

★ **Vitamin D level (Manousaki, 2020)**

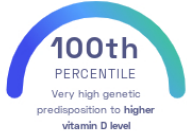
Despoina Manousaki, et al.
The American Journal of Human Genetics

Skin Bones

STUDY SUMMARY

Identification of 69 genetic regions associated with vitamin D level.

YOUR RESULT



STUDY DESCRIPTION

Vitamin D is known as the "sunshine vitamin" because it's produced by the skin when it's exposed to sunlight. Vitamin D helps ensure that the body absorbs and retains the minerals calcium and phosphorus, which are important for building strong bones. In this study, researchers aimed to understand the genetic determinants of vitamin D level by conducting a genome-wide association study of ~400,000 individuals of European ancestry. The study identified 69 genetic regions associated with vitamin D level, of which 63 are novel. Interestingly, the researchers discovered a link between vitamin D level and some socioeconomic traits, which may be related to how much time one spends outdoors.



The body produces vitamin D when the skin is exposed to the sun.

DID YOU KNOW?






























Individuals with darker skin are at a high risk of becoming vitamin D deficient. This is because melanin, which causes skin pigmentation, lowers the skin's ability to produce vitamin D in response to sunlight.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to higher vitamin D level we summed up the effects of genetic variants that were linked to higher vitamin D level 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 vitamin D level. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to higher vitamin D level. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to higher vitamin D level. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for higher vitamin D level to be 3.65**. 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 vitamin D level is in the **100th percentile**. This means that it is higher than the polygenic scores 100% of people. We consider this to be a **very high genetic predisposition to higher vitamin D level**. 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 [Ⓞ]
rs11723621_G	A / A	-0.16 (-)	29%	2.90 x 10 ⁻¹⁶⁸⁹
rs10832289_T	A / A	-0.09 (-)	41%	2.03 x 10 ⁻²⁶⁶
rs12803256_G	G / G	0.09 (↑)	78%	1.64 x 10 ⁻¹⁶⁵
rs567876843_G	G / G	0.54 (↑)	> 99%	3.35 x 10 ⁻¹¹⁶
rs3776150_C	T / T	-0.07 (-)	22%	3.46 x 10 ⁻¹⁰⁹
rs117913124_A	NA	-0.21 (-)	3%	2.94 x 10 ⁻¹⁰⁷
rs10859995_C	T / C	-0.04 (↓)	59%	3.03 x 10 ⁻⁹¹
rs112285002_T NEW	C / C	0.06 (-)	16%	1.49 x 10 ⁻⁹⁰
rs117576073_T	NA	-0.17 (-)	1%	1.40 x 10 ⁻⁷⁸
rs61816761_A NEW	NA	0.11 (-)	2%	5.39 x 10 ⁻⁵⁴
rs7699711_T NEW	T / T	-0.03 (↓)	45%	4.85 x 10 ⁻⁵⁰
rs549940584_T	NA	0.15 (-)	1%	1.93 x 10 ⁻⁴⁵
rs964184_C NEW	C / C	0.04 (↑)	87%	1.30 x 10 ⁻⁴³
rs222026_T	T / T	-0.05 (↓)	88%	1.09 x 10 ⁻⁴⁰
rs2011425_G NEW	T / T	-0.05 (-)	8%	9.93 x 10 ⁻³⁸
rs1800588_T NEW	C / T	-0.03 (↓)	21%	3.17 x 10 ⁻³⁷
rs188480917_G	NA	-0.17 (-)	1%	3.21 x 10 ⁻³⁷
rs577185477_C	NA	-0.15 (-)	1%	7.55 x 10 ⁻³⁷
rs8018720_C	G / C	-0.03 (↓)	82%	4.10 x 10 ⁻³⁶
rs7828742_G NEW	A / G	-0.02 (↓)	60%	2.85 x 10 ⁻³³
rs6127099_T	A / A	-0.03 (-)	27%	2.22 x 10 ⁻³²
rs538325438_C	C / C	-0.45 (↓)	> 99%	4.61 x 10 ⁻³²
rs261291_C NEW	T / T	-0.02 (-)	36%	2.46 x 10 ⁻²⁹
rs185433896_A NEW	A / A	-0.21 (↓)	> 99%	7.24 x 10 ⁻²⁸
rs705117_T	T / T	0.03 (↑)	85%	1.12 x 10 ⁻²⁷
rs150586703_G	G / G	0.24 (↑)	> 99%	1.56 x 10 ⁻²⁷
rs145432346_C	C / C	0.04 (↑)	87%	2.26 x 10 ⁻²⁷
rs10426_A NEW	G / G	0.03 (-)	21%	1.59 x 10 ⁻²⁶
rs2934744_A NEW	A / A	-0.02 (↓)	64%	4.13 x 10 ⁻²⁶
rs375984409_G NEW	G / G	-0.19 (↓)	> 99%	1.53 x 10 ⁻²⁵
rs12123821_T NEW	NA	0.05 (-)	5%	1.28 x 10 ⁻²⁴
rs3750296_C NEW	G / G	-0.02 (-)	34%	3.04 x 10 ⁻²⁴
rs560384646_C	NA	-0.09 (-)	1%	3.23 x 10 ⁻²⁴
rs2762942_A	A / A	0.04 (↑)	95%	1.69 x 10 ⁻²³
rs2585442_G	C / G	0.02 (↑)	24%	3.96 x 10 ⁻²³
rs200454003_T	T / T	-0.03 (↓)	25%	3.49 x 10 ⁻²¹
rs571484036_A	A / A	-0.25 (↓)	> 99%	3.43 x 10 ⁻²⁰
rs115045402_A NEW	NA	0.07 (-)	1%	1.58 x 10 ⁻¹⁹

