1/2020

Heart failure (Shah, 2020)

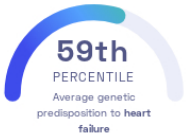
Sonia Shah, et al.
Nature Communications

Heart

STUDY SUMMARY

Identification of 12 genetic variants associated with the risk of heart failure.

YOUR RESULT



STUDY DESCRIPTION

Heart failure is a common condition affecting over 30 million people worldwide. It occurs when the heart is not strong enough to pump blood throughout the body. This typically results in fluid buildup in the body, which "congests" areas like the lungs and ankles. It is estimated that the heritability of heart failure is approximately 26%. This study examined the genomes of almost one million individuals of European ancestry to identify genetic regions associated with the risk of heart failure. The study identified 12 heart failure-associated genetic variants in 11 genomic regions, 10 of which are novel. Many of these regions are linked to heart development and function, body mass index, and coronary artery disease.

DID YOU KNOW?

A pacemaker is a device that uses electrical pulses to prompt the heart to beat at a normal rate. Pacemakers are used to treat multiple heart conditions including heart failure. In 1958, Arne Larrson received the first implantable pacemaker. He died at age 86 of a disease unrelated to his heart, outliving the surgeon who implanted his pacemaker.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to heart failure we summed up the effects of genetic variants that were linked to heart failure 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 heart failure. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to heart failure. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to heart failure. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for heart failure to be 0.66**. 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 heart failure is in the **59th percentile**. This means that it is higher than the polygenic scores 59% of people. We consider this to be an **average genetic predisposition to heart failure**. 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
rs17042102_A	G / G	0.11 (–)	12%	5.71×10^{-20}
rs1556516_C NEW	G / G	0.06 (–)	48%	1.57×10^{-15}
rs55730499_T NEW	C / C	0.10 (–)	7%	1.83×10^{-11}
rs140570886_C NEW	NA	0.22 (–)	2%	7.69×10^{-11}
rs660240_C NEW	C / C	0.06 (↑)	79%	3.25×10^{-10}
rs4746140_G NEW	G / G	0.07 (↑)	85%	1.10×10^{-9}
rs17617337_C	C / C	0.06 (↑)	78%	3.65×10^{-9}
rs600038_C NEW	C / T	0.06 (↑)	21%	3.68×10^{-9}
rs4135240_T NEW	T / C	0.05 (↑)	66%	6.84×10^{-9}
rs56094641_G NEW	A / G	0.05 (↑)	42%	1.21×10^{-8}
rs11745324_G NEW	G / G	0.05 (↑)	77%	2.35×10^{-8}
rs4766578_T NEW	T / A	0.04 (↑)	47%	4.90×10^{-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.