⭐ Breast cancer (Fachal, 2020)
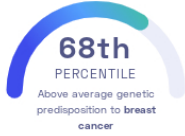
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`Cancer` `Breasts`

STUDY SUMMARY

Identification of 206 genetic variants associated with a risk of developing breast cancer.

YOUR RESULT

68th PERCENTILE

Above average genetic predisposition to **breast cancer**

STUDY DESCRIPTION

Breast cancer is currently the second most common cancer among women (behind skin cancer), affecting nearly 1 in 8 during their lifetime. Nearly 10% of all cases of breast cancer are thought to be hereditary. This study examined genetic data from over 215,000 women of European ancestry to identify genetic regions associated with an increased risk of developing breast cancer. The analysis discovered 206 variants across 129 genomic regions that are strongly associated with breast cancer risk. Collectively these genetic variants explain over 20% of the hereditary cancer risk. Many of the discovered variants are near genes that are related to the immune system, which indicates its importance in protecting us against cancer.

DID YOU KNOW?

Research suggests that long-term exposure to some plastics may increase the risk of developing breast cancer. In particular, plastics that contain bisphenol A (BPA). It is believed to interfere with the hormone system by mimicking the female sex hormone, estrogen. Look for the "BPA free" label on plastics and consider switching to a reusable water bottle made of metal or glass.

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 -0.51**. 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 **68th percentile**. This means that it is higher than the polygenic scores 68% of people. We consider this to be an **above average 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
rs4784227_T	C / T	0.23 (↑)	20%	4.63×10^{-160}
rs10941679_G	A / A	0.18 (–)	25%	6.48×10^{-90}
rs4442975_T	T / T	-0.15 (↓)	47%	2.35×10^{-89}
rs11249433_G	A / A	0.13 (–)	28%	4.00×10^{-63}
rs186430430_C	NA	1.07 (–)	< 1%	3.44×10^{-57}
rs659713_G	G / G	0.11 (↑)	70%	6.64×10^{-50}
rs62355902_T	A / A	0.17 (–)	16%	5.16×10^{-49}
rs7297051_T	C / C	-0.12 (–)	22%	2.18×10^{-40}
rs10995201_G	G / G	-0.12 (↓)	16%	1.40×10^{-37}
rs1353783_T	C / C	-0.09 (–)	31%	7.50×10^{-35}
rs10069690_T	C / T	0.16 (↑)	35%	1.56×10^{-31}
rs2403907_A	C / C	-0.09 (–)	31%	2.24×10^{-30}
rs754416_G	G / G	-0.07 (↓)	71%	7.83×10^{-30}
rs17356907_G	A / A	-0.08 (–)	28%	1.22×10^{-29}
rs244321_A	T / T	-0.09 (–)	34%	6.02×10^{-29}
rs1352944_A	A / A	-0.09 (↓)	38%	3.02×10^{-27}
rs620315_A	G / G	-0.07 (–)	37%	2.01×10^{-26}
rs45631563_T	NA	-0.39 (–)	3%	1.90×10^{-25}
rs55872725_T	C / T	-0.11 (↓)	31%	1.66×10^{-24}
rs4951401_A	G / G	-0.13 (–)	78%	1.43×10^{-23}
rs78540526_T	C / C	0.22 (–)	6%	3.54×10^{-23}
rs8105994_C	T / T	-0.07 (–)	45%	8.72×10^{-23}
rs7098100_A	G / A	0.07 (↑)	37%	1.38×10^{-22}
rs851984_A	G / A	0.08 (↑)	35%	3.93×10^{-22}
rs31864_G	A / A	0.07 (–)	59%	4.53×10^{-22}
rs12173562_T	C / C	0.21 (–)	6%	5.40×10^{-21}
rs7664956_T	G / G	-0.12 (–)	22%	1.11×10^{-20}
rs657244_G	A / A	0.12 (–)	77%	3.73×10^{-20}
rs7465364_G	A / A	-0.06 (–)	67%	5.29×10^{-20}
rs9938021_G	C / C	0.07 (–)	24%	5.98×10^{-20}
rs657686_G	A / G	0.16 (↑)	13%	9.86×10^{-20}
rs12881240_T	C / T	-0.07 (↓)	16%	3.53×10^{-19}
rs9421409_A	G / A	-0.07 (↓)	40%	1.50×10^{-18}
rs56344893_A	C / A	0.07 (↑)	30%	2.32×10^{-18}
rs2736107_T	C / T	-0.11 (↓)	21%	3.24×10^{-18}
rs10816625_G	A / A	0.13 (–)	7%	7.86×10^{-18}
rs2478777_T	T / T	-0.07 (↓)	82%	1.89×10^{-17}
rs6787391_T	C / C	0.05 (–)	27%	5.91×10^{-17}
rs2992756_C	T / C	-0.06 (↓)	52%	2.33×10^{-16}

