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Eye color (Simcoe, 2021)

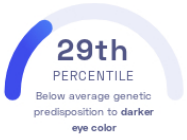
Mark Simcoe, et al.
Science Advances

Eyes | Appearance

STUDY SUMMARY

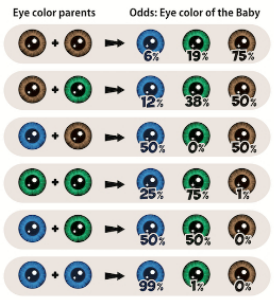
This report is based on a study that identified 115 genetic variants associated with eye color.

YOUR RESULT



STUDY DESCRIPTION

Much like a fingerprint, an individual's exact eye color is unique to them. To better understand the genetics that determine eye color, this genome-wide association study looked at nearly 200,000 individuals of European and Asian ancestry. The scientists identified 115 genetic variants associated with eye color, many of which are novel and have not been previously connected to pigmentation. This suggests that many more genes act to influence eye color than previously thought. For example, the SIK1 and GPR157 genes that both play a role in transmission of signals inside cells. The genetic variants that were discovered in this study collectively explain over 50% of eye color variation.



Prediction of a child's eye color based on the parents' eye color.

DID YOU KNOW?

Babies are usually born with little or no melanin, which is why they often have blue eyes. For some children, true eye color doesn't become apparent until they are over 3 years old.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to darker eye color we summed up the effects of genetic variants that were linked to darker eye color 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 darker eye color. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to darker eye color. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to darker eye color. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for darker eye color to be -54.63**. 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 darker eye color is in the **29th percentile**. This means that it is higher than the polygenic scores 29% of people. We consider this to be a **below average genetic predisposition to darker eye color**. 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
rs977589_T	C / T	-0.38 (↓)	46%	1.00×10^{-330}
rs117616283_G	G / G	-1.64 (↓)	98%	1.00×10^{-330}
rs8035315_T	G / T	-0.48 (↓)	58%	1.00×10^{-330}
rs4778218_G	A / G	-0.52 (↓)	83%	1.00×10^{-330}
rs145242923_T	T / T	-2.33 (↓)	99%	1.00×10^{-330}
rs749846_C	C / C	-0.87 (↓)	85%	1.00×10^{-330}
rs1470608_T	G / G	0.96 (-)	15%	1.00×10^{-330}
rs72712694_T	T / T	-1.36 (↓)	95%	1.00×10^{-330}
rs6497262_G	C / C	1.26 (-)	6%	1.00×10^{-330}
rs4778137_G	C / C	0.59 (-)	31%	1.00×10^{-330}
rs77542847_C	C / C	-1.59 (↓)	92%	1.00×10^{-330}
rs76415938_T	NA	1.59 (-)	3%	1.00×10^{-330}
rs4778239_T	T / T	-2.12 (↓)	99%	1.00×10^{-330}
rs8026089_C	C / C	-1.67 (↓)	97%	1.00×10^{-330}
rs59138695_T	T / T	-2.71 (↓)	99%	1.00×10^{-330}
rs141685696_C	C / C	-1.77 (↓)	92%	1.00×10^{-330}
rs1129038_T	T / T	-2.60 (↓)	73%	1.00×10^{-330}
rs77854840_G	G / G	-2.26 (↓)	98%	1.00×10^{-330}
rs12593929_G	A / A	2.30 (-)	7%	1.00×10^{-330}
rs150287021_T	NA	2.63 (-)	1%	1.00×10^{-330}
rs12901047_T	NA	1.35 (-)	2%	1.00×10^{-330}
rs146550637_T	NA	2.87 (-)	1%	1.00×10^{-330}
rs117504827_G	G / G	-2.17 (↓)	97%	1.00×10^{-330}
rs1667394_T	T / T	-2.24 (↓)	82%	1.00×10^{-330}
rs12203592_T	C / C	-0.39 (-)	17%	1.61×10^{-321}
rs17184180_T	T / A	0.27 (↑)	57%	1.34×10^{-284}
rs1126809_G	G / G	0.28 (↑)	72%	1.82×10^{-265}
rs16891982_G	G / G	-0.65 (↓)	96%	1.97×10^{-265}
rs13297008_G	G / A	0.26 (↑)	39%	4.99×10^{-260}
rs62389423_G	G / G	0.39 (↑)	86%	1.02×10^{-233}
rs35397_T	T / T	-0.58 (↓)	94%	1.25×10^{-212}
rs72963168_T	T / T	0.26 (↑)	74%	1.45×10^{-202}
rs151090307_T	NA	-0.90 (-)	2%	6.20×10^{-164}
rs4778224_G	A / G	-0.28 (↓)	79%	8.18×10^{-162}
rs35690998_G	C / C	0.55 (-)	5%	7.01×10^{-145}
rs62538956_T	T / C	-0.28 (↓)	88%	5.43×10^{-130}
rs4512823_G	A / A	-0.19 (-)	33%	1.39×10^{-122}
rs144161465_T	A / A	-0.25 (-)	16%	5.13×10^{-113}
rs74447445_G	NA	-0.89 (-)	1%	6.69×10^{-94}

