

★ Male-pattern baldness (Pirastu, 2017)

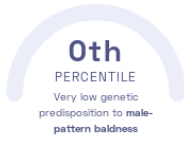
Nicola Pirastu, et al.
Nature Communications

Appearance Hormones

STUDY SUMMARY

Identification of 71 genetic regions associated with male-pattern baldness.

YOUR RESULT



STUDY DESCRIPTION

Hair loss is an extremely common condition. In fact, by the age of 50, about 50% of men experience major hair thinning, ultimately leading to a bald region surrounded by hair in a horseshoe-like pattern. This is known as male-pattern baldness. Male-pattern baldness is a common, heritable disorder that is linked to *testosterone* levels and is often associated with serious health conditions, such as increased risk of prostate cancer, heart disease, and diabetes. However, the underlying genetic basis of MPB remains poorly understood. This genome-wide association study examined the genomes of more than 70,000 men. The study identified 107 MPB-associated genetic variants across 71 genetic regions, 30 of which are novel. Collectively, these variants explain 38% of the heritability of MPB. Many of the discovered variants are within or near genes that play a role in hair growth and response of hair



Hairloss in a horseshoe-like pattern is characteristic for male-pattern baldness.

follicle cells to *testosterone*.





























DID YOU KNOW?

A common myth is that if you are male, MPB can be traced back to your maternal grandfather. However, this is not entirely accurate. One well-characterized gene related to MPB helps hair follicle cells detect testosterone, and testosterone is known to affect hair growth. This gene is located on the X chromosome, which means that for males, it is inherited from their mother. However, a number of studies, including this one, have highlighted that MPB is a polygenic disorder, meaning that there are a number of genes involved in MPB, many of which are not located on the sex chromosomes.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to male-pattern baldness we summed up the effects of genetic variants that were linked to male-pattern baldness 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 male-pattern baldness. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to male-pattern baldness. