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

[a]eGFR calculated using CKD-EPI 2021 equation [26]

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

Developmental Compartment	Genetic Marker
Early nephron development	***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*
Podocytes	**CLIC5, NPHS2, NPHS1, PODXL, PTPRO, *TGFBR3*
Tubulointerstitial cells	***ACTA2****, ALDH1A1, ANPEP, CD248*[a]*, CDH1, CLCN5, CLDN1,* ***CLDN2****, COL1A1, COL3A1, CSPG4, CUBN,* ***DCN****, DES, *FGF7, FOXD1, GDNF, LEF1, LRP2,* ***MAL****,* ***MCAM****, PAPPA2, PDGFRB, SERPINE2, SLC12A1, SLC12A3, SLC13A1,* ***SLC34A1****, *TACSTD2, TPM2, UMOD*
Collecting duct	***AQP2****, CALB1, CLDN7, GATA2, KRT8,* ***KRT18****,* ***MMP7****, RET*
Endothelium	*CDH5, FLT1, KDR, PECAM1*[b]*, TEK*

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

[a]*CD248* 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

[b]*PECAM1* 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 ≥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
ALDH1A1	20	12 (6-26)	-	6 (6-6)	12 (6.5-28)
ANPEP	55	11 (7-27.5)	-	16 (11.5-20.5)	11 (7-28)
CALB1	13	10 (6-23)	-	-	10 (6-23)
CCND1	9	21 (12-29)	6 (6-6)	-	22.5 (15.75-31.75)
CD248	24	7.5 (6-15.25)	-	-	7.5 (6-15.25)
CDH1	36	10 (7-14.5)	10 (7-17)	-	10 (6.75-12.5)
CDH5	64	8.5 (6-13.25)	6 (6-6)	7.5 (5.75-20)	9 (6-13.5)
CDH6	23	8 (6-13)	-	8.5 (6.75-10.25)	8 (6-14)
CITED1	8	13 (9-18.25)	-	-	13 (9-18.25)
CLCN5	35	7 (5.5-10.5)	9.5 (8-12.25)	7 (6-9.5)	6.5 (5.75-10.25)
CLDN1	11	9 (5.5-13.5)	-	-	9 (5.5-13.5)
CLDN7	16	14.5 (7-17.5)	-	7 (7-7)	15 (7-19)
COL1A1	95	9 (5-18)	15 (6.25-41.5)	-	8 (5-13)
COL2A1	73	9 (6-19)	6 (6-25)	-	9 (6-18.75)
COL3A1	63	7 (6-15)	11 (6.5-14.5)	6 (6-6)	7 (5-15)
CRABP2	11	9 (7-14.5)	-	12 (9-14.5)	9 (7.5-18.75)
CSPG4	126	10 (6.25-20.75)	84 (84-84)	5 (5-5)	10 (6.75-20.25)
CUBN	88	10.5 (6-25.5)	21 (10-33)	9 (6-16.75)	10 (6-23.5)
DES	31	7 (6-12.5)	10.5 (7.5-22.25)	6 (6-6)	6 (6-7)
ETV4	6	11.5 (7.25-18)	-	13 (10-16)	11.5 (7.5-16.75)
EYA1	40	7 (5-11.5)	11 (6.5-18.25)	6 (6-6)	7 (5-10)
FLT1	73	8 (6-15)	52 (52-52)	7.5 (7.25-7.75)	8 (6-14.75)
FOXD1	59	8 (6-13)	65 (63.5-66.5)	8 (7-9)	8 (5.75-13)
GATA2	18	8.5 (6.25-12.25)	40.5 (24.25-56.75)	-	8.5 (5.75-10.75)
GDNF	7	9 (7.5-14)	15 (12.5-17.5)	-	9 (6-9)
HES1	12	7 (5.75-26.25)	-	-	7 (5.75-26.25)
HNF1A	32	12.5 (8-16.5)	13 (8.5-18)	-	10 (8.25-15.75)
IRX3	20	9.5 (6.75-13)	-	-	9.5 (6.75-13)
ITGA8	98	7 (6-11.75)	-	6 (5.5-7.5)	7 (6-13)

