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Nasal polyps (Kristjansson, 2019)

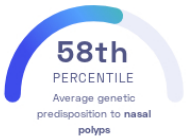
Ragnar Kristjansson, et al.
Nature Genetics

Nose

STUDY SUMMARY

Identification of 10 variants associated with the risk of developing nasal polyps.

YOUR RESULT



STUDY DESCRIPTION

Nasal polyps are growths that form along the lining of the nasal cavity. While not cancerous, they can eventually cause blockage of the nasal passage leading to breathing problems and a loss of smell. At the time of the publication of this study, no genetic risk factors for nasal polyp were known. This study examined the genomes of over 700,000 individuals of European descent and discovered 10 genetic variants, many near genes that play a role in inflammation. It was previously reported that chronic nasal inflammation increases the risk of developing nasal polyps. The findings of this study shed some light on this connection.

DID YOU KNOW?

Because dry air can trigger inflammation of the nasal cavity, the use of a humidifier may help prevent recurring inflammation and the development of polyps.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to nasal polyps we summed up the effects of genetic variants that were linked to nasal polyps 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 nasal polyps. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to nasal polyps. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to nasal polyps. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for nasal polyps to be -0.50**. 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 nasal polyps is in the **58th percentile**. This means that it is higher than the polygenic scores 58% of people. We consider this to be an **average genetic predisposition to nasal polyps**. 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
rs1391371_T NEW	A / A	0.39 (–)	19%	7.30×10^{-49}
rs1888909_T NEW	T / C	0.29 (↑)	25%	7.40×10^{-32}
rs1837253_T NEW	T / C	-0.30 (↓)	27%	3.70×10^{-29}
rs34210653_A NEW	NA	-1.14 (–)	3%	8.00×10^{-27}
rs1444782_A NEW	G / A	-0.17 (↓)	40%	1.10×10^{-14}
rs17718444_T NEW	C / T	-0.16 (↓)	30%	1.30×10^{-11}
rs338698_A NEW	C / A	-0.15 (↓)	50%	5.60×10^{-11}
rs6543124_A NEW	T / T	-0.14 (–)	38%	7.40×10^{-10}
rs174535_C NEW	T / T	-0.14 (–)	36%	3.50×10^{-9}
rs1050152_T NEW	C / C	-0.13 (–)	40%	1.10×10^{-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.