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PR interval (Ntalla, 2020)

Ioanna Ntalla, et al.
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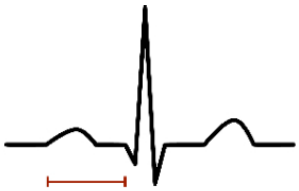
Heart

STUDY SUMMARY

Discovery of 202 regions of the genome associated with the heart's PR interval duration.



The PR interval in an electrocardiogram.

YOUR RESULT

9th
PERCENTILE
Low genetic predisposition to **longer PR interval**

STUDY DESCRIPTION

The heart beats at regular intervals to pump blood through the body. To control the timing of a heartbeat, the heart relies on a system that sends electrical signals to the heart's muscle cells. The electrocardiogram, or ECG, is a commonly used medical procedure to measure the electrical activity during a heartbeat. The PR interval is the time between the activation of the heart's *atria* and the activation of the *ventricles*. A normal PR interval duration is between 0.12 and 0.20 seconds. A PR interval duration that is too short, too long, or irregular can be an indication for heart disease. The genome-wide association study examined nearly 300,000 individuals of European, African, Hispanic, and Brazilian descent to identify variants associated with the heart's PR interval duration. The researchers identified 202 genomic regions, 141 of which are novel. Some of the variants are near genes involved in the development and contraction of the heart's muscles. Together, the identified variants may explain over 62% of the heritability of the heart's PR interval duration.

DID YOU KNOW?

The average human heart beats between 60 and 100 times per minute while resting. This adds up to over 100,000 times per day! Many factors influence the heart rate, including fitness, stress, body size, temperature, and diet.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to longer PR interval we summed up the effects of genetic variants that were linked to longer PR interval 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 longer PR interval. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to longer PR interval. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to longer PR interval. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for longer PR interval to be 128.02**. 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 longer PR interval is in the **9th percentile**. This means that it is higher than the polygenic scores 9% of people. We consider this to be a **low genetic predisposition to longer PR interval**. 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
rs6801957_T	T / C	3.49 (↑)	40%	5.69×10^{-634}
rs3807989_A	A / G	1.92 (↑)	41%	2.61×10^{-194}
rs2624021_T	A / T	1.98 (↑)	68%	1.73×10^{-178}
rs4246224_G	G / G	2.27 (↑)	86%	1.69×10^{-138}
rs3891585_A	G / G	1.35 (–)	39%	7.57×10^{-96}
rs1124477_T	C / C	1.22 (–)	31%	2.77×10^{-69}
rs6730558_T	C / C	1.14 (–)	39%	5.88×10^{-68}
rs29795_A	G / A	1.01 (↑)	57%	4.71×10^{-55}
rs2754171_C	C / T	4.26 (↑)	98%	5.23×10^{-55}
rs35712872_G	A / A	1.19 (–)	25%	1.71×10^{-54}
rs11153730_T	T / C	1.00 (↑)	51%	2.54×10^{-54}
rs10883908_T	C / T	0.98 (↑)	41%	5.44×10^{-52}
rs6441111_C	C / T	0.97 (↑)	51%	1.02×10^{-51}
rs2503715_G	A / G	1.60 (↑)	87%	1.07×10^{-51}
rs12869776_A	A / G	0.98 (↑)	60%	1.23×10^{-51}
rs116532272_G	G / G	3.74 (↑)	98%	6.67×10^{-49}
rs4245338_G	A / A	0.82 (–)	35%	4.03×10^{-35}
rs2732814_A	A / A	0.77 (↑)	49%	3.60×10^{-34}
rs4677294_T	T / T	0.83 (↑)	67%	4.80×10^{-34}
rs61989382_C	T / T	0.86 (–)	25%	1.01×10^{-31}
rs35680304_T	C / T	0.76 (↑)	58%	3.81×10^{-31}
rs10882644_T	C / T	0.76 (↑)	38%	8.85×10^{-31}
rs114555443_C	T / T	1.74 (–)	6%	2.15×10^{-29}
rs2042995_C	T / T	0.82 (–)	25%	8.30×10^{-28}
rs60325252_C NEW	C / C	0.75 (↑)	71%	9.10×10^{-27}
rs1531447_C	C / C	0.70 (↑)	62%	3.88×10^{-26}
rs72690486_T	T / T	2.31 (↑)	98%	1.19×10^{-25}
rs4834347_A	C / A	0.78 (↑)	25%	1.72×10^{-25}
rs4971089_A	G / G	0.66 (–)	50%	2.45×10^{-25}
rs757416_T NEW	T / C	0.69 (↑)	63%	2.50×10^{-25}
rs17496249_A NEW	G / G	0.64 (–)	55%	1.40×10^{-23}
rs10039283_A NEW	G / A	0.64 (↑)	41%	3.20×10^{-23}
rs340397_T	G / G	0.63 (–)	38%	6.23×10^{-22}
rs72671655_T	T / T	1.73 (↑)	96%	6.80×10^{-22}
rs4975572_T NEW	C / C	0.62 (–)	46%	5.50×10^{-21}
rs13131421_C	T / C	0.59 (↑)	53%	2.68×10^{-20}
rs6795775_T	C / T	0.66 (↑)	28%	1.03×10^{-19}

