

★ Beat synchronization (Niarchou, 2022)

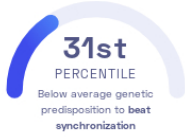
Maria Niarchou, et al.
Nature Human Behavior

Brain

STUDY SUMMARY

This report is based on a study that discovered 69 genetic variants associated with musical beat synchronization.

YOUR RESULT



STUDY DESCRIPTION

Music is an integral part of many cultures across the world. One feature of music that is present across cultures is the "beat", which is the rhythmic measure that helps to structure music. When listening to music, many people clap or tap along to the beat, but the ability to keep up with the beat varies widely. This genome-wide association study sought to identify genetic variants that affect an individual's ability to keep a beat by examining more than 600,000 individuals of European ancestry. Researchers identified 69 genetic variants that are linked with an individual's ability to keep a beat. One of the variants was near a gene known as GBE1 which encodes a protein that is produced inside muscle cells. It has previously been associated with reaction time. Overall, the study found that up to 16% of an individual's variation in keeping a beat can be explained by genetic variation.



Music is an important part of many cultures.

DID YOU KNOW?

Listening to music can help reduce the levels of the stress hormone known as cortisol.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to beat synchronization we summed up the effects of genetic variants that were linked to beat synchronization 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 beat synchronization. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to beat synchronization. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to beat synchronization. By adding up the effect sizes of the highlighted variants we calculated your polygenic score for beat synchronization to be **-0.58**. 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 beat synchronization is in the **31st percentile**. This means that it is higher than the polygenic scores 31% of people. We consider this to be a **below average genetic predisposition to beat synchronization**. 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
rs848293_G	G / G	VRK2	-0.06 (↓)	42%	9.23 x 10 ⁻¹⁸
rs62340585_G	A / A	GPM6A	-0.06 (-)	21%	1.81 x 10 ⁻¹⁴
rs10188817_G	G / G	-	-0.05 (↓)	49%	1.94 x 10 ⁻¹⁴
rs10779987_T	C / T	GBE1	-0.05 (↓)	38%	2.21 x 10 ⁻¹⁴
rs28392605_G	G / G	-	-0.05 (↓)	34%	8.93 x 10 ⁻¹⁴
rs1832909_T	T / C	-	0.05 (↑)	41%	1.78 x 10 ⁻¹³
rs34762587_T	T / C	FOXO6	0.05 (↑)	31%	2.25 x 10 ⁻¹³
rs7642_G	G / C	MAPK3	-0.05 (↓)	46%	2.41 x 10 ⁻¹³
rs10875125_C	C / C	DPYD	-0.07 (↓)	15%	2.61 x 10 ⁻¹³
rs9400241_C	A / A	FOXO3	-0.05 (-)	29%	4.49 x 10 ⁻¹³
rs4792891_T	G / G	MAPT	0.05 (-)	34%	7.07 x 10 ⁻¹³
rs1468701_G	A / A	SND1	-0.05 (-)	29%	3.62 x 10 ⁻¹²
rs10848660_G	C / C	SLC6A13	0.05 (-)	42%	6.04 x 10 ⁻¹²
rs2635634_T	C / C	CDH12	0.05 (-)	45%	9.54 x 10 ⁻¹²
rs9626920_G	G / A	MIRLET7BHG	0.05 (↑)	41%	1.04 x 10 ⁻¹¹
rs764299_G	G / G	PLEKHM3	0.05 (↑)	27%	1.47 x 10 ⁻¹¹
rs10984506_T	A / A	ANP32B	0.05 (-)	37%	1.66 x 10 ⁻¹¹
rs1426371_G	A / A	WSCD2	0.05 (-)	26%	1.67 x 10 ⁻¹¹
rs12913592_T	C / C	-	0.05 (-)	36%	6.13 x 10 ⁻¹¹
rs72700870_G	C / C	MCL1	-0.06 (-)	14%	1.42 x 10 ⁻¹⁰
rs9388171_G	C / G	-	-0.04 (↓)	48%	2.16 x 10 ⁻¹⁰
rs6572878_T	C / C	HAUS4	-0.04 (-)	39%	3.48 x 10 ⁻¹⁰
rs11210206_T	T / T	-	-0.04 (↓)	31%	3.93 x 10 ⁻¹⁰
rs72633496_T	T / A	-	-0.05 (↓)	43%	6.21 x 10 ⁻¹⁰
rs7586405_G	A / G	PPP1CB	0.04 (↑)	31%	7.19 x 10 ⁻¹⁰
rs3024293_T	T / T	C1QL1	0.05 (↑)	24%	8.26 x 10 ⁻¹⁰
rs2061843_G	A / A	CSMD2	-0.04 (-)	40%	1.19 x 10 ⁻⁹
rs1349028_T	T / A	EIF4E3	-0.05 (↓)	26%	1.54 x 10 ⁻⁹
rs4443239_T	T / T	C4orf27	0.05 (↑)	25%	1.68 x 10 ⁻⁹
rs1901739_T	T / T	-	0.04 (↑)	48%	2.14 x 10 ⁻⁹
rs55678522_G	G / G	LRRN2	-0.05 (↓)	22%	2.25 x 10 ⁻⁹
rs8079923_T	T / T	AKAP10	0.05 (↑)	25%	2.88 x 10 ⁻⁹
rs7501911_T	T / T	NLK	-0.05 (↓)	18%	3.34 x 10 ⁻⁹
rs6087848_G	A / G	POFUT1	-0.04 (↓)	44%	3.40 x 10 ⁻⁹
rs10744265_G	C / C	-	-0.04 (-)	23%	4.24 x 10 ⁻⁹
rs13163173_C	C / C	MEF2C	-0.05 (↓)	17%	4.51 x 10 ⁻⁹
rs2819333_T	A / T	PTPRF	0.04 (↑)	37%	4.54 x 10 ⁻⁹

