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QT interval (Arking, 2014)

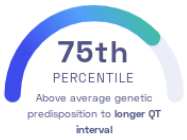
Dan Arking, et al.
Nature Genetics

Heart

STUDY SUMMARY

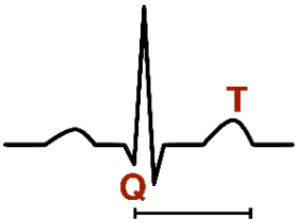
Identification of 22 novel genomic regions associated with QT interval duration, which is the time it takes for the heart to recharge for the next beat.

YOUR RESULT



STUDY DESCRIPTION

An electrical wave travels through your heart every time it beats. After every heartbeat, your heart needs time to repolarize, or "recharge," before the next beat. This time is known as the QT interval. The longer the QT interval, the longer it takes your heart to recharge between heartbeats. Overly long QT intervals are a risk factor for heart-related conditions, such as abnormal heartbeats and sudden cardiac death. This study examined the genomes of over 100,000 individuals, most of whom were of European descent, to better understand the genetic basis of QT interval duration. The study identified 35 genomic regions associated with QT interval duration, of which 22 are novel. Several of these genomic regions encode proteins involved in the calcium *signaling pathway*, highlighting the importance of calcium signaling in the recharging of the heart.



The QT interval is the time between the Q and the T wave in an electrocardiogram (ECG).

DID YOU KNOW?

The duration of the QT interval can be measured with an electrocardiogram (ECG). It is a common and painless test that only takes about five to ten minutes.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to longer QT interval we summed up the effects of genetic variants that were linked to longer QT 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 QT interval. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to longer QT interval. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to longer QT interval. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for longer QT interval to be 2.72**. 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 QT interval is in the **75th percentile**. This means that it is higher than the polygenic scores 75% of people. We consider this to be an **above average genetic predisposition to longer QT 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
rs12143842_T	C / T	3.50 (↑)	24%	1.00×10^{-213}
rs11153730_T	T / C	-1.65 (↓)	50%	2.00×10^{-67}
rs246196_C	T / T	-1.73 (–)	26%	2.00×10^{-67}
rs7122937_T	C / T	1.93 (↑)	19%	1.00×10^{-54}
rs2072413_T	C / C	-1.68 (–)	27%	1.00×10^{-49}
rs846111_C	G / C	1.73 (↑)	28%	7.00×10^{-40}
rs10919070_C	A / C	-1.68 (↓)	13%	1.00×10^{-31}
rs735951_A	G / G	-1.15 (–)	46%	2.00×10^{-28}
rs6793245_A	G / G	-1.12 (–)	32%	4.00×10^{-27}
rs1396515_C	G / C	-0.98 (↓)	52%	2.00×10^{-25}
rs1052536_C	T / T	0.98 (–)	53%	6.00×10^{-25}
rs1805128_T	NA	7.42 (–)	1%	2.00×10^{-18}
rs2298632_T NEW	T / T	0.70 (↑)	50%	1.00×10^{-14}
rs9892651_C NEW	T / T	-0.74 (–)	43%	3.00×10^{-14}
rs12997023_C	T / T	-1.69 (–)	5%	5.00×10^{-14}
rs246185_C NEW	T / T	0.72 (–)	34%	3.00×10^{-13}
rs3026445_C NEW	T / T	0.62 (–)	36%	3.00×10^{-12}
rs3105593_T NEW	C / C	0.66 (–)	45%	3.00×10^{-12}
rs295140_T NEW	T / C	0.57 (↑)	42%	2.00×10^{-11}
rs2273905_T NEW	T / C	0.61 (↑)	35%	4.00×10^{-11}
rs10040989_A NEW	G / G	-0.85 (–)	13%	5.00×10^{-11}
rs174583_T NEW	C / C	-0.57 (–)	34%	8.00×10^{-11}
rs11779860_C NEW	T / C	-0.61 (↓)	47%	2.00×10^{-10}
rs7765828_G NEW	C / C	0.55 (–)	40%	3.00×10^{-10}
rs1296720_C NEW	A / A	0.83 (–)	20%	4.00×10^{-10}
rs938291_G NEW	C / C	0.53 (–)	39%	6.00×10^{-10}
rs2363719_A NEW	G / G	0.97 (–)	11%	8.00×10^{-10}
rs3857067_A NEW	T / A	-0.51 (↓)	46%	1.00×10^{-9}
rs16936870_A NEW	T / T	0.99 (–)	10%	1.00×10^{-9}
rs1961102_T NEW	T / C	0.57 (↑)	33%	3.00×10^{-9}
rs7561149_C NEW	C / C	-0.52 (↓)	42%	7.00×10^{-9}
rs728926_T NEW	C / C	0.57 (–)	36%	2.00×10^{-8}
rs17784882_A NEW	C / C	-0.54 (–)	40%	3.00×10^{-8}
rs9920_C NEW	T / T	0.79 (–)	9%	3.00×10^{-8}
rs2485376_A NEW	A / A	-0.56 (↓)	39%	3.00×10^{-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.