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Testicular germ cell tumors (Pluta, 2021)

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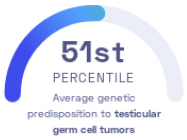
Cancer

STUDY SUMMARY

This report is based on a study that discovered 78 genetic variants associated with testicular germ cell tumors.

YOUR RESULT



STUDY DESCRIPTION

The testicles are two small, egg-shaped glands located close to the penis. Testicles contain many specialized types of cells, such as germ cells, that contribute to the production of sperm. While testicular cancer is relatively uncommon, affecting up to 90,000 men per year in the US, it is the most common cancer in men younger than 35. Overall, about 95 percent of testicular cancers begin in the sperm-producing germ cells. To better understand genetic factors that contribute to an individual's risk of testicular germ cell tumors (TGCT), this study examined nearly 190,000 men of European ancestry. The research identified 78 regions of the genome associated with TGCT, 22 of which were novel. Together these regions account for 44% of TGCT heritability. One of the genes linked to TGCT was AR. It provides instructions for making an androgen receptor. It detects androgen hormones such as testosterone which are important for male sexual development.

Doctors recommend that young men regularly examine their testicles for lumps.

DID YOU KNOW?

Testicular cancer can often be treated successfully. A man's lifetime risk of dying from testicular cancer is very low: about 1 in 5,000.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to testicular germ cell tumors we summed up the effects of genetic variants that were linked to testicular germ cell tumors 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 testicular germ cell tumors. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to testicular germ cell tumors. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to testicular germ cell tumors. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for testicular germ cell tumors to be 12.78**. 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 testicular germ cell tumors is in the **51st percentile**. This means that it is higher than the polygenic scores 51% of people. We consider this to be an **average genetic predisposition to testicular germ cell tumors**. 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
rs4474514_A	A / A	KITLG	0.75 (↑)	83%	1.42×10^{-164}
rs35409679_G	A / G	SPRY4	0.38 (↑)	51%	1.31×10^{-82}
rs36115365_C	G / G	CLPTM1L	0.43 (-)	22%	1.83×10^{-77}
rs755383_T	C / T	DMRT1	0.37 (↑)	64%	8.29×10^{-71}
rs7039737_C	C / T	DMRT1	0.39 (↑)	73%	3.67×10^{-64}
rs2735940_G	A / G	TERT	0.31 (↑)	51%	2.13×10^{-51}
rs210137_T	C / C	BAK1	0.36 (-)	20%	1.21×10^{-50}
rs55873183_G	A / A	DMRT1	0.53 (-)	8%	3.17×10^{-44}
rs7734992_T NEW	C / C	TERT	0.28 (-)	60%	5.17×10^{-40}
rs2711897_C	C / T	CENPE, BDH2	0.24 (↑)	62%	1.97×10^{-31}
rs12438394_A	A / A	PRTG	0.21 (↑)	54%	9.85×10^{-27}
rs11263762_A	A / A	HNF1B	0.22 (↑)	45%	2.72×10^{-26}
rs141079110_A NEW	A / A	BAK1	0.21 (↑)	75%	9.39×10^{-22}
rs2241965_A	G / G	UCK2	0.17 (-)	30%	1.21×10^{-21}
rs6949794_A	G / G	MAD1L1	0.20 (-)	37%	3.17×10^{-21}
rs304263_C	C / C	TEX14	0.18 (↑)	67%	3.70×10^{-20}
rs11076769_A	C / A	ZFPM1	0.19 (↑)	31%	3.50×10^{-19}
rs4898474_C NEW	T / T	TKTL1	0.17 (-)	31%	3.60×10^{-19}
rs55774410_A	A / G	ZNF728	0.24 (↑)	86%	1.67×10^{-17}
rs12485920_G	G / G	DAZL	0.17 (↑)	60%	5.54×10^{-17}
rs1052053_G	A / A	PMF1, SLC25A44	0.17 (-)	39%	1.03×10^{-16}
rs6441083_T	T / T	SSR3	0.18 (↑)	76%	2.19×10^{-16}
rs79350921_T	G / G	ZWILCH , RPL4	0.17 (-)	27%	1.03×10^{-15}
rs10976519_G NEW	G / T	DMRT1	0.15 (↑)	42%	1.04×10^{-15}
rs11055991_A	A / G	ATF7IP	0.17 (↑)	60%	1.48×10^{-15}
rs9824474_G	A / A	GPR160	0.16 (-)	39%	1.79×10^{-15}
rs34601376_T	A / A	-	0.20 (-)	21%	1.79×10^{-15}
rs2360670_A NEW	A / A	CENPI, DPR2	0.13 (↑)	54%	2.08×10^{-15}
rs12716769_T	T / C	RFWD3	0.17 (↑)	52%	2.11×10^{-15}
rs17021463_T	G / G	-	0.15 (-)	43%	4.82×10^{-15}
rs112251447_A	G / A	BMERB1, MPV17L	0.23 (↑)	11%	1.17×10^{-13}
rs7189510_C	C / C	GSPT1	0.15 (↑)	42%	2.12×10^{-13}
rs8131458_A	G / A	MCM3AP	0.16 (↑)	40%	3.37×10^{-13}
rs474853_T	T / C	PITX1	0.15 (↑)	64%	6.14×10^{-13}
rs739525_C	T / C	AIFM3, LZTR1	0.14 (↑)	54%	1.38×10^{-12}
rs2160570_A	C / A	HEATR3, CNEP1R1	0.16 (↑)	73%	1.75×10^{-12}
rs9718079_T	T / T	KATNA1	0.14 (↑)	65%	1.92×10^{-12}

