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Breast cancer (Michailidou, 2013)

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Breasts | Cancer

STUDY SUMMARY

41 novel genetic variants were determined to be associated with breast cancer, most of which are found in genes that play a role in cell death and differentiation.

YOUR RESULT

3rd
PERCENTILE
Very low genetic predisposition to **breast cancer**

STUDY DESCRIPTION

Breast cancer is the most common cancer for women worldwide. To identify genetic factors that correlate with a risk of developing breast cancer, this study analyzed genetic data from 9 previous genome-wide association studies. With this analysis, they selected 29,807 genetic variants for further study. These variants were studied in 45,290 cases and 41,880 controls of European ancestry. The analysis discovered 41 novel genetic variants that are associated with breast cancer risk. While 7 of these variants lie within or close to known breast cancer susceptibility genes, most of the variants are associated with genes that are linked to cell death and differentiation. In total, these variants explain approximately 30% of the familial risk of developing breast cancer.

DID YOU KNOW?

Women who give birth to their first child at age 35 or younger tend to have a lower risk of developing breast cancer compared to women who don't have children or those who have children at a later age. In addition, the more children you have the lower your risk of breast cancer.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to breast cancer we summed up the effects of genetic variants that were linked to breast cancer 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 breast cancer. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to breast cancer. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to breast cancer. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for breast cancer to be -0.39**. 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 breast cancer is in the **3rd percentile**. This means that it is higher than the polygenic scores 3% of people. We consider this to be a **very low genetic predisposition to breast cancer**. 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
rs2981579_A	G / G	0.30 (-)	40%	1.90×10^{-170}
rs3803662_A	A / G	0.25 (↑)	26%	2.10×10^{-114}
rs614367_T	C / T	0.27 (↑)	15%	2.20×10^{-63}
rs13387042_G	G / G	-0.19 (↓)	49%	2.20×10^{-57}
rs10941679_G	A / A	0.16 (-)	25%	1.70×10^{-37}
rs10995190_A	A / A	-0.17 (↓)	16%	1.30×10^{-36}
rs889312_C	A / A	0.15 (-)	28%	2.70×10^{-36}
rs865686_G	T / T	-0.12 (-)	38%	9.50×10^{-35}
rs10771399_G	A / A	-0.20 (-)	12%	8.10×10^{-31}
rs4973768_T	C / C	0.13 (-)	47%	2.30×10^{-30}
rs13281615_G	A / G	0.10 (↑)	41%	9.60×10^{-28}
rs11249433_G	A / A	0.13 (-)	40%	2.00×10^{-26}
rs17356907_G	A / A	-0.12 (-)	30%	1.80×10^{-22}
rs704010_T	C / C	0.11 (-)	38%	7.40×10^{-22}
rs1292011_G	A / A	-0.09 (-)	42%	8.90×10^{-22}
rs3757318_A	G / G	0.19 (-)	7%	2.20×10^{-21}
rs2046210_A	G / G	0.10 (-)	34%	2.00×10^{-19}
rs999737_T	C / C	-0.14 (-)	23%	2.50×10^{-19}
rs6001930_C NEW	T / T	0.16 (-)	11%	8.80×10^{-19}
rs6472903_G NEW	T / T	-0.13 (-)	18%	1.70×10^{-17}
rs13329835_G NEW	A / A	0.13 (-)	22%	2.10×10^{-16}
rs6828523_A NEW	C / C	-0.12 (-)	13%	3.50×10^{-16}
rs2823093_A	G / G	-0.08 (-)	27%	6.80×10^{-16}
rs11814448_C NEW	NA	0.30 (-)	2%	9.30×10^{-16}
rs16857609_T NEW	C / C	0.09 (-)	26%	1.10×10^{-15}
rs4808801_G NEW	A / A	-0.06 (-)	35%	4.60×10^{-15}
rs2943559_G NEW	A / A	0.16 (-)	7%	5.70×10^{-15}
rs1432679_C NEW	T / T	0.06 (-)	43%	2.00×10^{-14}
rs7072776_A NEW	G / G	0.10 (-)	29%	4.30×10^{-14}
rs17817449_G NEW	T / G	-0.05 (↓)	40%	6.40×10^{-14}
rs9693444_A NEW	A / A	0.07 (↑)	32%	9.20×10^{-14}
rs2236007_A NEW	G / A	-0.13 (↓)	21%	1.70×10^{-13}
rs6504950_A	G / G	-0.09 (-)	28%	2.30×10^{-13}
rs6762644_G NEW	A / A	0.06 (-)	40%	2.20×10^{-12}
rs3903072_T NEW	T / T	-0.08 (↓)	47%	8.60×10^{-12}
rs3817198_C	T / T	0.06 (-)	31%	1.50×10^{-11}
rs11780156_T NEW	C / C	0.12 (-)	16%	3.40×10^{-11}
rs4849887_T NEW	C / C	-0.11 (-)	10%	3.70×10^{-11}
rs720475_A NEW	G / G	-0.07 (-)	25%	7.00×10^{-11}

rs2588809_T	C / C	0.07 (-)	16%	1.40×10^{-10}
rs527616_C	G / G	-0.09 (-)	38%	1.60×10^{-10}
rs616488_G	G / G	-0.06 (↓)	33%	2.00×10^{-10}
rs3760982_A	A / G	0.06 (↑)	46%	2.10×10^{-10}
rs941764_G	A / A	0.05 (-)	34%	3.70×10^{-10}
rs11820646_T	C / C	-0.07 (-)	41%	1.10×10^{-9}
rs132390_C	NA	0.31 (-)	4%	3.10×10^{-9}
rs11242675_C	T / T	-0.03 (-)	39%	7.10×10^{-9}
rs10069690_T	C / T	0.04 (↑)	26%	7.20×10^{-9}
rs17530068_C	T / T	0.09 (-)	22%	8.20×10^{-9}
rs204247_G	A / A	0.06 (-)	43%	8.30×10^{-9}
rs2016394_A	G / G	-0.05 (-)	48%	1.20×10^{-8}
rs10759243_A	C / A	0.07 (↑)	39%	1.20×10^{-8}
rs11552449_T	C / C	0.08 (-)	17%	1.80×10^{-8}
rs11199914_T	C / T	-0.06 (↓)	32%	1.90×10^{-8}
rs12493607_C	G / C	0.04 (↑)	35%	2.30×10^{-8}
rs1353747_G	T / G	-0.11 (↓)	10%	2.50×10^{-8}
rs10472076_C	T / T	0.06 (-)	38%	2.90×10^{-8}
rs1550623_G	A / A	-0.09 (-)	16%	3.00×10^{-8}
rs7904519_G	A / G	0.06 (↑)	46%	3.10×10^{-8}
rs1436904_G	G / G	-0.07 (↓)	40%	3.20×10^{-8}
rs12422552_C	G / C	0.10 (↑)	26%	3.70×10^{-8}
rs9790517_T	C / C	0.09 (-)	23%	4.20×10^{-8}
rs11571833_T	NA	0.33 (-)	1%	4.90×10^{-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.