007 ]

**rs4149601:** Genetic variation in NEDD4L is associated with transverse and longitudinal blood pressure. Increases the risk of hypertension and adverse cardiovascular outcomes in patients with arterial hypertension treated with thiazide diuretics. Associated with favourable response to treatment with beta-blockers and diuretics in patients with arterial hypertension.
[ PMID 16788695 ] [ PMID 19635985 ] [ PMID 20038744 ] [ PMID 23353631 ] [ PMID 25098786 ]

**rs3865418:** A break in the NEDD4L gene is associated with significantly higher diastolic blood pressure.
[ PMID 18293164 ] [ PMID 20003179 ]

**rs3754777:** STK39 polymorphism is an independent risk factor for hypertension in men.
[ PMID 19114657 ] [ PMID 20003416 ] [ PMID 20889219 ] [ PMID 27082544 ]

**rs1126742:** The rs1126742 polymorphism of the cytochrome P450 gene is associated with essential hypertension in men.
[ PMID 18300855 ] [ PMID 24164311 ] [ PMID 32373936 ]

## Ischemic heart disease

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs3782218 | CG | CC |
| rs556621 | TT | GG |
| rs12425791 | GG | GG |
| rs1746048 | CC | TT |
| rs1412444 | CG | CC |
| rs2107595 | CG | GG |
| rs16851055 | AG | GG |
| rs879324 | GG | GG |
| rs2238151 | TC | CC |
| rs11984041 | TC | CC |
| rs13407662 | CC | CC |
| rs6843082 | AA | AA |
| rs646776 | TC | TT |
| rs886126 | CC | CC |
| rs17672135 | TT | TT |
| rs11066280 | TT | TT |
| rs2505083 | TC | TT |
| rs3798220 | TC | TT |
| rs2306374 | TT | TT |
| rs579459 | TT | TT |
| rs7586970 | TT | TT |
| rs6725887 | TC | TT |
| rs7808424 | TT | TT |
| rs1842896 | TG | TT |
| rs11066015 | CG | GG |
| rs671 | GG | GG |
| rs8055236 | TT | TT |
| rs10757274 | AG | AA |
| rs1333042 | AG | AA |

| | | |
|---|---|---|
| rs12740374 | TG | TT |
| rs12413409 | GG | AA |
| rs11671653 | CG | GG |
| rs2259816 | GG | GG |
| rs7203193 | AG | GG |
| rs10755578 | CC | CC |
| rs675026 | AA | GG |
| rs6504218 | AA | GG |
| rs11669133 | GG | GG |
| rs12200560 | AA | AA |
| rs9546711 | AA | GG |
| rs1994016 | TC | TT |
| rs7136259 | TT | CC |
| rs10953541 | TC | TT |
| rs8060686 | TT | CC |
| rs3729639 | CC | CC |
| rs2895811 | TC | TT |
| rs3127599 | CG | CC |
| rs7767084 | TA | TT |
| rs17465637 | CC | AA |
| rs9818870 | CC | CC |
| rs12526453 | CG | GG |
| rs6601299 | CC | CC |
| rs11206510 | TC | CC |
| rs11752643 | CC | CC |
| rs1333048 | TA | AA |
| rs1333049 | GC | GG |
| rs2123536 | CC | CC |
| rs4743150 | CC | CC |
| rs7569328 | CC | CC |
| rs974819 | CC | CC |
| rs9982601 | CG | CC |

| | | |
|---|---|---|
| rs12190287 | CG | CC |
| rs46522 | TT | CC |
| rs11556924 | TC | CC |
| rs964184 | CC | CC |
| rs11650066 | AA | GG |
| rs9268402 | AG | AA |
| rs4773144 | AA | AA |
| rs1165669 | AA | AA |
| rs1231206 | AG | GG |
| rs12936587 | AG | GG |
| rs2472299 | AG | GG |
| rs3869109 | GG | AA |
| rs7697839 | AA | AA |
| rs2515629 | TA | TT |
| rs514659 | N/A | AA |
| rs10933436 | CC | CC |
| rs9349379 | AG | AA |
| rs17114036 | TA | AA |
| rs17114046 | AG | AA |
| rs599839 | AG | GG |
| rs1263173 | AA | GG |
| rs2346177 | AA | GG |
| rs6905288 | AG | AA |
| rs2383207 | AG | GG |
| rs3135506 | GG | GG |
| rs10757278 | AG | AA |
| rs4665058 | CC | CC |
| rs708272 | AA | AA |
| rs1676232 | AA | GG |
| rs662799 | AA | AA |
| rs4977574 | AG | AA |
| rs6882776 | AG | AA |

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|---|---|---|
| rs28936670 | GG | CC |
| rs72554028 | CG | CC |
| rs703752 | CC | CC |
| rs1333040 | TC | CC |
| rs7025486 | AG | GG |
| rs1063192 | AG | AA |
| rs2811712 | AA | GG |
| rs2857657 | CG | CC |
| rs1024611 | AG | AA |
| rs10116277 | TA | TT |
| rs5443 | TC | CC |
| rs2383206 | AG | AA |
| rs6922269 | CG | GG |
| rs501120 | TT | CC |
| rs10455872 | AA | AA |
| rs20455 | AA | TT |
| rs1799983 | CG | GG |
| rs383830 | TA | TT |
| rs7250581 | GG | AA |
| rs688034 | CC | CC |
| rs2943634 | CC | AA |
| rs17228212 | TT | TT |
| rs2713604 | CC | CC |
| rs3803 | CG | CC |
| rs1800787 | CC | TT |
| rs4404477 | CG | CC |
| rs2331291 | CG | CC |
| rs3918242 | CG | CC |

Risk level: average

**rs556621:** The rs556621 variant on chromosome 6p21.1 is associated with large artery atherosclerotic stroke and ischaemic stroke.
[ PMID ]

**rs17465637:** SNP of the MIA3 gene associated with increased risk of myocardial infarction with odds ratios of 1.17 (CI: 1.04-1.32) and 1.37 (CI: 1.08-1.74) for carriers.
[ PMID 21463265 ] [ PMID 24125424 ] [ PMID 28400043 ]

**rs46522:** The rs46522 polymorphism of the E2Z ubiquitin-conjugating enzyme gene is associated with abnormal metabolic parameters in patients with myocardial infarction.
[ PMID ]

**rs1676232:** LSAMP tumour suppressor gene polymorphisms define a significant risk haplotype for left main artery coronary heart disease.
[ PMID 18318786 ] [ PMID 24143143 ]

**rs3782218:** A single nucleotide polymorphism of nitric oxide synthase (NOS) is associated with coronary heart disease.
[ PMID 24713495 ]

**rs1412444:** A single nucleotide polymorphism in the LIPA (lysosomal acidic lipase A) gene is associated with predisposition to premature coronary heart disease.
[ PMID 21606135 ]

**rs2107595:** HDAC9 Rs2107595 variant alters susceptibility to coronary heart disease and severity of coronary atherosclerosis.
[ PMID 26093197 ] [ PMID 27494404 ] [ PMID 29695241 ]

**rs11984041:** HDAC9 variant associated with large vessel ischaemic stroke contributes to carotid atherosclerosis.
[ PMID 22306652 ] [ PMID 23449258 ] [ PMID 27025970 ] [ PMID 27642596 ]

## Atherosclerosis

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs9632884 | CG | GG |
| rs1878406 | CC | CC |
| rs4712972 | GG | GG |
| rs17045031 | GG | GG |
| rs445925 | GG | GG |
| rs9515203 | TT | CC |
| rs958994 | AG | AA |
| rs17691394 | AG | AA |
| rs2229116 | AG | GG |
| rs17151904 | CG | GG |
| rs1697137 | AA | TT |
| rs588517 | CC | CC |
| rs13053817 | CC | CC |
| rs147555597 | CG | GG |
| rs9727451 | CG | GG |
| rs11413744 | TA | TT |
| rs4779614 | CG | CC |
| rs259140 | CG | GG |
| rs17398575 | AG | GG |
| rs11781551 | CG | GG |
| rs6601530 | AA | AA |
| rs6511720 | GG | GG |
| rs11726269 | AA | AA |
| rs682112 | CG | GG |
| rs2526620 | AA | AA |
| rs118039278 | CG | GG |
| rs8003602 | CG | CC |
| rs10841443 | CG | CC |
| rs112043140 | CG | CC |

| | | |
|---|---|---|
| rs2822693 | CC | CC |
| rs1108775 | GG | GG |
| rs1856746 | AG | GG |
| rs2791713 | AA | AA |
| rs291096 | AA | TT |
| rs11012265 | AC | CC |
| rs17366136 | TG | GG |
| rs10830090 | CG | GG |
| rs17078595 | AA | AA |
| rs6894083 | AG | AA |
| rs890710 | CC | CC |
| rs1035208 | CG | CC |
| rs6900057 | TA | AA |
| rs12285326 | GG | GG |



Risk level: average

**rs9632884:** Association of the 9p21-3 locus with coronary atherosclerosis and coronary heart disease.
[ PMID 24906238 ] [ PMID 26958643 ] [ PMID 27096864 ]

**rs2229116:** The RYR3 gene variant is associated with an increased risk of carotid atherosclerosis in immunocompromised individuals.
[ PMID 20009918 ] [ PMID 24561552 ] [ PMID 30182779 ]

**rs1856746:** Breakdown increases the risk of coronary atherosclerosis.
[ PMID 28355232 ]

## Rheumatic diseases

## Systemic lupus erythematosus

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1143679 | AG | GG |
| rs2004640 | CG | GG |
| rs13385731 | TT | TT |
| rs2230926 | TT | TT |
| rs7574865 | TG | GG |
| rs3821236 | GG | GG |
| rs13277113 | AG | GG |
| rs403016 | CC | CC |
| rs10954213 | AA | GG |
| rs10499197 | TT | TT |
| rs704840 | TT | TT |
| rs2275247 | TT | TT |
| rs2736340 | TC | CC |
| rs12711490 | TT | TT |
| rs13239597 | CC | CC |
| rs1635852 | CC | TT |
| rs11860650 | TC | CC |
| rs9303277 | TT | CC |
| rs960709 | AG | GG |
| rs2176082 | GG | GG |
| rs7172677 | CG | CC |
| rs10498070 | AA | AA |
| rs2051549 | AA | AA |
| rs10488631 | TT | TT |
| rs548234 | TC | TT |
| rs11574637 | TC | TT |
| rs9937837 | TG | TT |
| rs131654 | TT | TT |

| | | |
|---|---|---|
| rs6445975 | TT | TT |
| rs12537284 | GG | GG |
| rs2205960 | GG | GG |
| rs3131379 | GG | GG |
| rs558702 | GG | GG |
| rs2301271 | GG | GG |
| rs6049839 | TG | GG |
| rs4917014 | TG | GG |
| rs5754217 | GG | GG |
| rs4639966 | TC | TT |
| rs4963128 | TC | CC |
| rs10036748 | TC | TT |
| rs4684256 | TC | CC |
| rs1128334 | CC | CC |
| rs2618476 | TC | TT |
| rs2431697 | TC | CC |
| rs9271100 | CC | CC |
| rs10911628 | CC | CC |
| rs8023715 | CC | CC |
| rs5029939 | CC | CC |
| rs2187668 | CC | CC |
| rs1385374 | CC | CC |
| rs9888739 | TC | CC |
| rs1150754 | CC | CC |
| rs12949531 | CC | CC |
| rs2647012 | CC | CC |
| rs7812879 | CC | CC |
| rs7197475 | CC | CC |
| rs11101442 | TC | CC |
| rs4728142 | AA | GG |
| rs10516487 | GG | GG |
| rs10276619 | AA | AA |

| | | |
|---|---|---|
| rs6695567 | AA | AA |
| rs6590330 | GG | GG |
| rs7329174 | AA | AA |
| rs729302 | AA | AA |
| rs1801274 | GG | AA |
| rs1913517 | AG | GG |
| rs1800629 | GG | GG |
| rs1883832 | TC | CC |
| rs4948496 | TC | TT |
| rs12599402 | TC | CC |
| rs10857712 | TT | TT |
| rs2254546 | GG | GG |
| rs7097397 | CG | GG |
| rs4522865 | AA | GG |
| rs12629106 | CC | CC |
| rs3130320 | CG | CC |
| rs6705628 | CC | CC |
| rs340630 | GG | GG |
| rs11150610 | CC | CC |
| rs6804441 | N/A | AA |
| rs13306575 | GG | GG |
| rs2248932 | AG | GG |
| rs3024505 | GG | GG |
| rs3129860 | GG | GG |
| rs17266594 | TA | TT |
| rs633724 | TC | CC |
| rs2431099 | AA | AA |
| rs2327832 | AA | AA |
| rs3748079 | CC | CC |
| rs4794067 | TT | TT |
| rs1205 | TT | CC |
| rs907715 | AC | CC |