rs6442433_C	C / C	0.71 (↑)	79%	1.90×10^{-19}
rs2004851_A	C / C	0.63 (–)	33%	2.42×10^{-19}
rs7394152_C	C / C	0.79 (↑)	85%	2.64×10^{-19}
rs881299_C	T / C	0.58 (↑)	40%	2.79×10^{-19}
rs41306688_C	NA	1.65 (–)	5%	3.90×10^{-19}
rs17026114_G	A / A	1.23 (–)	8%	5.02×10^{-19}
rs4871397_G	C / C	1.19 (–)	6%	1.44×10^{-18}
rs982521_C	T / T	0.75 (–)	18%	1.70×10^{-18}
rs6922960_C	C / C	0.61 (↑)	28%	5.60×10^{-18}
rs1084537_T	C / C	0.56 (–)	39%	9.66×10^{-18}
rs6496452_A	A / A	0.55 (↑)	55%	1.30×10^{-17}
rs3759310_G	C / G	0.56 (↑)	36%	4.50×10^{-17}
rs763076_G	A / A	0.85 (–)	13%	5.33×10^{-17}
rs117443987_T	T / A	1.00 (↑)	92%	6.10×10^{-17}
rs2137897_T	C / C	0.65 (–)	21%	6.78×10^{-17}
rs4687352_A	A / A	0.53 (↑)	41%	1.30×10^{-16}
rs56352403_G	G / A	0.56 (↑)	64%	1.40×10^{-16}
rs1692144_C	C / C	0.65 (↑)	79%	1.70×10^{-16}
rs12443745_C	C / C	0.94 (↑)	91%	1.89×10^{-16}
rs72825038_A	G / G	0.94 (–)	9%	2.70×10^{-16}
rs2070464_G	G / G	0.54 (↑)	38%	6.20×10^{-16}
rs16989138_G	G / G	0.53 (↑)	43%	7.10×10^{-16}
rs11921457_T	G / G	0.69 (–)	81%	8.00×10^{-16}
rs871728_C	T / T	0.52 (–)	42%	1.30×10^{-15}
rs1285678_A	G / G	0.52 (–)	47%	2.60×10^{-15}
rs74772720_A	C / C	0.73 (–)	14%	4.59×10^{-15}
rs2970854_G	T / T	0.57 (–)	26%	5.13×10^{-15}
rs730506_C	G / G	0.62 (–)	20%	6.50×10^{-15}
rs35214871_T	G / G	0.72 (–)	15%	7.63×10^{-15}
rs7199856_G	T / T	0.56 (–)	26%	8.60×10^{-15}
rs12616546_A	G / A	0.53 (↑)	68%	9.20×10^{-15}
rs74537277_C	/	0.89 (–)	9%	1.48×10^{-14}
rs3768419_C	G / C	0.49 (↑)	48%	1.60×10^{-14}
rs4959193_A	G / G	0.49 (–)	44%	1.61×10^{-14}
rs57214150_C	G / G	0.59 (–)	21%	3.69×10^{-14}
rs1255908_T	T / T	0.52 (↑)	69%	6.00×10^{-14}
rs13006682_C	T / C	0.51 (↑)	34%	6.70×10^{-14}
rs4680046_T	C / C	0.47 (–)	49%	1.20×10^{-13}
rs2912774_T	G / G	0.48 (–)	42%	1.30×10^{-13}
rs12751675_G	G / G	0.56 (↑)	75%	1.80×10^{-13}
rs4894803_G	A / A	0.49 (–)	39%	1.80×10^{-13}
rs1816959_A	A / A	0.49 (↑)	66%	2.16×10^{-13}
rs62441680_C	T / T	0.62 (–)	17%	2.30×10^{-13}
rs4868384_T	A / T	0.47 (↑)	47%	2.50×10^{-13}
rs12808601_G	G / G	0.51 (↑)	70%	3.10×10^{-13}
rs62008078_C	C / C	0.48 (↑)	44%	4.40×10^{-13}
rs17441816_G	G / G	0.51 (↑)	29%	4.70×10^{-13}
rs6678632_T	T / C	0.47 (↑)	44%	4.90×10^{-13}
rs28414612_T	C / C	0.57 (–)	75%	5.16×10^{-13}
rs4584185_C	C / T	0.48 (↑)	45%	6.10×10^{-13}
rs61824886_C	C / C	0.67 (↑)	85%	6.20×10^{-13}
rs58577564_A	T / A	0.78 (↑)	10%	7.50×10^{-13}
rs28468565_A	A / A	0.49 (↑)	66%	8.90×10^{-13}
rs10862858_A	A / G	0.46 (↑)	43%	1.10×10^{-12}
rs78810186_T	C / T	0.74 (↑)	11%	1.40×10^{-12}
rs1015149_T	C / T	0.45 (↑)	47%	1.60×10^{-12}
rs35006907_A	C / C	0.48 (–)	31%	1.60×10^{-12}
rs2629745_A	A / G	0.69 (↑)	88%	1.70×10^{-12}
rs62003514_C	C / C	0.68 (↑)	82%	1.85×10^{-12}