rs534042887_G	G / G	0.19 (↑)	> 99%	2.21 × 10 ⁻¹⁹
rs58542926_T	C / C	0.03 (-)	8%	2.63 × 10 ⁻¹⁹
rs11127048_A	G / A	0.02 (↑)	62%	6.72 × 10 ⁻¹⁹
rs201501563_T	C / C	-0.04 (-)	7%	1.96 × 10 ⁻¹⁸
rs28364331_G	NA	0.06 (-)	2%	3.06 × 10 ⁻¹⁸
rs1972994_T	T / T	-0.02 (↓)	65%	8.04 × 10 ⁻¹⁸
rs138726443_A	NA	0.12 (-)	1%	1.36 × 10 ⁻¹⁷
rs1800775_A	C / A	-0.02 (↓)	49%	1.57 × 10 ⁻¹⁷
rs532836473_G	G / G	0.27 (↑)	> 99%	4.77 × 10 ⁻¹⁷
rs61937878_T	NA	0.10 (-)	1%	5.63 × 10 ⁻¹⁷
rs567415847_G	G / G	0.30 (↑)	> 99%	1.88 × 10 ⁻¹⁶
rs7528419_G	A / A	0.02 (-)	22%	2.43 × 10 ⁻¹⁶
rs201561609_T	T / T	-0.10 (↓)	> 99%	6.63 × 10 ⁻¹⁶
rs2229742_C	G / G	-0.03 (-)	11%	7.16 × 10 ⁻¹⁶
rs804280_A	A / A	0.02 (↑)	58%	9.90 × 10 ⁻¹⁶
rs11264360_A	A / A	0.02 (↑)	24%	1.12 × 10 ⁻¹⁵
rs3822868_G	G / G	0.02 (↑)	84%	1.41 × 10 ⁻¹⁵
rs186881826_A	T / T	0.02 (-)	19%	1.43 × 10 ⁻¹⁵
rs528776789_A	A / A	0.12 (↑)	> 99%	2.45 × 10 ⁻¹⁵
rs1149605_C	T / T	0.02 (-)	17%	3.36 × 10 ⁻¹⁵
rs157595_G	A / G	-0.02 (↓)	62%	4.25 × 10 ⁻¹⁵
rs148514005_T	NA	-0.14 (-)	< 1%	4.99 × 10 ⁻¹⁵
rs574615332_A	A / A	-0.21 (↓)	> 99%	5.87 × 10 ⁻¹⁵
rs190688847_C	C / C	0.25 (↑)	> 99%	1.26 × 10 ⁻¹⁴
rs186441690_G	G / G	-0.23 (↓)	> 99%	1.79 × 10 ⁻¹⁴
rs564377207_G	G / G	-0.16 (↓)	> 99%	2.23 × 10 ⁻¹⁴
rs1065853_T	G / G	0.03 (-)	8%	2.24 × 10 ⁻¹⁴
rs536006581_G	NA	-0.11 (-)	< 1%	5.64 × 10 ⁻¹⁴
rs73015021_G	A / A	0.02 (-)	12%	6.29 × 10 ⁻¹⁴
rs6123359_G	A / A	0.02 (-)	10%	7.48 × 10 ⁻¹⁴