| | | |
|---|---|---|
| rs17250932 | TA | TT |
| rs1800630 | AC | CC |
| rs419788 | CC | CC |
| rs3093061 | TA | TT |
| rs3733197 | GG | GG |
| rs6835457 | TA | AA |
| rs2304256 | AC | AA |
| rs2075799 | CC | CC |
| rs2280381 | TA | TT |
| rs2071278 | AA | AA |
| rs11569523 | CC | CC |
| rs11117956 | TT | TT |
| rs932859 | N/A | TT |
| rs2250656 | TC | TT |
| rs17047631 | TA | TT |
| rs677066 | TT | TT |
| rs423490 | AG | GG |
| rs3738468 | GG | GG |
| rs10779339 | CG | CC |
| rs2230205 | AC | CC |
| rs4310446 | AA | TT |
| rs11118131 | CG | CC |
| rs4807895 | AG | GG |
| rs3818361 | GG | GG |
| rs12034383 | AA | GG |
| rs6656401 | GG | GG |
| rs2025935 | GG | GG |
| rs1408077 | CG | CC |
| rs1571344 | AA | AA |
| rs1990760 | TC | CC |
| rs2618479 | GG | GG |
| rs1167796 | CG | GG |

| | | |
|---|---|---|
| rs610604 | TG | TT |
| rs9275596 | AA | TT |
| rs3024839 | TA | TT |
| rs5744168 | AG | GG |
| rs11889341 | TC | CC |
| rs10168266 | CC | CC |
| rs3024896 | CC | CC |
| rs1517352 | AC | AA |
| rs10181656 | CC | CC |
| rs7582694 | CG | GG |
| rs509749 | AG | GG |
| rs2241524 | CG | GG |
| rs172378 | AG | AA |
| rs9275572 | GG | GG |
| rs11717455 | TT | TT |
| rs9270984 | GG | GG |
| rs11073328 | CC | CC |
| rs12141391 | CC | CC |
| rs979233 | AC | CC |
| rs12822507 | GG | AA |
| rs4852324 | TT | TT |
| rs3734266 | TT | TT |
| rs17039212 | CC | CC |
| rs10845606 | AC | CC |
| rs10911390 | CC | CC |
| rs4622329 | AG | AA |
| rs7186852 | AA | AA |
| rs34015031 | TA | TT |
| rs35131781 | CA | AA |
| rs241428 | TT | TT |
| rs3745567 | TC | CC |
| rs9276606 | AA | AA |

| | | |
|---|---|---|
| rs4572884 | CC | CC |



Risk level: average

**rs4728142:** Validation of IRF5 as a multiple sclerosis risk gene: putative role in human herpes virus-6 infection.
[ PMID 18285424 ] [ PMID 20861862 ]

**rs1143679:** ITGAM coding variant (rs1143679) influences the risk of kidney disease, discoid rash and immunological manifestations in patients with systemic lupus erythematosus.
[ PMID 19129174 ] [ PMID 19939855 ] [ PMID 24269694 ] [ PMID 24608226 ] [ PMID 25315704 ]

**rs2004640:** The IRF5 rs2004640-T allele, a novel genetic factor in systemic lupus erythematosus, is not associated with rheumatoid arthritis.
[ PMID 15657875 ] [ PMID 16642019 ] [ PMID 17158136 ] [ PMID 17166181 ] [ PMID 19043711 ] [ PMID 31347288 ]

**rs7574865:** 1.3-fold risk of rheumatoid arthritis
[ PMID 17804842 ] [ PMID 17932559 ] [ PMID 18576330 ] [ PMID 18703106 ] [ PMID 19120275 ] [ PMID 19458352 ] [ PMID 19479340 ]

**rs13277113:** The rs13277113 genotype associated with the BLK pathway is more common in patients with systemic lupus erythematosus and is associated with low gene expression and increased frequency of exacerbations.
[ PMID 19180478 ] [ PMID 21152986 ] [ PMID 27864698 ]

**rs2736340:** The FAM167A-BLK rs2736340 polymorphism is associated with susceptibility to autoimmune diseases, particularly rheumatoid arthritis and systemic lupus erythematosus.
[ PMID 19838195 ] [ PMID 21068098 ] [ PMID 21905002 ] [ PMID 27105348 ]

**rs11860650:** ITGAM gene polymorphisms confer a higher risk of discoid cutaneous lupus erythematosus than systemic lupus erythematosus.
[ PMID 19129174 ] [ PMID 19838195 ] [ PMID 21068098 ] [ PMID 21151989 ]

**rs4639966:** Single nucleotide polymorphism rs4639966 at 11q23.3 is associated with clinical manifestations of systemic lupus erythematosus.
[ PMID 22291604 ] [ PMID 23002088 ] [ PMID 24001599 ]

## Rheumatoid arthritis

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs11676922 | AA | TT |
| rs26232 | TC | CC |
| rs10818488 | AG | GG |
| rs3218251 | TA | TT |
| rs13315591 | TT | TT |
| rs9372120 | TG | TT |
| rs67250450 | TT | CC |
| rs7765379 | TT | TT |
| rs11761231 | TC | TT |
| rs12529514 | TC | TT |
| rs4409785 | TT | TT |
| rs13142500 | TA | TT |
| rs998731 | CC | TT |
| rs10821944 | TG | TT |
| rs12831974 | TT | TT |
| rs13330176 | AA | TT |
| rs11089637 | TT | TT |
| rs4780401 | TG | TT |
| rs7574865 | TG | GG |
| rs231735 | TG | TT |
| rs13031237 | TG | GG |
| rs3093023 | GG | GG |
| rs2867461 | CG | GG |
| rs4750316 | CG | GG |
| rs2561477 | AG | GG |
| rs9826828 | GG | GG |
| rs6920220 | GG | GG |
| rs6732565 | AG | GG |
| rs678347 | AA | AA |

| | | |
|---|---|---|
| rs657075 | AG | GG |
| rs11889341 | TC | CC |
| rs1877030 | TC | CC |
| rs73013527 | TT | CC |
| rs3824660 | TC | TT |
| rs2736337 | TA | TT |
| rs2469434 | TA | TT |
| rs3184504 | TC | CC |
| rs615672 | CG | GG |
| rs6859219 | AC | CC |
| rs10499194 | CC | CC |
| rs71508903 | TC | CC |
| rs6496667 | AC | CC |
| rs2961663 | CG | CC |
| rs6679677 | CC | CC |
| rs6715284 | CG | CC |
| rs726288 | CC | CC |
| rs6457620 | CC | CC |
| rs4452313 | TT | AA |
| rs8133843 | AA | AA |
| rs11574914 | GG | GG |
| rs2664035 | AG | GG |
| rs2847297 | AA | AA |
| rs3087243 | AG | AA |
| rs2240335 | CC | CC |
| rs805297 | AC | CC |
| rs660895 | AA | AA |
| rs10865035 | AA | AA |
| rs10774624 | AA | AA |
| rs3761847 | AG | AA |
| rs2671692 | AG | GG |
| rs10985070 | AC | CC |

| | | |
|---|---|---|
| rs2104286 | TT | TT |
| rs6457617 | TT | TT |
| rs3816587 | TC | TT |
| rs2837960 | TT | TT |
| rs13192841 | GG | GG |
| rs6822844 | TG | GG |
| rs3890745 | TC | TT |
| rs2240340 | TT | CC |
| rs1953126 | TC | CC |
| rs7528684 | AG | GG |
| rs743777 | AA | AA |
| rs6684865 | AG | GG |
| rs9550642 | CG | GG |
| rs3738919 | CC | AA |
| rs2327832 | AA | AA |
| rs11162922 | AA | AA |
| rs11203366 | GG | AA |
| rs10488631 | TT | TT |
| rs8032939 | TT | TT |
| rs13192471 | TT | TT |
| rs331463 | TT | TT |
| rs2317230 | TA | TT |
| rs1950897 | CC | TT |
| rs2230926 | TT | TT |
| rs1571878 | TT | TT |
| rs3781913 | TG | TT |
| rs4810485 | TG | TT |
| rs4305317 | GG | GG |
| rs3093024 | GG | GG |
| rs12131057 | AG | GG |
| rs9275406 | GG | GG |
| rs8026898 | GG | GG |

| | | |
|---|---|---|
| rs1043099 | GG | GG |
| rs2075876 | AA | GG |
| rs2872507 | AG | GG |
| rs2841277 | TC | CC |
| rs1980422 | TC | TT |
| rs34695944 | TC | TT |
| rs2451258 | TC | TT |
| rs3125734 | CC | CC |
| rs1516971 | TT | TT |
| rs11933540 | TC | TT |
| rs2736340 | TC | CC |
| rs227163 | CC | TT |
| rs874040 | CG | GG |
| rs968567 | CC | CC |
| rs72634030 | CC | CC |
| rs11900673 | CC | CC |
| rs881375 | TC | CC |
| rs624988 | CC | CC |
| rs2233424 | CC | CC |
| rs9653442 | TT | CC |
| rs28411352 | CC | CC |
| rs73081554 | CC | CC |
| rs2582532 | CC | CC |
| rs1858037 | AT | TT |
| rs909685 | TT | AA |
| rs6910071 | AG | AA |
| rs9571178 | AG | GG |
| rs2812378 | AA | AA |
| rs11203203 | AA | GG |
| rs934734 | AG | AA |
| rs4272 | AA | AA |
| rs13017599 | AG | GG |

| | | |
|---|---|---|
| rs3806624 | GG | GG |
| rs10175798 | AA | GG |
| rs1893592 | AA | AA |
| rs13119723 | AA | AA |
| rs45475795 | AA | AA |
| rs951005 | AA | AA |
| rs947474 | AG | AA |
| rs12140275 | AA | AA |
| rs9268839 | AA | AA |
| rs2233434 | AA | AA |
| rs4678 | GG | GG |
| rs12525220 | GG | GG |
| rs7731626 | AA | GG |
| rs2072438 | TC | CC |
| rs1854853 | GG | AA |
| rs12379034 | AG | AA |
| rs3763309 | AC | CC |
| rs1160542 | CG | GG |
| rs1678542 | GG | GG |
| rs2476601 | GG | GG |
| rs5029937 | CG | GG |
| rs10760130 | CG | GG |
| rs3766379 | TC | CC |
| rs6682654 | AA | AA |
| rs2442728 | TT | GG |



Risk level: average

**rs11676922:** The combination of CD28 (rs1980422) and IRF5 (rs10488631) polymorphisms is associated with seropositivity in rheumatoid arthritis.
[ PMID 27092776 ]

**rs3738919:** The ITGAV rs3738919-C allele is associated with rheumatoid arthritis in Caucasians.
[ PMID 17615072 ] [ PMID 19818132 ]

**rs26232:** The C5orf30 rs26232 variant is a negative regulator of tissue damage in rheumatoid arthritis and is associated with joint damage in rheumatoid arthritis.
[ PMID 23817893 ] [ PMID 26316022 ]

**rs10818488:** The rs10818488 polymorphism in the TRAF1/C region is associated with genetic predisposition to rheumatoid arthritis and systemic lupus erythematosus.
[ PMID 23321589 ] [ PMID 27536202 ] [ PMID 31530986 ]

**rs7574865:** 1.3-fold risk of rheumatoid arthritis
[ PMID 17804842 ] [ PMID 17932559 ] [ PMID 18576330 ] [ PMID 18703106 ] [ PMID 19120275 ] [ PMID 19458352 ] [ PMID 19479340 ]

**rs3184504:** A variant of celiac disease genetic risk associated with immune response. Also carrier associated type 1 diabetes.
[ PMID 18311140 ] [ PMID 18978792 ] [ PMID 19073967 ] [ PMID 20546165 ] [ PMID 20854658 ] [ PMID 21873553 ] [ PMID 24936253 ]

**rs3087243:** The CTLA4 allelic variant alters T cell phosphorylation patterns and causes an increased risk of autoimmune diseases.
[ PMID 17554260 ] [ PMID 17606874 ] [ PMID 18940880 ] [ PMID 21121051 ]

