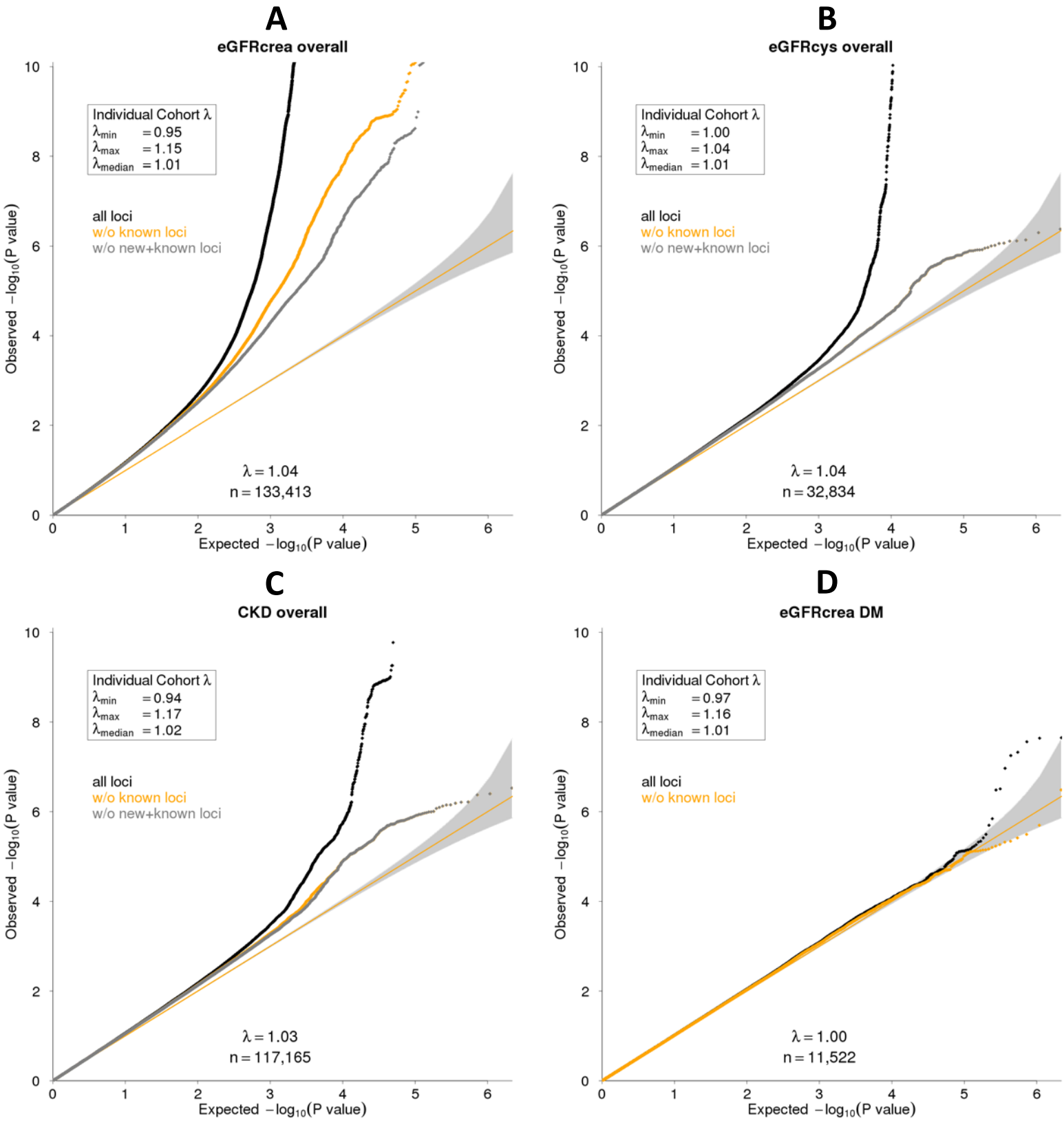
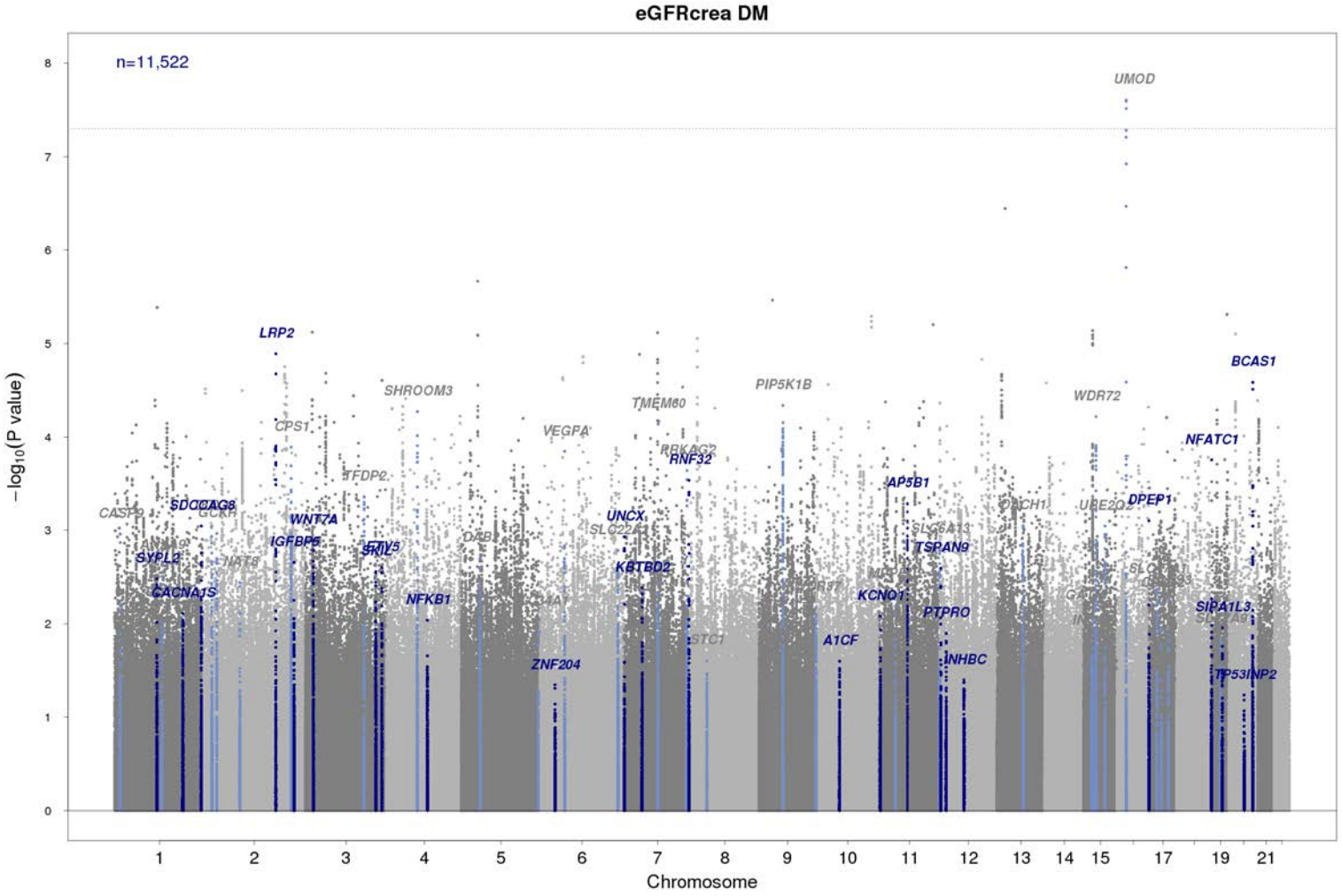
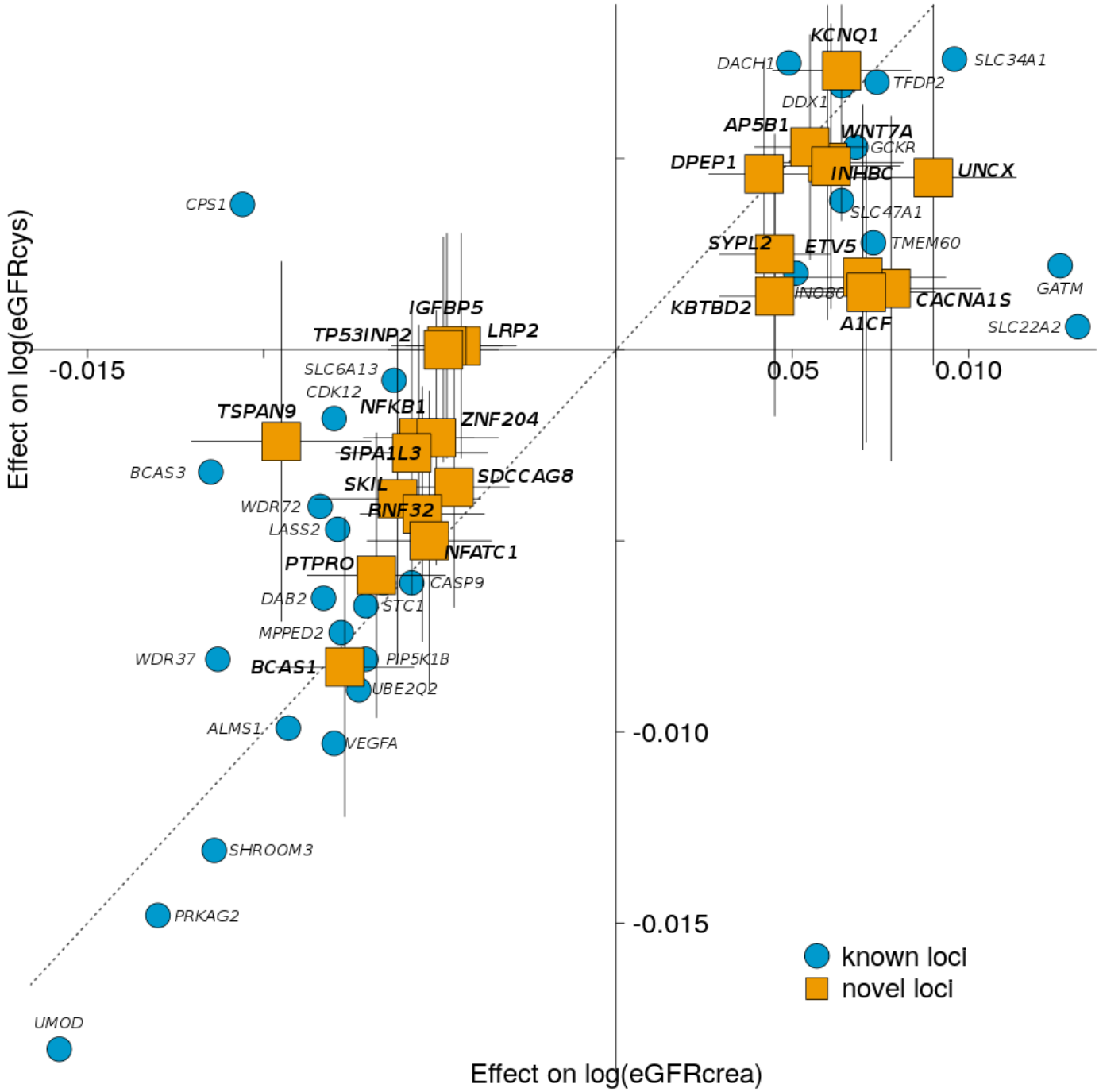
Supplementary Figure 1. Q-Q plots of eGFRcrea (**A**), eGFRcys (**B**), CKD (**C**), and eGFRcrea in diabetes (**D**). λ_{1000} = 1.00 for all four analyses.[1, 2]



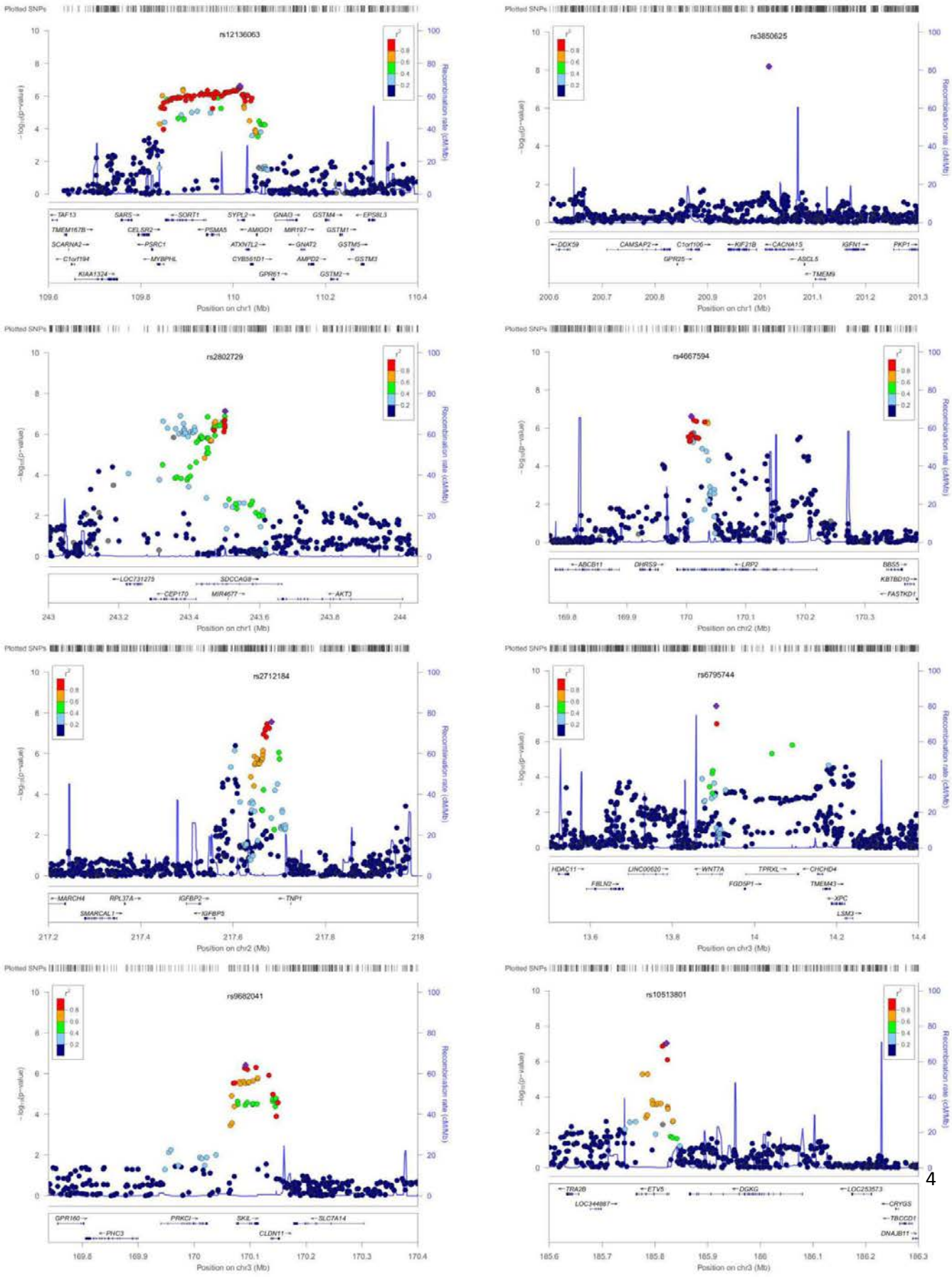
Supplementary Figure 2. Manhattan Plots of eGFRcrea in diabetes.

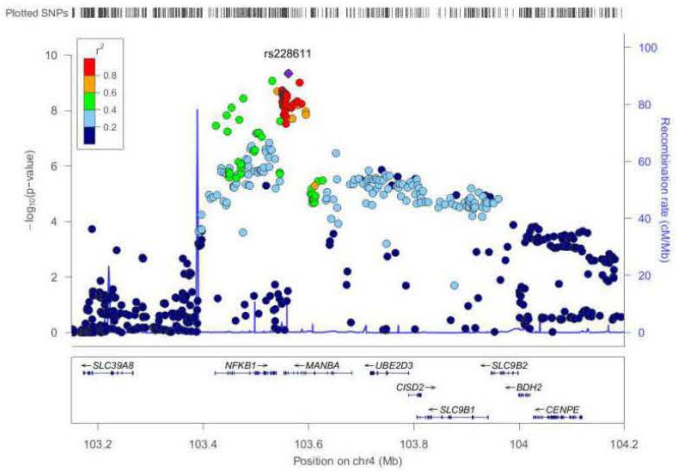


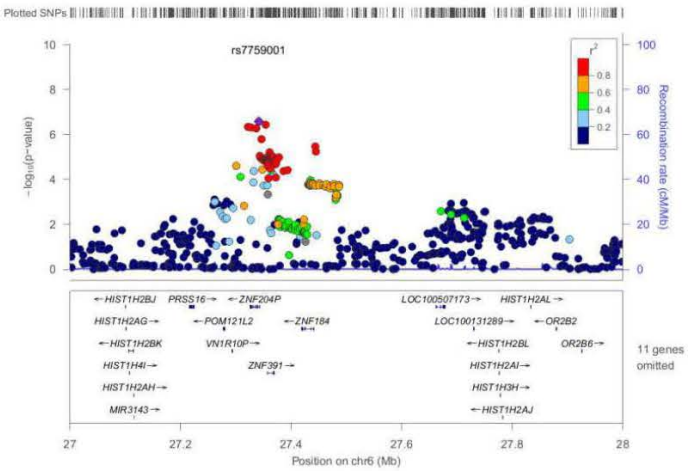
Supplementary Figure 3. All replicated loci comparing the effect sizes for eGFRcrea vs eGFRcys; known loci are in blue, new loci are in orange. 95% confidence intervals appear for the new loci only.

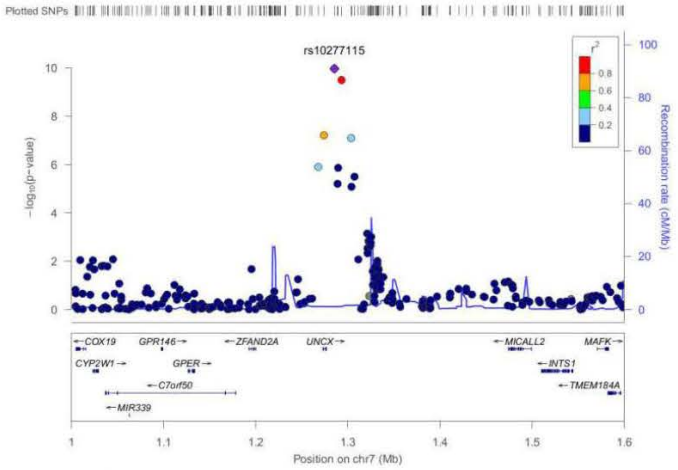


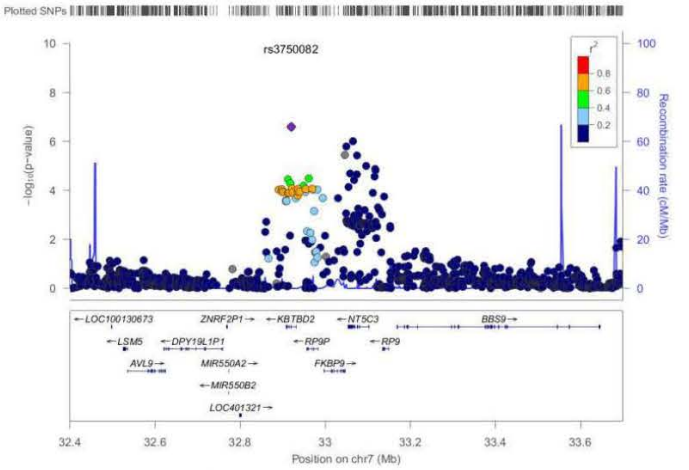
Supplementary Figure 4. Regional association plots for all 24 novel loci.

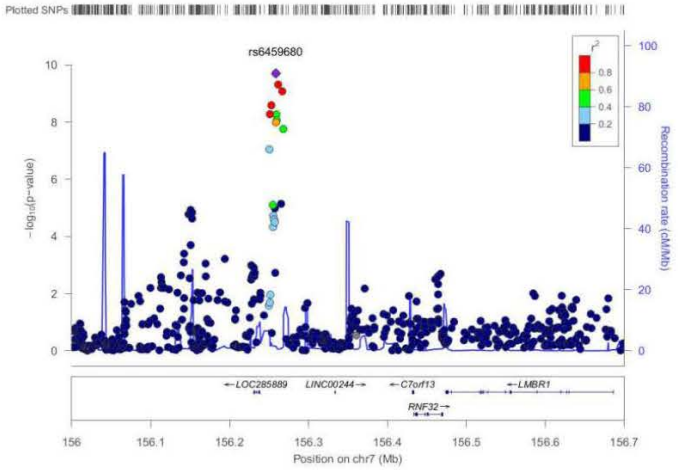


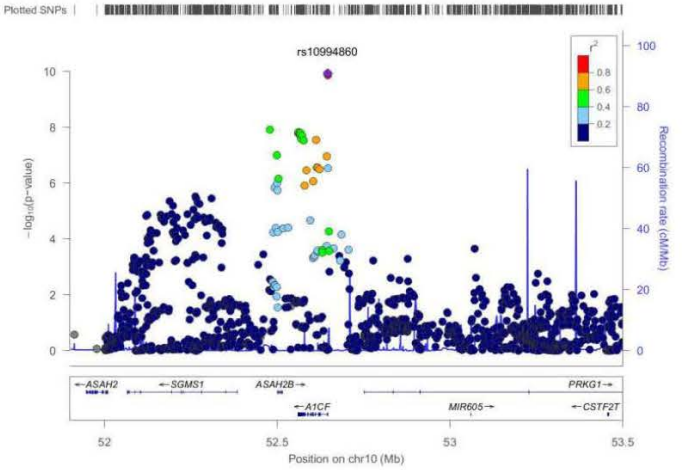

Plotted SNPs
rs228611
r²
0.8
0.6
0.4
0.2
−log10(p-value)
Recombination rate (cM/Mb)
SLC39A8
NFKB1
MANBA
UBE2D3
SLC9B2
CISD2
BDH2
SLC9B1
CENPE
103.2
103.4
103.6
103.8
104
104.2
Position on chr4 (Mb)

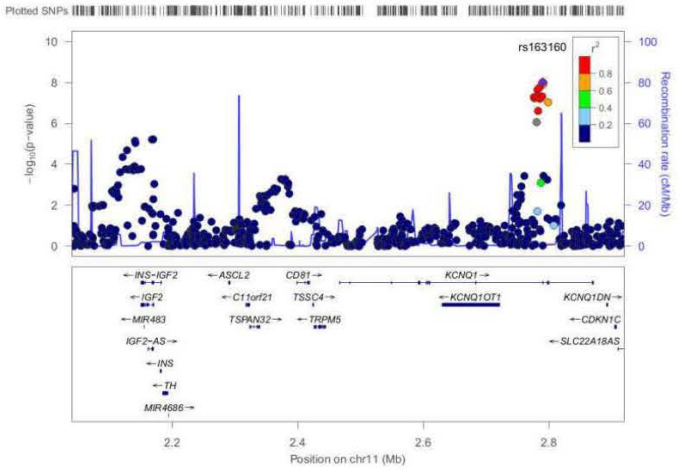

Plotted SNPs
rs7759001
r²
0.8
0.6
0.4
0.2
−log10(p-value)
Recombination rate (cM/Mb)
HIST1H2BJ
PRSS16
ZNF204P
LOC100507173
HIST1H2AL
HIST1H2AG
POM121L2
ZNF184
LOC100131289
OR2B2
HIST1H2BK
VN1R10P
HIST1H2BL
OR2B6
HIST1H4I
ZNF391
HIST1H2AI
HIST1H2AH
HIST1H3H
MIR3143
HIST1H2AJ
11 genes omitted
27
27.2
27.4
27.6
27.8
28
Position on chr6 (Mb)

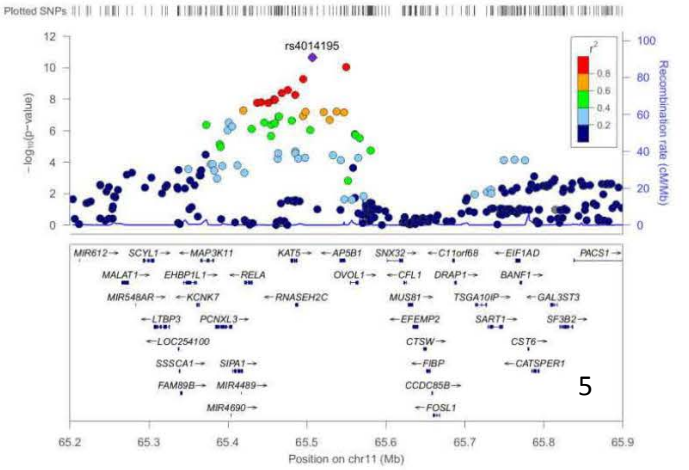

Plotted SNPs
rs10277115
r²
0.8
0.6
0.4
0.2
−log10(p-value)
Recombination rate (cM/Mb)
COX19
GPR146
ZFAND2A
UNCX
MICALL2
MAFK
CYP2W1
GPER
INTS1
C7orf50
TMEM184A
MIR339
1
1.1
1.2
1.3
1.4
1.5
1.6
Position on chr7 (Mb)

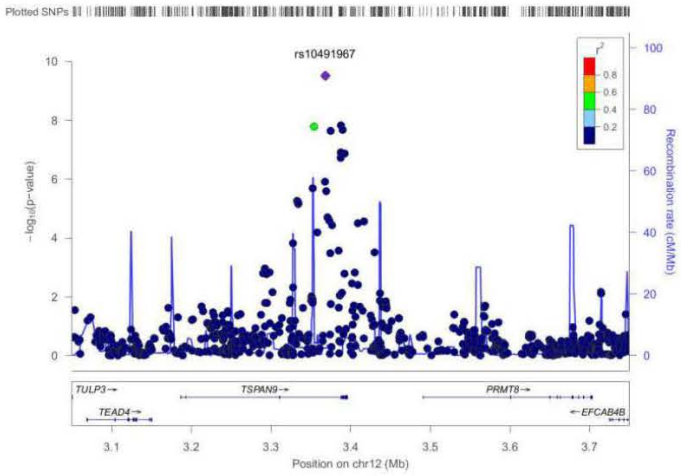

Plotted SNPs
rs3750082
r²
0.8
0.6
0.4
0.2
−log10(p-value)
Recombination rate (cM/Mb)
LOC100130673
ZNRF2P1
KBTBD2
NT5C3
BBS9
LSM5
DPY19L1P1
RP9P
RP9
AVL9
MIR550A2
FKBP9
MIR550B2
LOC401321
32.4
32.6
32.8
33
33.2
33.4
33.6
Position on chr7 (Mb)

