

☆ Age at first birth (Millis, 2021)

Melinda Millis, et al.
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Behavior Sex

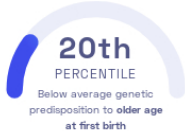
STUDY SUMMARY

This report is based on a study that discovered 89 genetic variants associated with an individual's age when they first become a parent.



The age at which an individual has their first child is influenced by genetics.

YOUR RESULT



STUDY DESCRIPTION

Historically, the age at which people become parents for the first time has been young, often in their 20s or earlier. With societal, cultural, and medical changes, people today often reach the age of 30 before having their first child. While many of the environmental and cultural factors influence the age at which person has their first child, genetics also plays a role. This study looked at the genetics of over 540,000 individuals of European ancestry and identified 89 variants associated with the age at which an individual has their first offspring. Among the many genes connected to this trait are FSHB and ESR1. FSHB encodes a hormone, that plays a role in the regulation of development and puberty. The ESR1 gene, on the other hand, is important for the development of the placenta during pregnancy. Combined, the genetic markers identified in this study may explain nearly 5% of the variability in the age at which a person becomes a parent for the first time.

DID YOU KNOW?

The average age at first childbirth in the United States can vary greatly by environment and geography. In major cities such as San Francisco and New York City, the average age at first birth is over 30 years old. In rural areas, such as in the central US, the average age at birth is nearly a decade younger.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to older age at first birth we summed up the effects of genetic variants that were linked to older age at first birth 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 older age at first birth. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to older age at first birth. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to older age at first birth. By adding up the effect sizes of the highlighted variants we calculated your polygenic score for older age at first birth to be **-0.96**. 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 older age at first birth is in the **20th percentile**. This means that it is higher than the polygenic scores 20% of people. We consider this to be a **below average genetic predisposition to older age at first birth**. 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 [Ⓞ]
rs9838987_A	A / A	CAMKV	0.12 (↑)	50%	5.55 x 10 ⁻³³
rs3172494_T	G / G	IP6K2	0.13 (-)	12%	8.63 x 10 ⁻¹⁰
rs199747428_A	A / A	CRTC2	-0.08 (↓)	30%	3.70 x 10 ⁻¹⁴
rs5932889_C	G / G	OR13H1	-0.09 (-)	65%	4.88 x 10 ⁻¹⁴
rs4443016_C	C / C	LINC01104	-0.07 (↓)	50%	1.02 x 10 ⁻¹³
rs34272260_A	A / AC	-	0.07 (↑)	36%	1.90 x 10 ⁻¹³
rs183103_T	C / C	HS6ST2	0.09 (-)	70%	4.27 x 10 ⁻¹³
rs293566_T	T / C	NOL4L, LOC101929698	0.07 (↑)	65%	2.18 x 10 ⁻¹²
rs17314804_T	C / C	MAML3	0.07 (-)	36%	2.67 x 10 ⁻¹²
rs111476533_G	/	TRAF3	0.09 (-)	80%	6.64 x 10 ⁻¹²
rs6585429_A	G / G	VAX1	-0.08 (-)	19%	1.08 x 10 ⁻¹¹
rs145678577_A	A / AAG	MIR4432HG	0.07 (↑)	37%	2.08 x 10 ⁻¹¹
rs10445366_C	G / C	MAPT-AS1	-0.09 (↓)	18%	6.69 x 10 ⁻¹¹
rs62262084_T	C / C	SMARCC1	-0.07 (-)	26%	7.09 x 10 ⁻¹¹
rs11249939_A	G / G	TNKS	0.06 (-)	61%	1.56 x 10 ⁻¹⁰
rs11887646_A	A / G	SOX11	-0.07 (↓)	76%	2.25 x 10 ⁻¹⁰
rs149047463_A	/	-	0.06 (-)	52%	2.26 x 10 ⁻¹⁰
rs8110682_T	C / C	IER2	-0.07 (-)	63%	2.59 x 10 ⁻¹⁰
rs2906457_A	A / C	ST3GAL3	-0.06 (↓)	27%	2.92 x 10 ⁻¹⁰
rs7516843_A	A / A	SYT14	-0.06 (↓)	68%	3.12 x 10 ⁻¹⁰
rs9818010_T	G / G	NPHP3-AS1	0.06 (-)	28%	5.63 x 10 ⁻¹⁰
rs11281490_A	A / AAGAAAATGG	LINC01029	0.06 (↑)	62%	5.82 x 10 ⁻¹⁰
rs34137317_T	NA	PRRC2A	0.25 (-)	3%	6.15 x 10 ⁻¹⁰
rs61750814_T	T / C	NUP54	0.08 (↑)	84%	6.32 x 10 ⁻¹⁰
rs17391694_T	C / T	GIPC2	-0.08 (↓)	14%	8.15 x 10 ⁻¹⁰
rs1702877_T	C / C	IKZF4	0.06 (-)	34%	8.22 x 10 ⁻¹⁰
rs1590949_C	G / G	LOC101929563	-0.06 (-)	59%	8.24 x 10 ⁻¹⁰
rs1464534_C	C / G	SDK1	-0.06 (↓)	30%	1.00 x 10 ⁻⁹
rs4244533_A	G / A	KIF18A	-0.07 (↓)	80%	1.33 x 10 ⁻⁹
rs7359501_T	C / T	TEX14	0.06 (↑)	41%	1.82 x 10 ⁻⁹
rs755895472_C	ATAT / ATAT	SORCS3	0.06 (-)	60%	1.99 x 10 ⁻⁹
rs11915934_A	G / G	-	0.07 (-)	18%	2.25 x 10 ⁻⁹
rs2069278_T	T / T	PDE4B	0.06 (↑)	68%	3.13 x 10 ⁻⁹
rs114142815_T	C / C	DOCK3	0.11 (-)	9%	3.58 x 10 ⁻⁹
rs9540715_A	C / C	PCDH9	0.06 (-)	46%	4.74 x 10 ⁻⁹
rs72779695_T	C / T	TRIB2	-0.08 (↓)	12%	4.87 x 10 ⁻⁹
rs763481319_C	/	LINC00971	0.06 (-)	43%	5.03 x 10 ⁻⁹
rs3832556_T	TC / TC	CYHR1	-0.06 (-)	10%	5.61 x 10 ⁻⁹

