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Male puberty timing (Hollis, 2020)

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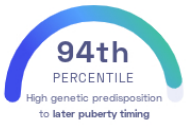
Aging | Hormones | Sex

STUDY SUMMARY

Identification of 29 novel genomic regions associated with male puberty timing.

YOUR RESULT



STUDY DESCRIPTION

The timing of puberty, which is the period of sexual maturation for teenage boys and girls, varies widely across individuals. It is a trait that is determined by a combination of environmental and genetic factors. This study aimed to understand the genetic basis of male puberty timing specifically, using voice breaking as a proxy for puberty. To this end, the researchers examined the genomes of over 200,000 males of European descent. The study discovered 76 genomic regions associated with male puberty timing, 29 of which are novel. These genomic regions are linked to genes, such as ALX4 and SRD5A2, which are involved in a growth factor signaling and the conversion of *testosterone* into a more potent male hormone, dihydrotestosterone. Moreover, the study identified unexpected genetic links between puberty timing and hair color. For example, males with darker hair colors were more likely to have earlier puberty timing relative to males with lighter hair color.

DID YOU KNOW?

During puberty, a male's larynx, or "voice-box," actually increases in size. This allows the vocal cords to grow thicker such that when they vibrate, the voice sounds deeper.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to later puberty timing we summed up the effects of genetic variants that were linked to later puberty timing 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 later puberty timing. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to later puberty timing. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to later puberty timing. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for later puberty timing to be 1.96**. 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 later puberty timing is in the **94th percentile**. This means that it is higher than the polygenic scores 94% of people. We consider this to be a **high genetic predisposition to later puberty timing**. 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	EFFECT SIZE	VARIANT FREQUENCY	SIGNIFICANCE
rs11156429_T	G / G	0.05 (-)	53%	3.49×10^{-62}
rs1659127_A	G / A	0.05 (↑)	35%	4.33×10^{-47}
rs142058842_G	G / G	0.05 (↑)	12%	8.57×10^{-36}
rs9408817_G	G / G	0.04 (↑)	67%	1.30×10^{-32}
rs6589961_T	T / T	0.04 (↑)	52%	2.40×10^{-30}
rs1856502_T	T / T	0.04 (↑)	27%	3.14×10^{-28}
rs71578952_C NEW	T / C	0.04 (↑)	46%	8.42×10^{-28}
rs2222746_T NEW	G / T	0.05 (↑)	8%	9.00×10^{-28}
rs73182377_C NEW	C / C	0.04 (↑)	77%	1.93×10^{-24}
rs2186245_C	C / C	0.04 (↑)	76%	6.07×10^{-22}
rs10980922_T NEW	A / A	0.06 (-)	11%	7.02×10^{-22}
rs3824915_G NEW	C / G	0.03 (↑)	43%	1.05×10^{-20}
rs77578010_A NEW	G / G	0.04 (-)	21%	1.05×10^{-20}
rs7402990_G NEW	G / G	0.05 (↑)	93%	1.35×10^{-18}
rs17833789_C NEW	A / A	0.03 (-)	64%	5.89×10^{-18}
rs17190166_C	C / A	0.03 (↑)	66%	7.56×10^{-18}
rs10919759_A	G / A	0.03 (↑)	49%	5.29×10^{-17}
rs62379978_G	T / T	0.04 (-)	13%	7.41×10^{-17}
rs34437050_A	NA	0.13 (-)	1%	2.31×10^{-16}
rs12203592_C NEW	C / C	0.04 (↑)	91%	9.58×10^{-16}
rs112881196_G NEW	NA	0.08 (-)	2%	2.02×10^{-15}
rs35063026_T NEW	NA	0.05 (-)	4%	2.08×10^{-15}
rs6014657_C	C / A	0.03 (↑)	83%	1.32×10^{-14}
rs6006984_C NEW	T / T	0.03 (-)	43%	2.48×10^{-14}
rs9690350_C NEW	G / C	0.03 (↑)	46%	3.19×10^{-14}
rs6560353_G	G / G	0.03 (↑)	75%	9.66×10^{-14}
rs138625771_C	NA	0.09 (-)	1%	8.78×10^{-13}
rs3743266_T	T / C	0.02 (↑)	70%	2.41×10^{-12}
rs2923177_T NEW	G / G	0.02 (-)	61%	3.41×10^{-12}
rs12766208_G NEW	G / C	0.03 (↑)	79%	3.60×10^{-12}
rs7905367_G NEW	C / C	0.03 (-)	37%	4.71×10^{-12}
rs6925777_T NEW	T / T	0.02 (↑)	50%	4.87×10^{-12}
rs7853970_T	T / T	0.02 (↑)	43%	6.84×10^{-12}
rs7136086_C NEW	T / C	0.03 (↑)	27%	1.35×10^{-11}
rs10110581_G NEW	A / A	0.03 (-)	25%	2.31×10^{-11}
rs767657_T NEW	T / T	0.02 (↑)	37%	2.32×10^{-11}
rs2842385_G	A / G	0.03 (↑)	21%	2.52×10^{-11}
rs1121980_G	G / A	0.02 (↑)	57%	3.32×10^{-11}

