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Kit: NTDNTEDYG

Healthy aging (Rosoff, 2023)

Daniel Rosoff, et al.
Nature Aging

Aging

Aging is an inevitable part of life

STUDY SUMMARY

This report is based on a study that discovered 52 genetic variants associated with healthy aging.

YOUR RESULT

STUDY DESCRIPTION

Aging is a natural and inevitable process that all individuals face as they grow older. This complex process involves several key components, including cognitive aging which encompasses changes in mental abilities such as memory and attention, and biological aging involving internal changes within cells and organs. The goal of all individuals is healthy aging, which can be measured in a number of ways, including frailty, lifespan, and healthspan. Frailty refers to a decline in physical strength and resilience, making older individuals more vulnerable to illness and injury. Lifespan measures how long a person lives, and healthspan focuses on the number of healthy and active years a person experiences within that lifespan. The differing measurements of healthy aging across individuals can be attributed to various factors, including lifestyle choices, environmental factors, psychological factors, and genetics. To better understand the genetic influence of healthy aging, this study examined over 1.9 million individuals of European ancestry. Scientists identified 52 genetic variants associated with healthy aging, 20 of which were newly identified by this study. One of the newly-associated variants is within the LPL gene, which functions to break down fat molecules called triglycerides that travel in your blood. Another new variant is within AFF3, a gene that controls the functions of other genes in the brain.

DID YOU KNOW?

The amount of blood pumped by your heart decreases by almost 50% by the time you're 90 years old.

