

## ☆ Hyperarousal in PTSD (Stein, 2021)

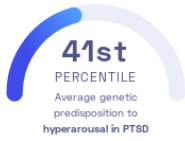
Murray Stein, et al.  
Nature Genetics

Mind Behavior

### STUDY SUMMARY

Identification of 15 genetic variants associated with hyperarousal, a symptom of post-traumatic stress disorder.

#### YOUR RESULT



#### STUDY DESCRIPTION

Post-traumatic stress disorder (PTSD) is a mental health condition caused by experiencing a traumatic event. Though many people associate PTSD with war veterans, anyone can experience the disorder. Common symptoms of PTSD include flashbacks and nightmares related to the traumatic event, avoidance of particular situations, and being easily startled. Being easily startled, and feeling tense in general, are collectively known as "hyperarousal". This genome-wide association study examined over 180,000 individuals of European ancestry to better understand the genetic factors associated with hyperarousal in PTSD. The study found 15 genetic variants associated with hyperarousal. Two genes linked to hyperarousal were TSNARE1 and FOXP2. While the function of TSNARE1 is largely unknown, FOXP2 is known to play a role in brain development, particularly areas of the brain involved in speech



Individuals suffering from PTSD are often easily startled.

and language.

#### DID YOU KNOW?

It is estimated that 7 out of every 100 people will develop PTSD at some point in their lives.

#### YOUR DETAILED RESULTS

To calculate your genetic predisposition to hyperarousal in PTSD we summed up the effects of genetic variants that were linked to hyperarousal in PTSD 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 hyperarousal in PTSD. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to hyperarousal in PTSD. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to hyperarousal in PTSD. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for hyperarousal in PTSD to be -0.35**. 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 hyperarousal in PTSD is in the **41st percentile**. This means that it is higher than the polygenic scores 41% of people. We consider this to be an **average genetic predisposition to hyperarousal in PTSD**. 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>⓪</sup>	YOUR GENOTYPE <sup>⓪</sup>	EFFECT SIZE <sup>⓪</sup>	VARIANT FREQUENCY <sup>⓪</sup>	SIGNIFICANCE <sup>⓪</sup>
rs56789728_G <span style="color: yellow;">NEW</span>	A / A	-0.13 (-)	28%	$4.62 \times 10^{-13}$
rs1496246_G <span style="color: yellow;">NEW</span>	A / A	0.10 (-)	38%	$1.77 \times 10^{-10}$
rs2887882_T <span style="color: yellow;">NEW</span>	C / C	-0.11 (-)	21%	$1.89 \times 10^{-9}$
rs7619147_T <span style="color: yellow;">NEW</span>	C / T	-0.09 (↓)	49%	$1.90 \times 10^{-9}$
rs13032994_C <span style="color: yellow;">NEW</span>	T / T	-0.10 (-)	23%	$3.73 \times 10^{-9}$
rs12420134_G <span style="color: yellow;">NEW</span>	C / C	0.12 (-)	11%	$6.45 \times 10^{-9}$
rs17209774_C <span style="color: yellow;">NEW</span>	G / C	-0.09 (↓)	24%	$7.97 \times 10^{-9}$
rs4129585_C <span style="color: yellow;">NEW</span>	C / C	-0.08 (↓)	67%	$2.07 \times 10^{-8}$
rs549326362_T <span style="color: yellow;">NEW</span>	G / G	-0.09 (-)	69%	$4.46 \times 10^{-8}$