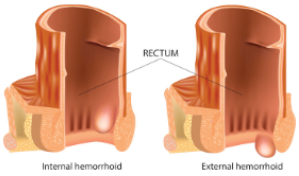
03/2021

Hemorrhoids (Zheng, 2021)

Tenghao Zheng, et al.
Gut

Intestines



Hemorrhoids can be internal or external.

STUDY SUMMARY

This report is based on a study that discovered more than 100 genetic variants associated with hemorrhoids.

YOUR RESULT

17th
PERCENTILE
Below average genetic predisposition to **hemorrhoids**

STUDY DESCRIPTION

Hemorrhoids occur when veins in and around the anus become swollen and inflamed which can lead to pain and bleeding.
Hemorrhoids are extremely common, potentially affecting up to 1 in every 20 individuals, and the likelihood of developing the condition increases with age. This genome-wide association included 944,000 individuals of European ancestry and discovered 102 genetic variants associated with the development of hemorrhoids. One of the genes linked to hemorrhoids in this study was ABO. It is the gene that determines the blood groups and the results of this study suggest that individuals with a type O blood group may have an increased risk of developing hemorrhoids.

DID YOU KNOW?

Individuals suffering from hemorrhoids are recommended to adopt a high-fiber diet or take fiber supplements. Fiber can help to soften stool, reducing the pain that is caused by hemorrhoids.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to hemorrhoids we summed up the effects of genetic variants that were linked to hemorrhoids 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 hemorrhoids. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to hemorrhoids. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to hemorrhoids. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for hemorrhoids to be -0.02**. 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 hemorrhoids is in the **17th percentile**. This means that it is higher than the polygenic scores 17% of people. We consider this to be a **below average genetic predisposition to hemorrhoids**. 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	GENE	EFFECT SIZE	VARIANT FREQUENCY	SIGNIFICANCE
rs11176001_A	C / C	HMGA2	-0.08 (–)	13%	2.50×10^{-46}
rs676996_G	G / G	ABO	-0.06 (↓)	34%	5.30×10^{-43}
rs1838392_T	T / G	XKR9	0.05 (↑)	39%	4.60×10^{-39}
rs11585073_T	A / T	BMP8B	0.06 (↑)	25%	3.90×10^{-33}
rs17293632_T	C / C	SMAD3	0.06 (–)	24%	6.90×10^{-32}
rs722687_T	T / T	GMDS	-0.05 (↓)	28%	1.50×10^{-31}
rs145163454_C	NA	ATP1B1	-0.14 (–)	3%	5.90×10^{-28}
rs1333047_A	A / A	CDKN2B	0.04 (↑)	50%	7.80×10^{-28}
rs9847710_C	C / C	SFMBT1	0.04 (↑)	41%	1.20×10^{-23}
rs4556017_C	T / T	MUC12	0.06 (–)	14%	1.30×10^{-22}
rs11770437_T	T / T	WBSCR28	-0.04 (↓)	36%	3.20×10^{-18}
rs900400_C	T / T	NA	-0.03 (–)	41%	5.00×10^{-18}
rs7778418_C	T / T	FAM185A	0.04 (–)	34%	6.40×10^{-18}
rs847148_T	A / T	HOXD11	-0.04 (↓)	32%	1.10×10^{-17}
rs7994724_A	A / G	DLEU7	0.04 (↑)	37%	1.70×10^{-17}
rs2912053_G	G / C	NA	0.04 (↑)	40%	2.30×10^{-17}
rs4910165_C	C / G	MRVI1	0.03 (↑)	32%	3.90×10^{-16}
rs62368263_C	T / C	ISL1	-0.04 (↓)	14%	5.90×10^{-16}
rs7594056_A	G / G	GDF7	-0.03 (–)	31%	7.20×10^{-16}
rs6792493_G	A / G	PLCXD2	0.03 (↑)	41%	9.50×10^{-16}
rs2421206_G	G / G	SPC24	0.03 (↑)	35%	2.30×10^{-14}
rs2597301_C	C / G	FOXP1	0.03 (↑)	32%	6.30×10^{-14}
rs2218793_A	C / C	AMPD3	0.03 (–)	29%	1.10×10^{-13}
rs4345978_T	G / T	CLMP	-0.03 (↓)	25%	1.20×10^{-13}
rs7183672_G	G / G	NA	0.03 (↑)	32%	1.20×10^{-13}
rs72707023_A	G / G	TPPP	-0.04 (–)	18%	2.40×10^{-13}
rs4579999_T	T / T	NA	0.03 (↑)	47%	3.30×10^{-13}
rs7795564_A	G / A	EGFR	-0.03 (↓)	39%	3.40×10^{-13}
rs11635984_C	T / C	GREM1	-0.03 (↓)	39%	4.10×10^{-13}
rs11578225_A	G / A	SLC44A3	-0.03 (↓)	21%	6.40×10^{-13}
rs6462976_T	C / C	SUGCT	-0.03 (–)	46%	1.20×10^{-12}
rs2180811_A	T / A	DCBLD1	0.03 (↑)	48%	1.90×10^{-12}
rs10807610_C	A / A	CAP2	0.04 (–)	18%	2.30×10^{-12}
rs1542726_A	A / A	HHIP	0.03 (↑)	42%	2.50×10^{-12}
rs4843407_A	G / G	FOXL1	-0.03 (–)	27%	4.00×10^{-12}
rs34161672_A	G / A	RBM38	-0.03 (↓)	32%	4.20×10^{-12}
rs6839705_A	A / C	TET2	0.03 (↑)	37%	5.00×10^{-12}
rs3253_T	T / T	THBS2	0.03 (↑)	32%	5.00×10^{-12}
rs6498573_T	C / C	MYH11	0.04 (–)	14%	5.20×10^{-12}

