

★ 25-hydroxyvitamin D level (Revez, 2020)

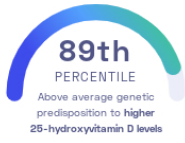
Joana Revez, et al.
Nature Communications

Metabolism Bones

STUDY SUMMARY

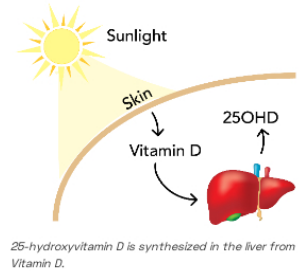
Discovery of 143 genomic regions associated with 25-hydroxyvitamin D levels, an indicator of vitamin D levels in the body.

YOUR RESULT



STUDY DESCRIPTION

Vitamin D is essential for the body. It helps to maintain strong bones, healthy teeth, and may also protect against an array of diseases such as type 1 diabetes. While vitamin D is not present in many foods we eat, our bodies naturally produce it as a response to sun exposure, giving vitamin D the nickname "sunshine vitamin". Produced vitamin D is further processed by the body in a series of chemical reactions. One of these reactions turns vitamin D into 25-hydroxyvitamin D (25OHD), which is commonly measured as an indicator of vitamin D levels in the body. This genome-wide association study examined over 417,000 individuals of European ancestry to identify genetic variants linked with 25OHD levels. The study found 143 variants. While many of the variants are found near genes active in the liver, the organ responsible for turning vitamin D into 25OHD, some other variants were located in genes related to processes in the skin.



DID YOU KNOW?

Low vitamin D levels can lead to a range of health issues, including tiredness, aches, and bone pain. Individuals who spend large amounts of time indoors, live in areas with high levels of pollution, and those with darker skin are all at an increased risk of low vitamin D levels. In addition to more sun, increased consumption of salmon, shrimp, milk fortified with vitamin D, and taking vitamin supplements are commonly recommended.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to higher 25-hydroxyvitamin D levels we summed up the effects of genetic variants that were linked to higher 25-hydroxyvitamin D levels 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 higher 25-hydroxyvitamin D levels. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to higher 25-hydroxyvitamin D levels. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to higher 25-hydroxyvitamin D levels. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for higher 25-hydroxyvitamin D levels to be 1.36**. 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 higher 25-hydroxyvitamin D levels is in the **89th percentile**. This means that it is higher than the polygenic scores 89% of people. We consider this to be an **above average genetic predisposition to higher 25-hydroxyvitamin D levels**. 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
rs1352846_A	A / A	0.20 (↑)	71%	1.00 x 10 ⁻⁹⁹⁹
rs116970203_G	G / G	0.43 (↑)	97%	1.00 x 10 ⁻⁹⁹⁹
rs12794714_G	G / G	0.11 (↑)	58%	1.00 x 10 ⁻⁹⁹⁹
rs212100_T	C / C	0.07 (-)	16%	3.80 x 10 ⁻¹³²
rs117576073_G	G / G	0.21 (↑)	99%	1.60 x 10 ⁻¹²⁴
rs10859995_T	T / C	0.04 (↑)	42%	3.80 x 10 ⁻⁹⁸
rs12803256_A	G / G	-0.07 (-)	22%	8.10 x 10 ⁻⁶⁷
rs12123821_C	C / C	-0.07 (↓)	95%	1.70 x 10 ⁻⁵⁴
rs8018720_G	G / C	0.04 (↑)	18%	6.80 x 10 ⁻⁴⁸
rs1800588_C	C / T	0.03 (↑)	78%	2.50 x 10 ⁻⁴⁴
rs281291_T	T / T	0.03 (↑)	64%	4.10 x 10 ⁻⁴²
rs2012736_C	C / C	0.05 (↑)	92%	1.20 x 10 ⁻³⁹
rs12056768_T	G / G	0.03 (-)	42%	2.30 x 10 ⁻³⁵
rs2762943_T	G / G	-0.04 (-)	8%	3.10 x 10 ⁻³³
rs17216707_T	T / T	0.03 (↑)	82%	8.30 x 10 ⁻³³
rs139148694_G	G / GTGCTTTTATCAA	0.03 (↑)	28%	6.60 x 10 ⁻³¹
rs12798050_C	T / T	-0.05 (-)	17%	8.40 x 10 ⁻²⁹
rs2131925_G	T / T	0.02 (-)	36%	4.70 x 10 ⁻²⁸
rs2585442_C	C / G	-0.03 (↓)	76%	8.90 x 10 ⁻²⁸
rs705117_C	T / T	-0.03 (-)	15%	9.60 x 10 ⁻²⁸
rs964184_G	C / C	-0.04 (-)	13%	2.00 x 10 ⁻²⁷
rs10426_G	G / G	-0.03 (↓)	79%	3.50 x 10 ⁻²⁶
rs1260326_T	T / C	-0.02 (↓)	39%	1.20 x 10 ⁻²⁴
rs35408430_C	C / C	0.02 (↑)	66%	2.30 x 10 ⁻²⁴
rs28364331_A	A / A	-0.07 (↓)	98%	6.80 x 10 ⁻²¹
rs55829990_T	C / C	0.02 (-)	66%	3.90 x 10 ⁻¹⁹
rs10908465_C	T / T	-0.02 (-)	73%	1.80 x 10 ⁻¹⁸
rs2248551_G	G / G	0.02 (↑)	83%	3.10 x 10 ⁻¹⁸
rs1149605_T	T / T	-0.02 (↓)	83%	4.30 x 10 ⁻¹⁸
rs6782190_G	A / A	0.02 (-)	35%	5.70 x 10 ⁻¹⁸
rs140371183_A	A / A	-0.06 (↓)	97%	2.20 x 10 ⁻¹⁷
rs13104260_G	G / A	-0.02 (↓)	74%	2.70 x 10 ⁻¹⁷
rs7412_C	C / C	-0.03 (↓)	92%	7.40 x 10 ⁻¹⁷
rs7528419_A	A / A	-0.02 (↓)	78%	1.40 x 10 ⁻¹⁶
rs11542462_G	G / A	0.02 (↑)	87%	2.90 x 10 ⁻¹⁶
rs142158911_G	G / G	-0.03 (↓)	89%	5.40 x 10 ⁻¹⁶