**rs6822844:** Combined with the rs13119723 breakage, the study showed the strongest association with celiac disease among Caucasian patients.
[ PMID 17558408 ]

## Women's diseases

## Endometriosis

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs10965235 | CC | CC |
| rs10859871 | AA | AA |
| rs16826658 | TT | TT |
| rs1537377 | TT | TT |
| rs7739264 | TC | TT |
| rs12700667 | AA | GG |
| rs7521902 | CG | CC |
| rs2235529 | CC | CC |
| rs13394619 | AA | AA |
| rs9340799 | AA | AA |
| rs6907340 | TC | TT |
| rs801112 | TT | TT |
| rs12449465 | TT | TT |
| rs7816936 | CC | TT |
| rs10431397 | CG | CC |
| rs11193561 | TC | CC |
| rs10508881 | GG | AA |



Risk level: average

**rs12700667:** Increased risk of ovarian endometriosis disease.
[ PMID 21151130 ] [ PMID 23104006 ] [ PMID 23142796 ] [ PMID 23315067 ] [ PMID 24676469 ] [ PMID 26337243 ] [ PMID 27233752 ] [ PMID 30010178 ] [ PMID 30988702 ] [ PMID 32232822 ]

**rs7739264:** Polymorphisms associated with infertility risk and endometriosis.
[ PMID 23104006 ] [ PMID 24676469 ] [ PMID 25678572 ] [ PMID 26337243 ] [ PMID 30010178 ] [ PMID 30988702 ]

**rs7521902:** Genetic variant underlying the risk of endometriosis.
[ PMID 21151130 ] [ PMID 23104006 ] [ PMID 23142796 ] [ PMID 23315067 ] [ PMID 24319535 ] [ PMID 24676469 ] [ PMID 25678572 ] [ PMID 26139156 ] [ PMID 26337243 ] [ PMID 28901453 ] [ PMID 30770928 ] [ PMID 30988702 ] [ PMID 32143537 ] [ PMID 33113402 ]

## Infertility and miscarriage

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs955988 | N/A | TT |
| rs12097821 | GG | GG |
| rs35576928 | CG | CC |
| rs9814870 | AG | AA |
| rs6068020 | TC | CC |
| rs10841496 | AC | CC |
| rs10917151 | CG | GG |
| rs10122243 | CG | CC |
| rs3129878 | AA | AA |
| rs498422 | TA | TT |
| rs6836703 | CG | GG |
| rs2293275 | TC | TT |
| rs2301365 | CG | GG |
| rs10910078 | TC | CC |
| rs2477686 | CC | CC |
| rs10842262 | GC | GG |
| rs2010963 | CG | GG |
| rs3918188 | CG | CC |
| rs1053023 | TA | TT |
| rs1799983 | CG | GG |
| rs360717 | GG | GG |
| rs2070744 | TC | CC |
| rs187238 | CG | CC |
| rs4680 | AG | GG |
| rs1052133 | CG | CC |
| rs9939609 | TT | TT |
| rs3025039 | TC | CC |
| rs17880664 | AA | AA |
| rs1048943 | TT | TT |

| | | |
|---|---|---|
| rs1799963 | GG | GG |
| rs6025 | CC | CC |
| rs2232365 | TC | CC |
| rs6505162 | CC | CC |
| rs2275913 | GG | GG |
| rs763780 | TT | TT |
| rs4646903 | AA | AA |
| rs1805087 | AA | AA |
| rs113588187 | CG | CC |
| rs146350366 | TA | AA |
| rs138993181 | CG | CC |
| rs7859844 | CG | GG |
| rs143445068 | CG | GG |
| rs183453668 | CG | GG |
| rs10270417 | TA | TT |



Risk level: average

**rs35576928:** Protamine gene polymorphism is associated with asthenozoospermia in men.
[ PMID 30123866 ]

**rs2293275:** A polymorphism of the chorionic gonadotropin luteinising hormone receptor gene (rs2293275) is associated with polycystic ovary syndrome.
[ PMID 25565299 ]

**rs1053023:** STAT3 polymorphism is associated with idiopathic habitual miscarriages.
[ PMID 20059466 ] [ PMID 23065274 ] [ PMID 23193966 ]

**rs1799983:** Decreases the activity of the NOS3 gene and may reduce the efficiency of the methylation process. Also associated with increased risk markers for cardiovascular problems, such as total cholesterol and low-density lipoprotein (LDL) levels, and with an increased risk of high blood pressure, especially in pregnant women.
[ PMID 20409549 ]

**rs4680:** The study showed a 10% increase in total plasma homocysteine (tHcy)
[ PMID 18064318 ]

# Cancer

## Cancer of respiratory organs

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs8034191 | TC | TT |
| rs2808630 | TT | TT |
| rs1051730 | AG | GG |
| rs763317 | AA | GG |
| rs7086803 | AG | GG |
| rs4488809 | TT | TT |
| rs4324798 | AG | GG |
| rs61764370 | AA | AA |
| rs2853677 | AG | AA |
| rs4254535 | TC | TT |
| rs3117582 | TT | TT |
| rs7216064 | GG | GG |
| rs2395185 | GG | GG |
| rs1530057 | GG | GG |
| rs10197940 | TC | CC |
| rs2352028 | CG | CC |
| rs402710 | TC | TT |
| rs10849605 | TC | TT |
| rs36600 | TT | CC |
| rs401681 | TC | TT |
| rs8042374 | AA | AA |
| rs753955 | AG | AA |
| rs2736100 | AC | AA |
| rs9387478 | AC | AA |
| rs1926203 | AA | CC |
| rs4975616 | AG | AA |
| rs12613938 | TT | CC |
| rs1267601 | TT | TT |

| | | |
|---|---|---|
| rs6740703 | AG | AA |
| rs1267622 | GG | AA |
| rs7591913 | GG | GG |
| rs13314271 | TT | CC |
| rs17879961 | CA | AA |
| rs11571833 | AA | AA |
| rs3749971 | AG | GG |
| rs3131379 | GG | GG |
| rs13180 | TC | CC |
| rs31489 | AC | AA |
| rs1270942 | AA | AA |
| rs2684807 | TC | TT |
| rs2684799 | TC | CC |
| rs7170035 | AA | AA |
| rs10508266 | CG | GG |
| rs3750861 | TC | CC |
| rs17576 | AG | AA |
| rs2250889 | CC | GG |
| rs7727912 | TA | TT |
| rs805297 | AC | CC |
| rs805293 | TA | TT |
| rs707939 | AC | CC |
| rs1802127 | CC | CC |
| rs4461039 | AA | AA |
| rs16969968 | AG | GG |
| rs12914385 | TC | CC |
| rs12440014 | CC | CC |
| rs1316971 | GG | GG |
| rs10937405 | CC | TT |
| rs3817963 | TC | TT |
| rs1663689 | TA | TT |
| rs6489769 | TC | TT |

| | | |
|---|---|---|
| rs12296850 | AA | GG |
| rs4809957 | AA | AA |
| rs6141383 | CG | GG |
| rs31490 | AG | GG |
| rs2895680 | TA | TT |



Risk level: average

**rs763317:** SNP of EGFR intron 1 increases 3.5-fold the risk of lung adenocarcinoma disease.
[ PMID 19026460 ] [ PMID 20068085 ]

**rs10937405:** TP63 variations are associated with predisposition to lung adenocarcinoma.
[ PMID 24092572 ] [ PMID 27162544 ] [ PMID 31204706 ] [ PMID 35222588 ]

**rs8034191:** A region of chromosome 5p15 associated with the risk of adenocarcinoma.
[ PMID 18385676 ] [ PMID 19641473 ] [ PMID 19836008 ] [ PMID 24254305 ]

**rs1051730:** CHRNA3 single nucleotide polymorphism increases the risk of lung cancer by 1.8 times. It also contributes to a decreased response to alcohol, so there may be an increased risk of alcohol abuse.
[ PMID 19465454 ] [ PMID 19733931 ] [ PMID 23056235 ]

**rs7086803:** Single nucleotide polymorphisms in the VTI1A gene contribute to susceptibility to non-small cell lung cancer.
[ PMID 25744365 ] [ PMID 28949031 ]

**rs4324798:** The TERT-CLPTM1L lung cancer susceptibility variant is associated with higher DNA adduct formation in the lungs and lung cancer susceptibility.
[ PMID 19465454 ] [ PMID 20548021 ] [ PMID 23959479 ]

**rs2853677:** Genetic variation in the TERT gene is associated with predisposition to non-small cell lung cancer and leukaemia.
[ PMID 21771723 ] [ PMID 27191258 ] [ PMID 31126249 ]

**rs16969968:** The nicotinic acetylcholine receptor risk allele in CHRNA5 causes a higher risk of nicotine dependence, lung cancer, but a lower risk of cocaine dependence.
[ PMID 18227835 ] [ PMID 18385738 ] [ PMID 18519132 ] [ PMID 18519524 ] [ PMID 18957677 ] [ PMID 19010884 ] [ PMID 20581870 ] [ PMID 29993116 ]

## Melanoma

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs12203592 | CC | CC |
| rs885479 | GG | GG |
| rs258322 | GG | GG |
| rs3219090 | CC | TT |
| rs16953002 | GG | GG |
| rs1110400 | TT | TT |
| rs872071 | AG | AA |
| rs2228479 | GG | GG |
| rs154659 | TT | TT |
| rs61996344 | TA | TT |
| rs3212361 | CG | GG |
| rs1805009 | GG | GG |
| rs1805005 | TT | GG |
| rs11547464 | GG | GG |
| rs1805008 | CC | CC |
| rs1805007 | CC | CC |
| rs17119461 | TT | TT |
| rs1393350 | GG | GG |
| rs2284063 | GG | AA |
| rs13016963 | AG | GG |
| rs45430 | TC | TT |
| rs7412746 | TC | CC |
| rs4785763 | CC | CC |
| rs7023329 | AA | GG |
| rs35390 | AA | AA |
| rs910873 | AG | GG |
| rs1800407 | CC | CC |
| rs1885120 | CG | GG |
| rs861539 | AA | GG |

| | | |
|---|---|---|
| rs13181 | TG | TT |
| rs1267601 | TT | TT |



Risk level: average

**rs3219090:** A common intronic variant of PARP1 increases the risk of melanoma.
[ PMID 28759004 ]

**rs1805005:** A variant of the melanocyte-stimulating hormone receptor gene responsible for a significant proportion of the risk of malignant melanoma of the skin
[ PMID 9302268 ] [ PMID 10631149 ] [ PMID 16601669 ] [ PMID 19585506 ]

**rs872071:** The IRF4 rs872071 polymorphism causes susceptibility to chronic lymphocytic leukaemia, Hodgkin's lymphoma, skin cancer and haematological malignancies.
[ PMID 19804451 ] [ PMID 20332261 ] [ PMID 20602913 ] [ PMID 24906573 ]

**rs910873:** There is a 3-fold increased risk of malignant melanoma.
[ PMID 18488026 ] [ PMID 20224305 ]

## Sarcoma

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs5742909 | CG | CC |
| rs2279744 | TT | TT |
| rs1800795 | GG | CC |
| rs231775 | AA | AA |
| rs11203289 | GG | GG |
| rs587776649 | CG | GG |
| rs587776653 | CG | GG |
| rs104886003 | GG | GG |
| rs878854590 | CG | GG |
| rs80338843 | CC | CC |
| rs878854591 | CG | CC |
| rs80338845 | GG | GG |
| rs878854594 | CC | CC |
| rs201372601 | GG | GG |
| rs11540652 | CC | CC |
| rs6734469 | CG | GG |



Risk level: average

**rs5742909:** Cytotoxic T-lymphocyte cytotoxic antigen-4 polymorphism increases susceptibility to Ewing's sarcoma.
[ PMID 22905924 ] [ PMID 30235774 ]

**rs6734469:** Polymorphisms in the p53 14-3-3tau and CD44 network genes influence sarcoma incidence and survival.
[ PMID 19996285 ]

# Cancer of the thyroid gland

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs199752932 | AA | AA |
| rs1800860 | AG | AA |
| rs9282834 | GG | GG |
| rs17158558 | CC | CC |
| rs1800858 | GG | AA |
| rs6983267 | TG | TT |
| rs944289 | CC | CC |
| rs2961920 | AC | CC |
| rs965513 | AG | GG |
| rs966423 | TC | TT |
| rs2439302 | CG | CC |
| rs116909374 | CC | CC |
| rs1867277 | CG | GG |
| rs2910164 | CG | GG |
| rs1443434 | TA | TT |



