

Supplement 1 Criteria for inclusion of primary outcomes of interest and clinical covariates

Phenotypes of interest	Criteria
Elevated blood pressure	-ICD-10: I10, I11, I11.0, I11.9, I12, I12.0, I12.9, I13, I13.0, I13.1, I13.2, I15, I15.0, I15.1, I15.2, I15.8, I15.9, I16, I16.0, I16.1, I16.9 -ICD-9: 401, 401.0, 401.1, 401.9, 402, 402.0, 402.1, 402.9, 403, 403.0, 403.1, 403.9, 404, 404.0, 404.1, 404.9, 405, 405.0, 405.01, 405.09, 405.1, 405.11, 405.19, 405.9, 405.91, 405.99 -Self-reported diagnosis of high blood pressure -Self-reported use of antihypertensive medication -Value for age at which high blood pressure diagnosed -Systolic blood pressure ≥ 130 mmHg -Diastolic blood pressure ≥ 80 mmHg
CKD stage 3+	-ICD-10: N18.0, N18.3, N18.4, N18.5, Z99.2, Z94.0 -ICD-9: 585.3, 585.4, 585.5, 585.6, V45.11, 55.6 -ESKD report present - ^a eGFR < 60 mL/min/1.73 m ²
Clinical covariates	
Current smoking status	-ICD-10: Z72.0, F17.200, F17.210 -ICD-9: 305.1 -Self-reported as current smoker -Self-reported as occasional or almost every day smoker
Diabetes mellitus	-ICD-10: E11, E11.0-11.9, E10, E10.0-10.9 -ICD-9: 250, 250.0-250.9 -Self-reported diagnosis of diabetes mellitus -Self-reported use of insulin -Value for age at which diabetes mellitus diagnosed
Vascular heart disease (stroke, angina, myocardial infarction)	-ICD-10: I20, I20.0, I20.1, I20.8, I20.9, I21, I21.0-I21.4, I22, I22.0, I22.1, I22.2, I22.8, I22.9, I23, I23.0-I23.8, I24, I24.0, I24.1, I24.8, I24.9, I25, I25.1-I25.9, I63, I63.0-I63.9 -ICD-9: 413, 414, 410, 410.0-410.9, 411, 411.0, 411.1, 411.8, 412, 429.2, 434, 434.0, 434.1, 434.9 -Self-reported as history of stroke, angina, myocardial infarction
Hyperlipidemia	-ICD-10: E78, E78.0-E78.5 -ICD9: 272, 272.0-272.4 -Self-reported use of cholesterol lowering medication
Overweight	-ICD-10: E66, E66.01, E66.09, E66.1, E66.2, E66.3, E66.8, E66.9, Z68.25-Z68.45 -ICD-9: 278.02 -Body mass index ≥ 25.0 kg/m ²

^aeGFR calculated using CKD-EPI 2021 equation²⁶

Supplement 2 List of genes selected with annotations of reason for exclusion from analysis where relevant

Developmental Compartment	Genetic Marker
Early nephron development	<i>AMN, CCND1, CDH6, CITED1, COL2A1, CRABP2, *DLL1, ETV4, EYA1, FOXC2, GDNF, HES1, HNF1A, HNF1B, IRX2, IRX3, ITGA8, JAG1, LEF1, LHX1, MAFB, MEOX1, *OLFM3, OSR1, PAX2, PAX8, POU3F3, SALL1, SFRP2, SIM2, SIX1, SIX2, SOX9, *WNT4, WT1</i>
Podocytes	<i>*CLIC5, NPHS2, NPHS1, PODXL, PTPRO, *TGFB3</i>
Tubulointerstitial cells	<i>ACTA2, ALDH1A1, ANPEP, CD248^a, CDH1, CLCN5, CLDN1, CLDN2, COL1A1, COL3A1, CSPG4, CUBN, DCN, DES, *FGF7, FOXD1, GDNF, LEF1, LRP2, MAL, MCAM, PAPP2, PDGFRB, SERPINE2, SLC12A1, SLC12A3, SLC13A1, SLC34A1, *TACSTD2, TPM2, UMOD</i>
Collecting duct	<i>AQP2, CALB1, CLDN7, GATA2, KRT8, KRT18, MMP7, RET</i>
Endothelium	<i>CDH5, FLT1, KDR, PECAM1^b, TEK</i>

Items in **bold face** represent genes excluded from analysis due to missing whole exome data in >30% of individuals being assessed

*Genes excluded from analysis due to lack of availability from UK Biobank

^aCD248 was excluded from subgroup analysis of those who are of non-White British ancestry as whole exome data was available in <70% of individuals within this subgroup

^bPECAM1 was not included in any model as there were no individuals with a qualifying variant in this gene

Supplement 3 RUNES Category classification. Those with MAF <0.1% and Categories 1-3 were designated as qualifying variants, while those variants with MAF \geq 0.1% or Categories 4-5 were designated as non-qualifying.

