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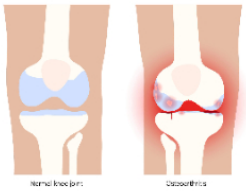
Osteoarthritis (Boer, 2021)

Cindy Boer, et al.
Cell

Bones Joints



Osteoarthritis leads to inflammation in joints.

STUDY SUMMARY

This report is based on a study that discovered 21 genetic variants associated with osteoarthritis.

YOUR RESULT

11th
PERCENTILE
Below average genetic predisposition to **osteoarthritis**

STUDY DESCRIPTION

Joints, including the knee and shoulder, are areas where 2 or more bones meet. Arthritis is a condition that is characterized by inflammation in the joints that leads to painful movement. Osteoarthritis is the most common form of arthritis, and it is often seen in older people. In individuals with osteoarthritis, the protective covering of the joints becomes worn down, causing the bones within the joint to rub together. This causes pain, stiffness, and other symptoms. This genome-wide association study sought to identify genetic associations that predispose individuals to osteoarthritis by examining more than 826,000 individuals of European and East Asian ancestry. The researchers identified 21 variants associated with osteoarthritis, 8 of which were newly identified by this study. A number of genes were linked to osteoarthritis. This included FBN2 and LTBP1, two genes which are associated with bone growth and development.

DID YOU KNOW?

Osteoarthritis is most common in the knee, affecting nearly 20% of individuals over the age of 45.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to osteoarthritis we summed up the effects of genetic variants that were linked to osteoarthritis 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 osteoarthritis. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to osteoarthritis. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to osteoarthritis. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for osteoarthritis to be 0.32**. 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 osteoarthritis is in the **11th percentile**. This means that it is higher than the polygenic scores 11% of people. We consider this to be a **below average genetic predisposition to osteoarthritis**. 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
rs13107325_T	C / C	SLC39A8	0.08 (–)	7%	3.25×10^{-17}
rs3771501_A	G / G	TGFA	0.04 (–)	47%	4.05×10^{-16}
rs1913707_A	A / A	RP11	0.03 (↑)	61%	1.39×10^{-12}
rs2425061_A	A / G	-	0.03 (↑)	63%	2.14×10^{-12}
rs216175_A	A / C	-	0.04 (↑)	83%	2.74×10^{-12}
rs2622873_T	T / T	-	0.05 (↑)	88%	4.24×10^{-11}
rs10405617_A	G / G	-	0.03 (–)	32%	9.33×10^{-11}
rs12901372_C	G / G	SMAD3	0.03 (–)	53%	1.02×10^{-10}
rs11731421_A	G / A	-	0.03 (↑)	35%	1.88×10^{-10}
rs4979341_T	C / C	-	0.03 (–)	27%	1.39×10^{-9}
rs12667224_A NEW	G / A	FOXP2	-0.03 (↓)	52%	1.66×10^{-9}
rs62242105_A NEW	A / A	RNU6	-0.03 (↓)	33%	2.93×10^{-9}
rs201194999_T NEW	C / C	RNU2	-0.13 (–)	30%	3.05×10^{-9}
rs62182810_A	G / A	RAPH1	0.03 (↑)	54%	3.82×10^{-9}
rs11729628_T NEW	G / G	RP11	-0.03 (–)	24%	4.74×10^{-9}
rs10831476_A NEW	A / A	MAML2	0.03 (↑)	81%	7.77×10^{-9}
rs1401795_A NEW	A / A	-	0.03 (↑)	50%	6.19×10^{-9}
rs17677555_C NEW	G / G	-	0.03 (–)	25%	1.10×10^{-8}