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C-reactive protein level (Ligthart, 2018)

Symen Ligthart, et al.
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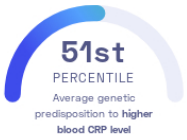
Inflammation

STUDY SUMMARY

Identification of 58 genetic variants associated with the blood level of C-reactive protein, a marker of inflammation.

YOUR RESULT



STUDY DESCRIPTION

Inflammation is a defense mechanism our body induces as a response to infections. However, chronic inflammation has been associated with many diseases including type 2 diabetes and cardiovascular disease. Inflammation can be assessed by measuring the level of C-reactive protein (CRP) in the blood which are typically increased if there is inflammation in the body. To identify genetic variants associated with the CRP level and therefore inflammation-related disorders, this genome-wide association study examined over 200,000 individuals of European ancestry. The study discovered 58 novel genetic variants, many of which are near genes involved in immune system pathways and metabolic processes in the liver.

DID YOU KNOW?

To reduce chronic inflammation, eat plenty of anti-inflammatory foods, exercise regularly, maintain a healthy weight, and reduce stress levels.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to higher blood CRP level we summed up the effects of genetic variants that were linked to higher blood CRP level 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 higher blood CRP level. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to higher blood CRP level. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to higher blood CRP level. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for higher blood CRP level to be 1.75**. 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 higher blood CRP level is in the **51st percentile**. This means that it is higher than the polygenic scores 51% of people. We consider this to be an **average genetic predisposition to higher blood CRP level**. 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
rs2794520_C	C / C	0.18 (↑)	33%	4.17×10^{-523}
rs4420638_A	A / A	0.23 (↑)	18%	1.23×10^{-305}
rs7310409_G	A / G	0.14 (↑)	39%	2.54×10^{-299}
rs1805096_G	G / G	0.10 (↑)	39%	2.17×10^{-183}
rs4129267_C	T / T	0.09 (–)	39%	1.20×10^{-129}
rs1260326_T	T / C	0.07 (↑)	39%	2.72×10^{-92}
rs13409371_A	G / G	0.05 (–)	43%	5.07×10^{-36}
rs2836878_G NEW	G / A	0.04 (↑)	27%	7.71×10^{-28}
rs4841132_G	A / G	0.07 (↑)	9%	2.00×10^{-25}
rs13233571_C	C / C	0.06 (↑)	12%	2.95×10^{-25}
rs1800961_C	NA	0.11 (–)	3%	4.63×10^{-23}
rs10521222_C	C / C	0.10 (↑)	5%	2.06×10^{-22}
rs10925027_T	T / C	0.04 (↑)	40%	4.25×10^{-21}
rs10778215_T	T / A	0.03 (↑)	49%	1.86×10^{-20}
rs1558902_A NEW	T / A	0.03 (↑)	41%	5.20×10^{-20}
rs2239222_G NEW	A / G	0.04 (↑)	36%	9.87×10^{-20}
rs9271608_G NEW	A / A	0.04 (–)	22%	2.33×10^{-17}
rs340005_A	A / A	0.03 (↑)	38%	1.01×10^{-16}
rs2064009_C NEW	T / T	-0.03 (–)	42%	2.28×10^{-14}
rs10512597_T NEW	C / C	-0.04 (–)	18%	4.44×10^{-14}
rs11108056_G NEW	C / G	-0.03 (↓)	42%	5.42×10^{-14}
rs6001193_G NEW	A / G	-0.03 (↓)	35%	6.53×10^{-14}
rs1880241_G NEW	G / G	-0.03 (↓)	48%	8.41×10^{-14}
rs1736060_T NEW	T / T	0.03 (↑)	60%	2.60×10^{-13}
rs2293476_C	G / G	0.03 (–)	23%	8.27×10^{-13}
rs10838687_G NEW	T / G	-0.03 (↓)	22%	9.12×10^{-13}
rs1490384_T NEW	C / T	-0.03 (↓)	51%	2.65×10^{-12}
rs10832027_G NEW	A / A	-0.03 (–)	33%	4.43×10^{-12}
rs469772_T NEW	C / T	-0.03 (↓)	19%	5.54×10^{-12}
rs2852151_A	G / A	0.03 (↑)	40%	1.36×10^{-11}
rs9385532_T NEW	T / C	-0.03 (↓)	33%	1.90×10^{-11}
rs1441169_G NEW	A / G	-0.03 (↓)	53%	2.27×10^{-11}
rs9284725_C NEW	C / A	0.03 (↑)	24%	7.34×10^{-11}
rs12995480_T NEW	C / C	-0.03 (–)	17%	1.24×10^{-10}
rs112635299_T NEW	NA	-0.11 (–)	2%	2.10×10^{-10}
rs687339_T NEW	T / T	-0.03 (↓)	78%	2.80×10^{-10}
rs12202641_T NEW	C / T	-0.02 (↓)	39%	3.00×10^{-10}
rs4092465_A NEW	A / G	-0.03 (↓)	35%	3.11×10^{-10}
rs75460349_A NEW	A / A	0.09 (↑)	97%	4.50×10^{-10}

rs4246598_A	C / A	0.02 (↑)	46%	5.11×10^{-10}
rs2315008_T	G / G	-0.02 (–)	31%	5.36×10^{-10}
rs2352975_C	T / T	0.03 (–)	30%	6.43×10^{-10}
rs643434_A	A / A	0.02 (↑)	37%	1.02×10^{-9}
rs12960928_C	T / C	0.02 (↑)	27%	1.91×10^{-9}
rs1051338_G	T / T	0.02 (–)	31%	2.27×10^{-9}
rs1582763_A	A / A	-0.02 (↓)	37%	2.37×10^{-9}
rs1514895_A	A / G	-0.03 (↓)	71%	2.70×10^{-9}
rs1189402_A	G / G	0.03 (–)	62%	3.90×10^{-9}
rs7121935_A	G / A	-0.02 (↓)	38%	5.28×10^{-9}
rs17658229_C	T / T	0.06 (–)	5%	5.50×10^{-9}
rs2710804_C	T / T	0.02 (–)	37%	1.30×10^{-8}
rs9611441_C	G / C	-0.02 (↓)	49%	1.40×10^{-8}
rs2891677_C	C / T	-0.02 (↓)	46%	1.59×10^{-8}
rs4774590_A	G / A	-0.02 (↓)	35%	2.71×10^{-8}
rs178810_T	C / C	0.02 (–)	56%	2.95×10^{-8}
rs7795281_A	G / A	0.03 (↑)	76%	3.10×10^{-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.