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Proteinuria (Teumer, 2019)

Alexander Teumer, et al.
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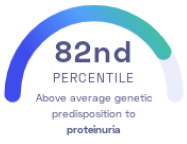
Kidneys

STUDY SUMMARY

Genome-wide identification of 68 variants associated with protein in urine, a key indicator of chronic kidney disease.

YOUR RESULT



STUDY DESCRIPTION

The kidneys have an important role of filtering blood to remove wastes from the body. When the kidneys become damaged, important proteins that normally stay in our blood can leak out into our urine. Increased urinary levels of proteins, called proteinuria, are used to diagnose chronic kidney disease. To date, only a few genetic risk factors contributing to heightened levels of protein in urine have been identified. This trans-ethnic study examined over 560,000 individuals of European, African, East Asian, South Asian, and Hispanic ancestry to improve our understanding of genetic predisposition to kidney damage. The study identified 68 genetic variants associated with elevated levels of proteins in urine. These variants help explain less than 1% of the heritability of proteinuria. Some of these variants are also correlated with elevated fat levels in the blood, high blood pressure, and gout (a type of inflammatory arthritis).

DID YOU KNOW?

Cooking meals from "scratch" instead of eating prepared foods can help to limit excess salt and sugar intake, reducing your chances of developing chronic kidney disease.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to proteinuria we summed up the effects of genetic variants that were linked to proteinuria 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 proteinuria. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to proteinuria. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to proteinuria. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for proteinuria 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 proteinuria is in the **82nd percentile**. This means that it is higher than the polygenic scores 82% of people. We consider this to be an **above average genetic predisposition to proteinuria**. 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
rs45561835_A	NA	0.20 (–)	2%	2.80×10^{-126}
rs1337526_A	G / G	-0.03 (–)	21%	9.60×10^{-29}
rs2470893_T	C / C	0.02 (–)	33%	7.50×10^{-27}
rs4410790_T	T / C	-0.02 (↓)	38%	6.70×10^{-25}
rs4665972_T	T / C	0.02 (↑)	39%	1.20×10^{-18}
rs1047891_A	C / A	-0.02 (↓)	31%	4.00×10^{-18}
rs17158386_A	G / A	0.02 (↑)	26%	4.80×10^{-18}
rs2070803_A	G / G	-0.02 (–)	57%	4.50×10^{-17}
rs8031650_A NEW	A / A	-0.02 (↓)	73%	4.30×10^{-16}
rs1145078_T	C / C	-0.02 (–)	27%	8.90×10^{-16}
rs3734692_A NEW	A / T	-0.02 (↓)	69%	1.00×10^{-15}
rs28601761_C	C / C	0.02 (↑)	58%	1.70×10^{-14}
rs11882796_A	A / T	-0.02 (↓)	47%	2.10×10^{-14}
rs10207567_C	G / C	0.02 (↑)	81%	3.30×10^{-14}
rs776434_A	A / A	0.02 (↑)	65%	3.50×10^{-14}
rs6535694_A	G / A	0.01 (↑)	50%	4.60×10^{-14}
rs2023843_T	C / T	0.03 (↑)	91%	5.50×10^{-14}
rs112607182_T	C / C	0.03 (–)	8%	6.80×10^{-14}
rs12714144_A	A / A	0.02 (↑)	87%	7.60×10^{-14}
rs3784283_A	A / T	0.01 (↑)	59%	1.70×10^{-13}
rs10023335_T	T / C	0.01 (↑)	60%	5.30×10^{-13}
rs67339103_A	G / A	0.02 (↑)	23%	1.30×10^{-12}
rs1544935_T NEW	T / G	-0.02 (↓)	79%	2.80×10^{-12}
rs1688031_T NEW	C / C	-0.02 (–)	16%	6.00×10^{-12}
rs11158763_T	C / T	-0.01 (↓)	46%	7.40×10^{-12}
rs73065147_T NEW	T / T	-0.03 (↓)	93%	7.50×10^{-12}
rs147215801_T	NA	0.06 (–)	2%	2.80×10^{-11}
rs11659764_A NEW	T / T	0.03 (–)	5%	2.80×10^{-11}
rs508205_A NEW	G / A	-0.01 (↓)	56%	3.00×10^{-11}
rs57858280_T	C / T	0.02 (↑)	13%	9.40×10^{-11}
rs40480_C	G / G	-0.01 (–)	63%	1.50×10^{-10}
rs15052_T NEW	T / T	0.02 (↑)	83%	2.40×10^{-10}
rs78444298_A NEW	NA	-0.05 (–)	2%	2.50×10^{-10}
rs2240060_A NEW	A / G	0.01 (↑)	29%	2.90×10^{-10}
rs2068888_A NEW	G / A	-0.01 (↓)	45%	3.20×10^{-10}
rs677888_T NEW	T / T	-0.01 (↓)	76%	4.90×10^{-10}
rs13230845_C NEW	G / G	-0.02 (–)	19%	5.10×10^{-10}
rs11078597_T NEW	T / T	-0.02 (↓)	81%	5.70×10^{-10}
rs113139575_C	C / C	-0.03 (↓)	94%	6.40×10^{-10}

rs34071855_C	C / C	-0.01 (↓)	65%	6.70×10^{-10}
rs162890_T	T / T	0.01 (↑)	34%	8.40×10^{-10}
rs7115200_T	T / T	-0.01 (↓)	56%	9.20×10^{-10}
rs78999781_T	T / C	0.02 (↑)	90%	1.10×10^{-9}
rs1309550_A	T / A	-0.01 (↓)	45%	1.40×10^{-9}
rs2880119_A	A / A	-0.02 (↓)	86%	1.90×10^{-9}
rs10110261_A	G / A	-0.01 (↓)	50%	3.00×10^{-9}
rs1010553_T	C / C	0.01 (–)	51%	4.10×10^{-9}
rs28412751_T	C / T	-0.01 (↓)	45%	6.40×10^{-9}
rs146311723_T	T / T	-0.01 (↓)	82%	8.80×10^{-9}
rs3850625_A	G / A	0.02 (↑)	12%	1.10×10^{-8}
rs819636_T	T / T	-0.01 (↓)	66%	1.40×10^{-8}
rs10491967_A	G / G	-0.02 (–)	12%	1.80×10^{-8}
rs6142630_A	G / A	0.01 (↑)	40%	1.90×10^{-8}
rs16864515_A	C / C	-0.02 (–)	10%	2.30×10^{-8}
rs6998967_A	G / G	-0.01 (–)	17%	2.30×10^{-8}
rs11030024_T	C / C	-0.01 (–)	22%	2.40×10^{-8}
rs2760995_A	G / G	-0.01 (–)	20%	3.60×10^{-8}
rs2460448_A	G / G	-0.01 (–)	44%	3.60×10^{-8}
rs2793351_A	A / A	0.01 (↑)	69%	4.30×10^{-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.