rs8039168_A	A / T	0.60 (↑)	83%	2.00×10^{-12}
rs28634651_T	T / C	0.51 (↑)	61%	2.10×10^{-12}
rs6560168_T	T / T	0.45 (↑)	45%	2.20×10^{-12}
rs11894252_T	T / C	0.45 (↑)	42%	2.30×10^{-12}
rs1188285_C	C / C	0.45 (↑)	56%	2.40×10^{-12}
rs4519566_G	G / G	0.54 (↑)	79%	4.70×10^{-12}
rs2625322_G	G / G	0.52 (↑)	77%	4.94×10^{-12}
rs7146955_G	G / G	0.44 (↑)	59%	6.70×10^{-12}
rs6023939_C	C / A	0.44 (↑)	54%	6.70×10^{-12}
rs17099893_A	G / G	0.95 (–)	6%	9.90×10^{-12}
rs1769758_T	T / T	0.50 (↑)	50%	1.00×10^{-11}
rs12961264_C	T / T	0.51 (–)	23%	1.10×10^{-11}
rs7972416_A	A / A	0.45 (↑)	66%	1.80×10^{-11}
rs206708_A	T / T	0.47 (–)	70%	1.90×10^{-11}
rs9513995_T	T / T	0.50 (↑)	74%	2.10×10^{-11}
rs442177_T	G / G	0.43 (–)	59%	2.57×10^{-11}
rs11786896_T	NA	1.09 (–)	5%	2.69×10^{-11}
rs10776558_C	T / T	0.42 (–)	53%	2.80×10^{-11}
rs3784192_A	G / A	0.55 (↑)	20%	3.00×10^{-11}
rs55866125_T	T / T	0.42 (↑)	52%	3.20×10^{-11}
rs603901_T	T / T	0.43 (↑)	58%	3.30×10^{-11}
rs2004359_G	G / G	0.42 (↑)	47%	5.00×10^{-11}
rs10770646_T	T / T	0.53 (↑)	79%	6.40×10^{-11}
rs62472627_C	T / T	0.61 (–)	14%	6.70×10^{-11}
rs1786595_C	C / T	0.47 (↑)	74%	6.90×10^{-11}
rs3795063_C	G / G	0.49 (–)	65%	7.30×10^{-11}
rs214502_A	C / C	0.42 (–)	58%	9.90×10^{-11}
rs13023533_T	T / C	0.41 (↑)	55%	1.10×10^{-10}
rs3759579_A	A / G	0.42 (↑)	41%	1.20×10^{-10}
rs3935716_A	G / G	0.61 (–)	15%	1.20×10^{-10}
rs76611452_T	NA	1.19 (–)	4%	1.50×10^{-10}
rs76909456_G	A / A	0.48 (–)	24%	1.80×10^{-10}
rs17712080_G	A / A	0.47 (–)	75%	2.00×10^{-10}
rs7629220_C	T / C	0.58 (↑)	84%	2.10×10^{-10}
rs78518764_T	T / T	0.61 (↑)	86%	2.10×10^{-10}
rs79321945_C	C / C	0.50 (↑)	78%	2.10×10^{-10}
rs94111_G	G / G	0.42 (↑)	64%	2.13×10^{-10}
rs4869412_G	A / A	0.40 (–)	49%	2.30×10^{-10}
rs67234920_G	G / G	0.67 (↑)	89%	2.30×10^{-10}
rs28540500_C	C / C	0.42 (↑)	38%	2.40×10^{-10}
rs1037100_G	G / G	0.40 (↑)	51%	2.70×10^{-10}
rs12654442_T	C / T	0.46 (↑)	27%	2.80×10^{-10}
rs12190287_G	C / G	0.43 (↑)	37%	2.90×10^{-10}
rs287606_A	G / A	0.44 (↑)	29%	3.27×10^{-10}
rs74813029_A	G / G	0.54 (–)	17%	3.30×10^{-10}
rs4720244_C	C / G	0.42 (↑)	64%	3.60×10^{-10}
rs9865051_T	T / T	0.49 (↑)	78%	3.70×10^{-10}
rs2947080_G	G / G	0.41 (↑)	64%	4.60×10^{-10}
rs179145_A	G / G	0.41 (–)	38%	5.20×10^{-10}
rs77422711_A	NA	1.85 (–)	2%	6.40×10^{-10}
rs17816356_A	C / C	0.96 (–)	5%	7.90×10^{-10}
rs904199_G	A / A	0.73 (–)	8%	7.90×10^{-10}
rs111551996_G	G / G	0.95 (↑)	95%	8.00×10^{-10}
rs7043482_A	A / C	0.42 (↑)	65%	8.30×10^{-10}
rs12885183_G	A / G	0.49 (↑)	22%	8.50×10^{-10}
rs7774_A	C / C	0.43 (–)	33%	8.60×10^{-10}
rs35816944_G	G / G	2.70 (↑)	99%	1.30×10^{-9}
rs10106406_C	G / G	0.40 (–)	45%	1.40×10^{-9}
rs111739590_C	C / T	0.50 (↑)	81%	1.50×10^{-9}

