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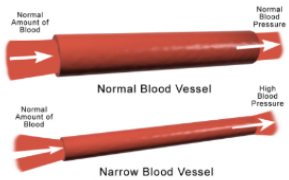
High blood pressure (Surendran, 2016)

Praveen Surendran, et al.
Nature Genetics

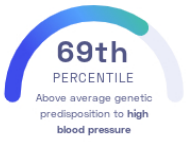
Vasculature | Blood



STUDY SUMMARY

This study links several cell signaling pathways to the risk of developing high blood pressure.

YOUR RESULT



STUDY DESCRIPTION

High blood pressure, also called hypertension, is a major risk factor for many diseases, including heart disease and stroke. High blood pressure is thought to be highly heritable, but the genetic factors that influence the risk of high blood pressure are not well understood. This large meta-analysis included ~350,000 individuals and identified 31 novel genetic variants associated with high blood pressure. These variants help explain ~2% of the heritability of high blood pressure. Several variants were linked to the solute carrier transporter pathway, which is responsible for the transport of many molecules across cell membranes. Notch signaling and the *RNA polymerase* I promoter clearance pathway also had genetic variants associated with high blood pressure. Notch signaling plays a role in the division of *neurons* and is crucial to normal embryonic development. The *RNA polymerase* I promoter clearance pathway is involved in transcription, which is part of the process that produces proteins.

DID YOU KNOW?

A healthy lifestyle can help reduce your risk of high blood pressure. Eating a healthy diet, exercising frequently, and limiting your alcohol consumption are all ways to prevent high blood pressure.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to high blood pressure we summed up the effects of genetic variants that were linked to high blood pressure 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 high blood pressure. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to high blood pressure. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to high blood pressure. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for high blood pressure to be 0.40**. 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 high blood pressure is in the **69th percentile**. This means that it is higher than the polygenic scores 69% of people. We consider this to be an **above average genetic predisposition to high blood pressure**. 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	COMMENTS	EFFECT SIZE	VARIANT FREQUENCY	SIGNIFICANCE
rs9349379_A	A / G	all ancestry	0.28 (↑)	57%	5.56×10^{-10}
rs7406910_T	C / C	all ancestry	-0.45 (–)	11%	6.51×10^{-10}
rs4387287_A NEW	A / C	all ancestry	0.36 (↑)	16%	9.12×10^{-10}
rs1008058_A	G / G	all ancestry	0.50 (–)	13%	2.86×10^{-9}
rs11229457_T	C / C	all ancestry	-0.30 (–)	23%	1.10×10^{-8}
rs35529250_T NEW	NA	all ancestry	-1.55 (–)	1%	2.42×10^{-8}
rs4728142_A NEW	G / A	all ancestry	-0.24 (↓)	43%	3.45×10^{-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.