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Mosaic loss of chromosome Y (Terao, 2019)

Chikashi Terao, et al.
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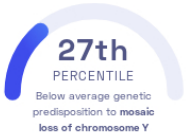
Blood | Sex

STUDY SUMMARY

Identification of 46 genetic variants associated with mosaic loss of chromosome Y.

YOUR RESULT



STUDY DESCRIPTION

Cells in the human body store genetic information in 23 pairs of chromosomes. Mosaic loss of chromosome Y (mLOY) is a male-specific condition characterized by the loss of chromosome Y by some cells. mLOY has been linked to various medical conditions, including cancer, and is most commonly observed in the white blood cells of ageing men. This genome-wide association study analyzed the genetic data of 95,380 Japanese men to better understand the genetic factors that contribute to the loss of the *Y chromosome*. The study discovered 46 genetic variants of which 35 are novel, and collectively these variants explain an estimated 9% of the heritability of mLOY. Many of the identified genetic variants are near genes that are active in blood *stem cells*.

DID YOU KNOW?

Studies have shown that smoking may significantly increase the risk of mosaic loss of chromosome Y.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to mosaic loss of chromosome Y we summed up the effects of genetic variants that were linked to mosaic loss of chromosome Y 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 mosaic loss of chromosome Y. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to mosaic loss of chromosome Y. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to mosaic loss of chromosome Y. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for mosaic loss of chromosome Y to be -0.08**. 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 mosaic loss of chromosome Y is in the **27th percentile**. This means that it is higher than the polygenic scores 27% of people. We consider this to be a **below average genetic predisposition to mosaic loss of chromosome Y**. 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
rs56116444_G	T / T	-0.09 (-)	31%	9.20×10^{-81}
rs80277818_G	A / G	-0.07 (↓)	26%	7.80×10^{-65}
rs2842873_T	C / C	-0.06 (-)	37%	1.50×10^{-36}
rs72698721_A	G / G	0.06 (-)	32%	4.20×10^{-33}
rs59543286_C NEW	A / A	0.06 (-)	23%	8.00×10^{-32}
rs4709819_A	G / A	0.05 (↑)	41%	1.30×10^{-30}
rs227079_A	C / A	-0.04 (↓)	48%	5.90×10^{-26}
rs4721217_T	C / C	-0.04 (-)	42%	6.80×10^{-23}
rs2237896_A NEW	G / G	0.04 (-)	40%	1.70×10^{-22}
rs78997619_T	C / C	0.08 (-)	6%	2.50×10^{-21}
rs55727837_T NEW	G / G	0.06 (-)	11%	9.70×10^{-20}
rs34324_A NEW	A / A	-0.04 (↓)	43%	3.10×10^{-19}
rs11769630_A NEW	T / T	-0.06 (-)	13%	3.70×10^{-19}
rs4681200_G	G / G	0.07 (↑)	92%	3.80×10^{-19}
rs4683900_T	C / T	0.04 (↑)	37%	7.90×10^{-19}
rs10849448_G NEW	A / G	-0.05 (↓)	81%	1.50×10^{-18}
rs728739_G	A / G	0.08 (↑)	6%	3.80×10^{-18}
rs871134_T NEW	C / T	-0.03 (↓)	49%	1.40×10^{-14}
rs35355140_A NEW	C / C	0.04 (-)	14%	2.30×10^{-13}
rs138423884_G NEW	NA	0.08 (-)	4%	1.30×10^{-12}
rs10948011_A NEW	G / G	0.04 (-)	23%	4.00×10^{-12}
rs9921295_G NEW	T / T	0.03 (-)	33%	4.00×10^{-12}
rs17049722_T NEW	C / C	0.04 (-)	17%	4.40×10^{-12}
rs11251_T	G / G	0.03 (-)	54%	3.40×10^{-11}
rs77406149_G NEW	A / A	0.04 (-)	20%	2.50×10^{-10}
rs2646425_T NEW	C / C	0.03 (-)	31%	4.30×10^{-10}
rs2811487_A NEW	G / G	0.03 (-)	36%	6.80×10^{-10}
rs1859259_T NEW	T / T	-0.03 (↓)	58%	1.10×10^{-9}
rs12668837_T NEW	C / C	-0.03 (-)	46%	1.80×10^{-9}
rs2853677_A NEW	G / A	0.03 (↑)	70%	2.10×10^{-9}
rs9299129_G NEW	A / A	0.03 (-)	23%	2.20×10^{-9}
rs527504_A NEW	G / A	-0.03 (↓)	19%	4.10×10^{-9}
rs77874075_G	T / G	-0.03 (↓)	22%	4.60×10^{-9}
rs117687217_C NEW	NA	-0.10 (-)	2%	9.70×10^{-9}
rs201753350_T	NA	-0.15 (-)	1%	1.00×10^{-8}
rs12225799_G NEW	C / G	-0.04 (↓)	13%	1.10×10^{-8}
rs79058858_T NEW	NA	0.16 (-)	1%	1.40×10^{-8}
rs74843651_T NEW	G / G	0.06 (-)	5%	2.20×10^{-8}

rs189309686_T	**C / C**	0.03 (–)	25%	4.40×10^{-8}
rs2804301_A	**G / G**	-0.03 (–)	24%	4.40×10^{-8}
rs2979469_C	**G / G**	-0.04 (–)	88%	4.90×10^{-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.