

☆ Bipolar disorder (Mullins, 2021)

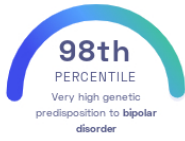
Niamh Mullins, et al.
Nature Genetics

Brain Mind Behavior

STUDY SUMMARY

This report is based on a study that discovered 64 genetic variants associated with bipolar disorder.

YOUR RESULT



STUDY DESCRIPTION

Bipolar disorder is a mental health condition that causes sharp shifts in an individual's mood, energy, and activity. The condition is characterized by periods of manic episodes, where the patient may feel energetic and irritable, and periods of depressive episodes, where the same person may feel down and hopeless. Like many mental health conditions, genetic factors are known to contribute to an individual's risk of developing bipolar disorder. For example, studies have shown that bipolar disorder is more common in people who have a first-degree relative, such as a parent or sibling, with the condition. This genome-wide association study of more than 413,000 individuals of European ancestry sought to identify regions of the genome associated with bipolar disorder. The researchers discovered 64 genetic variants associated with the condition, 33 of which have not been previously described. However, many of these variants have been connected to other mental health disorders including schizophrenia and depression.



Bipolar disorder is characterized by alternating manic and depressive episodes.

















DID YOU KNOW?

The median age of onset for bipolar disorder is 25 years, though the illness can begin any time from early childhood to the 50s or after.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to bipolar disorder we summed up the effects of genetic variants that were linked to bipolar disorder 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 bipolar disorder. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to bipolar disorder. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to bipolar disorder. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for bipolar disorder to be 4.57**. 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 bipolar disorder is in the **98th percentile**. This means that it is higher than the polygenic scores 98% of people. We consider this to be a **very high genetic predisposition to bipolar disorder**. 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
rs9834970_C	C / C	TRANK1	0.08 (↑)	48%	6.60 x 10 ⁻¹⁹
rs1487445_T	C / T	POU3F2	0.08 (↑)	49%	1.50 x 10 ⁻¹⁶
rs11062170_C	G / C	CACNA1C	0.08 (↑)	33%	1.90 x 10 ⁻¹⁶
rs13195402_G	G / G	MHC	0.14 (↑)	92%	5.80 x 10 ⁻¹⁶
rs174592_G	A / G	FADS2	0.07 (↑)	40%	9.90 x 10 ⁻¹⁴
rs113779084_A	G / A	THSD7A	0.08 (↑)	30%	1.40 x 10 ⁻¹³
rs2336147_T	T / C	ITIH1	0.07 (↑)	50%	3.60 x 10 ⁻¹³
rs10994415_C	T / T	ANK3	0.12 (-)	8%	1.10 x 10 ⁻¹¹
rs2273738_T	C / T	ADD3	0.09 (↑)	14%	1.60 x 10 ⁻¹¹
rs62489493_G	C / C	miR124-1	0.09 (-)	13%	2.60 x 10 ⁻¹¹
rs10866641_T	C / C	DOCK2	0.06 (-)	57%	2.80 x 10 ⁻¹¹
rs67712856_T	T / G	STK4	0.07 (↑)	69%	4.20 x 10 ⁻¹¹
rs4619651_G	G / G	LMAN2L	0.07 (↑)	67%	4.80 x 10 ⁻¹¹
rs748455_T	T / C	ZNF592	0.07 (↑)	72%	5.00 x 10 ⁻¹¹
rs12576685_A	G / G	SHANK2	0.06 (-)	33%	1.20 x 10 ⁻¹⁰
rs28456634_G	G / G	C16orf72	0.06 (↑)	62%	2.60 x 10 ⁻¹⁰
rs228768_G	G / G	HDAC5	0.06 (↑)	29%	2.80 x 10 ⁻¹⁰
rs6954854_G	A / A	SP4	0.06 (-)	43%	5.90 x 10 ⁻¹⁰
rs6032110_A	A / G	WFDC12	0.06 (↑)	51%	1.00 x 10 ⁻⁹
rs2126180_A	A / A	LINC01748	0.06 (↑)	46%	1.60 x 10 ⁻⁹
rs6992333_G	A / A	PLEC	0.06 (-)	41%	1.60 x 10 ⁻⁹
rs112481526_G	A / A	KIAA1109	0.06 (-)	26%	1.90 x 10 ⁻⁹
rs12668848_G	G / G	MAD1L1	0.06 (↑)	57%	1.90 x 10 ⁻⁹
rs28665162_A	G / A	SSBP2	0.07 (↑)	24%	2.00 x 10 ⁻⁹
rs476805_A	A / A	PACS1	0.07 (↑)	77%	2.00 x 10 ⁻⁹
rs4447398_A	C / C	STARD9	0.08 (-)	13%	2.60 x 10 ⁻⁹
rs12672003_G	A / A	MPP6	0.09 (-)	11%	2.70 x 10 ⁻⁹
rs4672_A	G / G	FKBP2	0.10 (-)	8%	3.40 x 10 ⁻⁹
rs11764361_A	A / A	SRPK2	0.06 (↑)	67%	3.50 x 10 ⁻⁹
rs4702_G	G / A	FURIN	0.06 (↑)	45%	3.50 x 10 ⁻⁹
rs35306827_G	G / A	CUL4A	0.07 (↑)	78%	3.60 x 10 ⁻⁹
rs10455979_G	G / G	RPS6KA2	0.06 (↑)	50%	4.20 x 10 ⁻⁹
rs237460_T	C / T	KCNB1	0.06 (↑)	41%	4.30 x 10 ⁻⁹
rs678397_T	T / C	PC	0.05 (↑)	46%	5.50 x 10 ⁻⁹
rs2953928_A	G / A	RP1-84015.2	0.12 (↑)	7%	6.30 x 10 ⁻⁹
rs12932628_T	G / G	RPL13	0.06 (-)	49%	6.70 x 10 ⁻⁹
rs10737496_C	C / C	NUF2	0.05 (↑)	44%	7.20 x 10 ⁻⁹
rs13044225_G	G / G	OSRP1-2	0.05 (↑)	44%	8.50 x 10 ⁻⁹

