01/2019

⭐ Well-being (Baselmans, 2019)
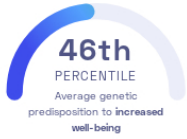
Bart M. L. Baselmans, et al.
Nature Genetics

`Behavior` `Mind`

STUDY SUMMARY

Novel method for multivariate traits identifies 304 genetic variants associated with well-being.

YOUR RESULT

46th
PERCENTILE
Average genetic predisposition to **increased well-being**

STUDY DESCRIPTION

Our well-being is a multivariate trait typically characterized by high life-satisfaction, positive affect, and absence of neuroticism as well as depressive symptoms. Determining genetic predispositions to our well-being can be difficult since a complex array of genetic variants contribute. Using a novel method, this study analyzed the genomes of 160,000 individuals of European ancestry to discover 304 variants associated with well-being. Some of these identified variants are near genes that are highly expressed in brain tissue, specifically in the hippocampus region that plays an important role in regulating memory, learning, and emotion. Also, this novel method increased the number of identified genetic variants associated with well-being by 26%!

DID YOU KNOW?

Studies have shown that exercising, sleeping well, spending time with loved ones, getting outside, helping others, practicing smiling, and planning trips can all increase your overall happiness!

YOUR DETAILED RESULTS

To calculate your genetic predisposition to increased well-being we summed up the effects of genetic variants that were linked to increased well-being 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 increased well-being. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to increased well-being. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to increased well-being. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for increased well-being to be 0.04**. 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 increased well-being is in the **46th percentile**. This means that it is higher than the polygenic scores 46% of people. We consider this to be an **average genetic predisposition to increased well-being**. 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
rs4938021_T NEW	C / C	0.01 (–)	63%	2.56×10^{-26}
rs483143_C NEW	G / G	-0.01 (–)	12%	1.19×10^{-22}
rs13213152_G NEW	A / A	-0.01 (–)	10%	6.48×10^{-21}
rs13212562_G NEW	A / A	-0.01 (–)	11%	7.08×10^{-21}
rs597462_C NEW	C / C	-0.01 (↓)	52%	2.21×10^{-19}
rs8084280_T NEW	A / A	0.01 (–)	51%	3.32×10^{-19}
rs11082011_T NEW	C / T	-0.01 (↓)	66%	6.51×10^{-19}
rs7010590_C NEW	T / T	0.01 (–)	51%	1.33×10^{-18}
rs2233980_A NEW	G / G	-0.01 (–)	13%	1.40×10^{-18}
rs13195401_T NEW	G / G	-0.01 (–)	9%	5.46×10^{-18}
rs2302832_C NEW	T / C	0.01 (↑)	52%	9.80×10^{-18}
rs433061_A NEW	G / G	-0.01 (–)	11%	4.08×10^{-17}
rs10491952_T NEW	C / T	-0.01 (↓)	22%	5.60×10^{-17}
rs17702602_T NEW	C / C	0.01 (–)	44%	1.10×10^{-16}
rs16903285_C NEW	T / T	0.01 (–)	14%	2.10×10^{-16}
rs7832708_T NEW	T / T	-0.01 (↓)	48%	3.00×10^{-16}
rs10774909_G NEW	C / C	0.01 (–)	20%	5.35×10^{-16}
rs12967143_C NEW	C / C	-0.01 (↓)	70%	7.28×10^{-16}
rs171697_G NEW	C / C	0.01 (–)	34%	1.26×10^{-15}
rs11599236_C NEW	C / C	-0.01 (↓)	42%	1.37×10^{-15}
rs716508_T NEW	T / T	-0.01 (↓)	68%	1.38×10^{-15}
rs55748329_G NEW	A / A	-0.01 (–)	14%	2.89×10^{-15}
rs11214441_A NEW	T / A	0.01 (↑)	40%	3.75×10^{-15}
rs3734572_C NEW	NA	0.02 (–)	4%	5.12×10^{-15}
rs2179744_A NEW	G / A	0.01 (↑)	29%	7.17×10^{-15}
rs2921036_C NEW	C / C	-0.01 (↓)	51%	7.22×10^{-15}
rs2149351_G NEW	G / G	-0.01 (↓)	76%	7.76×10^{-15}
rs28427480_C NEW	A / C	0.01 (↑)	10%	1.01×10^{-14}
rs4543289_G NEW	T / G	0.01 (↑)	52%	1.17×10^{-14}
rs782207_A NEW	G / A	-0.01 (↓)	37%	1.97×10^{-14}
rs3785234_T NEW	T / T	0.01 (↑)	62%	2.23×10^{-14}
rs7107356_G NEW	A / A	0.01 (–)	51%	2.31×10^{-14}
rs2458167_C NEW	A / C	-0.01 (↓)	69%	2.32×10^{-14}
rs4671459_C NEW	A / A	-0.01 (–)	19%	4.75×10^{-14}
rs1806153_T NEW	G / T	0.01 (↑)	22%	5.41×10^{-14}
rs115648484_A NEW	T / T	-0.01 (–)	9%	6.47×10^{-14}
rs2102341_C NEW	T / T	-0.01 (–)	70%	8.45×10^{-14}
rs3764512_T NEW	G / G	-0.01 (–)	23%	1.30×10^{-13}

