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Thyroid cancer (Liyanarachchi, 2020)

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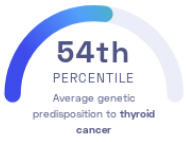
Metabolism | Thyroid | Cancer

STUDY SUMMARY

Development of a polygenic risk score for thyroid cancer based on 10 previously identified genetic variants.

YOUR RESULT



STUDY DESCRIPTION

The thyroid is a butterfly-shaped gland in the front of the neck that produces *hormones* which control important bodily functions like blood pressure, temperature, and heart rate. Thyroid cancer is more heritable than most other cancer types, and it affects over 50,000 individuals each year in the United States. This study developed a polygenic score based on 10 previously identified genetic variants to predict the risk of papillary thyroid cancer, the most common type of thyroid cancer. The researchers found that the score explained roughly 8% of the heritability of thyroid cancer in their study group. The prediction became more accurate when the polygenic score was used together with clinical factors to predict the risk of thyroid cancer risk. The study also showed that individuals in the 90th percentile had roughly a 7-times greater risk of thyroid cancer compared to the individuals in the 10th percentile.

DID YOU KNOW?

Despite being a highly heritable disease, radiation exposure, obesity, and consuming a diet high in iodine may all increase the risk of developing papillary thyroid cancer.

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 2.29**. 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 **54th percentile**. This means that it is higher than the polygenic scores 54% 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
rs12129938_A	A / A	0.18 (↑)	81%	5.00×10^{-8}
rs11693806_C	G / G	0.36 (-)	32%	5.00×10^{-8}
rs6793295_T	T / T	0.18 (↑)	76%	5.00×10^{-8}
rs73227498_A	A / A	0.25 (↑)	89%	5.00×10^{-8}
rs2466076_G	G / G	0.28 (↑)	53%	5.00×10^{-8}
rs1588635_A	C / C	0.49 (-)	48%	5.00×10^{-8}
rs7902587_T	C / T	0.22 (↑)	12%	5.00×10^{-8}
rs368187_G	G / C	0.29 (↑)	63%	5.00×10^{-8}
rs116909374_T	NA	0.54 (-)	4%	5.00×10^{-8}
rs2289261_C	G / G	0.13 (-)	70%	5.00×10^{-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.