Risk level: average

**rs1800858:** RET signalling pathway initiator polymorphisms are associated with susceptibility to sporadic papillary thyroid carcinoma.
[ PMID 11950855 ] [ PMID 16091499 ] [ PMID 18284634 ] [ PMID 23059849 ]

**rs1800860:** RET tagSNP polymorphism is associated with clinical severity and thyroid function in patients with differentiated thyroid cancer.
[ PMID 29131865 ]

**rs6983267:** SNP on chromosome 8q24 associated with increased risk of prostate cancer and colorectal cancer amenable to aspirin.
[ PMID 17618282 ] [ PMID 18172290 ] [ PMID 18362937 ] [ PMID 18372901 ] [ PMID 18768513 ] [ PMID 19047180 ] [ PMID 19561607 ] [ PMID 21483638 ] [ PMID 21567271 ] [ PMID 33432117 ] [ PMID 33713253 ]

**rs2961920:** Breakdown associated with papillary thyroid cancer, which is the most common form of thyroid cancer and is well-treated.
[ PMID ]

**rs965513:** Genetic predisposition to familial non-medullary thyroid cancer.

[ PMID 20628519 ]  [ PMID 21730105 ]  [ PMID 24723258 ]

**rs966423:** The rs966423 polymorphism in DIRC3 is associated with papillary thyroid carcinoma.
[ PMID 26490305 ]  [ PMID 32059462 ]

**rs2439302:** The rs2439302 polymorphism is associated with thyroid cancer.
[ PMID 25562676 ]  [ PMID 35558387 ]

## Cancer of the hematopoietic system

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs4129267 | TC | CC |
| rs4537545 | TC | CC |
| rs1801282 | GG | CC |
| rs7089424 | TA | TT |
| rs4132601 | TG | TT |
| rs17505102 | GG | GG |
| rs563507 | GG | GG |
| rs2239633 | AG | AA |
| rs674313 | TT | CC |
| rs4987852 | TC | TT |
| rs305061 | TC | TT |
| rs2466035 | TC | TT |
| rs13397985 | TT | TT |
| rs2511714 | TG | TT |
| rs31490 | AG | GG |
| rs4406737 | AA | AA |
| rs6858698 | GG | GG |
| rs210134 | GG | AA |
| rs9273012 | AA | AA |
| rs7944004 | GG | GG |
| rs1439287 | AG | GG |
| rs4368253 | TC | TT |
| rs1044873 | TC | TT |
| rs17246404 | TC | TT |
| rs10936599 | CC | CC |
| rs11022157 | CC | CC |
| rs757978 | CC | CC |
| rs210142 | CC | TT |
| rs1679013 | TT | TT |

| | | |
|---|---|---|
| rs9273363 | CC | CC |
| rs391023 | TC | TT |
| rs11636802 | AA | AA |
| rs11083846 | GG | GG |
| rs735665 | AG | GG |
| rs872071 | AG | AA |
| rs391525 | AG | AA |
| rs3769825 | AG | AA |
| rs2456449 | AA | AA |
| rs926070 | AA | GG |
| rs9378805 | CC | AA |
| rs2236256 | AA | AA |
| rs898518 | AA | CC |
| rs17483466 | AA | AA |
| rs1800682 | GG | GG |
| rs7176508 | GG | GG |
| rs13401811 | GG | AA |
| rs76428106 | AA | TT |
| rs35602083 | CG | CC |
| rs61756766 | CG | GG |
| rs2075726 | GG | AA |
| rs1036935 | CG | GG |
| rs1800566 | GG | GG |
| rs2858870 | TA | TT |
| rs9268528 | GG | AA |
| rs9268542 | GG | AA |
| rs6903608 | CC | TT |
| rs204999 | AA | AA |
| rs2019960 | TT | TT |
| rs501764 | TT | TT |
| rs2395185 | GG | GG |
| rs2069757 | GG | GG |

| | | |
|---|---|---|
| rs2248462 | GG | GG |
| rs27524 | GG | GG |
| rs20541 | GG | GG |
| rs444929 | TA | TT |
| rs7745098 | CC | TT |
| rs1860661 | AG | GG |
| rs3806624 | GG | GG |
| rs1432295 | AA | AA |
| rs6691170 | TG | GG |
| rs11249433 | AA | AA |
| rs16754 | TC | TT |
| rs10821936 | TC | TT |
| rs11978267 | AG | AA |
| rs3731217 | AA | AA |
| rs796065343 | GG | CC |
| rs1057519753 | CG | GG |
| rs77375493 | GG | GG |
| rs121913459 | CC | CC |
| rs121913461 | TT | TT |
| rs121913237 | CG | CC |
| rs662463 | CG | GG |
| rs924607 | TC | CC |
| rs361525 | GG | GG |
| rs909253 | AA | AA |
| rs2239704 | AC | AA |
| rs1801274 | GG | AA |

Risk level: average

**rs1801282:** Peroxisome proliferator-activated receptor gamma gene variation on the progression of type 2 diabetes and obesity. Also higher risk of cardiovascular disease with a diet high in saturated fat.
[ PMID 17213274 ] [ PMID 18091023 ] [ PMID 18598350 ] [ PMID 18694974 ] [ PMID 19020323 ]

**rs7089424:** Variations in 7p12.2 and 10q21.2 affect the risk of childhood acute lymphoblastic leukaemia.
[ PMID 19684604 ] [ PMID 20460642 ] [ PMID 20919861 ] [ PMID 28381164 ]

**rs4132601:** The IKZF1 rs4132601 polymorphism causes susceptibility to acute lymphoblastic leukaemia.
[ PMID 19684604 ] [ PMID 20453839 ] [ PMID 24597983 ] [ PMID 25012940 ] [ PMID 35932035 ]

**rs2239633:** CEBPE polymorphism increases the risk of acute lymphoblastic leukaemia in children.
[ PMID 20919861 ] [ PMID 22422485 ] [ PMID 25195121 ] [ PMID 26388693 ]

**rs735665:** 50% higher risk of chronic lymphocytic leukaemia.
[ PMID 20332261 ] [ PMID 20389242 ] [ PMID 20731705 ]

**rs872071:** The IRF4 rs872071 polymorphism causes susceptibility to chronic lymphocytic leukaemia, Hodgkin's lymphoma, skin cancer and haematological malignancies.
[ PMID 19804451 ] [ PMID 20332261 ] [ PMID 20602913 ] [ PMID 24906573 ]

**rs16754:** Single nucleotide polymorphism rs16754 of the WT1 gene is associated with acute myeloleukaemia in children.
[ PMID 20644087 ] [ PMID 21189390 ] [ PMID 23070125 ] [ PMID 30468432 ]

**rs10821936:** A variant of the ARID5B gene is associated with the development of acute lymphoblastic leukaemia in Mexican children.
[ PMID 20054350 ] [ PMID 20460642 ] [ PMID 23975371 ] [ PMID 31111395 ] [ PMID 31227872 ]

## Cancer of the mammary gland

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs3757318 | GG | GG |
| rs2363956 | GG | TT |
| rs10069690 | CC | CC |
| rs4245739 | AA | AA |
| rs10771399 | AA | AA |
| rs10822013 | TT | CC |
| rs1562430 | TT | TT |
| rs13393577 | TT | TT |
| rs865686 | GG | GG |
| rs10995190 | GG | AA |
| rs13281615 | AG | AA |
| rs2981582 | AA | GG |
| rs1011970 | GG | GG |
| rs9485372 | GG | GG |
| rs2981579 | AA | GG |
| rs2046210 | GG | GG |
| rs11249433 | AA | AA |
| rs8170 | GG | GG |
| rs3803662 | AA | GG |
| rs704010 | CC | CC |
| rs3817198 | TT | TT |
| rs4973768 | TT | CC |
| rs4784227 | TC | CC |
| rs3112612 | AG | GG |
| rs889312 | AA | AA |
| rs2981575 | GG | AA |
| rs13387042 | AA | GG |
| rs2180341 | AA | AA |
| rs1219648 | GG | AA |

| | | |
|---|---|---|
| rs11242675 | TT | CC |
| rs2380205 | CC | TT |
| rs10510102 | TC | TT |
| rs1436904 | TG | GG |
| rs9383938 | GG | GG |
| rs7072776 | GG | GG |
| rs2823093 | GG | GG |
| rs6788895 | GG | GG |
| rs720475 | AG | GG |
| rs4849887 | TA | TT |
| rs909116 | CC | CC |
| rs1432679 | TT | TT |
| rs999737 | TC | CC |
| rs11199914 | TC | CC |
| rs12922061 | CC | CC |
| rs2284378 | TC | CC |
| rs17530068 | CC | TT |
| rs17356907 | AA | GG |
| rs10941679 | GG | AA |
| rs7904519 | AG | AA |
| rs6504950 | AA | AA |
| rs3760982 | AA | GG |
| rs3734805 | AA | AA |
| rs8100241 | AA | AA |
| rs2588809 | TC | CC |
| rs2981578 | CC | CC |
| rs6472903 | TT | GG |
| rs16886165 | TT | TT |
| rs3903072 | GG | GG |
| rs6556756 | TG | TT |
| rs737387 | AG | GG |
| rs4455437 | AA | AA |

| | | |
|---|---|---|
| rs12493607 | GC | GG |
| rs527616 | GC | CC |
| rs7535752 | GG | GG |
| rs16857609 | CC | CC |
| rs10853029 | TT | TT |
| rs12422552 | GG | GG |
| rs10759243 | CC | CC |
| rs11780156 | CC | CC |
| rs12355688 | CC | CC |
| rs12710696 | TT | CC |
| rs1926657 | CC | CC |
| rs11820646 | TT | TT |
| rs9790517 | TC | CC |
| rs10472076 | TT | TT |
| rs9693444 | AA | CC |
| rs11075995 | TA | TT |
| rs13329835 | AG | AA |
| rs1078806 | TA | AA |
| rs11571833 | AA | AA |
| rs941764 | AG | AA |
| rs4808801 | AA | GG |
| rs1550623 | AA | GG |
| rs458685 | AA | AA |
| rs11814448 | AA | AA |
| rs6678914 | GG | GG |
| rs63750330 | TT | TT |
| rs1805812 | TT | TT |
| rs41295284 | TT | TT |
| rs78378222 | TT | TT |
| rs769420 | GG | GG |
| rs55819519 | CC | CC |
| rs1799977 | AA | AA |

| | | |
|---|---|---|
| rs6470522 | GG | GG |
| rs4986761 | TT | TT |
| rs1800056 | TT | TT |
| rs1799950 | TC | TT |
| rs2227945 | TT | TT |
| rs11571746 | TT | TT |
| rs16942 | TT | TT |
| rs1799954 | CC | CC |
| rs3218695 | CC | CC |
| rs1800058 | CC | CC |
| rs4987117 | CC | CC |
| rs3092856 | CC | CC |
| rs17879961 | CA | AA |
| rs144848 | AC | AA |
| rs11571747 | AA | AA |
| rs1801673 | AA | AA |
| rs4987047 | AA | AA |
| rs1801426 | AA | AA |
| rs28897708 | TT | TT |
| rs28897680 | TT | TT |
| rs1801499 | TT | TT |
| rs11571707 | TT | TT |
| rs28897689 | TT | TT |
| rs4986844 | TT | TT |
| rs56012641 | TT | TT |
| rs28897683 | GG | GG |
| rs8176260 | GG | GG |
| rs11571769 | GG | GG |
| rs1800709 | CG | GG |
| rs28897727 | GG | GG |
| rs1799965 | GG | GG |
| rs28897728 | GG | GG |

| | | |
|---|---|---|
| rs28897701 | GG | GG |
| rs8176316 | GG | GG |
| rs56158747 | GG | GG |
| rs9534262 | CC | CC |
| rs4942486 | CC | CC |
| rs1800704 | CC | CC |
| rs1799967 | CC | CC |
| rs4986852 | CG | CC |
| rs28897706 | CC | CC |
| rs55638633 | CC | CC |
| rs169547 | CC | CC |
| rs8176320 | CC | CC |
| rs55716624 | CC | CC |
| rs3092994 | CC | CC |
| rs8176318 | CC | CC |
| rs799923 | AA | GG |
| rs28897710 | AA | AA |
| rs9943888 | AG | AA |
| rs4986854 | AA | AA |
| rs1799944 | AA | AA |
| rs55953736 | AA | AA |
| rs11571640 | AA | AA |
| rs517118 | AA | AA |
| rs1801439 | AA | AA |
| rs11571653 | AA | AA |
| rs56128296 | AA | AA |
| rs28897745 | AA | AA |
| rs2909430 | TT | TT |
| rs17883862 | GG | GG |
| rs1800371 | GG | GG |
| rs2912774 | CG | GG |
| rs2420946 | TT | CC |

