

🌟 Coronary artery disease (Koyama, 2020)

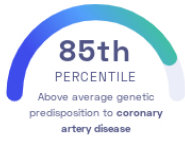
Satoshi Koyama, et al.
Nature Genetics

Heart Vasculature

STUDY SUMMARY

Identification of 175 genomic regions associated with the risk of coronary artery disease.

YOUR RESULT



STUDY DESCRIPTION

Like all other organs and tissues in the body, the heart requires a supply of blood to function. For the heart, the system that supplies its blood is known as the coronary circulation. Coronary artery disease occurs when the coronary arteries become damaged or diseased. As a consequence of decreased blood flow, less oxygen can reach the heart. Over time, this may result in heart attacks, making coronary artery disease the leading cause of death for both men and women. To identify the genetic factors that contribute to the development of coronary artery disease, this study examined over 168,000 individuals of Japanese ancestry. A trans-ethnic analysis that also included data from Europeans found 175 genomic regions that are associated with coronary artery disease across different ethnicities. This included 40 genetic variants that had not previously been known. Together, the identified variants may explain nearly 13% of the heritability of coronary artery disease.









DID YOU KNOW?



























A major avoidable risk factor for coronary artery disease is smoking. Even individuals who inhale smoke second-hand, have an increased risk of developing coronary artery disease.







YOUR DETAILED RESULTS

To calculate your genetic predisposition to coronary artery disease we summed up the effects of genetic variants that were linked to coronary artery disease 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 coronary artery disease. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to coronary artery disease. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to coronary artery disease. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for coronary artery disease to be 0.75**. 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 coronary artery disease is in the **85th percentile**. This means that it is higher than the polygenic scores 85% of people. We consider this to be an **above average genetic predisposition to coronary artery disease**. 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 [Ⓞ]
rs2891168_G	A / A	0.18 (-)	48%	3.80×10^{-296}
rs9349379_G	A / G	0.11 (↑)	40%	4.30×10^{-104}
rs56393506_T	C / C	0.15 (-)	17%	3.30×10^{-103}
rs12740374_T	G / G	-0.11 (-)	22%	1.50×10^{-62}
rs35158675_A	A / A	0.08 (↑)	70%	5.10×10^{-48}
rs11065783_G	NA	0.15 (-)	1%	3.80×10^{-47}
rs2327429_C	T / C	-0.07 (↓)	30%	1.50×10^{-46}
rs7173743_C	T / C	-0.07 (↓)	46%	4.20×10^{-44}
rs2839812_A	T / A	-0.07 (↓)	71%	4.40×10^{-43}
rs6841473_T	C / T	0.08 (↑)	14%	1.10×10^{-38}
rs7177338_A	G / A	-0.06 (↓)	53%	1.80×10^{-34}
rs61194703_T	A / A	-0.10 (-)	12%	8.60×10^{-34}
rs141622900_A	G / G	-0.14 (-)	6%	1.20×10^{-31}
rs2107595_A	G / A	0.07 (↑)	16%	1.40×10^{-31}
rs7691175_T	G / T	0.06 (↑)	46%	1.80×10^{-30}
rs72664335_T	G / G	-0.11 (-)	9%	2.80×10^{-30}
rs1412444_T	C / C	0.06 (-)	34%	4.00×10^{-29}
rs16986953_A	G / G	0.08 (-)	8%	7.20×10^{-29}
rs1870634_G	G / G	0.06 (↑)	66%	9.70×10^{-29}
rs9515203_C	C / C	-0.06 (↓)	26%	5.10×10^{-27}
rs3796587_G	C / C	-0.07 (-)	18%	5.20×10^{-27}
rs140244541_A	G / A	0.08 (↑)	15%	5.50×10^{-27}
rs10406816_G	A / G	-0.05 (↓)	51%	9.80×10^{-27}
rs745386_G	C / C	-0.07 (-)	10%	1.60×10^{-26}
rs8046696_G	T / G	0.05 (↑)	59%	1.10×10^{-26}
rs2681472_G	A / A	0.06 (-)	17%	6.80×10^{-26}
rs11107903_A	G / G	-0.08 (-)	7%	3.60×10^{-24}
rs11191447_T	C / C	-0.07 (-)	8%	1.50×10^{-23}
rs12893887_A	A / A	-0.06 (↓)	17%	2.20×10^{-22}
rs28601761_G	C / C	-0.05 (-)	41%	7.40×10^{-22}
rs72874178_A	G / A	-0.05 (↓)	23%	1.00×10^{-20}
rs185244_T	C / C	0.06 (-)	16%	1.30×10^{-20}
rs507666_A	A / A	0.06 (↑)	18%	2.00×10^{-20}
rs2296285_A	T / A	0.05 (↑)	33%	4.50×10^{-20}
rs17228058_G	A / A	-0.06 (-)	23%	1.40×10^{-19}
rs10488763_T	A / T	0.06 (↑)	13%	2.80×10^{-19}
rs1133773_G	A / G	0.06 (↑)	24%	4.00×10^{-19}
rs8072532_A	G / A	0.05 (↑)	70%	5.30×10^{-19}
rs16998073_T	T / T	0.05 (↑)	29%	6.40×10^{-19}

