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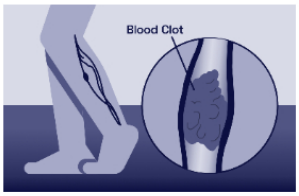
Venous thromboembolism (Lindstrom, 2019)

Sara Lindstrom, et al.
Blood

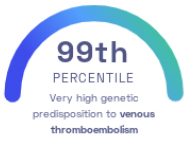
Vasculature



STUDY SUMMARY

Identification of novel genetic variants associated with venous thromboembolism.

YOUR RESULT



STUDY DESCRIPTION

Venous thromboembolism describes a condition where blood clots form in veins and block the flow of blood. Blood clots that break off and travel to organs can result in life-threatening conditions. Though venous thromboembolism is common, the contributing genetic risk factors are poorly understood. This genome-wide association study examined 200,000 individuals of European and African-American ancestry to identify genetic variants associated with venous thromboembolism. The study discovered 14 new variants, including 11 variants within genes not previously associated with venous thromboembolism. Many of these genes have been previously linked to counts and sizes of different types of blood cells. This suggests that blood traits may contribute to determining the risk of venous thromboembolism. Collectively, the genotyped variants explained 15% of the heritability of venous thromboembolism assuming disease *prevalence* of 0.5%.

DID YOU KNOW?

Movements such as walking and stretching can help blood circulate, which can reduce risks of clot formation.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to venous thromboembolism we summed up the effects of genetic variants that were linked to venous thromboembolism 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 venous thromboembolism. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to venous thromboembolism. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to venous thromboembolism. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for venous thromboembolism to be 1.24**. 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 venous thromboembolism is in the **99th percentile**. This means that it is higher than the polygenic scores 99% of people. We consider this to be a **very high genetic predisposition to venous thromboembolism**. 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
rs6025_T	NA	0.87 (-)	3%	1.40×10^{-188}
rs2519093_T	T / T	0.34 (↑)	21%	3.80×10^{-169}
rs579459_C	C / T	0.31 (↑)	23%	3.90×10^{-145}
rs2289252_T	C / C	0.17 (-)	40%	3.00×10^{-65}
rs2066864_A	G / A	0.18 (↑)	24%	2.00×10^{-59}
rs2036914_T	T / T	-0.15 (↓)	47%	1.60×10^{-54}
rs4253421_A NEW	A / G	-0.22 (↓)	12%	8.10×10^{-41}
rs191945075_A	NA	0.62 (-)	1%	9.50×10^{-32}
rs8176749_T	C / C	0.21 (-)	8%	2.30×10^{-30}
rs78707713_C	T / T	-0.19 (-)	12%	2.60×10^{-30}
rs4524_C	T / C	-0.13 (↓)	26%	3.10×10^{-29}
rs4548995_G	C / C	-0.11 (-)	22%	3.70×10^{-19}
rs3136516_G	G / A	0.08 (↑)	47%	1.00×10^{-15}
rs4541868_A	C / C	-0.08 (-)	25%	7.10×10^{-14}
rs1558519_G	A / A	0.08 (-)	35%	3.70×10^{-13}
rs12445050_T NEW	C / C	0.10 (-)	14%	6.70×10^{-13}
rs10886430_G NEW	A / A	0.11 (-)	13%	2.20×10^{-12}
rs1867312_C NEW	C / A	0.06 (↑)	43%	2.50×10^{-10}
rs6088735_T	C / T	0.08 (↑)	23%	3.00×10^{-10}
rs2842700_A NEW	C / C	0.13 (-)	6%	3.10×10^{-10}
rs4869589_T NEW	T / G	0.07 (↑)	26%	7.60×10^{-10}
rs7508633_G NEW	A / G	0.06 (↑)	45%	2.00×10^{-9}
rs12675621_G NEW	A / G	0.07 (↑)	29%	2.40×10^{-9}
rs1671135_G	C / C	-0.07 (-)	21%	2.90×10^{-9}
rs1048483_T NEW	T / T	0.06 (↑)	49%	3.40×10^{-9}
rs9373523_T	G / G	-0.06 (-)	42%	5.40×10^{-9}
rs867186_G	A / A	0.10 (-)	10%	6.80×10^{-9}
rs11158204_T NEW	C / C	-0.06 (-)	25%	1.50×10^{-8}
rs145470028_T NEW	NA	-0.25 (-)	2%	3.00×10^{-8}
rs143478537_G	G / G	0.08 (↑)	14%	3.10×10^{-8}
rs2851436_G NEW	T / T	-0.06 (-)	21%	3.90×10^{-8}
rs12450494_A NEW	T / A	0.06 (↑)	47%	1.00×10^{-7}
rs216311_T NEW	C / C	-0.02 (-)	39%	1.80×10^{-2}

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.