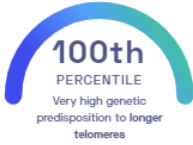


STUDY SUMMARY

Identification of 6 novel genomic regions associated with leukocyte telomere length (LTL).

YOUR RESULT



STUDY DESCRIPTION







Telomeres are protective caps at the ends of *chromosomes* which get shorter as our bodies age. Telomere length, typically measured in *leukocytes* from blood samples, can be used as a *biomarker* for aging and age-related diseases like coronary artery disease and some cancers. This genome-wide *meta-analysis* of over 78,000 individuals of European descent sought to identify genomic regions associated with leukocyte telomere length (LTL) to better understand how telomere length is regulated. The study reported 20 genomic regions associated with LTL, including 6 that are reported for the first time. Some of the genes in these regions have been previously linked to DNA damage repair.

DID YOU KNOW?

Regular exercise has been shown to extend telomere length. Drinking alcohol, smoking, and eating red meats fried in oil accelerates the shortening of telomeres.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to longer telomeres we summed up the effects of genetic variants that were linked to longer telomeres 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 telomeres. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to longer telomeres. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to longer telomeres. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for longer telomeres to be 0.39**. 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 telomeres is in the **100th percentile**. This means that it is higher than the polygenic scores 100% of people. We consider this to be a **very high genetic predisposition to longer telomeres**. 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 [Ⓢ]
rs10936600_T	A / A	-0.09 (-)	24%	7.18 x 10 ⁻⁵¹
rs7705526_A	A / A	0.08 (↑)	33%	5.34 x 10 ⁻⁴⁶
rs2853677_A	G / G	-0.06 (-)	59%	3.35 x 10 ⁻³¹
rs4691895_C	C / C	0.06 (↑)	78%	1.58 x 10 ⁻²¹
rs9419958_C	C / C	-0.06 (↓)	86%	5.05 x 10 ⁻¹⁹
rs75691080_T	C / T	-0.07 (↓)	9%	5.99 x 10 ⁻¹⁴
rs59294613_A	C / A	-0.04 (↓)	29%	1.17 x 10 ⁻¹³
rs8105767_G	A / G	0.04 (↑)	30%	5.42 x 10 ⁻¹³
rs73624724_C	T / C	0.05 (↑)	13%	6.33 x 10 ⁻¹²
rs3219104_C	C / C	0.04 (↑)	83%	9.60 x 10 ⁻¹¹
rs2736176_C 	G / G	0.04 (-)	31%	3.53 x 10 ⁻¹⁰
rs3785074_G 	G / G	0.04 (↑)	26%	4.64 x 10 ⁻¹⁰
rs7194734_T	C / T	-0.04 (↓)	78%	6.94 x 10 ⁻¹⁰
rs34978822_G	NA	-0.14 (-)	2%	7.26 x 10 ⁻¹⁰
rs34991172_G 	T / T	-0.06 (-)	7%	6.19 x 10 ⁻⁹
rs228595_A	G / A	-0.03 (↓)	42%	1.43 x 10 ⁻⁸
rs2302588_C	G / C	0.05 (↑)	10%	1.68 x 10 ⁻⁸
rs13137667_C 	C / C	0.08 (↑)	96%	2.43 x 10 ⁻⁸
rs55749605_A 	C / A	-0.04 (↓)	58%	2.45 x 10 ⁻⁸
rs62053580_G 	A / A	-0.04 (-)	17%	4.08 x 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%. These are limitations of low-coverage whole-genome sequencing. Please consider upgrading to high-coverage whole-genome sequencing.