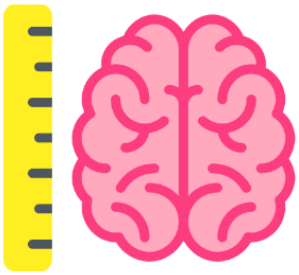
11/2019

Brain volume (Zhao, 2019)

Bingxin Zhao, et al.
Nature Genetics

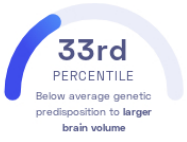
Brain



STUDY SUMMARY

Identification of 23 genetic variants associated with total brain volume.

YOUR RESULT



STUDY DESCRIPTION

Differences in brain volume among people 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 gain a deeper understanding of the contribution of genetics to the brain's total volume, this study examined the genomes of 19,629 individuals of European ancestry. The researchers found 23 genetic variants that correlate with total brain volume, many of which had not previously been discovered. The study also examined the correlation between brain volume and other traits, and found positive correlations between total brain volume and cognitive function, educational attainment, and proficiency working with numbers.

DID YOU KNOW?

While this study identified a correlation between brain volume and cognitive function, there are many things we can do to "train our brain". Practicing a musical instrument has been shown to improve cognitive function by forming strong connections between different parts of the brain. Reading and writing are also ways to give your brain a good workout!

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 effects 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 -0.18**. 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 **33rd percentile**. This means that it is higher than the polygenic scores 33% 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
rs11759026_G NEW	A / G	0.08 (↑)	25%	1.34×10^{-16}
rs1490384_C NEW	C / T	-0.06 (↓)	49%	2.26×10^{-15}
rs6584542_A NEW	A / A	0.07 (↑)	34%	2.56×10^{-14}
rs8756_C NEW	C / C	0.06 (↑)	45%	7.10×10^{-14}
rs118087478_G NEW	G / G	-0.07 (↓)	24%	7.74×10^{-14}
rs2764264_C NEW	T / T	-0.06 (-)	37%	5.06×10^{-13}
rs55938136_G NEW	NA	-0.07 (-)	2%	8.35×10^{-13}
rs7966895_G NEW	A / A	-0.06 (-)	34%	2.44×10^{-12}
rs12525327_G NEW	A / A	-0.06 (-)	24%	4.96×10^{-11}
rs117170334_G NEW	NA	0.21 (-)	2%	4.93×10^{-10}
rs199470_C NEW	C / C	-0.06 (↓)	38%	9.07×10^{-10}
rs8067056_C NEW	C / C	-0.05 (↓)	41%	6.05×10^{-9}
rs12202204_G NEW	A / A	-0.05 (-)	29%	1.88×10^{-8}
rs77126132_A NEW	G / G	0.08 (-)	12%	2.70×10^{-8}
rs7955865_A NEW	T / T	0.05 (-)	34%	2.76×10^{-8}
rs12938031_G NEW	G / G	-0.05 (↓)	39%	3.05×10^{-8}
rs796620802_A NEW	/	0.07 (-)	17%	3.84×10^{-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.