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Chronic kidney disease (Hellwege, 2019)

Jacklyn Hellwege, et al.
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Kidneys

STUDY SUMMARY

A study of over 1 million participants identified 82 novel genetic variants associated with chronic kidney disease.

YOUR RESULT

STUDY DESCRIPTION

Kidneys have the crucial roles of filtering blood to remove waste and maintaining electrolyte levels in the body. Damage to the kidneys can cause waste to accumulate in the body, leading to higher risks of kidney failure which contributes to heart disease and other conditions. Much of the genetic contribution to kidney diseases is not well understood. This trans-ethnic genome-wide association study examined over 1 million individuals of East Asian, South Asian, African American, Hispanic, and European ancestries. 82 novel variants associated with chronic kidney disease were discovered. One of the most significant novel variants is near NRIP1. Mutations in this gene have been reported to cause birth defects in the kidneys, which can increase the risk of chronic kidney disease in young adults.

DID YOU KNOW?

To help prevent kidney disease, eat healthily (in particular, consume less salt), exercise regularly, get sufficient sleep, and avoid alcohol as well as drugs.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to chronic kidney disease we summed up the effects of genetic variants that were linked to chronic kidney disease 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 chronic kidney disease. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to chronic kidney disease. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to chronic kidney disease. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for chronic kidney disease to be 8.88**. 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 chronic kidney disease is in the **100th percentile**. This means that it is higher than the polygenic scores 100% of people. We consider this to be a **very high genetic predisposition to chronic kidney disease**. 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
rs77924615_A	G / G	1.54 (–)	19%	3.55×10^{-139}
rs13146355_A	G / A	-0.74 (↓)	42%	2.56×10^{-93}
rs1047891_A	C / A	-0.65 (↓)	32%	1.83×10^{-62}
rs963837_T	T / T	-0.68 (↓)	57%	7.36×10^{-62}
rs9895661_T	T / T	0.68 (↑)	75%	2.42×10^{-57}
rs35610898_C	G / C	-0.70 (↓)	31%	9.79×10^{-57}
rs2279463_A	A / A	0.81 (↑)	86%	1.58×10^{-48}
rs13230509_C	C / C	-0.60 (↓)	63%	1.70×10^{-48}
rs56376587_A	A / A	0.62 (↑)	54%	7.51×10^{-43}
rs80282103_A	A / A	0.94 (↑)	89%	8.58×10^{-38}
rs1260326_T	T / C	0.42 (↑)	39%	9.65×10^{-35}
rs7007761_T	C / T	-0.47 (↓)	40%	1.05×10^{-33}
rs11072567_A	A / G	0.47 (↑)	52%	2.18×10^{-33}
rs1556751_A	G / A	0.42 (↑)	62%	5.43×10^{-33}
rs541524196_G	TTTTTTTTTTT / TTTTTTTTTTT	0.48 (–)	20%	2.77×10^{-26}
rs2252281_T	T / T	0.37 (↑)	60%	5.08×10^{-25}
rs948494_A	G / G	-0.52 (–)	33%	7.00×10^{-25}
rs1045463_T	C / C	-0.45 (–)	26%	2.03×10^{-23}
rs10774020_T	C / C	0.26 (–)	38%	6.52×10^{-21}
rs12509595_T	C / C	-0.39 (–)	72%	1.57×10^{-20}
rs2472297_T	C / C	0.45 (–)	23%	1.52×10^{-18}
rs81205_A	A / A	0.34 (↑)	49%	7.21×10^{-18}
rs12722725_T	T / T	0.41 (↑)	88%	8.94×10^{-18}
rs2925345_T	C / C	-0.40 (–)	51%	9.69×10^{-18}
rs7956634_T	T / C	-0.41 (↓)	74%	1.61×10^{-17}
rs2143919_C NEW	G / C	-0.36 (↓)	52%	1.71×10^{-17}
rs807624_T	G / T	0.28 (↑)	40%	4.91×10^{-17}
rs2823139_A NEW	G / A	-0.45 (↓)	34%	6.61×10^{-17}
rs77805826_T	C / C	-0.47 (–)	14%	7.86×10^{-16}
rs700750_A NEW	C / A	-0.30 (↓)	62%	3.25×10^{-15}
rs7914178_A	G / G	-0.29 (–)	54%	6.87×10^{-15}
rs10994856_A	G / G	0.37 (–)	18%	1.48×10^{-14}
rs7253870_A	A / A	0.31 (↑)	48%	2.08×10^{-14}
rs12471433_A NEW	A / A	0.36 (↑)	70%	2.20×10^{-14}
rs1785418_A	G / A	-0.32 (↓)	46%	4.75×10^{-14}
rs7635449_T	T / T	0.27 (↑)	54%	9.84×10^{-14}
rs1371810_T	C / C	-0.34 (–)	44%	2.05×10^{-13}
rs72929935_T	T / T	1.32 (↑)	98%	2.68×10^{-13}
rs953492_A	G / G	-0.30 (–)	49%	3.28×10^{-13}

