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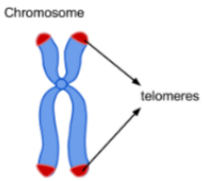
Thyroid cancer (Gudmundsson, 2017)

Julius Gudmundsson, et al.
Nature Communications

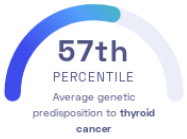
Cancer Thyroid



STUDY SUMMARY

Thyroid cancer is associated with genetic variants linked to the regulation of telomere length.

YOUR RESULT



STUDY DESCRIPTION

The thyroid is a gland at the bottom of the neck that produces hormones that regulate blood pressure, weight, and heart rate. Thyroid cancer is known to have one of the strongest genetic components of any cancer. Therefore, this study examined patients with thyroid cancer in order to identify genetic variants associated with the disease. In addition to confirming previously identified genetic variants, the study found 5 new variants by examining over 290,000 individuals of European descent. Interestingly, 3 of the identified variants are near genes that play a role in regulating telomere length. Telomeres are repetitive sequences of DNA that protect chromosomes from degradation or damage.

DID YOU KNOW?

Eating a healthy diet rich in fruits and vegetables may reduce your risk of thyroid cancer among other diseases.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to thyroid cancer we summed up the effects of genetic variants that were linked to thyroid cancer 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 thyroid cancer. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to thyroid cancer. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to thyroid cancer. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for thyroid cancer to be 2.83**. 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 thyroid cancer is in the **57th percentile**. This means that it is higher than the polygenic scores 57% of people. We consider this to be an **average genetic predisposition to thyroid cancer**. 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
rs1588635_A	C / C	0.52 (–)	40%	2.00×10^{-58}
rs11693806_C	G / G	0.36 (–)	32%	1.50×10^{-24}
rs368187_G	G / C	0.33 (↑)	58%	5.10×10^{-23}
rs2466076_G	G / G	0.28 (↑)	48%	1.50×10^{-17}
rs116909374_T	NA	0.59 (–)	3%	1.10×10^{-16}
rs12129938_A NEW	A / A	0.28 (↑)	80%	4.00×10^{-11}
rs7902587_T NEW	C / T	0.34 (↑)	11%	5.40×10^{-11}
rs73227498_A NEW	A / A	0.31 (↑)	87%	3.00×10^{-10}
rs2289261_C NEW	G / G	0.21 (–)	68%	3.10×10^{-9}
rs6793295_T NEW	T / T	0.21 (↑)	80%	2.70×10^{-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.