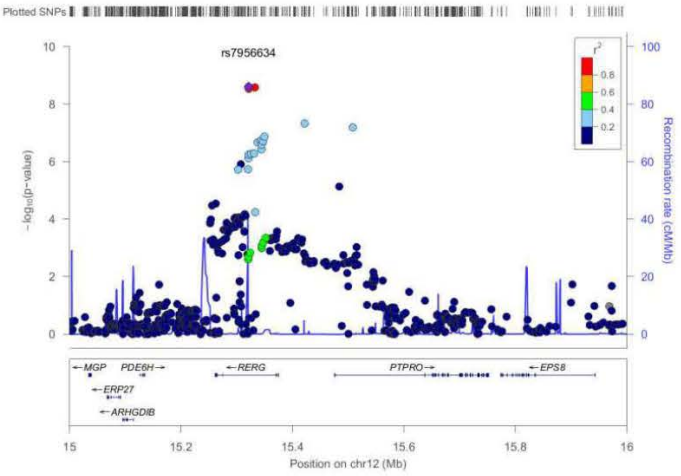

Plotted SNPs
rs6459680
r²
0.8
0.6
0.4
0.2
−log10(p-value)
Recombination rate (cM/Mb)
LOC285889
LINC00244
C7orf13
LMBR1
RNF32
156
156.1
156.2
156.3
156.4
156.5
156.6
156.7
Position on chr7 (Mb)

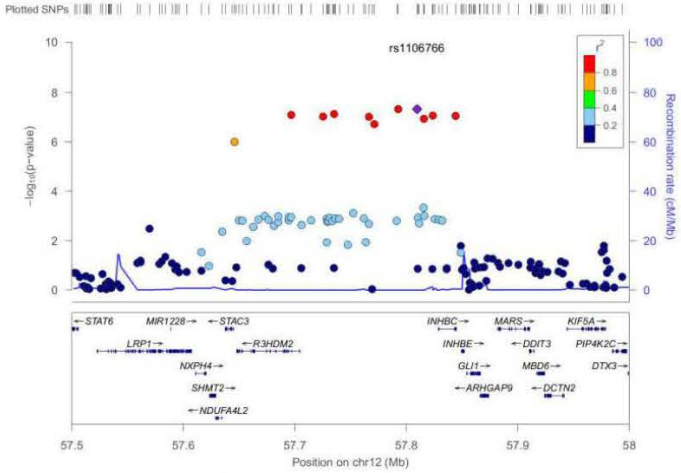

Plotted SNPs
rs10994860
r²
0.8
0.6
0.4
0.2
−log10(p-value)
Recombination rate (cM/Mb)
ASAH2
SGMS1
ASAH2B
PRKG1
A1CF
MIR605
CSTF2T
52
52.5
53
53.5
Position on chr10 (Mb)

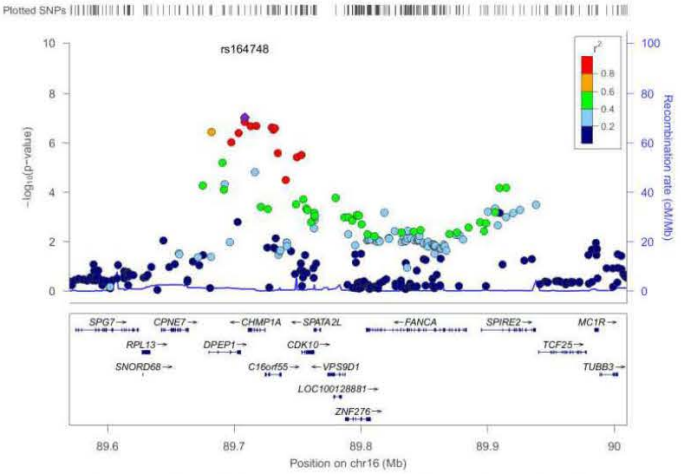

Plotted SNPs
rs163160
r²
0.8
0.6
0.4
0.2
−log10(p-value)
Recombination rate (cM/Mb)
INS-IGF2
ASCL2
CD81
KCNQ1
IGF2
C11orf21
TSSC4
KCNQ1OT1
KCNQ1DN
MIR483
TSPAN32
TRPM5
CDKN1C
IGF2-AS
SLC22A18AS
INS
TH
MIR4686
2.2
2.4
2.6
2.8
Position on chr11 (Mb)

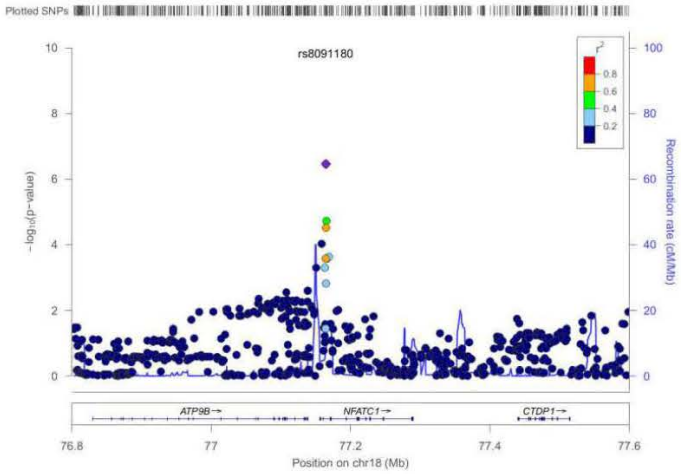

Plotted SNPs
rs4014195
r²
0.8
0.6
0.4
0.2
−log10(p-value)
Recombination rate (cM/Mb)
MIR612
SCYL1
MAP3K11
KAT5
AP5B1
SNX32
C11orf68
EIF1AD
PACS1
MALAT1
EHBP1L1
RELA
OVOL1
CFL1
DRAP1
BANF1
MIR548AR
KCNK7
RNASEH2C
MUS81
TSGA10IP
GAL3ST3
LTBP3
PCNXL3
EFEMP2
SART1
SF3B2
LOC254100
CTSW
CST6
SSSCA1
SIPA1
FIBP
CATSPER1
FAM89B
MIR4489
CCDC85B
MIR4690
FOSL1
65.2
65.3
65.4
65.5
65.6
65.7
65.8
65.9
Position on chr11 (Mb)

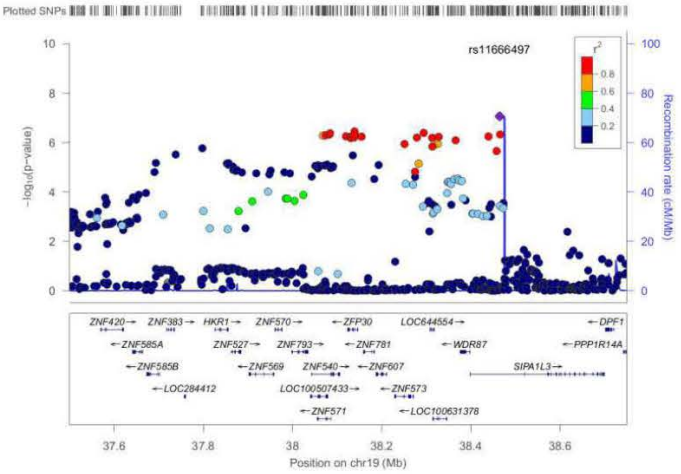

Plotted SNPs
rs10491967
$-\log_{10}$(p-value)
Recombination rate (cM/Mb)
r^2
0.8
0.6
0.4
0.2
TULP3→
TSPAN9→
PRMT8→
TEAD4→
←EFCAB4B
Position on chr12 (Mb)

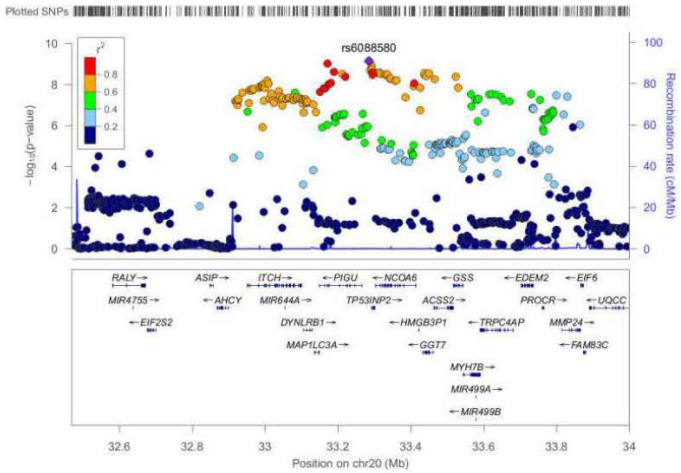

Plotted SNPs
rs7956634
$-\log_{10}$(p-value)
Recombination rate (cM/Mb)
r^2
0.8
0.6
0.4
0.2
←MGP
PDE6H→
←RERG
PTPRO→
←EPS8
←ERP27
←ARHGDIB
Position on chr12 (Mb)

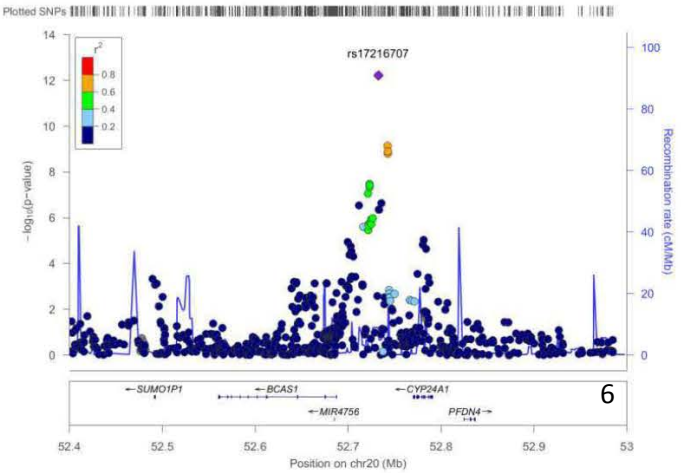

Plotted SNPs
rs1106766
$-\log_{10}$(p-value)
Recombination rate (cM/Mb)
r^2
0.8
0.6
0.4
0.2
←STAT6
MIR1228→
←STAC3
INHBC→
MARS→
KIF5A→
LRP1→
←R3HDM2
INHBE→
←DDIT3
PIP4K2C→
NXPH4→
GLI1→
MBD6→
DTX3→
SHMT2→
←ARHGAP9
←DCTN2
←NDUFA4L2
Position on chr12 (Mb)


Plotted SNPs
rs164748
$-\log_{10}$(p-value)
Recombination rate (cM/Mb)
r^2
0.8
0.6
0.4
0.2
SPG7→
CPNE7→
←CHMP1A
←SPATA2L
←FANCA
SPIRE2→
MC1R→
RPL13→
DPEP1→
CDK10→
TCF25→
SNORD68→
C16orf55→
←VPS9D1
TUBB3→
LOC100128881→
ZNF276→
Position on chr16 (Mb)

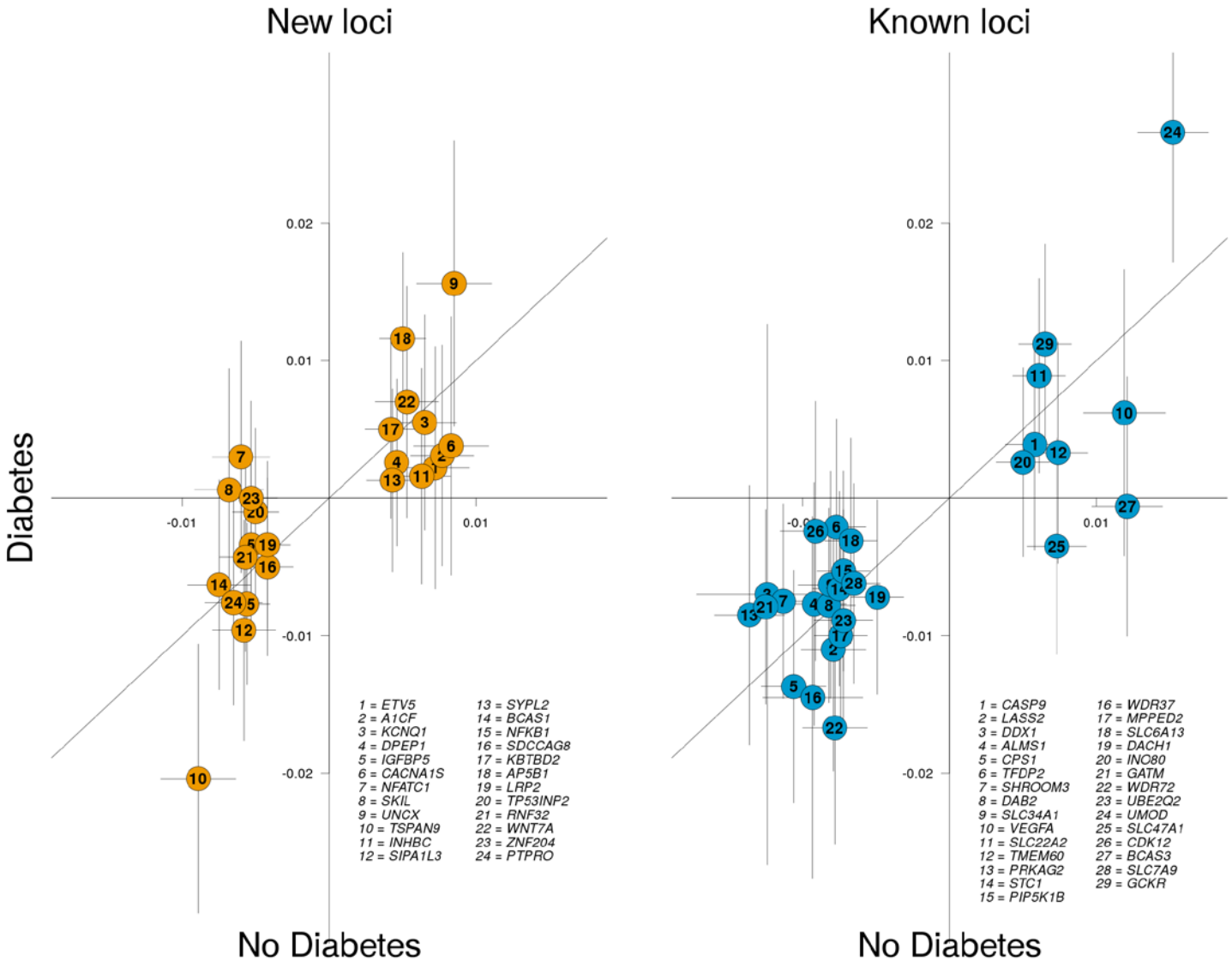

Plotted SNPs
rs8091180
$-\log_{10}$(p-value)
Recombination rate (cM/Mb)
r^2
0.8
0.6
0.4
0.2
ATP9B→
NFATC1→
CTDP1→
Position on chr18 (Mb)


Plotted SNPs
rs11666497
$-\log_{10}$(p-value)
Recombination rate (cM/Mb)
r^2
0.8
0.6
0.4
0.2
ZNF420→
ZNF383→
HKR1→
ZNF570→
←ZFP30
LOC644554→
←DPF1
←ZNF585A
ZNF527→
ZNF793→
←ZNF781
←WDR87
←PPP1R14A
←ZNF585B
←ZNF569
ZNF540→
←ZNF607
SIPA1L3→
←LOC284412
LOC100507433→
←ZNF573
←ZNF571
←LOC100631378
Position on chr19 (Mb)

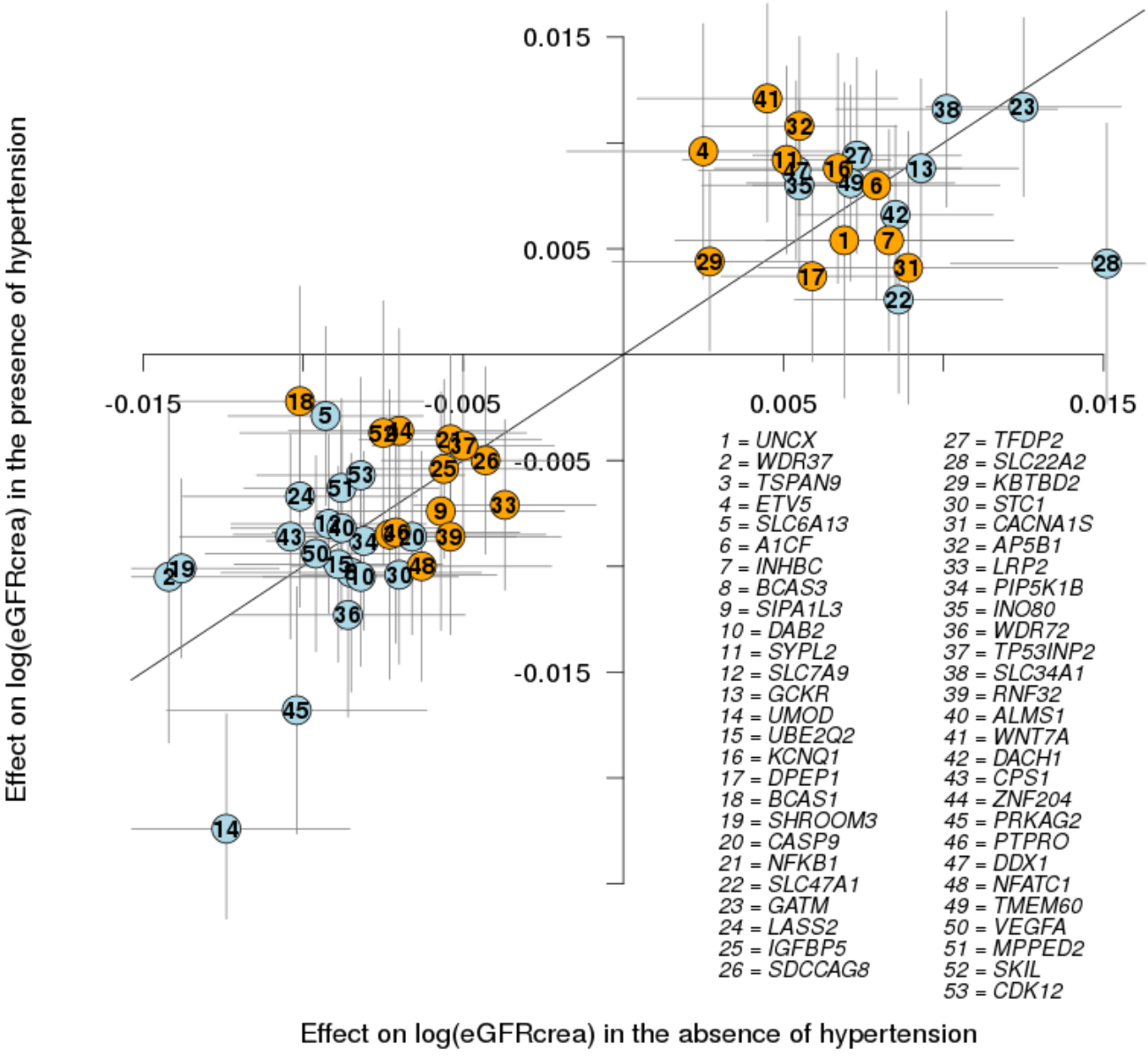

Plotted SNPs
rs6088580
$-\log_{10}$(p-value)
Recombination rate (cM/Mb)
r^2
0.8
0.6
0.4
0.2
RALY→
ASIP→
ITCH→
←PIGU
←NCOA6
←GSS
←EDEM2
←EIF6
MIR4755→
←AHCY
MIR644A→
TP53INP2→
ACSS2→
PROCR→
←UQCC
←EIF2S2
DYNLRB1→
←HMGB3P1
←TRPC4AP
MMP24→
MAP1LC3A→
←GGT7
←FAM83C
MYH7B→
MIR499A→
←MIR499B
Position on chr20 (Mb)


Plotted SNPs
rs17216707
$-\log_{10}$(p-value)
Recombination rate (cM/Mb)
r^2
0.8
0.6
0.4
0.2
←SUMO1P1
←BCAS1
←CYP24A1
←MIR4756
PFDN4→
Position on chr20 (Mb)

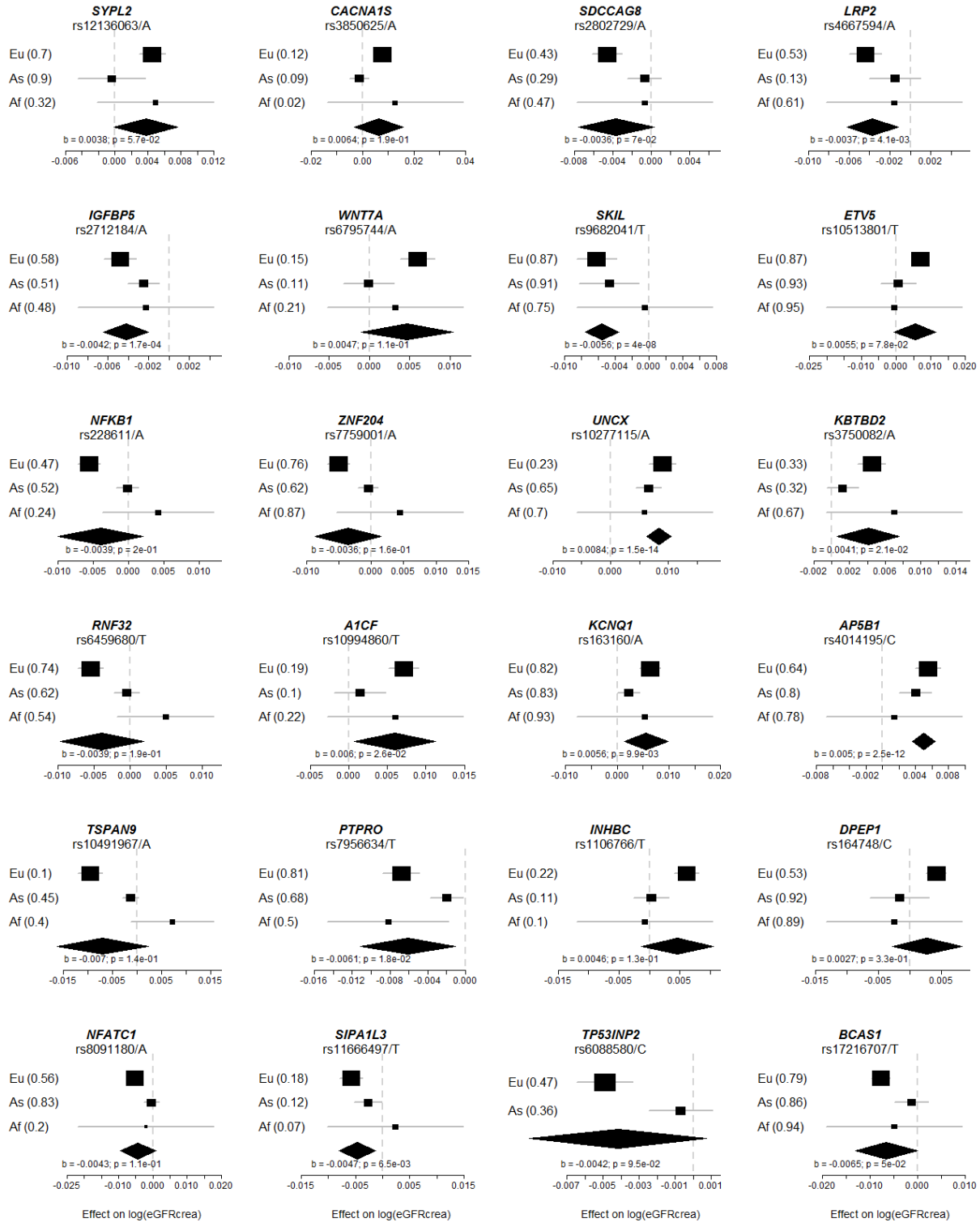
Supplementary Figure 5. Effects of known and novel loci on eGFRcrea in individuals with (n=16,477) and without (n=154,881) diabetes. The Pearson's correlation coefficient between the effects in the two groups was 0.80 across all loci (95% confidence interval: 0.67, 0.88). The corresponding correlation coefficient when considering all ~2.5 million genetic variants was of 0.044 (see "Test for differential effects on eGFRcrea between diabetes and hypertension strata", in the Methods), highlighting that most of replicated loci are associated with eGFRcrea regardless of the presence or absence of diabetes.



Supplementary Figure 6. Effect of the 53 known (light blue) and new (orange) loci on log(eGFRcrea) in the absence versus presence of hypertension. Data are derived from our previous analysis[3] and based on n = 29,592 and 44,319 hypertensive and non-hypertensive subjects, respectively.



Supplementary Figure 7. Forest plots from trans-ethnic random-effect meta-analysis for all 24 novel loci. Indicated are: index SNP and effect allele; ancestry (Eu = European, As = Asian; Af = African) along with effect allele frequencies in parenthesis. Dot sizes are proportional to study sample sizes. Bars indicate 95% confidence intervals. The random-effect estimate is reported as a rhomb and as a number (b) followed by the p-value (p).



Supplementary Table 1. Sample characteristics of discovery and replication studies.

