

★ Brain volume (Jansen, 2020)

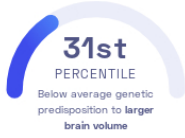
Phillip Jansen, et al.
Nature Communications

Brain

STUDY SUMMARY

Identification of 14 new genetic variants associated with brain volume.

YOUR RESULT



STUDY DESCRIPTION

Differences in brain volume among individuals appear to be connected with differences in numerous cognitive and behavioral traits, including intelligence and emotional processing. Furthermore, genes involved in determining brain volume have been linked to diseases such as schizophrenia and bipolar disorder. To identify genetic variants associated with brain volume, this study examined over 47,000 individuals of European descent. Researchers discovered 18 regions of the genome associated with brain volume, 14 of which were novel. Multiple genetic variants were linked to genes, including WNT3, PTEN, and AKT3, that have been previously implicated in conditions characterized by abnormal brain development. The researchers also found that 5 of the variants linked to brain volume in this study were previously associated with intelligence.

DID YOU KNOW?

Humans have the largest brain size relative to body size of any animal. However, in terms of absolute brain size, the sperm whale wins with a brain weighing in at 20 pounds.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to larger brain volume we summed up the effects of genetic variants that were linked to larger brain volume 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 larger brain volume. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to larger brain volume. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to larger brain volume. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for larger brain volume to be -8.43**. 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 larger brain volume is in the **31st percentile**. This means that it is higher than the polygenic scores 31% of people. We consider this to be a **below average genetic predisposition to larger brain volume**. 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 [Ⓞ] |
|----------------------|----------------------------|--------------------------|--------------------------------|---------------------------|
| rs62057149_A | G / G | 9.94 (-) | 87% | 2.72 x 10 ⁻²³ |
| rs2764264_T | T / T | 9.36 (↑) | 52% | 7.92 x 10 ⁻²¹ |
| rs288326_A | G / G | 6.94 (-) | 8% | 3.99 x 10 ⁻¹² |
| rs7297175_T | C / C | 6.84 (-) | 42% | 7.98 x 10 ⁻¹² |
| rs10927041_T | T / T | -6.84 (↓) | 88% | 8.16 x 10 ⁻¹² |
| rs1628768_T | C / C | -6.81 (-) | 82% | 9.71 x 10 ⁻¹² |
| rs42035_A | A / G | 6.70 (↑) | 81% | 2.10 x 10 ⁻¹¹ |
| rs34514405_A | A / A | -6.65 (↓) | 12% | 2.94 x 10 ⁻¹¹ |
| rs7970368_T | T / G | -6.41 (↓) | 84% | 1.42 x 10 ⁻¹⁰ |
| rs151057105_T | C / C | 6.32 (-) | 9% | 2.54 x 10 ⁻¹⁰ |
| rs41288837_T | NA | -5.97 (-) | 2% | 2.40 x 10 ⁻⁹ |
| rs3217870_T | C / C | -5.93 (-) | 33% | 3.02 x 10 ⁻⁹ |
| rs28675824_C | G / G | 5.90 (-) | 26% | 3.70 x 10 ⁻⁹ |
| rs73390208_T | C / T | -5.84 (↓) | 37% | 5.17 x 10 ⁻⁹ |
| rs112204843_T | C / C | -5.83 (-) | 5% | 5.65 x 10 ⁻⁹ |
| rs2237468_T | C / C | 5.81 (-) | 23% | 6.27 x 10 ⁻⁹ |
| rs11154343_T | C / T | -5.56 (↓) | 21% | 2.66 x 10 ⁻⁸ |
| rs478839_A | A / A | 5.47 (↑) | 65% | 4.55 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.