| | | |
|---|---|---|
| rs1219643 | AC | CC |
| rs1017226 | TT | TT |
| rs16886113 | TT | TT |
| rs16886181 | TT | TT |
| rs7726354 | CC | CC |
| rs2229882 | CC | CC |
| rs16886448 | CC | CC |
| rs653465 | TT | TT |
| rs16886364 | AA | AA |
| rs4784223 | AG | AA |
| rs2392780 | AA | AA |
| rs12655019 | AA | AA |
| rs16886397 | AA | AA |
| rs3822625 | AA | AA |
| rs28897693 | TT | TT |
| rs11571657 | TT | TT |
| rs55969723 | AA | AA |
| rs2842347 | TC | TT |
| rs132390 | TC | TT |
| rs1810320 | CG | GG |
| rs2236007 | GG | GG |
| rs6835704 | CC | TT |
| rs6001930 | TT | TT |
| rs6828523 | CC | AA |
| rs616488 | GG | GG |
| rs6797852 | GG | AA |
| rs2943559 | AA | AA |
| rs6762644 | GG | AA |
| rs204247 | AG | AA |
| rs4322600 | GG | GG |
| rs1292011 | AA | GG |
| rs1045487 | AG | GG |

| | | |
|---|---|---|
| rs3769825 | AG | AA |
| rs16941 | TT | TT |
| rs56039126 | GG | GG |
| rs62625307 | GG | GG |
| rs28897692 | CC | CC |
| rs28897677 | CC | CC |
| rs614367 | CC | CC |
| rs41293521 | TT | TT |

Risk level: low

**rs2981582:** Estrogen receptor-positive (ER+) breast cancer risk is 1.7 times higher.
[ PMID 17529967 ] [ PMID 18437204 ] [ PMID 18845558 ]

**rs2981579:** FGFR2 gene variation and the effect of low-fat diet on invasive breast cancer.
[ PMID 17529973 ] [ PMID 20056625 ] [ PMID 22452962 ] [ PMID 26175953 ]

**rs3803662:** The risk allele SNP rs3803662 and mRNA levels of the nearby TOX3 and LOC643714 genes predict unfavourable outcome for breast cancer patients.
[ PMID 21475997 ] [ PMID 23270421 ] [ PMID 29578175 ]

**rs1436904:** The CHST9 rs1436904 genetic variant contributes to the prognosis of triple negative breast cancer.
[ PMID 28924212 ]

## Cancer of the digestive organs

## Colorectal cancer

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs6983267 | TG | TT |
| rs4987188 | GG | GG |
| rs433852 | TC | CC |
| rs8111500 | GG | GG |
| rs3760775 | GG | GG |
| rs12608544 | GG | GG |
| rs2071699 | GG | GG |
| rs11880333 | CC | CC |
| rs441810 | AG | AA |
| rs7030248 | GG | GG |
| rs1047781 | AA | AA |
| rs12603526 | TT | TT |
| rs2423279 | TA | TT |
| rs10849432 | TT | TT |
| rs12309274 | TT | TT |
| rs11903757 | TT | TT |
| rs367615 | AT | TT |
| rs39453 | TC | TT |
| rs4939827 | TC | CC |
| rs6691170 | TG | GG |
| rs7758229 | GG | GG |
| rs4246215 | TG | GG |
| rs9929218 | AG | GG |
| rs10505477 | AG | GG |
| rs7229639 | GG | GG |
| rs7014346 | AG | GG |
| rs34245511 | CG | GG |
| rs1800469 | AG | GG |

| | | |
|---|---|---|
| rs11169552 | TC | TT |
| rs10774214 | TC | CC |
| rs1665650 | TC | CC |
| rs10411210 | TC | CC |
| rs10936599 | CC | CC |
| rs2241714 | TC | CC |
| rs2427308 | TC | CC |
| rs4779584 | CC | CC |
| rs961253 | CC | CC |
| rs4591517 | TC | CC |
| rs4925386 | TC | TT |
| rs3217810 | CC | CC |
| rs140355816 | CC | CC |
| rs11255841 | TT | AA |
| rs6687758 | AA | AA |
| rs10795668 | GG | AA |
| rs73376930 | AG | AA |
| rs2057314 | AG | GG |
| rs704017 | GG | AA |
| rs9365723 | AG | AA |
| rs1321311 | CC | CC |
| rs6469656 | AA | AA |
| rs16892766 | AA | AA |
| rs3217901 | AG | AA |
| rs11196172 | GG | GG |
| rs3802842 | AA | AA |
| rs10911251 | CC | AA |
| rs63749924 | CC | CC |
| rs1799977 | AA | AA |
| rs1800734 | AG | GG |
| rs2229995 | GG | GG |
| rs465899 | AA | AA |

| | | |
|---|---|---|
| rs719725 | AC | CC |
| rs36053993 | CC | CC |
| rs4464148 | TT | TT |
| rs396991 | CA | AA |



Risk level: average

**rs6983267:** SNP on chromosome 8q24 associated with increased risk of prostate cancer and colorectal cancer amenable to aspirin.
[ PMID 17618282 ] [ PMID 18172290 ] [ PMID 18362937 ] [ PMID 18372901 ] [ PMID 18768513 ] [ PMID 19047180 ] [ PMID 19561607 ] [ PMID 21483638 ] [ PMID 21567271 ] [ PMID 33432117 ] [ PMID 33713253 ]

**rs2423279:** A genetic variant associated with colorectal cancer risk.
[ PMID 23946381 ] [ PMID 24587672 ] [ PMID 28084440 ]

**rs367615:** Variant predisposition to colorectal and oesophageal cancer.
[ PMID 26078566 ]

**rs4939827:** Increased risk of colorectal cancer associated with SMAD7 genetic polymorphism.
[ PMID 17934461 ] [ PMID 19155440 ] [ PMID 19395656 ] [ PMID 20124488 ] [ PMID 28467803 ]

**rs10505477:** Genetic variation in 8q24 is associated with colorectal cancer risk.
[ PMID 17630503 ] [ PMID 18056436 ] [ PMID 18839428 ] [ PMID 22363440 ]

## Stomach cancer

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs2276330 | TT | TT |
| rs33935154 | GG | GG |
| rs16260 | AC | CC |
| rs55819519 | CC | CC |
| rs4074785 | GG | GG |
| rs2071543 | GG | GG |
| rs1045487 | AG | GG |
| rs61756766 | CG | GG |
| rs9357155 | GG | GG |
| rs1518111 | CG | CC |
| rs1800896 | TT | TT |
| rs3024493 | CC | CC |
| rs3810936 | TC | CC |
| rs763110 | TT | TT |
| rs4561508 | CC | CC |
| rs4985726 | CC | CC |
| rs11574514 | CC | CC |
| rs2234978 | TC | CC |
| rs3731249 | CC | CC |
| rs2834167 | AA | AA |
| rs735299 | AG | GG |
| rs6924102 | AG | AA |
| rs9276810 | CG | GG |
| rs1800871 | AG | GG |
| rs2157453 | CG | GG |
| rs229527 | CC | CC |
| rs3024490 | CG | CC |
| rs4273077 | AA | AA |
| rs3754935 | AA | AA |

| | | |
|---|---|---|
| rs3731217 | AA | AA |
| rs1800682 | GG | GG |
| rs3731211 | AA | AA |
| rs429358 | TA | TT |
| rs140501787 | TA | TT |
| rs4783244 | TG | GG |
| rs2858331 | GG | AA |
| rs7551188 | TC | TT |
| rs1607237 | TT | TT |
| rs2236851 | CG | CC |
| rs870995 | AC | CC |
| rs11706842 | CG | CC |
| rs113613074 | CG | CC |
| rs7501331 | CC | CC |
| rs2236225 | AG | GG |
| rs231775 | AA | AA |
| rs162036 | AA | AA |
| rs63750123 | TT | TT |
| rs3816587 | TC | TT |
| rs35831931 | GG | GG |
| rs7576974 | CC | CC |
| rs12112229 | CG | CC |
| rs6504663 | AG | AA |
| rs87938 | GG | GG |
| rs8057927 | TT | TT |
| rs11245936 | GG | GG |
| rs28360974 | CG | GG |
| rs10514585 | GG | GG |
| rs7934606 | CC | CC |
| rs3765695 | CC | CC |
| rs2517415 | CC | CC |
| rs2517416 | CC | CC |

| | | |
|---|---|---|
| rs4728142 | AA | GG |
| rs2274223 | AA | AA |
| rs4072037 | TA | TT |
| rs2294008 | CC | CC |
| rs2976392 | GG | GG |

Risk level: low

**rs2858331:** Together with the rs4988889 gene breakage, it is a diagnostic criterion for celiac disease.

**rs4728142:** Validation of IRF5 as a multiple sclerosis risk gene: putative role in human herpes virus-6 infection.
[ PMID 18285424 ] [ PMID 20861862 ]

**rs429358:** The APOE-E4 allele has a strong influence on the risk of developing Alzheimer's disease. One meta-analysis estimated the odds ratio for individuals homozygous for rs429358 to be 12 times higher for late-onset Alzheimer's disease and 61 times higher for early-onset disease. People with APOE4-4 allele C genotype should avoid eating animals raised on plants/grains that have higher levels of omega-6 compared to omega-3. It is advisable to practice vegetarianism to avoid all animal fats and measure the ratio of omega-3 to omega-6 in these people. Also, people with APOE 4 may do better on unmethylated forms of B12.
[ PMID 21263195 ] [ PMID 30665447 ]

**rs2236225:** Possible increased risk of fetal birth defects. A 1.5-fold higher risk for Caucasian mothers to give birth to children with DNT (neural tube defect). The association in children with this mutation with an increased risk of heart defects is greater if their mother did not get enough folic acid during pregnancy. The risk is reduced with adequate levels of folic acid and vitamin B6.
[ PMID 18767138 ] [ PMID 20544798 ] [ PMID 20890936 ]

**rs4072037:** Polymorphism affecting serum levels of magnesium, potassium and sodium. Also associated with risk of gastric cancer.
[ PMID 20700443 ] [ PMID 21427165 ] [ PMID 24782603 ] [ PMID 24810688 ] [ PMID 32269683 ] [ PMID 32595997 ]

## Other cancers of the digestive system

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs9543325 | CC | TT |
| rs372883 | TT | CC |
| rs9573163 | CC | CC |
| rs1547374 | AG | AA |
| rs2255280 | AA | AA |
| rs5768709 | AA | AA |
| rs12413624 | TT | AA |
| rs225190 | TC | TT |
| rs3016539 | TT | TT |
| rs9502893 | TC | CC |
| rs1585440 | TG | GG |
| rs1000589 | CG | GG |
| rs9874556 | CG | GG |
| rs9363918 | TG | TT |
| rs6464375 | CC | CC |
| rs4924935 | TC | TT |
| rs1886449 | CG | CC |
| rs2257205 | AC | CC |
| rs12615966 | CC | CC |
| rs6879627 | TC | CC |
| rs12456874 | AA | AA |
| rs6736997 | CG | CC |
| rs3790844 | AA | GG |
| rs6971499 | TC | TT |
| rs9581943 | AG | GG |
| rs7190458 | GG | GG |
| rs1561927 | TC | CC |
| rs16986825 | TC | CC |
| rs1169310 | CG | GG |

| | | |
|---|---|---|
| rs2259816 | GG | GG |
| rs7310409 | GG | GG |
| rs1183910 | GG | GG |
| rs144848 | AC | AA |
| rs1047972 | CC | CC |
| rs12953717 | TC | TT |
| rs2274223 | AA | AA |
| rs17655 | GG | CC |
| rs121909229 | CG | GG |
| rs13181 | TG | TT |
| rs11614913 | CC | TT |
| rs3746444 | AA | AA |
| rs11615 | AA | AA |
| rs1229984 | CC | CC |
| rs1048943 | TT | TT |
| rs505922 | TA | TT |
| rs121908291 | CG | CC |
| rs521102 | CG | GG |
| rs9895829 | AA | AA |