Study[1]	Sample size			Women % (N)	Age Mean (SD)	eGFRcrea Mean(SD) ml / min / 1.73m^2	eGFRcys Mean(SD) ml / min / 1.73m^2	CKD % (N)	HTN % (N)	DM % (N)
	eGFRcrea	CKD	eGFRcys							
Discovery studies										
3C	6431	6431	1243	60.8 (3911)	74(5)	73.1(16.9)	90.5(22.7)	20.4 (1311)	79.0 (6431)	9.7 (623)
Advance	2287	2287	NA	32.8 (755)	67(7)	85.1(29.2)	NA	14.7 (337)	47.6 (1096)	100.0 (2287)
AGES	3219	3219	NA	58.0 (1867)	76(5)	73.0(20.0)	NA	24.2 (781)	80.6 (2595)	11.5 (368)
Amish	1211	NA	783	48.9 (592)	49(17)	93.7(19.7)	114.9(18.0)	3.1 (37)	18.9 (229)	1.7 (20)
ARIC	8982	8982	7145	53.1 (4767)	62(6)	81.4(17.5)	84.2(19.7)	8.7 (782)	40.7 (3643)	14.2 (1276)
ASPS	848	848	NA	56.8 (482)	65(8)	96.5(39.9)	NA	8.1 (69)	72.5 (615)	9.2 (78)
AUSTWIN	9592	3320	NA	60.9 (5846)	46(13)	98.3(26.2)	NA	10.5 (350)	NA	NA
BLSA	723	723	NA	46.1 (333)	70(15)	80.3(23.1)	NA	17.4 (126)	21.9 (147)	7.7 (55)
BMES	2437	2437	NA	56.8 (1385)	69(9)	78.7(20.2)	NA	13.2 (322)	76.4 (1861)	10.9 (265)
CHS	2820	2353	2475	61.3 (1729)	72(5)	77.3(20.8)	81.0(17.9)	9.5 (224)	51.4 (1441)	11.0 (307)
CROATIA-KORCULA	888	888	NA	64.0 (568)	56(14)	87.3(20.6)	NA	7.5 (67)	54.2 (474)	13.1 (116)
CROATIA-SPLIT	478	478	NA	59.8 (286)	49(15)	104.8(23.8)	NA	5.0 (24)	39.4 (186)	5.0 (24)
CROATIA-VIS	768	768	NA	58.6 (450)	57(15)	88.2(22.1)	NA	6.9 (53)	52.2 (396)	12.0 (91)
DESIR	715	NA	NA	75.2 (550)	50(8)	92.0(16.9)	NA	0.7 (5)	NA	0.0 (0)
EGCUT 370K	863	NA	NA	51.2 (442)	37(16)	101.5(20.3)	NA	1.7 (15)	18.7 (161)	2.2 (19)
EGCUT Omni	261	261	NA	73.4 (193)	81(9)	71.2(24.1)	NA	34.2 (90)	82.5 (217)	21.8 (57)
ERF	2561	2561	NA	55.3 (1416)	49(14)	93.3(21.4)	NA	3.7 (96)	52.9 (1355)	6.1 (155)
FamHS	3838	3838	521	52.4 (2012)	52(14)	91.6(20.1)	86.3(33.5)	4.2 (161)	25.5 (979)	7.7 (291)
FHS	7782	4142	3002	54.3 (4229)	51(14)	92.1(21.7)	83.8(17.8)	10.7 (445)	57.5 (2390)	9.7 (405)
GENOA	1163	1163	NA	56.3 (655)	59(10)	87.7(24.0)	NA	10.7 (125)	73.3 (852)	15.3 (178)
HABC	1663	1663	1663	47.1 (784)	74(3)	71.2(14.8)	77.0(19.9)	25.0 (415)	63.7 (1060)	13.0 (216)
HCS	1235	1235	NA	49.6 (630)	66(7)	79.9(18.1)	NA	11.3 (144)	45 (544)	10.5 (127)
HPFS	818	818	NA	0.0 (0)	65(8)	85.2(22.7)	NA	9.5 (78)	59 (479)	100.0 (818)
HYPERGENES HTN cases	1591	1591	NA	33.0 (525)	48(10)	94.5(23.1)	NA	3.7 (59)	100.0 (1591)	0.0 (0)
HYPERGENES HTN ctrls	1662	1662	NA	39.6 (659)	60(10)	87.8(19.0)	NA	4.9 (81)	0.0 (0)	0.0 (0)
INCIPE	940	940	875	52.7 (495)	61(11)	82.6(18.5)	88.5(22.1)	8.6 (81)	69.6 (654)	10.6 (100)

Supplementary Table 1 (continued)**.**

Study[1]	Sample size			Women % (N)	Age Mean (SD)	eGFRcrea Mean(SD) ml / min / 1.73m^2	eGFRcys Mean(SD) ml / min / 1.73m^2	CKD % (N)	HTN % (N)	DM % (N)
	eGFRcrea	CKD	eGFRcys							
Discovery studies										
INGI-CARLANTINO	447	NA	NA	60.8 (272)	50(16)	93.9(22.4)	NA	NA	34.9 (156)	9.4 (42)
INGI-CILENTO	821	821	NA	54.9 (451)	54(18)	88.7(21.8)	NA	8.0 (66)	38.4 (315)	10.5 (86)
INGI-FVG	874	874	NA	59.4 (519)	52(16)	90.6(21.8)	NA	6.0 (52)	48.8 (427)	6.7 (59)
INGI-VAL BORBERA	1636	1636	NA	55.8 (913)	55(18)	89.2(23.3)	NA	8.5 (139)	43.8 (717)	6.5 (107)
JUPITER	8780	8780	NA	32.2 (2827)	66(8)	80.1(18.1)	NA	11.5 (1008)	55.8 (4901)	0.4 (37)
KORA-F3	1641	1641	1642	50.5 (831)	62(10)	83.9(21.0)	111.8(26.3)	10.8 (177)	41.1 (674)	11.1 (179)
KORA-F4	1814	1814	1811	51.3 (930)	61(9)	85.1(20.2)	109.7(26.2)	7.0 (127)	20.9 (379)	9.2 (167)
MESA	2521	2521	2521	52.0 (1311)	63(10)	82.4(18.3)	90.0(21.7)	9.7 (245)	38.6 (974)	6.0 (151)
MICROS	1201	1201	1198	56.5 (678)	46(16)	94.6(20.9)	107.4(23.8)	3.8 (46)	37.7 (437)	4.3 (49)
NESDA	1856	NA	1856	67.5 (1253)	42(12)	98.4(20.7)	112.4(24.9)	1.1 (20)	30.3 (563)	5.1 (95)
NHS	786	786	NA	100.0 (786)	59(6)	86.2(22.1)	NA	10.7 (84)	70 (554)	100.0 (786)
NSPHS	565	565	NA	53.1 (300)	52(18)	91.0(22.1)	NA	5.7 (32)	43.4 (242)	7.8 (44)
OGP-TALANA	862	862	NA	57.3 (494)	51(19)	91.2(23.6)	NA	7.5 (65)	37.3 (322)	5.1 (44)
ORCADES	704	704	NA	53.6 (377)	54(15)	89.4(20.7)	NA	6.8 (48)	41.8 (287)	4.0 (28)
POPGEN	1163	1163	NA	44.4 (516)	55(14)	88.1(18.8)	NA	5.1 (59)	46.8 (541)	3.8 (44)
PREVEND	NA	NA	1885	48.9 (923)	50(12)	NA	105.4(25.3)	NA	33.5 (631)	3.7 (70)
PROSPER-PHASE	5236	5236	NA	51.7 (2718)	75(3)	72.0(21.4)	NA	29.6 (1549)	62.1 (3251)	10.4 (544)
RS-I	4390	4390	NA	61.4 (2696)	70(9)	77.1(17.2)	NA	13.7 (600)	34.1 (1497)	10.7 (470)
RS-II	1863	1863	NA	54.5 (1015)	65(8)	81.3(17.2)	NA	9.1 (169)	28.4 (530)	11.1 (207)
SAPALDIA	1444	1444	NA	51.0 (737)	52(11)	90.3(17.3)	NA	3.1 (44)	27.4 (389)	2.8 (40)
SHIP	3228	3228	3228	51.7 (1670)	54(15)	90.4(23.6)	97.1(25.3)	7.7 (248)	51.1 (1649)	11.2 (362)
SHIP-TREND	986	986	986	56.2 (554)	50(14)	92.4(22.1)	122.1(22.1)	4.3 (42)	39.6 (390)	1.8 (18)
SORBS	856	856	NA	58.5 (501)	49(16)	92.2(19.0)	NA	4.1 (35)	53.2 (455)	9.3 (80)
WGHS	21940	23186	NA	100.0 (21,940)	55(7)	90.0(22.5)	NA	6.1 (1329)	24.5 (5374)	2.5 (554)
YFS	2023	NA	NA	54.7 (1107)	38(5)	100.3(15.8)	NA	0.2 (5)	20.0 (404)	1.9 (39)

Supplementary Table 1 (continued).

Study[1]	Sample size			Women % (N)	Age Mean (SD)	eGFRcrea Mean(SD) ml / min / 1.73m^2	eGFRcys Mean(SD) ml / min / 1.73m^2	CKD % (N)	HTN % (N)	DM % (N)
	eGFRcrea	CKD	eGFRcys							
Replication studies										
Bus Santé	4408	4408	NA	49.4 (2178)	58(11)	85.6(15.6)	NA	4.3 (186)	28.3 (1249)	7.4 (327)
EGCUT_replic	1519	1519	1037	46.2 (703)	58(17)	97.4(29.3)	85.5(16.9)	8.8 (134)	59.5 (905)	6.3 (97)
ESTHER	3604	3604	NA	55.6 (2004)	62(7)	90.3(34.4)	NA	15.7 (565)	57.5 (2073)	15.9 (572)
GENDIAN	450	450	450	47.1 (212)	65(10)	69.1(20.2)	85.3(27.1)	32.3 (145)	53.0 (237)	100.0 (450)
GHS 1	2995	2995	NA	48.5 (1452)	56(11)	87.3(16.5)	NA	3.7 (112)	52.6 (1575)	7.2 (215)
GHS 2	1179	1179	NA	50.0 (590)	55(11)	86.7(16.2)	NA	4.5 (53)	48.4 (570)	7.6 (90)
GSK	1721	1721	NA	66.6 (1147)	51(13)	92.3(22.6)	NA	5.5 (95)	43.7 (752)	4.6 (80)
HRS	NA	NA	7700	58.9 (4537)	68(10)	NA	102.5(20.3)	2.9 (221)	66.1 (5087)	20.5 (1557)
KORA-F3 non-GWAS	1494	NA	1493	52.5 (787)	52(13)	92.6(21.3)	123.5(29.1)	2.6 (39)	29.4 (437)	5.1 (76)
KORA-F4 non-GWAS	1199	1200	1196	52.4 (629)	49(15)	92.6(22.4)	118.4(27.5)	5.8 (70)	13.3 (159)	4.0 (48)
IPM_EA_Affy	440	NA	NA	30.2 (133)	62(13)	94.8(36.8)	NA	19.1 (84)	60.5 (266)	26.0 (99)
IPM_EA_Illu	1307	1307	NA	48.6 (635)	68(9)	86.1(27.8)	NA	14.8 (194)	55.1 (720)	15.0 (185)
LURIC	3056	3056	3054	30.0 (917)	63(11)	86.0(21.7)	84.7(22.6)	10.0 (305)	72.7 (2223)	32.6 (996)
OGP	9554	5884	NA	56.9 (5440)	50(17)	98.6(35.0)	NA	8.1 (776)	36.0 (3443)	6.2 (596)
SAPHIR	1721	NA	NA	37.1 (639)	51(6)	91.7(16.1)	NA	6.9 (19)	55.7 (959)	3.3 (56)
SKIPOGH	870	NA	NA	52.3 (455)	47(18)	94.2(24.6)	NA	5.7 (50)	22.9 (198)	4.5 (39)
Vanderbilt Omni1	3221	3221	NA	47.3 (1525)	54(19)	80.0(36.9)	NA	27.7 (891)	70.5 (2271)	18.0 (581)
Vanderbilt Omni5	1129	1129	NA	46.9 (529)	50(21)	89.0(44.4)	NA	21.7 (245)	58.2 (657)	33.3 (376)
Vanderbilt 660W	2299	2299	NA	56.5 (1298)	56(17)	78.6(23.9)	NA	20.6 (474)	57.2 (1316)	17.9 (411)

[1] Extended study names are given in the Acknowledgements section.

Supplementary Table 2. Association of previously identified loci. For each locus, we report the best SNP from the current discovery GWAS (current best SNP). The previously reported best SNP is reported for comparison.

ID of current best SNP in the locus	Chr	Position (Build 37)	Locus name*	Ref. / Non-Ref. All. (Ref All Freq)	eGFRcrea		CKD		Previously reported SNP in the locus		
					beta(SE)†	P-value†	Odds Ratio (95%CI) †	P-value†	ID of previously reported SNP[REF]	LD[#] with current best SNP r^2/D'	P-value in current GWAS†
rs1800615	1	15,832,281	*CASP9*	T/C(0.30)	-0.0058(0.0009)	1.90E-09	1.04 (1.00,1.07)	3.40E-02	rs12124078[3]	1.00/1.00	3.09E-09
rs267734	1	150,951,477	*LASS2*	T/C(0.79)	-0.0079(0.0011)	4.01E-13	1.06 (1.02,1.10)	3.52E-03	same[4]		
rs807601	2	15,793,014	*DDX1*	T/G(0.34)	0.0064(0.0009)	6.60E-12	0.99 (0.96,1.02)	5.28E-01	rs6431731[3]	0.04/0.60	2.95E-07
rs1260326	2	27,730,940	*GCKR*	T/C(0.42)	0.0068(0.0009)	3.38E-14	0.98 (0.95,1.01)	1.36E-01	same[4]		
rs6546838	2	73,679,280	*ALMS1*	A/G(0.76)	-0.0093(0.0010)	7.72E-20	1.05 (1.02,1.09)	4.63E-03	rs13538[4]	0.95/1.00	3.15E-17
rs7422339	2	211,540,507	*CPS1*	A/C(0.32)	-0.0106(0.0010)	2.18E-23	1.11 (1.07,1.15)	7.54E-09	same[5]		
rs2861422	3	141,724,644	*TFDP2*	T/C(0.27)	0.0074(0.0010)	9.12E-14	0.96 (0.92,0.99)	7.59E-03	rs347685[4]	0.96/1.00	1.87E-13
rs17319721	4	77,368,847	*SHROOM3*	A/G(0.43)	-0.0114(0.0009)	1.32E-37	1.07 (1.04,1.10)	7.71E-06	same[5]		
rs11959928	5	39,397,132	*DAB2*	A/T(0.44)	-0.0083(0.0009)	1.66E-20	1.06 (1.02,1.09)	4.20E-04	same[4]		
rs6420094	5	176,817,636	*SLC34A1*	A/G(0.66)	0.0096(0.0010)	4.92E-22	0.91 (0.88,0.94)	3.68E-09	same[4]		
rs9472135	6	43,809,802	*VEGFA*	T/C(0.71)	-0.0080(0.0010)	3.34E-15	1.07 (1.04,1.11)	3.37E-05	rs881858[4]	0.88/0.96	7.51E-15
rs316009	6	160,675,764	*SLC22A2*	T/C(0.10)	0.0131(0.0014)	4.38E-19	0.96 (0.91,1.01)	9.71E-02	rs2279463[4]	0.01/1.00	2.94E-16
rs848490	7	77,555,005	*TMEM60*	C/G(0.73)	0.0073(0.0010)	7.80E-13	0.93 (0.90,0.97)	1.44E-04	rs6465825[4]	0.41/1.00	4.91E-12
rs7805747	7	151,407,801	*PRKAG2*	A/G(0.25)	-0.0130(0.0011)	7.96E-29	1.16 (1.11,1.20)	2.06E-14	same[4]		
rs3758086	8	23,714,992	*STC1*	A/G(0.42)	-0.0071(0.0009)	1.71E-15	1.06 (1.02,1.09)	4.13E-04	rs10109414[5]	1.00/1.00	2.31E-15
rs4744712	9	71,434,707	*PIP5K1B*	A/C(0.40)	-0.0071(0.0009)	4.29E-15	1.06 (1.03,1.09)	7.59E-05	same[4]		
rs1044261	10	1,065,710	*WDR37*	T/C(0.08)	-0.0113(0.0016)	1.21E-11	1.15 (1.09,1.22)	3.62E-07	rs10794720[4]	0.42/0.69	3.23E-09
rs963837	11	30,749,090	*MPPED2*	T/C(0.54)	-0.0078(0.0009)	5.69E-18	1.09 (1.05,1.12)	9.03E-08	rs3925584[3]	0.93/0.97	7.58E-18
rs10774021	12	349,298	*SLC6A13*	T/C(0.65)	-0.0063(0.0009)	4.77E-12	1.04 (1.01,1.07)	1.17E-02	same[4]		
rs716877	13	72,347,448	*DACH1*	C/G(0.40)	0.0049(0.0009)	6.22E-08	0.97 (0.94,1.00)	3.15E-02	rs626277[4]	1.00/1.00	7.98E-08
rs476633	15	41,392,134	*INO80*	C/G(0.57)	0.0051(0.0009)	8.90E-09	0.94 (0.91,0.97)	2.84E-05	rs2928148[3]	0.84/1.00	1.28E-07
rs2467853	15	45,698,793	*GATM*	T/G(0.62)	0.0126(0.0009)	1.05E-42	0.90 (0.87,0.93)	1.88E-11	rs2453533[5]	1.00/1.00	4.26E-42
rs491567	15	53,946,593	*WDR72*	A/C(0.78)	-0.0084(0.0010)	2.86E-15	1.08 (1.04,1.12)	7.48E-05	same[4]		
rs1394125	15	76,158,983	*UBE2Q2*	A/G(0.35)	-0.0073(0.0010)	5.47E-14	1.07 (1.04,1.11)	3.02E-05	same[4]		
rs13329952	16	20,366,507	*UMOD*	T/C(0.81)	-0.0158(0.0011)	9.47E-43	1.24 (1.19,1.29)	1.98E-25	rs12917707[5]	0.95/1.00	1.16E-41
rs2453580	17	19,438,321	*SLC47A1*	T/C(0.59)	0.0064(0.0009)	2.93E-11	0.94 (0.91,0.97)	2.60E-04	same[3]		
rs9916302	17	37,499,949	*CDK12 / FBXL20*	T/C(0.74)	-0.008(0.0010)	4.78E-15	1.03 (0.99,1.07)	9.43E-02	rs7208487[3] rs11078903[6]	0.49/1.00 0.87/1.00	1.53E-12 5.09E-13
rs11657044	17	59,450,105	*BCAS3*	T/C(0.19)	-0.0115(0.0012)	7.89E-22	1.06 (1.02,1.10)	6.56E-03	rs9895661[4]	0.94/1.00	2.76E-21
rs12460876	19	33,356,891	*SLC7A9*	T/C(0.60)	-0.0066(0.0009)	1.86E-13	1.05 (1.02,1.08)	2.19E-03	same[4]		

*Based on previously reported index gene to facilitate comparison.

†Beta is the effect on log(eGFRcrea in ml/min/1.73 m^2); all reported standard errors, confidence intervals, and P-values, are based on the twice-GC corrected results from discovery GWAS meta-analysis.

#LD lookup is based on HapMap 22 CEU obtained using SNAP[7] version 2.2.

Supplementary Table 3. All SNPs tested for replication.

SNPID Locus name*	Chr	Position (bp) (Build 37)	Eff./ Non Eff All (EAF)[#]	STAGE 1 (discovery)[†]			STAGE 2 (replication)[‡]				Combined analysis					
				N	Beta (SE)	P-value	N	Beta (SE)	1-sided P-value	q-value	N	Beta (SE)	P-value	I^2 (%)	Power	Median Rsq
eGFRcrea in the non-diabetes group																
rs3850625 *CACNA1S*	1	201,016,296	A/G(0.12)	116,689	0.0086 (0.0014)	2.55E-09	36,418	0.0071 (0.0028)	5.10E-03	5.46E-03	153,107	0.0083 (0.0013)	6.82E-11	0	0.997	1.00
rs2712184 *IGFBP5*	2	217,682,779	A/C(0.58)	118,440	-0.0052 (0.0009)	1.65E-08	35,414	-0.0055 (0.0018)	1.20E-03	2.06E-03	153,854	-0.0053 (0.0008)	1.33E-10	0	0.983	1.00
rs9682041 *SKIL*	3	170,091,902	T/C(0.87)	118,454	-0.0072 (0.0013)	1.36E-07	32,457	-0.0046 (0.0031)	6.81E-02	2.33E-02	150,911	-0.0068 (0.0012)	2.58E-08	2	0.948	1.00
rs10513801 *ETV5*	3	185,822,353	T/G(0.87)	118,374	0.0079 (0.0013)	3.80E-09	36,400	0.0046 (0.0026)	3.96E-02	1.79E-02	154,774	0.0072 (0.0012)	1.03E-09	0	0.992	1.00
rs10994860 *A1CF*	10	52,645,424	T/C(0.18)	118,358	0.0082 (0.0012)	1.00E-11	36,286	0.0061 (0.0024)	5.10E-03	5.46E-03	154,644	0.0077 (0.0011)	1.07E-12	2	0.999	0.93
rs163160 *KCNQ1*	11	2,789,955	A/G(0.82)	118,373	0.0069 (0.0012)	9.02E-09	36,311	0.0050 (0.0023)	1.62E-02	9.89E-03	154,684	0.0065 (0.0011)	2.26E-09	14	0.992	0.98
rs164748 *DPEP1*	16	89,708,292	C/G(0.53)	118,373	0.0053 (0.0009)	9.92E-09	36,124	0.0019 (0.0018)	1.42E-01	4.19E-02	154,497	0.0046 (0.0008)	1.95E-08	17	0.991	0.99
rs8091180 *NFATC1*	18	77,164,243	A/G(0.56)	117,447	-0.0062 (0.0011)	1.43E-08	36,268	-0.0052 (0.0020)	5.10E-03	5.46E-03	153,715	-0.0060 (0.0010)	1.28E-09	0	0.999	0.81
rs437065 *ADAMTS5*	21	28,527,399	C/G(0.14)	118,358	0.0066 (0.0013)	8.64E-07	35,562	-0.0026 (0.0026)	1.63E-01	4.62E-02	153,920	0.0047 (0.0012)	6.78E-05	0	0.904	0.99
eGFRcrea in the overall sample																
rs12136063 *SYPL2*	1	110,014,170	A/G(0.70)	133,723	0.0049 (0.0009)	2.33E-07	41,703	0.0028 (0.0019)	6.48E-02	2.31E-02	175,426	0.0045 (0.0008)	4.71E-08	0	0.922	1.00
rs2802729 *SDCCAG8*	1	243,501,763	A/C(0.44)	133,608	-0.0050 (0.0009)	7.37E-08	41,200	-0.0029 (0.0018)	5.02E-02	2.05E-02	174,808	-0.0046 (0.0008)	2.20E-08	9	0.983	0.88
rs2888875 *THADA*	2	43,788,092	A/G(0.69)	129,114	0.0048 (0.0009)	7.75E-07	41,571	0.0012 (0.0018)	2.60E-01	5.72E-02	170,685	0.0041 (0.0008)	6.92E-07	0	0.894	0.99
rs17050272 *GLI2*	2	121,306,440	A/G(0.43)	132,764	-0.0048 (0.0009)	6.63E-07	41,681	-0.0024 (0.0018)	8.88E-02	2.93E-02	174,445	-0.0043 (0.0008)	1.36E-07	19	0.964	0.90
rs3820716 *ACVR2A*	2	148,680,260	A/G(0.53)	133,751	-0.0052 (0.0009)	2.73E-09	41,642	0.0006 (0.0017)	6.36E-01	1.22E-01	175,393	-0.0039 (0.0008)	1.36E-06	17	0.994	1.00
rs4667594 *LRP2*	2	170,008,506	A/T(0.53)	133,715	-0.0045 (0.0009)	2.37E-07	41,622	-0.0043 (0.0017)	5.90E-03	5.62E-03	175,337	-0.0044 (0.0008)	3.52E-08	4	0.922	1.00
rs6795744 *WNT7A*	3	13,906,850	A/G(0.15)	133,718	0.0071 (0.0012)	9.60E-09	41,772	0.0019 (0.0024)	2.10E-01	5.15E-02	175,490	0.0060 (0.0011)	3.33E-08	18	0.990	0.98

Supplementary Table 3 (continued).

