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## ☆ Lung adenocarcinoma (McKay, 2017)

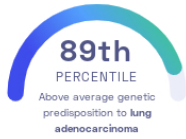
James McKay, et al.  
Nature Genetics

Cancer Lung

### STUDY SUMMARY

Identification of 6 novel genomic regions associated with lung adenocarcinoma.

#### YOUR RESULT



#### STUDY DESCRIPTION







Lung cancer is a condition in which cells in the lungs divide uncontrollably. Lung adenocarcinoma is a subtype that accounts for ~40% of all lung cancers. It is caused by mutations in mucus-producing glandular cells of the lungs. On average, lung adenocarcinoma tends to grow more slowly than other subtypes of lung cancer. To better understand the genetic basis of lung adenocarcinoma, this study examined the genomes of ~67,000 individuals. The researchers identified 6 new regions associated with lung adenocarcinoma. Half of these regions are located near genes related to *telomere* length, which shortens with age. Overall, the genetic variants identified help explain 6.7% of the heritability of lung adenocarcinoma.

#### DID YOU KNOW?

The most common type of lung cancer in women is adenocarcinoma. Moreover, adenocarcinoma is least associated with smoking.

#### YOUR DETAILED RESULTS

To calculate your genetic predisposition to lung adenocarcinoma we summed up the effects of genetic variants that were linked to lung adenocarcinoma 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 adenocarcinoma. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to lung adenocarcinoma. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to lung adenocarcinoma. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for lung adenocarcinoma to be 0.53**. 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 adenocarcinoma is in the **89th percentile**. This means that it is higher than the polygenic scores 89% of people. We consider this to be an **above average genetic predisposition to lung adenocarcinoma**. 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 <sup>Ⓞ</sup>	YOUR GENOTYPE <sup>Ⓞ</sup>	EFFECT SIZE <sup>Ⓞ</sup>	VARIANT FREQUENCY <sup>Ⓞ</sup>	SIGNIFICANCE <sup>Ⓞ</sup>
rs7705526_A	C / A	0.22 (↑)	34%	$3.80 \times 10^{-35}$
rs77468143_G 	T / T	-0.15 (-)	25%	$1.70 \times 10^{-16}$
rs13080835_T	G / T	-0.11 (↓)	49%	$7.50 \times 10^{-12}$
rs11591710_C 	A / C	0.15 (↑)	14%	$6.30 \times 10^{-11}$
rs4236709_G 	A / A	0.12 (-)	22%	$1.30 \times 10^{-10}$
rs1056562_T 	T / C	0.10 (↑)	47%	$2.80 \times 10^{-10}$
rs885518_G 	A / G	0.16 (↑)	10%	$1.00 \times 10^{-9}$
rs41309931_T 	G / G	0.16 (-)	12%	$1.30 \times 10^{-9}$