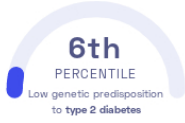⭐ **Type 2 diabetes (Spracklen, 2020)**

Cassandra Spracklen, et al.
Nature

Metabolism

STUDY SUMMARY

Identification of 301 genetic variants associated with type 2 diabetes in East Asian populations.

YOUR RESULT

6th
PERCENTILE
Low genetic predisposition
to **type 2 diabetes**

STUDY DESCRIPTION

Blood sugar, or glucose, is the body's main source of energy. Its concentration in the blood is controlled by the hormone insulin which is produced in the _pancreas_. Insulin promotes the intake of blood sugar by the cells in the body which reduces its concentration in the blood. Type 2 diabetes occurs when cells don't respond to insulin and/or the _pancreas_ does not produce enough insulin. This results in increased blood glucose concentration which damages organs, nerves, and blood vessels. Most previous studies examined genetic predisposition to type 2 diabetes in European populations, potentially missing many genetic variants that are less common in individuals of European ancestry. Also, previous research has shown that adjusted for _BMI_, East Asian individuals have higher rates of diabetes than Europeans. Thus, this study looked at type 2 diabetes in people with East Asian ancestry: 77,418 individuals with type 2 diabetes and 356,122 healthy controls. The study identified 301 genetic variants across 183 genomic locations of which 61 are novel. Most of the identified variants were found to influence type 2 diabetes risk in Europeans in a similar way.

DID YOU KNOW?

The glycemic index is a measurement of how fast a type of food will cause an increase in blood sugar. Glucose, the form of sugar your body uses, has a glycemic index of 100. White rice has a glycemic index of 73, nearly as high as white bread at 75. Eating lower glycemic index foods can help patients control their diabetes.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to type 2 diabetes we summed up the effects of genetic variants that were linked to type 2 diabetes 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 type 2 diabetes. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to type 2 diabetes. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to type 2 diabetes. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for type 2 diabetes to be 16.76**. 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 type 2 diabetes is in the **6th percentile**. This means that it is higher than the polygenic scores 6% of people. We consider this to be a **low genetic predisposition to type 2 diabetes**. 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ⓘ
rs2237897_C	C / C	0.27 (↑)	63%	2.08×10^{-246}
rs10965248_T	T / T	0.23 (↑)	56%	1.10×10^{-98}
rs2233580_T	C / C	0.27 (−)	9%	3.41×10^{-93}
rs9350271_A	G / G	0.15 (−)	42%	4.93×10^{-82}
rs7901695_C	NA	0.52 (−)	4%	5.83×10^{-81}
rs13266634_C	C / C	0.11 (↑)	59%	4.51×10^{-67}
rs13092876_A	G / G	0.12 (−)	31%	2.32×10^{-66}
rs8064454_A	C / C	0.11 (−)	31%	1.06×10^{-56}
rs11257657_G	C / C	0.10 (−)	48%	3.45×10^{-53}
rs1421085_C	T / C	0.13 (↑)	17%	1.71×10^{-48}
rs10757283_T	C / C	0.13 (−)	64%	5.94×10^{-46}
rs4073288_G	G / A	0.38 (↑)	95%	1.30×10^{-39}
rs8037894_G	G / G	0.09 (↑)	59%	3.35×10^{-37}
rs256904_T	T / T	0.08 (↑)	49%	5.89×10^{-34}
rs80234489_C	A / A	0.10 (−)	17%	4.53×10^{-32}
rs17072370_T	T / T	0.09 (↑)	72%	1.37×10^{-31}
rs35906730_G	G / A	0.10 (↑)	27%	1.08×10^{-30}
rs3824004_T	NA	0.22 (−)	3%	1.10×10^{-30}
rs2796441_G	G / A	0.08 (↑)	39%	4.96×10^{-29}
rs79748283_A	A / A	0.13 (↑)	90%	3.08×10^{-28}
rs10011838_G	G / G	0.08 (↑)	49%	1.47×10^{-27}
rs234866_G	G / G	0.11 (↑)	85%	3.56×10^{-27}
rs476828_C	T / C	0.09 (↑)	24%	4.95×10^{-27}
rs7656416_C	C / C	0.09 (↑)	68%	6.11×10^{-27}
rs952471_G	G / G	0.07 (↑)	40%	1.67×10^{-26}
rs4148646_C	G / G	0.08 (−)	39%	1.75×10^{-26}
rs11926494_G	G / G	0.10 (↑)	82%	2.72×10^{-26}
rs6585201_A	NA	0.25 (−)	4%	8.08×10^{-26}
rs4237150_C	G / C	0.07 (↑)	43%	2.57×10^{-25}
rs186568031_T	C / C	0.11 (−)	9%	9.19×10^{-24}
rs742762_A	A / C	0.08 (↑)	71%	1.68×10^{-23}
rs10886863_C	C / C	0.07 (↑)	66%	9.44×10^{-23}
rs8026714_A	G / G	0.07 (−)	49%	1.08×10^{-22}
rs142395395_A	A / A	0.22 (↑)	97%	1.42×10^{-22}
rs568052023_C	/	0.07 (−)	58%	2.68×10^{-22}
rs1260326_C	T / C	0.07 (↑)	46%	1.03×10^{-21}
rs60410861_A	G / G	0.10 (−)	14%	1.69×10^{-21}
rs7109575_G	G / G	0.14 (↑)	95%	5.55×10^{-21}