rs2195987_T	T / T	-	0.17 (↑)	78%	6.62 x 10^{-12}
rs17336718_T	C / C	TKTL1	0.22 (–)	8%	8.32 x 10^{-12}
rs990706_T	C / C	GAB2, NARS2	0.17 (–)	18%	8.54 x 10^{-12}
rs6992772_T	T / T	PRDM14	0.14 (↑)	60%	1.14 x 10^{-11}
rs28393706_T NEW	T / T	SSNA1, ANAPC2, TPRN	0.17 (↑)	75%	1.20 x 10^{-11}
rs2335864_G NEW	G / G	AR	0.14 (↑)	20%	3.39 x 10^{-11}
rs35969688_A NEW	G / A	SP1, AMRH2	0.16 (↑)	18%	4.32 x 10^{-11}
rs548059_G	A / G	ZNF257	0.13 (↑)	58%	8.51 x 10^{-11}
rs56151783_C	C / G	G3BP2, USO1	0.21 (↑)	89%	1.03 x 10^{-10}
rs55779573_C NEW	T / C	CYTH1, USP36	0.12 (↑)	53%	1.08 x 10^{-10}
rs8104804_C NEW	T / T	LOC101927151	0.16 (–)	19%	1.38 x 10^{-10}
rs2887532_C NEW	C / C	RAD52	0.16 (↑)	82%	6.23 x 10^{-10}
rs10818964_G NEW	A / G	-	0.12 (↑)	67%	7.92 x 10^{-10}
rs12830125_C NEW	G / G	-	0.13 (–)	34%	2.18 x 10^{-9}
rs9987332_A NEW	G / G	DEPTOR	0.11 (–)	44%	2.34 x 10^{-9}
rs72620486_T NEW	C / C	SUPT20HL1, PDK3	0.13 (–)	15%	2.74 x 10^{-9}
rs9469079_T NEW	C / C	TNXB	0.17 (–)	13%	3.93 x 10^{-9}
rs11698165_C	A / A	ZFP64	0.15 (–)	20%	3.99 x 10^{-9}
rs7255867_C	C / C	-	0.13 (↑)	74%	4.30 x 10^{-9}
rs2713206_C	C / C	TFCP2L1	0.15 (↑)	16%	1.12 x 10^{-8}
rs6068588_A NEW	C / C	ZNF217	0.17 (–)	12%	1.32 x 10^{-8}
rs7912968_C NEW	G / G	-	0.10 (–)	38%	1.50 x 10^{-8}
rs351418_T NEW	C / C	PPP2R5A, PACC1	0.10 (–)	38%	2.85 x 10^{-8}
rs6708784_G NEW	A / G	BCL2L11	0.10 (↑)	50%	3.91 x 10^{-8}
rs7927974_G NEW	A / A	ARL14EP, MPPED2	0.11 (–)	29%	4.03 x 10^{-8}
rs2847334_G NEW	G / G	ENOSF1	0.10 (↑)	57%	4.16 x 10^{-8}
rs614265_C	A / C	PKNOX2	0.12 (↑)	71%	4.23 x 10^{-8}
rs113406766_A	A / A	TFDP2	0.14 (↑)	80%	4.80 x 10^{-8}
rs2241024_G	G / G	-	0.14 (↑)	80%	4.85 x 10^{-8}
rs4901569_T	C / T	-	0.10 (↑)	59%	1.29 x 10^{-7}
rs7315956_A	G / G	-	0.10 (–)	33%	1.62 x 10^{-7}
rs4852784_G	G / C	-	0.11 (↑)	26%	6.11 x 10^{-7}
rs17689040_G	C / G	-	0.10 (↑)	43%	1.73 x 10^{-6}
rs61408740_G	NA	-	0.29 (–)	3%	1.84 x 10^{-6}
rs4931000_A	A / G	-	0.11 (↑)	21%	2.49 x 10^{-6}
rs17153755_C	G / G	-	0.10 (–)	64%	7.68 x 10^{-6}
rs6553123_G	G / A	-	0.10 (↑)	37%	1.08 x 10^{-5}
rs9966612_A	A / G	-	0.09 (↑)	29%	3.46 x 10^{-5}
rs4842864_C	C / C	-	0.09 (↑)	69%	4.01 x 10^{-5}
rs4240895_T	C / T	-	0.08 (↑)	40%	2.52 x 10^{-4}
rs13225986_T	C / C	-	0.07 (–)	69%	9.96 x 10^{-4}

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.