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Colorectal cancer (Huyghe, 2018)

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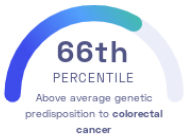
Intestines | Cancer

STUDY SUMMARY

Genetic variants in genes involved in *transcription*, cell signaling, and the immune system are associated with the risk of colorectal cancer.

YOUR RESULT



STUDY DESCRIPTION

Colorectal cancer occurs in either the colon or rectum, which are parts of the large intestine. It is the third most common cancer in the United States, but genetic risk factors of colorectal cancer remain poorly understood. This study examined 125,478 individuals of European and East Asian descent and discovered 30 novel genetic variants associated with the risk of colorectal cancer. A particularly strong association was detected for a genetic variant near the CHD1 gene which is involved in the regulation of *transcription*. Other discovered variants were in genes that play a role in cell signaling and the immune system.

DID YOU KNOW?

Regular colorectal cancer screening, especially after the age of 45, is recommended. Maintaining a healthy weight and limiting red or processed meats may also help lower your risk of colorectal cancer.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to colorectal cancer we summed up the effects of genetic variants that were linked to colorectal 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 colorectal cancer. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to colorectal cancer. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to colorectal cancer. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for colorectal cancer to be 7.38**. 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 colorectal cancer is in the **66th percentile**. This means that it is higher than the polygenic scores 66% of people. We consider this to be an **above average genetic predisposition to colorectal 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
rs11874392_A	A / T	0.16 (↑)	54%	3.80×10^{-74}
rs6983267_G	G / T	0.15 (↑)	52%	3.40×10^{-64}
rs58658771_A	T / A	0.14 (↑)	19%	6.00×10^{-37}
rs16892766_C	A / A	0.18 (–)	80%	3.90×10^{-32}
rs3087967_T	C / C	0.11 (–)	29%	1.90×10^{-31}
rs1741640_C	T / C	0.11 (↑)	76%	1.10×10^{-26}
rs2735940_G	A / G	0.09 (↑)	49%	5.10×10^{-25}
rs12372718_G	A / A	0.09 (–)	39%	1.90×10^{-23}
rs28840750_T	T / T	0.19 (↑)	94%	3.70×10^{-23}
rs189583_G	G / C	0.10 (↑)	32%	1.20×10^{-22}
rs35107139_C	A / A	0.09 (–)	42%	1.80×10^{-22}
rs11255841_T	T / T	0.09 (↑)	70%	2.10×10^{-21}
rs12514517_A	A / A	0.10 (↑)	28%	3.70×10^{-21}
rs7121958_G	G / G	0.08 (↑)	51%	1.40×10^{-20}
rs3217810_T	C / C	0.12 (–)	12%	3.60×10^{-19}
rs75954926_G NEW	A / G	0.09 (↑)	65%	3.00×10^{-18}
rs704017_G	G / G	0.08 (↑)	58%	5.20×10^{-18}
rs35470271_G	A / A	0.10 (–)	15%	1.20×10^{-16}
rs6678617_A	A / G	0.08 (↑)	58%	2.40×10^{-16}
rs597808_G	A / G	0.08 (↑)	51%	2.60×10^{-16}
rs61389091_C NEW	C / C	0.19 (↑)	96%	3.70×10^{-16}
rs17011141_G	A / A	0.09 (–)	20%	6.10×10^{-16}
rs4976270_C	T / T	0.07 (–)	55%	4.80×10^{-15}
rs6066825_A	A / G	0.07 (↑)	64%	5.90×10^{-15}
rs11190164_G	A / G	0.08 (↑)	26%	6.80×10^{-15}
rs28488_T NEW	C / T	0.07 (↑)	63%	2.60×10^{-14}
rs4813802_G	T / G	0.07 (↑)	35%	7.10×10^{-14}
rs7300312_C	T / C	0.07 (↑)	57%	7.50×10^{-14}
rs9271695_G NEW	A / G	0.09 (↑)	79%	1.10×10^{-13}
rs56324967_C NEW	T / C	0.07 (↑)	67%	1.10×10^{-13}
rs16969681_T	C / C	0.10 (–)	90%	1.40×10^{-13}
rs11087784_G	A / A	0.09 (–)	15%	2.70×10^{-13}
rs7333607_G NEW	A / A	0.08 (–)	24%	6.30×10^{-13}
rs6063514_C	C / T	0.07 (↑)	60%	7.60×10^{-13}
rs4968127_G	G / A	0.07 (↑)	36%	1.30×10^{-12}
rs755229494_G	NA	0.63 (–)	< 1%	2.10×10^{-12}
rs12246635_C	T / T	0.10 (–)	90%	4.90×10^{-12}
rs1078643_A NEW	A / A	0.08 (↑)	76%	6.60×10^{-12}
rs983402_T NEW	C / C	0.07 (–)	33%	7.70×10^{-12}