SNPID Locus name*	Chr	Position (bp) (Build 37)	Eff./ Non Eff All (EAF)#	STAGE 1 (discovery)†			STAGE 2 (replication)‡				Combined analysis					
				N	Beta (SE)	P-value	N	Beta (SE)	1-sided P-value	q-value	N	Beta (SE)	P-value	I^2 (%)	Power	Median Rsq
eGFRcrea in the overall sample																
rs6795744 *WNT7A*	3	13,906,850	A/G(0.15)	133,718	0.0071 (0.0012)	9.60E-09	41,772	0.0019 (0.0024)	2.10E-01	5.15E-02	175,490	0.0060 (0.0011)	3.33E-08	18	0.990	0.98
rs16852193 *EGFEM1P*	3	168,074,912	T/C(0.09)	133,691	0.0076 (0.0015)	8.72E-07	41,664	0.0005 (0.0030)	4.34E-01	8.86E-02	175,355	0.0061 (0.0014)	6.64E-06	0	0.885	0.95
rs228611 *NFKB1*	4	103,561,709	A/G(0.48)	133,788	-0.0055 (0.0009)	4.66E-10	41,657	-0.0060 (0.0017)	2.08E-04	8.91E-04	175,445	-0.0056 (0.0008)	3.58E-12	4	0.998	1.00
rs7735249 *ARL15*	5	53,310,139	C/G(0.92)	132,513	-0.0109 (0.0018)	2.09E-09	41,662	-0.0012 (0.0028)	3.28E-01	6.86E-02	174,175	-0.0079 (0.0015)	2.08E-07	8	1.000	0.98
rs11960179 *PIK3R1*	5	67,820,217	A/G(0.12)	133,714	-0.0072 (0.0014)	2.47E-07	23,693	-0.0051 (0.0033)	6.16E-02	2.31E-02	157,407	-0.0069 (0.0013)	1.57E-07	9	0.908	0.94
rs836788 *DHFR*	5	79,912,044	T/C(0.35)	133,810	-0.0045 (0.0009)	8.56E-07	41,731	-0.0038 (0.0018)	1.73E-02	9.89E-03	175,541	-0.0043 (0.0008)	9.89E-08	11	0.868	1.00
rs7759001 *ZNF204*	6	27,341,409	A/G(0.76)	133,723	-0.0053 (0.0010)	2.64E-07	41,760	-0.0045 (0.0020)	1.38E-02	9.10E-03	175,483	-0.0051 (0.0009)	1.75E-08	0	0.930	1.00
rs10277115 *UNCX*	7	1,285,195	A/T(0.24)	115,895	0.0095 (0.0014)	1.05E-10	40,626	0.0079 (0.0023)	3.16E-04	9.03E-04	156,521	0.0090 (0.0012)	8.72E-14	0	1.000	0.53
rs2290263 *MIR148A*	7	25,887,278	A/G(0.73)	132,930	0.0053 (0.0010)	2.35E-07	41,756	0.0016 (0.0019)	2.04E-01	5.15E-02	174,686	0.0045 (0.0009)	6.70E-07	5	0.959	1.00
rs3750082 *KBTBD2*	7	32,919,927	A/T(0.34)	127,284	0.0049 (0.0009)	2.52E-07	41,210	0.0031 (0.0018)	4.58E-02	1.96E-02	168,494	0.0045 (0.0008)	3.22E-08	2	0.934	1.00
rs1004402 *GRB10*	7	50,755,208	A/C(0.12)	127,292	0.0068 (0.0013)	4.79E-07	41,801	-0.0026 (0.0027)	8.31E-01	1.52E-01	169,093	0.0050 (0.0012)	2.93E-05	11	0.882	1.00
rs868055 *UBE2H*	7	129,435,191	T/C(0.10)	133,608	0.0082 (0.0016)	3.48E-07	41,843	-0.0008 (0.0029)	6.14E-01	1.22E-01	175,451	0.0060 (0.0014)	2.17E-05	22	0.981	0.83
rs6459680 *RNF32*	7	156,258,568	T/G(0.74)	133,692	-0.0065 (0.0010)	1.96E-10	41,655	-0.0019 (0.0019)	1.67E-01	4.62E-02	175,347	-0.0055 (0.0009)	1.07E-09	0	1.000	0.98
rs913423 *CYP26A1*	10	94,845,036	A/G(0.54)	132,861	-0.0052 (0.0009)	5.10E-09	41,638	-0.0014 (0.0017)	2.07E-01	5.15E-02	174,499	-0.0043 (0.0008)	7.65E-08	10	0.993	1.00
rs4014195 *AP5B1*	11	65,506,822	C/G(0.64)	133,723	0.0061 (0.0009)	2.19E-11	41,677	0.0034 (0.0018)	2.65E-02	1.42E-02	175,400	0.0055 (0.0008)	1.10E-11	0	1.000	1.00
rs10491967 *TSPAN9*	12	3,368,093	A/G(0.11)	133,800	-0.0092 (0.0014)	3.03E-10	41,870	-0.0106 (0.0027)	4.59E-05	3.93E-04	175,670	-0.0095 (0.0013)	5.18E-14	0	1.000	0.99
rs7956634 *PTPRO*	12	15,321,194	T/C(0.81)	133,722	-0.0068 (0.0011)	2.46E-09	41,726	-0.0069 (0.0022)	7.04E-04	1.51E-03	175,448	-0.0068 (0.0010)	7.17E-12	0	0.997	1.00

Supplementary Table 3 (continued).

SNPID Locus name*	Chr	Position (bp) (Build 37)	Eff./ Non Eff All (EAF)#	STAGE 1 (discovery)†			STAGE 2 (replication)‡				Combined analysis					
				N	Beta (SE)	P-value	N	Beta (SE)	1-sided P-value	q-value	N	Beta (SE)	P-value	I^2 (%)	Power	Median Rsq
eGFRcrea in the overall sample																
rs1106766 *INHBC*	12	57,809,456	T/C(0.22)	133,660	0.0062 (0.0011)	4.67E-08	21,005	0.0058 (0.0026)	1.23E-02	8.79E-03	154,665	0.0061 (0.0010)	2.41E-09	11	0.973	0.84
rs11180732 *PHLDA1*	12	76,283,354	T/G(0.31)	133,656	0.0049 (0.0009)	4.65E-07	41,586	0.0008 (0.0018)	3.26E-01	6.86E-02	175,242	0.0041 (0.0008)	6.23E-07	0	0.930	0.95
rs2071047 *BMP4*	14	54,418,411	A/G(0.41)	133,647	0.0044 (0.0009)	9.15E-07	41,772	0.0016 (0.0017)	1.85E-01	4.95E-02	175,419	0.0038 (0.0008)	3.20E-06	13	0.879	1.00
rs8056893 *SLC7A6*	16	68,304,392	A/C(0.72)	133,711	0.0051 (0.0010)	2.03E-07	41,695	0.0035 (0.0019)	3.21E-02	1.53E-02	175,406	0.0047 (0.0009)	1.28E-07	0	0.940	0.98
rs9807656 *SETBP1*	18	42,346,956	T/C(0.91)	133,688	-0.0081 (0.0016)	6.06E-07	40,684	0.0020 (0.0029)	7.61E-01	1.42E-01	174,372	-0.0056 (0.0014)	7.26E-05	22	0.947	0.99
rs9945268 *RNF152*	18	59,340,526	A/T(0.70)	127,290	-0.0048 (0.0010)	7.05E-07	41,612	-0.0020 (0.0018)	1.32E-01	4.05E-02	168,902	-0.0042 (0.0009)	3.18E-06	0	0.876	1.00
rs11666497 *SIPA1L3*	19	38,464,262	T/C(0.18)	127,271	-0.0064 (0.0012)	8.58E-08	41,640	-0.0041 (0.0022)	3.06E-02	1.53E-02	168,911	-0.0058 (0.0011)	4.25E-08	24	0.973	0.97
rs12975033 *IZUMO1*	19	49,249,443	A/T(0.55)	133,724	-0.0052 (0.0009)	4.75E-09	38,469	0.0006 (0.0017)	6.43E-01	1.22E-01	172,193	-0.0039 (0.0008)	1.31E-06	26	0.992	1.00
rs6088580 *TP53INP2*	20	33,285,053	C/G(0.47)	132,773	-0.0055 (0.0009)	7.17E-10	34,592	-0.0027 (0.0017)	6.28E-02	2.31E-02	167,365	-0.0049 (0.0008)	1.79E-09	0	0.997	0.99
rs2235808 *JPH2*	20	42,815,795	C/G(0.85)	129,605	0.0071 (0.0013)	1.50E-07	25,036	0.0020 (0.0025)	2.17E-01	5.17E-02	154,641	0.0060 (0.0012)	3.21E-07	0	0.967	0.87
rs17216707 *BCAS1*	20	52,732,362	T/C(0.79)	133,656	-0.0084 (0.0011)	5.96E-13	39,971	-0.0051 (0.0021)	7.80E-03	6.69E-03	173,627	-0.0077 (0.0010)	8.83E-15	1	1.000	0.85
CKD in the overall sample																
rs1032843 *FIGN*	2	164,184,329	T/C(0.07)	118,131	0.1508 (0.0299)	4.48E-07	32,338	0.0332 (0.0486)	2.47E-01	5.72E-02	150,469	0.1174 (0.0259)	5.70E-06	2	0.915	0.95
rs11039182 *MADD*	11	47,346,723	T/C(0.70)	118,130	-0.0818 (0.0167)	9.07E-07	35,062	-0.0325 (0.0271)	1.15E-01	3.66E-02	153,192	-0.0678 (0.0144)	2.64E-06	0	0.722	0.99
rs593790 *OR4C45*	11	48,391,116	A/T(0.82)	118,137	-0.1045 (0.0209)	5.96E-07	35,015	-0.0213 (0.0320)	2.53E-01	5.72E-02	153,152	-0.0788 (0.0178)	9.77E-06	0	0.956	0.99
rs2832559 *GRIK1*	21	31,417,144	T/C(0.91)	117,017	-0.1435 (0.0292)	9.56E-07	30,577	0.0668 (0.0540)	8.92E-01	1.61E-01	147,594	-0.0941 (0.0262)	3.31E-04	0	0.889	0.97

Supplementary Table 3 (continued).

SNPID Locus name*	Chr	Position (bp) (Build 37)	Eff./ Non Eff All (EAF)#	STAGE 1 (discovery)†			STAGE 2 (replication)‡				Combined analysis					
				N	Beta (SE)	P-value	N	Beta (SE)	1-sided P-value	q-value	N	Beta (SE)	P-value	I^2 (%)	Power	Median Rsq
eGFRcys in the overall sample																
rs12428035 *DZIP1*	13	96,300,872	T/C(0.12)	33,145	-0.0144 (0.0029)	7.28E-07	14,919	-0.0089 (0.0039)	1.13E-02	8.79E-03	48,064	-0.0125 (0.0023)	6.33E-08	0	0.588	1.00

*Based on Table 1 for replicated loci and on the closest gene name for the non-replicated loci, according to the UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly.
#Effect Allele Frequency as estimated in the combined sample.
†All P-values and SEs reported from the STAGE 1 analysis were twice-GC corrected, to account for possible genomic inflation.
‡ In Stage 2 analysis, 1-sided P-values were computed to assess direction consistent effects with Stage 1; q-values were estimated based on the 1-sided P-values.

Supplementary Table 4. Association of replicated novel loci with eGFRcrea, CKD, and eGFRcys, in the overall combined sample.

					eGFRcrea			CKD		eGFRcys	
SNP ID	**Chr**	**Position (bp) (Build 37)**	**Locus name***	**Eff./ Non Eff. All. (EAF)**	**beta (SE)**	**P-value**	**beta (SE) from random-effect meta-analysis**	**OR (95%CI)**	**P-value**	**beta (SE)**	**P-value**
rs12136063	1	110,014,170	*SYPL2*	A/G(0.70)	0.0045(0.0008)	4.71E-08	0.0045(0.0008)	0.98(0.96,1.01)	2.37E-01	0.0025(0.0016)	1.25E-01
rs3850625	1	201,016,296	*CACNA1S*	A/G(0.12)	0.0078(0.0013)	5.53E-10	0.0079(0.0012)	0.95(0.91,0.99)	2.31E-02	0.0016(0.0023)	4.95E-01
rs2802729	1	243,501,763	*SDCCAG8*	A/C(0.43)	-0.0046(0.0008)	2.20E-08	-0.0047(0.0009)	1.05(1.02,1.08)	4.10E-04	-0.0036(0.0016)	2.49E-02
rs4667594	2	170,008,506	*LRP2*	A/T(0.53)	-0.0044(0.0008)	3.52E-08	-0.0045(0.0008)	1.05(1.02,1.07)	5.43E-04	0.0001(0.0015)	9.63E-01
rs2712184	2	217,682,779	*IGFBP5*	A/C(0.58)	-0.0048(0.0008)	3.02E-09	-0.0047(0.0009)	1.02(0.99,1.05)	1.54E-01	0.0001(0.0015)	9.39E-01
rs6795744	3	13,906,850	*WNT7A*	A/G(0.15)	0.0060(0.0011)	3.33E-08	0.0057(0.0013)	0.96(0.93,1.00)	3.98E-02	0.0049(0.0021)	1.84E-02
rs9682041	3	170,091,902	*SKIL*	T/C(0.87)	-0.0062(0.0012)	2.95E-07	-0.0062(0.0012)	1.02(0.98,1.06)	2.53E-01	-0.0039(0.0022)	7.99E-02
rs10513801	3	185,822,353	*ETV5*	T/G(0.87)	0.0070(0.0012)	2.47E-09	0.0069(0.0012)	0.93(0.89,0.96)	5.08E-05	0.0019(0.0023)	3.92E-01
rs228611	4	103,561,709	*NFKB1*	A/G(0.47)	-0.0056(0.0008)	3.58E-12	-0.0056(0.0008)	1.03(1.00,1.05)	3.36E-02	-0.0023(0.0015)	1.23E-01
rs7759001	6	27,341,409	*ZNF204*	A/G(0.76)	-0.0051(0.0009)	1.75E-08	-0.0052(0.0009)	1.03(1.00,1.06)	5.66E-02	-0.0023(0.0017)	1.71E-01
rs10277115	7	1,285,195	*UNCX*	A/T(0.23)	0.0090(0.0012)	8.72E-14	0.0090(0.0012)	0.96(0.92,1.00)	4.09E-02	0.0045(0.0025)	7.62E-02
rs3750082	7	32,919,927	*KBTBD2*	A/T(0.33)	0.0045(0.0008)	3.22E-08	0.0045(0.0009)	0.97(0.95,1.00)	5.76E-02	0.0014(0.0016)	3.95E-01
rs6459680	7	156,258,568	*RNF32*	T/G(0.74)	-0.0055(0.0009)	1.07E-09	-0.0055(0.0009)	1.04(1.01,1.07)	2.08E-02	-0.0043(0.0017)	1.06E-02
rs10994860	10	52,645,424	*A1CF*	T/C(0.19)	0.0071(0.0010)	1.66E-12	0.0069(0.0011)	0.99(0.95,1.02)	5.14E-01	0.0015(0.0020)	4.41E-01
rs163160	11	2,789,955	*KCNQ1*	A/G(0.82)	0.0064(0.0010)	1.72E-10	0.0063(0.0011)	0.95(0.92,0.99)	5.30E-03	0.0073(0.0020)	2.35E-04
rs4014195	11	65,506,822	*AP5B1*	C/G(0.64)	0.0055(0.0008)	1.10E-11	0.0056(0.0004)	0.93(0.91,0.96)	2.35E-07	0.0053(0.0015)	5.58E-04
rs10491967	12	3,368,093	*TSPAN9*	A/G(0.10)	-0.0095(0.0013)	5.18E-14	-0.0095(0.0013)	1.06(1.02,1.11)	6.54E-03	-0.0024(0.0024)	3.24E-01
rs7956634	12	15,321,194	*PTPRO*	T/C(0.81)	-0.0068(0.0010)	7.17E-12	-0.0066(0.0011)	1.03(1.00,1.06)	8.94E-02	-0.0059(0.0019)	2.17E-03
rs1106766	12	57,809,456	*INHBC*	T/C(0.22)	0.0061(0.0010)	2.41E-09	0.0060(0.0011)	0.98(0.95,1.02)	3.07E-01	0.0048(0.0019)	1.03E-02
rs164748	16	89,708,292	*DPEP1*	C/G(0.53)	0.0042(0.0008)	1.63E-07	0.0040(0.0010)	0.99(0.96,1.01)	3.27E-01	0.0046(0.0015)	1.80E-03
rs8091180	18	77,164,243	*NFATC1*	A/G(0.56)	-0.0053(0.0009)	5.57E-09	-0.0053(0.0009)	1.03(1.00,1.06)	3.57E-02	-0.0050(0.0020)	1.19E-02
rs11666497	19	38,464,262	*SIPA1L3*	T/C(0.18)	-0.0058(0.0011)	4.25E-08	-0.0061(0.0013)	1.00(0.97,1.04)	9.70E-01	-0.0027(0.0019)	1.70E-01
rs6088580	20	33,285,053	*TP53INP2*	C/G(0.47)	-0.0049(0.0008)	1.79E-09	-0.0049(0.0008)	1.04(1.01,1.07)	5.25E-03	0.0000(0.0015)	9.92E-01
rs17216707	20	52,732,362	*BCAS1*	T/C(0.79)	-0.0077(0.0010)	8.83E-15	-0.0076(0.0011)	1.05(1.01,1.09)	8.18E-03	-0.0083(0.0020)	3.25E-05

* Conventional locus name based on relevant genes in the region as identified by bioinformatic investigation (Suppl. Tab. 12) or closest gene. A complete overview of the genes in each locus is given in the regional association plots (Suppl. Fig. 4)

Supplementary Table 5. SNP associations for novel and known loci stratified by diabetes status**.**

SNP ID (effect allele)	Locus name	No Diabetes			Diabetes			P-value for difference*
		N	beta (SE)	P-value	N	beta (SE)	P-value	
Novel loci: sample size based on the combined (discovery and replication) sample								
rs3850625 (A)	*CACNA1S*	153,107	0.0083 (0.0013)	6.82E-11	16,275	0.0038 (0.0048)	4.34E-01	0.27
rs2712184 (A)	*IGFBP5*	153,854	-0.0053 (0.0004)	1.33E-10	16,463	-0.0034 (0.0031)	2.70E-01	0.22
rs9682041 (T)	*SKIL*	150,911	-0.0068 (0.0012)	2.58E-08	16,161	0.0006 (0.0045)	8.86E-01	0.20
rs10513801 (T)	*ETV5*	154,774	0.0072 (0.0012)	1.03E-09	16,470	0.0022 (0.0045)	6.19E-01	0.28
rs10994860 (T)	*A1CF*	154,644	0.0077 (0.0011)	1.07E-12	16,451	0.0031 (0.0041)	4.57E-01	0.27
rs163160 (A)	*KCNQ1*	154,684	0.0065 (0.0011)	2.26E-09	16,457	0.0055 (0.0040)	1.68E-01	0.81
rs164748 (C)	*DPEP1*	154,497	0.0046 (0.0004)	1.95E-08	16,416	0.0026 (0.0031)	4.07E-01	0.52
rs8091180 (A)	*NFATC1*	153,715	-0.0060 (0.0010)	1.28E-09	13,764	0.0030 (0.0043)	4.85E-01	0.04
rs12136063 (A)	*SYPL2*	152,998	0.0043 (0.0009)	2.25E-06	16,253	0.0013 (0.0034)	7.02E-01	0.38
rs2802729 (A)	*SDCCAG8*	152,501	-0.0042 (0.0009)	2.65E-06	16,156	-0.0050 (0.0033)	1.24E-01	0.81
rs4667594 (A)	*LRP2*	154,570	-0.0042 (0.0008)	2.09E-07	16,449	-0.0034 (0.0031)	2.67E-01	0.80
rs6795744 (A)	*WNT7A*	154,716	0.0053 (0.0011)	1.23E-06	16,462	0.0070 (0.0043)	1.02E-01	0.70
rs228611 (A)	*NFKB1*	154,683	-0.0056 (0.0008)	7.39E-12	16,454	-0.0077 (0.0030)	1.07E-02	0.49
rs7759001 (A)	*ZNF204*	154,713	-0.0053 (0.0009)	1.02E-08	16,458	-0.0000 (0.0036)	9.92E-01	0.15
rs10277115 (A)	*UNCX*	141,932	0.0085 (0.0013)	4.97E-11	13,565	0.0156 (0.0053)	3.30E-03	0.19
rs3750082 (A)	*KBTBD2*	148,429	0.0042 (0.0009)	3.82E-06	15,754	0.0050 (0.0033)	1.32E-01	0.81
rs6459680 (T)	*RNF32*	154,586	-0.0057 (0.0009)	4.64E-10	16,454	-0.0043 (0.0035)	2.25E-01	0.70
rs4014195 (C)	*AP5B1*	154,634	0.0050 (0.0008)	1.02E-09	16,452	0.0116 (0.0032)	2.52E-04	0.04
rs10491967 (A)	*TSPAN9*	154,881	-0.0089 (0.0013)	3.18E-11	16,477	-0.0204 (0.0050)	3.80E-05	0.02
rs7956634 (T)	*PTPRO*	154,677	-0.0065 (0.0010)	1.11E-10	16,460	-0.0076 (0.0038)	4.82E-02	0.78
rs1106766 (T)	*INHBC*	138,058	0.0063 (0.0010)	1.75E-09	14,990	0.0016 (0.0040)	6.89E-01	0.25
rs11666497 (T)	*SIPA1L3*	148,770	-0.0058 (0.0011)	6.04E-08	15,831	-0.0096 (0.0041)	2.01E-02	0.37
rs6088580 (C)	*TP53INP2*	150,326	-0.0050 (0.0008)	1.51E-09	15,387	-0.0010 (0.0031)	7.48E-01	0.21
rs17216707 (T)	*BCAS1*	153,362	-0.0075 (0.0011)	2.25E-12	15,977	-0.0063 (0.0039)	1.06E-01	0.76
Known loci: sample size based on the discovery sample								
rs12917707 (T)	*UMOD*	118,365	0.0152 (0.0012)	4.68E-36	11,522	0.0266 (0.0048)	2.48E-08	0.02
rs1260326 (T)	*GCKR*	118,415	0.0065 (0.0009)	1.86E-12	11,525	0.0112 (0.0037)	2.21E-03	0.21
rs6465825 (T)	*SLC22A2*	118,448	0.0061 (0.0009)	4.80E-11	11,529	0.0089 (0.0036)	1.44E-02	0.45
rs2279463 (A)	*VEGFA*	118,368	0.0119 (0.0014)	6.98E-18	11,521	0.0062 (0.0053)	2.43E-01	0.30
rs12124078 (A)	*CASP9*	116,718	0.0058 (0.0010)	4.54E-09	11,315	0.0039 (0.0039)	3.18E-01	0.63
rs848490 (C)	*TMEM60*	112,566	0.0074 (0.0010)	1.35E-12	10,897	0.0033 (0.0041)	4.30E-01	0.33
rs2928148 (A)	*INO80*	118,368	0.0050 (0.0009)	2.82E-08	11,521	0.0026 (0.0035)	4.73E-01	0.50
rs9895661 (T)	*BCAS3*	118,188	0.0121 (0.0012)	2.80E-22	11,520	-0.0006 (0.0048)	9.00E-01	0.01
rs347685 (A)	*TFDP2*	118,374	-0.0077 (0.0010)	1.70E-14	11,522	-0.0021 (0.0040)	5.93E-01	0.17
rs7208487 (T)	*CDK12*	118,453	-0.0091 (0.0012)	8.60E-14	11,526	-0.0024 (0.0048)	6.20E-01	0.17

Supplementary Table 5 (continued).

SNP ID (effect allele)	Locus name	No Diabetes			Diabetes			P-value for difference*
		N	beta (SE)	P-value	N	beta (SE)	P-value	
Known loci: sample size based on the discovery sample								
rs10774021 (T)	*SLC6A13*	118,448	-0.0067 (0.0009)	1.48E-12	11,526	-0.0031 (0.0038)	4.13E-01	0.35
rs2453580 (T)	*SLC47A1*	117,386	0.0073 (0.0010)	2.56E-13	11,474	-0.0035 (0.0040)	3.93E-01	0.01
rs4744712 (A)	*PIP5K1B*	118,374	-0.0072 (0.0009)	7.45E-15	11,518	-0.0053 (0.0037)	1.48E-01	0.62
rs12460876 (T)	*SLC7A9*	118,361	-0.0065 (0.0009)	2.86E-12	11,521	-0.0062 (0.0037)	9.16E-02	0.94
rs881858 (A)	*SLC34A1*	118,324	-0.0081 (0.0011)	4.03E-14	11,521	-0.0063 (0.0042)	1.35E-01	0.68
rs10109414 (T)	*STC1*	118,342	-0.0075 (0.0009)	3.53E-16	11,521	-0.0066 (0.0036)	6.75E-02	0.81
rs6431731 (T)	*DDX1*	109,308	-0.0124 (0.0025)	4.70E-07	10,419	-0.0070 (0.0100)	4.89E-01	0.60
rs626277 (A)	*DACH1*	118,450	-0.0049 (0.0009)	1.44E-07	11,528	-0.0072 (0.0036)	4.53E-02	0.53
rs17319721 (A)	*SHROOM3*	118,359	-0.0113 (0.0009)	5.08E-35	11,522	-0.0075 (0.0036)	3.64E-02	0.30
rs13538 (A)	*ALMS1*	115,154	-0.0092 (0.0011)	2.79E-16	11,135	-0.0077 (0.0045)	8.45E-02	0.74
rs11959928 (A)	*DAB2*	118,359	-0.0082 (0.0009)	7.14E-19	11,521	-0.0078 (0.0036)	3.33E-02	0.91
rs2453533 (A)	*GATM*	118,374	-0.0125 (0.0009)	4.83E-41	11,520	-0.0079 (0.0036)	3.16E-02	0.21
rs7805747 (A)	*PRKAG2*	116,602	-0.0136 (0.0012)	1.53E-29	11,378	-0.0085 (0.0048)	7.37E-02	0.30
rs1394125 (A)	*UBE2Q2*	118,404	-0.0072 (0.0010)	5.83E-13	11,525	-0.0089 (0.0041)	2.92E-02	0.69
rs3925584 (T)	*MPPED2*	118,345	-0.0074 (0.0009)	5.35E-16	11,521	-0.0100 (0.0035)	5.00E-03	0.47
rs267734 (T)	*LASS2*	116,718	-0.0079 (0.0011)	2.81E-12	11,315	-0.0110 (0.0045)	1.39E-02	0.50
rs7422339 (A)	*CPS1*	115,499	-0.0106 (0.0011)	3.25E-22	11,422	-0.0137 (0.0043)	1.61E-03	0.48
rs10794720 (T)	*WDR37*	118,433	-0.0093 (0.0017)	4.95E-08	11,528	-0.0145 (0.0067)	3.06E-02	0.45
rs491567 (A)	*WDR72*	118,374	-0.0078 (0.0011)	1.45E-12	11,521	-0.0167 (0.0043)	1.25E-04	0.04

* P-value of a two-sample *t* test for correlated data (see Methods: “Associations Stratified by Diabetes and Hypertension Status“).