rs17765311_C	C / C	-0.01 (↓)	34%	1.18 × 10 ⁻¹³
rs1229984_C	C / C	-0.05 (↓)	98%	2.43 × 10 ⁻¹³
rs10793129_A	G / G	0.03 (-)	9%	4.11 × 10 ⁻¹³
rs373514022_C	C / C	0.21 (↑)	> 99%	4.15 × 10 ⁻¹³
rs558560635_G	G / G	-0.24 (↓)	> 99%	4.45 × 10 ⁻¹³
rs554808052_C	C / C	0.20 (↑)	> 99%	7.88 × 10 ⁻¹³
rs3814995_T	C / C	-0.01 (-)	31%	1.08 × 10 ⁻¹²
rs117206369_T	T / T	0.23 (↑)	> 99%	1.10 × 10 ⁻¹²
rs1011468_A	G / A	-0.01 (↓)	47%	1.39 × 10 ⁻¹²
rs571618690_A	A / A	0.23 (↑)	> 99%	1.40 × 10 ⁻¹²
rs144613541_G	A / A	0.02 (-)	29%	1.62 × 10 ⁻¹²
rs150597413_T	NA	0.11 (-)	< 1%	1.56 × 10 ⁻¹²
rs2847500_A	G / G	-0.02 (-)	12%	1.93 × 10 ⁻¹²
rs62130059_C	C / A	-0.02 (↓)	32%	2.64 × 10 ⁻¹²
rs2909218_T	C / T	0.02 (↑)	80%	2.82 × 10 ⁻¹²
rs192785674_A	A / A	0.18 (↑)	> 99%	3.48 × 10 ⁻¹²
rs200641845_T	T / T	0.02 (↑)	55%	5.23 × 10 ⁻¹²
rs5235583_C	A / C	0.01 (↑)	47%	6.60 × 10 ⁻¹²
rs2074735_C	G / C	0.03 (↑)	7%	7.12 × 10 ⁻¹²
rs12317268_G	A / A	-0.02 (-)	15%	9.20 × 10 ⁻¹²
rs1047891_A	C / A	-0.01 (↓)	32%	1.16 × 10 ⁻¹¹
rs191379475_G	G / G	-0.09 (↓)	> 99%	1.22 × 10 ⁻¹¹
rs113938679_A	NA	-0.10 (-)	< 1%	2.21 × 10 ⁻¹¹
rs1858889_C	A / C	0.01 (↑)	50%	3.03 × 10 ⁻¹¹
rs188838036_A	A / A	0.12 (↑)	> 99%	3.14 × 10 ⁻¹¹
rs867772_G	A / G	-0.01 (↓)	68%	3.31 × 10 ⁻¹¹
rs62007299_A	A / A	-0.01 (↓)	71%	3.33 × 10 ⁻¹¹
rs7519574_A	G / G	0.02 (-)	18%	4.03 × 10 ⁻¹¹
rs561089663_G	G / G	0.20 (↑)	> 99%	4.31 × 10 ⁻¹¹
rs111529171_C	C / C	-0.01 (↓)	22%	6.26 × 10 ⁻¹¹