SNP	Genotype	Effect	Frequency	p-value
rs4841662_A	A / A	-0.01 (↓)	48%	1.47×10^{-13}
rs61687445_A	A / A	-0.01 (↓)	44%	2.28×10^{-13}
rs11693031_G	G / G	-0.01 (↓)	33%	2.97×10^{-13}
rs1360692_T	T / T	0.01 (↑)	60%	3.38×10^{-13}
rs11604333_G	C / G	0.01 (↑)	32%	3.75×10^{-13}
rs12962538_C	T / T	-0.01 (–)	18%	4.25×10^{-13}
rs10244364_C	C / C	0.01 (↑)	32%	7.07×10^{-13}
rs3793577_G	A / G	0.01 (↑)	53%	7.39×10^{-13}
rs3783007_G	T / G	0.01 (↑)	38%	8.06×10^{-13}
rs2105841_C	T / C	0.01 (↑)	38%	8.19×10^{-13}
rs7805419_C	T / C	0.01 (↑)	42%	8.69×10^{-13}
rs2276825_C	T / T	-0.01 (–)	25%	1.21×10^{-12}
rs11214596_G	C / C	-0.01 (–)	54%	1.24×10^{-12}
rs13198298_T	C / C	0.01 (–)	10%	2.27×10^{-12}
rs619466_G	G / G	0.01 (↑)	90%	2.31×10^{-12}
rs301806_T	T / T	-0.01 (↓)	57%	2.35×10^{-12}
rs10487459_G	A / G	0.01 (↑)	39%	3.02×10^{-12}
rs1431071_T	G / G	-0.01 (–)	29%	5.05×10^{-12}
rs261909_C	C / C	0.01 (↑)	44%	5.15×10^{-12}
rs2093623_A	G / A	-0.01 (↓)	49%	5.29×10^{-12}
rs60045856_G	T / T	-0.01 (–)	11%	5.38×10^{-12}
rs6601426_G	G / G	-0.01 (↓)	84%	6.92×10^{-12}
rs11610143_G	C / C	0.01 (–)	20%	7.34×10^{-12}
rs2678897_A	A / A	0.01 (↑)	61%	8.14×10^{-12}
rs11644362_C	C / C	0.01 (↑)	55%	9.44×10^{-12}
rs942866_T	G / T	0.01 (↑)	66%	9.53×10^{-12}
rs1493914_T	C / T	0.01 (↑)	51%	9.73×10^{-12}
rs6131010_G	A / G	-0.01 (↓)	74%	9.81×10^{-12}
rs10812851_C	T / C	-0.01 (↓)	37%	9.93×10^{-12}
rs6925748_G	A / A	0.01 (–)	42%	1.20×10^{-11}
rs35609938_C	C / C	0.01 (↑)	51%	1.29×10^{-11}
rs6943746_G	T / T	-0.01 (–)	39%	1.39×10^{-11}
rs9564496_A	T / A	0.01 (↑)	32%	1.53×10^{-11}
rs7841297_C	C / C	0.01 (↑)	85%	1.97×10^{-11}
rs215815_A	G / A	0.01 (↑)	30%	2.07×10^{-11}
rs12552533_T	G / G	0.01 (–)	27%	2.34×10^{-11}
rs910187_A	G / A	-0.01 (↓)	37%	2.43×10^{-11}
rs2398144_A	A / A	0.01 (↑)	40%	3.05×10^{-11}
rs2273653_C	A / C	-0.01 (↓)	41%	3.62×10^{-11}
rs210914_C	C / C	-0.01 (↓)	81%	3.71×10^{-11}
rs6776145_C	T / T	0.01 (–)	12%	4.93×10^{-11}
rs72808287_T	C / C	-0.01 (–)	23%	5.09×10^{-11}
rs11633354_C	T / C	-0.01 (↓)	51%	5.13×10^{-11}
rs4955417_C	C / C	-0.01 (↓)	74%	5.36×10^{-11}
rs12125942_G	T / T	-0.01 (–)	18%	6.19×10^{-11}
rs72694263_C	G / G	-0.01 (–)	8%	6.95×10^{-11}
rs6705939_T	T / T	0.01 (↑)	30%	9.15×10^{-11}
rs1371325_G	G / G	0.01 (↑)	60%	9.35×10^{-11}
rs827123_C	C / C	0.01 (↑)	58%	9.36×10^{-11}
rs2721811_G	A / G	0.01 (↑)	42%	9.86×10^{-11}
rs7989827_G	T / G	-0.01 (↓)	49%	1.05×10^{-10}
rs12817055_T	C / C	0.01 (–)	26%	1.12×10^{-10}
rs7243332_G	A / A	0.01 (–)	31%	1.12×10^{-10}
rs4654874_G	G / G	0.01 (↑)	56%	1.22×10^{-10}
rs164640_T	C / T	-0.01 (↓)	53%	1.25×10^{-10}
rs6721577_T	A / T	0.01 (↑)	58%	1.29×10^{-10}
rs7422667_C	T / C	-0.01 (↓)	56%	1.55×10^{-10}
rs2744228_G	T / T	-0.01 (–)	38%	1.76×10^{-10}
rs4554778_T	C / C	-0.01 (–)	80%	1.90×10^{-10}