rs6420484_G	A / G	-0.16 (↓)	65%	7.53×10^{-90}
rs62330021_G	G / G	-0.33 (↓)	95%	1.36×10^{-80}
rs34422827_T	T / G	-0.14 (↓)	47%	1.29×10^{-75}
rs76375770_G	G / G	0.52 (↑)	98%	3.42×10^{-71}
rs12440428_T	C / T	-0.14 (↓)	60%	8.05×10^{-71}
rs4778208_G	G / G	-0.18 (↓)	82%	1.53×10^{-64}
rs3797201_G	G / G	-0.94 (↓)	99%	6.42×10^{-66}
rs56411871_T	C / C	-0.26 (–)	7%	2.18×10^{-53}
rs78542430_T	A / A	-0.10 (–)	45%	5.93×10^{-53}
rs12837220_G	G / G	0.10 (↑)	58%	4.94×10^{-52}
rs622330_G	A / A	0.11 (–)	51%	3.87×10^{-49}
rs619484_G	G / G	-0.11 (↓)	63%	4.18×10^{-48}
rs3949960_T	T / T	-0.14 (↓)	75%	5.56×10^{-47}
rs142639084_G	NA	0.87 (–)	1%	5.94×10^{-47}
rs34931502_G	G / G	0.11 (↑)	38%	2.18×10^{-46}
rs6696511_T	T / T	0.11 (↑)	38%	1.35×10^{-45}
rs76519749_T	T / T	0.20 (↑)	90%	1.54×10^{-41}
rs10830237_T	T / T	0.10 (↑)	59%	3.27×10^{-41}
rs73734205_T	T / G	-0.16 (↓)	88%	5.91×10^{-41}
rs145750983_T	NA	0.50 (–)	2%	7.94×10^{-40}
rs35167426_T	C / C	0.11 (–)	22%	4.45×10^{-35}
rs72928978_G	G / G	0.14 (↑)	88%	6.42×10^{-32}
rs79335104_G	NA	-0.28 (–)	3%	2.33×10^{-31}
rs187887338_G	NA	-0.50 (–)	1%	6.06×10^{-29}
rs181994037_C	C / C	-0.08 (↓)	47%	8.31×10^{-29}
rs351385_G	G / G	-0.08 (↓)	58%	2.31×10^{-28}
rs9971729_C	A / C	0.08 (↑)	57%	5.03×10^{-27}
rs1426654_G	A / A	0.68 (–)	10%	2.72×10^{-26}
rs142680396_T	T / G	-0.14 (↓)	90%	9.44×10^{-25}
rs6910861_G	A / G	0.08 (↑)	46%	1.20×10^{-24}
rs1042713_G	A / A	-0.08 (–)	62%	1.26×10^{-24}
rs5957354_T	T / T	-0.09 (↓)	86%	5.43×10^{-23}
rs77816393_C	A / A	0.11 (–)	13%	6.14×10^{-23}
rs76033022_T	T / T	0.32 (↑)	98%	4.79×10^{-22}
rs116359091_G	G / G	-0.23 (↓)	97%	1.02×10^{-20}
rs74409360_T	C / C	-0.13 (–)	8%	8.09×10^{-20}
rs2835660_G	G / C	-0.06 (↓)	55%	1.62×10^{-17}
rs10900944_G	G / G	0.31 (↑)	99%	6.21×10^{-17}
rs116527520_G	G / G	-0.20 (↓)	95%	1.18×10^{-16}
rs9301973_G	G / G	0.07 (↑)	67%	1.48×10^{-16}
rs35051352_G	C / G	-0.06 (↓)	55%	3.33×10^{-14}
rs72777200_T	T / C	0.07 (↑)	83%	1.22×10^{-13}
rs12552712_T	T / C	-0.06 (↓)	60%	2.79×10^{-13}
rs2385028_T	C / C	0.06 (–)	25%	2.43×10^{-12}
rs1800888_T	NA	-0.23 (–)	1%	5.20×10^{-12}
rs73488486_T	G / G	0.09 (–)	10%	2.40×10^{-11}
rs112747614_G	G / G	0.05 (↑)	70%	3.69×10^{-11}
rs148336621_T	T / T	-0.65 (↓)	> 99%	4.14×10^{-11}
rs6997494_T	T / G	0.05 (↑)	48%	1.07×10^{-10}
rs12335410_T	C / T	-0.06 (↓)	22%	1.28×10^{-10}
rs6944702_T	T / T	0.05 (↑)	51%	1.71×10^{-10}
rs13016869_G	C / G	-0.06 (↓)	21%	2.23×10^{-10}
rs2095645_G	G / G	0.05 (↑)	67%	3.26×10^{-10}
rs2748901_G	G / A	-0.05 (↓)	46%	3.37×10^{-10}
rs12614022_G	G / G	0.05 (↑)	64%	4.26×10^{-10}
rs790464_T	T / C	0.06 (↑)	19%	4.50×10^{-10}
rs188004381_C	C / C	0.07 (↑)	89%	4.73×10^{-10}
rs138777265_C	NA	-0.11 (–)	5%	6.21×10^{-10}
rs147068120_T	NA	-0.12 (–)	4%	8.34×10^{-10}
rs6693258_T	T / T	-0.06 (↓)	22%	9.86×10^{-10}