rs6887473_G	G / G	SSBP2	0.06 (↑)	74%	8.80×10^{-9}
rs62011709_T 	A / A	HOMER2	0.06 (-)	76%	1.40×10^{-8}
rs10255167_A	A / A	MRPS33	0.07 (↑)	78%	1.60×10^{-8}
rs61554907_T	G / T	ERBB2	0.09 (↑)	12%	1.60×10^{-8}
rs6865469_T 	G / T	HOMER1	0.06 (↑)	27%	1.70×10^{-8}
rs7199910_G	T / T	GRIN2A	0.06 (-)	31%	1.70×10^{-8}
rs4331993_A	T / A	SYNE1	0.05 (↑)	38%	2.00×10^{-8}
rs2693698_G 	G / G	BCL11B	0.05 (↑)	55%	2.00×10^{-8}
rs5758064_T 	T / T	SLC25A17	0.05 (↑)	52%	2.00×10^{-8}
rs13417268_C 	C / G	CERS6	0.06 (↑)	76%	2.10×10^{-8}
rs3088186_T 	T / T	MSRA	0.06 (↑)	29%	2.10×10^{-8}
rs115694474_T 	T / T	MDFC2	0.07 (↑)	80%	2.40×10^{-8}
rs10973201_C 	T / T	ZCCHC7	0.10 (-)	11%	2.50×10^{-8}
rs17183814_G	G / G	SCN2A	0.10 (↑)	92%	2.70×10^{-8}
rs62581014_T 	C / T	TUBBP5	0.06 (↑)	37%	2.80×10^{-8}
rs11870683_T	T / A	ERBB2	0.06 (↑)	65%	2.80×10^{-8}
rs4790841_T 	C / T	RTN4RL1	0.07 (↑)	15%	3.10×10^{-8}
rs12289486_T	C / C	ODZ4	0.08 (-)	12%	3.30×10^{-8}
rs10043984_T 	C / C	KDM3B	0.06 (-)	24%	3.70×10^{-8}
rs6946056_C 	A / C	PLXNA4	0.05 (↑)	62%	3.70×10^{-8}
rs35958438_G 	G / A	C15orf63	0.06 (↑)	77%	3.80×10^{-8}
rs1998820_T 	T / T	CACNB2	0.08 (↑)	89%	4.10×10^{-8}
rs2011302_A 	T / A	PGEM1	0.05 (↑)	38%	4.30×10^{-8}
rs696366_C	C / A	OD47	0.05 (↑)	55%	4.50×10^{-8}
rs10761661_T 	C / T	ADO	0.05 (↑)	47%	4.70×10^{-8}
rs2719164_A	A / G	NA	0.05 (↑)	56%	4.90×10^{-8}