RUNES Category	Classification Criteria
Category 1	Previously reported in ClinVar or HGMD and recognized as pathogenic
Category 2	Unreported but expected to cause disorder due to prediction of nonsense mutation, disruption of stop/start site, splice donor/acceptor mutation, frameshift mutation, or whole transcript deletion
Category 3	Unreported and may or may not cause disease including any missense mutation, in-frame insertion/deletion including whole exon, intronic or synonymous variant possibly affecting splicing, or any variant in a mitochondrial gene
Category 4	Novel and probably not causative of disease including synonymous mutations and intronic mutations far from the splice site, or variants with MAF >2%
Category 5	Known neutral variant in external database or variant with MAF >5%

Supplement 4A Count of number of qualifying rare variants identified in each gene included in analysis (n), and number of individuals possessing each qualifying rare variant with further subdivision by RUNES category, displayed as median (IQR).

Gene	Qualifying variants (n)	Individuals per variant	Category 1	Category 2	Category 3
<i>ALDH1A1</i>	20	12 (6-26)	-	6 (6-6)	12 (6.5-28)
<i>ANPEP</i>	55	11 (7-27.5)	-	16 (11.5-20.5)	11 (7-28)
<i>CALBI</i>	13	10 (6-23)	-	-	10 (6-23)
<i>CCND1</i>	9	21 (12-29)	6 (6-6)	-	22.5 (15.75-31.75)
<i>CD248</i>	24	7.5 (6-15.25)	-	-	7.5 (6-15.25)
<i>CDH1</i>	36	10 (7-14.5)	10 (7-17)	-	10 (6.75-12.5)
<i>CDH5</i>	64	8.5 (6-13.25)	6 (6-6)	7.5 (5.75-20)	9 (6-13.5)
<i>CDH6</i>	23	8 (6-13)	-	8.5 (6.75-10.25)	8 (6-14)
<i>CITED1</i>	8	13 (9-18.25)	-	-	13 (9-18.25)
<i>CLCN5</i>	35	7 (5.5-10.5)	9.5 (8-12.25)	7 (6-9.5)	6.5 (5.75-10.25)
<i>CLDN1</i>	11	9 (5.5-13.5)	-	-	9 (5.5-13.5)
<i>CLDN7</i>	16	14.5 (7-17.5)	-	7 (7-7)	15 (7-19)
<i>COL1A1</i>	95	9 (5-18)	15 (6.25-41.5)	-	8 (5-13)
<i>COL2A1</i>	73	9 (6-19)	6 (6-25)	-	9 (6-18.75)
<i>COL3A1</i>	63	7 (6-15)	11 (6.5-14.5)	6 (6-6)	7 (5-15)
<i>CRABP2</i>	11	9 (7-14.5)	-	12 (9-14.5)	9 (7.5-18.75)
<i>CSPG4</i>	126	10 (6.25-20.75)	84 (84-84)	5 (5-5)	10 (6.75-20.25)
<i>CUBN</i>	88	10.5 (6-25.5)	21 (10-33)	9 (6-16.75)	10 (6-23.5)
<i>DES</i>	31	7 (6-12.5)	10.5 (7.5-22.25)	6 (6-6)	6 (6-7)
<i>ETV4</i>	6	11.5 (7.25-18)	-	13 (10-16)	11.5 (7.5-16.75)
<i>EYAI</i>	40	7 (5-11.5)	11 (6.5-18.25)	6 (6-6)	7 (5-10)
<i>FLT1</i>	73	8 (6-15)	52 (52-52)	7.5 (7.25-7.75)	8 (6-14.75)
<i>FOXD1</i>	59	8 (6-13)	65 (63.5-66.5)	8 (7-9)	8 (5.75-13)
<i>GATA2</i>	18	8.5 (6.25-12.25)	40.5 (24.25-56.75)	-	8.5 (5.75-10.75)
<i>GDNF</i>	7	9 (7.5-14)	15 (12.5-17.5)	-	9 (6-9)
<i>HES1</i>	12	7 (5.75-26.25)	-	-	7 (5.75-26.25)
<i>HNFA1</i>	32	12.5 (8-16.5)	13 (8.5-18)	-	10 (8.25-15.75)
<i>IRX3</i>	20	9.5 (6.75-13)	-	-	9.5 (6.75-13)
<i>ITGA8</i>	98	7 (6-11.75)	-	6 (5.5-7.5)	7 (6-13)