rs994308_C	C / C	0.06 (↑)	59%	8.60×10^{-12}
rs174533_G	G / G	0.07 (↑)	67%	1.20×10^{-11}
rs3731861_T	C / C	0.06 (–)	62%	1.50×10^{-11}
rs35808169_C	T / T	0.08 (–)	17%	1.50×10^{-11}
rs12144319_C	T / T	0.07 (–)	25%	3.30×10^{-11}
rs17094983_G	G / G	0.09 (↑)	87%	4.60×10^{-11}
rs17816465_A	G / A	0.07 (↑)	20%	1.40×10^{-10}
rs2516420_C	C / C	0.11 (↑)	92%	2.00×10^{-10}
rs78341008_C	T / T	0.11 (–)	7%	3.20×10^{-10}
rs2250430_T	A / A	0.07 (–)	70%	3.30×10^{-10}
rs7160450_T	T / T	0.06 (↑)	37%	4.00×10^{-10}
rs34797592_T	C / C	0.09 (–)	11%	4.20×10^{-10}
rs10821907_C	C / C	0.08 (↑)	82%	5.00×10^{-10}
rs3133285_G	G / G	0.07 (↑)	82%	6.00×10^{-10}
rs11610543_G	G / G	0.05 (↑)	50%	1.30×10^{-9}
rs2186607_T	T / A	0.05 (↑)	52%	1.50×10^{-9}
rs8000189_T	C / T	0.06 (↑)	64%	1.80×10^{-9}
rs4313119_G	G / G	0.06 (↑)	74%	2.10×10^{-9}
rs3217874_T	T / T	0.06 (↑)	38%	2.40×10^{-9}
rs62404966_C	C / T	0.06 (↑)	76%	2.60×10^{-9}
rs10980628_C	T / T	0.07 (–)	21%	2.80×10^{-9}
rs11884596_C	T / T	0.06 (–)	38%	3.60×10^{-9}
rs7708610_A	G / G	0.06 (–)	45%	3.80×10^{-9}
rs4360494_G	G / C	0.05 (↑)	45%	3.80×10^{-9}
rs78368589_T	C / C	0.11 (–)	6%	4.10×10^{-9}
rs12149163_T	T / T	0.05 (↑)	49%	5.40×10^{-9}
rs983318_A	G / A	0.06 (↑)	25%	5.60×10^{-9}
rs145364999_T	T / T	0.55 (↑)	99%	6.30×10^{-9}
rs6031311_T	T / T	0.06 (↑)	76%	6.80×10^{-9}
rs4759277_A	C / C	0.05 (–)	35%	9.40×10^{-9}
rs13149359_A	A / A	0.05 (↑)	36%	1.20×10^{-8}
rs1391441_A	A / A	0.05 (↑)	67%	1.60×10^{-8}
rs9930005_C	C / A	0.05 (↑)	43%	2.10×10^{-8}
rs72942485_G	G / G	0.17 (↑)	98%	2.10×10^{-8}
rs11727676_C	T / C	0.09 (↑)	10%	2.90×10^{-8}
rs9924886_A	A / C	0.06 (↑)	73%	3.10×10^{-8}
rs34405347_T	T / T	0.09 (↑)	90%	3.10×10^{-8}
rs16878812_A	A / A	0.08 (↑)	88%	3.60×10^{-8}
rs73068325_T	C / T	0.07 (↑)	18%	4.20×10^{-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.