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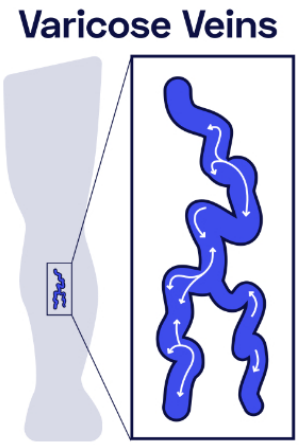
Varicose veins (Fukaya, 2018)

Eri Fukaya, et al.
Circulation

Vasculature



STUDY SUMMARY

Identification of 30 novel genetic variants linked with the development of varicose *vein*s.

YOUR RESULT

STUDY DESCRIPTION

Varicose *vein*s are a condition characterized by swollen and twisted *vein*s that occurs when blood pools, typically in the legs. Though varicose *vein*s are sometimes considered a cosmetic concern, they can also increase the risk of blood clots. To identify genetic variants that may predispose an individual to varicose *vein*s, this study examined the genomes of over 490,000 individuals of European ancestry. 30 newly discovered genetic loci were correlated with a predisposition to developing varicose *vein*s. Some of these variants are located near genes that play a role in the formation of arteries and *vein*s, while other variants are in proximity to genes that relate to the growth and development of our bones. This study also uncovered a new risk factor for the condition: the taller you are, the greater your risk of developing varicose *vein*s.

DID YOU KNOW?

You may be able to prevent or reduce the appearance of varicose veins by exercising regularly, wearing compression stockings during the day, and eating potassium-rich foods such as almonds and leafy vegetables.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to varicose veins we summed up the effects of genetic variants that were linked to varicose veins 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 varicose veins. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to varicose veins. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to varicose veins. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for varicose veins to be -1.31**. 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 varicose veins is in the **47th percentile**. This means that it is higher than the polygenic scores 47% of people. We consider this to be an **average genetic predisposition to varicose veins**. 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
rs11121615_T	C / T	-0.26 (↓)	48%	3.71×10^{-65}
rs2911463_A	A / A	-0.17 (↓)	72%	4.81×10^{-29}
rs2861819_C	G / C	0.16 (↑)	61%	1.40×10^{-23}
rs28558138_C	G / G	-0.14 (–)	42%	5.00×10^{-19}
rs8053360_A	G / A	-0.13 (↓)	66%	6.78×10^{-19}
rs3101725_C	C / C	-0.14 (↓)	84%	8.93×10^{-18}
rs11135046_T	T / T	-0.12 (↓)	45%	3.11×10^{-16}
rs7773004_G	A / G	-0.11 (↓)	62%	2.30×10^{-14}
rs12625547_G	T / G	-0.15 (↓)	18%	6.88×10^{-13}
rs236597_T	C / C	-0.12 (–)	75%	1.63×10^{-12}
rs7614922_C	G / G	0.14 (–)	16%	3.67×10^{-12}
rs73107980_T	C / T	0.11 (↑)	16%	7.61×10^{-11}
rs7469817_C	G / C	0.11 (↑)	66%	9.63×10^{-11}
rs2241173_G	G / G	-0.10 (↓)	56%	1.62×10^{-10}
rs816943_G	A / G	-0.09 (↓)	52%	1.98×10^{-10}
rs1061539_C	C / C	-0.11 (↓)	80%	1.59×10^{-9}
rs1549063_T	A / T	0.09 (↑)	35%	2.11×10^{-9}
rs16828263_C	NA	1.12 (–)	4%	4.37×10^{-9}
rs9719461_T	C / T	0.09 (↑)	69%	7.36×10^{-9}
rs2263321_A	G / G	-0.09 (–)	30%	8.42×10^{-9}
rs247749_C	T / C	0.10 (↑)	41%	8.77×10^{-9}
rs75522736_G	A / A	-0.12 (–)	16%	1.07×10^{-8}
rs553399706_A	NA	1.06 (–)	< 1%	1.32×10^{-8}
rs62512472_A	G / G	0.08 (–)	30%	1.38×10^{-8}
rs584768_A	A / A	0.08 (↑)	43%	1.43×10^{-8}
rs2089657_T	C / T	-0.10 (↓)	18%	2.41×10^{-8}
rs12594708_T	C / C	-0.17 (–)	10%	3.72×10^{-8}
rs186005582_T	NA	1.34 (–)	< 1%	4.24×10^{-8}
rs192647746_G	NA	0.86 (–)	< 1%	4.73×10^{-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.