<i>JAG1</i>	50	8 (6-11.75)	6 (6-7.5)	-	8 (6-12)
<i>KDR</i>	104	7.5 (6-12)	19 (16.5-30.5)	6 (5.5-7)	7 (6-11.75)
<i>KRT8</i>	44	9 (7-26.25)	25 (9-28)	41 (21.5-61)	7 (6-15.25)
<i>LEF1</i>	29	9 (6-18)	-	-	9 (6-18)
<i>LRP2</i>	264	9 (6-21)	20.5 (11.5-30.25)	6 (6-7)	9 (6-21)
<i>NPHS1</i>	96	11.5 (6-24.25)	11 (7-19.75)	11 (11-11)	12 (6-24.5)
<i>NPHS2</i>	15	10 (6-21.5)	9 (6-19.5)	-	10 (7-21)
<i>OSR1</i>	6	6 (5-13)	-	-	6 (5-13)
<i>PAPPA2</i>	104	7 (6-13.25)	-	6 (5-11.5)	7 (6-13.25)
<i>PAX2</i>	16	8.5 (6-22.5)	16 (9.5-31)	-	7.5 (5.75-13.5)
<i>PAX8</i>	14	12.5 (6.25-41.25)	46 (25.5-48)	-	11 (6.5-27.5)
<i>PDGFRB</i>	87	7 (5-12.5)	21 (15.5-26.5)	8 (5-30)	7 (5-12)
<i>PODXL</i>	44	9.5 (7-17)	-	34 (14-40)	9 (7-15.5)
<i>POU3F3</i>	31	12 (7-28)	-	7 (7-7)	12 (7-28)
<i>PTPRO</i>	128	6 (5-9)	31.5 (8-64.75)	5 (5-6.25)	6 (5-9)
<i>RET</i>	62	9 (7-14.75)	13 (5.5-16.5)	-	8 (7-12.5)
<i>SALL1</i>	52	7 (6-12)	31.5 (18.75-44.25)	20.5 (14.75-26.25)	7 (6-12)
<i>SERPINE2</i>	23	7 (6-9)	-	-	7 (6-9)
<i>SFRP2</i>	11	9 (5.5-15.5)	-	-	9 (5.5-15.5)
<i>SIM2</i>	47	8 (6-15.5)	-	68 (68-68)	8 (6-14.5)
<i>SIX1</i>	8	6 (6-17.75)	28 (17-39)	6 (6-6)	6 (6-7)
<i>SIX2</i>	12	12.5 (7-19.25)	20 (20-20)	6 (6-6)	12.5 (8.25-18.25)
<i>SLC12A1</i>	71	7 (5-15.5)	5 (5-7)	7 (6-10.5)	7 (5-17)
<i>SLC12A3</i>	133	9 (6-17)	8 (6-19.5)	-	10 (6-17)
<i>SLC13A1</i>	52	9.5 (6-18)	-	6 (5-7)	10 (6-18)
<i>SOX9</i>	31	9 (6-12)	27 (13.25-28.75)	11 (8-11.5)	8 (6-9)
<i>TEK</i>	50	9.5 (6-13.5)	6 (5.5-14)	5 (5-5)	10 (6.25-13.5)
<i>TPM2</i>	17	11 (6-21)	-	6.5 (5.75-8)	12 (9-38)
<i>UMOD</i>	54	9 (6.25-21)	52 (39.5-64.5)	7 (6-9)	9 (6-21)
<i>WT1</i>	20	9 (5-14.5)	32 (18.5-41.5)	-	9 (5-12)

Supplement 4B Count of number of qualifying rare variants identified in each gene included in analysis (n), and number of individuals possessing each qualifying rare variant with further subdivision by functional impact as identified by RUNES software, displayed as median (IQR).

