

☆ Tourette's syndrome (Yu, 2019)

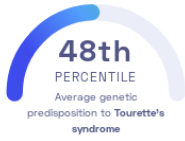
Dongmei Yu, et al.
The American Journal of Psychiatry

Behavior Mind

STUDY SUMMARY

Discovery of multiple genetic variants associated with Tourette's Syndrome.

YOUR RESULT



STUDY DESCRIPTION

Tourette's syndrome is a disorder of the nervous system characterized by uncontrollable movements or sounds that are known as tics. It affects about 1 out of every 160 people to varying degrees. Tourette's syndrome is known to be highly heritable, with up to 80% of the disease risk being inherited from the parents. This genome-wide association study sought to identify genetic variants associated with Tourette's Syndrome by examining over 20,000 individuals of European ancestry. One of the top variants is located in the FLT3 gene, which encodes a *receptor* protein that is believed to play a role in immune system functions. The authors also report 9 other genetic variants that are significantly associated with Tourette's Syndrome.

DID YOU KNOW?

Tourette's Syndrome is typically diagnosed early in life. Though it is a chronic condition, many affected individuals experience a peak in symptoms in the teenage years followed by a gradual improvement through adulthood.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to Tourette's syndrome we summed up the effects of genetic variants that were linked to Tourette's syndrome 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 Tourette's syndrome. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to Tourette's syndrome. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to Tourette's syndrome. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for Tourette's syndrome to be -0.06**. 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 Tourette's syndrome is in the **48th percentile**. This means that it is higher than the polygenic scores 48% of people. We consider this to be an **average genetic predisposition to Tourette's syndrome**. 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 [Ⓞ]	COMMENTS	EFFECT SIZE [Ⓞ]	VARIANT FREQUENCY [Ⓞ]	SIGNIFICANCE [Ⓞ]
rs2604235_A	G / G	In the FLT3 gene	0.16 (-)	38%	2.10×10^{-8}
rs191044310_A	NA	-	-0.62 (-)	2%	1.50×10^{-7}
rs13407215_T	NA	-	0.79 (-)	2%	1.90×10^{-7}
rs2708146_G	A / G	-	-0.13 (↓)	46%	3.20×10^{-7}
rs1906252_A	C / A	-	-0.13 (↓)	49%	7.00×10^{-7}
rs12459560_T	G / G	-	0.17 (-)	16%	8.20×10^{-7}
rs117648881_A	NA	-	-0.53 (-)	2%	8.80×10^{-7}
rs6670211_A	A / C	-	-0.13 (↓)	47%	1.40×10^{-6}
rs72653320_A	G / A	-	0.18 (↑)	13%	1.70×10^{-6}
rs73205493_T	C / T	-	0.15 (↑)	34%	1.80×10^{-6}

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.