Supplementary Table 6. Association between replicated SNPs and additional kidney related phenotypes**.***

			Myocardial Infarction		Left Ventricular Mass		Incident Heart Failure		DBP		SBP		UACR		Fasting glucose	
SNPID	**Locus name**	**All.** [#]	**OR (95%CI)**	**P-value**	**beta (SE)**	**P-value**	**beta (SE)**	**P-value**	**beta (SE)**	**P-value**	**beta (SE)**	**P-value**	**beta(SE)**	**P-value**	**beta (SE)**	**P-value**
rs3850625	*CACNA1S*	A/G	1.03 (0.99,1.08)	0.15	0.390 (0.680)	0.57	-0.034 (0.044)	0.44	0.003 (0.094)	0.97	-0.068 (0.147)	0.64	0.017 (0.011)	0.11	0.012 (0.005)	0.013
rs2712184	*IGFBP5*	A/C	1.00 (0.97,1.03)	0.81	-0.183 (0.449)	0.68	-0.051 (0.034)	0.14	-0.087 (0.062)	0.16	-0.016 (0.098)	0.87	-0.001 (0.006)	0.88	-0.001 (0.003)	0.77
rs9682041	*SKIL*	T/C	0.99 (0.95,1.04)	0.79	-0.036 (0.639)	0.96	-0.003 (0.043)	0.95	-0.026 (0.093)	0.78	-0.092 (0.147)	0.53	-0.015 (0.009)	0.11	-0.006 (0.005)	0.18
rs10513801	*ETV5*	T/G	0.97 (0.94,1.01)	0.18	0.255 (0.649)	0.69	0.019 (0.044)	0.67	-0.021 (0.091)	0.82	0.004 (0.145)	0.98	0.027 (0.011)	0.014	0.002 (0.005)	0.71
rs10994860	*A1CF*	T/C	0.99 (0.96,1.03)	0.56	0.294 (0.595)	0.62	-0.081 (0.041)	0.05	-0.064 (0.081)	0.43	-0.162 (0.127)	0.20	-0.006 (0.009)	0.55	0.004 (0.004)	0.28
rs163160	*KCNQ1*	A/G	0.98 (0.95,1.02)	0.39	0.360 (0.577)	0.53	-0.063 (0.038)	0.10	-0.040 (0.082)	0.62	0.032 (0.129)	0.80	0.011 (0.010)	0.26	0.001 (0.004)	0.86
rs164748	*DPEP1*	C/G	0.99 (0.97,1.02)	0.65	0.668 (0.439)	0.13	0.062 (0.029)	0.04	0.173 (0.063)	0.01	0.361 (0.099)	0.00026[§]	0.021 (0.006)	0.0004	-0.003 (0.003)	0.30
rs8091180	*NFATC1*	A/G	NA	NA	0.307 (0.816)	0.71	0.056 (0.044)	0.21	0.122 (0.103)	0.23	0.181 (0.162)	0.27	-0.018 (0.015)	0.21	0.006 (0.005)	0.19
rs12136063	*SYPL2*	A/G	1.03 (1.00,1.06)	0.08	-0.192 (0.478)	0.69	0.023 (0.032)	0.47	0.032 (0.066)	0.62	-0.033 (0.104)	0.75	0.010 (0.008)	0.19	-0.007 (0.003)	0.05
rs2802729	*SDCCAG8*	A/C	NA	NA	-0.127 (0.470)	0.79	-0.005 (0.032)	0.88	0.147 (0.067)	0.03	0.239 (0.105)	0.02	0.008 (0.007)	0.23	0.002 (0.003)	0.53
rs4667594	*LRP2*	A/T	0.99 (0.97,1.02)	0.59	0.940 (0.440)	0.03	0.019 (0.029)	0.51	0.098 (0.062)	0.11	0.152 (0.097)	0.12	-0.008 (0.006)	0.18	0.000 (0.003)	0.89
rs6795744	*WNT7A*	A/G	0.98 (0.94,1.02)	0.27	0.298 (0.643)	0.64	-0.071 (0.045)	0.12	-0.022 (0.088)	0.80	-0.110 (0.139)	0.43	-0.005 (0.009)	0.57	0.005 (0.004)	0.30
rs228611	*NFKB1*	A/G	0.98 (0.95,1.01)	0.18	0.165 (0.440)	0.71	0.008 (0.028)	0.78	0.090 (0.061)	0.14	0.003 (0.097)	0.98	0.008 (0.006)	0.20	0.011 (0.003)	0.00026[§]
rs7759001	*ZNF204*	A/G	0.99 (0.96,1.02)	0.51	0.172 (0.524)	0.74	-0.031 (0.034)	0.36	-0.022 (0.071)	0.75	-0.085 (0.112)	0.45	0.002 (0.007)	0.83	0.006 (0.004)	0.10
rs10277115	*UNCX*	A/T	NA	NA	-1.058 (0.777)	0.17	0.012 (0.052)	0.82	-0.099 (0.141)	0.48	-0.232 (0.219)	0.29	0.013 (0.012)	0.27	-0.009 (0.006)	0.15
rs3750082	*KBTBD2*	A/T	0.99 (0.96,1.02)	0.48	0.641 (0.470)	0.17	-0.005 (0.031)	0.86	-0.024 (0.066)	0.72	0.094 (0.104)	0.37	0.019 (0.006)	0.0036	-0.001 (0.003)	0.88
rs6459680	*RNF32*	T/G	0.98 (0.95,1.01)	0.14	-0.234 (0.514)	0.65	-0.010 (0.034)	0.76	-0.155 (0.071)	0.03	-0.184 (0.112)	0.10	-0.001 (0.008)	0.90	0.002 (0.004)	0.60
rs4014195	*AP5B1*	C/G	0.98 (0.95,1.01)	0.20	-0.825 (0.458)	0.07	-0.052 (0.035)	0.14	-0.079 (0.064)	0.22	-0.176 (0.101)	0.08	0.007 (0.006)	0.29	0.001 (0.003)	0.70

Supplementary Table 6 (continued).

			Myocardial Infarction		Left Ventricular Mass		Incident Heart Failure		DBP		SBP		UACR		Fasting glucose	
SNPID	**Locus name**	**All.** #	**OR (95%CI)**	**P-value**	**beta (SE)**	**P-value**	**beta (SE)**	**P-value**	**beta (SE)**	**P-value**	**beta (SE)**	**P-value**	**beta(SE)**	**P-value**	**beta (SE)**	**P-value**
rs10491967	*TSPAN9*	A/G	0.95 (0.91,1.00)	0.04	0.087 (0.696)	0.90	-0.033 (0.047)	0.48	0.003 (0.101)	0.98	-0.205 (0.160)	0.20	0.002 (0.011)	0.86	-0.003 (0.005)	0.60
rs7956634	*PTPRO*	T/C	1.01 (0.98,1.05)	0.49	0.528 (0.564)	0.35	0.010 (0.036)	0.79	0.047 (0.083)	0.57	0.113 (0.130)	0.39	-0.017 (0.008)	0.03	0.006 (0.004)	0.17
rs1106766	*INHBC*	T/C	0.99 (0.96,1.02)	0.56	-0.322 (0.584)	0.58	0.027 (0.037)	0.46	0.069 (0.079)	0.39	0.093 (0.125)	0.46	0.011 (0.009)	0.22	-0.001 (0.004)	0.82
rs11666497	*SIPA1L3*	T/C	1.02 (0.98,1.05)	0.42	0.624 (0.590)	0.29	0.058 (0.041)	0.15	-0.056 (0.081)	0.49	-0.034 (0.127)	0.79	0.000 (0.008)	1.00	0.002 (0.004)	0.72
rs6088580	*TP53INP2*	C/G	1.02 (0.99,1.05)	0.14	-0.864 (0.456)	0.06	0.014 (0.028)	0.63	-0.126 (0.061)	0.04	-0.066 (0.097)	0.49	0.010 (0.006)	0.10	0.010 (0.003)	0.0016
rs17216707	*BCAS1*	T/C	1.02 (0.98,1.05)	0.40	0.238 (0.605)	0.69	0.038 (0.041)	0.35	0.136 (0.084)	0.11	0.195 (0.132)	0.14	-0.000 (0.009)	0.98	0.004 (0.004)	0.36

* ***Myocardial infarction***: results from CARDIoGRAM meta-analysis[8] of up to 14 studies, for a total sample size comprised between 72,649 and 83,231, except for SNPs rs4014195 (N=61,259) and rs2712184 (N=61,275). SNPs not reported did not pass CARDIoGRAM internal quality control checks and were not assessed. ***Left Ventricular Mass*****:** per-allele effect on left ventricular mass in grams, from a meta-analysis of five community-based studies within the EchoGen consortium, totaling 12,612 European ancestry individuals.[9] ***Incident heart failure***: CHARGE consortium meta-analysis on incident heart failure:[10] four studies on European ancestry individuals totaling a sample size of 20,926, except for SNPs rs2712184 and rs4014195 (N=13,282). ***DBP*** and ***SBP***: diastolic and systolic blood pressure results from the ICBP consortium:[11] meta-analysis of up to 43 studies, for a total sample size of 53,302 to 69,671 samples, except for SNPs rs10277115 (27 studies; N=17,644) and rs8091180 (21 studies; N=23,456). ***UACR***: urinary albumin-to-creatinine ratio, results from the CKDGen consortium (personal communication): meta-analysis of up to 29 studies, for a total sample size of 39,130 to 54,450. ***Fasting glucose***: per-allele effect on fasting glucose (mmol/L) not adjusted for BMI in 29 studies on up 58,074 non-diabetic participants of European ancestry.[12]

All.: first is the effect and second is the non-effect allele, respectively.

§ P-values that are significant at a Bonferroni corrected level of 0.0003, corresponding to 0.05 over 165 tests.

Supplementary Table 7. NHGRI GWAS catalog query of novel loci associated with different traits at a genome-wide significant level.

Locus name	Index SNP	Published SNP	Chr	Position (Build 37)	Region	LD (r^2)*	Disease or Quantitative Trait[REF]	P-value
SDCCAG8	rs2802729	rs6703335	1	243,608,967	1q43	0.44	Schizophrenia[13]	5.00E-08
ETV5	rs10513801	rs1516725	3	185,824,004	3q27.2	1.00	Body mass index[14]	4.00E-08
		rs1516725	3	185,824,004	3q27.2	1.00	Obesity[14]	3.00E-09
		rs7647305	3	185,834,290	3q27.2	0.39	Body mass index[15]	7.00E-11
		rs7647305	3	185,834,290	3q27.2	0.39	Weight[15]	4.00E-09
		rs9816226	3	185,834,499	3q27.2	0.49	Obesity[14]	2.00E-13
		rs9816226	3	185,834,499	3q27.2	0.49	Obesity[14]	2.00E-14
		rs9816226	3	185,834,499	3q27.2	0.49	Body mass index[16]	2.00E-18
NFKB1	rs228611	rs3774959	4	103,511,114	4q24	0.29	Ulcerative colitis[17]	4.00E-12
		rs7665090	4	103,551,603	4q24	0.87	Primary biliary cirrhosis[18]	4.00E-12
UNCX	rs10277115	rs10275044	7	1,273,845	7p22.3	0.73	Blood Urea Nitrogen[19]	4.00E-09
		rs10277115	7	1,285,195	7p22.3	1.00	eGRFcrea[19]	1.00E-10
		rs10277115	7	1,285,195	7p22.3	1.00	Serum creatinine[19]	5.00E-11
A1CF	rs10994860	rs10821905	10	52,646,093	10q11.23	1.00	Urate levels[20]	7.00E-17
AP5B1	rs4014195	rs479844	11	65,551,957	11q13.1	0.37	Atopic dermatitis[21]	1.00E-13
		rs642803	11	65,560,620	11q13.1	0.40	Urate levels[20]	3.00E-13
INHBC	rs1106766	rs11613352	12	57,792,580	12q13.3	1.00	HDL cholesterol[22]	2.00E-08
		rs11613352	12	57,792,580	12q13.3	1.00	Triglycerides[22]	4.00E-10
		rs1106766	12	57,809,456	12q13.3	1.00	Urate levels[23]	2.00E-11
		rs3741414	12	57,844,049	12q13.3	0.97	Urate levels[20]	2.00E-25
DPEP1	rs164748	rs154657	16	89,708,096	16q24.3	1.00	Homocysteine levels[24]	2.00E-43
		rs258322	16	89,755,903	16q24.3	0.30	Melanoma[25]	3.00E-27
		rs258322	16	89,755,903	16q24.3	0.30	Melanoma[26]	3.00E-27
		rs258322	16	89,755,903	16q24.3	0.30	Black vs. red hair color[27]	2.00E-23
		rs12921383	16	89,859,753	16q24.3	0.25	Homocysteine levels[24]	8.00E-11
		rs1805007	16	89,986,117	16q24.3	0.25	Hair color[28]	3.00E-09
		rs1805007	16	89,986,117	16q24.3	0.25	Non-melanoma skin cancer[28]	3.00E-10
		rs1805007	16	89,986,117	16q24.3	0.25	Sunburns[28]	2.00E-19
		rs1805007	16	89,986,117	16q24.3	0.25	Tanning[28]	1.00E-65
		rs1805007	16	89,986,117	16q24.3	0.25	Basal cell carcinoma[29]	4.00E-17
		rs1805007	16	89,986,117	16q24.3	0.25	Blond vs. brown hair color[30]	2.00E-13
		rs1805007	16	89,986,117	16q24.3	0.25	Freckles[30]	1.00E-96
		rs1805007	16	89,986,117	16q24.3	0.25	Red vs non-red hair color[30]	2.00E-142
		rs1805007	16	89,986,117	16q24.3	0.25	Skin sensitivity to sun[30]	2.00E-55
TP53INP2	rs6088580	rs2284378	20	32,588,095	20q11.22	0.25	Breast cancer[31]	1.00E-08
		rs4911414	20	32,729,444	20q11.22	0.25	Tanning[28]	4.00E-09
		rs4911414	20	32,729,444	20q11.22	0.25	Burning and freckling[32]	6.00E-37
		rs4911414	20	32,729,444	20q11.22	0.25	Freckles[32]	8.00E-29
		rs4911414	20	32,729,444	20q11.22	0.25	Red vs. non-red hair color[32]	3.00E-09
		rs4911414	20	32,729,444	20q11.22	0.25	Skin sensitivity to sun[32]	2.00E-24
		rs910873	20	33,171,772	20q11.22	0.21	Melanoma[33]	1.00E-15
		rs8114671	20	33,789,142	20q11.22	0.47	Height[14]	1.00E-15
		rs6088765	20	33,799,280	20q11.22	0.34	Ulcerative colitis[17]	2.00E-08

* LD between published and index SNPs**.**

Supplementary Table 8. Study sample characteristics, African ancestry meta-analysis**.**

Study	**Sample Size**	**European Ancestry % - change to median with 25/75th percentiles**	**Women %**	**Mean age** (years)	**Mean eGFRcrea** (ml/min/1.73 m^2)	**CKD %**
ARIC	2786	15.3 (10.7, 22.1)	63.1	53.3	100	3.7
CARDIA	821	16.7 (12.2, 23.2)	61.1	39.4	111	0.9
CHS	728	20.6 (12.4, 32.7)	62.8	72.9	81	18.4
JHS	2135	15.7 (11.8, 21.1)	60.8	50	101	4.2
MESA	1640	18.8 (11.5, 29.7)	54.8	62.2	87	8.6
GENOA	1217	12.6 (7.2, 18.9)	71.7	63.2	88	13.0
HANDLS	989	16.1 (11.2, 22.0)	55.0	48.4	121	5.3
Health ABC	1139	22.4 (12.2, 32.6)	57.2	73.4	76	17.1
HUFS	1013	19.7 (14.3, 27.0)	58.8	48.3	104	4.9
IPM	712	12.5 (7.1, 19.5)	60.0	59.7	76	36.4
SIGNET-Sea Islands	1275	7.0 (4.3, 11.7)	77.1	53.7	106	9.6
SIGNET-REGARDS	2385	14.8 (9.0, 22.9)	63.7	63	100	10.0

Abbreviations: eGFRcrea: estimated glomerular filtration rate by serum creatinine, CKD: chronic kidney disease.

Supplementary Table 9. Evaluation of replicated SNPs among individuals of Asian (AGEN) and the African Ancestry Renal meta-analysis**.**

Locus name	SNPID	Eff. All.	Non Eff. All.	AGEN Consortium[19]				African Ancestry Renal Meta-Analysis			
				N	Eff. All. Freq.	Beta (SE)	P-value	N	Ref. all freq.	Beta (SE)	P-value
SYPL2	rs12136063	A	G	36,057	0.90	-0.0004 (0.0021)	0.85	16,349	0.32	0.0049 (0.0036)	0.16
CACNA1S	rs3850625	A	G	41,963	0.09	-0.0012 (0.0019)	0.53	11,194	0.02	0.0127 (0.0135)	0.35
SDCCAG8	rs2802729	A	C	42,296	0.29	-0.0007 (0.0009)	0.42	15,461	0.47	-0.0007 (0.0036)	0.85
LRP2	rs4667594	A	T	40,415	0.13	-0.0015 (0.0013)	0.24	15,417	0.61	-0.0016 (0.0034)	0.63
IGFBP5	rs2712184	A	C	40,415	0.51	-0.0025 (0.0008)	0.0024	16,210	0.48	-0.0023 (0.0034)	0.50
WNT7A	rs6795744	A	G	42,296	0.11	-0.0001 (0.0016)	0.94	16,420	0.21	0.0032 (0.0043)	0.46
SKIL	rs9682041	T	C	42,296	0.91	-0.0047 (0.0018)	0.0074	15,460	0.75	-0.0005 (0.0041)	0.91
ETV5	rs10513801	T	G	37,250	0.93	0.0006 (0.0026)	0.82	14,243	0.95	-0.0006 (0.0100)	0.95
NFKB1	rs228611	A	G	42,296	0.52	-0.0001 (0.0008)	0.88	16,450	0.24	0.0042 (0.0040)	0.29
ZNF204	rs7759001	A	G	40,415	0.62	-0.0005 (0.0008)	0.56	16,435	0.87	0.0044 (0.0050)	0.38
UNCX	rs10277115	A	T	40,415	0.65	0.0066 (0.0011)	7.30E-10	11,801	0.70	0.0059 (0.0060)	0.32
KBTBD2	rs3750082	A	T	39,440	0.32	0.0012 (0.0009)	0.19	15,461	0.67	0.0070 (0.0039)	0.07
RNF32	rs6459680	T	G	40,415	0.62	-0.0005 (0.0009)	0.56	16,435	0.54	0.0049 (0.0034)	0.15
A1CF	rs10994860	T	C	41,963	0.10	0.0014 (0.0017)	0.42	15,461	0.22	0.0060 (0.0045)	0.18
KCNQ1	rs163160	A	G	40,415	0.83	0.0022 (0.0011)	0.04	16,467	0.93	0.0053 (0.0067)	0.43
AP5B1	rs4014195	G	C	40,415	0.20	-0.0040 (0.0010)	0.00012	15,297	0.22	-0.0014 (0.0042)	0.74
TSPAN9	rs10491967	A	G	40,415	0.45	-0.0013 (0.0008)	0.13	15,460	0.40	0.0072 (0.0043)	0.09
PTPRO	rs7956634	T	C	40,415	0.68	-0.0020 (0.0009)	0.03	16,403	0.50	-0.0082 (0.0033)	0.01
INHBC	rs1106766	T	C	42,296	0.11	0.0003 (0.0015)	0.85	16,415	0.10	-0.0008 (0.0057)	0.89
DPEP1	rs164748	G	C	39,164	0.08	0.0016 (0.0024)	0.49	16,471	0.11	0.0025 (0.0055)	0.65
NFATC1	rs8091180	A	G	40,415	0.83	-0.0004 (0.0011)	0.69	3,838	0.20	-0.0021 (0.0101)	0.84
SIPA1L3	rs11666497	T	C	40,415	0.12	-0.0027 (0.0013)	0.03	16,422	0.07	0.0023 (0.0064)	0.72
TP53INP2	rs6088580	G	C	36,275	0.64	0.0007 (0.0009)	0.45	NA	NA	NA	NA
BCAS1	rs17216707	T	C	35,492	0.86	-0.0012 (0.0018)	0.52	15,399	0.94	-0.0049 (0.0073)	0.50

Supplementary Table 10. Transethnic meta-analysis of CKDGen and the African Ancestry Renal Meta-Analysis**.***

SNPID	Locus name	Chr.	Effect Allele	Non-Effect Allele	log10BF#	Posterior Probability
rs17216707	*BCAS1*	20	T	C	11.63	0.038
rs4014195	*AP5B1*	11	C	G	9.66	0.025
rs10994860	*A1CF*	10	T	C	9.52	0.025
rs7956634	*PTPRO*	12	T	C	9.07	0.015
rs10277115	*UNCX*	7	A	T	8.84	0.023
rs228611	*NFKB1*	4	A	G	7.65	0.07
rs6088580	*TP53INP2*	20	C	G	7.44	0.021
rs163160	*KCNQ1*	11	A	G	7.38	0.026
rs3850625	*CACNA1S*	1	A	G	7.34	0.046
rs6795744	*WNT7A*	3	A	G	7.04	0.046
rs10491967	*TSPAN9*	12	A	G	6.93	0.725
rs2712184	*IGFBP5*	2	A	C	6.72	0.021
rs3750082	*KBTBD2*	7	A	T	6.65	0.01
rs6459680	*RNF32*	7	T	G	6.42	0.701
rs12136063	*SYPL2*	1	A	G	6.18	0.012
rs2802729	*SDCCAG8*	1	A	C	6.00	0.021
rs10513801	*ETV5*	3	T	G	5.88	0.03
rs164748	*DPEP1*	16	C	G	5.83	0.045
rs4667594	*LRP2*	2	A	T	5.72	0.027
rs11666497	*SIPA1L3*	19	T	C	5.72	0.031
rs1106766	*INHBC*	12	T	C	5.56	0.053
rs7759001	*ZNF204*	6	A	G	5.23	0.051
rs9682041	*SKIL*	3	T	C	5.04	0.032
rs8091180	*NFATC1*	18	A	G	4.87	0.044

*The analysis was performed using the MANTRA (Meta-Analysis of Trans-ethnic Association studies) software.[34] The posterior probability is a measure of heterogeneity of allelic effects across the individual studies.

#Log_{10} Bayes Factor

Supplementary Table 11. SNP associations with transcript expression.*****

Locus name; index SNP	*eSNP*									*Best eSNP*			
	eSNP rsID	*Dist. index SNP*	*r^2*	*eQTL tissue[REF]*	*P-value*	*Chr*	*position*	*Probe**	*Transcript***	*Best eSNP rsID*	*P-value*	*r^2 to eSNP*	*r^2 to index SNP*
SYPL2 rs12136063	rs12136063	0	1.00	Prefrontal cortex - all samples[35]	1.3E-05	1	109,815,693	10031920561	SYPL2	rs12136063	1.3E-05	Same	Same
	rs10494040	1,562	1.00	SubCutAdipose[36]	6.5E-50	1	109,817,255	10031920561	SYPL2	rs10494040	6.5E-50	Same	0.96
	rs10494040	1,562	1.00	Liver[36]	5.4E-47	1	109,817,255	10031920561	SYPL2	rs10494040	5.4E-47	Same	0.96
	rs10857787	3,881	1.00	Liver[37]	2.9E-35	1	109,811,812		SYPL2	rs10857787	2.9E-35	Same	0.96
	rs4970767	1,013	1.00	Liver (UChicago)[38]	8.9E-16	1	109,816,706	A_23_P317200	ATXN7L2	rs4970767	8.9E-16	Same	0.96
	rs10494040	1,562	1.00	OmentalAdipose[36]	9.4E-13	1	109,817,255	10031920561	SYPL2	rs10494040	9.4E-13	Same	0.96
	rs10494040	1,562	1.00	Liver[39]	1.1E-12	1	109,817,255		SYPL2	rs10494040	1.1E-12	Same	0.96
	rs4970767	1,013	1.00	Liver (UWash)[38]	3.3E-02	1	109,816,706	5360451	ATXN7L2	rs4970767	3.3E-02	Same	0.96
	rs4970729	34,968	0.92	Liver[36]	2.3E-24	1	109,780,725	10025910902	PSMA5	rs4970729	2.3E-24	Same	0.89
	rs12073497	39,720	0.92	Liver[36]	6.2E-09	1	109,775,973	10023805980	Contig42599_RC	rs12073497	6.2E-09	Same	0.89
	rs12073497	39,720	0.92	Visual cortex - all samples[35]	3.1E-06	1	109,775,973	10031920561	SYPL2	rs12073497	3.1E-06	Same	0.89
	rs4970729	34,968	0.92	Cerebellum - all samples[35]	1.1E-05	1	109,780,725	10025932473	AMIGO1	rs4970729	1.1E-05	Same	0.89
	rs2781553	12,819	0.85	Liver[36]	4.8E-05	1	109,828,512	10025909878	PRPF38B	rs2781553	4.8E-05	Same	0.85
SDCCAG8 rs2802729	rs2802723	3,451	1.00	Periph artery plaque‡	4.1E-07	1	241,564,935	100142973_TGI_at	SDCCAG8	rs2802723	4.1E-07	Same	1.00
	rs2490395	42,841	0.83	Blood[40]	9.2E-06	1	241,525,545	460458	SDCCAG8	rs2490395	9.2E-06	Same	0.83
	rs2484639	39,396	0.81	Visual cortex - all samples[35]	3.2E-07	1	241,528,990	10025912019	SDCCAG8	rs2484639	3.2E-07	Same	0.80
NFKB1 rs228611	rs228611	0	1.00	LCL MuTHER [41]	1.6E-19	4	103,780,757	ILMN_1800733	MANBA	rs228611	1.6E-19	Same	Same
	rs228611	0	1.00	Prefrontal cortex (Huntington's)[35]	1.4E-08	4	103,780,757	10025907439	MANBA	rs228611	1.4E-08	Same	Same
	rs228611	0	1.00	Lymphocytes[42]	2.0E-08	4	103,780,757		MANBA	rs228611	2.0E-08	Same	Same
	rs228611	0	1.00	Visual cortex (Alzheimer's)[35]	5.6E-05	4	103,780,757	10025907439	MANBA	rs228611	5.6E-05	Same	Same
	rs228611	0	1.00	Cerebellum - all samples[35]	6.7E-02	4	103,780,757	10025907439	MANBA	rs228611	6.7E-02	Same	Same
	rs909349	5,393	0.97	Monocytes[43]	2.5E-121	4	103,775,364		MANBA	rs909349	2.5E-121	Same	0.97
	rs7665090	10,106	0.97	OmentalAdipose[36]	6.5E-42	4	103,770,651	10025907439	MANBA	rs7665090	6.5E-42	Same	0.97
	rs228611	0	1.00	Blood[40]	1.3E-30	4	103,780,757	4230168	MANBA	rs7665090	3.9E-37	0.97	0.97
	rs7665090	10,106	0.97	Prefrontal cortex - all samples[35]	2.4E-26	4	103,770,651	10025907439	MANBA	rs7665090	2.4E-26	Same	0.97

Supplementary Table 11 (continued).