JAG1	50	8 (6-11.75)	6 (6-7.5)	-	8 (6-12)
KDR	104	7.5 (6-12)	19 (16.5-30.5)	6 (5.5-7)	7 (6-11.75)
KRT8	44	9 (7-26.25)	25 (9-28)	41 (21.5-61)	7 (6-15.25)
LEF1	29	9 (6-18)	-	-	9 (6-18)
LRP2	264	9 (6-21)	20.5 (11.5-30.25)	6 (6-7)	9 (6-21)
NPHS1	96	11.5 (6-24.25)	11 (7-19.75)	11 (11-11)	12 (6-24.5)
NPHS2	15	10 (6-21.5)	9 (6-19.5)	-	10 (7-21)
OSR1	6	6 (5-13)	-	-	6 (5-13)
PAPPA2	104	7 (6-13.25)	-	6 (5-11.5)	7 (6-13.25)
PAX2	16	8.5 (6-22.5)	16 (9.5-31)	-	7.5 (5.75-13.5)
PAX8	14	12.5 (6.25-41.25)	46 (25.5-48)	-	11 (6.5-27.5)
PDGFRB	87	7 (5-12.5)	21 (15.5-26.5)	8 (5-30)	7 (5-12)
PODXL	44	9.5 (7-17)	-	34 (14-40)	9 (7-15.5)
POU3F3	31	12 (7-28)	-	7 (7-7)	12 (7-28)
PTPRO	128	6 (5-9)	31.5 (8-64.75)	5 (5-6.25)	6 (5-9)
RET	62	9 (7-14.75)	13 (5.5-16.5)	-	8 (7-12.5)
SALL1	52	7 (6-12)	31.5 (18.75-44.25)	20.5 (14.75-26.25)	7 (6-12)
SERPINE2	23	7 (6-9)	-	-	7 (6-9)
SFRP2	11	9 (5.5-15.5)	-	-	9 (5.5-15.5)
SIM2	47	8 (6-15.5)	-	68 (68-68)	8 (6-14.5)
SIX1	8	6 (6-17.75)	28 (17-39)	6 (6-6)	6 (6-7)
SIX2	12	12.5 (7-19.25)	20 (20-20)	6 (6-6)	12.5 (8.25-18.25)
SLC12A1	71	7 (5-15.5)	5 (5-7)	7 (6-10.5)	7 (5-17)
SLC12A3	133	9 (6-17)	8 (6-19.5)	-	10 (6-17)
SLC13A1	52	9.5 (6-18)	-	6 (5-7)	10 (6-18)
SOX9	31	9 (6-12)	27 (13.25-28.75)	11 (8-11.5)	8 (6-9)
TEK	50	9.5 (6-13.5)	6 (5.5-14)	5 (5-5)	10 (6.25-13.5)
TPM2	17	11 (6-21)	-	6.5 (5.75-8)	12 (9-38)
UMOD	54	9 (6.25-21)	52 (39.5-64.5)	7 (6-9)	9 (6-21)
WT1	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
ALDH1A1	20	8 (6-16)	6 (6-6)	28 (14.25-38.25)	-	-	-	-	-	-
ANPEP	55	18 (5-32)	25 (25-25)	11 (8-28)	6 (5.5-6.5)	7 (7-7)	12 (12-12)	-	-	-
CALB1	13	12 (6.75-23.75)	-	10 (5-10)	-	-	-	-	-	-
CCND1	9	19 (10.75-25.25)	-	-	45 (45-45)	-	-	-	-	-
CD248	24	-	-	7 (6-15.5)	10 (10-10)	-	-	-	-	-
CDH1	36	10 (8-12)	-	10 (6.25-15.5)	10 (10-10)	-	-	-	-	-
CDH5	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)	-	-
CDH6	23	15 (7.5-22)	12 (12-12)	8 (6-10)	6 (6-6)	-	-	5 (5-5)	-	-
CITED1	8	-	-	13 (9-18.25)	-	-	-	-	-	-
CLCN5	35	6 (6-11.5)	12 (8.5-15.5)	7.5 (5.75-10)	-	6 (5.5-6.5)	-	-	-	-
CLDN1	11	7 (5.75-9.5)	-	10 (7-14.5)	-	-	-	-	-	-
CLDN7	16	28 (16.5-29)	7 (7-7)	14.5 (7-16)	-	-	-	-	-	-
COL1A1	95	9 (6-15.5)	5 (5-5)	9 (5-22)	9.5 (8.75-10.25)	-	26 (15.5-36.5)	-	-	-
COL2A1	73	8 (6-20)	5 (5-5)	9.5 (6-19)	-	-	5 (5-12)	-	-	-