rs703410_A NEW	G / A	-0.01 (↓)	26%	1.97×10^{-10}
rs59211589_C NEW	T / T	-0.01 (–)	16%	2.50×10^{-10}
rs2051293_G NEW	A / G	0.01 (↑)	34%	2.59×10^{-10}
rs11068917_A NEW	C / C	0.01 (–)	18%	2.67×10^{-10}
rs166418_T NEW	T / T	-0.01 (↓)	48%	2.79×10^{-10}
rs247911_G NEW	G / G	0.01 (↑)	47%	3.74×10^{-10}
rs1187257_G NEW	A / A	0.01 (–)	29%	4.33×10^{-10}
rs12794371_T NEW	G / G	0.01 (–)	33%	4.33×10^{-10}
rs9957512_T NEW	G / T	0.01 (↑)	39%	5.05×10^{-10}
rs8001600_C NEW	T / C	0.01 (↑)	35%	5.14×10^{-10}
rs77648771_T NEW	NA	0.01 (–)	5%	5.22×10^{-10}
rs9380700_A NEW	G / G	-0.01 (–)	25%	5.33×10^{-10}
rs9298995_A NEW	G / A	-0.01 (↓)	41%	5.68×10^{-10}
rs297346_G NEW	A / G	-0.01 (↓)	64%	6.82×10^{-10}
rs7523829_A NEW	G / A	0.01 (↑)	49%	7.24×10^{-10}
rs12436091_C NEW	C / C	0.01 (↑)	76%	8.06×10^{-10}
rs1484680_G NEW	A / G	-0.01 (↓)	58%	8.71×10^{-10}
rs4461738_C NEW	T / C	0.01 (↑)	46%	9.22×10^{-10}
rs10879715_A NEW	A / A	0.01 (↑)	55%	9.27×10^{-10}
rs10913160_A NEW	T / A	-0.01 (↓)	40%	1.01×10^{-9}
rs61905363_T NEW	NA	-0.01 (–)	4%	1.04×10^{-9}
rs651245_C NEW	C / C	0.01 (↑)	60%	1.12×10^{-9}
rs308805_T NEW	C / C	-0.01 (–)	20%	1.18×10^{-9}
rs7789405_T NEW	C / T	-0.01 (↓)	57%	1.23×10^{-9}
rs4886920_G NEW	G / G	0.01 (↑)	70%	1.37×10^{-9}
rs2715147_T NEW	C / T	0.01 (↑)	50%	1.40×10^{-9}
rs17150537_G NEW	C / G	-0.01 (↓)	18%	1.45×10^{-9}
rs9967747_C NEW	C / C	0.01 (↑)	86%	1.46×10^{-9}
rs4581549_T NEW	C / C	-0.01 (–)	12%	1.50×10^{-9}
rs17041417_A NEW	G / G	0.01 (–)	18%	1.52×10^{-9}
rs12374076_G NEW	G / G	0.01 (↑)	51%	1.54×10^{-9}
rs815710_G NEW	A / A	0.01 (–)	41%	1.62×10^{-9}
rs61867341_A NEW	A / A	-0.01 (↓)	24%	1.70×10^{-9}
rs769688_T NEW	T / T	-0.01 (↓)	67%	1.73×10^{-9}
rs4836189_G NEW	C / C	0.01 (–)	41%	1.87×10^{-9}
rs17622606_A NEW	NA	-0.01 (–)	5%	1.95×10^{-9}
rs1019706_G NEW	A / G	-0.01 (↓)	29%	1.96×10^{-9}
rs3811935_G NEW	A / A	-0.01 (–)	50%	2.16×10^{-9}
rs6019826_T NEW	C / C	0.01 (–)	13%	2.17×10^{-9}
rs60157091_T NEW	C / T	0.01 (↑)	52%	2.22×10^{-9}
rs34517207_C NEW	T / T	-0.01 (–)	31%	2.26×10^{-9}
rs204883_A NEW	G / G	0.01 (–)	40%	2.29×10^{-9}
rs6773869_G NEW	G / A	0.01 (↑)	35%	2.32×10^{-9}
rs198457_T NEW	C / C	-0.01 (–)	19%	2.59×10^{-9}
rs3134012_C NEW	T / T	0.01 (–)	72%	2.65×10^{-9}
rs17583539_G NEW	A / A	0.01 (–)	22%	2.76×10^{-9}
rs1964390_G NEW	C / G	0.01 (↑)	75%	2.81×10^{-9}
rs7200826_T NEW	C / C	0.01 (–)	26%	3.05×10^{-9}
rs111871194_C NEW	T / T	-0.01 (–)	10%	3.21×10^{-9}
rs7191427_T NEW	G / G	0.01 (–)	25%	3.80×10^{-9}
rs2589341_C NEW	T / C	0.01 (↑)	34%	3.85×10^{-9}
rs9601120_T NEW	T / T	0.01 (↑)	19%	4.10×10^{-9}
rs13409834_G NEW	G / G	-0.01 (↓)	50%	4.43×10^{-9}
rs10967509_A NEW	G / G	-0.01 (↓)	38%	4.81×10^{-9}
rs66511648_C NEW	T / C	0.01 (↑)	27%	4.86×10^{-9}
rs9592461_G NEW	A / G	-0.01 (↓)	52%	5.02×10^{-9}
rs10746509_T NEW	T / T	0.01 (↑)	41%	5.07×10^{-9}
rs78324365_A NEW	G / G	-0.01 (–)	8%	5.14×10^{-9}
rs10936879_C NEW	T / T	-0.01 (–)	35%	5.93×10^{-9}

