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Vitiligo (Jin, 2017)

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Autoimmunity | Skin

STUDY SUMMARY

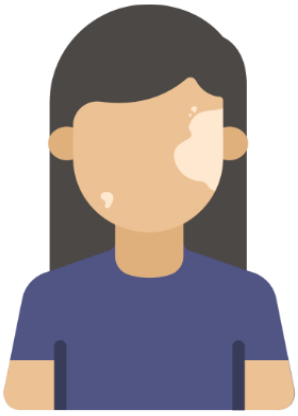
Identification of 23 novel genetic variants associated with vitiligo, an autoimmune disease that causes loss of skin color.

YOUR RESULT

1st
PERCENTILE
Very low genetic predisposition to **vitiligo**

STUDY DESCRIPTION

The color of a person's skin is determined by the amount of melanin, a dark pigment that is produced by cells called melanocytes. Vitiligo is a rare disease characterized by the destruction of melanocytes by the body's own immune system. This causes patches of skin to lose their color. To better understand the genetic susceptibility to vitiligo, this genome-wide association study examined the genomes of over 44,000 individuals of European ancestry. The study identified 50 genetic variants of which 23 are newly discovered. Together, the identified variants explain about 17% of vitiligo heritability and many can be linked to the immune system and melanocyte function.



Vitiligo is characterized by patches of discolored skin.

DID YOU KNOW?

In the past, vitiligo was believed to be contagious and has lead to social stigma. Unfortunately, people who are affected by vitiligo today still encounter discrimination. Many debunked myths still persist.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to vitiligo we summed up the effects of genetic variants that were linked to vitiligo in the study that this report is based on. These variants can be found in the table below. The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to vitiligo. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to vitiligo. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to vitiligo. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for vitiligo to be -1.18**. To determine whether your score is high or low, we compared it to the scores of 5,000 other Nebula Genomics users. We found that your polygenic score for vitiligo is in the **1st percentile**. This means that it is higher than the polygenic scores 1% of people. We consider this to be a **very low genetic predisposition to vitiligo**. However, please note that genetic predispositions do not account for important non-genetic factors like lifestyle. Furthermore, the genetics of most traits has not been fully understood yet and many associations between traits and genetic variants remain unknown. For additional explanations, click on the column titles in the table below and visit our Nebula Library tutorial.

VARIANT	YOUR GENOTYPE	EFFECT SIZE	VARIANT FREQUENCY	SIGNIFICANCE
rs9271597_A	T / T	0.57 (–)	43%	3.15×10^{-89}
rs1126809_A	G / G	-0.40 (–)	27%	1.16×10^{-43}
rs4268748_C	T / T	-0.34 (–)	27%	2.88×10^{-33}
rs2017445_A	G / G	0.29 (–)	33%	6.62×10^{-31}
rs229527_A	C / A	0.28 (↑)	43%	1.14×10^{-30}
rs13076312_T	T / T	0.28 (↑)	46%	1.61×10^{-30}
rs12482904_A	T / A	0.30 (↑)	22%	5.84×10^{-29}
rs706779_C	T / C	-0.26 (↓)	47%	7.20×10^{-27}
rs117744081_G NEW	NA	0.61 (–)	3%	8.72×10^{-26}
rs2111485_A	A / G	-0.26 (↓)	39%	6.40×10^{-25}
rs11021232_C	T / T	0.29 (–)	19%	2.10×10^{-23}
rs10774624_A	G / A	-0.24 (↓)	50%	6.22×10^{-23}
rs6059655_A NEW	A / G	-0.49 (↓)	7%	1.04×10^{-19}
rs10200159_C NEW	T / T	0.41 (–)	6%	3.73×10^{-19}
rs34346645_A	A / A	-0.22 (↓)	42%	7.99×10^{-19}
rs2476601_A	G / G	0.32 (–)	10%	1.21×10^{-18}
rs2247314_C	C / C	-0.24 (↓)	33%	1.72×10^{-18}
rs1043101_G	A / G	0.21 (↑)	40%	5.26×10^{-18}
rs78037977_G NEW	A / A	0.28 (–)	13%	6.74×10^{-17}
rs8192917_C	C / T	0.22 (↑)	24%	8.91×10^{-16}
rs9611565_C	T / C	-0.24 (↓)	24%	3.13×10^{-15}
rs301807_A	G / G	0.19 (–)	45%	4.14×10^{-15}
rs72928038_A	G / A	0.24 (↑)	17%	1.00×10^{-14}
rs4807000_A NEW	G / G	0.19 (–)	40%	1.94×10^{-14}
rs1635168_A	C / C	0.31 (–)	7%	8.78×10^{-14}
rs2687812_A	T / T	0.17 (–)	48%	2.19×10^{-13}
rs12771452_A	A / A	-0.20 (↓)	26%	4.43×10^{-12}
rs13136820_C	C / T	0.17 (↑)	33%	3.60×10^{-11}
rs231725_A NEW	G / A	0.17 (↑)	33%	1.49×10^{-10}
rs8083511_C NEW	A / A	0.19 (–)	19%	2.81×10^{-10}
rs12203592_T NEW	C / C	-0.24 (–)	14%	2.95×10^{-10}
rs11079035_A NEW	G / A	0.19 (↑)	17%	6.77×10^{-10}
rs73456411_T NEW	NA	0.57 (–)	1%	7.34×10^{-10}
rs16843742_C NEW	T / C	-0.19 (↓)	23%	1.02×10^{-9}
rs5952553_C	T / T	-0.15 (–)	41%	1.05×10^{-9}
rs2304206_A NEW	A / A	-0.17 (↓)	25%	2.36×10^{-9}
rs41342147_A NEW	G / A	-0.22 (↓)	13%	3.70×10^{-9}
rs4308124_C NEW	T / T	0.14 (–)	41%	3.96×10^{-9}

rs35860234_G NEW	T / T	0.16 (–)	27%	4.76×10^{-9}
rs71508903_T NEW	C / T	0.17 (↑)	20%	6.93×10^{-9}
rs10087240_T	C / T	0.17 (↑)	46%	7.74×10^{-9}
rs6012953_G NEW	A / G	0.14 (↑)	48%	9.47×10^{-9}
rs10986311_C NEW	T / T	0.14 (–)	37%	1.01×10^{-8}
rs6583331_A NEW	A / A	-0.14 (↓)	45%	2.53×10^{-8}
rs78521699_G NEW	A / A	-0.24 (–)	10%	2.54×10^{-8}
rs1031034_A NEW	C / C	-0.15 (–)	28%	3.43×10^{-8}
rs561079_C	T / T	0.13 (–)	38%	3.76×10^{-8}
rs12421615_A NEW	G / A	-0.14 (↓)	35%	4.81×10^{-8}

N/A indicates variants that could not be imputed using the 1000 genomes project datasets and variants that have a frequency of < 5%. Your genome was sequenced at 30x/100x coverage and is not imputed. However, to calculate percentiles, we need to compare your data with other users imputed data. To make the data comparable, we need to exclude some of the variants from your data.