

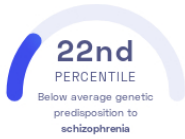
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Nature Genetics

Brain Behavior Mind

STUDY SUMMARY

Discovery of 53 novel schizophrenia-associated genetic loci in East Asian and European populations.

YOUR RESULT



schizophrenia patients.

STUDY DESCRIPTION

Schizophrenia is a mental disorder that affects how an individual perceives and interacts with reality. It is characterized by hallucinations, delusions, as well as abnormal thinking and behavior that impairs daily function. To discover novel genetic determinants of schizophrenia, this genome-wide association study included genomes of over 68,000 individuals of East Asian ancestry in addition to a cohort of European ancestry. The study identified a total of 208 genetic variants across 178 genetic loci of which 53 were novel. Together the variants identified in this study explain ~ 3% of schizophrenia risk. The study also revealed that the genetic basis of schizophrenia and its biology is shared across populations.

DID YOU KNOW?

Symptoms of schizophrenia typically begin to appear during childhood. Daily living support, social skills training, as well as individual and family therapy have been shown to help

YOUR DETAILED RESULTS

To calculate your genetic predisposition to schizophrenia we summed up the effects of genetic variants that were linked to schizophrenia 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 schizophrenia. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to schizophrenia. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to schizophrenia. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for schizophrenia to be -3.49**. 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 schizophrenia is in the **22nd percentile**. This means that it is higher than the polygenic scores 22% of people. We consider this to be a **below average genetic predisposition to schizophrenia**. 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 [Ⓞ]
rs9267666_T	C / C	-0.21 (-)	8%	7.26 x 10 ⁻³⁰
rs75970938_T	T / T	0.13 (↑)	74%	1.53 x 10 ⁻²⁶
rs1718180_A	A / A	-0.09 (↓)	65%	1.79 x 10 ⁻²³
rs7596038_T	C / C	-0.08 (-)	46%	7.24 x 10 ⁻²²
rs2159100_T	C / T	0.10 (↑)	37%	1.40 x 10 ⁻¹⁹
rs7478192_T	T / T	0.09 (↑)	60%	9.44 x 10 ⁻¹⁹
rs58120505_T	T / T	0.08 (↑)	54%	1.39 x 10 ⁻¹⁸
rs2949006_T	G / G	0.09 (-)	31%	2.88 x 10 ⁻¹⁸
rs66691851_T	C / T	-0.08 (↓)	48%	4.02 x 10 ⁻¹⁸
rs17592552_T	C / C	-0.13 (-)	22%	1.06 x 10 ⁻¹⁷
rs1198588_A	T / T	-0.10 (-)	17%	1.40 x 10 ⁻¹⁶
rs11210892_A	G / A	-0.07 (↓)	61%	1.07 x 10 ⁻¹⁶
rs4666990_T	T / C	0.07 (↑)	52%	1.64 x 10 ⁻¹⁶
rs4702_A	G / A	-0.07 (↓)	54%	2.42 x 10 ⁻¹⁶
rs7786663_A	G / A	-0.07 (↓)	41%	4.21 x 10 ⁻¹⁶
rs3929747_T	C / T	-0.08 (↓)	28%	5.15 x 10 ⁻¹⁶
rs4855019_T	C / C	-0.09 (-)	30%	6.43 x 10 ⁻¹⁶
rs13262696_A	A / A	0.07 (↑)	45%	2.57 x 10 ⁻¹⁴
rs2577831_A	C / A	-0.06 (↓)	49%	3.22 x 10 ⁻¹⁴
rs1926026_A	A / A	0.12 (↑)	75%	3.67 x 10 ⁻¹⁴
rs214475_A	A / G	-0.07 (↓)	41%	4.27 x 10 ⁻¹⁴
rs10873538_T	T / T	-0.07 (↓)	67%	5.98 x 10 ⁻¹⁴
rs11633534_T	C / T	-0.08 (↓)	35%	7.90 x 10 ⁻¹⁴
rs6694545_A	G / G	0.08 (-)	25%	8.25 x 10 ⁻¹⁴
rs217289_A	G / A	-0.06 (↓)	46%	1.05 x 10 ⁻¹³
rs302321_A	C / A	-0.07 (↓)	40%	1.37 x 10 ⁻¹³
rs6804239_T	T / T	-0.06 (↓)	43%	1.39 x 10 ⁻¹³
rs7001340_T	T / T	0.07 (↑)	67%	2.03 x 10 ⁻¹³
rs117325001_T	G / G	0.07 (-)	30%	2.25 x 10 ⁻¹³
rs13107325_T	C / C	0.15 (-)	7%	3.89 x 10 ⁻¹³
rs6874127_A	A / A	-0.07 (↓)	68%	9.49 x 10 ⁻¹³
rs2190864_T	T / C	0.06 (↑)	43%	1.03 x 10 ⁻¹²
rs28735056_A	A / A	-0.06 (↓)	58%	1.18 x 10 ⁻¹²
rs9890128_T	C / T	-0.07 (↓)	37%	1.21 x 10 ⁻¹²
rs4632296_T	T / T	0.07 (↑)	64%	1.22 x 10 ⁻¹²
rs2153960_A	A / A	-0.07 (↓)	63%	1.47 x 10 ⁻¹²
rs3802924_A	C / C	0.09 (-)	70%	1.69 x 10 ⁻¹²
rs7926389_A	A / A	-0.09 (↓)	72%	2.06 x 10 ⁻¹²
rs72934570_T	T / T	-0.14 (↓)	8%	2.65 x 10 ⁻¹²
rs28681284_T	C / T	-0.08 (↓)	20%	3.18 x 10 ⁻¹²