Gene	Qualifying variants (n)	NA	Frameshift	Non-synonymous	In-frame insertion/deletion	Premature stop	Synonymous	Loss of initiation	Disruption of splicing	Disruption of stop
<i>ALDH1A1</i>	20	8 (6-16)	6 (6-6)	28 (14.25-38.25)	-	-	-	-	-	-
<i>ANPEP</i>	55	18 (5-32)	25 (25-25)	11 (8-28)	6 (5.5-6.5)	7 (7-7)	12 (12-12)	-	-	-
<i>CALBI</i>	13	12 (6.75-23.75)	-	10 (5-10)	-	-	-	-	-	-
<i>CCND1</i>	9	19 (10.75-25.25)	-	-	45 (45-45)	-	-	-	-	-
<i>CD248</i>	24	-	-	7 (6-15.5)	10 (10-10)	-	-	-	-	-
<i>CDH1</i>	36	10 (8-12)	-	10 (6.25-15.5)	10 (10-10)	-	-	-	-	-
<i>CDH5</i>	64	14 (6-20)	5 (5-5)	8 (6-12)	6 (6-6)	7.5 (6.75-8.25)	6 (6-6)	53 (53-53)	-	-
<i>CDH6</i>	23	15 (7.5-22)	12 (12-12)	8 (6-10)	6 (6-6)	-	-	5 (5-5)	-	-
<i>CITED1</i>	8	-	-	13 (9-18.25)	-	-	-	-	-	-
<i>CLCN5</i>	35	6 (6-11.5)	12 (8.5-15.5)	7.5 (5.75-10)	-	6 (5.5-6.5)	-	-	-	-
<i>CLDN1</i>	11	7 (5.75-9.5)	-	10 (7-14.5)	-	-	-	-	-	-
<i>CLDN7</i>	16	28 (16.5-29)	7 (7-7)	14.5 (7-16)	-	-	-	-	-	-
<i>COL1A1</i>	95	9 (6-15.5)	5 (5-5)	9 (5-22)	9.5 (8.75-10.25)	-	26 (15.5-36.5)	-	-	-
<i>COL2A1</i>	73	8 (6-20)	5 (5-5)	9.5 (6-19)	-	-	5 (5-12)	-	-	-

<i>COL3A1</i>	63	6 (5-8.25)	10.5 (8.25-12.75)	11 (6-19)	5 (5-5)	-	21 (21-21)	-	-	-
<i>CRABP2</i>	11	6 (6-6)	6 (6-6)	9 (8.25-10.5)	-	12 (12-12)	42 (42-42)	-	17 (17-17)	-
<i>CSPG4</i>	126	7 (6.5-7.5)	-	10 (7-20)	21 (21-21)	5 (5-5)	-	-	-	-
<i>CUBN</i>	88	10 (6-23.75)	12 (7-28)	-	16.5 (10.75-22.25)	-	-	-	-	-
<i>DES</i>	31	16 (13-17)	6 (6-6)	6 (6-9.25)	-	-	6 (6-6)	-	-	-
<i>ETV4</i>	6	15 (10.5-18.5)	-	8 (8-8)	-	19 (19-19)	-	7 (7-7)	-	-
<i>EYAI</i>	40	9 (6.5-12)	6 (6-6)	6 (5-8.75)	-	8 (8-8)	23 (23-23)	-	-	-
<i>FLT1</i>	73	8 (5.25-14.25)	-	7.5 (6-16.75)	8 (8-9.5)	7.5 (7.25-7.75)	-	-	-	-
<i>FOXD1</i>	59	-	8 (7-9)	7 (5.25-12)	9 (6.75-17)	-	-	-	-	-
<i>GATA2</i>	18	9 (6-29)	-	8.5 (6.5-10.75)	-	-	8 (8-8)	-	-	-
<i>GDNF</i>	7	13.5 (11.25-15.75)	-	9 (6-10)	-	-	-	-	-	-
<i>HES1</i>	12	24 (14.5-33.5)	-	7 (5.75-15)	7 (7-7)	-	-	-	-	-
<i>HNFI1A</i>	32	13 (10-14.5)	8 (8-8)	12.5 (6.75-17.5)	-	-	30 (19-41)	-	-	-
<i>IRX3</i>	20	11 (8-14)	-	9 (7-12)	13 (13-13)	-	-	-	-	-
<i>ITGA8</i>	98	7 (6-11.75)	-	7 (6-11.75)	-	-	-	-	-	-
<i>JAG1</i>	50	8.5 (5.25-11)	-	8 (6-12)	-	-	7 (7-7)	-	-	-
<i>KDR</i>	104	7 (6-10)	-	8 (6-14)	-	6 (5.5-7)	6 (6-6)	-	-	-