rs17168486_T	C / T	0.06 (↑)	42%	6.10×10^{-21}
rs3751236_G	G / A	0.07 (↑)	67%	6.69×10^{-21}
rs12907887_C	G / G	0.08 (−)	23%	2.23×10^{-20}
rs2583934_T	G / G	0.07 (−)	34%	1.55×10^{-19}
rs35099099_A	G / A	0.06 (↑)	41%	3.32×10^{-19}
rs1832886_G	G / A	0.08 (↑)	21%	7.17×10^{-19}
rs10950550_T	T / G	0.07 (↑)	68%	1.30×10^{-18}
rs7983505_T	A / A	0.08 (−)	16%	1.61×10^{-18}
rs4711389_A	A / A	0.10 (↑)	89%	2.89×10^{-18}
rs9523295_G	G / A	0.08 (↑)	83%	7.32×10^{-18}
rs28691713_C	T / T	0.07 (−)	56%	1.22×10^{-17}
rs11199753_G	G / T	0.08 (↑)	81%	4.45×10^{-17}
rs697743_G	G / G	0.12 (↑)	90%	6.27×10^{-17}
rs1575972_T	T / T	0.13 (↑)	95%	1.41×10^{-16}
rs117267808_A	G / G	0.10 (−)	8%	1.60×10^{-16}
rs117624659_T	T / T	0.21 (↑)	98%	1.98×10^{-16}
rs7250869_T	T / C	0.06 (↑)	53%	2.31×10^{-16}
rs28599782_A	G / G	0.07 (−)	21%	4.69×10^{-16}
rs7925578_T	G / T	0.07 (↑)	79%	8.06×10^{-16}
rs6831006_G	G / C	0.07 (↑)	27%	1.09×10^{-15}
rs75536691_A	A / A	0.18 (↑)	98%	1.17×10^{-15}
rs12454712_T	C / C	0.06 (−)	51%	1.41×10^{-15}
rs111246699_A	G / A	0.06 (↑)	26%	1.55×10^{-15}
rs243018_G	C / C	0.06 (−)	67%	1.80×10^{-15}
rs7787720_T	T / T	0.06 (↑)	42%	2.27×10^{-15}
rs12698877_G	A / A	0.06 (−)	34%	2.59×10^{-15}
rs12712928_C 🆕	G / C	0.06 (↑)	40%	5.64×10^{-15}
rs76868685_C	C / C	0.37 (↑)	99%	6.69×10^{-15}
rs11205766_T	T / A	0.09 (↑)	90%	7.56×10^{-15}
rs12625671_C	T / T	0.06 (−)	44%	8.09×10^{-15}
rs13040225_A	A / A	0.05 (↑)	51%	1.65×10^{-14}
rs8043085_T	G / G	0.05 (−)	45%	2.07×10^{-14}
rs9379084_G	G / G	0.07 (↑)	80%	2.22×10^{-14}
rs62508166_G	G / G	0.09 (↑)	87%	2.52×10^{-14}
rs376993806_G	A / A	0.10 (−)	88%	3.86×10^{-14}
rs4273712_G	A / G	0.05 (↑)	47%	4.00×10^{-14}
rs10965239_A	A / A	0.10 (↑)	83%	6.12×10^{-14}
rs61509816_C	C / C	0.14 (↑)	96%	7.58×10^{-14}
rs139034871_C	NA	0.22 (−)	2%	8.60×10^{-14}
rs201308301_A	G / G	0.09 (−)	22%	1.23×10^{-13}
rs138205568_C	C / C	0.19 (↑)	98%	1.38×10^{-13}
rs11023072_A	C / C	0.06 (−)	47%	1.45×10^{-13}
rs6416749_C	T / T	0.06 (−)	38%	3.94×10^{-13}
rs184356106_C	C / C	0.07 (↑)	75%	7.28×10^{-13}
rs80196932_T	T / C	0.06 (↑)	79%	7.62×10^{-13}
rs10852123_A	C / C	0.06 (−)	20%	8.43×10^{-13}
rs147834269_G	G / G	0.22 (↑)	98%	1.23×10^{-12}
rs3135911_A	A / A	0.05 (↑)	43%	1.52×10^{-12}
rs55783344_T	C / C	0.07 (−)	18%	2.17×10^{-12}
rs3735567_G	G / G	0.06 (↑)	78%	3.07×10^{-12}
rs562138031_C	/	0.06 (−)	73%	4.01×10^{-12}
rs2524113_G	T / G	0.07 (↑)	20%	5.28×10^{-12}
rs7900112_T	T / A	0.05 (↑)	49%	5.39×10^{-12}
rs60054445_C	C / C	0.05 (↑)	66%	5.65×10^{-12}
rs7313668_T	T / T	0.05 (↑)	37%	5.89×10^{-12}
rs12403994_C	A / A	0.05 (−)	62%	6.09×10^{-12}
rs1426371_G	A / A	0.05 (−)	49%	7.80×10^{-12}
rs117809958_A	NA	0.19 (−)	2%	9.55×10^{-12}
rs532504_A	G / G	0.06 (−)	21%	1.01×10^{-11}
rs201018682_T	T / C	0.06 (↑)	82%	1.02×10^{-11}
rs188520200_C	NA	0.25 (−)	1%	1.02×10^{-11}