rs35225048_T	T / T	-0.06 (↓)	49%	4.72 × 10 ⁻¹²
rs172531_A	G / G	-0.07 (-)	63%	4.76 × 10 ⁻¹²
rs7605813_C	C / G	0.07 (↑)	37%	5.01 × 10 ⁻¹²
rs17164_T	C / T	-0.07 (↓)	61%	5.35 × 10 ⁻¹²
rs4132385_T	G / T	0.07 (↑)	40%	5.72 × 10 ⁻¹²
rs61937595_T	C / T	-0.14 (↓)	7%	6.07 × 10 ⁻¹²
rs3814881_A	G / G	-0.06 (-)	46%	7.39 × 10 ⁻¹²
rs6633421_A	A / A	0.07 (↑)	79%	1.39 × 10 ⁻¹¹
rs2057884_T	T / C	0.06 (↑)	40%	1.48 × 10 ⁻¹¹
rs17194490_T	G / G	0.10 (-)	29%	1.82 × 10 ⁻¹¹
rs9607782_A	T / A	0.08 (↑)	20%	2.16 × 10 ⁻¹¹
rs13230421_A	T / T	-0.10 (-)	11%	2.20 × 10 ⁻¹¹
rs2514218_T	T / T	-0.07 (↓)	37%	2.47 × 10 ⁻¹¹
rs11685299_A	C / A	-0.06 (↓)	39%	2.69 × 10 ⁻¹¹
rs3732386_T	T / T	0.07 (↑)	38%	3.46 × 10 ⁻¹¹
rs1792709_A	G / G	-0.07 (-)	35%	3.48 × 10 ⁻¹¹
rs374528934_C	C / C	-0.12 (↓)	58%	3.64 × 10 ⁻¹¹
rs6995307_C	C / C	-0.08 (↓)	81%	4.61 × 10 ⁻¹¹
rs55661361_A	G / G	-0.06 (-)	39%	4.93 × 10 ⁻¹¹
rs57346805_T	T / T	-0.06 (↓)	52%	5.58 × 10 ⁻¹¹
rs12031518_T	T / T	-0.07 (↓)	70%	6.43 × 10 ⁻¹¹
rs8188203_T	T / C	0.06 (↑)	46%	7.74 × 10 ⁻¹¹
rs5767730_A	A / A	-0.07 (↓)	45%	7.90 × 10 ⁻¹¹
rs13376709_T	T / T	-0.06 (↓)	40%	9.32 × 10 ⁻¹¹
rs7733403_A	A / A	0.05 (↑)	48%	9.47 × 10 ⁻¹¹
rs58146172_A	T / T	-0.06 (-)	33%	1.14 × 10 ⁻¹⁰
rs11663602_A	C / C	0.06 (-)	37%	1.15 × 10 ⁻¹⁰
rs7499362_C	C / C	-0.07 (↓)	80%	1.32 × 10 ⁻¹⁰
rs41356645_T	C / C	0.07 (-)	34%	1.45 × 10 ⁻¹⁰
rs2333321_A	A / A	0.07 (↑)	31%	1.58 × 10 ⁻¹⁰
rs2801578_A	A / A	0.06 (↑)	50%	1.82 × 10 ⁻¹⁰