<i>KRT8</i>	44	8 (7-21)	61 (46.25-74.5)	8 (6.5-17.5)	-	-	-	-	-	-
<i>LEF1</i>	29	6.5 (5.75-9)	-	16 (7.5-36.5)	5 (5-5)	-	47 (47-47)	-	-	-
<i>LRP2</i>	264	9 (6-21.5)	6 (6-8)	9 (6-20)	-	5 (5-5)	-	-	-	-
<i>NPHS1</i>	96	14.5 (8-28)	8.5 (5.75-17)	11 (6-24.5)	-	11 (11-11)	7 (7-7)	-	-	-
<i>NPHS2</i>	15	12 (7-27)	6 (6-6)	10 (6.75-15.25)	-	-	6 (6-6)	-	-	-
<i>PAPPA2</i>	104	6 (5-13.75)	16 (6.5-38.75)	7 (6-13)	-	5.5 (5.25-5.75)	5 (5-5)	-	-	-
<i>PAX2</i>	16	8 (6.25-9.75)	-	8 (5.75-40)	-	-	16 (13-19)	-	-	-
<i>PAX8</i>	14	9 (7.5-24)	-	14 (6-44)	-	-	-	-	-	-
<i>PDGFRB</i>	87	6 (5-7)	8 (6.5-9.5)	9 (6-15.5)	-	46 (25.5-66.5)	9 (9-9.5)	-	-	-
<i>PODXL</i>	44	9.5 (9-10)	37 (28.25-40)	9 (7-16)	9 (9-12)	14 (14-14)	-	-	-	-
<i>POU3F3</i>	31	-	7 (7-7)	8 (6.25-12.25)	19 (8-49.5)	-	-	-	-	-
<i>PTPRO</i>	128	6 (5-8)	5 (5-5)	7 (5-10)	19 (19-19)	6 (5.75-6.25)	-	-	-	-
<i>RET</i>	62	12 (8-21)	-	8 (5-14)	7 (7-7)	-	13 (7-17)	-	-	-
<i>SALL1</i>	52	6 (6-6)	33 (21-45)	7 (6-11.75)	8.5 (5-20.5)	-	-	32 (32-32)	-	-
<i>SERPINE2</i>	23	8 (7-9)	-	7 (6-8)	-	-	-	-	-	-
<i>SFRP2</i>	11	7 (6-8)	-	8.5 (5.75-20.5)	13 (13-13)	-	-	-	-	-
<i>SIM2</i>	47	6 (6-15)	-	9 (6-13)	-	68 (68-68)	-	-	-	-
<i>SIX1</i>	8	6.5 (6.25-6.75)	6 (6-6)	6 (6-50)	-	-	-	-	-	-

<i>SLC12A1</i>	71	6 (5-8)	10.5 (8.75-12.25)	10 (5.25-17.75)	-	5 (5-5)	9 (9-9)	-	-	-
<i>SLC12A3</i>	133	9 (6-19.5)	6 (6-6)	9 (7-17)	-	-	42 (25-59)	-	-	-
<i>SLC13A1</i>	52	12 (7.25-26.75)	5.5 (5.25-5.75)	7 (5.5-10)	-	99 (99-99)	-	-	-	-
<i>SOX9</i>	31	8.5 (6-14.25)	11 (10-26)	8 (5.75-9)	9 (6-9)	-	28 (28-28)	-	-	-
<i>TEK</i>	50	11 (9-21)	5 (5-5)	9 (6-11.25)	-	-	-	-	-	-
<i>TPM2</i>	17	11.5 (6.75-33.75)	-	8 (6.5-9.5)	-	7 (7-7)	-	-	-	-
<i>UMOD</i>	54	10.5 (7.25-21.75)	-	8.5 (6.75-22.25)	6 (6-6)	7 (6-9)	-	-	-	-
<i>WT1</i>	20	9 (5-11)	-	9.5 (6-20.5)	14 (14-14)	-	-	-	-	-

Supplement 5A Distribution of functional impacts of qualifying rare variants between those with *versus* without elevated BP, as determined by Chi-square analysis. Values are displayed as % (n).

All														X ²	P
Gene	Frameshift		In-frame insertion/deletion		Non-synonymous		Synonymous		Premature Stop		NA				
	Control	BP	Control	BP	Control	BP	Control	BP	Control	BP	Control	BP			
<i>SIX1</i>	0%(0)	5.2%(6)	-	-	88.9%(24)	86.2%(100)	-	-	-	-	11.1%(3)	8.6%(10)	1.6	0.46	
<i>WT1</i>	-	-	8.6%(3)	4.9%(11)	57.1%(20)	58.9%(132)	-	-	-	-	34.3%(12)	36.2%(81)	0.80	0.67	
<i>NPHS1</i>	3.1%(8)	4.0%(49)	-	-	60.5%(155)	64.5%(785)	0.8%(2)	0.4%(5)	1.6%(4)	1.5%(18)	34.0%(87)	29.6%(361)	2.9	0.58	

White British														X ²	P
Gene	Frameshift		Non-synonymous		NA										
	Control	BP	Control	BP	Control	BP									
<i>SIX1</i>	0%(0)	5.9%(6)	89.5%(17)	86.1%(87)	10.5%(2)	7.9%(8)							1.3	0.53	

Non-White British														X ²	P
Gene	Non-synonymous		In-frame insertion/deletion		NA										
	Control	BP	Control	BP	Control	BP									
<i>WT1</i>	50%(3)	58.9%(33)	0%(0)	3.6%(2)	50%(3)	37.5%(21)							0.51	0.78	

Supplement 5B Distribution of functional impacts of qualifying rare variants between those with *versus* without CKD, as determined by chi-square analysis. Values are displayed as % (n).