rs35551980_C	T / T	0.05 (−)	25%	1.07×10^{-11}
rs7895872_T 🆕	G / T	0.05 (↑)	58%	1.37×10^{-11}
rs7739842_G	T / T	0.05 (−)	36%	1.56×10^{-11}
rs6806156_T 🆕	C / C	0.05 (−)	61%	1.60×10^{-11}
rs538698072_A	NA	0.27 (−)	1%	1.69×10^{-11}
rs7171507_T	T / C	0.05 (↑)	61%	1.82×10^{-11}
rs4739515_G 🆕	G / G	0.05 (↑)	54%	2.84×10^{-11}
rs75990271_T	T / T	0.07 (↑)	82%	3.23×10^{-11}
rs3963364_C	C / A	0.11 (↑)	95%	3.51×10^{-11}
rs7502556_T	T / C	0.05 (↑)	54%	3.81×10^{-11}
rs1182444_G	A / G	0.05 (↑)	50%	3.83×10^{-11}
rs2151282_C	C / T	0.05 (↑)	66%	4.01×10^{-11}
rs2908279_G	T / T	0.05 (−)	63%	4.59×10^{-11}
rs238763_T	A / A	0.05 (−)	68%	5.07×10^{-11}
rs73347525_A 🆕	A / A	0.06 (↑)	76%	7.50×10^{-11}
rs879882_C	T / C	0.05 (↑)	43%	8.56×10^{-11}
rs118074491_G	NA	0.14 (−)	3%	8.93×10^{-11}
rs10748694_A 🆕	T / T	0.05 (−)	31%	9.24×10^{-11}
rs2800734_G	G / G	0.07 (↑)	89%	1.23×10^{-10}
rs61021634_A 🆕	A / A	0.05 (↑)	44%	1.35×10^{-10}
rs988748_G 🆕	G / G	0.04 (↑)	56%	1.62×10^{-10}
rs529565_C	C / C	0.04 (↑)	45%	1.69×10^{-10}
rs561837820_A	NA	0.53 (−)	1%	1.76×10^{-10}
rs56687477_A	G / G	0.05 (−)	32%	1.91×10^{-10}
rs123378_G	G / A	0.05 (↑)	20%	2.23×10^{-10}
rs1955163_G	G / A	0.04 (↑)	54%	3.38×10^{-10}
rs10938398_A	G / G	0.05 (−)	29%	3.86×10^{-10}
rs60573766_C 🆕	C / C	0.04 (↑)	64%	4.31×10^{-10}
rs1236816_A	C / A	0.04 (↑)	50%	4.32×10^{-10}
rs77045000_C	C / C	0.43 (↑)	> 99%	5.28×10^{-10}
rs75179644_T 🆕	T / T	0.08 (↑)	90%	5.38×10^{-10}
rs2269245_G 🆕	G / G	0.06 (↑)	82%	5.42×10^{-10}
rs149265787_G 🆕	NA	0.13 (−)	2%	5.70×10^{-10}
rs6021276_T	C / C	0.04 (−)	41%	6.68×10^{-10}
rs9998835_G	C / C	0.11 (−)	96%	7.00×10^{-10}
rs61910828_C	C / C	0.08 (↑)	91%	8.00×10^{-10}
rs9948462_T	C / C	0.05 (−)	71%	8.73×10^{-10}
rs4716673_T	T / T	0.06 (↑)	81%	8.98×10^{-10}
rs12437434_C 🆕	C / C	0.05 (↑)	71%	1.02×10^{-9}
rs475002_G	C / C	0.04 (−)	52%	1.08×10^{-9}
rs1850421_A	A / C	0.05 (↑)	28%	1.41×10^{-9}
rs231917_T	C / C	0.05 (−)	31%	1.44×10^{-9}
rs9866168_T 🆕	A / A	0.05 (−)	64%	1.55×10^{-9}
rs34642578_T 🆕	C / C	0.09 (−)	5%	1.61×10^{-9}
rs10860209_C	C / C	0.04 (↑)	59%	1.63×10^{-9}
rs7136054_C	G / C	0.07 (↑)	88%	1.64×10^{-9}
rs73085586_G	G / G	0.04 (↑)	64%	1.66×10^{-9}
rs149336329_G 🆕	G / G	0.10 (↑)	95%	1.71×10^{-9}
rs2925979_T	C / C	0.04 (−)	36%	1.71×10^{-9}
rs61975988_A	A / A	0.04 (↑)	46%	1.98×10^{-9}
rs7289813_A 🆕	A / G	0.06 (↑)	85%	2.03×10^{-9}
rs111826047_T	NA	0.10 (−)	4%	2.23×10^{-9}
rs10125947_A	G / G	0.04 (−)	63%	2.46×10^{-9}
rs6885132_C	C / C	0.04 (↑)	56%	2.59×10^{-9}
rs58524310_G 🆕	A / G	0.04 (↑)	33%	2.70×10^{-9}
rs2240885_A	G / G	0.04 (−)	40%	2.80×10^{-9}
rs12379111_C	C / C	0.08 (↑)	79%	2.84×10^{-9}
rs9859381_G	T / G	0.04 (↑)	49%	2.87×10^{-9}
rs28637892_T 🆕	G / T	0.05 (↑)	22%	3.09×10^{-9}
rs261982_T 🆕	T / T	0.04 (↑)	41%	3.12×10^{-9}

