

🌟 Parkinson's disease (Nalls, 2019)

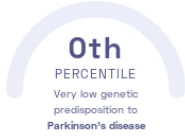
Mike A. Nalls, et al.
The Lancet Neurology

Dementia Brain

STUDY SUMMARY

Identification of 90 genetic variants associated with Parkinson's disease.

YOUR RESULT



STUDY DESCRIPTION

Parkinson's disease is a neurodegenerative disorder caused by reduced *dopamine* signaling in some regions of the brain that leads to tremors. This can impair various activities that involve muscle movements including walking, speaking and eating. To date, Parkinson's disease remains largely a genetic mystery. To advance our understanding of genetic risk factors for Parkinson's, this study analyzed the genomes of almost 1.5 million individuals of European ancestry and identified 90 genetic variants, of which 38 were novel. Many variants were in genes that are active in regions of the brain involved in movement control. The study also identified genetic associations between Parkinson's and smoking as well as Parkinson's and educational attainment.


































DID YOU KNOW?

Diets rich in antioxidants, omega-3 fatty acids and vitamin D3 and CoQ10 are believed to reduce the risk of Parkinson's disease. Reducing stress and exercising may also help.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to Parkinson's disease we summed up the effects of genetic variants that were linked to Parkinson's disease 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 Parkinson's disease. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to Parkinson's disease. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to Parkinson's disease. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for Parkinson's disease to be -6.30**. 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 Parkinson's disease is in the **0th percentile**. This means that it is higher than the polygenic scores 0% of people. We consider this to be a **very low genetic predisposition to Parkinson's disease**. 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
rs356182_A	G / A	-0.28 (↓)	63%	3.89 x 10 ⁻¹⁶⁴
rs356203_T	T / T	-0.25 (↓)	61%	5.16 x 10 ⁻¹⁴⁹
rs34637584_A	NA	2.43 (-)	< 1%	3.61 x 10 ⁻¹⁴⁸
rs35749011_A	NA	0.61 (-)	2%	1.72 x 10 ⁻⁷⁰
rs34311866_T	T / T	-0.21 (↓)	81%	9.98 x 10 ⁻⁷⁰
rs62053943_T	T / T	-0.27 (↓)	16%	3.58 x 10 ⁻⁶⁸
rs199453_T	T / T	-0.20 (↓)	23%	8.62 x 10 ⁻⁶⁷
rs356228_C	C / G	0.15 (↑)	46%	9.53 x 10 ⁻⁴⁹
rs7225002_A	G / G	0.14 (-)	61%	1.84 x 10 ⁻⁴⁰
rs1474055_T	C / C	0.18 (-)	13%	2.54 x 10 ⁻³⁹
rs7221167_T	C / C	0.14 (-)	58%	1.36 x 10 ⁻³⁷
rs10847864_T	G / G	0.15 (-)	36%	1.47 x 10 ⁻³⁷
rs5019538_A	A / A	-0.16 (↓)	68%	1.13 x 10 ⁻³⁶
rs10513789_T	T / G	0.15 (↑)	81%	1.22 x 10 ⁻³⁴
rs823118_T	C / T	0.11 (↑)	57%	1.11 x 10 ⁻²⁹
rs76904798_T	C / C	0.14 (-)	14%	1.52 x 10 ⁻²⁸
rs4698412_A	A / A	0.10 (↑)	55%	2.06 x 10 ⁻²⁸
rs117896735_A	NA	0.44 (-)	2%	2.36 x 10 ⁻²⁸
rs17686238_T	G / T	-0.19 (↓)	11%	8.25 x 10 ⁻²⁷
rs199351_A	A / C	0.10 (↑)	59%	5.25 x 10 ⁻²⁶
rs1867598_A	A / A	-0.16 (↓)	90%	2.52 x 10 ⁻²³
rs12456492_A	A / G	-0.10 (↓)	68%	3.80 x 10 ⁻²³
rs76763715_T	T / T	-0.75 (↓)	> 99%	1.59 x 10 ⁻²²
rs11557080_A	G / G	0.13 (-)	14%	2.50 x 10 ⁻²²
rs35643925_A	NA	0.39 (-)	2%	8.11 x 10 ⁻²²
rs873786_T	C / T	-0.17 (↓)	10%	1.79 x 10 ⁻²¹
rs6854006_T	C / T	-0.09 (↓)	36%	5.82 x 10 ⁻²¹
rs117073808_T	T / T	-0.40 (↓)	98%	1.59 x 10 ⁻²⁰
rs11150601_A	A / A	0.09 (↑)	64%	5.12 x 10 ⁻²⁰
rs3802920_T	G / G	0.11 (-)	21%	6.26 x 10 ⁻²⁰
rs4101061_A	G / G	-0.09 (-)	71%	4.97 x 10 ⁻¹⁹
rs2251086_T	C / C	-0.12 (-)	14%	6.08 x 10 ⁻¹⁸
rs13294100_T	T / T	-0.09 (↓)	34%	8.72 x 10 ⁻¹⁸
rs10756907_A	A / A	-0.09 (↓)	77%	5.06 x 10 ⁻¹⁷
rs10797576_T	C / T	0.11 (↑)	14%	6.84 x 10 ⁻¹⁷
rs11158026_T	C / C	-0.08 (-)	32%	1.66 x 10 ⁻¹⁶
rs1293298_A	A / A	0.09 (↑)	74%	3.99 x 10 ⁻¹⁶
rs117615688_A	G / G	-0.23 (-)	7%	6.71 x 10 ⁻¹⁶
rs4653767_T	T / C	0.08 (↑)	72%	1.38 x 10 ⁻¹⁶
rs200547_T	G / G	0.00 (-)	27%	2.70 x 10 ⁻¹⁵