All											X ²	P
Gene	Frameshift		Non-synonymous		Premature Stop		NA					
	Control	CKD	Control	CKD	Control	CKD	Control	CKD				
<i>CLCN5</i>	5.2%(23)	4.8%(1)	57.0%(253)	47.6%(10)	2.5%(11)	4.8%(1)	35.4%(157)	42.9%(9)	1.0	0.79		

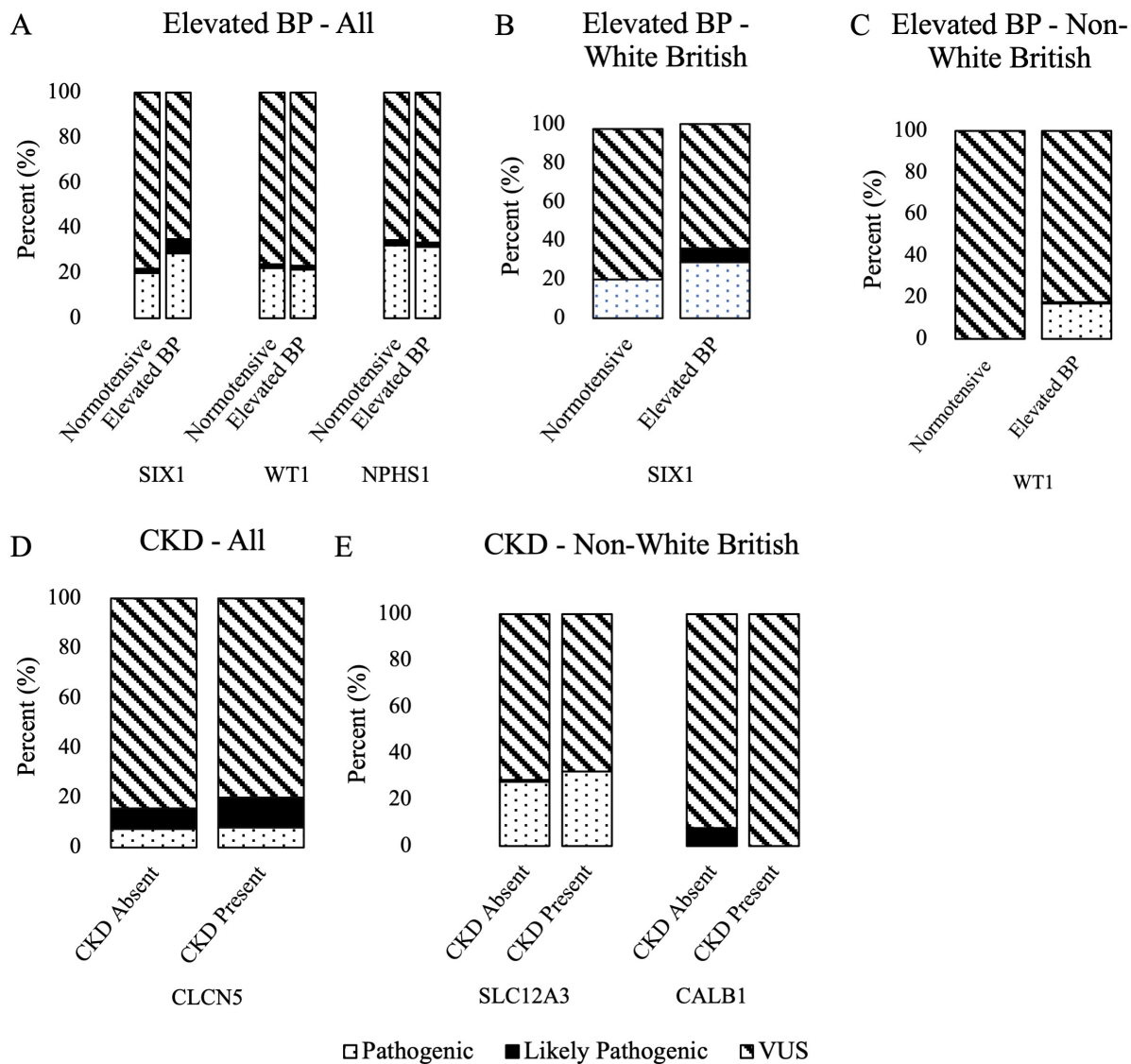
Non-White British											X ²	P
Gene	Frameshift		Synonymous		Non-synonymous		NA					
	Control	CKD	Control	CKD	Control	CKD	Control	CKD				
<i>SLC12A3</i>	0.2%(1)	0%(0)	11.6%(53)	25%(5)	51.4%(235)	50%(10)	36.8%(168)	25%(5)	3.6	0.31		
<i>CALB1</i>	-	-	-	-	21.4%(12)	33.3%(2)	78.6%(44)	66.6%(4)	0.022	0.88		