Locus name; index SNP	*eSNP*									*Best eSNP*			
	eSNP rsID	*Dist. index SNP*	*r^2*	*eQTL tissue^{REF}*	*P-value*	*Chr*	*position*	*Probe**	*Transcript***	*Best eSNP rsID*	*P-value*	*r^2 to eSNP*	*r^2 to index SNP*
NFKB1 rs228611	rs228614	16,928	0.91	Blood[40]	2.0E-22	4	103,797,685	4230168	MANBA	rs7665090	3.9E-37	0.87	0.97
	rs2866413	4,632	0.97	Prefrontal cortex - all samples[35]	5.8E-17	4	103,776,125	10025907439	MANBA	rs7665090	2.4E-26	1	0.97
	rs2866413	4,632	0.97	Visual cortex - all samples[35]	5.8E-08	4	103,776,125	10025907439	MANBA	rs2866413	5.8E-08	Same	0.97
	rs228614	16,928	0.91	Blood[44]	2.1E-05	4	103,797,685	HSG00228144	MANBA	rs228614	2.1E-05	Same	0.91
	rs404574	21,499	0.90	SubCutAdipose MuTHER[41]	1.7E-14	4	103,802,256	ILMN_1800733	MANBA	rs404574	1.7E-14	Same	0.84
	rs7674640	20,929	0.81	Lung[45]	<2E-16	4	103,759,828	100150393_TGI_at	CISD2	rs7674640	<2E-16	Same	0.81
ZNF204 rs7759001	rs7759001	0	1.00	Intestine normal ileum[46]	1.3E-10	6	27,341,409		ZNF391	rs7759001	1.3E-10	Same	Same
	rs7759001	0	1.00	Cerebellum - normal samples[35]	5.5E-09	6	27,449,388	10025913649	BC035154	rs7759001	5.5E-09	Same	Same
	rs2143062	12,443	1.00	Cerebellum (Alzheimer's)[35]	1.6E-11	6	27,461,831	10025913649	BC035154	rs2143062	1.6E-11	Same	1.00
	rs2143062	12,443	1.00	Prefrontal cortex (Huntington's)[35]	1.4E-05	6	27,461,831	10025913649	BC035154	rs2143062	1.4E-05	Same	1.00
	rs9368508	19,561	1.00	Cerebellum (Huntington's)[35]	3.4E-06	6	27,429,827	10025913649	BC035154	rs9368508	3.4E-06	Same	0.95
	rs10755644	4,696	1.00	SubCutAdipose[36]	7.0E-05	6	27,444,692	10025933640	ZNF391	rs10755644	7.0E-05	Same	0.90
	rs10807021	15,516	0.95	OmentalAdipose[36]	1.5E-08	6	27,464,904	10025913649	BC035154	rs10807021	1.5E-08	Same	0.86
	rs4713086	9,037	0.95	Periph artery plaque‡	1.9E-07	6	27,458,425	100139132_TGI_at	BC035154	rs4713086	1.9E-07	Same	0.86
	rs980963	19,528	0.86	Cerebellum - all samples[35]	2.3E-05	6	27,468,916	10025933640	ZNF391	rs980963	2.3E-05	Same	0.86
	rs10807020	15,493	0.95	Cerebellum - normal samples[35]	5.3E-05	6	27,464,881	10025907341	NM_178534	rs10807020	5.3E-05	Same	0.86
	rs10807021	15,516	0.95	Visual cortex - all samples[35]	1.3E-03	6	27,464,904	10025908866	ZNF184	rs10807021	1.3E-03	Same	0.86
KBTBD2 rs3750082	rs6462431	15,512	0.93	Blood[40]	2.3E-38	7	32,901,964	4920372	KBTBD2	rs6462431	2.3E-38	Same	0.89
	rs3750082	0	1.00	LCL asthmatics [47]	8.1E-17	7	32,886,452	212447_at	KBTBD2	rs7785065	8.1E-17	0.89	0.89
	rs3750082	0	1.00	LCL MuTHER[41]	1.1E-06	7	32,886,452	ILMN_1784540	KBTBD2	rs13230763	8.3E-08	0.80	0.89
	rs2392152	19,378	0.89	Liver[37]	2.0E-10	7	32,867,074		HSS00226368	rs2392152	2.0E-10	Same	0.85
	rs4723221	34,280	0.82	Lung[45]	6.4E-08	7	32,920,732	100132413_TGI_at	KBTBD2	rs4723221	6.4E-08	Same	0.82

Supplementary Table 11 (continued).

Locus name; index SNP	*eSNP*									*Best eSNP*			
	eSNP rsID	*Dist. index SNP*	*r^2*	*eQTL tissue[REF]*	*P-value*	*Chr*	*position*	*Probe**	*Transcript***	*Best eSNP rsID*	*P-value*	*r^2 to eSNP*	*r^2 to index SNP*
AP5B1 rs4014195	rs11227281	10,264	1.00	Intestine -normal ileum[46]	3.8E-05	11	65,496,558		EIF1AD	rs11227281	3.8E-05	Same	1.00
	rs11604451	44,888	1.00	LCL (Degner - DNAse QTLs)[48]	2.9E-04	11	65,308,286		DNAse QTL 65308500-65308600	rs11604451	2.9E-04	Same	1.00
PTPRO rs7956634	rs2193172	11,148	1.00	Liver (UChicago)[38]	6.6E-03	12	15,223,609	A_23_P204304	PTPRO	rs2193172	6.6E-03	Same	1.00
INHBC rs1106766	rs1106766	0	1.00	ER+ breast tumor cells[49]	7.7E-06	12	56,095,723		GLS2	rs11614506	3.4E-07	0.80	0.80
DPEP1 rs164748	rs164749	68	1.00	Liver[37]	2.5E-09	16	88,235,725		C16orf55 (SPATA33)	rs164749	2.5E-09	Same	1.00
	rs460879	4,597	1.00	Prefrontal cortex (Huntington's)[35]	3.0E-08	16	88,240,390	10025907286	C16orf55 (SPATA33)	rs460879	3.0E-08	Same	1.00
	rs460879	4,597	1.00	OmentalAdipose[36]	2.7E-06	16	88,240,390	10025902450	CHMP1A	rs460879	2.7E-06	Same	1.00
	rs154657	196	1.00	Periph artery plaque‡	1.7E-05	16	88,235,597	100143418_TGI_at	SPATA2L	rs154657	1.7E-05	Same	1.00
	rs460879	4,597	1.00	Cerebellum (Huntington's)[35]	3.1E-05	16	88,240,390	10025902450	CHMP1A	rs460879	3.1E-05	Same	1.00
	rs459920	22,535	0.97	OmentalAdipose[36]	3.7E-44	16	88,258,328	10025907286	C16orf55 (SPATA33)	rs459920	3.7E-44	Same	0.97
	rs459920	22,535	0.97	SubCutAdipose[36]	1.2E-30	16	88,258,328	10025907286	C16orf55 (SPATA33)	rs459920	1.2E-30	Same	0.97
	rs459920	22,535	0.97	Cerebellum -all samples[35]	1.8E-30	16	88,258,328	10025907286	C16orf55 (SPATA33)	rs459920	1.8E-30	Same	0.97
	rs459920	22,535	0.97	Prefrontal cortex - all samples[35]	4.8E-23	16	88,258,328	10025907286	C16orf55 (SPATA33)	rs459920	4.8E-23	Same	0.97
	rs459920	22,535	0.97	Liver[36]	2.1E-21	16	88,258,328	10025907286	C16orf55 (SPATA33)	rs459920	2.1E-21	Same	0.97
	rs459920	22,535	0.97	Visual cortex -all samples[35]	2.7E-17	16	88,258,328	10025907286	C16orf55 (SPATA33)	rs459920	2.7E-17	Same	0.97
	rs2115401	32,317	0.97	Peripheral artery plaque‡	3.6E-07	16	88,268,110	100138862_TGI_at	C16orf55 (SPATA33)	rs2115401	3.6E-07	Same	0.97
	rs467035	31,993	0.97	Peripheral artery plaque‡	6.0E-06	16	88,267,786	100131451_TGI_at	SNAI3	rs467035	6.0E-06	Same	0.97
	rs258319	23,732	0.97	Temporal cortex[50]	4.8E-05	16	88,259,525	ILMN_1759261	C16orf55 (SPATA33)	rs258319	4.8E-05	Same	0.97
	rs2115401	32,317	0.97	Liver (UWash)[38]	1.7E-04	16	88,268,110	1300411	C16orf55 (SPATA33)	rs2115401	1.7E-04	Same	0.97

Supplementary Table 11 (continued).

Locus name; index SNP	*eSNP*									*Best eSNP*			
	eSNP rsID	*Dist. index SNP*	*r^2*	*eQTL tissue^{REF}*	*P-value*	*Chr*	*position*	*Probe**	*Transcript***	*Best eSNP rsID*	*P-value*	*r^2 to eSNP*	*r^2 to index SNP*
DPEP1 rs164748	rs2115401	32,317	0.97	Liver (UChicago)[38]	<1e-16	16	88,268,110	A_24_P159335	C16orf55 (SPATA33)	rs2115401	<1e-16	Same	0.97
	rs459920	22,535	0.97	Liver (UChicago)[38]	<1e-16	16	88,258,328	A_23_P106694	CHMP1A	rs459920	<1e-16	Same	0.97
TP53INP2 rs6088580	rs2273684	244,713	0.94	Blood[40]	7.6E-08	20	32,993,427	7150537	ACSS2	rs2273684	7.6E-08	Same	0.94
	rs2273684	244,713	0.94	Blood[40]	1.5E-06	20	32,993,427	2680161	GSS	rs2273684	1.5E-06	Same	0.94
	rs6059909	145,362	0.84	Lymphocytes[51]	2.2E-03	20	32,603,352	GI_31563517-A	MAP1LC3A	rs6059909	2.2E-03	Same	0.81

* Expression QTL results were identified for our index SNPs or their proxies within the following dataset sources: whole blood samples,[40, 44] Epstein-Barr transformed B-lymphoblastoid cell lines (LCL) from population samples,[41, 42, 47] DNase-I QTLs in LCLs,[48] fresh lymphocytes,[51] peripheral blood monocytes,[43] ER+ breast cancer tumor cells,[49] omental and/or subcutaneous adipose,[36, 41] peripheral artery plaque intestine,[46] lung,[45] brain,[35, 50] and liver.[36-39]

‡ Unpublished (Emilsson)

Supplementary Table 12. Background information on novel replicated loci**.**

SNPID (Locus name)	Evidence from functional databases		Gene prioritized for functional work	Description of Genes in each Region*
	Source	Gene		
rs228611 (*NFKB1*)	**eSNP**	*MANBA*	*NFKB1* closest gene	*MANBA* encodes beta-mannosidase, a lysosomal enzyme that catalyzes the final exoglycosidase step in the degradation pathway for N-linked oligosaccharide moieties of glycoproteins (RefSeq). Rare mutations have been identified as the cause for beta-mannosidosis (OMIM #248510). A mouse model has linked *MANBA* to lysosomal storage disease in multiple organs, including the kidney.[52] *NFKB1* encodes a pleiotropic transcription factor that is present in almost all cell types and is the endpoint of a series of signal transduction events that are initiated by a vast array of stimuli related to many biological processes such as inflammation, immunity, differentiation, cell growth, tumorigenesis and apoptosis (RefSeq).
	GRAIL	NO		
	DEPICT	NO		
rs7759001 (*ZNF204*)	**eSNP**	NA	NO	ZNF204 is known as a transcribed pseudogene (RefSeq). ZNF391 and ZNF184 are two neighboring zinc finger protein-coding genes (RefSeq). Little is known about other nearby genes in the region.
	GRAIL	NO		
	DEPICT	NO		
rs1106766 (*INHBC*)	**eSNP**	NO	NO	*R3HDM2* encodes a protein with R3H domain. *INHBC* encodes the beta C chain of inhibin, which forms heterodimers with beta A and beta B subunits. Inhibins are involved in hormonal secretion and growth and differentiation of various cell types (RefSeq). *GLI1* encodes a transcription factor that is activated by the sonic hedgehog signal transduction cascade that regulates stem cell proliferation (RefSeq). The hedgehog-GlI pathway has been implicated in kidney fibrosis in mouse studies.[53] *ARHGAP9* encodes a member of the Rho-GAP family of GTPase activating proteins, converting them to an inactive GDP-bound state (RefSeq).
	GRAIL	NO		
	DEPICT	NO		
rs10513801 (*ETV5*)	**eSNP**	NA	NO	The *ETV5* gene is a ubiquitously expressed transcription factor. A role in renal development has been shown in a mouse model[54]. In humans, it has not yet been connected to kidney disease. *DGKG* encodes diacylglycerol Kinase, Gamma, a glycerol kinase that metabolizes 1,2,diacylglycerol to produce the second messenger phosphatidic acid. The transcript is expressed in kidney.
	GRAIL	NO		
	DEPICT	NO		
rs3850625 (*CACNA1S*)	**eSNP**	NA	NO	*CACNA1S* encodes one of five subunits of the slowly inactivating L-type voltage-dependent calcium channel, which plays a role in skeletal muscle contraction. Known mutations in *CACNA1S* have been associated with susceptibility to malignant hyperthermia, hypokalemic periodic paralysis, and thyrotoxic periodic paralysis. The identified variant is a non-synonymous coding SNP at a highly conserved position (R1539C on protein level) that is predicted as damaging or pathogenic by 3 out of 4 prediction software.
	GRAIL	NO		
	DEPICT	NO		
rs10491967 (*TSPAN9*)	**eSNP**	NA	*TSPAN9*	*TSPAN9* encodes for a member of the tetraspanin family, which assemble in complexes with additional proteins such as integrins to transduct signals. Its association to renal function is unclear; mutations in some integrins cause monogenic kidney disease, as do mutations in the gene paralog CD151. Other genes in the region have not specifically been connected to kidney disease.
	GRAIL	NO		
	DEPICT	*TSPAN9* FDR<0.05		

Supplementary Table 12 (continued).

SNPID (Locus name)	Evidence from functional databases		Gene prioritized for functional work	Description of Genes in each Region*
	Source	**Gene**		
rs164748 (*DPEP1*)	**eSNP**	*C16orf55* (also known as *SPATA33*)	*DPEP1*	*DPEP1* encodes dipeptidase 1, an enzyme responsible for hydrolysis of glutathione and certain types of antibiotics in the kidney membrane[55,56] and is highly expressed in the kidney and pancreas (GeneCards), but there are no studies linking this gene to kidney function. *RPL13* encodes ribosomal protein L13, a protein within the large 60S ribosomal subunit complex[57]. There are no publications linking RPL13 to the kidney or kidney function. *SNORD68* encodes small nucleolar RNA C/D box 68 a class molecules that modify other RNAs. This particular class of snoRNA is responsible for RNA methylation. There are no known connections to kidney function or disease. *SPG7* encodes paraplegin, an enzyme component of m-AAA protease (a mitochondrial enzyme responsible for degradation of malformed or misfolded proteins).[58] Mutations in the *SPG7* gene lead to monogenic forms of spastic paraplegia.[59, 60, 60, 61, 61] There are no reported studies linking *SPG7* and kidney function. *ANKRD11* encodes ankyrin repeat domain protein 11, a protein inhibiting ligand-dependent activation of transcription. Variation in *ANKRD11* can lead to KBG syndrome (a disorder with abnormal skeletal development and delay in neurological development.[62, 63, 63] No associations of *ANKRD*11 and kidney function have been published. *C16orf55* (also known as *SPATA33*) encodes spermatogenesis-associated protein 33 and is thought to be involved in spermatogenesis. No associations with kidney disease have been identified.
	GRAIL	NO		
	DEPICT	DPEP1 FDR<0.05		
rs8091180 (*NFATC1*)	**eSNP**	NA	*NFATC1*	*NFATC1* encodes for nuclear factor of activated T-cells (cytoplasmic, calcineurin dependent 1) and is a part of a complex involved in the activation of immune response, specifically activation of the T-cell antigen receptor.[64] In rodents, *NFAT1C* is potentially involved in proximal tubules after injury[65] and activation of this nuclear factor may lead to glomeruloscerosis by mutant forms of *TRPC6* - a podocyte protein involved in maintaining the filtration barrier.[66] *NFAT*1C has not been linked with kidney function in humans. *ATP9B* encodes an ATPase, class II, type 9b - a transmembrane transporter. No association with kidney disease has been previously reported. *CTDP1* encodes the c-terminal domain of RNA polymerase II subunit A phosphatase. Variations in *CTDP1* have been associated with congenital cataracts, facial dimorphism and neuropathy in Bulgarian gypsy populations.[67] There have been no previous reports of *CTDP1* and kidney disease.
	GRAIL	*NFATC1* p=0.03		
	DEPICT	NO		
rs11666497 (*SIPA1L3*)	**eSNP**	NA	NO	*SIPA1L3* encodes the signal-induced proliferation-associated 1 like 3 protein. There are no published reports in the literature describing this gene or its protein product. *WDR87* encodes the WD repeat-containing protein 87, a protein 2.8K amino acids in length. There are no published reports of this gene or gene product in the literature.
	GRAIL	NO		
	DEPICT	NO		

Supplementary Table 12 (continued).

SNPID (Locus name)	Evidence from functional databases		Gene prioritized for functional work	Description of Genes in each Region*
	Source	**Gene**		
rs4667594 (*LRP2*)	**eSNP**	NA	NO	*LRP2* encodes the megalin receptor, which plays an important role in the reabsorption of albumin and other low-molecular-weight proteins[68] along with cubilin (*CUBN*) and amnionless (*AMN*). *LRP2* mutations are associated with Donnai-Barrow and facio-oculo-acoustico-renal syndromes.[69] *DHRS9* is a protein-coding gene that encodes dehydrogenase/reductase member 9 (GeneCards). It is a 3-alpha-hydroxysteroid dehydrogenase that is responsible for the synthesis of dihydroxyprotesterone; low levels of activity with retinoids have also been identified (UCSC). There are no published studies linking this gene to kidney function. *ABCB11* belongs to the ATP-binding cassette superfamily. The protein is involved in bile salt export (www.genecards.org), and mutations are involved in familial intrahepatic cholestasis (OMIM). In addition, this gene may be involved with bile acid transport in the kidney.[70]
	GRAIL	*LRP2* p=0.0004		
	DEPICT	*LRP2* FDR<0.05		
rs6795744 (*WNT7A*)	**eSNP**	NA	*WNT7A* closest gene	*WNT7A* is a member of set of genes that are signaling proteins, specifically those that are involved in embryogenesis (www.genecards.org). Mutations in this gene have been associated with Fuhrmann syndrome (OMIM #228930) and the Al-Awadi/Raas-Rothschild/Schinzel phocomelia syndrome (AARRS; OMIM #276820), disorders characterized by limb malformation. Wnt-7a signalling may allow for the development of sexual dimorphism via development of the mullerian ducts.[71] *TPRXL* is a homeobox gene thought to be involved in embryonic development (GeneCards). There are no published papers linking this gene to kidney function. Of the remaining genes in the region, only *XPC* has been previously linked to kidney function in the published literature. *XPC* is a DNA repair gene. Mutations result in Xeroderma pigmentosum, a disease characterized by sunlight sensitivity and early carcinomas. Mutations in *XPC* may be associated with renal cell carcinoma.[72]
	GRAIL	NO		
	DEPICT	NO		
rs7956634 (*PTPRO*)	**eSNP**	*PTPRO*	*PTPRO* closest gene	*RERG* belongs to the RAS superfamily and is involved with cell proliferation and tumor pathogenesis (GeneCards). *RERG* expression may be lost in kidney cancer.[73] *PTPRO* is expressed in the podocyte foot processes of the kidney; mutations in *PTPRO* are associated with autosomal-recessive nephrotic syndrome.[74] Knock-out mice display reduced eGFR but no proteinuria[75]. *EPS8 i*s an epidermal growth factor receptor pathway substrate gene (GeneCards). Eps8 proteins are involved in the organization of actin filaments.[76]
	GRAIL	NO		
	DEPICT	NO		
rs10277115 (*UNCX*)	**eSNP**	NA	*UNCX* (no other genes in the LD block)	*UNCX* is a transcription factor that is involved in neurogenesis and somitogenesis (GeneCards). In addition, it may be involved in differentiation of the axial skeleton (GeneCards). There is no published literature linking it to kidney function. *ZFAND2A* is a protein coding gene involved in zinc ion binding (GeneCards). It has been shown to be part of a network of genes expressed in human renal epithelial cells in response to cadium exposure, a known nephrotoxin.[77] *GPER* is a member of the G-protein coupled receptor family with a primary role of binding estrogen (GeneCards). *GPER* may mediate the effects of estrogen (but not aldosterone)[78] on the vasculature[79] including the rat kidney.[80] *GPER* binds estrogen in addition to other substances including endocrine disruptors.[81]
	GRAIL	NO		
	DEPICT	NO		

Supplementary Table 12 (continued).

SNPID (Locus name)	Evidence from functional databases		Gene prioritized for functional work	Description of Genes in each Region*
	Source	Gene		
rs12136063 (*SYPL2*)	**eSNP**	*SYPL2*	*SYPL2*	*SYPL2* encodes synaptophysin-like 2 protein (also known as mitsugumin 29), a membrane protein involved in the communication between the transverse tubular and junctional sarcoplasmatic reticulum membranes (Entrez Gene). It is expressed in the kidney (www.proteinatlas.org). There are no publications linking this gene to kidney function. *PSMA5* encodes proteasome (prosome, macropain) subunit alpha type 5, which is a proteosome involved in the processing of MHC class I peptides (Entrez Gene) and is expressed in many tissues including the kidney (ProteinAtlas). There are no publications linking this gene to kidney function. There is no disease linked to this gene in OMIM. *ATXN7L2* encodes for ataxin 7-like 2 protein (GeneCards), which is expressed in several tissues including the kidney (ProteinAtlas). There is no publication linking this gene to kidney function. *AMIGO1* encodes adhesion molecule with Ig-like domain 1, which is part of a family of transmembrane proteins involved in axon tract development.[82] It is expressed in the kidney. *CELSR2* encodes cadherin EGF LAG seven-pass G-type receptor 2, which is a member of the flamingo subfamily cadherins which does not interact with catenins (Entrez Gene). It is a plasma membrane protein postulated to be involved in contact-mediated communication and expressed in many tissues including the kidney.
	GRAIL	NO		
	DEPICT	*SYPL2* FDR<0.05		
rs2802729 (*SDCCAG8*)	**eSNP**	*SDCCAG8*	NO	*SDCCAG8* encodes serologically defined colon cances antigen 8, a centrosome associated protein involved in interphase and mitosis (Entrez Gene). Truncating mutations cause Senior-Loken syndrome 7 (OMIM #613615), an autosomal recessive ciliopathy with nephronophthisis and Leber congenital amaurosis. *CEP170* encodes centrosomal protein 170kDa, which is the major microtubule-organizing center in animals (Entrez Gene). It is expressed in several tissues including the kidney, but has not been linked to kidney function in any publication. *AKT3* encodes v-akt murine thymoma viral oncogene homolog 3, which is a kinase regulating cell signaling in response to insulin and rowth factors; it is stimulated by PDGF, insulin and IGF-1 (Entrez Gene). It shows low-level expression in the kidney (ProteinAtlas). Rare mutations cause megalencephaly-polymicrogyria-polydactyly-hydrocephalus syndrome (MPPH, OMIM #603387), which does not show organ involvement beyond central nervous defects. There are no publications linking this gene to kidney function.
	GRAIL	NO		
	DEPICT	NO		
rs17216707 (*BCAS1*)	**eSNP**	NA	*BCAS1* but no fish orthologs	*BCAS1* encodes breat carcinoma amplified sequence 1, which has been implicated as a breast cancer oncogene (Entrez Gene). There is no expression in the kidney (ProteinAtlas). *CYP24A1* encodes cytochrome P450, family 24, subfamily A, polypeptide 1, which initiates the degradation of 1,25 hydrox-Vitamin D3, thus regulating calcium homeostasis (Entrez Gene). Rare mutations in this gene cause infantile hypercalcemia (OMIM #143880). *CYP24A1* is expressed in the kidney. *PFDN4* encodes prefoldin subunit 4, which is part of a molecular chaperone complex needed for correct folding of newly synthesised polypeptides (Entrez Gene). There are no publications linking *PFDN4* to kidney function. *SUMO1P1* encodes *SUMO1* (small ubiquitin-like modifier 1) pseudogene 1 (Entrez Gene); *SUMO1* is part of a post-translational modification system regulating NFKB under high glucose conditions in kidney mesangial cells;[83] sumoylation protects from oxidative stress.[84] There is no publication linking *SUMO1P1* to kidney function.
	GRAIL	NO		
	DEPICT	NO		

Supplementary Table 12 (continued).

SNPID (Locus name)	Evidence from functional databases		Gene prioritized for functional work	Description of Genes in each Region*
	Source	**Gene**		
rs3750082 (*KBTBD2*)	**eSNP**	*KBTBD2*	*KBTBD2*	*AVL9* plays a role in late exocytic transport,[85] at the level of the Golgi.[86] This gene has not formally been associated with kidney function in the published literature. *LSM5* is a Sm-like protein that plays a role in pre-mRNA splicing (GeneCards). It has not previously been linked to kidney function in the published literature. There is little known about *KBTBD2*, and no published literature linking it to kidney function. There are several other genes in the region.
	GRAIL	NO		
	DEPICT	*KBTBD2* FDR<0.05		
rs6088580 (*TP53INP2*)	**eSNP**	NO	NO	*TP53INP2* regulates both transcription and autophagy (UCSC). It is a scaffold protein that interacts with *VMP1.*[87] It has not been formally linked to kidney function in the literature. There are dozens of additional genes in the region.
	GRAIL	NO		
	DEPICT	*ACSS2* and *NCOA6* FDR<0.05		
rs6459680 (*RNF32*)	**eSNP**	NA	NO	*RNF32* plays a role in spermatogenesis. The gene has not previously been identified in associaiton with kidney function. *LMBR1* plays a role in limb malformation, which may occur via altered Sonic hedgehog signaling. The gene has not been connected to kidney function or disease.
	GRAIL	NO		
	DEPICT	NO		
rs4014195 (*AP5B1*)	**eSNP**	NA	*AP5B1* but no existing Morpholino	*KAT5* encodes for K(Lysine) acetyltransferase 5, which is important in transcriptional regulation. It has not been previously identified in association with kidney function. OVOL1 encodes for a transcription factor. *OVOL1* deficient mice of C57BL/6 background show increased perinatal lethality and other abnomalities, including cystic kidneys.[88]
	GRAIL	NO		
	DEPICT	*AP5B1* FDR<0.05		
rs2712184 (*IGFBP5*)	**eSNP**	NA	NO	*IGFBP5* (insulin-like growth factor binding protein 5) is a protein-coding gene that either induces or suppresses cell proliferation. *IGFBP5* participates in cellular pathways of adaptation to hypertonicity in renal medulla under TonEBP control.[89] *IGFBP2* (insulin-like growth factor binding protein 2, 36kDA) regulates cell growth by enhancing or suppressing IGF bioavailability. RNA and protein are ubiquitously expressed. IGFBP2 is the most expressed among IGF binding proteins, particularly in glomerular mesangial cells where it is controlled by angiotensin and glucose concentrations.[90] *TNP1* (transition protein 1) is a protein-coding gene. In the course of spermiogenesis, *TNP1* is a spermatid-specific product that replaces histone and is itself replaced in the mature sperm by protamines. It is expressed in testis. There is no published literature relating this gene or its protein product to kidney function.
	GRAIL	NO		
	DEPICT	NO		
rs10994860 (*A1CF*)	**eSNP**	NA	*A1CF*	*A1CF* is a protein coding gene that mediates the deamination of apolipoprotein B mRNA through a multi-componenent enzyme complex including *APOBEC-1* and a complementation factor coded by *A1CF* gene. It is expressed in the gastrointestinal tract, liver, pancreas, brain and kidneys. One publication[20] links this gene to kidney reabsorption of urate (elevated serum urate concentrations). ASAH2B (N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2B) is a protein-coding gene. Ceramidases are a group of enzymes which catalyze the hydrolysis of ceramides to produce sphingosine but ASAH2B lacks the active site and therefore could be catalytically inactive. No publications link this gene to kidney function. *PRKG1* encodes the soluble alpha and I beta1 isoforms of the cGMP dependent protein kinase, involved in the regulation of cardiovascular and neuronal functions, smooth muscle relaxation, platelet aggregation, and in cell growth by modulating cellular calcium.
	GRAIL	NO		
	DEPICT	*A1CF* FDR<0.05		

Supplementary Table 12 (continued).