Risk level: average

**rs9543325:** Pancreatic cancer predisposition locus.
[ PMID 20101243 ] [ PMID 22125638 ] [ PMID 26929738 ] [ PMID 28172817 ]

**rs372883:** The BACH1 polymorphism causes a predisposition to pancreatic cancer.
[ PMID 23250936 ] [ PMID 29930735 ]

**rs3790844:** NR5A2 variation is associated with pancreatic cancer risk, especially among Caucasian individuals.
[ PMID 21498636 ] [ PMID 22125638 ] [ PMID 26592175 ] [ PMID 29785120 ]

**rs11614913:** A variant of the MIR196A2 gene increases the risk of gastrointestinal cancer.
[ PMID 19834808 ] [ PMID 19851984 ] [ PMID 19926640 ] [ PMID 20722507 ] [ PMID 23160898 ] [ PMID 26215064 ]

**rs505922:** There is a 1.2-fold increased risk of pancreatic cancer.
[ PMID ]

## Bronchial asthma

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs7216389 | CC | CC |
| rs1051931 | AG | AA |
| rs4950928 | CC | CC |
| rs1805018 | AA | AA |
| rs7009110 | CC | CC |
| rs1837253 | TC | TT |
| rs4833095 | CC | CC |
| rs62026376 | TC | TT |
| rs1438673 | TA | TT |
| rs17294280 | AA | AA |
| rs72699186 | AA | AA |
| rs10197862 | AA | GG |
| rs6754459 | CC | CC |
| rs20541 | GG | GG |
| rs1800925 | AC | CC |
| rs2066960 | CC | CC |
| rs1295686 | CC | CC |
| rs848 | CG | CC |
| rs17218161 | TT | TT |
| rs2473967 | TA | TT |
| rs16929097 | GG | GG |
| rs7927044 | GG | GG |
| rs12570188 | CC | CC |
| rs9815663 | CC | CC |
| rs4658627 | GG | GG |
| rs7328278 | AA | AA |
| rs10521233 | AA | AA |
| rs2303067 | AG | AA |
| rs17334242 | AA | AA |

| | | |
|---|---|---|
| rs4986790 | AA | AA |
| rs4986791 | CC | CC |
| rs1801105 | AC | CC |
| rs2280089 | GG | GG |
| rs2280090 | CG | GG |
| rs612709 | CG | GG |
| rs574174 | CC | CC |
| rs44707 | TG | TT |
| rs2787094 | GG | CC |
| rs569108 | AA | AA |
| rs324981 | AA | AA |
| rs1154404 | AA | AA |
| rs4794067 | TT | TT |
| rs2074190 | AA | AA |
| rs9910408 | CG | GG |
| rs2240017 | CG | CC |
| rs16947078 | TA | AA |
| rs11650354 | CC | CC |
| rs2070874 | CC | CC |
| rs2241712 | CG | CC |
| rs2278206 | CG | GG |
| rs4378650 | CG | GG |
| rs12603332 | TT | TT |
| rs8067378 | GG | AA |
| rs6591255 | AT | TT |
| rs1800896 | TT | TT |
| rs3024492 | TA | TT |
| rs3024496 | AA | AA |
| rs3802780 | CG | GG |
| rs1978331 | GG | AA |
| rs11569562 | AG | AA |
| rs1042713 | GG | GG |

| | | |
|---|---|---|
| rs1446495 | AA | AA |
| rs3918396 | CC | TT |
| rs689465 | TT | CC |
| rs2407992 | CC | CC |
| rs320995 | AA | GG |
| rs2251746 | TT | CC |
| rs2427837 | GG | AA |
| rs8069176 | AG | AA |
| rs2305480 | AG | GG |
| rs4795400 | CG | CC |
| rs3741240 | AG | GG |
| rs12422149 | GG | GG |
| rs3804100 | TT | TT |
| rs11650680 | CG | CC |
| rs8193036 | TT | TT |
| rs1420101 | CC | CC |
| rs7740529 | CC | CC |
| rs10402876 | CC | CC |
| rs366510 | CG | GG |
| rs1334710 | AA | AA |
| rs4959389 | AA | AA |
| rs977785 | AC | AA |
| rs11558538 | TC | CC |



Risk level: average

**rs1837253:** A variant of the estrogen receptor I (ESR1) gene is associated with anorexia nervosa and eating disorders.
[ PMID 19539984 ] [ PMID 20560908 ] [ PMID 31066119 ] [ PMID 33879431 ]

**rs1800925:** Interleukin-13 SNP rs1800925 variation associated with asthma and allergic rhinitis.
[ PMID 19796199 ] [ PMID 20444268 ] [ PMID 22750299 ]

**rs2280090:** ADAM33 gene polymorphism identified as associated with asthma and rhinitis in adults.

[ PMID 18778489 ]  [ PMID 22851202 ]  [ PMID 24141861 ]

**rs16947078:** 8-fold risk of developing allergic asthma.
[ PMID  ]

## HIV

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs8321 | AC | AA |
| rs2395029 | TT | TT |
| rs10484554 | CC | CC |
| rs3108919 | TA | TT |
| rs1020064 | TT | TT |
| rs1522232 | TC | TT |
| rs4118325 | GG | AA |
| rs10800098 | GG | GG |
| rs1360517 | CC | CC |
| rs1556032 | CC | TT |
| rs1015164 | CG | GG |
| rs11239930 | AA | GG |
| rs6467710 | CG | GG |
| rs11884476 | CC | CC |
| rs7217319 | TC | TT |
| rs6441975 | AC | CC |
| rs477687 | AG | GG |
| rs572880838 | TA | TT |
| rs6076463 | CG | CC |
| rs9264942 | TT | TT |
| rs2572886 | GG | GG |
| rs1799864 | CG | GG |
| rs4418214 | TT | TT |
| rs3131018 | CC | AA |
| rs9261174 | TA | TT |
| rs9368699 | TT | TT |
| rs8069770 | CG | GG |
| rs17762192 | CG | CC |
| rs2234358 | TT | TT |

| | | |
|---|---|---|
| rs12483205 | AA | AA |
| rs152363 | CC | CC |
| rs1265112 | TT | TT |
| rs1127888 | CG | CC |
| rs667859 | CG | GG |
| rs2306242 | TA | TT |
| rs444772 | GG | GG |
| rs3796375 | GG | GG |



Risk level: average

**rs8321:** The HLA-C single nucleotide polymorphism is associated with increased viral load in HIV-1-infected individuals.
[ PMID 24240316 ] [ PMID 28494720 ] [ PMID 33252547 ]

**rs1799864:** There is a 58% greater risk of developing AIDS in the first 4 years after a positive HIV test.
[ PMID 9252328 ] [ PMID 9662369 ]

**rs17762192:** The 1q41 locus associated with the rate of HIV-1 disease progression to clinical AIDS.
[ PMID 20064070 ] [ PMID 20149939 ] [ PMID 24240316 ]

## Obesity

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs1421085 | TC | TT |
| rs1558902 | TA | TT |
| rs9930506 | TA | AA |
| rs9939609 | TT | TT |
| rs17817449 | TG | TT |
| rs9940128 | AG | GG |
| rs1121980 | AG | GG |
| rs12149832 | AG | GG |
| rs3751812 | TG | GG |
| rs8044769 | TC | CC |
| rs11642841 | AC | CC |
| rs8050136 | AC | CC |
| rs6499662 | AA | AA |
| rs6499640 | AG | GG |
| rs16953002 | GG | GG |
| rs8043757 | AT | AA |
| rs1861868 | CC | CC |
| rs34114122 | TA | TT |
| rs4994 | AA | AA |
| rs11075990 | AG | AA |
| rs5082 | AG | AA |
| rs2229616 | CC | CC |
| rs16964465 | AA | AA |
| rs16964476 | TA | AA |
| rs3764220 | AA | AA |
| rs1528133 | TT | TT |
| rs2272382 | CG | GG |
| rs2272383 | AG | AA |
| rs3865188 | AT | AA |

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|---|---|---|
| rs6971091 | GG | GG |
| rs4142322 | TA | TT |
| rs17573102 | AG | GG |
| rs9028 | TC | CC |
| rs7149926 | CC | CC |
| rs11753543 | CG | GG |
| rs9736016 | AA | TT |
| rs7635777 | CG | CC |
| rs9384860 | AA | AA |
| rs2470315 | AT | TT |
| rs6093921 | AG | GG |
| rs2283208 | AA | GG |
| rs6928576 | AA | TT |
| rs10945918 | CG | CC |
| rs6902153 | CG | CC |
| rs12925846 | CC | CC |
| rs10954428 | GG | GG |
| rs10797020 | AG | GG |
| rs1578761 | CA | AA |
| rs10489833 | TA | TT |
| rs11264997 | TA | AA |
| rs12540206 | CG | GG |
| rs975118 | TA | AA |
| rs7512592 | AA | AA |
| rs1873511 | TA | TT |
| rs6697656 | CG | GG |
| rs6963221 | TG | TT |
| rs6679056 | AG | GG |
| rs6976491 | TA | TT |
| rs7800006 | AG | AA |
| rs1776012 | CG | GG |
| rs2173676 | AA | TT |

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|---|---|---|
| rs2060457 | CG | CC |
| rs2948300 | TT | CC |
| rs2953802 | CG | GG |
| rs435581 | AG | GG |
| rs666595 | AG | GG |
| rs2241005 | AT | TT |
| rs750456 | AA | TT |
| rs12295638 | TT | TT |
| rs1435703 | CG | GG |
| rs6726292 | GG | GG |
| rs2274459 | AG | GG |
| rs999943 | AA | AA |
| rs9941349 | TC | CC |
| rs10433903 | TT | TT |
| rs6110577 | TA | TT |
| rs7603514 | GG | GG |
| rs12635698 | TT | TT |
| rs10999409 | CC | TT |
| rs7474896 | CC | CC |
| rs374748 | TA | AA |
| rs11624704 | AC | AA |
| rs17126232 | CC | CC |
| rs16867321 | TC | CC |
| rs11680012 | CG | GG |
| rs17773430 | TT | TT |
| rs12463617 | CC | CC |
| rs1993709 | GG | GG |
| rs1957894 | TG | GG |
| rs11208659 | TT | TT |
| rs11109072 | CC | CC |
| rs3101336 | TC | TT |
| rs16923476 | GG | GG |

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|---|---|---|
| rs17025867 | GG | GG |
| rs3782724 | AA | AA |
| rs2275848 | CG | GG |
| rs1631486 | AG | GG |
| rs12408810 | TC | TT |
| rs476828 | TC | TT |
| rs564343 | AG | GG |
| rs1048466 | GG | AA |
| rs9328321 | CG | GG |
| rs1704198 | CG | GG |
| rs988712 | GG | TT |
| rs2116830 | TG | TT |
| rs17700144 | AG | GG |
| rs4756846 | TT | TT |
| rs297325 | TT | TT |
| rs1424233 | TC | CC |
| rs17782313 | TC | TT |
| rs1805081 | TC | CC |
| rs4712652 | CG | GG |
| rs734597 | GG | GG |
| rs699363 | AA | AA |
| rs970843 | GG | GG |
| rs10401969 | TC | TT |
| rs4823173 | CG | GG |
| rs12145833 | TT | GG |
| rs11127485 | TT | CC |
| rs17150703 | GG | GG |
| rs10105606 | CC | CC |
| rs651821 | TT | TT |
| rs972317 | TG | TT |
| rs1808579 | TC | CC |
| rs2605100 | AG | AA |

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|---|---|---|
| rs987237 | AA | AA |
| rs6429082 | TC | TT |
| rs2943650 | CG | CC |
| rs534870 | CG | GG |
| rs9568856 | GG | GG |
| rs9299 | TC | CC |
| rs7132908 | GG | GG |
| rs6567160 | TC | TT |
| rs13130484 | TC | CC |
| rs10182181 | AA | AA |
| rs2030323 | CC | AA |
| rs2112347 | TG | GG |
| rs7498665 | AA | AA |
| rs887912 | CG | CC |
| rs2531995 | TC | CC |
| rs9816226 | TT | AA |
| rs7138803 | GG | GG |
| rs7141420 | CC | CC |
| rs1800437 | GG | CC |
| rs10968576 | AA | AA |
| rs7185735 | AG | AA |
| rs2207139 | AA | AA |
| rs10938397 | AG | AA |
| rs10871777 | AG | AA |
| rs2568958 | AG | GG |
| rs13078807 | AG | AA |

