

★ Resting heart rate (Eppinga, 2016)

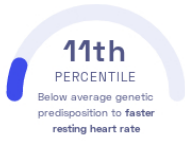
Ruben Eppinga, et al.
Nature Genetics

Heart

STUDY SUMMARY

Identification of 64 genetic loci that are associated with resting heart rate, a key predictor of cardiovascular health.

YOUR RESULT



STUDY DESCRIPTION

The heart rate is the number of times that the heart beats per minute. In adults, the resting heart rate is typically 60 to 100 beats per minute. A lower resting heart rate indicates a more efficient function of the heart and better health. People who are physically very fit, for example professional runners, may have a resting heart rate as low as 40 beats per minute! Conversely, an elevated resting heart rate can be a predictor of high blood pressure, heart disease, and heart failure. This study aimed to better understand the genetic influence on resting heart rate by analyzing the genomes of over 265,000 individuals of various ancestries. The study identified 64 genetic loci, including 46 novel loci, that correlate with resting heart rate. Together, all the identified genetic variants explain around 2.5% of the total variance in resting heart rate. The study also found that an elevated resting heart rate is linked to an increased mortality risk. A fast genetically predicted heart rate was associated with a reduction of life expectancy by multiple years.

DID YOU KNOW?


























Physical activity, such as running, biking, or swimming, is an effective way to decrease resting heart rate. Get your heart pumping today to decrease your resting heart rate and potentially live a longer, healthier life!

YOUR DETAILED RESULTS

To calculate your genetic predisposition to faster resting heart rate we summed up the effects of genetic variants that were linked to faster resting heart rate 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 faster resting heart rate. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to faster resting heart rate. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to faster resting heart rate. By adding up the effect sizes of the highlighted variants we calculated your polygenic score for faster resting heart rate to be **-2.94**. 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 faster resting heart rate is in the **11th percentile**. This means that it is higher than the polygenic scores 11% of people. We consider this to be a **below average genetic predisposition to faster resting heart rate**. 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 [Ⓞ]
rs422068_C	T / T	0.73 (-)	36%	1.52 x 10 ⁻¹⁰⁰
rs151041685_T	G / G	1.06 (-)	9%	7.86 x 10 ⁻⁷⁵
rs6123471_C	T / C	-0.59 (↓)	46%	6.63 x 10 ⁻⁷²
rs1320761_T	C / C	0.90 (-)	11%	1.22 x 10 ⁻⁶⁴
rs3951016_A	T / A	0.52 (↑)	47%	2.95 x 10 ⁻⁵⁵
rs4963772_A	G / G	-0.71 (-)	15%	3.23 x 10 ⁻⁵³
rs17881696_A	G / G	0.58 (-)	18%	1.18 x 10 ⁻⁴¹
rs1994135_C	T / C	0.40 (↑)	47%	7.19 x 10 ⁻³⁴
rs7173389_T	A / T	-0.54 (↓)	16%	1.31 x 10 ⁻³²
rs41317993_A	G / G	0.63 (-)	10%	5.42 x 10 ⁻³¹
rs174536_C NEW	A / A	0.40 (-)	66%	1.65 x 10 ⁻³⁰
rs17201923_G	A / G	-0.41 (↓)	28%	6.55 x 10 ⁻²⁹
rs7612445_T	G / G	-0.43 (-)	19%	2.41 x 10 ⁻²⁴
rs272564_C NEW	A / A	0.35 (-)	28%	4.51 x 10 ⁻²¹
rs180239_C	G / C	-0.33 (↓)	35%	4.54 x 10 ⁻²¹
rs907683_T NEW	G / T	-0.33 (↓)	43%	1.02 x 10 ⁻²⁰
rs12889267_G NEW	A / G	0.42 (↑)	16%	3.61 x 10 ⁻²⁰
rs2283274_C NEW	G / C	-0.41 (↓)	18%	7.21 x 10 ⁻²⁰
rs867400_C NEW	T / C	0.30 (↑)	43%	4.58 x 10 ⁻¹⁹
rs17180489_C NEW	G / G	-0.49 (-)	14%	9.15 x 10 ⁻¹⁹
rs73158705_G	A / A	0.39 (-)	16%	2.81 x 10 ⁻¹⁸
rs7194801_C NEW	T / C	-0.29 (↓)	43%	3.58 x 10 ⁻¹⁸
rs2152735_A NEW	G / A	-0.31 (↓)	33%	7.23 x 10 ⁻¹⁸
rs3915499_A NEW	G / G	0.30 (-)	32%	1.24 x 10 ⁻¹⁷
rs13002735_C	A / C	-0.33 (↓)	24%	1.29 x 10 ⁻¹⁷
rs75190942_A NEW	C / A	-0.50 (↓)	9%	1.19 x 10 ⁻¹⁶
rs4868243_A	G / G	-0.36 (-)	16%	4.08 x 10 ⁻¹⁶
rs1260326_C NEW	T / C	-0.28 (↓)	39%	4.29 x 10 ⁻¹⁶
rs2076028_A NEW	G / A	-0.29 (↓)	29%	5.45 x 10 ⁻¹⁶
rs62172372_G	A / A	0.34 (-)	19%	5.99 x 10 ⁻¹⁶
rs10739663_G NEW	G / G	-0.27 (↓)	45%	9.62 x 10 ⁻¹⁶
rs236349_G NEW	G / G	0.28 (↑)	34%	1.01 x 10 ⁻¹⁶
rs56233017_A NEW	NA	-0.67 (-)	4%	1.09 x 10 ⁻¹⁶
rs12501032_G NEW	C / C	0.29 (-)	31%	1.83 x 10 ⁻¹⁶
rs1483890_G NEW	A / G	0.28 (↑)	30%	2.54 x 10 ⁻¹⁶
rs61735998_T NEW	NA	-0.83 (-)	2%	2.06 x 10 ⁻¹⁴
rs6845865_C NEW	T / T	-0.34 (-)	16%	2.25 x 10 ⁻¹⁴