rs7500448_G	A / A	-0.05 (-)	25%	1.60 x 10 ⁻¹⁸
rs13200993_T	T / T	0.04 (↑)	37%	2.60 x 10 ⁻¹⁸
rs56714120_T	G / G	0.05 (-)	32%	1.20 x 10 ⁻¹⁷
rs11566924_T	C / C	-0.05 (-)	37%	1.30 x 10 ⁻¹⁷
rs11752218_T	C / T	0.09 (↑)	7%	1.50 x 10 ⁻¹⁷
rs3741380_A	G / A	0.04 (↑)	47%	2.00 x 10 ⁻¹⁷
rs35462537_G	A / G	-0.04 (↓)	53%	2.60 x 10 ⁻¹⁷
rs13702_C	T / C	-0.05 (↓)	29%	3.80 x 10 ⁻¹⁷
rs4845625_C	C / C	-0.04 (↓)	58%	6.40 x 10 ⁻¹⁷
rs10841443_G	G / G	0.04 (↑)	66%	7.50 x 10 ⁻¹⁷
rs11066707_A	NA	0.13 (-)	1%	8.20 x 10 ⁻¹⁷
rs7277800_A	G / A	0.05 (↑)	26%	1.10 x 10 ⁻¹⁶
rs1476098_C	C / C	-0.05 (↓)	79%	3.00 x 10 ⁻¹⁶
rs781668_A	G / G	0.05 (-)	19%	1.20 x 10 ⁻¹⁶
rs10947786_A	G / A	-0.05 (↓)	21%	1.60 x 10 ⁻¹⁶
rs11601507_A	C / C	0.08 (-)	7%	3.70 x 10 ⁻¹⁶
rs7251815_T	G / T	0.05 (↑)	22%	4.20 x 10 ⁻¹⁶
rs1169288_C	A / C	0.04 (↑)	31%	5.80 x 10 ⁻¹⁶
rs2505083_C	T / C	0.04 (↑)	42%	5.90 x 10 ⁻¹⁶
rs1154988_A	A / A	0.05 (↑)	77%	6.70 x 10 ⁻¹⁶
rs13134800_C	T / C	-0.04 (↓)	71%	9.90 x 10 ⁻¹⁶
rs1050382_A	A / A	0.04 (↑)	53%	1.20 x 10 ⁻¹⁴
rs998584_A	C / C	0.04 (-)	48%	2.40 x 10 ⁻¹⁴
rs34372836_G	A / A	0.04 (-)	30%	2.70 x 10 ⁻¹⁴
rs56215311_C	T / C	-0.04 (↓)	60%	5.00 x 10 ⁻¹⁴
rs7090277_A	T / A	-0.04 (↓)	51%	7.80 x 10 ⁻¹⁴
rs604723_C	C / C	0.04 (↑)	73%	8.40 x 10 ⁻¹⁴
rs662799_A	A / A	-0.05 (↓)	93%	8.90 x 10 ⁻¹⁴
rs61776719_A	C / A	0.04 (↑)	54%	9.20 x 10 ⁻¹⁴
rs1967604_G	G / G	-0.04 (↓)	72%	9.80 x 10 ⁻¹⁴
rs10985348_C	G / G	0.04 (-)	26%	1.10 x 10 ⁻¹³
rs378825_G	A / G	0.04 (↑)	57%	1.30 x 10 ⁻¹³
rs11099493_G	A / G	-0.04 (↓)	32%	1.60 x 10 ⁻¹³
rs12469768_A	NA	0.10 (-)	2%	2.10 x 10 ⁻¹³
rs35093463_A 	C / C	0.06 (-)	6%	3.40 x 10 ⁻¹³
rs9624456_T	NA	-0.09 (-)	2%	3.90 x 10 ⁻¹³
rs7486666_G	A / A	0.04 (-)	15%	4.20 x 10 ⁻¹³
rs4678145_C	G / C	0.06 (↑)	13%	4.40 x 10 ⁻¹³
rs948386_C 	G / C	0.04 (↑)	58%	8.10 x 10 ⁻¹³
rs34042070_G	C / C	0.04 (-)	19%	9.40 x 10 ⁻¹³
rs175040_G	A / G	-0.04 (↓)	48%	1.10 x 10 ⁻¹²
rs7229520_A	G / A	0.04 (↑)	66%	1.10 x 10 ⁻¹²
rs34232196_T	C / C	-0.04 (-)	25%	1.50 x 10 ⁻¹²
rs2421028_G	A / A	0.04 (-)	45%	1.90 x 10 ⁻¹²
rs7566501_T 	C / C	-0.04 (-)	42%	1.90 x 10 ⁻¹²
rs2074164_C	G / C	0.04 (↑)	20%	3.00 x 10 ⁻¹²
rs6704_A	C / C	0.04 (-)	30%	3.10 x 10 ⁻¹²
rs11204892_G	G / G	0.04 (↑)	83%	5.20 x 10 ⁻¹²
rs10797374_G	C / C	-0.05 (-)	13%	5.60 x 10 ⁻¹²
rs11968400_T	C / C	0.07 (-)	6%	6.30 x 10 ⁻¹²
rs11080107_C	C / C	0.03 (↑)	49%	9.90 x 10 ⁻¹²
rs28522673_C 	G / G	0.04 (-)	17%	1.80 x 10 ⁻¹¹
rs12469628_C 	T / T	-0.04 (-)	16%	1.90 x 10 ⁻¹¹
rs7703260_C	T / C	0.04 (↑)	17%	2.40 x 10 ⁻¹¹
rs1250259_A	A / A	-0.04 (↓)	74%	2.70 x 10 ⁻¹¹
rs4561781_G	A / G	0.04 (↑)	31%	2.80 x 10 ⁻¹¹
rs73392700_C 	NA	0.06 (-)	5%	3.30 x 10 ⁻¹¹
rs11000448_G 	T / T	-0.05 (-)	7%	3.90 x 10 ⁻¹¹
rs2161967_G	T / G	-0.03 (↓)	56%	6.60 x 10 ⁻¹¹
rs8124182_A	G / G	0.04 (-)	15%	6.80 x 10 ⁻¹¹
rs9556903_A 	G / G	-0.04 (-)	11%	7.90 x 10 ⁻¹¹