rs72997623_C	C / C	-0.03 (↓)	92%	6.40 × 10 ⁻¹⁵
rs2229742_G	G / G	0.03 (↑)	90%	1.50 × 10 ⁻¹⁴
rs35057908_A	A / A	-0.02 (↓)	57%	2.60 × 10 ⁻¹⁴
rs78168201_C	C / C	-0.07 (↓)	99%	2.80 × 10 ⁻¹⁴
rs484195_A	A / G	0.02 (↑)	38%	4.30 × 10 ⁻¹⁴
rs368637654_G	TTTTTTTT / TTTTTTTT	0.02 (-)	86%	4.80 × 10 ⁻¹⁴
rs12317268_A	A / A	0.02 (↑)	85%	6.20 × 10 ⁻¹⁴
rs6123359_A	A / A	-0.03 (↓)	90%	6.70 × 10 ⁻¹⁴
rs61816761_G	G / G	-0.08 (↓)	98%	1.40 × 10 ⁻¹³
rs76798800_G	G / G	0.02 (↑)	73%	1.60 × 10 ⁻¹³
rs11732896_G	G / G	0.02 (↑)	70%	1.80 × 10 ⁻¹³
rs6671730_G	G / G	0.01 (↑)	57%	1.90 × 10 ⁻¹³
rs1229984_T	NA	0.05 (-)	2%	2.40 × 10 ⁻¹³
rs2847500_G	G / G	0.02 (↑)	88%	2.50 × 10 ⁻¹³
rs804281_A	G / G	-0.01 (-)	42%	2.60 × 10 ⁻¹³
rs4575545_G	G / G	0.02 (↑)	70%	2.70 × 10 ⁻¹³
rs1933064_G	G / A	-0.01 (↓)	53%	6.90 × 10 ⁻¹³
rs187429064_A	A / A	-0.07 (↓)	99%	7.60 × 10 ⁻¹³
rs2952289_C	C / T	-0.02 (↓)	20%	1.20 × 10 ⁻¹²
rs1047891_C	C / A	0.01 (↑)	68%	1.20 × 10 ⁻¹²
rs6672758_C	T / T	-0.02 (-)	20%	3.40 × 10 ⁻¹²
rs4121823_T	T / A	0.02 (↑)	16%	3.80 × 10 ⁻¹²
rs2074735_G	G / C	-0.03 (↓)	94%	9.60 × 10 ⁻¹²
rs727857_G	G / A	0.01 (↑)	39%	1.10 × 10 ⁻¹¹
rs2037511_G	G / G	-0.02 (↓)	83%	1.50 × 10 ⁻¹¹
rs867772_A	A / G	0.01 (↑)	32%	1.60 × 10 ⁻¹¹
rs11108368_A	A / G	-0.01 (↓)	39%	2.10 × 10 ⁻¹¹
rs7784802_A	A / A	-0.01 (↓)	64%	2.60 × 10 ⁻¹¹
rs7522116_C	T / T	0.01 (-)	43%	3.30 × 10 ⁻¹¹
rs8091117_C	C / C	0.03 (↑)	93%	6.00 × 10 ⁻¹¹
rs77924615_G	G / G	0.02 (↑)	81%	7.00 × 10 ⁻¹¹
rs78649910_T	T / T	0.02 (↑)	89%	7.20 × 10 ⁻¹¹
rs10085881_T	C / C	0.01 (-)	72%	7.80 × 10 ⁻¹¹
rs7604788_C	C / C	-0.04 (↓)	97%	7.90 × 10 ⁻¹¹
rs28692966_G	G / G	-0.01 (↓)	75%	8.10 × 10 ⁻¹¹
rs34290760_C	C / C	0.04 (↑)	97%	9.20 × 10 ⁻¹¹
rs61891388_T	T / G	-0.01 (↓)	54%	9.70 × 10 ⁻¹¹
rs72834856_T	G / G	0.03 (-)	93%	1.00 × 10 ⁻¹⁰
rs1660539_G	G / A	-0.01 (↓)	75%	1.00 × 10 ⁻¹⁰
rs11076175_A	A / A	-0.02 (↓)	82%	1.20 × 10 ⁻¹⁰
rs7569755_G	G / A	-0.01 (↓)	71%	1.20 × 10 ⁻¹⁰
rs28367476_A	A / A	0.01 (↑)	81%	1.30 × 10 ⁻¹⁰
rs613808_A	A / G	-0.02 (↓)	28%	1.60 × 10 ⁻¹⁰
rs325384_C	C / T	0.01 (↑)	72%	1.70 × 10 ⁻¹⁰
rs11264322_G	A / A	0.01 (-)	57%	2.00 × 10 ⁻¹⁰
rs4364259_G	G / A	-0.02 (↓)	80%	2.20 × 10 ⁻¹⁰
rs3925446_G	G / G	-0.02 (↓)	80%	2.50 × 10 ⁻¹⁰
rs7149014_T	C / C	0.01 (-)	37%	2.80 × 10 ⁻¹⁰
rs11182428_T	T / C	0.01 (↑)	48%	3.20 × 10 ⁻¹⁰
rs541041_G	A / A	0.02 (-)	18%	3.90 × 10 ⁻¹⁰
rs9861009_T	C / C	-0.01 (-)	27%	4.90 × 10 ⁻¹⁰
rs2207132_G	G / G	0.04 (↑)	97%	5.60 × 10 ⁻¹⁰
rs17231506_C	C / T	0.01 (↑)	68%	6.90 × 10 ⁻¹⁰
rs3849374_G	G / G	0.02 (↑)	82%	7.50 × 10 ⁻¹⁰
rs77532868_C	C / C	-0.03 (↓)	95%	8.50 × 10 ⁻¹⁰
rs10454087_C	C / C	0.01 (↑)	72%	8.70 × 10 ⁻¹⁰
rs4616820_C	C / C	0.01 (↑)	54%	1.10 × 10 ⁻⁹
rs10908419_G	G / G	0.01 (↑)	51%	1.20 × 10 ⁻⁹