rs79121763_T 	C / T	-0.47 (↓)	9%	7.17×10^{-14}
rs1468333_C 	T / T	-0.26 (-)	63%	9.53×10^{-14}
rs3749237_A 	G / G	0.26 (-)	32%	3.08×10^{-13}
rs11920570_A 	G / A	0.27 (↑)	26%	5.18×10^{-13}
rs12576326_G 	A / G	0.25 (↑)	34%	1.20×10^{-12}
rs4608502_C 	T / C	0.25 (↑)	33%	1.85×10^{-12}
rs58437978_C 	T / T	-0.24 (-)	50%	2.61×10^{-12}
rs16974196_A 	A / A	0.24 (↑)	32%	1.10×10^{-11}
rs41312411_G 	C / C	-0.32 (-)	15%	1.34×10^{-11}
rs13165531_T 	A / T	-0.22 (↓)	42%	4.31×10^{-11}
rs12721051_G 	C / C	-0.29 (-)	18%	5.23×10^{-11}
rs11563648_C 	C / C	-0.23 (↓)	27%	4.42×10^{-10}
rs12579753_T 	C / C	-0.25 (-)	23%	4.80×10^{-10}
rs11083258_C 	A / A	-0.28 (-)	17%	5.51×10^{-10}
rs10880689_G 	A / G	0.21 (↑)	60%	8.10×10^{-10}
rs1050288_T 	C / C	-0.21 (-)	34%	2.74×10^{-9}
rs10841486_C 	T / T	-0.24 (-)	22%	2.98×10^{-9}
rs2358740_T 	G / T	-0.21 (↓)	32%	3.58×10^{-9}
rs4900069_C 	A / C	0.20 (↑)	37%	5.38×10^{-9}
rs41748_G 	T / G	-0.19 (↓)	45%	7.14×10^{-9}
rs12713404_T 	T / T	-0.20 (↓)	38%	9.33×10^{-9}
rs17265513_C 	T / T	0.24 (-)	19%	1.12×10^{-8}
rs748802_A 	G / G	-0.20 (-)	34%	1.13×10^{-8}
rs11081761_A 	G / G	-0.27 (-)	15%	1.25×10^{-8}
rs1549118_T 	C / C	0.20 (-)	28%	4.67×10^{-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.