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Breast cancer (Shu, 2020)

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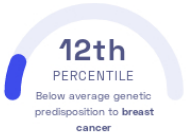
Cancer Breasts

STUDY SUMMARY

Discovery of 28 novel genomic regions associated with breast cancer risk.

YOUR RESULT



STUDY DESCRIPTION

Breast cancer is the second most commonly diagnosed cancer in the United States. Much research has been done to find genetic variants associated with predisposition to breast cancer. However, most studies have been conducted in women of European ancestry, potentially missing breast cancer-associated variants that are less common in Europeans. This genome-wide association study combined genomic data from over 310,000 women of Asian and European descent and identified 28 novel variants associated with breast cancer risk. The study also confirmed over 100 previously identified genetic variants and found differences in genetic risk for breast cancer based on race.

DID YOU KNOW?

Lifestyle changes can reduce the risk of breast cancer, even for women with a genetic predisposition to the disease. Some ways to lower the risk include consuming less alcohol, not smoking, controlling weight, and being physically active.

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 0.38**. 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 **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 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
rs2981578_T	C / T	-0.21 (↓)	51%	2.30×10^{-291}
rs4784227_T	C / T	0.22 (↑)	24%	2.10×10^{-240}
rs4442975_T	T / T	-0.13 (↓)	54%	2.30×10^{-97}
rs75915166_A	C / C	0.26 (–)	6%	1.30×10^{-96}
rs62355902_A	A / A	-0.14 (↓)	83%	2.40×10^{-86}
rs10941679_A	A / A	-0.12 (↓)	73%	1.30×10^{-80}
rs2046210_A	G / G	0.10 (–)	35%	3.20×10^{-74}
rs7297051_T	C / C	-0.12 (–)	24%	5.50×10^{-72}
rs4973768_T	C / C	0.10 (–)	48%	4.90×10^{-62}
rs13281615_A	A / G	-0.09 (↓)	58%	2.30×10^{-55}
rs11249433_A	A / A	-0.09 (↓)	61%	7.80×10^{-54}
rs676256_T	T / T	0.10 (↑)	62%	2.80×10^{-53}
rs10995201_A	G / G	0.13 (–)	84%	5.10×10^{-52}
rs1292011_A	A / A	0.09 (↑)	58%	1.00×10^{-47}
rs34005590_A	C / C	-0.20 (–)	5%	5.30×10^{-41}
rs17356907_A	A / A	0.09 (↑)	71%	1.30×10^{-40}
rs999737_T	C / C	-0.09 (–)	22%	1.20×10^{-38}
rs704010_T	C / C	0.08 (–)	37%	3.40×10^{-38}
rs1432679_T	T / T	-0.07 (↓)	56%	5.10×10^{-37}
rs45631563_A	A / T	0.19 (↑)	96%	1.10×10^{-35}
rs2787486_A	A / A	0.08 (↑)	70%	2.10×10^{-34}
rs6001930_T	T / T	-0.11 (↓)	90%	5.40×10^{-34}
rs16857609_T	C / C	0.07 (–)	27%	2.20×10^{-31}
rs4808801_A	A / A	0.07 (↑)	63%	2.30×10^{-31}
rs13329835_A	A / A	-0.08 (↓)	75%	2.90×10^{-28}
rs2747652_T	T / C	-0.06 (↓)	49%	5.90×10^{-28}
rs10822013_T	C / T	0.06 (↑)	51%	2.90×10^{-27}
rs6828523_A	C / C	-0.09 (–)	16%	4.70×10^{-27}
rs10816625_A	A / A	-0.11 (↓)	93%	7.70×10^{-27}
rs9693444_A	A / A	0.07 (↑)	32%	8.10×10^{-26}
rs2236007_A	G / A	-0.07 (↓)	16%	1.10×10^{-25}
rs4849887_T	C / C	-0.09 (–)	12%	2.10×10^{-25}
rs17817449_T	T / G	0.06 (↑)	60%	5.40×10^{-24}
rs1830298_T	C / C	-0.06 (–)	72%	6.10×10^{-24}
rs6472903_T	T / T	0.08 (↑)	84%	1.10×10^{-23}
rs13365225_A	A / A	0.07 (↑)	79%	1.40×10^{-23}
rs616488_A	G / G	0.06 (–)	68%	1.60×10^{-23}
rs2823093_A	G / G	-0.06 (–)	28%	1.70×10^{-21}
rs10759243_A	C / A	0.06 (↑)	34%	3.40×10^{-21}
rs3817198_T	T / T	-0.06 (↓)	69%	5.50×10^{-21}