rs35263707_A	G / A	0.07 (↑)	36%	3.04 x 10⁻¹⁶
rs13294895_T	T / T	0.09 (↑)	12%	3.04 x 10⁻¹⁶
rs4849879_G	G / G	0.11 (↑)	83%	3.10 x 10⁻¹⁶
rs10762851_G	A / A	0.06 (−)	26%	3.47 x 10⁻¹⁶
rs4286946_G	C / C	-0.09 (−)	15%	4.95 x 10⁻¹⁶
rs5995543_A	G / A	-0.06 (↓)	30%	3.59 x 10⁻¹⁵
rs7813150_A	G / G	0.06 (−)	30%	5.87 x 10⁻¹⁵
rs2003526_G	G / G	0.06 (↑)	58%	1.53 x 10⁻¹⁴
rs11571833_T	NA	0.40 (−)	< 1%	2.06 x 10⁻¹⁴
rs9925952_G	A / G	-0.11 (↓)	76%	2.08 x 10⁻¹⁴
rs13153426_A	NA	0.17 (−)	4%	7.64 x 10⁻¹⁴
rs143384623_T	AAAAAAAAAAA / AAAAAAAAAAA	-0.06 (−)	30%	1.15 x 10⁻¹³
rs71403627_A	NA	-0.09 (−)	< 1%	1.16 x 10⁻¹³
rs62334412_G	A / G	0.06 (↑)	25%	1.28 x 10⁻¹³
rs4950774_A	G / G	-0.08 (−)	34%	1.54 x 10⁻¹³
rs2016394_A	G / G	-0.05 (−)	41%	1.87 x 10⁻¹³
rs984113_C	C / C	-0.06 (↓)	60%	2.95 x 10⁻¹³
rs3769821_T	C / C	-0.06 (−)	59%	3.66 x 10⁻¹³
rs56387622_C	T / T	-0.10 (−)	16%	3.87 x 10⁻¹³
rs35422_A	G / G	0.05 (−)	65%	3.89 x 10⁻¹³
rs78955132_G	A / A	-0.12 (−)	6%	4.04 x 10⁻¹³
rs405447_G	G / G	-0.05 (↓)	60%	7.67 x 10⁻¹³
rs12706954_T	C / C	-0.06 (−)	37%	8.90 x 10⁻¹³
rs2059891_C	C / C	0.05 (↑)	19%	8.92 x 10⁻¹³
rs12250948_C	C / C	-0.06 (↓)	59%	1.14 x 10⁻¹²
rs7625643_G	G / G	0.06 (↑)	49%	1.30 x 10⁻¹²
rs12048493_C	A / A	0.05 (−)	29%	1.49 x 10⁻¹²
rs1964292_C	T / T	-0.08 (−)	24%	1.73 x 10⁻¹²
rs28539243_A	G / A	0.04 (↑)	59%	1.83 x 10⁻¹²
rs527616_G	G / G	0.06 (↑)	69%	2.03 x 10⁻¹²
rs56722914_C	T / T	0.06 (−)	17%	4.16 x 10⁻¹²
rs9952980_C	T / C	-0.05 (↓)	35%	5.39 x 10⁻¹²
rs12594752_T	C / C	-0.07 (−)	17%	6.37 x 10⁻¹²
rs7796917_A	A / A	-0.07 (↓)	9%	6.54 x 10⁻¹²
rs1057941_A	A / A	0.05 (↑)	45%	9.12 x 10⁻¹²
rs190443933_C	NA	0.30 (−)	1%	2.09 x 10⁻¹¹
rs72755295_G	NA	0.12 (−)	2%	3.64 x 10⁻¹¹
rs548082010_C	G / G	-0.05 (−)	32%	3.73 x 10⁻¹¹
rs1882155_C	T / T	-0.06 (−)	20%	3.83 x 10⁻¹¹
rs13294352_T	G / G	-0.05 (−)	37%	4.85 x 10⁻¹¹
rs848088_C	T / C	-0.04 (↓)	65%	4.92 x 10⁻¹¹
rs7017073_C	T / T	0.05 (−)	23%	7.56 x 10⁻¹¹
rs12039667_C	T / C	0.06 (↑)	71%	8.27 x 10⁻¹¹
rs4076654_T	A / T	-0.04 (↓)	49%	9.79 x 10⁻¹¹
rs148509105_T	NA	0.36 (−)	< 1%	1.66 x 10⁻¹⁰
rs17879961_G	NA	0.30 (−)	< 1%	2.03 x 10⁻¹⁰
rs4871411_A	G / A	0.05 (↑)	35%	2.11 x 10⁻¹⁰
rs74174203_A	G / A	-0.05 (↓)	42%	2.22 x 10⁻¹⁰
rs17625845_C	T / T	-0.11 (−)	15%	2.43 x 10⁻¹⁰
rs419018_G	A / G	0.07 (↑)	41%	3.72 x 10⁻¹⁰
rs150957507_T	C / T	-0.07 (↓)	11%	4.35 x 10⁻¹⁰
rs6854739_T	T / T	-0.05 (↓)	50%	4.75 x 10⁻¹⁰
rs571173399_G	T / T	-0.06 (−)	18%	6.46 x 10⁻¹⁰
rs17617028_A	G / G	0.06 (−)	21%	7.02 x 10⁻¹⁰
rs745382_G	G / G	0.05 (↑)	66%	1.28 x 10⁻⁹
rs7763102_A	C / C	0.06 (−)	22%	1.47 x 10⁻⁹
rs1879854_G	G / G	-0.04 (↓)	79%	1.54 x 10⁻⁹
rs112497245_A	G / G	0.10 (−)	6%	1.73 x 10⁻⁹
rs10034903_G	C / C	0.05 (−)	33%	1.73 x 10⁻⁹
rs61862474_A	NA	0.28 (−)	3%	3.04 x 10⁻⁹
rs78440108_T	C / C	-0.06 (−)	10%	3.20 x 10⁻⁹
rs67397300_G	C / C	0.10 (−)	38%	3.28 x 10⁻⁹