SNPID (Locus name)	Evidence from functional databases		Gene prioritized for functional work	Description of Genes in each Region*
	Source	**Gene**		
rs9682041 (*SKIL*)	**eSNP**	NA	*SKIL*	The protein encoded by SKI-like oncogene is a component of the SMAD pathway, that has a regulatory role on the cell division and differentiation through TGFß. RNA and protein are expressed in most human tissues except pancreas. *SKIL* is implicated in ubiquitin dependent tubulointerstitial fibrosis along with TGFbeta1.[91] Claudin 11 is a member of the claudin family of tight junction associated proteins. The protein encoded by this gene is a major component of the central nervous system (CNS) myelin and plays an important role in regulating proliferation and migration of oligodendrocytes. RNA and protein are expressed in Sertoli cells in testis and oligodendrocytes in the CNS. CLDN11 Claudin family is differentially expressed in tight junctions of human cortical nephron and influences pathologies involving abnormalities of absorption.[92] Its expression is significantly unregulated in genetic model of polycystic kidney in early stages.[93] RNA is expressed in cerebral cortex, while the protein is strongly expressed in hyppocampus and prostate. There are no publications linking this gene to kidney function.
	GRAIL	*SKIL* p=0.02		
	DEPICT	*SKIL* FDR<0.05		
rs163160 (*KCNQ1*)	**eSNP**	NA	*KCNQ1* work already completed	*KCNQ1* encodes a voltage-gated potassium channel required for cardiac repolarization. RNA is ubiquitously expressed but the protein product is mostly expressed in glandular cells. In addition to be recognized as a gene conferring risk of T2D in Caucasians and more recently in African Americans,[94] it is also reported as a gene conferring susceptibility to diabetic nephropathy in Asians[95] and CKD in African Americans.[96] *TRPM5* encodes the transient receptor potential cation channel, subfamily M, member 5 gene, a member of the transient receptor potential (TRP) protein family with structural features typical of ion channels (non-selctive cations except Ca2+) and mediates a transient membrane depolarization in the presence of low concentrations of intracellular calcium. mRNA is found mainly in the prostate, testis, ovary, colon and leukocytes but the protein is expressed in the majority of human tissues. There are no publications linking this gene or its protein to kidney function. The tumor suppressing subtransferable candidate 4 (*TSSC4*) gene is located in the p15.5 region of the chromosome 11, a region involved in Wilm's tumor and a known important tumor-supressor gene region. TSSC4 RNA is widely expressed in human tissues while protein is strongly expressed in renal tubules and moderately in digestive system as well as male and female reproductive systems.
	GRAIL	NO		
	DEPICT	*IGF2* (FDR<0.05) but very far away from lead SNP		

*Cited web resources: Entrez Gene: http://www.ncbi.nlm.nih.gov/gene; GenCards: www.genecards.org; OMIM: http://www.ncbi.nlm.nih.gov/omim; ProteinAtlas: www.proteinatlas.org; RefSeq: http://www.ncbi.nlm.nih.gov/refseq/; UCSC: www.genome.ucsc.edu.

Supplementary Table 13. DEPICT tissue and cell-type enrichment**.***

MeSH ID	Name	MeSH# first level term	MeSH second level term	P-value	FDR	Genes at associated loci§
A05.810	Urinary Tract	Urogenital System	Urinary Tract	0.000226	<0.025	*NAT8, SLC17A3, SLC22A2, SLC17A1, LRP2, UMOD, SLC7A9, SLC6A13, SLC34A1, ENSG00000204872, PCK1, SLC47A1, WDR72*
A05.810.453	Kidney	Urogenital System	Urinary Tract	0.000292	<0.025	*NAT8, SLC17A3, SLC22A2, SLC17A1, LRP2, UMOD, SLC7A9, SLC6A13, SLC34A1, ENSG00000204872, PCK1, SLC47A1, WDR72*
A03.620	Liver	Digestive System	Liver	0.000663	<0.025	*ITIH1, LPA, SLC17A2, SLC22A1, ITIH3, KNG1, LEAP2, GCKR, SLC22A7, CPS1, A1CF*
A11.436.348	Hepatocytes	Cells	Epithelial Cells	0.001338	<0.025	*ITIH3, A1CF, LEAP2, SLC17A2, GCKR, AGMAT, ITIH1, SCGN, LCAT, SLC22A3, SLC7A9, SLC22A1*
A06.407.071.140	Adrenal Cortex	Endocrine System	Endocrine Glands	0.001574	<0.025	*ENSG00000256731, SLC47A1, FNDC4, KCNQ1, RERG, CASP9*
A06.407.071	Adrenal Glands	Endocrine System	Endocrine Glands	0.002988	0.025	*SLC47A1, FNDC4, ENSG00000256731, KCNQ1, RERG, MAMSTR, CASP9*

*DEPICT was used to assess whether genes at associated loci were highly expressed in any of 209 tissue and cell type annotations. In total we found 6 significantly enriched tissues (FDR < 0.05). Only significant tissues are shown in the table.

MeSH: Medical Subject Headings.

§ Lists of genes that are within an associated region and highly expressed in the given tissue or cell type.

Supplementary Table 14. DEPICT pathway analysis**.** Gene sets with P-value < 1e–05 are shown.

Reconstituted gene set ID	Reconstituted gene set name	Part of meta gene set	P-value	FDR	Reconstituted gene set genes at associated loci
ENSG00000186350	RXRA protein complex	NCOA1 protein complex	5.94E-08	<0.002	*NCOA6, SKIL, TRIB1, MED1, CDK12, EDC4, RELA, ARNT, ERBB2, PGAP3, NFATC1, PTPN12, NFKB1, A1CF, NRBP1, TPRKB, AFF4, NRIP1, NFATC3, INO80*
MP:0011423	Kidney Cortex Atrophy	Dilated Renal Tubules	3.40E-07	<0.002	*SLC7A9, SLC22A2, SLC34A1, VEGFA, NAT8, UMOD, DPEP1, AGMAT, PCK1, LRP2, PTPRO, IGF2, ENSG00000204872, ADAMTS5, DAB2, BMP4, SLC12A4, CA12, SLC6A13, TRIB1*
ENSG00000125124	BBS2 protein complex	BBS4 protein complex	4.76E-07	<0.002	*KNG1, UMOD, CPS1, ITIH3, ESRP2, RASIP1, PCK1, SLC7A9, AGMAT, SLC22A1, NAT8, LRP2, NUTF2, DACH1, ITIH4, EDC4, SLC22A2, ENSG00000204872, PSMD12, SGMS1*
ENSG00000124151	NCOA3 protein complex	NCOA1 protein complex	7.21E-07	<0.002	*TRIB1, MED1, NCOA6, FBXL20, ETV5, CDK12, VEGFA, GCKR, GLI2, RAI1, PSKH1, GTF3C2, MOV10, PIK3R1, PHLDA1, PGAP3, ITIH3, NFATC1, SETBP1, RMND5A*
MP:0003918	Decreased Kidney Weight	Dilated Renal Tubules	8.75E-07	0.002	*RAPSN, IGF2-AS, ACVR2A, NFATC3, PCK1, NAT8, SLC7A9, SLC6A13, IGF2, SLC34A1, PTPRO, ADAMTS5, PAPPA, IGF2R, UMOD, GSS, LCAT, TCEA3, SVEP1, AGMAT*
GO:0015145	Monosaccharide Transmembrane Transporter Activity	Monosaccharide Trans-membrane Transporter Activity	1.21E-06	0.002	*SLC7A9, ENSG00000204872, SLC34A1, AGMAT, LEAP2, NAT8, SLC22A2, TSPAN9, TRIM58, SLC2A9, DPEP1, C12orf68, ENSG00000230288, VEGFA, SLC28A2, DAB2, UMOD, SLC6A13, XYLB, OR2W3*
GO:0008514	Organic Anion Transmembrane Transporter Activity	Organic Cationanionzwitterion Transport	2.08E-06	0.006	*SLC34A1, SLC22A2, NAT8, SLC6A13, KNG1, SLC22A7, UMOD, SLC22A1, ITIH1, SLC7A9, AGMAT, WDR72, ENSG00000204872, INHBC, SLC47A1, A1CF, LRP2, XYLB, PCK1, DPEP1*
MP:0000521	Abnormal Kidney Cortex Morphology	Dilated Renal Tubules	2.60E-06	0.005	*UMOD, SLC7A9, SLC22A2, SLC34A1, AGMAT, VEGFA, NAT8, CA12, IGF2-AS, STC1, KNG1, GLI2, RASIP1, LRP2, DPEP1, EYA4, DACH1, SETBP1, PCK1, TSPAN9*
GO:2000117	Negative Regulation Of Cysteine-Type Endopeptidase Activity	Negative Regulation Of Cysteine-Type Endopeptidase Activity	3.26E-06	0.004	*OR2W3, UMOD, SLC34A1, NRIP1, RMND5A, PSMA5, PRELID1, PTPN12, ENSG00000187446, SNX17, SLC7A6, ENSG00000232656, PSKH1, IZUMO1, SLC22A2, TRIB1, IDI1, NFE2L2, DCDC5, LRP2*

Supplementary Table 14 (continued).

Reconstituted gene set ID	Reconstituted gene set name	Part of meta gene set	P-value	FDR	Reconstituted gene set genes at associated loci
MP:0001698	Decreased Embryo Size	Complete Embryonic Lethality During Organogenesis	4.30E-06	0.006	*PTPN12, HNRNPR, NCOA6, HSPA4, IGF2, AFF4, IGF2R, ACVR2B, NSD1, VEGFA, MED1, CELF1, NRF1, BMP4, SETDB1, LAMA5, JARID2, RIF1, RMND5A, INO80*
MP:0011108	Partial Embryonic Lethality During Organogenesis	Complete Embryonic Lethality During Organogenesis	4.61E-06	0.005	*IGF2, LAMA5, VEGFA, BMP4, TRIB1, RARB, PHLDA1, R3HDM2, RHOC, TSPAN9, JARID2, ACVR2B, AFF4, NSD1, PTPN12, SIPA1L3, RASIP1, A1CF, GLI2, GRB10*
MP:0001711	Abnormal Placenta Morphology	Abnormal Placenta Labyrinth Morphology	4.80E-06	0.005	*VEGFA, ITIH1, GRHL2, TRIB1, KNG1, IGF2, SPATA5L1, NSD1, ITIH3, ESRP2, INO80, RHOC, LEAP2, LAMA5, CELF1, ARNT, ITCH, ERBB2, NCOA6, PAPPA*
GO:0005355	Glucose Transmembrane Transporter Activity	Monosaccharide Transmembrane Transporter Activity	5.07E-06	0.005	*SLC7A9, ENSG00000204872, SLC34A1, AGMAT, SLC2A9, DPEP1, NAT8, SLC22A2, C12orf68, LEAP2, TRIM58, ENSG00000230288, VEGFA, SLC28A2, TSPAN9, GGT7, UMOD, SLC22A7, TFDP2, SLC6A13*
GO:0001655	Urogenital System Development	Kidney Development	5.43E-06	0.006	*UMOD, EYA4, DACH1, SLC34A1, SLC22A2, RARB, DPEP1, IGF2-AS, ADAMTS5, IGF2, SETBP1, GRHL2, ERBB2, GLI2, LRP2, SHH, PAPPA, ACVR2B, BMP4, STC1*
GO:0015149	Hexose Transmembrane Transporter Activity	Monosaccharide Transmembrane Transporter Activity	6.45E-06	0.006	*SLC7A9, ENSG00000204872, SLC34A1, AGMAT, SLC2A9, NAT8, SLC22A2, DPEP1, TSPAN9, LEAP2, C12orf68, TRIM58, ENSG00000230288, VEGFA, SLC28A2, GGT7, UMOD, PRELID1, SLC22A7, OR2W3*
MP:0002981	Increased Liver Weight	Decreased Circulating Cholesterol Level	7.33E-06	0.006	*ITIH1, PCK1, KNG1, CPS1, LEAP2, SLC22A1, SLC22A7, ACSS2, SLC7A9, ITIH3, GCKR, IDI1, LPA, INHBC, FASN, A1CF, DPEP1, ITIH4, GSS, IGF2R*
GO:0072001	Renal System Development	Kidney Development	7.35E-06	0.005	*UMOD, DPEP1, DACH1, SLC22A2, RARB, SLC34A1, ADAMTS5, EYA4, IGF2, IGF2-AS, SETBP1, BMP4, LRP2, NAT8, GLI2, SHH, CLDN11, ERBB2, LAMA5, CA12*
MP:0011346	Renal Tubule Atrophy	Dilated Renal Tubules	8.41E-06	0.005	*UMOD, SLC34A1, SLC7A9, DPEP1, VEGFA, PTPRO, SLC47A1, AGMAT, SLC22A2, SLC22A7, KNG1, PCK1, MANBA, CPS1, ENSG00000204872, NAT8, WDR72, SLC2A9, LEAP2, SLC22A3*
MP:0005459	Decreased Percent Body Fat	Abnormal Glucose Homeostasis	8.78E-06	0.005	*CTRL, CELA2B, TRIB1, PCK1, RAPSN, SORT1, ACSS2, SLC34A1, SLC7A9, ENSG00000187446, RSBN1L, FASN, STC1, THADA, LPA, PIK3R1, LMAN2, CASP9, IGF2R, PIGU*

Supplementary Table 15. Zebrafish knock-down results**.***

	MO	Dose	*Pax2a*	*Nephrin*	*Slc20a1a*
Clutch 1	**Control**	N/A	0/33 (0%)	0/36 (0%)	0/51 (0%)
	Wnt7aa	250 uM	3/38 (8%) p= 0.24	0/29 (0%)	0/29 (0%)
	Nfkb1	250 uM	0/33 (0%)	0/32 (0%)	0/30 (0%)
	Ptpro	250 uM	0/22 (0%)	0/27 (0%)	0/14 (0%)
	A1cf	250 uM	0/31 (0%)	0/36 (0%)	0/23 (0%)
	Tspan9a+b	125 uM each	1/25 (4%) p=0.43	0/22 (0%)	1/19 (5%) p=0.27
Clutch 2	**Control**	N/A	3/18 (17%)	0/21 (0%)	0/20 (0%)
	Kbtbd2	250 uM	0/20 (0%) p=0.10	0/22 (0%)	0/17 (0%)
	Uncx	250 uM	3/30 (10%) p=0.66	1/26 (4%) p=1.00	0/19 (0%)
	Dpep	250 uM	1/26 (4%) p=0.29	1/23 (4%) p=1.00	0/24 (0%)
	Sypl2a+b	250 uM each	7/35 (20%) p=1.00	1/25 (4%) p=1.00	0/29 (0%)
Clutch 3	**Control**	N/A	0/37 (0%)	0/55 (0%)	0/41 (0%)
	Nfatc1	250 uM	2/26 (8%) p=0.17	0/29 (0%)	0/31 (0%)
	Skila+b	62.5 uM each	0/41 (0%)	0/46 (0%)	0/32 (0%)

Zebrafish embryos were injected with morpholinos (MOs) targeting orthologous loci, and renal gene expression was assessed at 48 hours post-fertilization (hpf) by whole mount *in situ* hybridization. Renal markers examined include *pax2a* (global kidney), *nephrin* (podocyte), and *slc20a1a* (proximal tubule). Data are presented as the number of observed abnormalities per total number of embryos scored.

*P-values provided for non-0 results only.

Supplementary Table 16. Study information: discovery. Extensive study names are reported in the Acknowledgements section.

Study[REF]	Study Design	N[§]	Study characteristics	Creatinine Measurement	Cystatin measurement
3C[97, 98]	Prospective population-based	6440	**Study exclusions or disease enrichment**. None. **Exclusions**. Of the 6440, those with genotypes and creatinine were 6431 and those with genotypes and cystatin C were 1243.	Modified kinetic Jaffe reaction.	Particle-enhanced immuno-nephelometric method (BNII, Dade-Behring/ Siemens)
Advance[99]	Randomised controlled trial	11,140	**Study exclusions or disease enrichment**. Multicenter trial done by 215 collaborating centres in 20 countries. All patients had T2D and were of Caucasian origin. Those with genotypes and creatinine were 2301. **Exclusions**. NA	Serum creatinine was measured in local laboratories at individual study sites.	NA
AGES[100]	Population based	3664	**Study exclusions or disease enrichment**. None. **Exclusions**. Sample exclusion criteria included sample failure, genotype mismatch with reference panel, and sex mismatch, resulting in clean genotype data on 3219 individuals.	Jaffé reaction.	NA
Amish[101, 102]	Population based "founder" cohort	1264	**Study exclusions or disease enrichment**. None. **Exclusions**. Age <20, severe chronic disease, call rate <95%, pHWE<10E-6.	Modified kinetic Jaffe reaction.	Particle-enhanced immunonephelometric method (BNII, Dade-Behring).
ARIC[103]	Prospective, population-based	9713	**Study exclusions or disease enrichment**. None. **Exclusions**. Of the 9713 genotyped individuals of European ancestry, we excluded 658 individuals based on discrepancies with previous genotypes, disagreement between reported and genotypic sex, one randomly selected member of a pair of first-degree relatives, or outlier based on measures of average DST or >8 SD away on any of the first 10 principal components.	Modified kinetic Jaffé reaction.	Particle enhanced immunonephelometric assay (N Latex Cystatin C, Dade Behring).
ASPS[104, 105]	Prospective study	922	**Study exclusions or disease enrichment**. Excluded were subjects with histrory of neuropsychiatric disease, previous stroke and/or TIA, and dementia. **Exclusions**. Of the 922 participants who underwent genotyping, we made the following exclusions: sample call rate <98% (74). This resulted in 848 genotyped individuals.	Modified kinetic Jaffé reaction.	NA
AUSTWIN[106]	Families, population-based	9592	**Study exclusions or disease enrichment**. NA. **Exclusions**. NA.	Jaffé method, Hitachi 917 analyser.	NA
BLSA[107]	Population based study	1200	**Study exclusions or disease enrichment**. None. **Exclusions**. Those of non-European descent or with missing phenotype information.	Modified kinetic Jaffé reaction.	NA
BMES[108-110]	Prospective cohort study	2761	**Study exclusions or disease enrichment**. None. **Exclusions**. Sample call rate <95% (n=9), outlying autosomal heterozygosity (n=28), sex discrepancies or ambiguous sample identification (n=69), cryptic relatedness (average IBD sharing proportion > 0.1875: n=121), non-European ancestry (n=13). This resulted in 2534 genotyped individuals.	Measured within 4 hours of collection using a Hitachi 747 Biochemistry analyser (Roche reagents, modified kinetic Jaffé).	NA

Abbreviations: T2D = type 2 diabetes. §Total genotyped sample size.

Supplementary Table 16 (continued).

Study[REF]	Study Design	N[§]	Study characteristics	Creatinine Measurement	Cystatin measurement
CHS[111, 112]	Prospective population-based	3397	**Study exclusions or disease enrichment**. A total of 1908 persons excluded from the GWAS study sample due to the presence at study baseline of coronary heart disease, congestive heart failure, peripheral vascular disease, valvular heart disease, stroke or transient ischemic attack or lack of available DNA. **Exclusions**. The present report is based upon genotyping results from 3329 Caucasian participants, who were free of clinical cardiovascular disease at baseline, consented to genetic testing, and had DNA available for genotyping. Genotyping was successful in 3291 persons.	Colorimetric method (Ektachem 700, Eastman Kodak).	Particle-enhanced immunonephelometric assay [N Latex Cystatin C, Dade Behring (now Siemens), Deerfield, Ill, USA] with a nephelometer [BNII, Dade Behring (now Siemens)].
CROATIA-KORCULA[113]	Cross-sectional, family-based	888	**Study exclusions or disease enrichment**. None. **Exclusions**. Subjects were excluded if they fulfilled any of the following criteria: genotypic call rate <97%; reported vs. genotypic sex mismatch; unexpectedly low genomic sharing with 1st degree relatives; excess of autosomal heterozygosity; outliers identified by IBS clustering analysis; pregnant women.	Jaffé rate method in plasma.	NA
CROATIA-SPLIT[114]	Population-based	499	**Study exclusions or disease enrichment**. Fasting urine and blood samples were collected from 1012 healthy volunteers aged 18+ from Split on the Dalmatian coast in Croatia in 2008/2011. **Exclusions**. Missing creatinine levels	Jaffé protein compensated method in the serum.	NA
CROATIA-VIS[115, 116]	Cross-sectional, family-based	768	**Study exclusions or disease enrichment**. None. **Exclusions**. Subjects were excluded if they fulfilled any of the following criteria: genotypic call rate <97%, mismatch between reported and genotypic sex, unexpectedly low genomic sharing with first degree relatives, excess autosomal heterozygosity, or outliers identified by IBS clustering analysis. Pregnant women were excluded from the study.	Enzymatic photometric assay using an ADVIA1650 clinical chemistry analyzer (Siemens Healthcare Diagnostics GmbH, Eschborn, Germany)[117] at the Institute for Clinical Chemistry and Laboratory Medicine, Regensburg University Medical Center, Germany.	NA
DESIR[118]	Population-based	731	**Study exclusions or disease enrichment**. Excluded 15 ethnicity outliers. **Exclusions**. Individuals with genotype call rate <0.90, outlying heterozygosity, gender discrepancies, missing clinical data, cryptic relationships, non-European.	Kinetic colorimetry using Jaffé's Method. The assay utilized a Technicon DAX24 automated analyser from Bayer Diagnostics, Puteaux, France or a Specific or a Delta from Konelab, Evry, France.	NA
EGCUT 370K[119, 120] EGCUT Omni[119, 120]	Population-based	2700 9500	**Study exclusions or disease enrichment**. None. **Exclusions**. Missing creatinine levels; genetic outliers; cryptic relatedness (one random member up to 2nd cousins was only included)	Modified Jaffé protein compensated method in the serum.	NA

Abbreviations: T2D = type 2 diabetes. §Total genotyped sample size.

Supplementary Table 16 (continued).

Study[REF]	Study Design	N[§]	Study characteristics	Creatinine Measurement	Cystatin measurement
ERF[121]	Population based family study	2834	**Study exclusions or disease enrichment**. None. **Exclusions**. NA.	Jaffé rate method using a Synchron LX20.	NA
FamHS[122]	Family based	3838	**Study exclusions or disease enrichment**. None. **Exclusions**. Age <18, call rate <98%, pHWE <10E-6, sex mismatch, non-European ancestry.	Thin film adaptation of the amidohydrolase enzymatic method using the Vitros analyzer (Johnson & Johnson Clinical Diagnostics, Inc. Rochester NY 14650).	Immune particle-enhanced turbidimetric (PET) kit (DAKO A/S, Produktionsvej 42, DK-2600 Glostrup, Denmark. Code no. K0071)
FHS[123-125]	Prospective family-based	9300	**Study exclusions or disease enrichment**. None. **Exclusions**. Of the 9,274 participants who underwent genotyping, we made the following exclusions: sample call rate <97% (n=666), genotype heterozygosity > 5 SDs, and ambiguous family data (n=127). This resulted in 8481 genotyped individuals.	Modified kinetic Jaffé reaction.	Particle-enhanced immunonephelometric method, Cystatin C was measured (BNII, Dade-Behring).
GENOA[126-128]	Family-based	1553	**Study exclusions or disease enrichment**. 5 Non-white, 1 Missing Exam. **Exclusions**. For the Affymetrix 6.0 data, we excluded 25 subjects who failed pre-processing, 123 with Contrast QC<0.4, 2 for inconsistent relatedness, 11 identical twins. We re-ran the samples that failed pre-processing or the Contrast QC filter on the Affymetrix 6.0 data along with 50 that had passed. Of these samples, 19 failed genotyping completely, 9 had call rate <0.95, 2 had inconsistent relatedness, and 2 were identical twins. Of the 1509 remaining samples, 346 had no serum creatinine information. Our final data had 1163 samples with genotype and phenotype data.	Compensated rate Jaffé reaction.	NA
HABC	prospective cohort study	1663	**Study exclusions or disease enrichment**. None. **Exclusions**. Sample failure, genotypic sex mismatch, and first-degree relative of an included individual based on genotype data.	Colorimetric technique on a Johnson & Johnson VITROS 950 Chemistry Analyzer (Johnson & Johnson, New Brunswick, N.J., USA) using the enzymatic method.	BNII nephelometer (Dade Behring Inc., Deerfield, Ill., USA) that utilized a particleenhanced immunonephelometric assay (N Latex Cystatin C).
HCS[129]	Population-based	2204	**Study exclusions or disease enrichment**. None. **Exclusions**. Individuals with genotype call rate <0.95, outlying heterozygosity, gender discrepancies, missing clinical data, cryptic relationships, non-European ancestry or missing creatinine measurement.	Siemens Dimension Vista 1500 Intelligent Lab System using a modified Jaffé assay in a NATA accredited lab.	NA
HPFS[130-134]	Nested case-control study of T2D	2487	**Study exclusions or disease enrichment**. All subjects had T2D. **Exclusions**. Of the 2487 subjects with genome-wide scans, 818 (all T2D cases) had creatinine measured.	Modified kinetic Jaffé reaction in plasma.	NA

Abbreviations: T2D = type 2 diabetes. §Total genotyped sample size.