YOUR DETAILED RESULTS

To calculate your genetic score to healthy aging we summed up the effects of genetic variants that were linked to healthy aging 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 score to healthy aging. The variants highlighted in blue have **negative effects sizes** and decrease your genetic score to healthy aging. Variants that are not highlighted are not found in your genome and do not affect your genetic score to healthy aging. By adding up the effect sizes of the highlighted variants (twice for homozygous variants) **we calculated your personal genetic score for healthy aging to be 0.11.** To determine whether your score is high or low, we compared this to the proprietary database of Nebula Genomics users. We found that your personal genetic score for healthy aging is in the **61st percentile.** This means that it is higher than the personal genetic scores 61% of people. We consider this to be an **above average genetic score to healthy aging.** Note that on average every user will have ~10% of the reports with scores that are in the >90th percentile, another ~10% of reports with scores in the 80th-90th percentile etc. Hence, having some reports with very high/low percentiles is expected and no reason for concern. However, please note that genetic scores 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	GENE	EFFECT SIZE	VARIANT FREQUENCY	SIGNIFICANCE
rs157581_T	T / C	TOMM40	0.02 (↑)	21%	1.25×10^{-27}
rs55730499_C	C / C	LPA	0.02 (↑)	8%	2.41×10^{-24}
rs7412_C	C / C	APOE	-0.02 (↓)	6%	1.45×10^{-20}
rs7859727_C	C / T	CDKN2B-AS1	0.01 (↑)	49%	3.45×10^{-18}
rs35198068_T	T / C	TCF7L2	0.01 (↑)	32%	5.39×10^{-18}
rs9295128_G	NA	SLC22A3	0.04 (–)	1%	2.52×10^{-15}
rs6859_A	G / G	PVRL2	-0.01 (–)	44%	6.88×10^{-14}
rs16843836_G	G / G	HTT	-0.01 (↓)	31%	7.24×10^{-13}
rs8042849_C	T / T	HYKK	-0.01 (–)	39%	1.03×10^{-12}
rs4766578_T	T / A	ATXN2	-0.01 (↓)	48%	1.10×10^{-12}
rs12203592_C	C / C	IRF4	0.01 (↑)	12%	6.88×10^{-12}
rs1230666_A	G / G	MAGI3	-0.01 (–)	14%	1.84×10^{-11}
rs61905747_A	A / C	ZW10	0.01 (↑)	15%	2.48×10^{-10}
rs16843603_T	T / C	ADD1	-0.01 (↓)	31%	4.16×10^{-10}
rs34891485_T	T / T	DHX58	0.01 (↑)	5%	4.97×10^{-10}
rs405509_T	T / G	APOE	-0.01 (↓)	48%	5.11×10^{-10}
rs159428_T	C / C	C20orf112	0.01 (–)	49%	6.13×10^{-10}
rs3768321_G NEW	G / G	PABPC4	0.01 (↑)	19%	6.46×10^{-10}
rs2643826_C NEW	C / C	AC137675.1	0.01 (↑)	45%	9.66×10^{-10}
rs142158911_G	G / G	LDLR	-0.01 (↓)	11%	1.13×10^{-9}
rs2186800_G	G / G	TTC12	-0.01 (↓)	46%	1.36×10^{-9}
rs9355297_C	C / C	LPA	-0.01 (↓)	26%	1.39×10^{-9}
rs980183_G NEW	A / A	LINC01122	-0.01 (–)	38%	1.76×10^{-9}
rs6907508_A NEW	A / A	C6orf106	0.01 (↑)	10%	1.90×10^{-9}
rs11066320_A	G / G	PTPN11	-0.01 (–)	43%	1.99×10^{-9}
rs1275922_A	A / G	KCNK3	-0.01 (↓)	27%	3.02×10^{-9}
rs2271961_T	T / T	TRAIP	0.01 (↑)	47%	3.05×10^{-9}
rs1126809_G	G / A	TYR	0.01 (↑)	25%	6.90×10^{-9}
rs472103_A	A / A	NLGN1	0.01 (↑)	47%	7.41×10^{-9}
rs2613508_C NEW	T / T	RPL31P12	0.01 (–)	18%	7.77×10^{-9}
rs12706966_A	A / A	FOXP2	-0.01 (↓)	37%	9.10×10^{-9}
rs78438918_A NEW	A / A	AFF3	-0.01 (↓)	17%	1.07×10^{-8}
rs13141210_C NEW	C / C	RNU6	-0.01 (↓)	50%	1.46×10^{-8}
rs114298671_G NEW	G / G	MSANTD1	0.01 (↑)	12%	1.57×10^{-8}
rs28455998_T	T / A	INO80	0.01 (↑)	50%	1.87×10^{-8}
rs2863671_T NEW	T / G	RNU6	0.01 (↑)	29%	1.95×10^{-8}
rs79570361_A	A / G	PLG	0.01 (↑)	8%	1.99×10^{-8}
rs36072649_T NEW	T / A	MAML3	-0.01 (↓)	37%	2.01×10^{-8}
rs940088_T NEW	T / C	IGF2BP1	-0.01 (↓)	29%	2.27×10^{-8}
rs9364552_G	G / G	SLC22A3	0.01 (↑)	50%	2.47×10^{-8}
rs7742789_C NEW	C / T	ZNF318	0.01 (↑)	35%	3.30×10^{-8}
rs6062322_A NEW	T / T	ZBTB46	-0.01 (–)	19%	3.30×10^{-8}
rs268_A NEW	NA	LPL	0.02 (–)	1%	3.38×10^{-8}
rs55686423_A NEW	A / A	PRPF40B	-0.01 (↓)	9%	3.45×10^{-8}
rs449647_A	A / T	APOE	-0.01 (↓)	17%	3.49×10^{-8}
rs17499404_G NEW	A / A	RP11	-0.01 (–)	46%	3.57×10^{-8}
rs9277988_T NEW	T / T	MYL8P	0.01 (↑)	20%	3.59×10^{-8}
rs6690632†_T	C / C	TMEM18	0.01 (–)	18%	3.60×10^{-8}
rs2972566_G	C / C	PVRL2	0.01 (–)	15%	4.02×10^{-8}
rs12769128_C NEW	C / T	MLLT10	0.01 (↑)	32%	4.56×10^{-8}
rs7174250_C NEW	C / C	ABHD17C	0.01 (↑)	46%	4.82×10^{-8}
rs1889406_A NEW	A / G	RP11	0.01 (↑)	20%	4.95×10^{-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.