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Acute lymphoblastic leukaemia (Vijayakrishnan, 2019)

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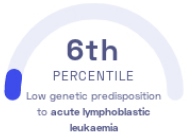
Cancer Blood

STUDY SUMMARY

Discovery of 4 novel genetic variants associated with acute lymphoblastic leukaemia (ALL).

YOUR RESULT



STUDY DESCRIPTION

Acute lymphoblastic leukaemia (ALL) is a type of blood cancer that leads to a debilitating overproduction of lymphocytes, a type white blood cells. ALL is the most common cancer for young children, accounting for around 85% of all cases. To identify genetic variants that may contribute to the development of ALL, this genome-wide association study analyzed the genomes of nearly 22,000 individuals of European ancestry. The study discovered 16 ALL-associated genetic variants, of which 4 were novel. The study estimated that the identified loci collectively explain 31% of the variance in genetic risk of ALL.

DID YOU KNOW?

Chemotherapy is an effective treatment for ALL. The overall cure rate is ~ 40%.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to acute lymphoblastic leukaemia we summed up the effects of genetic variants that were linked to acute lymphoblastic leukaemia 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 acute lymphoblastic leukaemia. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to acute lymphoblastic leukaemia. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to acute lymphoblastic leukaemia. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for acute lymphoblastic leukaemia to be 2.48**. 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 acute lymphoblastic leukaemia is in the **6th percentile**. This means that it is higher than the polygenic scores 6% of people. We consider this to be a **low genetic predisposition to acute lymphoblastic leukaemia**. 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
rs10821936_C	T / T	0.59 (–)	33%	1.19×10^{-106}
rs17133805_G	T / T	0.50 (–)	32%	5.28×10^{-71}
rs113650570_A	NA	0.84 (–)	2%	8.06×10^{-35}
rs2239630_A	A / G	0.25 (↑)	45%	1.72×10^{-21}
rs2296624_C	C / T	0.22 (↑)	67%	2.79×10^{-16}
rs3824662_A	C / C	0.25 (–)	19%	3.57×10^{-14}
rs12779301_C	C / C	0.20 (↑)	66%	5.72×10^{-13}
rs75777619_G	A / A	0.23 (–)	12%	2.30×10^{-9}
rs17481869_A	C / C	0.55 (–)	8%	2.37×10^{-9}
rs9976326_T	A / A	0.29 (–)	25%	4.79×10^{-9}
rs886285_T NEW	T / C	0.25 (↑)	34%	1.56×10^{-8}
rs10853104_T NEW	C / C	0.29 (–)	47%	1.82×10^{-8}
rs76925697_A NEW	A / A	0.42 (↑)	96%	2.11×10^{-8}
rs210143_C NEW	C / C	0.26 (↑)	73%	2.21×10^{-8}
rs4762284_T	A / A	0.14 (–)	32%	3.75×10^{-7}

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.