rs620615_T	G / G	-0.09 (-)	27%	2.72 x 10 ⁻¹⁴
rs57891859_A	A / A	0.08 (↑)	72%	4.55 x 10 ⁻¹⁴
rs141128804_T	NA	0.35 (-)	2%	6.38 x 10 ⁻¹⁴
rs9912362_T	C / C	0.08 (-)	36%	1.62 x 10 ⁻¹³
rs896435_T	T / T	0.07 (↑)	69%	3.41 x 10 ⁻¹³
rs73038319_A	A / A	-0.17 (↓)	96%	5.94 x 10 ⁻¹³
rs11683001_A	T / T	0.07 (-)	34%	8.04 x 10 ⁻¹³
rs13117519_T	C / C	0.09 (-)	17%	9.82 x 10 ⁻¹³
rs3104783_A	C / A	0.07 (↑)	43%	1.29 x 10 ⁻¹²
rs4140646_A	G / G	0.08 (-)	21%	5.62 x 10 ⁻¹²
rs6658353_C 	G / C	0.07 (↑)	50%	6.10 x 10 ⁻¹²
rs138017112_C	NA	0.41 (-)	1%	7.29 x 10 ⁻¹²
rs6808178_T 	C / C	0.07 (-)	38%	8.09 x 10 ⁻¹²
rs55961674_T 	C / C	0.09 (-)	17%	9.98 x 10 ⁻¹²
rs850738_A 	A / A	-0.07 (↓)	61%	1.29 x 10 ⁻¹¹
rs72840788_A	G / G	0.08 (-)	22%	1.57 x 10 ⁻¹¹
rs2248244_A 	G / A	0.07 (↑)	28%	2.74 x 10 ⁻¹¹
rs6497339_A	A / T	0.06 (↑)	45%	2.76 x 10 ⁻¹¹
rs9267659_A	A / G	0.08 (↑)	20%	3.65 x 10 ⁻¹¹
rs979812_T	T / T	0.06 (↑)	44%	6.19 x 10 ⁻¹¹
rs181609621_A	A / A	-0.42 (↓)	99%	7.69 x 10 ⁻¹¹
rs2295545_T	C / C	0.06 (-)	61%	8.45 x 10 ⁻¹¹
rs75859381_T 	T / T	-0.22 (↓)	97%	1.04 x 10 ⁻¹⁰
rs10221156_A	G / G	-0.12 (-)	9%	1.08 x 10 ⁻¹⁰
rs11707416_A 	T / T	-0.06 (-)	37%	1.13 x 10 ⁻¹⁰
rs12497850_T	G / G	0.06 (-)	65%	1.36 x 10 ⁻¹⁰
rs12528068_T 	C / C	0.07 (-)	28%	1.63 x 10 ⁻¹⁰
rs11610045_A 	G / A	0.06 (↑)	49%	1.77 x 10 ⁻¹⁰
rs144755950_T	T / T	-0.40 (↓)	99%	1.82 x 10 ⁻¹⁰
rs62333164_A 	G / G	-0.06 (-)	33%	2.00 x 10 ⁻¹⁰
rs12283611_A	C / A	-0.06 (↓)	41%	2.61 x 10 ⁻¹⁰
rs34025766_A 	T / T	-0.08 (-)	16%	2.87 x 10 ⁻¹⁰
rs55818311_T	T / T	-0.07 (↓)	69%	4.18 x 10 ⁻¹⁰
rs1450522_A 	A / G	-0.06 (↓)	67%	5.01 x 10 ⁻¹⁰
