



STUDY SUMMARY

This study identified hundreds of new genetic variants associated with risky behavior in genes, most of which are highly expressed in the brain.

YOUR RESULT



STUDY DESCRIPTION

Risk tolerance varies widely within the human population. Although it is known to be a moderately heritable trait, few genetic variants that correlate with this tolerance have been identified. In this study, several genome-wide association analyses examined 1 million individuals with European ancestry who self-reported their inclinations towards risky behavior. *Risk tolerance* was measured using various behaviors: adventurousness, automobile speeding propensity, drinks per week, smoking, and the number of sexual partners. Hundreds of genetic variants were identified in or near genes that are highly expressed in the brain and play a role in signaling between neurons. These variants collectively explained an estimated 5% of the heritability in general *risk tolerance*.




















































DID YOU KNOW?

Risky behavior is thought to play a role in many psychiatric disorders. For example, patients with anxiety disorders and obsessive-compulsive disorder may perceive more situations as risky than other individuals.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to increased risk tolerance we summed up the effects of genetic variants that were linked to increased risk tolerance 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 risk tolerance. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to increased risk tolerance. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to increased risk tolerance. By adding up the effect sizes of the highlighted variants we calculated your polygenic score for increased risk tolerance to be **0.10**. 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 risk tolerance is in the **32nd percentile**. This means that it is higher than the polygenic scores 32% of people. We consider this to be a **below average genetic predisposition to increased risk tolerance**. 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 [Ⓞ]
rs993137_T	T / T	-0.02 (↓)	62%	2.14 x 10 ⁻⁴⁰
rs7783012_A	G / A	0.02 (↑)	58%	7.57 x 10 ⁻²⁶
rs9641536_A	A / A	0.01 (↑)	49%	5.01 x 10 ⁻²³
rs2409095_A	A / A	0.02 (↑)	76%	1.01 x 10 ⁻²⁰
rs35424804_T	T / T	0.01 (↑)	50%	5.57 x 10 ⁻¹⁷
rs2409669_A	A / A	0.01 (↑)	40%	3.04 x 10 ⁻¹⁶
rs3764002_T	T / T	-0.01 (↓)	26%	1.15 x 10 ⁻¹⁶
rs4271249_T	G / G	0.01 (-)	59%	6.71 x 10 ⁻¹⁶
rs3781373_T	T / T	-0.01 (↓)	62%	7.42 x 10 ⁻¹⁶
rs58560561_T	T / G	-0.01 (↓)	35%	1.07 x 10 ⁻¹⁴
rs6748341_C	C / G	0.01 (↑)	67%	8.70 x 10 ⁻¹⁴
rs1531518_A	A / A	-0.01 (↓)	33%	1.58 x 10 ⁻¹³
rs13095117_A	A / G	0.01 (↑)	39%	1.82 x 10 ⁻¹³
rs10865313_A	G / G	-0.01 (-)	42%	2.61 x 10 ⁻¹³
rs4551267_T	C / T	-0.01 (↓)	45%	9.84 x 10 ⁻¹³
rs1233508_T	T / T	-0.01 (↓)	46%	2.72 x 10 ⁻¹²
rs940174_T	T / C	-0.01 (↓)	60%	3.70 x 10 ⁻¹²
rs10190777_C	G / C	0.01 (↑)	57%	4.57 x 10 ⁻¹²
rs12202969_A	G / A	0.01 (↑)	48%	4.63 x 10 ⁻¹²
rs6426658_A	G / G	0.01 (-)	40%	6.94 x 10 ⁻¹²
rs992493_T	C / C	0.01 (-)	20%	8.45 x 10 ⁻¹²
rs55745410_A	A / G	0.01 (↑)	64%	1.21 x 10 ⁻¹¹
rs12546540_A	A / A	0.01 (↑)	83%	1.53 x 10 ⁻¹¹
rs56738524_A	G / G	0.01 (-)	17%	1.70 x 10 ⁻¹¹
rs6987057_T	T / T	0.01 (↑)	18%	1.94 x 10 ⁻¹¹
rs2176263_C	G / C	0.01 (↑)	60%	2.17 x 10 ⁻¹¹
rs1799796_T	T / T	-0.01 (↓)	68%	2.19 x 10 ⁻¹¹
rs75254175_C	NA	-0.02 (-)	4%	2.84 x 10 ⁻¹¹
rs1211538_A	A / C	-0.01 (↓)	77%	3.47 x 10 ⁻¹¹
rs77182875_A	T / T	0.01 (-)	20%	3.60 x 10 ⁻¹¹
rs4762097_A	A / A	0.01 (↑)	64%	3.77 x 10 ⁻¹¹
rs10191477_T	T / C	-0.01 (↓)	39%	5.01 x 10 ⁻¹¹
rs12751210_C	C / C	-0.01 (↓)	40%	5.73 x 10 ⁻¹¹
rs786250_T	T / T	-0.01 (↓)	35%	5.90 x 10 ⁻¹¹
rs1051920_T	C / C	0.01 (-)	24%	8.46 x 10 ⁻¹¹
rs2239030_A	G / A	0.01 (↑)	43%	8.80 x 10 ⁻¹¹
rs2172845_A	A / A	0.01 (↑)	69%	1.01 x 10 ⁻¹⁰

