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Long QT syndrome (Lahrouchi, 2020)

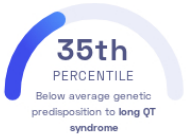
Najim Lahrouchi, et al.
Circulation

Heart

STUDY SUMMARY

Identification of 3 genomic regions associated with long QT syndrome.

YOUR RESULT



STUDY DESCRIPTION

The heartbeat is controlled by electrical impulses which normally pause between beats. During that pause, the heart muscles recharge for the next beat. If this recharge takes too long, an *electrocardiogram* will show a long QT interval. People with long QT intervals can be affected by a fast and chaotic heartbeat which may cause fainting, seizures, and even death. This study compared 1,656 European or Japanese individuals with long QT syndrome to 9,890 healthy controls and found three associated genomic regions.

DID YOU KNOW?

Some drugs can cause long QT syndrome.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to long QT syndrome we summed up the effects of genetic variants that were linked to long QT syndrome 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 long QT syndrome. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to long QT syndrome. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to long QT syndrome. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for long QT syndrome to be 0.27**. 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 long QT syndrome is in the **35th percentile**. This means that it is higher than the polygenic scores 35% of people. We consider this to be a **below average genetic predisposition to long QT syndrome**. 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
rs12143842_T NEW	C / T	0.27 (↑)	26%	1.09×10^{-11}
rs179405_A NEW	G / G	0.32 (-)	14%	1.92×10^{-8}
rs17061696_C NEW	G / G	0.22 (-)	37%	4.33×10^{-8}