COL3A1	63	6 (5-8.25)	10.5 (8.25-12.75)	11 (6-19)	5 (5-5)	-	21 (21-21)	-	-	-
CRABP2	11	6 (6-6)	6 (6-6)	9 (8.25-10.5)	-	12 (12-12)	42 (42-42)	-	17 (17-17)	-
CSPG4	126	7 (6.5-7.5)	-	10 (7-20)	21 (21-21)	5 (5-5)	-	-	-	-
CUBN	88	10 (6-23.75)	12 (7-28)	-	16.5 (10.75-22.25)	-	-	-	-	-
DES	31	16 (13-17)	6 (6-6)	6 (6-9.25)	-	-	6 (6-6)	-	-	-
ETV4	6	15 (10.5-18.5)	-	8 (8-8)	-	19 (19-19)	-	7 (7-7)	-	-
EYA1	40	9 (6.5-12)	6 (6-6)	6 (5-8.75)	-	8 (8-8)	23 (23-23)	-	-	-
FLT1	73	8 (5.25-14.25)	-	7.5 (6-16.75)	8 (8-9.5)	7.5 (7.25-7.75)	-	-	-	-
FOXD1	59	-	8 (7-9)	7 (5.25-12)	9 (6.75-17)	-	-	-	-	-
GATA2	18	9 (6-29)	-	8.5 (6.5-10.75)	-	-	8 (8-8)	-	-	-
GDNF	7	13.5 (11.25-15.75)	-	9 (6-10)	-	-	-	-	-	-
HES1	12	24 (14.5-33.5)	-	7 (5.75-15)	7 (7-7)	-	-	-	-	-
HNF1A	32	13 (10-14.5)	8 (8-8)	12.5 (6.75-17.5)	-	-	30 (19-41)	-	-	-
IRX3	20	11 (8-14)	-	9 (7-12)	13 (13-13)	-	-	-	-	-
ITGA8	98	7 (6-11.75)	-	7 (6-11.75)	-	-	-	-	-	-
JAG1	50	8.5 (5.25-11)	-	8 (6-12)	-	-	7 (7-7)	-	-	-
KDR	104	7 (6-10)	-	8 (6-14)	-	6 (5.5-7)	6 (6-6)	-	-	-

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

SLC12A1	71	6 (5-8)	10.5 (8.75-12.25)	10 (5.25-17.75)	-	5 (5-5)	9 (9-9)	-	-	-
SLC12A3	133	9 (6-19.5)	6 (6-6)	9 (7-17)	-	-	42 (25-59)	-	-	-
SLC13A1	52	12 (7.25-26.75)	5.5 (5.25-5.75)	7 (5.5-10)	-	99 (99-99)	-	-	-	-
SOX9	31	8.5 (6-14.25)	11 (10-26)	8 (5.75-9)	9 (6-9)	-	28 (28-28)	-	-	-
TEK	50	11 (9-21)	5 (5-5)	9 (6-11.25)	-	-	-	-	-	-
TPM2	17	11.5 (6.75-33.75)	-	8 (6.5-9.5)	-	7 (7-7)	-	-	-	-
UMOD	54	10.5 (7.25-21.75)	-	8.5 (6.75-22.25)	6 (6-6)	7 (6-9)	-	-	-	-
WT1	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														
Gene	**Frameshift**		**In-frame insertion/deletion**		**Non-synonymous**		**Synonymous**		**Premature Stop**		**NA**		**X^2**	***P***
	Control	BP	Control	BP	Control	BP	Control	BP	Control	BP	Control	BP		
SIX1	0%(0)	5.2%(6)	-	-	88.9%(24)	86.2%(100)	-	-	-	-	11.1%(3)	8.6%(10)	1.6	0.46
WT1	-	-	8.6%(3)	4.9%(11)	57.1%(20)	58.9%(132)	-	-	-	-	34.3%(12)	36.2%(81)	0.80	0.67
NPHS1	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								
Gene	**Frameshift**		**Non-synonymous**		**NA**		**X^2**	***P***
	Control	BP	Control	BP	Control	BP		
SIX1	0%(0)	5.9%(6)	89.5%(17)	86.1%(87)	10.5%(2)	7.9%(8)	1.3	0.53