rs2153515_A 	A / A	-0.01 (↓)	75%	1.09 x 10 ⁻¹⁰
rs12705985_A 	G / G	0.01 (-)	41%	1.20 x 10 ⁻¹⁰
rs475125_A 	A / A	-0.01 (↓)	51%	1.80 x 10 ⁻¹⁰
rs12210560_T 	C / T	-0.01 (↓)	35%	1.90 x 10 ⁻¹⁰
rs11080149_T 	C / C	-0.01 (-)	13%	2.30 x 10 ⁻¹⁰
rs2325036_A 	A / C	0.01 (↑)	62%	2.56 x 10 ⁻¹⁰
rs1417998_A 	T / T	-0.01 (-)	14%	2.92 x 10 ⁻¹⁰
rs62519839_T 	C / T	-0.01 (↓)	11%	3.92 x 10 ⁻¹⁰
rs624244_A 	A / A	-0.01 (↓)	66%	4.17 x 10 ⁻¹⁰
rs74068655_T 	T / G	0.01 (↑)	83%	4.24 x 10 ⁻¹⁰
rs983583_T 	C / C	0.01 (-)	39%	5.73 x 10 ⁻¹⁰
rs7387531_C 	G / G	-0.01 (-)	22%	8.60 x 10 ⁻¹⁰
rs11655325_A 	A / A	-0.01 (↓)	48%	9.19 x 10 ⁻¹⁰
rs689086_T 	T / C	-0.01 (↓)	72%	9.58 x 10 ⁻¹⁰
rs7594447_A 	A / C	0.01 (↑)	85%	1.10 x 10 ⁻⁹
rs6884452_A 	A / C	-0.01 (↓)	37%	1.30 x 10 ⁻⁹
rs6874731_T 	T / G	-0.01 (↓)	52%	1.33 x 10 ⁻⁹
rs7003528_T 	T / T	0.01 (↑)	33%	1.40 x 10 ⁻⁹
rs2350771_A 	G / G	-0.01 (-)	44%	1.41 x 10 ⁻⁹
rs114459574_A 	A / A	0.03 (↑)	97%	1.56 x 10 ⁻⁹
rs4605551_T 	T / T	-0.01 (↓)	64%	1.69 x 10 ⁻⁹
rs13327339_C 	C / C	0.01 (↑)	48%	1.78 x 10 ⁻⁹
rs8091761_A 	G / G	0.01 (-)	38%	1.78 x 10 ⁻⁹
rs12037322_A 	A / A	-0.01 (↓)	81%	1.84 x 10 ⁻⁹
rs12487748_A 	T / T	0.01 (-)	14%	2.16 x 10 ⁻⁹
rs7145844_C 	C / G	0.02 (↑)	91%	2.20 x 10 ⁻⁹
rs7818737_A 	G / G	-0.01 (-)	19%	2.28 x 10 ⁻⁹
rs10043722_A 	A / A	-0.01 (↓)	59%	2.37 x 10 ⁻⁹
rs2798421_A 	C / C	-0.01 (-)	28%	2.39 x 10 ⁻⁹
rs58400863_A 	G / A	-0.01 (↓)	34%	2.77 x 10 ⁻⁹
rs12413701_T 	T / C	0.01 (↑)	74%	2.83 x 10 ⁻⁹
rs140116958_A 	A / A	0.01 (↑)	82%	2.85 x 10 ⁻⁹
rs10007598_T 	T / C	-0.02 (↓)	92%	2.88 x 10 ⁻⁹
rs4782274_C 	C / C	0.01 (↑)	83%	3.00 x 10 ⁻⁹
rs114600294_C 	G / G	-0.01 (-)	19%	3.07 x 10 ⁻⁹
rs28361032_A 	A / A	0.01 (↑)	60%	3.25 x 10 ⁻⁹
rs918765_T 	G / G	0.01 (-)	35%	3.26 x 10 ⁻⁹
rs3849046_T 	C / C	0.01 (-)	53%	3.27 x 10 ⁻⁹
rs13273716_T 	C / C	0.01 (-)	14%	3.33 x 10 ⁻⁹
rs67361341_A 	A / A	-0.01 (↓)	39%	3.36 x 10 ⁻⁹
rs10860328_T 	T / T	-0.01 (↓)	80%	3.40 x 10 ⁻⁹
rs35606600_A 	A / G	-0.01 (↓)	65%	4.60 x 10 ⁻⁹
rs72965482_T 	C / C	-0.01 (-)	9%	4.65 x 10 ⁻⁹
rs163503_A 	G / G	-0.01 (-)	37%	4.99 x 10 ⁻⁹
rs17573719_T 	T / C	-0.01 (↓)	57%	6.35 x 10 ⁻⁹
rs4537316_T 	T / T	-0.01 (↓)	83%	6.37 x 10 ⁻⁹
rs6880870_T 	T / T	0.01 (↑)	42%	6.47 x 10 ⁻⁹
rs55678495_A 	G / G	0.01 (-)	16%	7.59 x 10 ⁻⁹
rs1110320_A 	A / A	0.01 (↑)	61%	8.55 x 10 ⁻⁹
rs198801_T 	C / C	-0.01 (-)	63%	9.21 x 10 ⁻⁹
rs2357023_T 	T / T	0.01 (↑)	59%	9.66 x 10 ⁻⁹
rs77706698_A	G / G	0.01 (-)	14%	9.86 x 10 ⁻⁹
rs1328110_T	T / C	0.01 (↑)	39%	9.86 x 10 ⁻⁹
rs6778487_T	G / G	0.01 (-)	68%	1.03 x 10 ⁻⁸
rs4671351_A	C / C	-0.01 (-)	37%	1.30 x 10 ⁻⁸
rs12547439_T	T / C	-0.01 (↓)	80%	1.30 x 10 ⁻⁸
rs741273_A	G / A	-0.01 (↓)	50%	1.36 x 10 ⁻⁸
rs7624230_C	G / G	0.01 (-)	11%	1.72 x 10 ⁻⁸
rs253754_T	T / T	-0.01 (↓)	74%	1.73 x 10 ⁻⁸

