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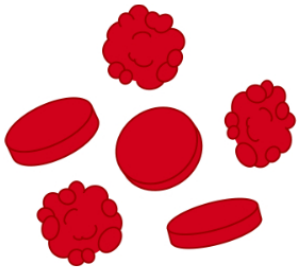
Chronic lymphocytic leukemia (Berndt, 2016)

Sonja I. Berndt, et al.
Nature Communications

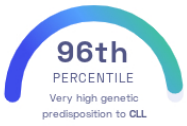
Cancer Blood



STUDY SUMMARY

Discovery of novel genetic variants associated with an increased risk of chronic lymphocytic leukemia.

YOUR RESULT



STUDY DESCRIPTION

Chronic lymphocytic leukemia (CLL) is a form of cancer that is characterized by an overproduction of lymphocytes (a type of white blood cells) that makes it difficult for the other blood cells to function properly. This study found multiple genetic variants that are associated with an increased risk of developing CLL after examining the genomes of 10,767 individuals of European ancestry. These newly discovered variants explain roughly 1% of the heritability for CLL, and nearly 17% when combined with previously discovered variants. The identified variants are found in genes that are involved in the process of apoptosis, or programmed cell death. Deregulation of apoptosis is known to contribute to many forms of cancer.

DID YOU KNOW?

Environmental factors, including some herbicides, pesticides, and radon exposure, have been linked to an increased risk of developing chronic lymphocytic leukemia.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to CLL we summed up the effects of genetic variants that were linked to CLL 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 CLL. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to CLL. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to CLL. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for CLL to be 2.63**. 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 CLL is in the **96th percentile**. This means that it is higher than the polygenic scores 96% of people. We consider this to be a **very high genetic predisposition to CLL**. 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
rs735665_A	G / G	0.49 (–)	15%	4.94×10^{-62}
rs872071_G	A / G	0.31 (↑)	31%	3.50×10^{-38}
rs13397985_G	T / G	0.38 (↑)	14%	2.32×10^{-34}
rs7176508_G	A / A	-0.30 (–)	66%	1.61×10^{-33}
rs17483466_G	A / A	0.33 (–)	15%	6.93×10^{-28}
rs13395354_T	C / T	-0.31 (↓)	18%	3.24×10^{-23}
rs4406737_G	A / G	0.22 (↑)	49%	3.26×10^{-19}
rs210134_G	G / G	0.21 (↑)	73%	8.68×10^{-16}
rs4987852_C	T / T	0.34 (–)	6%	7.00×10^{-13}
rs2466024_A	G / G	0.18 (–)	46%	8.70×10^{-13}
rs4987855_T	C / C	-0.30 (–)	6%	3.51×10^{-12}
rs9308731_A NEW	G / A	0.17 (↑)	54%	1.00×10^{-11}
rs10936599_T	C / C	-0.19 (–)	22%	1.04×10^{-11}
rs9880772_A NEW	G / A	0.17 (↑)	47%	2.55×10^{-11}
rs7169431_G	G / G	-0.27 (↓)	87%	1.27×10^{-10}
rs10069690_T	C / T	0.18 (↑)	35%	2.54×10^{-10}
rs757978_T	C / T	0.24 (↑)	10%	5.33×10^{-10}
rs305061_T	T / T	0.16 (↑)	74%	1.92×10^{-9}
rs7944004_G	T / T	-0.15 (–)	48%	2.00×10^{-9}
rs9273012_G	A / G	0.17 (↑)	30%	5.21×10^{-9}
rs7231647_A	G / A	0.15 (↑)	56%	5.59×10^{-9}
rs17246404_T	C / C	-0.15 (–)	20%	6.38×10^{-9}
rs3769825_G	A / A	-0.14 (–)	46%	1.03×10^{-8}
rs898518_A	A / A	0.15 (↑)	57%	1.09×10^{-8}
rs2511714_G	T / G	0.15 (↑)	42%	1.47×10^{-8}
rs2236256_A	C / C	-0.13 (–)	53%	1.91×10^{-8}
rs73718779_T NEW	C / C	0.23 (–)	11%	1.97×10^{-8}
rs9815073_C NEW	C / C	0.17 (↑)	65%	3.62×10^{-8}