Supplement 6A Logistic regression models of RUNES Category 3 variants as a predictor of elevated blood pressure

Compartment	All			White British			Non-White British		
	Gene	OR (99% CI)	P	Gene	OR (99% CI)	P	Gene	OR (99% CI)	P
Early nephron development	<i>AMN</i>	0.867 (0.615-1.222)	0.3	<i>AMN</i>	0.803 (0.542-1.190)	0.2	<i>CDH6</i>	0.862 (0.487-1.525)	0.5
	<i>CITED1</i>	0.707 (0.400-1.249)	0.1	<i>CITED1</i>	0.605 (0.326-1.122)	0.04	<i>CRABP2</i>	0.631 (0.261-1.528)	0.2
	<i>COL2A1</i>	0.846 (0.691-1.034)	0.03	<i>COL2A1</i>	0.917 (0.729-1.153)	0.3	<i>EYA1</i>	1.566 (0.846-2.900)	0.06
	<i>ETV4</i>	1.606 (0.688-3.745)	0.2	<i>CRABP2</i>	1.731 (0.747-4.010)	0.1	<i>PAX2</i>	1.879 (0.793-4.449)	0.06
	<i>JAG1</i>	0.931 (0.721-1.203)	0.5	<i>ETV4</i>	2.256 (0.801 -6.355)	0.04	<i>SIX1</i>	0.530 (0.169-1.666)	0.2
	<i>LEF1</i>	0.886 (0.669-1.203)	0.3	<i>HNF1A</i>	1.463 (0.790-2.709)	0.1	<i>WT1</i>	1.747 (0.741-4.118)	0.1
	<i>SIX1</i>	0.416 (0.230-0.751)	<0.001	<i>JAG1</i>	0.949 (0.708-1.272)	0.6			
	<i>WT1</i>	1.561 (0.949-2.567)	0.02	<i>LEF1</i>	0.840 (0.609-1.158)	0.2			
Podocytes	<i>NPHS1</i>	0.844 (0.696-1.023)	0.02	<i>NPHS1</i>	0.816 (0.647-1.028)	0.02	-	-	-
Tubulointerstitial cells	<i>ANPEP</i>	0.943 (0.746-1.192)	0.5	<i>CSPG4</i>	0.916 (0.762-1.102)	0.2	<i>CLCN5</i>	0.653 (0.416-1.024)	0.02
	<i>CD248</i>	1.215 (0.865-1.706)	0.1	<i>DES</i>	1.419 (0.746-2.698)	0.2	<i>COL1A1</i>	1.146 (0.774-1.696)	0.4
	<i>CLCN5</i>	0.891 (0.707-1.124)	0.2	<i>FOXD1</i>	0.869 (0.636-1.186)	0.2	<i>CUBN</i>	1.244 (0.883-1.753)	0.1
	<i>CSPG4</i>	0.900 (0.764-1.061)	0.1	<i>LEF1</i>	0.813 (0.588-1.124)	0.1	<i>FOXD1</i>	1.196 (0.739-1.938)	0.3
	<i>DES</i>	1.217 (0.701-2.113)	0.4	<i>PAPPA2</i>	1.094 (0.873-1.370)	0.3	<i>MCAM</i>	1.153 (0.705-1.883)	0.5
	<i>LEF1</i>	0.814 (0.614-1.079)	0.06	<i>SLC12A1</i>	1.232 (0.966-1.571)	0.03	<i>SLC13A1</i>	1.041 (0.656-1.653)	0.8
	<i>SLC12A1</i>	1.212 (0.974 -1.509)	0.02	<i>TPM2</i>	1.669 (0.934 -2.983)	0.02	<i>TPM2</i>	1.426 (0.759-2.679)	0.1
	<i>TPM2</i>	1.333 (0.840-2.113)	0.1						
Collecting duct	-	-	-	<i>CALB1</i>	1.166 (0.801-1.697)	0.3	<i>RET</i>	1.253 (0.774-2.029)	0.2
Endothelium	<i>FLT1</i>	0.910 (0.773-1.072)	0.1	-	-	-	<i>KDR</i>	1.156 (0.828-1.614)	0.3