rs10861879_A	A / A	0.06 (↑)	41%	1.99 × 10 ⁻¹⁰
rs13142920_A	C / C	-0.07 (-)	29%	2.36 × 10 ⁻¹⁰
rs11587347_C	C / C	-0.11 (↓)	92%	2.66 × 10 ⁻¹⁰
rs7067170_A	A / A	0.07 (↑)	13%	2.92 × 10 ⁻¹⁰
rs160593_A	A / A	-0.05 (↓)	55%	2.96 × 10 ⁻¹⁰
rs7676765_T	T / T	-0.05 (↓)	51%	3.10 × 10 ⁻¹⁰
rs999494_T	C / C	-0.07 (-)	30%	3.46 × 10 ⁻¹⁰
rs2381760_A	A / A	-0.08 (↓)	86%	3.50 × 10 ⁻¹⁰
rs148415900_T	G / G	-0.08 (-)	25%	3.62 × 10 ⁻¹⁰
rs2927176_A	T / A	0.06 (↑)	56%	4.33 × 10 ⁻¹⁰
rs6994019_T	T / G	0.07 (↑)	34%	4.35 × 10 ⁻¹⁰
rs2189806_A	T / A	-0.06 (↓)	59%	4.72 × 10 ⁻¹⁰
rs9841616_A	T / T	-0.08 (-)	16%	4.73 × 10 ⁻¹⁰
rs13355485_A	A / A	-0.06 (↓)	61%	4.81 × 10 ⁻¹⁰
rs12363019_A	T / A	0.06 (↑)	40%	5.15 × 10 ⁻¹⁰
rs117074560_T	C / C	-0.17 (-)	5%	5.31 × 10 ⁻¹⁰
rs6986895_T	C / T	-0.06 (↓)	64%	5.58 × 10 ⁻¹⁰
rs13335685_T	C / C	0.06 (-)	36%	5.67 × 10 ⁻¹⁰
rs77502336_C	G / C	0.06 (↑)	35%	5.81 × 10 ⁻¹⁰
rs71428218_T	C / T	-0.07 (↓)	30%	6.36 × 10 ⁻¹⁰
rs76442143_T	C / C	0.11 (-)	44%	6.40 × 10 ⁻¹⁰
rs6721549_T	T / C	0.06 (↑)	68%	6.49 × 10 ⁻¹⁰
rs17687067_A	A / C	-0.06 (↓)	69%	6.94 × 10 ⁻¹⁰
rs9567393_A	A / A	0.08 (↑)	77%	7.47 × 10 ⁻¹⁰
rs758129_A	A / A	-0.06 (↓)	41%	7.60 × 10 ⁻¹⁰
rs9342117_T	T / T	-0.06 (↓)	64%	8.53 × 10 ⁻¹⁰
rs2319280_A	C / A	-0.09 (↓)	17%	9.64 × 10 ⁻¹⁰
rs62152284_T	C / T	0.06 (↑)	31%	1.07 × 10 ⁻⁹
rs13164092_A	A / A	-0.06 (↓)	50%	1.10 × 10 ⁻⁹
rs13261217_A	A / A	-0.06 (↓)	67%	1.20 × 10 ⁻⁹