rs4521336_T	C / C	0.05 (–)	36%	1.28×10^{-9}
rs3912104_T	T / A	0.04 (↑)	54%	1.47×10^{-9}
rs747572_G	G / G	-0.05 (↓)	37%	2.01×10^{-9}
rs761063_G	G / G	-0.05 (↓)	28%	2.07×10^{-9}
rs348613_G	NA	0.73 (–)	< 1%	2.54×10^{-9}
rs2386579_G	G / A	0.05 (↑)	73%	3.86×10^{-9}
rs3809761_G	G / G	0.06 (↑)	81%	5.08×10^{-9}
rs341147_G	A / A	-0.04 (–)	34%	6.45×10^{-9}
rs12543326_G	G / A	0.07 (↑)	88%	9.07×10^{-9}
rs2854746_G	G / G	-0.04 (↓)	59%	1.24×10^{-8}
rs139838980_G	G / G	0.27 (↑)	99%	1.29×10^{-8}
rs121908120_T	T / T	0.14 (↑)	98%	1.54×10^{-8}
rs141318671_G	G / G	-0.32 (↓)	99%	2.09×10^{-8}
rs11957757_G	G / G	0.04 (↑)	55%	2.94×10^{-8}
rs4790309_T	C / T	0.04 (↑)	46%	3.71×10^{-8}
rs6828137_T	G / T	-0.04 (↓)	46%	3.93×10^{-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.