rs62007299_G	A / A	0.01 (↓)	29%	1.30 x 10 ⁻⁹
rs10070734_T	T / T	-0.01 (↓)		
rs11591147_G	G / G	-0.04 (↓)	98%	2.10 x 10 ⁻⁹
rs11606_C	C / G	-0.01 (↓)	67%	2.20 x 10 ⁻⁹
rs1038185_C	C / T	-0.01 (↓)	42%	2.30 x 10 ⁻⁹
rs61883501_A	A / A	-0.03 (↓)	97%	4.00 x 10 ⁻⁹
rs9476310_C	C / T	-0.01 (↓)	49%	4.20 x 10 ⁻⁹
rs115621755_C	C / T	0.01 (↑)	67%	4.80 x 10 ⁻⁹
rs8113404_C	C / T	-0.01 (↓)	70%	4.90 x 10 ⁻⁹
rs4738684_A	A / G	-0.01 (↓)	33%	5.90 x 10 ⁻⁹
rs35230619_T	T / TA	0.01 (↑)	72%	6.30 x 10 ⁻⁹
rs3814995_C	C / C	0.01 (↑)	69%	6.60 x 10 ⁻⁹
rs13060130_C	C / C	0.02 (↑)	86%	6.70 x 10 ⁻⁹
rs28374650_C	C / T	0.01 (↑)	76%	7.70 x 10 ⁻⁹
rs2710651_G	G / A	0.01 (↑)	47%	9.80 x 10 ⁻⁹
rs6966728_C	C / T	0.01 (↑)	54%	9.80 x 10 ⁻⁹
rs75741381_C	C / G	0.02 (↑)	85%	1.10 x 10 ⁻⁸
rs590215_C	C / T	0.01 (↑)	73%	1.20 x 10 ⁻⁸
rs2346264_A	A / C	0.01 (↑)	22%	1.20 x 10 ⁻⁸
rs12372115_G	G / G	0.02 (↑)	93%	1.40 x 10 ⁻⁸
rs7341359_T	T / T	-0.02 (↓)	93%	1.40 x 10 ⁻⁸
rs556230166_A	A / ATT	-0.01 (↓)	51%	1.70 x 10 ⁻⁸
rs112943319_A	ATATCTG / ATATCTG	-0.01 (-)	58%	1.70 x 10 ⁻⁸
rs4327060_C	C / C	0.03 (↑)	95%	1.80 x 10 ⁻⁸
rs78151190_A	A / C	0.02 (↑)	87%	2.00 x 10 ⁻⁸
rs13284054_T	T / T	-0.02 (↓)	88%	2.10 x 10 ⁻⁸
rs4418728_G	G / T	-0.01 (↓)	55%	2.20 x 10 ⁻⁸
rs6003456_T	T / T	0.01 (↑)	77%	2.30 x 10 ⁻⁸
rs10887718_C	T / T	0.01 (-)	47%	2.30 x 10 ⁻⁸
rs11127186_T	T / T	-0.01 (↓)	50%	2.40 x 10 ⁻⁸
rs12881545_G	C / C	-0.01 (-)	33%	3.50 x 10 ⁻⁸
rs9490317_T	T / T	-0.01 (↓)	55%	4.00 x 10 ⁻⁸
rs31612_T	T / C	0.01 (↑)	83%	4.20 x 10 ⁻⁸
rs2725371_A	A / G	-0.01 (↓)	30%	4.20 x 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.