rs9316706_A 🆕	A / A	0.04 (↑)	35%	3.34×10^{-9}
rs60089934_A 🆕	G / G	0.04 (–)	38%	3.34×10^{-9}
rs16902871_G 🆕	A / A	0.06 (–)	15%	3.35×10^{-9}
rs62405419_T	G / G	0.05 (–)	27%	3.79×10^{-9}
rs77816939_C	C / C	0.16 (↑)	98%	4.10×10^{-9}
rs602652_A	A / A	0.06 (↑)	81%	4.65×10^{-9}
rs77978149_T 🆕	C / C	0.08 (–)	9%	5.71×10^{-9}
rs12600132_T 🆕	C / T	0.04 (↑)	43%	5.96×10^{-9}
rs9390022_T 🆕	C / C	0.05 (–)	80%	6.37×10^{-9}
rs896852_G	G / T	0.04 (↑)	30%	6.43×10^{-9}
rs3731600_C	C / C	0.12 (↑)	97%	6.88×10^{-9}
rs1327123_C 🆕	C / C	0.04 (↑)	46%	7.01×10^{-9}
rs13086331_T	T / T	0.05 (↑)	82%	7.31×10^{-9}
rs2074120_A 🆕	A / C	0.04 (↑)	32%	8.40×10^{-9}
rs12109081_T	T / T	0.04 (↑)	36%	1.08×10^{-8}
rs76541615_T	T / T	0.06 (↑)	80%	1.25×10^{-8}
rs2706710_T	C / C	0.07 (–)	8%	1.38×10^{-8}
rs55700915_A 🆕	G / G	0.04 (–)	43%	1.50×10^{-8}
rs77065181_A 🆕	NA	0.09 (–)	5%	1.57×10^{-8}
rs2126736_A	G / G	0.04 (–)	43%	1.84×10^{-8}
rs74998300_T 🆕	T / T	0.06 (↑)	87%	1.89×10^{-8}
rs1016565_A 🆕	A / A	0.04 (↑)	42%	2.19×10^{-8}
rs329122_A	G / A	0.04 (↑)	39%	2.22×10^{-8}
rs9376382_C 🆕	T / T	0.04 (–)	60%	2.57×10^{-8}
rs12673470_A	G / G	0.06 (–)	25%	2.77×10^{-8}
rs9266658_G	G / G	0.04 (↑)	60%	2.82×10^{-8}
rs144239281_C	C / C	0.17 (↑)	98%	2.97×10^{-8}
rs349359_C 🆕	A / C	0.04 (↑)	24%	3.06×10^{-8}
rs9935994_C	C / G	0.05 (↑)	79%	3.08×10^{-8}
rs4776970_A	A / A	0.04 (↑)	22%	3.42×10^{-8}
rs188775221_T	T / T	0.07 (↑)	77%	3.52×10^{-8}
rs113154802_C 🆕	C / T	0.06 (↑)	89%	3.52×10^{-8}
rs7307263_G 🆕	C / G	0.04 (↑)	43%	3.65×10^{-8}
rs572817245_T	/	0.06 (–)	19%	3.79×10^{-8}
rs12438302_G 🆕	G / G	0.05 (↑)	74%	3.81×10^{-8}
rs8101064_T	C / C	0.07 (–)	13%	3.88×10^{-8}
rs75759932_C	NA	0.16 (–)	2%	4.01×10^{-8}
rs10505581_C 🆕	T / T	0.04 (–)	25%	4.42×10^{-8}
rs10830963_G	C / G	0.04 (↑)	42%	4.49×10^{-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.