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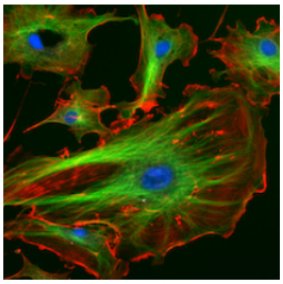
Prostate cancer (Schumacher, 2011)

Fredrick R. Schumacher, et al.
Human Molecular Genetics

Prostate | Cancer



Cytoplasmic filaments that form the cytoskeleton.

STUDY SUMMARY

Prostate cancer may be linked to variants in the MLPH gene and genes that encode proteins of cytoplasmic filaments.

YOUR RESULT

49th
PERCENTILE
Average genetic predisposition to **prostate cancer**

STUDY DESCRIPTION

Prostate cancer is the most common cancer among men after skin cancer. It occurs in the prostate - a gland in males that produces the seminal fluid. To identify novel genetic variants associated with prostate cancer, this study examined the genomes of 7,240 individuals. The most significant variant found was in the MLPH gene which plays an essential role in the development of skin and hair pigmentation. The study also identified variants in nearby genes that play a role in the formation of cytoplasmic filaments which are strands of protein molecules that are important for cell shape, movement, and signaling.

DID YOU KNOW?

Although there are no known prevention methods for prostate cancer, living a healthy lifestyle should reduce your risk for this disease. Increasing fruits and vegetables while reducing dairy products in your diet and exercising for 30 minutes most days of the week may help prevent prostate cancer.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to prostate cancer we summed up the effects of genetic variants that were linked to prostate 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 prostate cancer. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to prostate cancer. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to prostate cancer. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for prostate cancer to be 0.09**. 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 prostate cancer is in the **49th percentile**. This means that it is higher than the polygenic scores 49% of people. We consider this to be an **average genetic predisposition to prostate 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
rs651164_A	G / G	-0.16 (–)	68%	1.40×10^{-13}
rs13252298_G	A / A	-0.16 (–)	76%	4.50×10^{-12}
rs7629490_T	C / C	0.14 (–)	68%	1.90×10^{-10}
rs11228594_G	G / G	-0.14 (↓)	24%	1.20×10^{-9}
rs902774_A NEW	G / G	0.16 (–)	16%	4.70×10^{-9}
rs742134_G	G / G	0.18 (↑)	13%	5.60×10^{-9}
rs2292884_G NEW	A / A	0.13 (–)	25%	4.30×10^{-8}