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Squamous cell carcinoma (Sarin, 2020)

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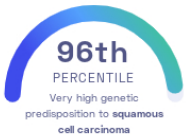
Skin Cancer

STUDY SUMMARY

Identification of 8 novel genomic variants associated with cutaneous *squamous cell* carcinoma (SCC).

YOUR RESULT



STUDY DESCRIPTION

Cutaneous *squamous cell* carcinoma (SCC) is the second most common form of skin cancer. Most SCCs can be easily removed, but if left untreated, they can grow deeper into the skin and the cancer cells can spread to other parts of the body. This study combined data from nearly 700,000 individuals of European descent to identify genetic variants associated with SCC. The researchers discovered 14 previously known genetic variants, as well as 8 novel variants. Collectively, these genetic variants explain roughly 9% of the heritability of SCC. Many of the variants are near genes related to skin functions and the immune system, as well as genes known to play a role in other cancers.

DID YOU KNOW?

To reduce your risk of skin cancer, dermatologists recommend seeking shade when appropriate, wearing protective clothing and using sunscreen.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to squamous cell carcinoma we summed up the effects of genetic variants that were linked to squamous cell carcinoma 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 squamous cell carcinoma. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to squamous cell carcinoma. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to squamous cell carcinoma. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for squamous cell carcinoma to be 1.08**. 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 squamous cell carcinoma 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 squamous cell carcinoma**. 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
rs12203592_T	C / C	0.44 (-)	17%	1.33×10^{-221}
rs1805007_T	C / T	0.38 (↑)	8%	5.55×10^{-87}
rs6059655_A	A / G	0.25 (↑)	8%	8.42×10^{-40}
rs1126809_A	G / G	0.15 (-)	28%	2.21×10^{-38}
rs35407_A	NA	-0.47 (-)	4%	5.81×10^{-31}
rs4455710_T	T / T	0.14 (↑)	37%	5.57×10^{-21}
rs10810657_T	A / A	-0.10 (-)	40%	1.26×10^{-17}
rs6791479_T	T / A	0.09 (↑)	43%	6.09×10^{-16}
rs1800407_T	C / T	0.16 (↑)	7%	5.12×10^{-14}
rs7939541_C NEW	T / T	0.08 (-)	41%	9.23×10^{-12}
rs57994353_C	T / T	0.09 (-)	28%	1.84×10^{-11}
rs62246017_A	A / A	0.07 (↑)	33%	1.65×10^{-9}
rs657187_G NEW	A / G	-0.07 (↓)	42%	1.80×10^{-9}
rs7834300_G NEW	G / C	0.07 (↑)	44%	2.01×10^{-9}
rs10200279_T NEW	T / T	0.07 (↑)	29%	2.67×10^{-9}
rs10944479_A NEW	G / A	-0.09 (↓)	19%	3.75×10^{-9}
rs10399947_A NEW	A / A	-0.07 (↓)	36%	6.65×10^{-9}
rs117132860_A	NA	0.25 (-)	2%	7.97×10^{-9}
rs721199_T NEW	T / C	-0.06 (↓)	46%	3.55×10^{-8}
rs1325118_C NEW	C / T	-0.07 (↓)	30%	4.38×10^{-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.