Non-White British								
Gene	**Non-synonymous**		**In-frame insertion/deletion**		**NA**		**X^2**	***P***
	Control	BP	Control	BP	Control	BP		
WT1	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										
Gene	**Frameshift**		**Non-synonymous**		**Premature Stop**		**NA**		**X^2**	***P***
	Control	CKD	Control	CKD	Control	CKD	Control	CKD		
CLCN5	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

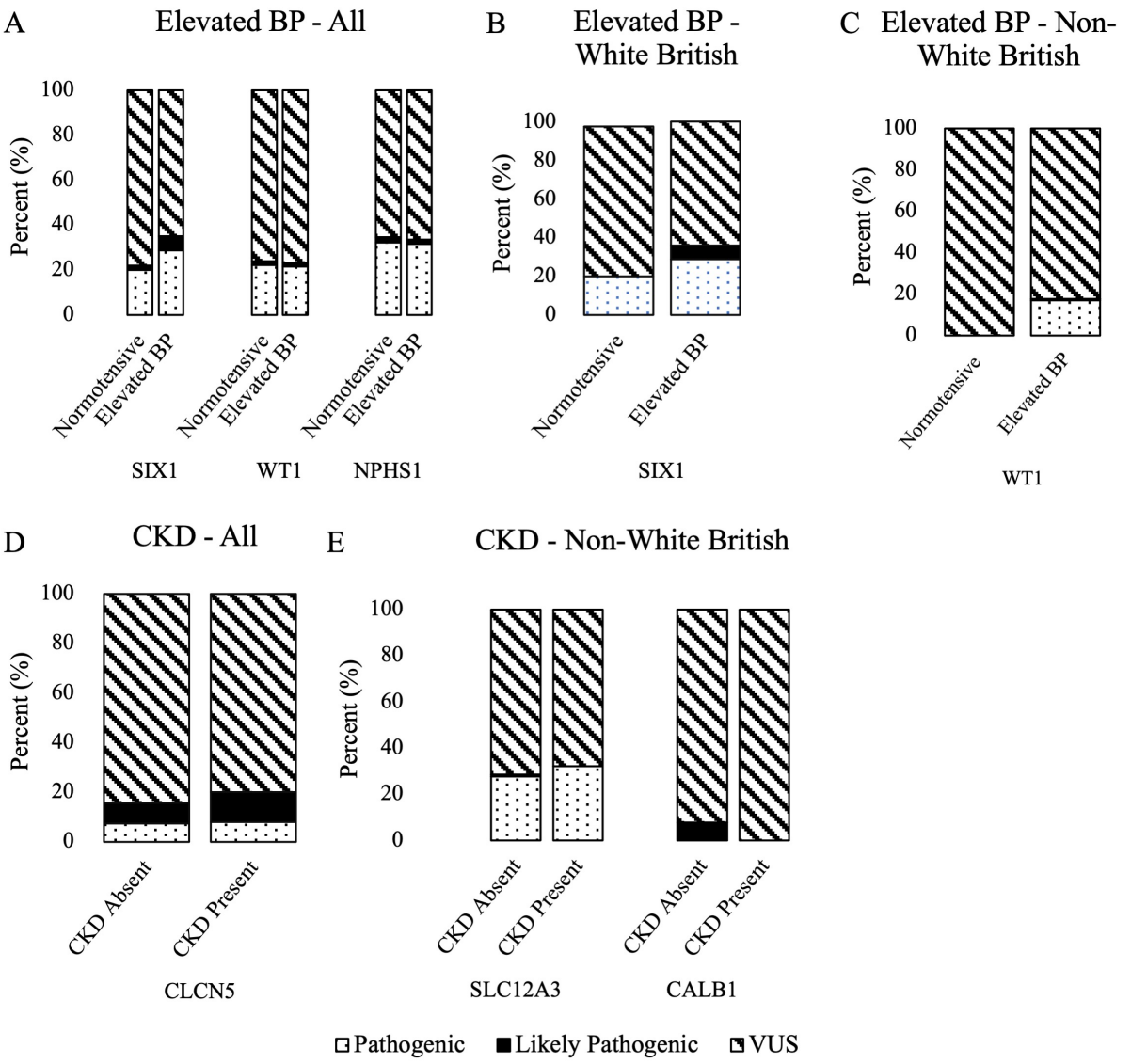
Non-White British										
Gene	**Frameshift**		**Synonymous**		**Non-synonymous**		**NA**		**X^2**	***P***
	Control	CKD	Control	CKD	Control	CKD	Control	CKD		
SLC12A3	0.2%(1)	0%(0)	11.6%(53)	25%(5)	51.4%(235)	50%(10)	36.8%(168)	25%(5)	3.6	0.31
CALB1	-	-	-	-	21.4%(12)	33.3%(2)	78.6%(44)	66.6%(4)	0.022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