rs57116599_A	G / A	MERTK	0.03 (↑)	23%	1.50×10^{-11}
rs58579887_C	T / T	PLEC	0.03 (–)	40%	1.70×10^{-11}
rs4233681_C	T / T	ITGB6	-0.03 (–)	48%	2.00×10^{-11}
rs6482359_A	G / G	KIAA1217	0.03 (–)	39%	3.10×10^{-11}
rs35318931_A	G / G	SRPX	-0.04 (–)	8%	3.20×10^{-11}
rs17824374_C	T / T	NA	-0.03 (–)	20%	3.30×10^{-11}
rs806169_C	C / G	SND1	-0.03 (↓)	33%	3.60×10^{-11}
rs2832279_A	C / C	BACH1	0.03 (–)	36%	4.50×10^{-11}
rs2212450_C	T / C	NCAM1	0.03 (↑)	43%	5.40×10^{-11}
rs1858015_C	C / T	PAPPA	-0.03 (↓)	32%	6.10×10^{-11}
rs13632_A	G / G	HDAC7	0.03 (–)	24%	6.10×10^{-11}
rs62061554_A	G / A	NA	0.04 (↑)	12%	2.60×10^{-10}
rs728327_T	T / T	SRBD1	-0.03 (↓)	34%	3.00×10^{-10}
rs13271626_G	C / C	CCAR2	0.03 (–)	33%	3.40×10^{-10}
rs3851366_C	T / T	KPNA4	-0.02 (–)	47%	3.50×10^{-10}
rs13017210_T	A / A	MAP3K20	-0.03 (–)	39%	3.80×10^{-10}
rs2631752_C	C / G	ACOX3	0.02 (↑)	50%	4.40×10^{-10}
rs28663472_T	C / C	BMPR1B	-0.02 (–)	45%	4.70×10^{-10}
rs78378222_G	NA	TP53	0.11 (–)	1%	4.70×10^{-10}
rs2555004_G	G / G	NA	-0.02 (↓)	49%	5.40×10^{-10}
rs2525570_A	A / G	NF1	-0.02 (↓)	39%	6.80×10^{-10}
rs920778_G	A / A	HOXC11	-0.03 (–)	36%	6.90×10^{-10}
rs5942977_A	A / A	CHRDL1	-0.02 (↓)	40%	6.90×10^{-10}
rs12153515_T	C / C	NA	0.04 (–)	13%	7.30×10^{-10}
rs12594232_G	A / G	PIAS1	-0.02 (↓)	45%	1.00×10^{-9}
rs2581260_A	T / A	NA	-0.03 (↓)	16%	1.10×10^{-9}
rs4670149_T	A / A	FEZ2	0.03 (–)	31%	1.30×10^{-9}
rs10956488_G	A / A	GSDMC	0.03 (–)	15%	1.70×10^{-9}
rs10838738_G	A / G	MTCH2	0.03 (↑)	35%	1.70×10^{-9}
rs11045079_G	A / G	NA	-0.03 (↓)	14%	1.80×10^{-9}
rs9853475_G	A / A	ZBTB20	-0.03 (–)	28%	2.00×10^{-9}
rs3020338_A	G / A	ESR1	-0.03 (↓)	25%	2.20×10^{-9}