Risk level: average

**rs1421085:** Variation in the FTO gene contributes to obesity in children and severe obesity in adults.
[ PMID 17496892 ] [ PMID 17658951 ] [ PMID 18159244 ] [ PMID 18379722 ] [ PMID 20381893 ] [ PMID 26440677 ]

**rs1558902:** Variants in the FTO gene are associated with increased body mass index, obesity and diabetes. A high-protein diet was more beneficial for people with risk allele A. These findings suggest significant genetic heterogeneity in weight loss in response to dietary interventions.
[ PMID 18379722 ] [ PMID 20075932 ] [ PMID 20430937 ] [ PMID 21357378 ] [ PMID 21466928 ] [ PMID 21976109 ] [ PMID 23316347 ] [ PMID 24992585 ]

**rs17817449:** The FTO genetic variant affects obesity, insulin sensitivity, leptin levels and resting metabolic rate.
[ PMID 18316358 ] [ PMID 18599522 ] [ PMID 18719664 ] [ PMID 18833210 ] [ PMID 21651756 ] [ PMID 22187296 ] [ PMID 24392269 ]

**rs1121980:** SNP rs1121980 in the FTO gene showed the strongest association with obesity risk (2.76-fold increase).
[ PMID 18159244 ] [ PMID 18379722 ] [ PMID 18454148 ] [ PMID 18487448 ]

**rs8050136:** Obesity-related heterogeneity in models of predisposition to type 2 diabetes.
[ PMID 17786212 ] [ PMID 17928989 ] [ PMID 18251005 ] [ PMID 18469204 ] [ PMID 18591388 ] [ PMID 19056611 ] [ PMID 20049090 ] [ PMID 20057365 ]

**rs2272382:** TUB gene polymorphisms are a candidate for late-life obesity in women.
[ PMID 17955208 ] [ PMID 18183286 ]

**rs17782313:** The rs17782313 (C) alleles are associated with higher body mass index (BMI), with an even larger effect in children. The average increase in BMI is 0.44 units.
[ PMID 19880856 ] [ PMID 20181787 ] [ PMID 20725061 ] [ PMID 24139164 ] [ PMID 27213003 ] [ PMID 31954858 ]

## Psoriasis

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs2523454 | GG | GG |
| rs3134792 | TT | TT |
| rs12586317 | TT | CC |
| rs240993 | TC | CC |
| rs1076160 | TC | CC |
| rs610604 | TG | TT |
| rs4085613 | TT | GG |
| rs17728338 | CG | GG |
| rs280519 | GG | GG |
| rs1265181 | GG | CC |
| rs27524 | GG | GG |
| rs4649203 | AG | GG |
| rs8016947 | TG | TT |
| rs458017 | TC | TT |
| rs702873 | TC | CC |
| rs3213094 | CC | CC |
| rs10484554 | CC | CC |
| rs33980500 | CC | CC |
| rs12191877 | CC | CC |
| rs842636 | AG | AA |
| rs2546890 | AG | GG |
| rs6809854 | AG | AA |
| rs2082412 | GG | AA |
| rs4112788 | AA | AA |
| rs465969 | AG | GG |
| rs12720356 | AC | AA |
| rs12580100 | AA | GG |
| rs2066808 | AA | GG |
| rs10782001 | AG | AA |

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|---|---|---|
| rs495337 | AG | GG |
| rs2201841 | AG | AA |
| rs4795067 | GG | AA |
| rs3212227 | TT | TT |
| rs1265159 | GG | GG |
| rs887466 | AA | AA |
| rs12634229 | TT | TT |
| rs6661961 | TC | CC |
| rs13015714 | TT | TT |
| rs479844 | GG | AA |
| rs878860 | CC | TT |
| rs10995251 | CC | TT |
| rs4722404 | TT | TT |
| rs593982 | CC | TT |
| rs2164983 | CC | CC |
| rs7927894 | CG | CC |
| rs3853601 | CC | CC |
| rs7613051 | GG | GG |
| rs176095 | AA | GG |
| rs3126085 | GG | GG |
| rs1444418 | AA | GG |
| rs7130588 | AG | AA |
| rs4406273 | GG | GG |
| rs144475004 | CG | GG |
| rs387907240 | TT | TT |
| rs281875215 | GG | GG |
| rs587777763 | GG | GG |
| rs281875214 | AA | AA |
| rs281875212 | CG | GG |
| rs281875213 | AA | AA |
| rs4379333 | TA | TT |
| rs734232 | CG | GG |

| | | |
|---|---|---|
| rs6887695 | GC | CC |
| rs7993214 | CC | CC |
| rs6701216 | CC | CC |
| rs3803369 | CC | CC |



Risk level: average

**rs17728338:** A genetic marker for the development or presence of psoriatic arthritis in psoriasis patients. [ PMID 21623003 ] [ PMID 25182136 ] [ PMID 32398022 ] [ PMID 34127053 ]

**rs144475004:** A significant (6-fold) increase in the risk of developing psoriasis, at least in Asians. [ PMID ]

## Diet susceptibility

## Keto diet and lchf

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs814628 | CG | GG |
| rs2306179 | CG | CC |
| rs5883 | CC | TT |
| rs694066 | CG | GG |
| rs5950584 | CG | GG |
| rs12204701 | CA | AA |
| rs9943291 | CG | GG |
| rs10060615 | AC | CC |
| rs274555 | TT | CC |
| rs2924679 | N/A | AA |
| rs7938117 | AG | GG |
| rs597539 | CG | GG |
| rs11161521 | TT | TT |
| rs2286963 | TG | TT |
| rs1799958 | AG | GG |
| rs3916 | CG | CC |
| rs1522813 | AA | AA |
| rs1801282 | GG | CC |
| rs1440581 | TC | CC |
| rs3764261 | AC | CC |
| rs1799883 | AA | AA |
| rs4994 | AA | AA |

Effectiveness of the diet: average

**rs5883:** CETP regulates reverse cholesterol transport, a process by which excess cholesterol is removed from peripheral tissues and returned to the liver. CETP may mediate the triglyceride-lowering and LDL and HDL remodelling effects observed with low-carbohydrate diets.
[ PMID 16700901 ] [ PMID 18254975 ]

**rs1801282:** Peroxisome proliferator-activated receptor gamma gene variation on the progression of type 2 diabetes and obesity. Also higher risk of cardiovascular disease with a diet high in saturated fat.
[ PMID 17213274 ] [ PMID 18091023 ] [ PMID 18598350 ] [ PMID 18694974 ] [ PMID 19020323 ]

**rs814628:** A polymorphism in the LIPF gene contributes to reduced breakdown of fat in the stomach and promotes more effective weight loss on high-fat diets.
[ PMID 16700901 ] [ PMID 18254975 ]

**rs2306179:** gene is responsible for hepatic glycogen synthase, which catalyses the formation of glycogen from glucose in the liver. According to the study carriers of the minor allele C lost more weight than homozygotes for the major allele T in response to a keto diet (8-13% carbohydrate, 60-63% fat and 28-30% protein) over a period of 4-12 years. This suggests that the liver glycogen response to carbohydrate restriction may influence the weight loss response to the keto diet.
[ PMID 16700901 ] [ PMID 18254975 ]

**rs5950584:** In the study, the minor G allele was associated with a greater reduction in body fat percentage in response to the keto diet, with ~12% of total energy derived from carbohydrates. Given that the AGTR2 gene is X-linked, its effect on fat loss in BC may be more prevalent and/or stronger in men than in women.
[ PMID 18254975 ]

**rs12204701:** The A allele of the CDY1L gene rs12204701 contributes to seizure reduction efficacy of more than 50% in patients with drug-resistant epilepsy in response to a keto diet.
[ PMID ]

**rs1440581:** Association of the rs1440581 variant of the PPM1K gene with improved insulin sensitivity in people who followed a high-fat diet.
[ PMID 23446828 ] [ PMID 28768654 ]

**rs3764261:** People with the CETP rs3764261 CC genotype may achieve a greater effect in raising HDL cholesterol and lowering triglyceride levels by choosing a low-carbohydrate, high-fat weight loss diet instead of a low-fat diet.
[ PMID 16700901 ] [ PMID 25548261 ]

## Low-calorie diet

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs13200531 | CG | GG |
| rs9344031 | AA | GG |
| rs481777 | AG | GG |
| rs1544241 | TG | TT |
| rs10132280 | AC | AA |
| rs1377985 | AC | CC |
| rs11113832 | CG | CC |
| rs7512601 | TA | TT |
| rs11185098 | TA | AA |
| rs2419621 | TC | TT |
| rs17300539 | AA | AA |
| rs1501299 | TG | GG |
| rs1801260 | AG | AA |
| rs179883 | AG | GG |
| rs9939609 | TT | TT |
| rs694066 | CG | GG |
| rs41423247 | CG | GG |
| rs659366 | TC | AA |
| rs1799883 | AA | AA |
| rs4994 | AA | AA |



Effectiveness of the diet: average

**rs659366:** More effective reduction in BMI and fat mass in A allele carriers.
[ PMID ]

**rs11185098:** Overweight and obese individuals carrying the AMY1-AMY2 rs11185098 genotype, associated with higher amylase activity, may have greater obesity loss during a low-calorie diet.
[ PMID 28659346 ]

**rs2419621:** More weight loss on a hypocaloric diet in T allele carriers.
[ PMID 32686444 ]

**rs1501299:** No reduction in waist circumference in TT compared with a 5.9 cm reduction in G allele carriers on diet.
[ PMID 22129377 ] [ PMID 29154912 ] [ PMID 29325772 ] [ PMID 31029921 ]

**rs9939609:** The common variant rs9939609 of the FTO gene, associated with fat mass and obesity, is associated with fat cell lipolysis as well as early onset of extreme obesity. Studies show that carriers of the risk allele A demonstrate significantly greater weight loss on a fat-restricted diet than non-carriers.
[ PMID 17942823 ] [ PMID 17959933 ] [ PMID 18048838 ] [ PMID 18159244 ] [ PMID 18249188 ] [ PMID 18325910 ] [ PMID 26888713 ]

**rs1799883:** This genotype is associated with increased sensitivity to both saturated fat and refined carbohydrates. Thus, allele A impairs the effectiveness of both low-carbohydrate and low-fat diets.
[ PMID ]

**rs4994:** A beta-3-adrenergic receptor mutation is associated with visceral obesity but lowers serum triglyceride levels. Carriers of the G allele necessarily need strength training to lose weight and keep the body in good shape.
[ PMID 7609752 ] [ PMID 9112025 ] [ PMID 9892244 ]

# Mediterranean diet

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs9939609 | TT | TT |
| rs1800795 | GG | CC |
| rs16147 | TC | AA |
| rs1501299 | TG | GG |
| rs1801260 | AG | AA |
| rs13702 | TC | CC |
| rs3812316 | GC | GG |
| rs1801282 | GG | CC |
| rs4343 | AG | AA |
| rs8061518 | AA | AA |
| rs1130864 | GG | GG |
| rs659366 | TC | AA |
| rs6131 | TC | CC |
| rs12535708 | CG | CC |
| rs708272 | AA | AA |
| rs2241766 | AA | TT |
| rs1799883 | AA | AA |
| rs4994 | AA | AA |



Effectiveness of the diet: average

**rs16147:** The A allele of the rs16147 variant causes a better metabolic response in terms of insulin resistance and basal insulin secondary to weight loss on two different hypocaloric diets in obese subjects, with improvement being greater on the Mediterranean diet.
[ PMID 22966009 ] [ PMID 28787737 ] [ PMID 32686440 ] [ PMID 34480216 ]

**rs1801282:** Peroxisome proliferator-activated receptor gamma gene variation on the progression of type 2 diabetes and obesity. Also higher risk of cardiovascular disease with a diet high in saturated fat.
[ PMID 17213274 ] [ PMID 18091023 ] [ PMID 18598350 ] [ PMID 18694974 ] [ PMID 19020323 ]

**rs659366:** More effective reduction in BMI and fat mass in A allele carriers.
[ PMID ]

**rs1501299:** No reduction in waist circumference in TT compared with a 5.9 cm reduction in G allele

carriers on diet.
[ PMID 22129377 ] [ PMID 29154912 ] [ PMID 29325772 ] [ PMID 31029921 ]

**rs13702:** Reduced risk of stroke following a Mediterranean diet high in unsaturated fat.
[ PMID 27089360 ] [ PMID 35387194 ]

**rs3812316:** Lower triglyceride levels, reduced cardiovascular disease risk depend on level of adherence to the Mediterranean diet in the PREDIMED study.
[ PMID 24448738 ]