rs11876796_T NEW	C / T	-0.01 (↓)	52%	6.04×10^{-9}
rs115091345_C NEW	NA	0.02 (–)	3%	6.30×10^{-9}
rs9332801_C NEW	A / A	0.01 (–)	6%	6.45×10^{-9}
rs4914930_C NEW	C / C	0.01 (↑)	74%	6.60×10^{-9}
rs35722835_A NEW	G / G	-0.01 (–)	26%	7.09×10^{-9}
rs4652676_A NEW	G / A	0.01 (↑)	25%	7.26×10^{-9}
rs7396827_C NEW	T / C	-0.01 (↓)	53%	7.51×10^{-9}
rs4712936_T NEW	T / T	0.01 (↑)	92%	7.65×10^{-9}
rs11605020_A NEW	G / A	0.01 (↑)	51%	7.96×10^{-9}
rs1147478_A NEW	G / A	-0.01 (↓)	36%	8.99×10^{-9}
rs7021901_T NEW	T / T	-0.01 (↓)	44%	9.97×10^{-9}
rs10838629_A NEW	G / A	0.01 (↑)	77%	1.03×10^{-8}
rs1329572_A NEW	T / T	0.01 (–)	37%	1.03×10^{-8}
rs12910872_T NEW	C / C	-0.01 (–)	12%	1.08×10^{-8}
rs41316748_C NEW	NA	0.01 (–)	4%	1.08×10^{-8}
rs1563245_G NEW	T / T	0.01 (–)	40%	1.12×10^{-8}
rs17049478_A NEW	G / G	0.01 (–)	7%	1.13×10^{-8}
rs977747_G NEW	T / T	-0.01 (–)	59%	1.18×10^{-8}
rs17186681_T NEW	A / A	0.01 (–)	20%	1.21×10^{-8}
rs7819525_T NEW	G / G	-0.01 (–)	42%	1.23×10^{-8}
rs285006_A NEW	G / A	0.01 (↑)	34%	1.26×10^{-8}
rs62041356_C NEW	G / G	0.01 (–)	13%	1.35×10^{-8}
rs7154329_G NEW	A / A	-0.01 (–)	50%	1.44×10^{-8}
rs1510386_C NEW	C / C	-0.01 (↓)	48%	1.57×10^{-8}
rs10485622_G NEW	A / G	-0.01 (↓)	19%	1.59×10^{-8}
rs9546806_T NEW	C / T	0.01 (↑)	61%	1.61×10^{-8}
rs17570807_G NEW	NA	0.01 (–)	4%	1.65×10^{-8}
rs74504435_G NEW	A / A	-0.01 (–)	10%	1.66×10^{-8}
rs4409766_C NEW	T / T	-0.01 (–)	9%	1.67×10^{-8}
rs16958292_G NEW	G / G	-0.01 (↓)	14%	1.67×10^{-8}