rs8904_G	G / A	0.40 (↑)	63%	1.60×10^{-9}
rs12031946_C	T / T	0.59 (-)	13%	2.40×10^{-9}
rs1000368_T	C / C	0.43 (-)	26%	2.50×10^{-9}
rs9909004_C	T / T	0.38 (-)	42%	2.90×10^{-9}
rs6961768_A	A / A	0.38 (↑)	43%	3.00×10^{-9}
rs10226357_G	G / G	0.39 (↑)	59%	3.10×10^{-9}
rs36034102_T	T / T	0.43 (↑)	27%	3.50×10^{-9}
rs2577531_C	T / C	0.38 (↑)	59%	3.80×10^{-9}
rs2642608_T	C / C	0.42 (-)	27%	3.80×10^{-9}
rs4921804_G	G / A	0.39 (↑)	63%	4.40×10^{-9}
rs9634754_G	G / G	0.41 (↑)	69%	4.40×10^{-9}
rs67968533_C	T / T	0.66 (-)	9%	4.80×10^{-9}
rs7588761_T	C / C	0.75 (-)	7%	5.30×10^{-9}
rs9607805_T	C / T	0.42 (↑)	70%	5.60×10^{-9}
rs2006122_T	A / T	0.42 (↑)	27%	5.80×10^{-9}
rs144789148_G	A / A	0.96 (-)	5%	6.40×10^{-9}
rs4026608_T	T / T	0.38 (↑)	62%	6.50×10^{-9}
rs10802580_G	G / G	0.45 (↑)	76%	6.90×10^{-9}
rs1186818_G	G / A	0.43 (↑)	24%	9.00×10^{-9}
rs1407243_C	C / C	0.37 (↑)	60%	9.10×10^{-9}
rs2172448_A	G / A	0.37 (↑)	55%	9.40×10^{-9}
rs56317071_C	G / G	0.57 (-)	12%	1.20×10^{-8}
rs7584373_A	G / G	0.38 (-)	35%	1.50×10^{-8}
rs13447455_A	A / G	0.38 (↑)	64%	1.70×10^{-8}
rs819636_C	T / T	0.38 (-)	33%	1.70×10^{-8}
rs6728830_C	C / C	1.02 (↑)	96%	1.90×10^{-8}
rs2179452_T	T / T	0.46 (↑)	80%	1.90×10^{-8}
rs4545054_C	T / T	0.36 (-)	49%	2.00×10^{-8}
rs1475267_G	C / C	0.50 (-)	16%	2.10×10^{-8}
rs113394178_A	C / C	0.46 (-)	60%	2.10×10^{-8}
rs6800641_G	A / A	0.41 (-)	25%	2.60×10^{-8}
rs6587924_A	C / C	0.35 (-)	49%	2.70×10^{-8}
rs531706_C	G / G	0.39 (-)	72%	3.40×10^{-8}
rs745570_G	A / G	0.35 (↑)	53%	3.40×10^{-8}
rs7916672_T	C / C	0.35 (-)	58%	3.80×10^{-8}
rs553951_C	C / C	0.39 (↑)	73%	3.80×10^{-8}
rs11083300_G	C / C	0.35 (-)	46%	3.80×10^{-8}
rs12801636_A	A / A	0.41 (↑)	24%	4.10×10^{-8}
rs11031737_G	G / A	0.35 (↑)	52%	4.50×10^{-8}
rs1424569_C	T / C	0.36 (↑)	53%	4.60×10^{-8}
rs138711926_G	NA	0.98 (-)	4%	4.70×10^{-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.