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Neuroticism (Luciano, 2017)

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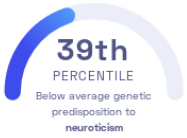
Behavior Mind

STUDY SUMMARY

Identification of 116 genetic variants associated with neuroticism.

YOUR RESULT



STUDY DESCRIPTION

Neuroticism is a personality trait characterized by negative emotionality (e.g. anger, guilt, anxiety) and associated with poorer mental and physical health. Though neuroticism is known to be highly heritable, most genetic factors remain unknown. This genome-wide association study analyzed the genomes of almost 330,000 individuals of European ancestry and discovered 116 genetic variants were found to be associated with neuroticism. Some of these variants are near or within genes associated with cell metabolism, as well as genes previously linked to major depression disorder and anxiety.

DID YOU KNOW?

Being mindful of your feelings and creating positive experiences may help overcome neuroticism.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to neuroticism we summed up the effects of genetic variants that were linked to neuroticism 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 neuroticism. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to neuroticism. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to neuroticism. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for neuroticism to be 0.53**. 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 neuroticism is in the **39th percentile**. This means that it is higher than the polygenic scores 39% of people. We consider this to be a **below average genetic predisposition to neuroticism**. 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
rs2921036_C	C / C	-0.06 (↓)	50%	8.04×10^{-26}
rs77804065_T	T / T	0.06 (↑)	25%	3.91×10^{-25}
rs10097870_A	A / A	-0.06 (↓)	44%	2.18×10^{-24}
rs7005884_G	A / A	0.06 (-)	46%	1.92×10^{-23}
rs2532386_A	A / A	0.06 (↑)	13%	2.00×10^{-23}
rs2953805_C	C / C	-0.05 (↓)	46%	3.02×10^{-22}
rs6982308_G	C / C	0.05 (-)	45%	6.46×10^{-21}
rs199534_G	G / G	0.05 (↑)	22%	1.13×10^{-20}
rs11082011_T	C / T	-0.05 (↓)	34%	1.25×10^{-16}
rs6601444_T	C / C	0.05 (-)	20%	5.48×10^{-16}
rs7111031_A	C / C	0.04 (-)	36%	1.06×10^{-15}
rs72700239_C	T / C	-0.04 (↓)	23%	3.15×10^{-14}
rs4936277_G	G / G	-0.04 (↓)	42%	2.13×10^{-13}
rs34862781_A	A / A	-0.04 (↓)	41%	2.40×10^{-13}
rs12896360_C	C / C	0.04 (↑)	30%	3.72×10^{-13}
rs6791611_C	G / C	-0.04 (↓)	46%	5.62×10^{-13}
rs11090045_A	G / G	0.04 (-)	31%	8.04×10^{-13}
rs6773869_G	G / A	0.04 (↑)	35%	1.09×10^{-12}
rs7107356_G	A / A	0.04 (-)	50%	1.52×10^{-12}
rs4731328_C	C / C	0.04 (↑)	49%	1.55×10^{-12}
rs2042555_A	A / A	0.04 (↑)	38%	2.49×10^{-12}
rs192083738_C	G / G	0.04 (-)	9%	3.07×10^{-12}
rs1542212_G	T / G	0.04 (↑)	38%	5.25×10^{-12}
rs11214589_A	G / G	-0.04 (-)	49%	5.40×10^{-12}
rs35169606_G	T / T	0.04 (-)	41%	6.56×10^{-12}
rs60150206_A	G / A	0.04 (↑)	10%	7.14×10^{-12}
rs7696796_A	G / G	0.04 (-)	25%	1.00×10^{-11}
rs4653218_C	T / T	-0.04 (-)	43%	1.17×10^{-11}
rs2269426_A	G / G	0.04 (-)	41%	1.49×10^{-11}
rs2071754_T	C / T	-0.04 (↓)	19%	2.02×10^{-11}
rs7502590_G	A / A	-0.04 (-)	14%	2.61×10^{-11}
rs6606710_C	T / T	0.04 (-)	42%	2.69×10^{-11}
rs56403421_C	A / C	0.04 (↑)	35%	4.38×10^{-11}
rs17662402_C	T / T	0.04 (-)	6%	1.36×10^{-10}
rs2380937_C	T / C	-0.04 (↓)	39%	1.57×10^{-10}
rs2149351_G	G / G	-0.04 (↓)	22%	1.64×10^{-10}
rs1870293_C	C / C	0.04 (↑)	36%	2.52×10^{-10}
rs17508548_G	T / T	0.04 (-)	11%	2.79×10^{-10}
rs13239186_T	T / T	0.04 (↑)	29%	3.07×10^{-10}

