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Migraines (Choquet, 2021)

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Brain Mind

STUDY SUMMARY

This report is based on a study that discovered 73 genetic variants associated with migraines.

YOUR RESULT

12th
PERCENTILE
Below average genetic predisposition to **migraines**

STUDY DESCRIPTION

A migraine is a headache characterized by throbbing head pain, usually located on one side of the head. It is often accompanied by nausea, vision troubles, and sensitivity to light and/or sound. Women are three times more likely to experience migraines than men. To identify genetic factors linked to migraines, this study examined almost 900,000 individuals of European ancestry. The scientists identified 73 regions of the genome associated with an individual's risk of migraines, 40 of which were newly identified. While there are no definite answers to what causes migraines, the genes identified in this study help to form a better understanding of how the condition arises. One gene identified in this study, TGFB1, is associated with inflammation and another, HOXB3, is involved in brain development.

Migraine pain is usually located on one side of the head.

DID YOU KNOW?

Patients who experience migraines are potentially at a higher risk for developing depression and anxiety. Migraines also seem to increase the chances that you may develop certain cardiac conditions such as high blood pressure.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to migraines we summed up the effects of genetic variants that were linked to migraines 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 migraines. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to migraines. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to migraines. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for migraines to be -0.37**. 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 migraines is in the **12th percentile**. This means that it is higher than the polygenic scores 12% of people. We consider this to be a **below average genetic predisposition to migraines**. 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
rs11172113_C	T / T	LRP1	-0.11 (-)	41%	6.94×10^{-75}
rs11153082_G	A / A	FHL5	0.09 (-)	33%	1.40×10^{-49}
rs10166942_C	T / C	TRPM8	-0.09 (↓)	19%	2.15×10^{-39}
rs9349379_G	A / G	PHACTR1	-0.07 (↓)	41%	3.80×10^{-38}
rs12134493_A	C / C	-	0.10 (-)	12%	5.50×10^{-36}
rs1925950_A	G / A	MEF2D	-0.06 (↓)	65%	2.72×10^{-30}
rs1075550_T	C / T	-	-0.06 (↓)	52%	1.61×10^{-28}
rs10234636_C	C / C	SUGCT	-0.09 (↓)	89%	1.52×10^{-26}
rs7858153_A	G / G	ASTN2	0.07 (-)	23%	2.35×10^{-24}
rs4814861_A	G / G	SLC24A3	0.06 (-)	26%	1.19×10^{-22}
rs4909945_C	T / C	IRAG1	0.06 (↑)	68%	7.67×10^{-22}
rs10786156_G	C / G	PLCE1	-0.05 (↓)	44%	6.16×10^{-19}
rs28455731_T	G / G	-	0.07 (-)	16%	2.54×10^{-17}
rs13078967_C	NA	-	-0.15 (-)	3%	1.30×10^{-16}
rs953588_T NEW	C / C	-	0.05 (-)	38%	2.24×10^{-16}
rs10456100_T	C / C	KCNK5	0.05 (-)	28%	3.16×10^{-16}
rs28451064_A NEW	G / G	-	-0.06 (-)	13%	3.20×10^{-14}
rs4704232_C NEW	T / C	POC5	0.05 (↑)	30%	2.50×10^{-13}
rs4888378_G	A / G	CFDP1	-0.04 (↓)	60%	3.74×10^{-13}
rs6693567_T	C / T	-	-0.04 (↓)	73%	4.15×10^{-13}
rs12260159_A	G / G	HPSE2	-0.07 (-)	8%	7.41×10^{-13}
rs2223089_C	G / G	LOC105378525	-0.07 (-)	9%	1.03×10^{-12}
rs7916911_G NEW	T / G	-	-0.04 (↓)	72%	2.56×10^{-12}
rs10927723_G NEW	C / G	TMEM51	0.04 (↑)	36%	3.68×10^{-12}
rs8075138_T NEW	C / T	-	0.04 (↑)	40%	3.81×10^{-12}
rs11096773_A NEW	G / A	-	-0.05 (↓)	19%	4.46×10^{-12}
rs28540738_G	A / A	-	-0.04 (-)	32%	4.47×10^{-12}
rs34653882_G NEW	A / A	-	-0.05 (-)	20%	7.16×10^{-12}
rs6906594_A NEW	G / G	-	0.04 (-)	45%	1.90×10^{-11}
rs138556413_T	NA	CARF	-0.12 (-)	4%	2.12×10^{-11}
rs76597087_T NEW	A / T	LOC105376157	0.06 (↑)	10%	2.29×10^{-11}
rs12787996_A	C / C	YAP1	0.04 (-)	33%	2.32×10^{-11}
rs11031122_C	T / T	MPPED2	0.04 (-)	24%	2.49×10^{-11}
rs6040095_T NEW	G / T	-	0.04 (↑)	35%	2.67×10^{-11}
rs28739509_C NEW	T / C	INPP5B	0.04 (↑)	27%	5.57×10^{-11}
rs293570_G	A / G	NOL4L	0.04 (↑)	32%	5.73×10^{-11}
rs4081947_G	A / A	-	0.04 (-)	35%	7.03×10^{-11}
rs2000660_A NEW	G / G	LOC101927712	0.06 (-)	9%	1.16×10^{-10}