rs6768735_C	T / T	0.10 (−)	28%	3.26 × 10⁻⁹
rs6973318_C	T / T	0.05 (−)	59%	3.55×10^{-9}
rs62485509_T	G / G	-0.06 (−)	11%	3.91×10^{-9}
rs58847641_A	G / G	0.07 (−)	22%	3.97×10^{-9}
rs506186_C	C / C	-0.05 (↓)	82%	4.24×10^{-9}
rs10096351_G	A / G	0.06 (↑)	59%	5.10×10^{-9}
rs117618124_C	NA	-0.13 (−)	4%	5.17×10^{-9}
rs2328531_G	G / G	-0.04 (↓)	70%	5.98×10^{-9}
rs5997389_A	G / A	0.08 (↑)	8%	6.07×10^{-9}
rs6569648_T	C / T	0.06 (↑)	83%	6.19×10^{-9}
rs7541276_A	C / A	-0.03 (↓)	38%	6.23×10^{-9}
rs12422552_C	G / C	0.05 (↑)	29%	7.43×10^{-9}
rs2822999_G	T / T	0.05 (−)	13%	7.98×10^{-9}
rs11102701_A	T / T	0.05 (−)	23%	9.65×10^{-9}
rs34810249_C	C / C	0.09 (↑)	21%	1.20×10^{-8}
rs10641009_A	CA / CA	-0.04 (−)	38%	1.38×10^{-8}
rs671888_G	G / G	-0.05 (↓)	54%	1.38×10^{-8}
rs1600346_C	T / C	-0.05 (↓)	17%	1.51×10^{-8}
rs10184522_A	C / C	-0.07 (−)	54%	1.78×10^{-8}
rs11117754_G	T / T	-0.05 (−)	21%	2.32×10^{-8}
rs7785971_A	T / A	0.04 (↑)	43%	2.79×10^{-8}
rs537267133_C	T / T	-0.07 (−)	5%	2.88×10^{-8}
rs199661266_T	/	-0.05 (−)	13%	3.19×10^{-8}
rs12652713_G	A / A	-0.04 (−)	45%	3.65×10^{-8}
rs2587505_C	T / T	-0.04 (−)	50%	3.83×10^{-8}
rs13015648_G	NA	0.08 (−)	5%	4.46×10^{-8}
rs2384061_A	A / A	-0.05 (↓)	44%	5.33×10^{-8}
rs12970390_C	T / C	-0.08 (↓)	27%	5.58×10^{-8}
rs2012709_T	C / T	0.04 (↑)	37%	5.80×10^{-8}
rs7589172_C	C / C	0.06 (↑)	84%	6.37×10^{-8}
rs1469713_G	A / G	0.04 (↑)	41%	7.60×10^{-8}
rs3819405_T	C / T	-0.04 (↓)	37%	1.14×10^{-7}
rs35383942_T	NA	0.09 (−)	4%	1.14×10^{-7}
rs7971_G	A / G	-0.04 (↓)	28%	1.32×10^{-7}
rs7081544_G	A / A	0.06 (−)	12%	1.35×10^{-7}
rs2981578_T	C / T	-0.16 (↓)	37%	1.58×10^{-7}
rs79309050_T	NA	0.10 (−)	1%	1.61×10^{-7}
rs13020413_T	C / C	-0.04 (−)	36%	1.63×10^{-7}
rs4800749_C	A / C	-0.03 (↓)	65%	1.81×10^{-7}
rs17303163_C	T / T	0.08 (−)	6%	1.81×10^{-7}
rs184486140_T	NA	0.30 (−)	1%	1.85×10^{-7}
rs9619765_T	NA	-0.13 (−)	2%	1.99×10^{-7}
rs8137282_G	NA	0.11 (−)	3%	2.43×10^{-7}
rs11583393_A	C / C	-0.05 (−)	22%	2.51×10^{-7}
rs13267382_G	G / G	-0.04 (↓)	46%	3.28×10^{-7}
rs4066743_A	A / A	0.04 (↑)	68%	3.32×10^{-7}
rs7529522_C	T / C	0.05 (↑)	26%	3.42×10^{-7}
rs6500580_G	A / A	0.08 (−)	53%	3.85×10^{-7}
rs62070949_G	G / G	-0.06 (↓)	6%	4.87×10^{-7}
rs555060306_T	/	0.05 (−)	12%	4.87×10^{-7}
rs17513613_C	T / C	0.07 (↑)	26%	5.63×10^{-7}
rs59867004_C	T / T	0.04 (−)	27%	6.24×10^{-7}
rs201000337_T	NA	0.16 (−)	2%	6.48×10^{-7}
rs8063564_A	G / A	0.04 (↑)	36%	7.45×10^{-7}
rs13066793_G	A / A	-0.06 (−)	7%	7.71×10^{-7}
rs78269692_C	NA	0.10 (−)	4%	7.83×10^{-7}
rs16991615_A	NA	0.08 (−)	4%	7.89×10^{-7}
rs11704298_A	NA	0.09 (−)	4%	1.08×10^{-6}
rs11067765_A	T / T	0.05 (−)	13%	1.29×10^{-6}
rs3846498_T	G / G	-0.03 (−)	39%	1.37×10^{-6}
rs17432750_A	C / C	-0.05 (−)	13%	1.37×10^{-6}
rs7730210_A	C / C	-0.03 (−)	38%	3.95×10^{-6}