**rs4343:** The GG genotype of the ACE rs4343 polymorphism represents a reliable nutrigenetic marker of adverse response to a diet high in saturated fat.
[ PMID 28096099 ] [ PMID 32398726 ]

**rs9939609:** The common variant rs9939609 of the FTO gene, associated with fat mass and obesity, is associated with fat cell lipolysis as well as early onset of extreme obesity. Studies show that carriers of the risk allele A demonstrate significantly greater weight loss on a fat-restricted diet than non-carriers.
[ PMID 17942823 ] [ PMID 17959933 ] [ PMID 18048838 ] [ PMID 18159244 ] [ PMID 18249188 ] [ PMID 18325910 ] [ PMID 26888713 ]

## Low-fat diet

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs2943641 | CC | CC |
| rs964184 | CC | CC |
| rs9939609 | TT | TT |
| rs6795735 | GG | GG |
| rs10182181 | AA | AA |
| rs266729 | CG | GG |
| rs987237 | AA | AA |
| rs2287019 | TT | TT |
| rs10830963 | CC | CC |
| rs11150675 | CG | GG |
| rs1799883 | AA | AA |
| rs4994 | AA | AA |

Effectiveness of the diet: high

**rs266729:** Carriers of the GC genotype (minor allele G) lose more weight on a low-fat diet than carriers of the CC genotype.
[ PMID 16871334 ]

**rs11150675:** AA genotype carriers (minor allele A) had less weight loss on a low-fat diet than AG and GG genotype carriers.
[ PMID 29693310 ]

**rs2943641:** People with the C allele may gain more weight loss and improved insulin resistance benefits than people without this genotype by choosing a high-carbohydrate, low-fat diet.
[ PMID 21747052 ] [ PMID 24009303 ] [ PMID 33170161 ]

**rs964184:** Involved in lipid and vitamin E metabolism. The genotype is a moderate risk factor for reduced vitamin E levels. A low-fat diet is suitable for people with this defect. On a low-fat diet (20% of energy comes from fat), carriers of the risk allele (allele G) had greater reductions in OX and LDL cholesterol levels. These studies showed better lipid profile improvement with long-term low-fat dietary intake in the risk allele G.
[ PMID 21729881 ] [ PMID 24623848 ] [ PMID 26981194 ] [ PMID 31505768 ]

**rs9939609:** The common variant rs9939609 of the FTO gene, associated with fat mass and obesity, is associated with fat cell lipolysis as well as early onset of extreme obesity. Studies show that carriers of the risk allele A demonstrate significantly greater weight loss on a fat-restricted diet than non-carriers.
[ PMID 17942823 ] [ PMID 17959933 ] [ PMID 18048838 ] [ PMID 18159244 ] [ PMID 18249188 ] [ PMID 18325910 ] [ PMID 26888713 ]

**rs6795735:** Carriers of the GG genotype (minor allele G) lose more weight on a low-fat diet than carriers of the AG or AA genotypes.
[ PMID ]

**rs987237:** The AA genotype of the TFAP2B gene was associated with greater weight loss on a low-fat, high-protein diet.
[ PMID 22952648 ] [ PMID 24081236 ]

**rs2287019:** The T allele of the GIPR gene is associated with greater improvements in glucose homeostasis in people who choose a low-fat, high-carbohydrate, high-fibre diet.
[ PMID 22237064 ]

## Vegetarian diet

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs174547 | TC | TT |
| rs602662 | AG | AA |
| rs429358 | TA | TT |
| rs7412 | CC | CC |
| rs12325817 | CG | CC |
| rs4646343 | CG | GG |
| rs3760188 | CG | CC |
| rs7946 | TT | CC |
| rs1531100 | GG | GG |
| rs4646365 | AC | CC |
| rs601338 | AG | GG |
| rs492602 | AG | AA |
| rs572169 | TT | CC |
| rs4684677 | TT | TT |
| rs26747 | CG | GG |
| rs7566605 | CG | GG |
| rs509325 | AT | TT |
| rs6545790 | AA | AA |
| rs7560575 | AT | TT |
| rs2196476 | CG | GG |
| rs587056 | CC | CC |
| rs1421085 | TC | TT |
| rs35867081 | CA | AA |
| rs60259426 | CG | GG |
| rs6089240 | GG | AA |
| rs12934922 | AA | AA |
| rs7501331 | CC | CC |
| rs1805087 | AA | AA |
| rs1801394 | GG | AA |

| | | |
|---|---|---|
| rs1799883 | AA | AA |
| rs4994 | AA | AA |



Effectiveness of the diet: average

**rs7946:** Genetic polymorphisms in methyl group metabolism DNA methylation in peripheral blood. Affect the human need for choline (vitamin B4).
[ PMID 18789905 ] [ PMID 22371529 ] [ PMID 16816108 ]

**rs1801394:** Polymorphism can lead to elevated homocysteine levels independent of folic acid, vitamin B12 or B6 levels. It is a risk factor for neural tube defects and Down syndrome in the setting of higher homocysteine levels.
[ PMID 10444342 ] [ PMID 10930360 ]

**rs174547:** Genetic variants that affect circulating lipid levels and risk of cardiovascular disease. People with the C gene variant have lower levels of long forms of fatty acids such as AA. Vegetarians and vegans with the C gene variant have lower plasma concentrations of EPA, DHA and AA than omnivores. Vegetarians with the C gene variant have been shown to benefit from omega-3 supplements or omega-3 rich foods such as chia seeds, flax seeds and canola oil.
[ PMID 19750004 ] [ PMID 20864672 ] [ PMID 20972250 ] [ PMID 29858861 ]

**rs602662:** The polymorphism is associated with reduced levels of vitamin B12 in the blood, this effect may be due to reduced absorption of vitamin B12, such people need additional vitamin B12 supplementation in the form of injections.
[ PMID 18776911 ]

**rs429358:** The APOE-E4 allele has a strong influence on the risk of developing Alzheimer's disease. One meta-analysis estimated the odds ratio for individuals homozygous for rs429358 to be 12 times higher for late-onset Alzheimer's disease and 61 times higher for early-onset disease. People with APOE4-4 allele C genotype should avoid eating animals raised on plants/grains that have higher levels of omega-6 compared to omega-3. It is advisable to practice vegetarianism to avoid all animal fats and measure the ratio of omega-3 to omega-6 in these people. Also, people with APOE 4 may do better on unmethylated forms of B12.
[ PMID 21263195 ] [ PMID 30665447 ]

**rs601338:** FUT2 gene fragment affects serum vitamin B12 concentration via hologaptocorrin. Presumably reduces the amount of vitamin B12 absorption from food and tablets. Administration of B12 in the form of injections is recommended.
[ PMID 29040465 ] [ PMID 18776911 ]

**rs492602:** B12 levels are 1.5 times higher in women.
[ PMID 18776911 ]

**rs7566605:** Sustained weight loss effect in carriers of the risk allele C polymorphism of the INSIG2 gene rs7566605 when following a vegetarian diet.
[ PMID ]

## High-protein diet

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs987237 | AA | AA |
| rs1558902 | TA | TT |
| rs12785878 | TT | GG |
| rs2970848 | TA | AA |
| rs2970853 | GG | GG |
| rs2932976 | GG | GG |
| rs11629199 | CG | GG |
| rs10507391 | CA | AA |
| rs4076128 | CG | GG |
| rs1058046 | CC | CC |
| rs4998 | CG | CC |
| rs838133 | AG | AA |
| rs1229984 | CC | CC |
| rs28712821 | CA | AA |
| rs1603977 | TA | AA |
| rs780094 | TC | CC |
| rs6601299 | CC | CC |
| rs579459 | TT | TT |
| rs34050136 | TA | AA |
| rs445551 | CG | GG |
| rs12402440 | CG | GG |
| rs59756727 | TA | TT |
| rs7760212 | AA | AA |
| rs2391333 | CC | CC |
| rs9512706 | TA | AA |
| rs668056 | CC | CC |
| rs5755279 | AA | AA |
| rs12405096 | CC | CC |
| rs74565497 | TA | AA |

| | | |
|---|---|---|
| rs117301188 | CG | CC |
| rs7833349 | CG | CC |
| rs2391331 | CC | TT |
| rs12715065 | AA | AA |
| rs11940694 | AG | GG |
| rs1799883 | AA | AA |
| rs4994 | AA | AA |



## Effectiveness of the diet: average

**rs12785878:** Has been associated with serum vitamin D concentrations in several studies. The T risk allele is associated with greater reductions in insulin and HOMA-IR levels in response to a high-protein diet.
[ PMID 23924835 ] [ PMID 22801813 ]

**rs1558902:** Variants in the FTO gene are associated with increased body mass index, obesity and diabetes. A high-protein diet was more beneficial for people with risk allele A. These findings suggest significant genetic heterogeneity in weight loss in response to dietary interventions.
[ PMID 18379722 ] [ PMID 20075932 ] [ PMID 20430937 ] [ PMID 21357378 ] [ PMID 21466928 ] [ PMID 21976109 ] [ PMID 23316347 ] [ PMID 24992585 ]

**rs838133:** FGF21 is a sugar-inducible hormone associated with the consumption and preference for sweets in humans. For carriers of the risk allele A, a diet high in protein and limiting carbohydrates has an effective response.
[ PMID 23372041 ] [ PMID 28467924 ] [ PMID 29641994 ] [ PMID 34836209 ]

**rs780094:** The GCKR rs780094 polymorphism is associated with increased fasting serum triacylglycerol, decreased fasting insulinaemia and reduced risk of type 2 diabetes. A diet restricting carbohydrates and increasing protein is particularly effective for carriers of the T risk allele.
[ PMID 18008060 ]

**rs987237:** The AA genotype of the TFAP2B gene was associated with greater weight loss on a low-fat, high-protein diet.
[ PMID 22952648 ] [ PMID 24081236 ]

**rs1058046:** According to research, a high-protein diet is more effective.
[ PMID 18254975 ]

**rs1799883:** This genotype is associated with increased sensitivity to both saturated fat and refined carbohydrates. Thus, allele A impairs the effectiveness of both low-carbohydrate and low-fat diets.
[ PMID ]

**rs4994:** A beta-3-adrenergic receptor mutation is associated with visceral obesity but lowers serum triglyceride levels. Carriers of the G allele necessarily need strength training to lose weight and keep the body in good shape.
[ PMID 7609752 ] [ PMID 9112025 ] [ PMID 9892244 ]

# Gluten-free diet

| SNP id | Your alleles | Allele norm |
|---|---|---|
| rs2187668 | CC | CC |
| rs2858331 | GG | AA |
| rs6441961 | CC | TT |
| rs6822844 | TG | GG |
| rs2395182 | TT | TT |
| rs9851967 | TT | CC |
| rs7775228 | TT | TT |
| rs4713586 | AA | AA |
| rs3184504 | TC | CC |
| rs231775 | AA | AA |
| rs2816316 | TA | AA |
| rs4994 | AA | AA |



Effectiveness of the diet: average

**rs2858331:** Together with the rs4988889 gene breakage, it is a diagnostic criterion for celiac disease.

**rs6441961:** Increased risk of gluten disease.
[ PMID 19693089 ] [ PMID 19542083 ] [ PMID 22087237 ]

**rs9851967:** Genetic risk of celiac disease associated with immune response.
[ PMID 18311140 ]

**rs6822844:** Combined with the rs13119723 breakage, the study showed the strongest association with celiac disease among Caucasian patients.
[ PMID 17558408 ]

**rs3184504:** A variant of celiac disease genetic risk associated with immune response. Also carrier associated type 1 diabetes.
[ PMID 18311140 ] [ PMID 18978792 ] [ PMID 19073967 ] [ PMID 20546165 ] [ PMID 20854658 ] [ PMID 21873553 ] [ PMID 24936253 ]

**rs2816316:** Genetic variant risk for type 1 diabetes and gluten disease.
[ PMID 18311140 ] [ PMID 19073967 ] [ PMID 19622889 ] [ PMID 20854658 ] [ PMID 21980299 ] [ PMID 27015091 ]

**rs2187668:** Risk of autoimmune diseases (lupus, gluten disease).
[ PMID 17997607 ] [ PMID 18509540 ]

**rs2395182:** HLA DQ2.2 genes play an important role in many autoimmune diseases such as celiac disease, type 1 diabetes, rheumatoid arthritis, multiple sclerosis, psoriasis and others.
[ PMID 18509540 ]

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