rs2453873_G	G / G	-	-0.05 (↓)	22%	5.17×10^{-9}
rs67264739_G	G / G	ADCY2	-0.04 (↓)	27%	5.54×10^{-9}
rs2284901_G	A / G	AKAP6	0.04 (↑)	37%	6.48×10^{-9}
rs1596431_T	T / T	-	0.05 (↑)	19%	7.42×10^{-9}
rs10978661_T	T / T	ZNF462	-0.06 (↓)	12%	7.74×10^{-9}
rs4263335_G	G / A	JAKMIP1	0.04 (↑)	49%	8.74×10^{-9}
rs7939759_T	C / C	CTSF	0.05 (-)	24%	1.23×10^{-8}
rs9710427_G	G / A	TECR	0.04 (↑)	42%	1.32×10^{-8}
rs12638746_G	G / G	EPHA3	-0.04 (↓)	34%	1.37×10^{-8}
rs12909047_G	G / G	UBL7	0.04 (↑)	48%	1.49×10^{-8}
rs2505344_G	A / G	EPC1	-0.05 (↓)	18%	1.51×10^{-8}
rs67816799_C	A / C	CCSER1	0.04 (↑)	38%	1.56×10^{-8}
rs10932201_G	G / A	CREB1	0.04 (↑)	46%	1.59×10^{-8}
rs526904_T	T / C	PICALM	-0.04 (↓)	35%	0.00×10^0
rs6548147_T	C / C	TSSC1	0.04 (-)	44%	2.05×10^{-8}
rs10877461_G	G / G	-	-0.04 (↓)	30%	2.44×10^{-8}
rs11996434_G	G / G	-	0.04 (↑)	27%	2.61×10^{-8}
rs1996148_G	G / G	PEBP4	-0.04 (↓)	32%	2.69×10^{-8}
rs10885458_G	A / G	-	-0.04 (↓)	28%	2.69×10^{-8}
rs191373913_T	G / G	NGEF	-0.04 (-)	44%	2.74×10^{-8}
rs12066186_C	A / A	ORC5	-0.04 (-)	43%	2.93×10^{-8}
rs7856850_C	C / C	PTPRD	-0.04 (↓)	22%	3.07×10^{-8}
rs13197257_T	G / T	PTPRK	-0.04 (↓)	27%	3.23×10^{-8}
rs10497355_T	A / A	UBR3	0.04 (-)	46%	3.43×10^{-8}
rs11692449_T	T / C	XPO1	0.04 (↑)	38%	3.45×10^{-8}
rs4704043_T	T / T	TNPO1	0.04 (↑)	28%	3.65×10^{-8}
rs43182_T	C / C	PTPRG	0.06 (-)	13%	0.00×10^0
rs62014217_G	A / A	HERC1	-0.04 (-)	20%	3.91×10^{-8}
rs476141_T	G / T	-	0.04 (↑)	50%	4.49×10^{-8}
rs2849543_G	G / G	PARK2	0.04 (↑)	42%	0.00×10^0