rs2269906_A 	C / C	0.06 (-)	65%	6.24 x 10 ⁻¹⁰
rs2904880_C 	C / G	-0.07 (↓)	31%	7.87 x 10 ⁻¹⁰
rs61169879_T 	C / T	0.08 (↑)	16%	9.28 x 10 ⁻¹⁰
rs10748818_A 	A / A	-0.08 (↓)	85%	1.05 x 10 ⁻⁹
rs6825004_C	C / G	0.06 (↑)	69%	1.17 x 10 ⁻⁹
rs12951632_T	T / T	0.06 (↑)	73%	1.40 x 10 ⁻⁹
rs4771268_T 	C / C	0.07 (-)	23%	1.45 x 10 ⁻⁹
rs26431_C 	C / C	0.06 (↑)	70%	1.57 x 10 ⁻⁹
rs6500328_A 	A / G	0.06 (↑)	60%	1.82 x 10 ⁻⁹
rs997368_A 	A / A	0.07 (↑)	80%	1.84 x 10 ⁻⁹
rs3742785_A 	A / C	0.07 (↑)	79%	1.92 x 10 ⁻⁹
rs7938782_A 	A / A	0.09 (↑)	88%	2.12 x 10 ⁻⁹
rs666463_A 	A / A	0.08 (↑)	83%	3.20 x 10 ⁻⁹
rs114138760_C	NA	0.28 (-)	1%	4.19 x 10 ⁻⁹
rs11578699_T 	C / T	-0.07 (↓)	19%	4.47 x 10 ⁻⁹
rs6476434_T 	T / T	-0.06 (↓)	73%	6.58 x 10 ⁻⁹
rs11950533_A 	C / C	-0.09 (-)	10%	7.16 x 10 ⁻⁹
rs77351827_T 	C / C	0.08 (-)	13%	8.87 x 10 ⁻⁹
rs12600861_A 	C / C	-0.06 (-)	65%	1.01 x 10 ⁻⁸
rs6875262_T	C / C	0.11 (-)	10%	1.02 x 10 ⁻⁸
rs9568188_T 	T / T	0.06 (↑)	74%	1.15 x 10 ⁻⁸
rs2280104_T	C / C	0.06 (-)	36%	1.16 x 10 ⁻⁸
rs76116224_A 	A / A	0.11 (↑)	90%	1.27 x 10 ⁻⁸
rs2042477_A 	T / T	-0.07 (-)	24%	1.38 x 10 ⁻⁸
rs8087969_T 	T / G	-0.06 (↓)	55%	1.41 x 10 ⁻⁸
rs76949143_A 	T / T	-0.14 (-)	5%	1.43 x 10 ⁻⁸

rs4954162_A	G / G	-0.07 (↓)	16%	1.60×10^{-8}
rs9261484_T	C / T	-0.06 (↓)	25%	1.62×10^{-8}
rs1941685_T	G / T	0.05 (↑)	50%	1.69×10^{-8}
rs2086641_T	T / T	-0.06 (↓)	72%	1.81×10^{-8}
rs11658976_A	A / A	-0.06 (↓)	58%	3.52×10^{-8}
rs12147950_T	T / T	-0.05 (↓)	44%	3.54×10^{-8}
rs7134559_T	T / T	-0.05 (↓)	40%	3.96×10^{-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.