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to male-pattern baldness. By adding up the effect sizes of the highlighted variants we calculated your polygenic score for male-pattern baldness to be **-2.61**. 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 male-pattern baldness is in the **0th percentile**. This means that it is higher than the polygenic scores 0% of people. We consider this to be a **very low genetic predisposition to male-pattern baldness**. 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
rs4827628_A	A / A	-1.24 (↓)	15%	1.00 x 10 ⁻⁹⁹⁹
rs71530654_G	A / A	0.24 (-)	41%	7.34 x 10 ⁻⁶³
rs12203592_T	C / C	0.26 (-)	22%	2.35 x 10 ⁻⁶²
rs7542354_A	G / G	-0.25 (-)	22%	6.04 x 10 ⁻⁴⁹
rs77410716_T	C / T	0.28 (↑)	24%	4.65 x 10 ⁻⁴⁵
rs1422798_G	G / G	-0.20 (↓)	38%	2.29 x 10 ⁻⁴⁴
rs939963_C	G / C	-0.19 (↓)	45%	2.06 x 10 ⁻⁴¹
rs11684254_G	C / G	0.19 (↑)	35%	1.43 x 10 ⁻³⁹
rs7061504_G	A / A	0.40 (-)	12%	2.65 x 10 ⁻³⁵
rs550618068_A	T / A	-0.16 (↓)	40%	3.10 x 10 ⁻²⁷
rs4718886_G	A / G	-0.17 (↓)	25%	7.93 x 10 ⁻²⁷
rs919462_T	T / T	-0.17 (↓)	23%	1.49 x 10 ⁻²⁸
rs13021718_A	G / G	-0.21 (-)	14%	1.90 x 10 ⁻²⁶
rs7680591_A	A / A	0.15 (↑)	42%	4.60 x 10 ⁻²⁶
rs8085664_A	C / C	-0.16 (-)	28%	8.03 x 10 ⁻²⁶
rs11593840_G	G / G	-0.14 (↓)	45%	9.31 x 10 ⁻²⁴
rs577845405_A	NA	-0.47 (-)	3%	3.73 x 10 ⁻²³
rs17833789_A	A / A	0.14 (↑)	45%	8.95 x 10 ⁻²³
rs79593277_C	NA	0.62 (-)	1%	2.13 x 10 ⁻²²
rs113436165_T	G / G	0.43 (-)	6%	1.40 x 10 ⁻²¹
rs7642536_C	T / C	0.20 (↑)	14%	2.26 x 10 ⁻²¹
rs2064251_A	G / A	0.15 (↑)	27%	1.28 x 10 ⁻²⁰
rs11578119_T	C / T	0.13 (↑)	39%	2.78 x 10 ⁻²⁰
rs62433864_A NEW	G / A	-0.18 (↓)	16%	6.00 x 10 ⁻²⁰
rs7349332_T	C / C	0.18 (-)	15%	1.07 x 10 ⁻¹⁹
rs9803723_T	C / C	-0.13 (-)	33%	2.04 x 10 ⁻¹⁹
rs11037975_G	C / G	-0.14 (↓)	31%	2.14 x 10 ⁻¹⁹
rs68088846_A	G / A	0.15 (↑)	21%	9.94 x 10 ⁻¹⁹
rs9692245_C NEW	T / T	-0.13 (-)	37%	2.33 x 10 ⁻¹⁸
rs16863765_A	G / G	0.13 (-)	28%	8.21 x 10 ⁻¹⁸
rs9398803_G	A / G	-0.12 (↓)	47%	1.66 x 10 ⁻¹⁷
rs3781452_T	C / T	-0.12 (↓)	37%	2.58 x 10 ⁻¹⁷
rs11249243_T	C / C	-0.21 (-)	9%	5.23 x 10 ⁻¹⁷
rs182973285_T	NA	0.94 (-)	1%	1.33 x 10 ⁻¹⁶
rs7974900_C	C / C	-0.13 (↓)	27%	1.62 x 10 ⁻¹⁶
rs2149150_A	C / C	0.16 (-)	14%	3.48 x 10 ⁻¹⁶