rs79487346_C	T / T	-0.04 (–)	7%	3.51×10^{-10}
rs13163891_A	C / C	-0.04 (–)	44%	3.62×10^{-10}
rs10896636_G	C / G	0.03 (↑)	32%	4.52×10^{-10}
rs10757410_C	T / C	-0.04 (↓)	36%	5.00×10^{-10}
rs1282545_C	T / T	0.03 (–)	42%	5.51×10^{-10}
rs496939_G	A / A	0.03 (–)	47%	5.55×10^{-10}
rs11152363_A	G / A	0.03 (↑)	20%	6.38×10^{-10}
rs2407746_G	C / G	0.03 (↑)	29%	8.17×10^{-10}
rs9398586_G	A / A	0.03 (–)	12%	8.34×10^{-10}
rs73190080_T	C / C	0.03 (–)	14%	9.25×10^{-10}
rs7175083_C	T / C	-0.03 (↓)	49%	1.15×10^{-9}
rs2056477_C	G / G	-0.03 (–)	26%	1.33×10^{-9}
rs9572015_A	G / A	0.03 (↑)	30%	1.40×10^{-9}
rs76333288_A	A / A	-0.03 (↓)	8%	1.52×10^{-9}
rs1422192_A	G / G	0.03 (–)	17%	1.68×10^{-9}
rs3741475_A	G / G	0.03 (–)	21%	1.73×10^{-9}
rs11068926_A	T / T	0.03 (–)	20%	1.97×10^{-9}
rs61361413_G	C / G	0.03 (↑)	17%	2.39×10^{-9}
rs4772079_C	G / C	0.03 (↑)	39%	2.60×10^{-9}
rs1521732_A	C / A	0.03 (↑)	37%	2.91×10^{-9}
rs75976_A	G / G	-0.03 (–)	43%	2.97×10^{-9}
rs4140799_A	A / A	-0.03 (↓)	45%	3.39×10^{-9}
rs117374667_G	T / T	0.03 (–)	8%	3.51×10^{-9}
rs2678897_A	A / A	0.03 (↑)	41%	3.56×10^{-9}
rs169235_G	A / G	0.03 (↑)	26%	3.97×10^{-9}
rs3793577_G	A / G	0.03 (↑)	49%	4.40×10^{-9}
rs112850127_G	NA	-0.03 (–)	3%	4.53×10^{-9}
rs76335349_A	G / G	0.03 (–)	9%	5.18×10^{-9}
rs240764_A	G / A	0.03 (↑)	47%	5.21×10^{-9}
rs802425_T	T / T	-0.03 (↓)	44%	5.24×10^{-9}
rs17711777_C	NA	-0.03 (–)	5%	5.40×10^{-9}
rs4362360_C	C / C	-0.03 (↓)	43%	5.48×10^{-9}
rs3785232_T	T / T	0.03 (↑)	32%	5.75×10^{-9}
rs57506017_T	A / T	0.03 (↑)	29%	5.75×10^{-9}
rs2690837_C	G / C	-0.03 (↓)	43%	7.57×10^{-9}
rs4841132_G	A / G	0.03 (↑)	7%	7.99×10^{-9}
rs77156030_A	G / G	-0.03 (–)	10%	8.30×10^{-9}
rs10789929_T	C / T	0.03 (↑)	43%	9.55×10^{-9}
rs9541687_C	C / C	0.03 (↑)	38%	1.02×10^{-8}
rs860626_G	T / G	-0.03 (↓)	31%	1.04×10^{-8}
rs4673866_G	G / G	0.03 (↑)	14%	1.07×10^{-8}
rs7814925_G	C / C	0.03 (–)	14%	1.22×10^{-8}
rs7567451_T	T / T	0.03 (↑)	27%	1.24×10^{-8}
rs10497655_C	T / C	-0.03 (↓)	32%	1.28×10^{-8}
rs8100891_G	C / G	-0.03 (↓)	30%	1.28×10^{-8}
rs1109451_A	G / G	-0.03 (–)	43%	1.31×10^{-8}
rs78323352_T	C / C	0.03 (–)	9%	1.32×10^{-8}
rs1050846_A	G / A	-0.03 (↓)	45%	1.33×10^{-8}
rs297346_G	A / G	-0.03 (↓)	36%	1.36×10^{-8}
rs11605020_A	G / A	0.03 (↑)	48%	1.37×10^{-8}
rs12441402_C	G / G	0.03 (–)	42%	1.41×10^{-8}
rs6986_C	G / C	0.03 (↑)	25%	1.65×10^{-8}
rs8039690_G	G / G	0.03 (↑)	30%	1.69×10^{-8}
rs4911448_T	C / T	0.03 (↑)	13%	1.78×10^{-8}
rs1275411_C	T / C	-0.03 (↓)	23%	1.84×10^{-8}
rs8063603_A	A / A	-0.03 (↓)	34%	1.84×10^{-8}
rs59143394_G	A / G	0.03 (↑)	30%	1.99×10^{-8}
rs189298483_A	NA	0.03 (–)	< 1%	2.01×10^{-8}
rs72694263_C	G / G	-0.03 (–)	9%	2.12×10^{-8}

rs80279740_C	NA	-0.03 (–)	4%	2.13×10^{-8}
rs4267411_T	C / C	-0.03 (–)	19%	2.20×10^{-8}
rs10507274_C	T / C	0.03 (↑)	7%	2.67×10^{-8}
rs7857183_G	A / A	0.03 (–)	13%	2.69×10^{-8}
rs76064345_G	T / T	0.03 (–)	8%	2.76×10^{-8}
rs1563245_G	T / T	0.03 (–)	39%	2.82×10^{-8}
rs77484855_G	T / T	0.03 (–)	8%	2.87×10^{-8}
rs11759026_G	A / G	-0.03 (↓)	25%	3.11×10^{-8}
rs2244497_T	C / T	0.03 (↑)	35%	3.30×10^{-8}
rs534666677_T	NA	0.03 (–)	< 1%	3.33×10^{-8}
rs7723944_A	G / G	-0.03 (–)	6%	3.36×10^{-8}
rs4585149_C	C / C	0.03 (↑)	19%	3.56×10^{-8}
rs72995548_T	NA	-0.03 (–)	5%	3.91×10^{-8}
rs7578651_C	T / T	0.03 (–)	49%	4.24×10^{-8}
rs72899043_T	C / T	-0.03 (↓)	40%	4.64×10^{-8}
rs2683653_C	G / G	-0.03 (–)	11%	4.82×10^{-8}
rs60668206_T	T / T	0.03 (↑)	16%	4.86×10^{-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.