

## ★ Resistance to severe malaria (Malaria Genomic Epidemiology Network, 2019)

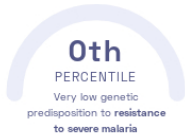
Malaria Genomic Epidemiology Network, et al.  
Nature Communications

Infection

### STUDY SUMMARY

Identification of 5 genomic loci associated with resistance to severe malaria.

#### YOUR RESULT



#### STUDY DESCRIPTION


Malaria is a disease caused by parasites transmitted via mosquito bites. Typical symptoms are chills, high fever and, in severe cases, organ failure. The World Health Organization estimated 219 million malaria cases in 2017, with the estimated number of deaths totaling 435,000. This study sought to identify genomic regions associated with resistance to severe malaria. Using DNA from over 17,000 individuals from Africa, Asia, and Oceania, researchers identified 5 genetic variants. Collectively, these variants explain roughly 10% of the heritability of resistance to severe malaria. One of the identified genetic variants is located in the ATP2B4 gene, which appears to play a role in the infection of red blood cells with malaria parasites.

#### DID YOU KNOW?

Sickle cell disease is an inherited blood disorder that is characterized by red blood cells that can take a sickle-like shape. While sickle cell disease can lead to various health problems, it also provides natural resistance against malaria.

#### YOUR DETAILED RESULTS

To calculate your genetic predisposition to resistance to severe malaria we summed up the effects of genetic variants that were linked to resistance to severe malaria 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 resistance to severe malaria. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to resistance to severe malaria. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to resistance to severe malaria. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for resistance to severe malaria to be -3.03**. 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 resistance to severe malaria is in the **0th percentile**. This means that it is higher than the polygenic scores 0% of people. We consider this to be a **very low genetic predisposition to resistance to severe malaria**. 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 <sup>Ⓞ</sup>	YOUR GENOTYPE <sup>Ⓞ</sup>	COMMENTS	EFFECT SIZE <sup>Ⓞ</sup>	VARIANT FREQUENCY <sup>Ⓞ</sup>	SIGNIFICANCE <sup>Ⓞ</sup>
rs334_T	T / T	-	-1.11 (↓)	93%	$1.31 \times 10^{-56}$
rs567544458_T	T / T	-	-0.59 (↓)	97%	$6.56 \times 10^{-11}$
rs4951377_A	G / G	In ATP2B4 gene	0.14 (-)	32%	$9.42 \times 10^{-8}$
rs62418762_C 	C / C	Statistically significant in Bayesian analysis	0.18 (↑)	95%	$1.15 \times 10^{-4}$