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

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

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

	All			White British			Non-White British		
Compartment	Gene	OR (99% CI)	*P*	Gene	OR (99% CI)	*P*	Gene	OR (99% CI)	*P*
Early nephron development	*CITED1*	1.811 (0.661-4.965)	0.1	*CITED1*	1.981 (0.664-5.910)	0.1	*AMN*	2.164 (0.640-7.319)	0.1
	HNF1A	0.384 (0.086-1.723)	0.1	*HNF1A*	0.187 (0.014-2.480)	0.1	*COL2A1*	0.522 (0.139-1.967)	0.2
	ITGA8	0.819 (0.555-1.207)	0.2	*ITGA8*	0.819 (0.527-1.273)	0.2	*CRABP2*	2.995 (0.434-20.652)	0.1
	WT1	0.594 (0.184-1.912)	0.3	*SIM2*	0.599 (0.250-1.434)	0.1	*LEF1*	1.679 (0.552-5.106)	0.2
							PAX2	0.000	0.9
							SALL1	2.305 (0.816-6.515)	0.04
							SIM2	1.334 (0.476-3.738)	0.5
							SOX9	2.385 (0.495-11.486)	0.2
Podocytes	*NPHS2*	0.516 (0.115-2.319)	0.3	*NPHS2*	0.438 (0.070-2.755)	0.2	*NPHS1*	1.953 (0.986-3.869)	0.01
	PODXL	1.455 (0.812-2.610)	0.1	*PTPRO*	0.713 (0.451-1.126)	0.06	*PODXL*	1.729 (0.722-4.139)	0.1
	PTPRO	0.803 (0.546-1.182)	0.1						
Tubulointerstitial cells	*CDH1*	1.456 (0.730-2.907)	0.2	*CLCN5*	1.414 (0.872-2.295)	0.07	***CDH1***	**3.502 (1.211-10.129)**	**0.002**
	CLCN5	1.555 (0.964-2.510)	0.02	*CSPG4*	0.809 (0.521-1.257)	0.2	*COL1A1*	1.701 (0.796-3.635)	0.07
	CLDN1	0.559 (0.088-3.528)	0.4	*LRP2*	0.769 (0.550-1.076)	0.04	*COL3A1*	1.374 (0.572-3.299)	0.4
	COL3A1	1.182 (0.711-1.965)	0.4	*SLC12A3*	0.644 (0.357-1.162)	0.06	*DES*	0.000	0.9
	FOXD1	1.437 (0.829-2.490)	0.09	*TPM2*	0.332 (0.053-2.078)	0.1	*FOXD1*	2.264 (1.004 -5.104)	0.01
							LEF1	1.952 (0.725-5.253)	0.08
							LRP2	1.151 (0.691-1.918)	0.5
							PAPPA2	1.521 (0.761-3.040)	0.1
							PDGFRB	1.216 (0.523-2.828)	0.6
							SLC12A3	1.686 (0.793-3.584)	0.07
							TPM2	2.441 (0.948-6.288)	0.02
Collecting duct	*CALB1*	1.525 (0.824-2.822)	0.08	-	-	-	***CALB1***	**3.508 (1.286-9.565)**	**0.001**
							GATA2	0.000	0.9
Endothelium	*FLT1*	1.379 (0.962 -1.977)	0.02	*KDR*	1.220 (0.811-1.834)	0.2	***FLT1***	**2.277 (1.250-4.149)**	**<0.001**
	KDR	1.171 (0.817-1.677)	0.3						



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).