rs7484641_T	A / A	-0.04 (-)	22%	7.90×10^{-11}
rs4723406_A 	C / C	-0.03 (-)	38%	7.90×10^{-11}
rs869396_A	C / A	-0.03 (↓)	47%	8.00×10^{-11}
rs302953_T	T / T	0.03 (↑)	56%	8.00×10^{-11}
rs61797063_A	C / A	-0.04 (↓)	16%	8.50×10^{-11}
rs2832232_G	A / A	0.04 (-)	17%	1.00×10^{-10}
rs6001960_G	A / G	-0.04 (↓)	74%	1.40×10^{-10}
rs76964792_T	C / T	0.04 (↑)	22%	1.50×10^{-10}
rs12714767_C 	T / T	-0.04 (-)	24%	1.50×10^{-10}
rs259990_C	A / C	0.05 (↑)	14%	2.20×10^{-10}
rs197907_C	G / C	0.03 (↑)	28%	2.40×10^{-10}
rs11552449_T 	C / C	0.04 (-)	17%	3.70×10^{-10}
rs6006426_A 	G / G	0.03 (-)	55%	4.10×10^{-10}
rs1879454_A 	A / A	-0.04 (↓)	82%	4.50×10^{-10}
rs1481345_C 	T / C	-0.03 (↓)	58%	4.70×10^{-10}
rs2952286_G 	T / G	0.04 (↑)	79%	5.30×10^{-10}
rs6102322_T	C / T	0.03 (↑)	32%	5.40×10^{-10}
rs9995627_T	T / T	-0.07 (↓)	96%	5.60×10^{-10}
rs2820315_T	C / T	0.04 (↑)	31%	7.10×10^{-10}
rs11977187_T	T / T	-0.03 (↓)	71%	8.10×10^{-10}
rs2623168_G 	A / G	0.05 (↑)	12%	1.10×10^{-9}
rs7115190_T 	C / T	0.03 (↑)	33%	1.60×10^{-9}
rs10806235_T	C / T	0.03 (↑)	39%	2.10×10^{-9}
rs12625329_A 	G / G	-0.03 (-)	44%	2.10×10^{-9}
rs35885398_T	C / T	-0.04 (↓)	17%	2.20×10^{-9}
rs13105983_A 	G / A	-0.03 (↓)	44%	2.80×10^{-9}
rs7998440_A	A / A	-0.03 (↓)	37%	3.10×10^{-9}
rs7926712_G	G / G	0.03 (↑)	70%	3.20×10^{-9}
rs35224956_G 	A / A	0.03 (-)	36%	3.20×10^{-9}
rs10006310_G	T / T	-0.03 (-)	48%	3.20×10^{-9}
rs7604403_A 	G / A	0.03 (↑)	30%	3.50×10^{-9}
rs663129_A	G / A	0.03 (↑)	24%	3.50×10^{-9}
rs12444314_G 	A / A	0.03 (-)	28%	3.60×10^{-9}
rs7580831_A	A / A	-0.03 (↓)	32%	3.60×10^{-9}
rs11167260_A	G / G	-0.05 (-)	9%	3.60×10^{-9}
rs7420881_C 	C / C	0.03 (↑)	69%	3.90×10^{-9}
rs4076834_G	T / G	-0.06 (↓)	7%	4.00×10^{-9}
rs6593297_T 	T / T	-0.03 (↓)	70%	4.00×10^{-9}
rs12028817_G	A / G	-0.03 (↓)	52%	4.60×10^{-9}
rs2607903_A 	A / A	-0.04 (↓)	91%	4.80×10^{-9}
rs603424_A 	G / A	0.04 (↑)	19%	5.80×10^{-9}
rs72822411_A 	G / G	0.04 (-)	25%	6.10×10^{-9}
rs582384_A	C / A	0.03 (↑)	53%	6.30×10^{-9}
rs1307145_G 	C / C	0.03 (-)	41%	7.20×10^{-9}
rs77620124_G	A / G	-0.04 (↓)	13%	8.60×10^{-9}
rs9549328_T	C / C	0.03 (-)	23%	8.70×10^{-9}
rs13255004_T 	T / T	0.03 (↑)	78%	1.10×10^{-8}
rs34880628_T	C / C	0.03 (-)	35%	1.20×10^{-8}
rs1051860_G	G / G	-0.03 (↓)	58%	1.20×10^{-8}
rs2286200_G	A / G	-0.03 (↓)	32%	1.40×10^{-8}
rs9693598_A 	G / G	-0.04 (-)	12%	1.60×10^{-8}
rs11947277_T	C / T	0.03 (↑)	26%	1.60×10^{-8}
rs9351209_G 	G / G	-0.03 (↓)	63%	1.80×10^{-8}
rs2493135_G	C / G	0.03 (↑)	42%	2.30×10^{-8}
rs2744427_T 	G / G	-0.04 (-)	10%	2.40×10^{-8}
rs1727949_C	C / C	0.04 (↑)	85%	2.40×10^{-8}
rs13354746_T 	T / T	0.03 (↑)	22%	2.50×10^{-8}
rs7928523_T	C / C	0.03 (-)	32%	3.00×10^{-8}
rs11509880_A	G / A	0.03 (↑)	35%	3.00×10^{-8}
rs7680806_C 	C / C	0.04 (↑)	20%	3.00×10^{-8}