rs1572668_G	A / G	-	0.04 (↑)	49%	1.61×10^{-10}
rs17434299_G	G / G	LOC105370420	-0.03 (↓)	54%	2.05×10^{-10}
rs10038882_C	T / T	-	-0.04 (-)	25%	2.18×10^{-10}
rs6791480_T	C / C	LOC101927995	0.04 (-)	31%	2.56×10^{-10}
rs1268083_C	C / C	LOC105377986	-0.03 (↓)	47%	3.15×10^{-10}
rs1800469_G	G / G	TGFB1	0.04 (↑)	70%	4.75×10^{-10}
rs12947578_T	C / C	RNF213	0.04 (-)	43%	8.47×10^{-10}
rs1019990_T	C / C	MIR4527HG	-0.04 (-)	30%	1.44×10^{-9}
rs4074957_C	T / T	-	-0.04 (-)	23%	1.68×10^{-9}
rs7684253_T	C / C	-	0.03 (-)	55%	1.75×10^{-9}
rs4790873_T	T / T	SMG6	-0.03 (↓)	59%	1.77×10^{-9}
rs4785967_A	A / A	HMOX2, NMRAL1	-0.04 (↓)	70%	2.03×10^{-9}
rs5763529_C	C / C	ASCC2	-0.04 (↓)	83%	2.17×10^{-9}
rs10156578_G	C / G	-	-0.03 (↓)	57%	2.19×10^{-9}
rs1472100_T	T / T	THADA	-0.03 (↓)	56%	2.98×10^{-9}
rs4278348_C	T / T	-	0.03 (-)	54%	3.48×10^{-9}
rs74182632_A	G / G	SUGP1	0.07 (-)	5%	4.73×10^{-9}
rs154516_A	G / A	SNX24	0.03 (↑)	52%	5.31×10^{-9}
rs2506142_G	A / A	NRP1	0.04 (-)	17%	5.53×10^{-9}
rs3911893_A	NA	SKIV2L	-0.08 (-)	4%	6.66×10^{-9}
rs10912903_G	G / G	KIAA0040	0.03 (↑)	57%	7.14×10^{-9}
rs10838634_G	G / G	LRP4	0.06 (↑)	90%	7.65×10^{-9}
rs9611522_T	C / T	CHADL	0.04 (↑)	26%	1.04×10^{-8}
rs10777901_A	C / C	-	-0.03 (-)	50%	1.29×10^{-8}
rs10902940_A	G / G	LINC02641	0.04 (-)	25%	1.31×10^{-8}
rs2145600_G	G / G	PSMA3-AS1	0.04 (↑)	76%	1.95×10^{-8}
rs4415679_A	A / A	-	0.04 (↑)	36%	2.03×10^{-8}
rs75002882_T	NA	IFT43	-0.15 (-)	1%	2.27×10^{-8}
rs12740105_G	G / G	-	-0.03 (↓)	67%	2.52×10^{-8}
rs7093087_A	G / G	CNNM2	0.04 (-)	18%	3.22×10^{-8}
rs7996252_C	T / C	OBI1-AS1	-0.03 (↓)	41%	3.34×10^{-8}
rs12936464_C	A / C	POLR2A	0.04 (↑)	79%	3.46×10^{-8}
rs8054079_T	C / C	-	0.04 (-)	14%	3.83×10^{-8}
rs1026332_C	C / C	-	-0.03 (↓)	27%	4.85×10^{-8}
rs1496332_G	A / A	-	-0.03 (-)	46%	4.96×10^{-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.