rs2861709_G	A / G	NA	0.05 (↑)	6%	2.40×10^{-9}
rs2327426_C	T / C	TCF21	-0.03 (↓)	29%	2.70×10^{-9}
rs4951080_A	A / A	MDM4	-0.03 (↓)	32%	2.80×10^{-9}
rs2060285_A	C / C	NA	0.02 (–)	34%	4.20×10^{-9}
rs2605097_C	A / A	NA	0.03 (–)	30%	4.30×10^{-9}
rs1689549_C	T / C	FGD5	-0.04 (↓)	11%	4.40×10^{-9}
rs111235435_T	C / C	NA	0.02 (–)	38%	5.00×10^{-9}
rs4485884_A	T / T	NA	0.02 (–)	43%	5.60×10^{-9}
rs2687965_A	A / A	UGDH	-0.02 (↓)	49%	5.90×10^{-9}
rs6867042_T	C / C	KIAA0825	-0.03 (–)	13%	6.00×10^{-9}
rs4671051_T	A / T	EHBP1	0.02 (↑)	36%	7.50×10^{-9}
rs61026653_G	A / A	FBXL7	-0.03 (–)	14%	7.60×10^{-9}
rs1563319_T	A / A	NA	-0.02 (–)	49%	9.50×10^{-9}
rs7423637_T	A / A	NA	0.02 (–)	31%	1.00×10^{-8}
rs16831319_C	T / T	COL5A2	0.05 (–)	6%	1.00×10^{-8}
rs11942410_T	C / C	BTC	-0.03 (–)	26%	1.10×10^{-8}
rs34532102_T	C / C	SERTAD2	-0.03 (–)	20%	1.30×10^{-8}
rs854786_G	A / G	MYO15A	-0.02 (↓)	32%	1.30×10^{-8}
rs174767_A	A / G	AP1B1	-0.02 (↓)	38%	1.40×10^{-8}
rs4959352_C	A / A	EXOC2	0.02 (–)	33%	1.50×10^{-8}
rs1156533_G	A / A	TRIM31	-0.02 (–)	30%	1.80×10^{-8}
rs6723226_G	A / A	TTC27	0.02 (–)	35%	2.00×10^{-8}
rs9322356_A	G / G	ESR1	0.04 (–)	8%	2.00×10^{-8}
rs34417560_T	A / A	TMEM194B	0.03 (–)	25%	2.50×10^{-8}
rs755209_A	A / A	BICD2	0.02 (↑)	28%	3.10×10^{-8}
rs8106090_G	A / A	ZNF404	0.02 (–)	49%	3.30×10^{-8}
rs4423457_A	G / A	PRKCA	0.02 (↓)	42%	3.40×10^{-8}

rs34425487_A	G / A	PRKCA	-0.02 (↓)	42%	3.40 x 10
rs35384758_G	A / G	NA	0.03 (↑)	24%	4.00×10^{-8}
rs3012065_C	T / C	CTBP2	0.02 (↑)	32%	4.10×10^{-8}
rs2186797_C	T / T	ANO1	-0.04 (–)	6%	4.50×10^{-8}
rs7559714_C	T / T	ACVR2A	-0.02 (–)	31%	5.00×10^{-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.