

☆ Loneliness (Abdellaoui, 2019)

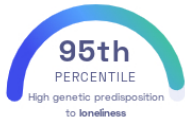
Abdel Abdellaoui, et al.
Human Molecular Genetics

Mind Behavior

STUDY SUMMARY

Detection of 19 genetic variants associated with feelings of loneliness.

YOUR RESULT



STUDY DESCRIPTION

Humans are social creatures and feelings of loneliness arise when we don't feel as socially connected as we want. Chronic loneliness has been correlated with elevated risks of various mental and physical diseases, and even premature death. While loneliness can be a result of social and environmental circumstances, some genetic factors may lead to a predisposition to loneliness. This study examined more than half a million people of European descent, discovering 19 genetic variants that may be associated with an increased propensity of feeling lonely. These variants help explain ~20% of the heritability of loneliness. Further, this study revealed that chronic loneliness is associated with a range of disorders, including heart disease, depression, and *obesity*.







DID YOU KNOW?

Volunteering is a great way to increase social connections while making an impact on the world around you. Find a cause you are passionate about and look for opportunities to get involved!

YOUR DETAILED RESULTS

To calculate your genetic predisposition to loneliness we summed up the effects of genetic variants that were linked to loneliness 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 loneliness. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to loneliness. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to loneliness. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for loneliness to be -0.08**. 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 loneliness is in the **95th percentile**. This means that it is higher than the polygenic scores 95% of people. We consider this to be a **high genetic predisposition to loneliness**. 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 [ⓘ]
rs599550_A	A / A	-0.03 (↓)	90%	5.88×10^{-14}
rs13291079_C	T / C	0.02 (↑)	40%	1.95×10^{-11}
rs4958586_A	G / A	-0.02 (↓)	56%	1.50×10^{-10}
rs12458015_C	T / T	-0.02 (-)	29%	1.16×10^{-9}
rs773020_A	A / A	-0.03 (↓)	93%	1.43×10^{-9}
rs74338595_C	C / C	0.02 (↑)	23%	2.19×10^{-9}
rs7826596_A	G / A	0.02 (↑)	61%	3.12×10^{-9}
rs171697_C	C / C	-0.02 (↓)	75%	4.84×10^{-9}
rs11867618_A	G / G	-0.02 (-)	13%	7.37×10^{-9}
rs7770860_C	T / C	-0.02 (↓)	31%	8.53×10^{-9}
rs348258_C	C / T	-0.02 (↓)	65%	1.06×10^{-8}
rs72627233_G	T / T	-0.02 (-)	19%	1.25×10^{-8}
rs10456089_A	G / G	0.04 (-)	7%	1.54×10^{-8}
rs11068917_A 	C / C	-0.02 (-)	20%	1.54×10^{-8}
rs82347916_A 	G / A	0.02 (↑)	35%	2.71×10^{-8}
rs2732660_C 	G / G	-0.02 (-)	87%	3.18×10^{-8}
rs11039265_A	C / A	0.02 (↑)	30%	4.57×10^{-8}
rs7209581_C	G / G	-0.02 (-)	54%	4.76×10^{-8}
rs159960_A 	A / G	0.02 (↑)	53%	4.77×10^{-8}