

★ Bladder cancer (Figueroa, 2014)

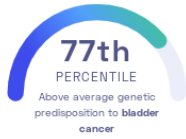
Jonine D. Figueroa, et al.
Human Molecular Genetics

Cancer Bladder

STUDY SUMMARY

Bladder cancer may be associated with genes linked to *telomere* length and inflammation.

YOUR RESULT



STUDY DESCRIPTION



Bladder cancer is one of the most common cancers worldwide. Men are three to four times more likely to develop bladder cancer than women. Prior to this study, 11 genetic variants were known to be associated with bladder cancer. This study identified 4 more variants in a cohort of 18,725 individuals of European descent. One of the genetic variants has previously been associated with colorectal cancer and is near a gene that affects *telomere* length. *Telomeres* are structures at the end of *chromosomes* that protect them from deterioration. *Telomere* length shortens with age, exposing the ends of *chromosomes* and allowing DNA damage to occur. The second significant variant is linked to a gene that controls inflammation, which is an important factor in bladder cancer development.

DID YOU KNOW?

Although age and gender are key risk factors, you can reduce your risk for bladder cancer by following all chemical safety rules (if you work with or around chemicals), staying properly hydrated, and eating a well-balanced diet.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to bladder cancer we summed up the effects of genetic variants that were linked to bladder 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 bladder cancer. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to bladder cancer. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to bladder cancer. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for bladder cancer to be 1.34**. 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 bladder cancer is in the **77th percentile**. This means that it is higher than the polygenic scores 77% of people. We consider this to be an **above average genetic predisposition to bladder 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 [Ⓞ]
rs9642880_T	G / T	0.22 (↑)	46%	3.55×10^{-38}
rs798766_T	C / C	0.20 (-)	20%	7.06×10^{-25}
rs2294008_T	C / T	0.12 (↑)	46%	2.75×10^{-16}
rs1014971_T	C / T	0.12 (↑)	62%	9.76×10^{-12}
rs8102137_C	T / C	0.12 (↑)	33%	1.22×10^{-11}
rs710521_T	T / T	0.13 (↑)	73%	1.92×10^{-11}
rs401681_C	C / C	0.11 (↑)	56%	4.27×10^{-11}
rs1495741_A	G / A	0.13 (↑)	78%	1.77×10^{-10}
rs10936599_T 	C / C	-0.16 (-)	24%	4.53×10^{-9}
rs907611_A 	G / A	0.14 (↑)	31%	4.11×10^{-8}