Supplement 6B Logistic regression models of RUNES Category 3 variants as a predictor of CKD

Compartment	All			White British			Non-White British		
	Gene	OR (99% CI)	P	Gene	OR (99% CI)	P	Gene	OR (99% CI)	P
Early nephron development	<i>CITED1</i>	1.811 (0.661-4.965)	0.1	<i>CITED1</i>	1.981 (0.664-5.910)	0.1	<i>AMN</i>	2.164 (0.640-7.319)	0.1
	<i>HNFI1A</i>	0.384 (0.086-1.723)	0.1	<i>HNFI1A</i>	0.187 (0.014-2.480)	0.1	<i>COL2A1</i>	0.522 (0.139-1.967)	0.2
	<i>ITGA8</i>	0.819 (0.555-1.207)	0.2	<i>ITGA8</i>	0.819 (0.527-1.273)	0.2	<i>CRABP2</i>	2.995 (0.434-20.652)	0.1
	<i>WT1</i>	0.594 (0.184-1.912)	0.3	<i>SIM2</i>	0.599 (0.250-1.434)	0.1	<i>LEF1</i>	1.679 (0.552-5.106)	0.2
Podocytes							<i>PAX2</i>	0.000	0.9
	<i>NPHS2</i>	0.516 (0.115-2.319)	0.3	<i>NPHS2</i>	0.438 (0.070-2.755)	0.2	<i>SALL1</i>	2.305 (0.816-6.515)	0.04
	<i>PODXL</i>	1.455 (0.812-2.610)	0.1	<i>PTPRO</i>	0.713 (0.451-1.126)	0.06	<i>SIM2</i>	1.334 (0.476-3.738)	0.5
	<i>PTPRO</i>	0.803 (0.546-1.182)	0.1				<i>SOX9</i>	2.385 (0.495-11.486)	0.2
							<i>NPHS1</i>	1.953 (0.986-3.869)	0.01
							<i>PODXL</i>	1.729 (0.722-4.139)	0.1
Tubulointerstitial cells	<i>CDHI</i>	1.456 (0.730-2.907)	0.2	<i>CLCN5</i>	1.414 (0.872-2.295)	0.07	<i>CDHI</i>	3.502 (1.211-10.129)	0.002
	<i>CLCN5</i>	1.555 (0.964-2.510)	0.02	<i>CSPG4</i>	0.809 (0.521-1.257)	0.2	<i>COL1A1</i>	1.701 (0.796-3.635)	0.07
	<i>CLDN1</i>	0.559 (0.088-3.528)	0.4	<i>LRP2</i>	0.769 (0.550-1.076)	0.04	<i>COL3A1</i>	1.374 (0.572-3.299)	0.4
	<i>COL3A1</i>	1.182 (0.711-1.965)	0.4	<i>SLC12A3</i>	0.644 (0.357-1.162)	0.06	<i>DES</i>	0.000	0.9
	<i>FOXD1</i>	1.437 (0.829-2.490)	0.09	<i>TPM2</i>	0.332 (0.053-2.078)	0.1	<i>FOXD1</i>	2.264 (1.004 -5.104)	0.01
							<i>LEF1</i>	1.952 (0.725-5.253)	0.08
Collecting duct							<i>LRP2</i>	1.151 (0.691-1.918)	0.5
	<i>CALB1</i>	1.525 (0.824-2.822)	0.08	-	-	-	<i>PAPPA2</i>	1.521 (0.761-3.040)	0.1
Endothelium							<i>PDGFRB</i>	1.216 (0.523-2.828)	0.6
	<i>FLT1</i>	1.379 (0.962 -1.977)	0.02	<i>KDR</i>	1.220 (0.811-1.834)	0.2	<i>SLC12A3</i>	1.686 (0.793-3.584)	0.07
	<i>KDR</i>	1.171 (0.817-1.677)	0.3				<i>TPM2</i>	2.441 (0.948-6.288)	0.02
							<i>CALB1</i>	3.508 (1.286-9.565)	0.001
							<i>GATA2</i>	0.000	0.9
							<i>FLT1</i>	2.277 (1.250-4.149)	<0.001



Supplement 7: Distribution of qualifying variants genes with statistically significant association with disease in cases and controls in all individuals (A, D), those of White British ancestry (B), and those with non-White British ancestry (C, E).