rs12815613_A	A / A	HNF1A-AS1	-0.06 (↓)	67%	5.75×10^{-9}
rs71149745_A	A / AAATTCAT	FOXP2	-0.06 (↓)	57%	5.76×10^{-9}
rs590076_A	G / G	TCF4	-0.06 (-)	35%	5.78×10^{-9}
rs11167753_T	T / C	DIAPH1	0.06 (↑)	71%	1.04×10^{-8}
rs35280105_C	C / CA	FNIP2	0.06 (↑)	63%	1.08×10^{-8}
rs933738_A	A / G	KCNH3	-0.07 (↓)	82%	1.10×10^{-8}
rs6925118_A	A / G	HIVEP2	-0.07 (↓)	81%	1.11×10^{-8}
rs17731405_A	A / G	VWC2	0.07 (↑)	85%	1.21×10^{-8}
rs13420733_A	T / T	MIR4431	0.06 (-)	38%	1.22×10^{-8}
rs693691_T	C / C	PKN2-AS1	0.08 (-)	14%	1.26×10^{-8}
rs8030494_A	A / A	C15orf69-AS1	0.05 (↑)	61%	1.30×10^{-8}
rs12837176_A	A / A	NUDT10	0.08 (↑)	81%	1.38×10^{-8}
rs112282597_A	A / A	SCN2A	-0.06 (↓)	75%	1.57×10^{-8}
rs11242222_A	A / A	JADE2	-0.07 (↓)	79%	1.67×10^{-8}
rs80153284_A	NA	-	0.23 (-)	3%	1.74×10^{-8}
rs5763436_A	A / A	CABP7	0.05 (↑)	59%	1.94×10^{-8}
rs6923535_A	G / G	ID4	-0.05 (-)	44%	2.12×10^{-8}
rs6574018_T	G / T	SIPA1L1	0.06 (↑)	36%	2.42×10^{-8}
rs113247159_T	T / T	MKRN1	-0.06 (↓)	70%	2.68×10^{-8}
rs62261746_C	C / G	CADM2	-0.06 (↓)	69%	2.85×10^{-8}
rs756368126_A	C / C	LGSN	-0.06 (-)	65%	2.88×10^{-8}
rs10962552_T	C / C	BNC2	-0.07 (-)	17%	3.12×10^{-8}
rs9276427_T	T / C	HLA-DQA2	0.05 (↑)	52%	3.29×10^{-8}
rs7865801_A	G / G	FREM1	0.05 (-)	63%	3.35×10^{-8}
rs2178487_A	T / T	-	-0.05 (-)	55%	3.37×10^{-8}
rs34361026_C	CA / CA	-	-0.07 (-)	19%	3.46×10^{-8}
rs144245162_A	G / G	-	0.16 (-)	8%	3.46×10^{-8}
rs112512729_T	T / T	RARB	-0.10 (↓)	91%	3.50×10^{-8}
rs60222682_T	C / C	MIR924HG	-0.06 (-)	20%	3.51×10^{-8}
rs6677536_A	C / C	LINC01360	0.06 (-)	62%	3.85×10^{-8}
rs33920398_T	T / C	LOC340107	0.06 (↑)	72%	3.93×10^{-8}
rs78928669_A	A / A	CALM1	-0.14 (↓)	96%	4.22×10^{-8}
rs12407439_A	A / A	LINC01635	-0.08 (↓)	83%	4.37×10^{-8}
rs57432042_T	T / T	TEFM	-0.09 (↓)	90%	4.57×10^{-8}
rs2253763_T	T / C	ADARB1	0.05 (↑)	40%	4.58×10^{-8}
rs1606974_A	G / G	LOC730100	0.07 (-)	13%	4.61×10^{-8}

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.