rs1893261_A	G / A	0.03 (↑)	38%	3.10×10^{-8}
rs2076438_C 	C / C	0.03 (↑)	37%	3.10×10^{-8}
rs2008603_T	C / C	-0.04 (-)	14%	3.20×10^{-8}
rs11230728_G 	A / G	-0.04 (↓)	11%	3.60×10^{-8}
rs4794213_T 	T / T	-0.03 (↓)	37%	3.60×10^{-8}
rs2111485_G 	A / G	0.03 (↑)	59%	3.70×10^{-8}
rs216168_G 	C / C	-0.03 (-)	42%	3.90×10^{-8}
rs12897_A	A / A	-0.03 (↓)	61%	4.10×10^{-8}
rs11133381_C 	T / T	-0.03 (-)	37%	4.80×10^{-8}
rs10268797_G	G / G	0.04 (↑)	81%	5.10×10^{-8}
rs4646248_T	C / T	-0.03 (↓)	71%	5.40×10^{-8}
rs11718165_G	G / G	-0.03 (↓)	29%	5.80×10^{-8}
rs1508798_C	T / C	-0.04 (↓)	19%	6.20×10^{-8}
rs10063823_C	T / C	-0.03 (↓)	34%	7.90×10^{-7}
rs7088704_C	T / C	-0.03 (↓)	34%	2.90×10^{-6}

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.