rs7569755_A 	G / A	0.01 (↑)	29%	8.35 x 10 ⁻¹¹
rs10887718_T 	T / T	-0.01 (↓)	53%	1.18 x 10 ⁻¹⁰
rs6724965_G 	A / A	-0.02 (-)	17%	1.34 x 10 ⁻¹⁰
rs7650253_A 	T / T	0.01 (-)	70%	1.76 x 10 ⁻¹⁰
rs557657187_G	G / G	0.29 (↑)	> 99%	2.19 x 10 ⁻¹⁰
rs529640451_C	C / C	0.17 (↑)	> 99%	2.20 x 10 ⁻¹⁰
rs77924815_A 	G / G	-0.02 (-)	19%	2.28 x 10 ⁻¹⁰
rs12997242_A 	G / G	-0.01 (-)	44%	2.32 x 10 ⁻¹⁰
rs576242124_A 	NA	0.09 (-)	< 1%	2.59 x 10 ⁻¹⁰
rs58073039_G 	A / A	-0.01 (-)	30%	2.84 x 10 ⁻¹⁰
rs10832218_C	C / C	-0.02 (↓)	11%	3.06 x 10 ⁻¹⁰
rs56044892_T 	C / C	0.01 (-)	20%	3.13 x 10 ⁻¹⁰
rs189918701_G 	G / G	-0.18 (↓)	> 99%	3.29 x 10 ⁻¹⁰
rs34726834_T 	C / C	0.01 (-)	25%	3.39 x 10 ⁻¹⁰
rs546541682_T	T / T	-0.11 (↓)	> 99%	3.45 x 10 ⁻¹⁰
rs8103262_C 	T / C	0.01 (↑)	30%	6.80 x 10 ⁻¹⁰
rs6698680_G 	A / A	-0.01 (-)	47%	7.47 x 10 ⁻¹⁰
rs2037511_A 	G / G	0.02 (-)	17%	8.35 x 10 ⁻¹⁰
rs8091117_A 	C / C	-0.02 (-)	6%	9.48 x 10 ⁻¹⁰
rs6438900_G 	C / G	0.01 (↑)	26%	1.16 x 10 ⁻⁹
rs184958517_T 	T / T	-0.10 (↓)	> 99%	1.21 x 10 ⁻⁹
rs57631352_G 	A / A	-0.01 (-)	30%	1.50 x 10 ⁻⁹
rs187443664_T	T / T	-0.08 (↓)	> 99%	1.52 x 10 ⁻⁹
rs7718395_G 	C / C	0.01 (-)	32%	1.68 x 10 ⁻⁹
rs574992951_C 	C / C	0.09 (↑)	> 99%	1.69 x 10 ⁻⁹
rs960596_T 	C / T	0.01 (↑)	34%	2.43 x 10 ⁻⁹
rs10500209_C 	T / T	-0.01 (-)	28%	2.73 x 10 ⁻⁹
rs10818769_G 	G / G	-0.02 (↓)	86%	2.99 x 10 ⁻⁹
rs10127775_T 	T / T	0.01 (↑)	61%	3.11 x 10 ⁻⁹
rs78649910_A 	T / T	-0.02 (-)	11%	3.41 x 10 ⁻⁹
rs565277381_T	T / T	0.28 (↑)	> 99%	3.55 x 10 ⁻⁹
rs186897112_G	G / G	0.20 (↑)	> 99%	3.81 x 10 ⁻⁹
rs3768013_A 	A / A	-0.01 (↓)	37%	3.86 x 10 ⁻⁹
rs8063706_T 	A / T	0.01 (↑)	27%	4.27 x 10 ⁻⁹
rs143106299_T	NA	-0.09 (-)	< 1%	4.62 x 10 ⁻⁹
rs184291421_C	C / C	0.09 (↑)	> 99%	5.03 x 10 ⁻⁹
rs9668081_T 	C / C	0.01 (-)	47%	5.40 x 10 ⁻⁹
rs6773343_T 	T / T	0.01 (↑)	72%	6.28 x 10 ⁻⁹

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.