rs4793885_A	G / G	0.06 (-)	31%	1.20 x 10 ⁻⁹
rs13284900_T	C / C	0.07 (-)	28%	1.22 x 10 ⁻⁹
rs12328348_A	G / G	0.06 (-)	65%	1.29 x 10 ⁻⁹
rs112222723_T	T / T	-0.09 (↓)	79%	1.42 x 10 ⁻⁹
rs72986630_T	C / C	0.14 (-)	6%	1.45 x 10 ⁻⁹
rs975025_T	C / C	-0.07 (-)	26%	1.50 x 10 ⁻⁹
rs1043009_T	C / T	0.06 (↑)	41%	1.51 x 10 ⁻⁹
rs5943630_A	C / C	0.05 (-)	40%	1.56 x 10 ⁻⁹
rs867743_A	G / A	-0.05 (↓)	56%	1.64 x 10 ⁻⁹
rs6128857_A	A / A	0.06 (↑)	76%	1.66 x 10 ⁻⁹
rs9636107_A	A / A	-0.06 (↓)	49%	1.78 x 10 ⁻⁹
rs6670165_T	C / C	0.07 (-)	30%	1.88 x 10 ⁻⁹
rs2010476_C	C / G	0.06 (↑)	66%	2.16 x 10 ⁻⁹
rs2767713_A	A / C	-0.06 (↓)	63%	2.42 x 10 ⁻⁹
rs10517289_A	A / A	-0.07 (↓)	83%	2.74 x 10 ⁻⁹
rs147786161_A	A / G	-0.05 (↓)	54%	2.87 x 10 ⁻⁹
rs1451488_A	A / A	-0.05 (↓)	52%	3.04 x 10 ⁻⁹
rs111589530_T	C / C	0.08 (-)	23%	3.25 x 10 ⁻⁹
rs942820_A	A / A	-0.06 (↓)	37%	3.47 x 10 ⁻⁹
rs3088186_T	T / T	0.06 (↑)	37%	3.98 x 10 ⁻⁹
rs1075195_T	T / T	0.06 (↑)	28%	4.12 x 10 ⁻⁹
rs7127399_A	G / G	-0.05 (-)	39%	4.17 x 10 ⁻⁹
rs2293018_T	C / C	0.13 (-)	19%	4.46 x 10 ⁻⁹
rs7673823_A	G / G	0.10 (-)	7%	4.91 x 10 ⁻⁹
rs419677_A	A / G	-0.05 (↓)	60%	5.13 x 10 ⁻⁹
rs6938026_A	A / A	0.06 (↑)	67%	5.47 x 10 ⁻⁹
rs215412_A	G / G	0.06 (-)	37%	5.87 x 10 ⁻⁹
rs72829007_T	T / T	0.17 (↑)	96%	6.19 x 10 ⁻⁹
rs79210963_T	T / T	-0.09 (↓)	75%	6.36 x 10 ⁻⁹
rs4479913_A	G / A	0.06 (↑)	66%	6.37 x 10 ⁻⁹
rs4243617_T	T / G	0.05 (↑)	41%	6.48 x 10 ⁻⁹
rs946106_T	C / C	-0.05 (-)	66%	6.60 x 10 ⁻⁹
rs4365348_T	C / T	0.06 (↑)	44%	6.69 x 10 ⁻⁹
rs78895722_C	C / C	-0.18 (↓)	97%	7.06 x 10 ⁻⁹
rs13019859_A	A / G	0.05 (↑)	49%	7.24 x 10 ⁻⁹
rs9420_A	A / G	0.06 (↑)	37%	7.44 x 10 ⁻⁹
rs10515678_T	C / T	-0.07 (↓)	22%	7.83 x 10 ⁻⁹
rs1676062_A	C / C	-0.05 (-)	43%	8.05 x 10 ⁻⁹
rs75365967_A	G / G	-0.05 (-)	44%	8.13 x 10 ⁻⁹
rs28419375_T	T / C	-0.05 (↓)	63%	8.14 x 10 ⁻⁹
rs11038391_T	G / T	-0.06 (↓)	29%	8.19 x 10 ⁻⁹
rs73477270_T	T / T	-0.18 (↓)	97%	8.42 x 10 ⁻⁹
rs2236989_T	C / C	-0.06 (-)	26%	8.60 x 10 ⁻⁹
rs59721702_C	C / C	-0.07 (↓)	80%	8.61 x 10 ⁻⁹
rs79527984_A	A / A	-0.05 (↓)	48%	8.66 x 10 ⁻⁹
rs11958187_A	G / A	0.05 (↑)	55%	9.39 x 10 ⁻⁹
rs73229090_A	C / C	-0.10 (-)	11%	9.54 x 10 ⁻⁹
rs10791099_C	G / C	-0.05 (↓)	54%	9.66 x 10 ⁻⁹
rs2917568_T	C / C	0.05 (-)	51%	9.70 x 10 ⁻⁹
rs337718_T	T / C	0.05 (↑)	37%	1.03 x 10 ⁻⁸
rs12104272_A	A / A	-0.06 (↓)	31%	1.09 x 10 ⁻⁸
rs1357318_T	T / T	0.06 (↑)	72%	1.11 x 10 ⁻⁸
rs62244881_T	T / C	0.09 (↑)	86%	1.17 x 10 ⁻⁸
rs61257528_A	A / A	0.07 (↑)	24%	1.19 x 10 ⁻⁸
rs6703335_A	A / G	-0.05 (↓)	44%	1.20 x 10 ⁻⁸
rs1483245_A	A / G	0.05 (↑)	45%	1.30 x 10 ⁻⁸
rs59159185_A	T / T	0.10 (-)	7%	1.31 x 10 ⁻⁸
rs4734654_A	A / A	0.05 (↑)	60%	1.50 x 10 ⁻⁸
rs783540_A	A / A	-0.05 (↓)	57%	1.52 x 10 ⁻⁸
rs2957582_T	C / T	-0.06 (↓)	29%	1.56 x 10 ⁻⁸
rs3849490_T	C / C	-0.05 (-)	45%	1.67 x 10 ⁻⁸

