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Crohn's disease (Franke, 2010)

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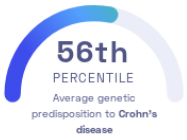
Inflammation | Intestines

STUDY SUMMARY

Identification of 71 genetic variants associated with Crohn's disease.

YOUR RESULT



STUDY DESCRIPTION

Crohn's disease is a type of inflammatory bowel disease, a condition characterized by chronic inflammation of the digestive tract. Nearly a million individuals in the United States alone are affected by Crohn's disease. Typical symptoms are pain, diarrhea and weight loss. To better understand the genetics of Crohn's disease, this study examined over 40,000 individuals of European descent. The analysis uncovered 71 Crohn's disease-associated genetic variants, including 39 variants that are reported for the first time. Together, these 71 variants explain about 23% of the heritability of Crohn's disease. Many of the identified genetic variants are near genes that play a role in controlling the body's immune system. Some of these genes have been previously implicated in other inflammatory conditions such as *ulcerative colitis* and *rheumatoid arthritis*.

DID YOU KNOW?

Because there is no cure for Crohn's disease, the condition is commonly managed through incorporating lifestyle changes that reduce inflammation. This may include dietary changes, such as limiting the intake of fats and dairy while increasing fiber consumption.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to Crohn's disease we summed up the effects of genetic variants that were linked to Crohn's disease 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 Crohn's disease. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to Crohn's disease. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to Crohn's disease. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for Crohn's disease to be 10.55**. 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 Crohn's disease is in the **56th percentile**. This means that it is higher than the polygenic scores 56% of people. We consider this to be an **average genetic predisposition to Crohn's disease**. 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
rs2076756_G	A / G	0.43 (↑)	26%	3.98×10^{-69}
rs11209026_G	G / G	0.98 (↑)	93%	1.00×10^{-64}
rs3792109_A	A / A	0.29 (↑)	53%	6.76×10^{-41}
rs4077515_T	C / C	0.17 (-)	41%	1.30×10^{-36}
rs11742570_C	T / C	0.29 (↑)	61%	7.08×10^{-36}
rs1250550_C	C / A	0.17 (↑)	67%	1.10×10^{-30}
rs2413583_C	C / C	0.21 (↑)	83%	1.10×10^{-26}
rs10761659_G	A / G	0.21 (↑)	54%	4.37×10^{-22}
rs11564258_A	NA	0.55 (-)	3%	6.17×10^{-21}
rs12521868_T	G / G	0.21 (-)	42%	1.41×10^{-20}
rs4409764_T	T / G	0.20 (↑)	49%	2.29×10^{-20}
rs17293632_T	C / C	0.11 (-)	23%	2.70×10^{-19}
rs7714584_G	A / A	0.31 (-)	9%	7.76×10^{-19}
rs6651252_T	T / T	0.21 (↑)	87%	3.90×10^{-18}
rs8005161_T	C / C	0.21 (-)	12%	4.20×10^{-18}
rs3197999_A	A / A	0.20 (↑)	30%	6.17×10^{-17}
rs1819658_C	C / T	0.17 (↑)	77%	9.10×10^{-17}
rs181359_A	G / A	0.10 (↑)	20%	4.80×10^{-16}
rs3810936_C	T / C	0.19 (↑)	68%	1.00×10^{-15}
rs7517810_T	C / C	0.20 (-)	25%	1.51×10^{-15}
rs4809330_G	G / G	0.11 (↑)	71%	2.70×10^{-15}
rs1893217_G	A / A	0.22 (-)	15%	1.29×10^{-14}
rs10495903_T	C / T	0.13 (↑)	13%	1.60×10^{-14}
rs3024505_A	G / G	0.11 (-)	16%	1.60×10^{-14}
rs2838519_G	G / G	0.17 (↑)	39%	2.09×10^{-14}
rs6556412_A	G / G	0.17 (-)	33%	5.37×10^{-14}
rs10758669_C	C / A	0.17 (↑)	35%	1.00×10^{-13}
rs3091315_A	A / G	0.18 (↑)	72%	1.70×10^{-13}
rs3180018_A	/	0.12 (-)	25%	2.30×10^{-13}
rs7423615_T	C / T	0.11 (↑)	19%	3.10×10^{-13}
rs7927997_T	C / C	0.16 (-)	39%	5.62×10^{-13}
rs12720356_C	A / A	0.11 (-)	8%	1.40×10^{-12}
rs4871611_A NEW	G / A	0.16 (↑)	61%	1.51×10^{-12}
rs2058660_G NEW	A / A	0.17 (-)	23%	1.58×10^{-12}
rs359457_T NEW	C / C	0.08 (-)	57%	2.50×10^{-12}
rs415890_C NEW	G / G	0.16 (-)	52%	2.51×10^{-12}
rs7702331_A NEW	A / G	0.11 (↑)	60%	5.90×10^{-12}
rs713875_C NEW	C / C	0.08 (↑)	47%	7.30×10^{-12}
rs281379_A NEW	A / A	0.07 (↑)	49%	7.40×10^{-12}

rs740495_G	A / A	0.15 (–)	25%	8.13×10^{-12}
rs1736020_C	A / A	0.15 (–)	58%	9.33×10^{-12}
rs151181_C	T / C	0.07 (↑)	39%	1.50×10^{-11}
rs102275_C	T / T	0.08 (–)	34%	2.30×10^{-11}
rs212388_C	C / C	0.10 (↑)	39%	2.30×10^{-11}
rs1799964_C	T / C	0.17 (↑)	21%	3.98×10^{-11}
rs780093_T	T / C	0.14 (↑)	42%	4.70×10^{-11}
rs2549794_C	T / T	0.05 (–)	41%	1.10×10^{-10}
rs3764147_G	A / A	0.16 (–)	25%	1.41×10^{-10}
rs4902642_G	G / A	0.07 (↑)	58%	1.60×10^{-10}
rs2062305_G	G / G	0.10 (↑)	35%	4.90×10^{-10}
rs694739_A	A / G	0.10 (↑)	63%	6.00×10^{-10}
rs13428812_G	A / G	0.06 (↑)	33%	8.50×10^{-10}
rs12242110_G	A / G	0.14 (↑)	32%	1.10×10^{-9}
rs2872507_A	G / A	0.13 (↑)	46%	1.51×10^{-9}
rs11167764_C	A / C	0.06 (↑)	80%	2.00×10^{-9}
rs12722489_C	C / T	0.10 (↑)	85%	2.90×10^{-9}
rs6738825_A	A / G	0.06 (↑)	47%	3.50×10^{-9}
rs2476601_G	G / G	0.23 (↑)	91%	4.47×10^{-9}
rs1847472_C	A / A	0.07 (–)	66%	5.10×10^{-9}
rs10181042_T	C / C	0.13 (–)	42%	6.61×10^{-9}
rs13073817_A	G / A	0.08 (↑)	32%	6.70×10^{-9}
rs17309827_T	T / T	0.10 (↑)	64%	6.70×10^{-9}
rs2797685_T	C / T	0.05 (↑)	19%	7.10×10^{-9}
rs1998598_G	A / G	0.04 (↑)	30%	8.70×10^{-9}
rs736289_T	T / C	0.06 (↑)	61%	8.70×10^{-9}
rs1456896_T	C / T	0.13 (↑)	69%	1.20×10^{-8}
rs6908425_C	C / C	0.16 (↑)	78%	1.41×10^{-8}
rs11871801_A	A / A	0.14 (↑)	76%	2.51×10^{-8}
rs6568421_G	G / G	0.12 (↑)	30%	4.37×10^{-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.