rs1514177_G	G / G	0.02 (↑)	55%	6.10×10^{-11}
rs2049045_C	G / G	0.03 (–)	16%	9.66×10^{-11}
rs4664605_C	C / C	0.02 (↑)	36%	9.91×10^{-11}
rs11836880_G NEW	NA	-0.05 (–)	4%	1.05×10^{-10}
rs4900184_T NEW	T / C	0.02 (↑)	39%	1.24×10^{-10}
rs58611096_A	T / T	0.02 (–)	30%	1.43×10^{-10}
rs10164550_A NEW	G / A	0.02 (↑)	37%	1.66×10^{-10}
rs12895406_A NEW	A / G	0.02 (↑)	48%	2.76×10^{-10}
rs10934420_C	T / C	0.02 (↑)	48%	3.03×10^{-10}
rs438830_A	A / G	0.03 (↑)	24%	3.20×10^{-10}
rs1598656_A	G / G	0.02 (–)	23%	3.56×10^{-10}
rs7896371_T	C / C	0.02 (–)	44%	3.77×10^{-10}
rs6486116_A	C / C	0.02 (–)	33%	4.89×10^{-10}
rs2473234_A	C / C	0.03 (–)	14%	4.98×10^{-10}
rs835648_A NEW	T / T	0.02 (–)	29%	5.25×10^{-10}
rs780094_T NEW	T / C	0.02 (↑)	39%	7.77×10^{-10}
rs6670873_C	C / C	0.03 (↑)	80%	9.04×10^{-10}
rs10188334_T	C / C	0.03 (–)	15%	1.44×10^{-9}
rs11190751_C	C / C	0.02 (↑)	67%	1.96×10^{-9}
rs1979835_A NEW	G / G	0.03 (–)	10%	2.52×10^{-9}
rs12930815_C NEW	C / C	0.02 (↑)	44%	2.55×10^{-9}
rs12940636_C NEW	T / C	0.02 (↑)	28%	3.59×10^{-9}
rs913588_G	G / G	0.02 (↑)	58%	5.91×10^{-9}
rs11603453_T	C / T	0.02 (↑)	36%	5.99×10^{-9}
rs11671893_T	T / T	0.03 (↑)	90%	6.01×10^{-9}
rs583269_T	T / C	0.02 (↑)	52%	1.13×10^{-8}
rs2311380_A	T / A	0.02 (↑)	77%	1.31×10^{-8}
rs60856990_A NEW	G / G	0.02 (–)	26%	1.33×10^{-8}
rs6473008_C	T / T	0.02 (–)	59%	1.39×10^{-8}
rs17193410_G NEW	G / A	0.03 (↑)	90%	1.51×10^{-8}
rs4911442_G NEW	G / A	0.03 (↑)	7%	1.69×10^{-8}
rs11761054_C NEW	C / C	-0.02 (↓)	70%	2.21×10^{-8}
rs10765711_C NEW	C / G	0.02 (↑)	64%	2.91×10^{-8}
rs61168554_A	A / G	0.02 (↑)	62%	3.76×10^{-8}
rs12983109_G NEW	G / G	0.02 (↑)	83%	3.82×10^{-8}
rs11873906_G	G / A	0.02 (↑)	26%	4.16×10^{-8}
rs4717905_C	C / C	0.02 (↑)	21%	4.26×10^{-8}
rs4801593_T NEW	A / T	0.02 (↑)	21%	4.51×10^{-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.