rs61847303_T	C / C	-0.06 (-)	35%	1.96 x 10 ⁻⁸
rs4766428_T	C / T	0.06 (↑)	50%	2.05 x 10 ⁻⁸
rs7811417_T	C / C	0.05 (-)	40%	2.08 x 10 ⁻⁸
rs3810449_T	C / T	-0.09 (↓)	22%	2.12 x 10 ⁻⁸
rs533123_A	G / A	0.08 (↑)	86%	2.25 x 10 ⁻⁸
rs12421382_T	C / T	-0.05 (↓)	39%	2.30 x 10 ⁻⁸
rs10777342_T	C / C	-0.05 (-)	42%	2.31 x 10 ⁻⁸
rs2634447_T	C / T	-0.06 (↓)	72%	2.34 x 10 ⁻⁸
rs7599488_T	C / C	-0.05 (-)	49%	2.60 x 10 ⁻⁸
rs138636117_A	A / A	-0.13 (↓)	83%	2.60 x 10 ⁻⁸
rs11878180_A	C / C	0.06 (-)	33%	2.62 x 10 ⁻⁸
rs76262184_A	A / A	0.08 (↑)	87%	2.63 x 10 ⁻⁸
rs9666169_T	C / T	-0.05 (↓)	41%	2.63 x 10 ⁻⁸
rs77441740_A	A / A	-0.16 (↓)	96%	2.65 x 10 ⁻⁸
rs9669820_T	G / T	0.06 (↑)	28%	2.69 x 10 ⁻⁸
rs323169_T	C / T	-0.05 (↓)	61%	2.75 x 10 ⁻⁸
rs12969453_A	A / A	0.05 (↑)	54%	2.83 x 10 ⁻⁸
rs112316332_A	T / A	-0.07 (↓)	18%	3.04 x 10 ⁻⁸
rs117465168_C	C / C	-0.13 (↓)	83%	3.21 x 10 ⁻⁸
rs5767773_A	G / A	0.06 (↑)	61%	3.25 x 10 ⁻⁸
rs793571_A	A / G	0.05 (↑)	65%	3.37 x 10 ⁻⁸
rs6797774_T	T / T	0.05 (↑)	57%	3.38 x 10 ⁻⁸
rs1191551_T	G / G	0.07 (-)	31%	3.40 x 10 ⁻⁸
rs11615992_A	A / G	-0.07 (↓)	83%	3.42 x 10 ⁻⁸
rs7271624_C	C / C	-0.06 (↓)	75%	3.42 x 10 ⁻⁸
rs4697446_T	G / G	0.05 (-)	45%	3.66 x 10 ⁻⁸
rs832190_T	C / T	-0.05 (↓)	57%	3.82 x 10 ⁻⁸
rs1999512_A	A / G	-0.05 (↓)	66%	3.84 x 10 ⁻⁸
rs61826793_A	G / G	-0.07 (-)	17%	3.94 x 10 ⁻⁸
rs76432012_T	T / T	0.14 (↑)	94%	3.98 x 10 ⁻⁸
rs6864084_T	T / T	0.07 (↑)	29%	4.06 x 10 ⁻⁸
rs2358740_T	G / T	-0.05 (↓)	39%	4.13 x 10 ⁻⁸
rs28886334_A	A / G	0.05 (↑)	62%	4.14 x 10 ⁻⁸
rs1997529_A	A / A	-0.05 (↓)	42%	4.24 x 10 ⁻⁸
rs9975024_A	G / G	-0.05 (-)	56%	4.24 x 10 ⁻⁸
rs6983764_A	G / A	0.05 (↑)	38%	4.36 x 10 ⁻⁸
rs12083902_A	G / A	-0.07 (↓)	29%	4.40 x 10 ⁻⁸
rs1440849_A	G / A	-0.06 (↓)	75%	4.56 x 10 ⁻⁸
rs17635239_T	G / G	0.07 (-)	27%	4.61 x 10 ⁻⁸
rs74912003_T	NA	-0.22 (-)	2%	4.64 x 10 ⁻⁸
rs11230827_A	G / G	0.10 (-)	21%	4.73 x 10 ⁻⁸
rs7951609_T	T / C	-0.05 (↓)	67%	4.87 x 10 ⁻⁸
rs28607014_T	C / T	-0.05 (↓)	41%	4.88 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.