rs10007784_T	T / T	0.01 (↑)	79%	1.74×10^{-8}
rs9329227_C	C / C	0.01 (↑)	63%	1.83×10^{-8}
rs17579930_T	C / C	-0.01 (-)	41%	2.27×10^{-8}
rs13030106_C	G / C	0.01 (↑)	30%	2.50×10^{-8}
rs1438026_T	T / T	0.01 (↑)	67%	2.59×10^{-8}
rs2470951_A	A / T	-0.01 (↓)	61%	2.74×10^{-8}
rs149934732_T	C / T	0.02 (↑)	8%	2.78×10^{-8}
rs62262269_C	G / G	0.01 (-)	16%	2.79×10^{-8}
rs1369420_A	A / A	0.01 (↑)	58%	2.79×10^{-8}
rs4709200_T	C / T	-0.01 (↓)	55%	3.00×10^{-8}
rs7965253_T	T / C	0.01 (↑)	35%	3.05×10^{-8}
rs13251864_A	G / G	-0.02 (-)	89%	3.23×10^{-8}
rs2003485_T	C / C	0.01 (-)	35%	3.37×10^{-8}
rs2063886_A	A / C	-0.01 (↓)	31%	3.40×10^{-8}
rs8078436_T	C / T	-0.01 (↓)	44%	3.46×10^{-8}
rs687790_T	C / T	0.01 (↑)	69%	3.61×10^{-8}
rs7192890_T	C / T	0.01 (↑)	52%	3.85×10^{-8}
rs62425620_T	C / C	-0.01 (-)	37%	3.90×10^{-8}
rs17328201_T	T / T	-0.01 (↓)	81%	3.92×10^{-8}
rs2249190_T	T / T	0.01 (↑)	78%	3.96×10^{-8}
rs60359704_A	G / G	-0.01 (-)	31%	4.07×10^{-8}
rs10905461_T	C / C	0.01 (-)	26%	4.22×10^{-8}
rs1374197_A	A / G	0.01 (↑)	53%	4.24×10^{-8}
rs9388490_T	C / T	0.01 (↑)	45%	4.44×10^{-8}
rs75681102_T	C / C	0.01 (-)	17%	4.57×10^{-8}
rs7099822_C	C / C	0.01 (↑)	42%	4.60×10^{-8}
rs13249227_C	C / G	0.01 (↑)	39%	4.68×10^{-8}
rs1935571_T	T / T	-0.01 (↓)	52%	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.