rs779995_C NEW	T / T	0.01 (–)	37%	1.69×10^{-8}
rs72932350_C NEW	T / T	0.01 (–)	15%	1.75×10^{-8}
rs10168771_A NEW	A / A	-0.01 (↓)	66%	1.81×10^{-8}
rs1191600_A NEW	C / A	-0.01 (↓)	59%	1.82×10^{-8}
rs1919159_G NEW	G / G	0.01 (↑)	79%	1.82×10^{-8}
rs12458596_G NEW	A / A	0.01 (–)	37%	1.91×10^{-8}
rs1983949_A NEW	T / T	0.01 (–)	54%	1.93×10^{-8}
rs1551840_A NEW	A / A	-0.01 (↓)	39%	2.05×10^{-8}
rs12513440_A NEW	G / A	0.01 (↑)	25%	2.09×10^{-8}
rs77414181_A NEW	G / G	0.01 (–)	8%	2.11×10^{-8}
rs13262595_G NEW	A / A	-0.01 (–)	56%	2.13×10^{-8}
rs1950835_T NEW	G / T	-0.01 (↓)	51%	2.16×10^{-8}
rs73190080_T NEW	C / C	0.01 (–)	13%	2.25×10^{-8}
rs71384258_G NEW	A / G	0.01 (↑)	18%	2.38×10^{-8}
rs34945223_G NEW	A / A	0.01 (–)	26%	2.39×10^{-8}
rs4968736_G NEW	G / G	0.01 (↑)	36%	2.51×10^{-8}
rs117599630_G NEW	NA	-0.02 (–)	3%	2.63×10^{-8}
rs310763_C NEW	C / C	-0.01 (↓)	78%	2.69×10^{-8}
rs3846828_A NEW	C / C	0.01 (–)	11%	2.77×10^{-8}
rs6433563_G NEW	A / A	-0.01 (–)	51%	2.81×10^{-8}
rs6771469_C NEW	T / C	-0.01 (↓)	40%	2.94×10^{-8}
rs28680958_A NEW	G / G	-0.01 (–)	22%	3.05×10^{-8}
rs35258156_G NEW	A / G	-0.01 (↓)	46%	3.05×10^{-8}
rs4271063_A NEW	C / A	-0.01 (↓)	45%	3.15×10^{-8}
rs306755_C NEW	T / T	-0.01 (–)	47%	3.19×10^{-8}
rs10061069_C NEW	G / G	-0.01 (–)	23%	3.38×10^{-8}
rs79367487_A NEW	G / G	0.01 (–)	20%	3.59×10^{-8}
rs5754712_G NEW	G / G	-0.01 (↓)	81%	3.63×10^{-8}
rs6535577_C NEW	A / C	0.01 (↓)	58%	3.70×10^{-8}

