6/2016

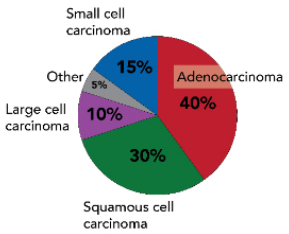
Lung cancer (McKay, 2017)

James McKay, et al.
Nature Genetics

Lung Cancer

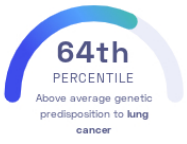
STUDY SUMMARY

Identification of 4 novel genomic regions associated with lung cancer.



Adenocarcinoma and squamous cell carcinoma are the most common types of lung cancer.

YOUR RESULT



Above average genetic predisposition to **lung cancer**

STUDY DESCRIPTION

Lung cancer is a condition in which cells in the lungs divide uncontrollably. It is the leading cause of cancer-related deaths in the United States. There are two main types of lung cancer: small cell lung cancer and non-small cell cancer, with the latter comprising 80 to 85% of all lung cancers. Although smoking is the most common risk factor associated with lung cancer, genetics is also thought to play a role. Therefore, by examining ~85,000 genomes, this study aimed to understand the genetic factors associated with the risk of developing lung cancer. The researchers identified 18 genetic variants associated with lung cancer, 10 of which are novel. Of the novel regions, 4 are associated with lung cancer overall. Some of these regions have been previously associated with addiction and smoking behavior. Overall, the genetic variants identified help explain 8.9% of the heritability of lung cancer.

DID YOU KNOW?

While smoking is the leading cause of lung cancer, exposure to radon, an invisible, radioactive gas also contributes to the risk. Radon is released from the normal decay of the elements uranium, thorium, and radium in rocks and soil. Houses that are built on soil rich in these elements can have higher radon levels in the air.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to lung cancer we summed up the effects of genetic variants that were linked to lung 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 lung cancer. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to lung cancer. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to lung cancer. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for lung cancer to be 0.26**. 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 lung cancer is in the **64th percentile**. This means that it is higher than the polygenic scores 64% of people. We consider this to be an **above average genetic predisposition to lung 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
rs55781567_G	C / C	0.26 (–)	37%	3.10×10^{-103}
rs56113850_T	C / C	-0.13 (–)	44%	5.00×10^{-19}
rs11571833_T	NA	0.47 (–)	1%	6.10×10^{-16}
rs71658797_A NEW	T / A	0.12 (↑)	10%	3.30×10^{-11}
rs6920364_C NEW	C / C	0.07 (↑)	46%	1.30×10^{-8}
rs11780471_A NEW	G / G	-0.14 (–)	6%	1.70×10^{-8}
rs66759488_A NEW	G / G	0.07 (–)	36%	2.80×10^{-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.