rs10069690_T	C / T	0.06 (↑)	35%	2.00×10^{-20}
rs12422552_C	G / C	0.06 (↑)	31%	2.40×10^{-20}
rs11977670_A	A / A	0.05 (↑)	40%	1.10×10^{-19}
rs2290203_G	G / G	0.06 (↑)	70%	2.40×10^{-19}
rs7072776_A	G / G	0.06 (–)	35%	2.40×10^{-19}
rs2943559_A	A / A	-0.09 (↓)	88%	6.90×10^{-19}
rs6762644_A	A / A	-0.05 (↓)	63%	1.00×10^{-18}
rs11814448_A	A / A	-0.17 (↓)	78%	4.00×10^{-18}
rs12628403_C	A / A	0.09 (–)	9%	3.10×10^{-17}
rs7107217_C	A / C	0.05 (↑)	54%	3.90×10^{-17}
rs2992756_T	T / C	0.05 (↑)	47%	5.20×10^{-17}
rs13294895_T	T / T	0.07 (↑)	12%	7.10×10^{-17}
rs10474352_C	C / C	0.06 (↑)	76%	1.10×10^{-16}
rs12493607_C	G / C	0.05 (↑)	29%	2.60×10^{-16}
rs1011970_T	G / G	0.06 (–)	23%	6.40×10^{-16}
rs6796502_A	G / G	-0.07 (–)	14%	7.10×10^{-16}
rs527616_C	G / G	-0.05 (–)	28%	7.70×10^{-16}
rs1436904_T	G / G	0.05 (–)	64%	7.80×10^{-16}
rs28539243_A	G / A	0.05 (↑)	61%	1.10×10^{-15}
rs11820646_T	C / C	-0.04 (–)	35%	3.30×10^{-15}
rs17268829_T	T / T	-0.05 (↓)	78%	4.10×10^{-15}
rs2588809_T	C / C	0.07 (–)	20%	1.30×10^{-14}
rs3760982_A	A / G	0.05 (↑)	43%	1.60×10^{-14}
rs204247_A	A / A	-0.04 (↓)	58%	3.00×10^{-14}
rs12048493_A	A / A	-0.05 (↓)	71%	3.60×10^{-14}
rs738321_C	C / G	0.05 (↑)	61%	7.20×10^{-14}
rs10760444_A	G / A	-0.04 (↓)	51%	8.30×10^{-14}
rs6507583_A	A / A	0.08 (↑)	84%	9.70×10^{-14}
rs1895062_A	A / A	0.04 (↑)	69%	1.10×10^{-13}
rs941764_A	A / A	-0.04 (↓)	54%	1.70×10^{-13}
rs7904519_A	A / G	-0.04 (↓)	47%	1.80×10^{-13}
rs4593472_T	C / C	-0.04 (–)	30%	2.40×10^{-13}
rs11199914_T	C / T	-0.04 (↓)	41%	4.20×10^{-13}
rs58847541_A	G / G	0.06 (–)	19%	4.60×10^{-13}
rs71559437_A	A / A	-0.07 (↓)	8%	9.70×10^{-13}
rs7707921_A	A / A	0.05 (↑)	81%	1.30×10^{-12}
rs6569648_T	C / T	0.05 (↑)	85%	1.90×10^{-12}
rs13267382_A	G / G	0.04 (–)	55%	2.00×10^{-12}
rs6597981_A	G / G	-0.04 (–)	39%	2.50×10^{-12}
rs2016394_A	G / G	-0.04 (–)	39%	2.60×10^{-12}
rs6964587_T	G / T	0.04 (↑)	41%	2.70×10^{-12}
rs58058861_A	G / A	0.05 (↑)	20%	3.40×10^{-12}
rs12546444_A	A / T	0.07 (↑)	92%	3.90×10^{-12}
rs3903072_T	T / T	-0.04 (↓)	34%	5.70×10^{-12}
rs9485372_G	G / G	0.05 (↑)	79%	7.60×10^{-12}
rs2965183_A	G / A	0.04 (↑)	44%	9.80×10^{-12}
rs117618124_T	T / T	0.10 (↑)	97%	1.10×10^{-11}
rs514192_A	T / T	0.04 (–)	41%	1.20×10^{-11}
rs6815814_A	A / A	-0.04 (↓)	54%	1.30×10^{-11}
rs720475_A	G / G	-0.05 (–)	19%	1.90×10^{-11}
rs11075995_A	A / T	0.04 (↑)	23%	3.20×10^{-11}
rs745570_A	A / G	0.04 (↑)	41%	3.30×10^{-11}
rs6122906_A	A / A	-0.05 (↓)	76%	3.70×10^{-11}
rs6725517_A	G / G	0.04 (–)	49%	4.50×10^{-11}
rs76535198_A NEW	A / A	0.05 (↑)	83%	5.40×10^{-11}
rs12710696_T	T / C	0.04 (↑)	41%	6.30×10^{-11}
rs73006998_A NEW	G / G	-0.07 (–)	22%	1.10×10^{-10}
rs35418111_A NEW	G / G	0.07 (–)	12%	1.10×10^{-10}
rs17350191_T	C / T	0.04 (↑)	50%	1.10×10^{-10}
rs4496150_A	C / C	-0.04 (–)	22%	1.90×10^{-10}
rs12207986_A	A / A	0.04 (↑)	36%	2.00×10^{-10}

