

★ Age-related hearing impairment (Wells, 2019)

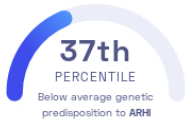
Helena R.R. Wells, et al.
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Aging Senses

STUDY SUMMARY

Identification of 44 genetic variants associated with age-related hearing impairment.

YOUR RESULT



STUDY DESCRIPTION

Hearing loss is one of the most common age-associated medical conditions. It has been associated with social isolation, depression, and can be a risk factor for *dementia*. Though believed to be highly heritable, the genetic factors associated with a predisposition to age-related hearing impairment (ARHI) remain largely unknown. This genome-wide association study discovered 44 variants associated with ARHI after examining more than 260,000 individuals of European ancestry aged 40 to 65. Many of these variants are near genes that play a role in development and function of the inner ear. Some of the variants have been previously associated with multiple personality disorder and psychological traits. These variants explain 10-20% of the heritability of ARHI.






DID YOU KNOW?

Depending on the severity of the hearing loss, you can use hearing aids, cochlear implants, bone anchored hearing systems, assistive listening devices, and learn how to lip or speech read.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to ARHI we summed up the effects of genetic variants that were linked to ARHI 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 ARHI. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to ARHI. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to ARHI. By adding up the effect sizes of the highlighted variants we **calculated your polygenic score for ARHI to be -0.32**. 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 ARHI is in the **37th percentile**. This means that it is higher than the polygenic scores 37% of people. We consider this to be a **below average genetic predisposition to ARHI**. 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 [Ⓞ]
rs38062310_G	G / G	-0.03 (↓)	96%	1.90 x 10 ⁻²²
rs6453022_C	C / A	-0.01 (↓)	50%	1.70 x 10 ⁻²¹
rs759016271_AGTAGTCCACTTTTCTCTT GCCTG	/	-0.01 (-)	39%	6.10 x 10 ⁻²¹
rs6890164_A	A / G	0.01 (↑)	51%	3.30 x 10 ⁻¹⁹
rs7951935_G	G / G	-0.01 (↓)	62%	7.80 x 10 ⁻¹⁷
rs35186928_G	A / A	-0.01 (-)	62%	1.70 x 10 ⁻¹⁶
rs9493627_G	A / A	-0.01 (-)	68%	1.40 x 10 ⁻¹⁵
rs132929_G	G / G	-0.01 (↓)	59%	2.20 x 10 ⁻¹³
rs5756795_T	C / C	-0.01 (-)	54%	5.10 x 10 ⁻¹²
rs1566129_T	C / C	0.01 (-)	41%	1.40 x 10 ⁻¹¹
rs35414371_T	T / T	-0.01 (↓)	87%	1.60 x 10 ⁻¹¹
rs12225399_G	G / C	-0.01 (↓)	65%	8.60 x 10 ⁻¹¹
rs55635402_A	G / G	0.01 (-)	81%	2.90 x 10 ⁻¹⁰
rs62033400_A	A / G	0.01 (↑)	61%	2.90 x 10 ⁻¹⁰
rs1327721_G	A / A	-0.01 (-)	49%	3.30 x 10 ⁻¹⁰
rs62188635_C	T / T	0.01 (-)	45%	4.70 x 10 ⁻¹⁰
rs2236401_C	C / T	-0.01 (↓)	49%	9.30 x 10 ⁻¹⁰
rs4947828_T	T / G	-0.01 (↓)	23%	1.00 x 10 ⁻⁹
rs6597883_T	T / C	0.01 (↑)	84%	1.00 x 10 ⁻⁹
rs34442808_T	TA / TA	-0.01 (-)	49%	1.30 x 10 ⁻⁹
rs835267_A	A / G	0.01 (↑)	53%	1.60 x 10 ⁻⁹
rs4948502_T	C / C	0.01 (-)	57%	1.70 x 10 ⁻⁹
rs10824108_G	T / T	-0.01 (-)	42%	3.00 x 10 ⁻⁹
rs12027345_G	A / A	0.01 (-)	57%	3.60 x 10 ⁻⁹
rs217289_G	G / A	-0.01 (↓)	56%	4.90 x 10 ⁻⁹
rs13093972_A	A / G	0.01 (↑)	55%	5.50 x 10 ⁻⁹
rs62015206_C	T / T	-0.01 (-)	41%	7.70 x 10 ⁻⁹
rs10475169_A	A / A	-0.01 (↓)	88%	9.30 x 10 ⁻⁹
rs17671352_T	C / C	0.01 (-)	38%	1.00 x 10 ⁻⁸
rs7525101_C	T / T	-0.01 (-)	56%	1.50 x 10 ⁻⁸
rs12938775_G	G / G	0.01 (↑)	50%	1.60 x 10 ⁻⁸
rs78837345_A	A / A	-0.01 (↓)	93%	1.90 x 10 ⁻⁸
rs9366417_G	G / A	0.01 (↑)	26%	2.10 x 10 ⁻⁸
rs3890736_G	A / A	-0.01 (-)	63%	2.20 x 10 ⁻⁸
rs143282422_G	G / G	-0.03 (↓)	99%	2.40 x 10 ⁻⁸
rs9691831_A	G / G	-0.01 (-)	42%	3.10 x 10 ⁻⁸
rs141403654_A	A / A	-0.03 (↓)	98%	3.50 x 10 ⁻⁸

rs4611562_T 	T / T	-0.01 (↓)	78%	3.60×10^{-8}
rs12552_A 	A / G	0.01 (↑)	44%	4.80×10^{-8}
rs10927035_C 	C / C	-0.01 (↓)	35%	4.90×10^{-8}