rs6635877_C	A / C	-0.01 (↓)	58%	3.76 x 10⁻⁸
rs655836_C 🆕	T / C	-0.01 (↓)	43%	3.71 x 10⁻⁸
rs4757136_A 🆕	A / A	-0.01 (↓)	58%	3.83 x 10⁻⁸
rs77129413_A 🆕	G / G	-0.01 (−)	10%	3.87 x 10⁻⁸
rs12517438_G 🆕	T / T	0.01 (−)	54%	3.91 x 10⁻⁸
rs9883788_A 🆕	G / G	0.01 (−)	37%	3.98 x 10⁻⁸
rs7633673_A 🆕	G / G	-0.01 (−)	41%	4.12 x 10⁻⁸
rs314262_A 🆕	A / A	0.01 (↑)	54%	4.14 x 10⁻⁸
rs2876520_G 🆕	C / C	0.01 (−)	47%	4.22 x 10⁻⁸
rs1892350_G 🆕	A / A	0.01 (−)	49%	4.25 x 10⁻⁸
rs2042395_A 🆕	A / A	-0.01 (↓)	76%	4.39 x 10⁻⁸
rs2469903_G 🆕	G / G	0.01 (↑)	69%	4.56 x 10⁻⁸
rs4739938_G 🆕	T / T	0.01 (−)	9%	4.58 x 10⁻⁸
rs6931902_C 🆕	C / C	0.01 (↑)	80%	4.87 x 10⁻⁸
rs1016306_T 🆕	G / T	-0.01 (↓)	53%	4.89 x 10⁻⁸
rs12910903_G 🆕	G / G	-0.01 (↓)	41%	4.93 x 10⁻⁸
rs1072880_T 🆕	C / T	-0.01 (↓)	31%	4.98 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.