rs9573140_G	G / G	0.04 (↑)	25%	1.05×10^{-5}
rs180952292_C	NA	0.22 (−)	1%	1.44×10^{-5}
rs149934734_T	NA	-0.16 (−)	1%	1.69×10^{-5}
rs2363956_G	T / G	-0.07 (↓)	48%	2.60×10^{-5}
rs9918437_T	G / G	0.09 (−)	10%	4.18×10^{-5}
rs144101714_G	NA	-0.14 (−)	2%	4.31×10^{-5}
rs7899765_C	T / C	0.12 (↑)	13%	7.61×10^{-5}
rs66496128_T	A / A	-0.06 (−)	24%	8.08×10^{-5}
rs17467658_C	NA	0.20 (−)	1%	1.26×10^{-4}
rs4587_C	C / C	-0.05 (↓)	64%	6.74×10^{-4}
rs184070480_T	NA	0.29 (−)	< 1%	1.17×10^{-3}
rs10472097_T	T / T	-0.15 (↓)	93%	2.30×10^{-3}
rs72764096_C	T / T	-0.03 (−)	12%	5.32×10^{-3}
rs7740686_T	A / A	0.87 (−)	34%	2.43×10^{-1}
rs7763637_A	G / G	-0.76 (−)	34%	3.57×10^{-1}

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.