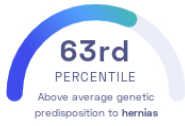


STUDY SUMMARY

This report is based on a study that discovered 22 genetic variants associated with the occurrence of hernias.

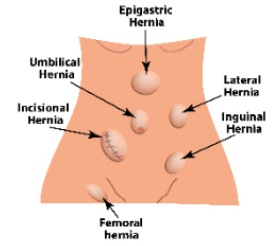
YOUR RESULT



STUDY DESCRIPTION

A hernia occurs when part of an internal organ or tissue bulges through a weak area of muscle. Many hernias happen in areas around the abdomen, including the groin, stomach, and belly button. Hernias are a fairly common occurrence and are often caused by lifting heavy objects or excessive coughing. When left untreated, they can cause pain and health problems. To discover genetic variants associated with the development of hernias, this study examined over 65,000 individuals of European ancestry.

Researchers identified 22 regions of the genome associated with the development of hernias at any location in the body. A number of genes belonging to the ADAMTS family (ADAMTS6, ADAMTS16, ADAMTSL3) were associated with hernias in this study. These genes have an important role in tissue organization and may contribute to strengthening the abdomen.



Hernias can occur in many parts of the body.

DID YOU KNOW?

Obesity is a risk factor for developing hernias. It can also complicate surgical repair and make recurrence more likely.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to hernias we summed up the effects of genetic variants that were linked to hernias 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 hernias. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to hernias. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to hernias. By adding up the effect sizes of the highlighted variants we **calculated your polygenic score for hernias to be -0.27**. 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 hernias is in the **63rd percentile**. This means that it is higher than the polygenic scores 63% of people. We consider this to be an **above average genetic predisposition to hernias**. 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 [Ⓞ]
rs3791679_G	A / A	EFEMP1	-0.18 (-)	23%	3.72×10^{-75}
rs6747490_G	A / G	MIR217HG	0.13 (↑)	59%	4.11×10^{-51}
rs1415288_C	A / A	-	0.13 (-)	30%	2.72×10^{-43}
rs6917403_G	A / A	AIG1	-0.08 (-)	57%	3.03×10^{-23}
rs10005540_T	T / T	-	-0.07 (↓)	61%	1.69×10^{-18}
rs7924571_A	C / C	-	-0.08 (-)	22%	9.04×10^{-17}
rs792829_A	G / A	COL8A1	-0.06 (↓)	63%	1.94×10^{-12}
rs7547760_G	C / C	-	0.06 (-)	50%	5.61×10^{-12}
rs1834922_A	A / A	ADAMTS16	-0.06 (↓)	65%	1.09×10^{-10}
rs56148717_G	A / A	SPSB1	0.07 (-)	21%	1.44×10^{-10}
rs2498527_A	G / A	-	-0.06 (↓)	79%	4.36×10^{-10}
rs2383920_A	T / T	-	-0.06 (-)	22%	1.18×10^{-9}
rs6123685_A	G / A	BMP7	-0.06 (↓)	25%	1.64×10^{-9}
rs10224499_T	T / T	-	0.05 (↑)	39%	8.23×10^{-9}
rs4974113_G	A / G	ERC2	0.06 (↑)	23%	8.91×10^{-9}
rs947510_C	T / C	HMCN2	-0.05 (↓)	72%	2.76×10^{-8}
rs9392136_G	A / A	-	0.05 (-)	30%	3.85×10^{-8}
rs146385050_A	C / A	TLK2	-0.06 (↓)	18%	4.76×10^{-8}