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# Frailty (Atkins, 2021)

Janice Atkins, et al.
Aging Cell

Aging

*Frailty is used to describe weakness and bad health that are typical for old age.*

## STUDY SUMMARY

This report is based on a study that discovered 14 genetic variants associated with an individual's predisposition to frailty.

## YOUR RESULT

**8th**
PERCENTILE
Low genetic predisposition to **frailty**

## STUDY DESCRIPTION

Frailty is a medical condition characterized by reduced ability to function and diminished health. Individuals experiencing frailty often experience weight loss, reduced strength, and low activity levels. As a result, these individuals are more susceptible to having major health declines from issues such as infections or falls. Age increases an individual's odds of becoming frail. This genome-wide association study aimed to identify regions of the genome that may predispose individuals to frailty. After examining more than 175,000 individuals of European ancestry, the researchers identified 14 genetic variants associated with the onset of frailty. Two of the genes found to be associated with frailty were FOXP2 and ANK3. The FOXP2 gene encodes instructions for making a protein that plays a role in the development of brain areas responsible for speech and language. ANK2 encodes a protein that helps cells in the nervous system maintain their physical structure.

## DID YOU KNOW?

Research suggests that positive thinking and an active mind are correlated with reduced risk of frailty. In one study, older volunteers who tutored at elementary schools were found to exhibit not only sharper thinking but also improved physical fitness.

## YOUR DETAILED RESULTS

To calculate your genetic predisposition to frailty we summed up the effects of genetic variants that were linked to frailty 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 frailty. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to frailty. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to frailty. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for frailty to be -0.03**. 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 frailty is in the **8th percentile**. This means that it is higher than the polygenic scores 8% of people. We consider this to be a **low genetic predisposition to frailty**. 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 | GENE | EFFECT SIZE | VARIANT FREQUENCY | SIGNIFICANCE |
|---|---|---|---|---|---|
| rs9275160_A NEW | G / G | HLA-DQB1, HLA-DQA2 | 0.04 (–) | 34% | $7.20 \times 10^{-28}$ |
| rs82334_A NEW | A / C | HTT | 0.02 (↑) | 68% | $3.10 \times 10^{-10}$ |
| rs2396766_A NEW | G / G | FOXP2 | 0.02 (–) | 47% | $1.20 \times 10^{-9}$ |
| rs12739243_T NEW | T / T | SYT14 | 0.02 (↑) | 78% | $1.30 \times 10^{-9}$ |
| rs583514_T NEW | T / C | NLGN1 | -0.02 (↓) | 49% | $1.70 \times 10^{-9}$ |
| rs8089807_T NEW | C / C | KC6, PIK3C3 | -0.03 (–) | 19% | $6.50 \times 10^{-9}$ |
| rs4146140_T NEW | C / T | ANK3 | -0.02 (↓) | 38% | $6.80 \times 10^{-9}$ |
| rs4952693_T NEW | C / T | LRPPRC | -0.02 (↓) | 37% | $1.50 \times 10^{-8}$ |
| rs2071207_T NEW | C / C | SEMA3F-AS1 | 0.02 (–) | 52% | $1.50 \times 10^{-8}$ |
| rs3959554_A NEW | A / A | IN080, EXD1 | -0.02 (↓) | 58% | $1.70 \times 10^{-8}$ |
| rs10891490_T NEW | T / C | NCAM1 | 0.02 (↑) | 41% | $2.00 \times 10^{-8}$ |
| rs1363103_T NEW | C / C | - | 0.02 (–) | 62% | $2.20 \times 10^{-8}$ |
| rs17612102_T NEW | T / C | LE01, MAPK6 | -0.02 (↓) | 41% | $2.80 \times 10^{-8}$ |
| rs56299474_A NEW | C / C | HR, REEP4 | 0.02 (–) | 17% | $3.90 \times 10^{-8}$ |