rs13393068_T	C / T	-0.30 (↓)	35%	4.49×10^{-13}
rs12920969_A	G / G	-0.26 (–)	43%	8.79×10^{-13}
rs11123169_T	C / T	0.30 (↑)	66%	1.26×10^{-12}
rs12927956_T	C / C	-0.29 (–)	22%	1.31×10^{-12}
rs7688014_T	T / C	-0.32 (↓)	44%	2.35×10^{-12}
rs2068888_A	G / A	-0.24 (↓)	44%	3.77×10^{-12}
rs115276619_A	NA	-1.53 (–)	2%	4.47×10^{-12}
rs10865282_A	A / A	0.39 (↑)	79%	2.76×10^{-11}
rs55878006_A	G / G	-0.42 (–)	13%	2.85×10^{-11}
rs11759908_T	C / T	-0.29 (↓)	41%	4.72×10^{-11}
rs760077_A	T / T	-0.34 (–)	38%	7.02×10^{-11}
rs41301394_T	C / T	0.29 (↑)	27%	7.21×10^{-11}
rs6933716_T	C / C	0.28 (–)	37%	1.05×10^{-10}
rs2921051_A	A / A	0.26 (↑)	47%	1.95×10^{-10}
rs10983324_A	C / C	-0.30 (–)	36%	2.82×10^{-10}
rs543179_A	G / A	-0.30 (↓)	41%	2.83×10^{-10}
rs112785404_T	T / T	-0.51 (↓)	92%	2.96×10^{-10}
rs28833881_A	A / A	-0.34 (↓)	66%	3.71×10^{-10}
rs12942059_A	G / G	-0.35 (–)	40%	6.22×10^{-10}
rs5763646_T	T / T	-0.27 (↓)	61%	8.80×10^{-10}
rs1264351_C	G / G	-0.47 (–)	11%	9.44×10^{-10}
rs755631_A	A / A	0.32 (↑)	50%	1.01×10^{-9}
rs2143668_A	A / A	0.58 (↑)	91%	1.25×10^{-9}
rs281380_T	T / T	-0.26 (↓)	63%	1.39×10^{-9}
rs872355_A	G / G	-0.27 (–)	35%	1.52×10^{-9}
rs2652806_T	T / T	0.31 (↑)	67%	2.97×10^{-9}
rs11103387_T	C / T	0.26 (↑)	37%	3.12×10^{-9}
rs28601761_C	C / C	0.28 (↑)	60%	3.27×10^{-9}
rs7681615_T	T / T	0.30 (↑)	36%	5.17×10^{-9}
rs3904941_A	G / G	-0.29 (–)	48%	6.03×10^{-9}
rs288762_T	T / C	0.29 (↑)	38%	7.52×10^{-9}
rs71559067_A	A / A	0.53 (↑)	92%	8.18×10^{-9}
rs72683923_T	T / T	-1.19 (↓)	98%	8.49×10^{-9}
rs116092985_A	A / A	-0.53 (↓)	14%	1.15×10^{-8}
rs11100781_A	G / G	-0.32 (–)	31%	1.29×10^{-8}
rs7107004_C	C / C	0.35 (↑)	73%	1.45×10^{-8}
rs4783720_T	T / T	0.41 (↑)	87%	1.84×10^{-8}
rs6055748_A	G / G	-0.27 (–)	70%	1.84×10^{-8}
rs3776712_T	T / C	-0.32 (↓)	73%	2.26×10^{-8}
rs58625759_A	A / A	0.36 (↑)	18%	2.46×10^{-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.