

☆ **Left-handedness (Cuellar-Partida, 2020)**

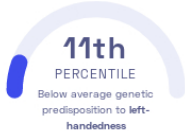
Gabriel Cuellar-Partida, et al.
Nature Human Behavior

Brain

STUDY SUMMARY

Identification of 41 genetic variants associated with left-handedness.

YOUR RESULT



STUDY DESCRIPTION

Handedness influences how we write, throw a ball and perform many other common activities. Right-handedness is much more common, with only 1 in 10 people being a lefty. Genetics appears to play a role in determining which hand is dominant, perhaps accounting for a quarter of all variation in handedness. To identify the regions of the genome that may determine handedness, this study examined the genomes of over 1.76 million individuals of European ancestry. The study found 41 unique regions associated with left-hand dominance. These regions harbor genes known to influence brain structure and function, such as CNTN3, SOX6, and NPAS4. The study also found a correlation between left-handedness and an increased prevalence of psychiatric conditions such as schizophrenia and bipolar disorder.

DID YOU KNOW?

A study by the National Bureau of Economic Research found left-handed men earned up to 15% more than their righty counterparts. On the other hand, the study found no effect of handedness on women's earnings.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to left-handedness we summed up the effects of genetic variants that were linked to left-handedness 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 left-handedness. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to left-handedness. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to left-handedness. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for left-handedness to be -0.19**. 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 left-handedness is in the **11th percentile**. This means that it is higher than the polygenic scores 11% of people. We consider this to be a **below average genetic predisposition to left-handedness**. 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 [Ⓞ]
rs62213410_A	A / A	-0.04 (↓)	71%	2.37 x 10 ⁻³⁰
rs55974014_A	A / A	-0.05 (↓)	21%	2.97 x 10 ⁻³⁰
rs3132584_T	G / G	-0.05 (-)	21%	6.12 x 10 ⁻²⁶
rs4550447_C	G / G	0.06 (-)	12%	4.67 x 10 ⁻²⁴
rs6224_T	G / T	-0.03 (↓)	47%	6.16 x 10 ⁻²¹
rs2233324_C	G / G	-0.04 (-)	16%	1.86 x 10 ⁻¹⁴
rs13107325_T	C / C	0.06 (-)	8%	4.62 x 10 ⁻¹⁴
rs62036618_A	A / C	-0.02 (↓)	61%	1.43 x 10 ⁻¹³
rs35551703_A	NA	-0.06 (-)	4%	1.93 x 10 ⁻¹²
rs66479618_T	C / T	-0.03 (↓)	20%	6.48 x 10 ⁻¹²
rs7132513_C	T / T	0.03 (-)	61%	2.10 x 10 ⁻¹¹
rs4953572_A	A / A	0.02 (↑)	66%	2.11 x 10 ⁻¹¹
rs1422070_A	A / A	-0.02 (↓)	60%	2.85 x 10 ⁻¹¹
rs1526194_T	T / C	-0.02 (↓)	58%	3.02 x 10 ⁻¹¹
rs13006483_T	G / G	0.03 (-)	28%	4.51 x 10 ⁻¹¹
rs2194028_T	C / C	0.02 (-)	34%	4.52 x 10 ⁻¹¹
rs9645660_T	C / C	-0.02 (-)	52%	7.43 x 10 ⁻¹¹
rs34550543_T	C / C	0.02 (-)	41%	1.40 x 10 ⁻¹⁰
rs8016028_T	T / T	-0.03 (↓)	81%	1.92 x 10 ⁻¹⁰
rs11168884_T	C / C	-0.02 (-)	34%	1.96 x 10 ⁻¹⁰
rs11820337_T	C / T	0.02 (↑)	35%	3.64 x 10 ⁻¹⁰
rs806188_T	T / C	0.02 (↑)	32%	5.65 x 10 ⁻¹⁰
rs9581731_T	T / T	-0.02 (↓)	71%	1.49 x 10 ⁻⁹
rs11227478_A	G / G	-0.02 (-)	21%	1.97 x 10 ⁻⁹
rs10081960_C	C / C	-0.02 (↓)	60%	2.96 x 10 ⁻⁹
rs5762532_T	T / T	-0.02 (↓)	59%	4.04 x 10 ⁻⁹
rs45527431_A	A / A	0.04 (↑)	91%	4.63 x 10 ⁻⁹
rs4676276_A	A / A	0.02 (↑)	52%	1.06 x 10 ⁻⁸
rs246628_C	C / C	0.02 (↑)	41%	1.06 x 10 ⁻⁸
rs1000565_A	A / G	0.02 (↑)	60%	1.66 x 10 ⁻⁸
rs4822384_T	T / T	-0.02 (↓)	39%	1.82 x 10 ⁻⁸
rs1398651_A	A / A	0.02 (↑)	56%	4.11 x 10 ⁻⁸
rs1424114_T	C / C	-0.02 (-)	35%	4.21 x 10 ⁻⁸
rs8012503_C	C / C	0.03 (↑)	88%	4.27 x 10 ⁻⁸
rs12414988_A	G / G	0.02 (-)	21%	4.75 x 10 ⁻⁸
rs6225113_A	C / C	0.02 (-)	37%	4.94 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.