rs17265613_C	T / T	-0.14 (-)	20%	4.04 x 10 ⁻¹⁶
rs534591951_T	NA	-0.97 (-)	1%	9.25 x 10 ⁻¹⁶
rs6788232_C	C / C	0.18 (↑)	11%	1.25 x 10 ⁻¹⁵
rs12902958_A	G / G	0.18 (-)	10%	4.25 x 10 ⁻¹⁵
rs78448052_T 	NA	-0.32 (-)	3%	8.57 x 10 ⁻¹⁵
rs534855217_T	NA	-0.98 (-)	1%	1.08 x 10 ⁻¹⁴
rs71421546_A	NA	0.27 (-)	5%	1.49 x 10 ⁻¹⁴
rs530010717_G	NA	1.00 (-)	< 1%	2.34 x 10 ⁻¹⁴
rs77767830_T	NA	0.31 (-)	3%	2.39 x 10 ⁻¹⁴
rs7976269_A 	G / G	-0.14 (-)	18%	5.73 x 10 ⁻¹⁴
rs12214131_A 	A / A	0.11 (↑)	37%	9.09 x 10 ⁻¹⁴
rs10930758_G	A / A	-0.10 (-)	48%	2.53 x 10 ⁻¹³
rs5934505_C	C / C	0.16 (↑)	27%	4.07 x 10 ⁻¹³
rs35892873_T	T / T	-0.11 (↓)	31%	4.84 x 10 ⁻¹³
rs10888690_C 	T / C	-0.10 (↓)	41%	6.47 x 10 ⁻¹³
rs16830188_T	NA	-0.34 (-)	2%	1.06 x 10 ⁻¹²
rs76972608_T	A / T	-0.15 (↓)	14%	1.73 x 10 ⁻¹²
rs191212334_G	NA	-0.85 (-)	1%	3.65 x 10 ⁻¹²
rs61784834_T	C / T	0.10 (↑)	42%	6.57 x 10 ⁻¹²
rs62146540_A	C / C	-0.11 (-)	27%	7.75 x 10 ⁻¹²
rs16877149_A	G / G	0.11 (-)	22%	8.43 x 10 ⁻¹²
rs79811440_C 	NA	0.24 (-)	4%	8.99 x 10 ⁻¹²
rs7164914_A	G / G	-0.12 (-)	20%	1.08 x 10 ⁻¹¹
rs12752809_T	C / C	0.11 (-)	25%	1.34 x 10 ⁻¹¹
rs115182912_A	NA	0.31 (-)	3%	2.50 x 10 ⁻¹¹
rs10225279_T	G / T	-0.09 (↓)	44%	4.61 x 10 ⁻¹¹
rs985546_T 	T / T	0.11 (↑)	22%	5.40 x 10 ⁻¹¹
rs76067940_T	NA	-0.25 (-)	4%	8.10 x 10 ⁻¹¹
rs12144907_C 	G / G	0.12 (-)	18%	1.08 x 10 ⁻¹⁰
rs9846246_A 	G / A	-0.09 (↓)	41%	1.18 x 10 ⁻¹⁰
rs2876167_A	G / G	-0.09 (-)	39%	1.87 x 10 ⁻¹⁰
rs77177529_T 	C / C	-0.14 (-)	11%	3.63 x 10 ⁻¹⁰
rs13405699_A 	NA	0.31 (-)	2%	4.61 x 10 ⁻¹⁰
rs200541723_A	/	0.09 (-)	31%	7.09 x 10 ⁻¹⁰
rs29073_C 	C / C	-0.09 (↓)	50%	7.09 x 10 ⁻¹⁰
rs6752754_G	A / A	-0.12 (-)	16%	8.24 x 10 ⁻¹⁰
rs10923528_G	A / G	-0.09 (↓)	46%	8.95 x 10 ⁻¹⁰
rs2256843_T 	T / T	0.09 (↑)	38%	1.06 x 10 ⁻⁹
rs998245_T 	C / C	-0.12 (-)	15%	1.35 x 10 ⁻⁹
rs1704529_T	C / T	-0.09 (↓)	32%	1.42 x 10 ⁻⁹
rs72809171_A 	NA	0.20 (-)	5%	1.54 x 10 ⁻⁹
rs12509636_T 	C / C	-0.09 (-)	31%	2.63 x 10 ⁻⁹
rs10843003_G	T / T	-0.10 (-)	20%	3.43 x 10 ⁻⁹
rs2807691_G 	A / A	0.08 (-)	42%	4.59 x 10 ⁻⁹
rs16827770_G 	A / A	0.09 (-)	33%	5.74 x 10 ⁻⁹
rs12686549_G 	A / A	0.17 (-)	6%	7.25 x 10 ⁻⁹
rs844193_T 	A / A	0.10 (-)	23%	7.66 x 10 ⁻⁹
rs149801367_T 	T / T	0.08 (↑)	42%	8.77 x 10 ⁻⁹
rs335145_G 	A / A	-0.09 (-)	29%	1.44 x 10 ⁻⁸
rs10928235_T 	T / T	0.09 (↑)	25%	1.90 x 10 ⁻⁸
rs7226979_T 	C / T	0.08 (↑)	46%	2.35 x 10 ⁻⁸
rs11714208_G 	A / G	-0.08 (↓)	36%	2.75 x 10 ⁻⁸
rs9719620_C 	T / C	-0.08 (↓)	46%	2.94 x 10 ⁻⁸
rs2040432_C 	A / C	0.08 (↑)	38%	3.03 x 10 ⁻⁸
rs417054_C 	C / C	-0.09 (↓)	21%	3.65 x 10 ⁻⁸
rs2706768_T 	C / C	0.08 (-)	40%	4.05 x 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.