rs11627032_T	T / C	0.04 (↑)	76%	2.00×10^{-10}
rs4971059_A	A / A	0.04 (↑)	43%	2.20×10^{-10}
rs2432539_A	A / G	0.04 (↑)	29%	2.70×10^{-10}
rs10022462_T	C / T	0.04 (↑)	29%	3.00×10^{-10}
rs9833888_T	G / G	0.04 (–)	17%	3.10×10^{-10}
rs1707302_A	G / G	-0.04 (–)	38%	3.40×10^{-10}
rs17529111_T	T / T	-0.04 (↓)	83%	3.40×10^{-10}
rs2594714_A	G / A	-0.04 (↓)	42%	3.80×10^{-10}
rs10838267_A NEW	G / G	0.04 (–)	51%	4.20×10^{-10}
rs8027365_A NEW	A / C	0.04 (↑)	71%	4.60×10^{-10}
rs4562056_T	G / G	0.04 (–)	39%	4.60×10^{-10}
rs8176636_T	/	0.05 (–)	17%	4.90×10^{-10}
rs113577745_C	C / C	-0.06 (↓)	94%	5.00×10^{-10}
rs7529522_T	T / C	-0.04 (↓)	68%	5.10×10^{-10}
rs1550623_A	A / A	0.05 (↑)	83%	5.60×10^{-10}
rs6882649_T	G / T	0.04 (↑)	39%	5.70×10^{-10}
rs1053338_A	A / A	-0.05 (↓)	89%	6.70×10^{-10}
rs77528541_T	G / G	-0.06 (–)	9%	7.20×10^{-10}
rs16992204_C	T / T	0.12 (–)	5%	7.80×10^{-10}
rs12481286_T NEW	G / G	0.04 (–)	26%	1.10×10^{-9}
rs11552449_T	C / C	0.04 (–)	24%	1.20×10^{-9}
rs6562760_A	G / G	-0.04 (–)	17%	1.30×10^{-9}
rs9790517_T	C / C	0.04 (–)	28%	1.50×10^{-9}
rs11780156_T	C / C	0.05 (–)	14%	1.50×10^{-9}
rs6940159_T NEW	T / T	-0.04 (↓)	43%	1.70×10^{-9}
rs6555134_T NEW	T / T	-0.03 (↓)	54%	2.90×10^{-9}
rs1353747_T	T / G	0.06 (↑)	95%	3.30×10^{-9}
rs2758598_A NEW	G / G	0.04 (–)	31%	3.60×10^{-9}
rs72906468_A NEW	A / A	0.04 (↑)	76%	4.00×10^{-9}
rs2901157_A NEW	A / A	0.05 (↑)	85%	4.00×10^{-9}
rs11117758_A	G / G	-0.04 (–)	17%	4.40×10^{-9}
rs12405132_T	G / A	-0.04 (–)	21%	5.20×10^{-9}
rs3790585_A NEW	A / A	0.04 (↑)	81%	5.30×10^{-9}
rs10820600_T NEW	T / T	-0.03 (↓)	48%	5.70×10^{-9}
rs855596_T NEW	NA	-0.09 (–)	4%	7.50×10^{-9}
rs66823261_T	C / C	-0.04 (–)	75%	1.10×10^{-8}
rs28512361_A	G / A	0.06 (↑)	14%	1.40×10^{-8}
rs6756513_A NEW	G / G	-0.04 (–)	29%	1.50×10^{-8}
rs17426269_A	G / G	0.05 (–)	8%	1.50×10^{-8}
rs11944638_T NEW	T / T	0.06 (↑)	85%	1.60×10^{-8}
rs4233486_T	C / T	0.04 (↑)	69%	1.60×10^{-8}
rs7765429_T NEW	T / T	-0.03 (↓)	49%	1.70×10^{-8}
rs4951011_G	A / A	0.04 (–)	20%	1.80×10^{-8}
rs7768862_A NEW	T / T	-0.03 (–)	48%	2.00×10^{-8}
rs2223621_T	C / C	0.03 (–)	32%	2.00×10^{-8}
rs9316500_T NEW	T / G	0.03 (↑)	64%	2.10×10^{-8}
rs6596100_T	C / C	-0.04 (–)	21%	2.10×10^{-8}
rs17156577_T	T / C	-0.05 (↓)	81%	2.30×10^{-8}
rs12479355_A	A / A	0.04 (↑)	79%	3.80×10^{-8}
rs6805189_T	C / C	0.03 (–)	70%	4.40×10^{-8}
rs11947923_T NEW	C / T	-0.03 (↓)	36%	4.50×10^{-8}
rs2849506_C NEW	G / C	-0.03 (↓)	41%	4.70×10^{-8}
rs75004998_A NEW	G / A	-0.03 (↓)	36%	4.90×10^{-8}
rs206966_T	C / T	0.05 (↑)	15%	5.00×10^{-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.