Supplementary Table 16 (continued).

Study[REF]	Study Design#	N*	Study characteristics	Creatinine Measurement	Cystatin measurement
HYPERGENES HTN cases[135]	Cases from a nested case-control study of Hypertension	2125	**Study exclusions or disease enrichment**. We excluded 81 samples with call rate <0.95, 33 with genotypic sex mis-match, 39 duplicated, 94 related subjects, and 13 outliers. **Exclusions**. Of the 1865 subjects with GWA data after QC, 1591 had creatine measured	Kinetic Jaffé reaction.	NA
HYPERGENES HTN controls[135]	Controls from a nested case-control study of Hypertension	1934	**Study exclusions or disease enrichment**. We excluded 62 samples with call rate <0.95, 23 with genotypic sex mismatch, 25 duplicated, 62 related subjects, and 12 outliers. **Exclusions**. Of the 1750 subjects with GWA data after QC, 1662 had creatine measured	Kinetic Jaffé reaction.	NA
INCIPE[136]	Cross-sectional, population based	940	**Study exclusions or disease enrichment**. Excluded were individuals <40 year old. **Exclusions**. Pregnant women	Kinetic rates using the Jaffé method, recalibrated to standardized creatinine determinations obtained at the Cleveland Clinic Research Laboratory.	Immunonephelometric method that used monospecific antisera on an Immage 800 (Beckman Coulter).
INGI-CARLANTINO [137-139]	Isolated population	679	**Study exclusions or disease enrichment**. None. **Exclusions**. We obtained the levels of creatinine of 447 participants; excluded were those with call rate <97%.	Jaffè reaction.	NA
INGI-CILENTO[140-147]	Cross-sectional population-based study of isolated populations with pedigree information	859	**Study exclusions or disease enrichment**. None. **Exclusions**. 38 individuals aged <20 years	Modified kinetic Jaffé reaction.	NA
INGI-FVG[137-139]	Isolated population	1376	**Study exclusions or disease enrichment**. None. **Exclusions**. We obtained the levels of creatinine of 874 participants; excluded were those with call rate <97%.	Jaffé reaction.	NA
INGI-VAL BORBERA[148]	Family Population-based	1665	**Study exclusions or disease enrichment**. None. **Exclusions**. Of the 1665 participants who underwent genotyping, one was excluded because of a sample call rate <95%.	Jaffé reaction.	NA

Abbreviations: T2D = type 2 diabetes. §Total genotyped sample size.

Supplementary Table 16 (continued).

Study[REF]	Study Design	N[§]	Study characteristics	Creatinine Measurement	Cystatin measurement
JUPITER[149, 150]	Randomized, placebo-controlled trial	8782	**Study exclusions or disease enrichment**. Excluded were subjects with LDL-C ≥ 130 mg/dl or CRP < 2 mg/l. **Exclusions**. None	Performed in JUPITER core central laboratories using the Roche Modular Analytics Chemistry System with Roche creatinine reagents (modified Jaffe reaction with rate blanking) (Roche Diagnostics, Township of Branchburg, New Jersey).	NA
KORA-F3[151, 152] KORA-F4[151, 152]	Prospective population based	1644 1814	**Study exclusions or disease enrichment**. None. **Exclusions**. None.	Modified kinetic Jaffe reaction.	Particle-enhanced immunonephelometric method (BNII, Dade-Behring).
MESA[153]	Community-based cohort study	2520	**Study exclusions or disease enrichment**. None. **Exclusions**. NA.	Serum creatinine was measured by rate reflectance spectrophotometry using thin film adaptation of the creatine amidinohydrolase method on the Vitros analyzer (Johnson & Johnson Clinical Diagnostics, Inc., Rochester, NY 14650). The laboratory analytical CV is 2.2%. All creatinine measurements for the MDRD Study were performed at Cleveland Clinic Labs using a CX3 assay. The Vitros analyzer used here was previously calibrated to a CX3 machine with the Cleveland Clinic lab and found the results were nearly identical.	BNII nephelometer (Dade Behring Inc., Deerfield, IL) that utilizes a particle enhanced immunonepholometric assay (N Latex Cystatin-C) 7 on fasting plasma specimens stored at -70°C. The assay is stable over 5 cycles of freeze / thaw. Among 61 healthy individuals with 3 cystatin-C measurements over a 6-month period, the intra-individual coefficient of variation was 7.7%.
MICROS[154-156]	Cross-sectional, population-based study on extended pedigrees	1391	**Study exclusions or disease enrichment**. None. **Exclusions**. Excluded were samples with overall SNP call rate <95%, showing excess of heterozygosity, or being classified as outliers by IBS clustering analysis.	Enzymatic photometric assay using an ADVIA1650 clinical chemistry analyzer (Siemens Healthcare Diagnostics GmbH, Eschborn, Germany).	BN-ProSpec analyzer (Dade Behring, Marburg, Germany) at the Institute for Clinical Chemistry and Laboratory Medicine, Regensburg University Medical Center, Germany.

Abbreviations: T2D = type 2 diabetes. §Total genotyped sample size.

Supplementary Table 16 (continued).

Study[REF]	Study Design	N[§]	Study characteristics	Creatinine Measurement	Cystatin measurement
NESDA[157, 158]	Longitudinal cohort study	1862	**Study exclusions or disease enrichment**. Individuals were almost all cases with major depression or anxiety disorder (N=1705) and of Western-European ancestry. **Exclusions**. Excluded were ethnic outliers, XO and XXY samples, and samples with a call rate <95%, high genome-wide homo- or heterozygosity, or excess of IBS.	Enzymatic assay from Roche Modular P unit (CREAplus; Roche Diagnostics, Ltd., Lewes, UK). Outliers (>4SD from mean) were excluded.	BNII nephelometer on plasma specimens (N Latex Cystatin C; Dade Behring Inc., Deerfield, IL). Excluded were values >4SD from the mean.
NHS[130, 132, 133, 159, 160]	Nested case-control study of T2D	3286	**Study exclusions or disease enrichment**. All individuals had T2D. **Exclusions**. Of the 3286 subjects with GWA data, 784 had creatinine measured.	Modified kinetic Jaffé reaction in plasma. Creatinine values were not normalized to the Cleveland Clinic standard.	NA
NSPHS[161, 162]	cross-sectional, family-based	565	**Study exclusions or disease enrichment**. None. **Exclusions**. Subjects were excluded if they fulfilled any of the following criteria: genotypic call rate <97%, mismatch between reported and genotypic sex, unexpectedly low genomic sharing with first degree relatives, excess of autosomal heterozygosity, or outliers identified by IBS clustering analysis.	Enzymatic photometric assay in plasma using an ADVIA1650 clinical chemistry analyzer (Siemens Healthcare Diagnostics GmbH, Eschborn, Germany).	NA
OGP-TALANA[163-165]	Isolated population	1376	**Study exclusions or disease enrichment**. None. **Exclusions**. We obtained the levels of creatinine of 874 participants; exclusions were samples with call rate<97%.	Jaffé reaction.	NA
ORCADES[166]	cross-sectional, family-based	704	**Study exclusions or disease enrichment**. None. **Exclusions**. Subjects were excluded if they fulfilled any of the following criteria: genotypic call rate <97%, mismatch between reported and genotypic sex, unexpectedly low genomic sharing with first degree relatives, excess autosomal heterozygosity, or outliers identified by IBS clustering analysis.	Enzymatic photometric assay in plasma using an ADVIA1650 clinical chemistry analyzer (Siemens Healthcare Diagnostics GmbH, Eschborn, Germany)[117] at the Institute for Clinical Chemistry and Laboratory Medicine, Regensburg University Medical Center, Germany.	NA
POPGEN[167]	Prospective population-based	1163	**Study exclusions or disease enrichment**. None. **Exclusions**. Samples with > 5% missing genotypes, showing excess genetic dissimilarity to the remaining subjects, or with evidence for a cryptic relatedness to other study participants were removed. These quality control measures left 1241 control samples for inclusion in the study. Of them, 1163 had serum creatinine available. All sex assignments could be verified by reference to the proportion of heterozygous SNPs on the X chromosome.	Enzymatic in vitro assay (CREAplus, Cobas®, Roche Diagnostics, Indianapolis, IN)	NA
PREVEND[168]	population based	3634	**Study exclusions or disease enrichment**. Subjects were aged 28 to 75 years and were enriched for microalbuminuria. **Exclusions**. NA	NA	BNII nephelometer (Dade Behring Inc.).

Abbreviations: T2D = type 2 diabetes. §Total genotyped sample size.

Supplementary Table 16 (continued).

Study[REF]	Study Design	N[§]	Study characteristics	Creatinine Measurement	Cystatin measurement
PROSPER-PHASE[169-171]	randomized placebo controlled trial	5763	**Study exclusions or disease enrichment**. Subjects were included when they had had a vascular event or were at increased risk of vascular disease; age: 70-82. **Exclusions**. After QC (sample rate <97.5%, genotype heterozygosity, ambigous family data), 5244 samples were available for analysis.	Measured at central laboratories, one in each of the three participating countries.	NA
RS-I[172-174]	Prospective population based study	5974	**Study exclusions or disease enrichment**. NA. **Exclusions**. Excluded were samples with call rate < 97.5%, excess autosomal heterozygosity >0.336 (~FDR <0.1%), mismatch between called and phenotypic gender, or outliers identified by the IBS clustering analysis with >3 SDs from population mean or IBS probabilities >97%.	Modified kinetic Jaffé reaction.	NA
RS-II[172-174]	Prospective population based study	1895	**Study exclusions or disease enrichment**. NA. **Exclusions**. Excluded were samples with call-rate <97.5%, excess of autosomal heterozygosity >0.336 (~FDR<0.1%), mismatch between called and phenotypic gender, and outliers identified by the IBS clustering analysis with >3 SDs from population mean or IBS probabilities >97%.	Modified kinetic Jaffé reaction.	NA
SAPALDIA	population based	1444	**Study exclusions or disease enrichment**. NA. **Exclusions**. Excluded were subjects with cryptic relatedness and call rate <95%.	Jaffé reaction (Roche) and calibrated to the Roche enzymatic gold standard reference yielding slightly lower serum creatinine measurements than the Cleveland Clinic Jaffé reaction.	NA
SHIP[175, 176]	Prospective population-based	4105	**Study exclusions or disease enrichment**. None. **Exclusions**. Excluded were samples with call rate <92%, duplicate samples (by IBS estimation), individuals with reported/genotyped gender mismatch.	Jaffè method. (A blood sample was drawn from the cubital vein in the supine position - the participants were non-fasting due to the duration of the cumulative examinations, 4-6 hours in total).	Siemens N Latex Cystatin C assay, a particle-enhanced nephelometric immunoassay, on the BN ProSpec® System.
SHIP-TREND	Prospective population-based	988	**Study exclusions or disease enrichment**. Excluded were individuals with no genotype and those with known T2D. **Exclusions**. Excluded were samples with call rate <94%, duplicate samples (by IBS estimation), individuals with reported/genotyped gender mismatch.	Jaffé method.	Dimension Vista® System, CYSC Flex® reagent cartridge, SIEMENS, Eschborn, Germany
SORBS[177-179]	Population-based	1097	**Study exclusions or disease enrichment**. None. **Exclusions**. Sample call rate<0.94; Ethnic outliers; duplicates; gender mismatch; IBS>0.2	Kinetic enzymatic method.	NA

Abbreviations: T2D = type 2 diabetes. §Total genotyped sample size.

Supplementary Table 16 (continued).

Study[REF]	Study Design	N[§]	Study characteristics	Creatinine Measurement	Cystatin measurement
WGHS[180]	Prospective population based	21,940	**Study exclusions or disease enrichment**. Excluded were individuals of non-European ancestry. **Exclusions**. Samples with <98% successful SNP calls were excluded. Data had been collected on 21940 individuals had successful genotype information and verified European ancestry at the time of the analysis.	Rate-blanked method based on the Jaffé reaction using Roche Diagnostics reagents with reproducibility of 3.67% and 1.60% at concentrations of 1.17 and 6.40 mg/dL, respectively.	NA
YFS	Population based	2023	**Study exclusions or disease enrichment**. NA. **Exclusions**. None.	Jaffé method (picric acid; Olympus Diagnostica GmbH) from frozen plasma samples in 2007.	NA

Abbreviations: T2D = type 2 diabetes. §Total genotyped sample size.

Supplementary Table 17. Study information, replication. Extensive study names are reported in the Acknowledgements section.

Study Name[REF]	Study Design	N§	Study characteristics	Creatinine Measurement	Cystatin measurement
Bus Santé[181, 182]	Cross-sectional population-based	5589	**Study exclusions or disease enrichment**. None. **Exclusions**. Unsuccessful genotyping (N=106). Analyses were restricted to Caucasians, defined as self-reported citizenship corresponding to South / North America, Europe, and Australia regions (N=4671). Creatinine was available in 4408 participants.	Modified kinetic Jaffé reaction (Abbott Architect).	NA
EGCUT replic[120]	Population-based	8576	**Study exclusions or disease enrichment**. None. **Exclusions**. Sample call rate <95% (N=279), genotype heterozygosity >5 SDs and ambiguous family data (N=264), gender mismatch (N=241).	Modified kinetic Jaffé reaction.	Immune turbidimetric method.
ESTHER[183-185]	Prospective cohort study	3490	**Study exclusions or disease enrichment**. Inclusion criteria: age ≥50 and good knowledge of German language. **Exclusions**. Samples with insufficient amount of DNA were not genotyped.	Modified kinetic Jaffé reaction.	NA
GENDIAN[186, 187]	Cohort study of T2D complications	1026	**Study exclusions or disease enrichment**. After exclusion of N=53 subjects due to subject QC, excluded were patients with ESRD (N=438) or advanced, histologically proven diabetic nephropathy (N=84) or missing phenotype (N=1). **Exclusions**: call-rate<95% (N=22); relatedness and duplicates (N=11); gender mismatch (N=16); ethnicity check (N=4).	Enzymatic assay.	Dade Behring assay (BNII)
GHS-I[188, 189] GHS-II[188, 189]	Population-based	3422 1438	**Study exclusions or disease enrichment**. Excluded if age <35 and >74. **Exclusions**: N=426 based on a call-rate <97%, a rate of heterorzygosity of 3 SDs away from the mean, disagreement between reported and genotypic sex, estimated IBD >0.25, IBS based principal components. This resulted in 2996 genotyped individuals.	Modified kinetic Jaffé reaction (Abbott).	NA
GSK[190-192]	Case-control study	1776	**Study exclusions or disease enrichment**. Cases were patients with unipolar recurrent depression; exclusion criteria: presence of manic or hypomanic episodes, mood incongruent psychotic symptoms, lifetime diagnosis of drug abuse and depressive symptoms secondary to alcohol or substance abuse or dependence or to a medical illness or medication. Controls: exclusion criteria: anxiety and affective disorders. **Exclusions**: call-rate<98% (N=2).	Standard clinical chemistry assays from Roche Hitachi.	NA
HRS	Population-based Longitudinal	12,507	**Study exclusions or disease enrichment**. Non-European participants were excluded. **Exclusions**. Sample call-rate<98%, gender discrepancy, unexpected duplicates and/or relatives with KC>1/32, missing cystatin C data.	NA	See note (1)
KORAF3 non-GWAS[151, 152] KORAF4 non-GWAS[151, 152]	Prospective Population based	1498 1202	**Study exclusions or disease enrichment**. None. **Exclusions**. None.	Modified kinetic Jaffé reaction.	Particle-enhanced immunonephelometric method (BNII, Dade-Behring).

§ Total genotyped sample size.

(1) Measured from dried blood spots (DBS) obtained during a face-to-face interview with the respondent at the same time as saliva collection. Blood was taken by pricking the participant's finger with a sterile lancet after cleansing the finger with an alcohol swab. Droplets of blood were extracted from the finger and directly placed on specially treated filter paper. Cystatin C for was assayed at the University of Vermont in 2006 and 2008. Serum equivalent values were calculated using a formula derived from a validation study done in conjunction with the USC/UCLA Center on Biodemography and Population Health.

Supplementary Table 17 (continued).

Study Name[REF]	Study Design	N§	Study characteristics	Creatinine Measurement	Cystatin measurement
IPM[193]	Hospital-based	1747	**Study exclusions or disease enrichment**. None. **Exclusions**. None.	Colorimetric method in (CPT82565) performed by the New York State / CLIA Clinical Chemistry Laboratory at Mount Sinai Medical Center.	NA
LURIC[194]	Case control	3061	**Study exclusions or disease enrichment**. Inclusion criteria: Caucasian, availability of coronary angiogram, stable condition except acute coronary syndrome. Exclusion criteria: any chronic disease other than cardiovascular, any acute illnesss other than ACS, any malignancy in the previous five years. **Exclusions**. Sample call-rate<95%, ambiguous sex, duplicates, relatedness. This resulted in 3061 genotyped individuals.	Jaffé method (CREA/Hitachi 717).	N LATEX Cystatin C/ Behring nephelometer II.
OGP[163-165]	Population-based study with pedigree information	9554	**Study exclusions or disease enrichment**. None. **Exclusions**. NA.	Modified kinetic Jaffé reaction or enzymatic reaction.	NA
SAPHIR[195, 196]	Healthy working population	1726	**Study exclusions or disease enrichment**. None. **Exclusions**. None.	Modified kinetic Jaffé reaction (CREA®, Roche Diagnostics GmbH, Mannheim, Germany).	NA
SKIPOGH[197]	cross-sectional family-based population-based	941	**Study exclusions or disease enrichment**. None. **Exclusions**. Excluded were 71 participants with call-rate <90%, resulting in 870 genotyped individuals.	IDMS-traceable Jaffé kinetic compensated method.	NA
Vanderbilt Omni1 Vanderbilt Omni5	Practice-based cohort	5184 2005	**Study exclusions or disease enrichment**. Samples chosen based on being a case or control for one of 31 pharmacogenetic analyses. **Exclusions**. Excluded individuals of non-white ancestry in the electronic medical record. Also excluded any lab measurements of individuals after initiation of dialysis or a kidney transplant. The median outpatient creatinine value was chosen.	Jaffé reaction.	NA
Vanderbilt 660W	Practice-based cohort	3021	**Study exclusions or disease enrichment**. Samples chosen for normal cardiac conduction, meaning that at some point in time they had a normal electrocardiogram without the presence of heart disease, arrhythmias, or electro-cardiographically-active medications. **Exclusions**. Children (age<18) and individuals of non-white ancestry in the electronic medical record. Also excluded any lab measurements from individuals after initiation of dialysis or a kidney transplant. The median outpatient creatinine value was chosen. At some point in their electronic medical record, the patients were absent of heart disease, but could later develop it.	Jaffé reaction.	NA

§ Total genotyped sample size.

Supplementary Table 18. Genotyping information, discovery studies.

Study name	Array type	Genotype calling	QC filters genotyped SNPs used for imputation‡	No. of SNPs used for imputation	Imputation software	Imputation Backbone (NCBI build)	Filtering of imputed genotypes†	Data management and statistical analysis
3C	Illumina Human610-Quad	Illumina BeadStudio	call rate < 98%, pHWE<10e-6, MAF<1%	492,897	MACH	1000 Genomes - CEU - Dec 2010 (build 37)	none	R, ProbABEL
Advance	Affymetrix 5.0 Affymetrix 6.0	Affymetrix	Affymetrix 5.0: call rate < 96% (<99% if MAF < 5%); Affymetrix 6.0: call rate < 97% (<99% if MAF<5%)	876,688	IMPUTE 2 v2.1.2	1000 Genomes - CEU Pilot - Jun 2010 plus HapMap3 rel. 2 (all available haplotypes) – Feb 2009 (build 36)	imputation info<0.5	SNPTEST
AGES	Illumina Hu370CNV	Illumina	pHWE<1e-6, call rate<97%, mishap p<1e-9, MAF<1%, SNPs not in Hapmap or with strand issues when merging with Hapmap	329,804	MACH v1.0.16	HapMap rel. 22 (build 36)	none	R, ProbABEL, Linear and Logistic Regression
Amish	Affymetrix 500K	BRLMM	MAF<1%, non-HapMap, call rate < 95%, pHWE<10e-6	338,598	MACH v1.0.15	HapMap rel. 22 - phased CEU haplotypes (build 36)	none	Measured genotype accounting for polygenic component
ARIC	Affy 6.0	Birdseed	call rate <95%, MAF<1%, pHWE <10e-5	669,450	MACH v1.0.16	HapMap rel. 22 (build 36)	none	R, ProbABEL, PLINK
ASPS	Illumina Human610-Quad BeadChip	Illumina	pHWE<1e-6, call rate < 98%, mishap p<1e-9, MAF<1%, Mendelian errors>100, SNPs not in Hapmap or with strand issues when merging with Hapmap	550,635	MACH v1.0.15	HapMap rel. 22 (build 36)	none	R, linear and logistic fixed effects model
AUSTWIN	Illumina370, iLLumina610	BeadStudio-gencall v3.0	call rate < 95%, pHWE<1e-6	271,069	MACH v1.0.15	HapMap rel. 22 - phased CEU haplotypes (build 36)	Rsq<0.3	Stata, SPSS
BLSA	Illumina Infinium HumanHap 550K	BeadStudio	call rate <99%, MAF <1%, pHWE<10e-4	501,764	MACH v1.0.15	HapMap rel. 21 - phased CEU haplotypes (build 35)	MAF<0.01, r2hat < 0.3	SAS, MERLIN, R

Supplementary Table 18 (continued).

Study name	Array type	Genotype calling	QC filters genotyped SNPs used for imputation‡	No. of SNPs used for imputation	Imputation software	Imputation Backbone (NCBI build)	Filtering of imputed genotypes†	Data management and statistical analysis
BMES	Illumina 670K-Quad	CHIAMO	call rate <95%, pHWE<10e-6, MAF<1%, genotype discrepancies in > 2.5% of 1356 samples independently genotyped for the Illumina 610K array	501,910	MACH v1.0.16	HapMap rel. 22 - phased CEU haplotypes (build 36.1)	none	Plink, mach2dat, SAS
CHS	Illumina 370CNV	Illumina BeadStudio	call rate<97%, heterozygotes=0, pHWE<10e-5, SNP not in HapMap	306,655	BimBam v0.99	HapMap CEU rel. 22 (build 36)	dosage variance < 0.01	R, linear and logistic regression, robust SE estimates
CROATIA-KORCULA	Illumina Infinium HumanCNV370 v1 SNP bead microarrays	BeadStudio	MAF<1%, pHWE<1e-6, call rate < 98%	317,896	MACH v1.0.16	HapMap rel. 22 (build 36)	none	R, GenABEL, ProbABEL;
CROATIA-SPLIT	Illumina HAP370CNV	Illumina	call rate <98%, pHWE<10e-10	330,997	MACH v1.0.15	HapMap rel. 22 - phased CEU haplotypes (build 36)	none	R (GenABEL, ProABEL)
CROATIA-VIS	Illumina HumanHap300 beadchip	BeadStudio	MAF≤1% , pHWE ≤1e-6 , call rate ≤ 98%	305,068	MACH v1.0.15	HapMap rel. 22 (build 36)	none	R, GenABEL, ProbABEL;
DESIR	Illumina Human CNV370-Duo Array and Illumina HAP300 array	Illumina Beadstation Genotyping Solution	call rate < 95% p HWE < 1e-4	291,609	IMPUTE v0.3.2 (genotyped SNPs used where available)	HapMap rel. 22 - phased CEU haplotypes (build 36)	none	SNPTEST v2.2.0
EGCUT 370K	Illumina 370CNV; Illumina OmniExpress	GenCall GenomeStudio	call rate <95%, pHWE<10e-6, MAF<1%	320784; 622800	IMPUTE v1.0	HapMap 2 CEU rel. 22	none	PLINK
EGCUT Omni	Illumina 370CNV; Illumina OmniExpress	GenCall GenomeStudio	call rate <95%, pHWE<10e-6, MAF<1%	320784; 622800	IMPUTE v1.0	HapMap 2 CEU rel. 22	none	PLINK
ERF	Illumina 6K/318K/380K, Affy 250K	BeadStudio (Affymetrix)	pHWE<1e-6, call rate<98%, MAF<1%, gender mismatch, excess heterozygosity	487,573	MACH v1.0.15	HapMap rel. 22 (build 36)	none	R, GenABEL, ProbABEL (linear mixed effect models)
FamHS	Illumina 550K, Illumina 610K, and Illumina 1M	BeadStudio-GenCall v3.0	call rate <98%, pHWE<10e-6, MAF<1%	499,979	MACH v1.0.16	HapMap rel. 22 - phased CEU haplotypes (build 36)	none	R (quantitative traits), SAS (qualitative trait)

Supplementary Table 18 (continued).

Study name	Array type	Genotype calling	QC filters genotyped SNPs used for imputation‡	No. of SNPs used for imputation	Imputation software	Imputation Backbone (NCBI build)	Filtering of imputed genotypes†	Data management and statistical analysis
FHS	Affymetrix 500K Affymetrix 50K Supplementary	Affymetrix	call rate <95%, pHWE<10e-6	503,526	MACH v1.0.15	HapMap rel. 22 - phased CEU haplotypes (build 36)	none	R
GENOA	Affymetrix 6.0 (primary), Illumina 610-Quad, Illumina 660-Quad, Illumina 1M-Duo	Birdseed (Affymetrix data), Genome Studio (Illumina data)	call rate < 95%, pHWE < 0.001, MAF<1%	1,233,495 (because of the different platforms, some SNPs may have had many missings)	MACH v1.0.16	HapMap CEU rel. 22 (build 36)	none	R, multic and GEE
HABC	Illumina 1M	BeadStudio v3.3.7	MAF<1%, call rate < 97%, pHWE<1e-6	914,263	MACH v1.0.16	HapMap CEU rel. 22 (build 36)	None	R, linear regression and logistic regression
HCS	Illumina 610K-Quad	Illumina	call rate <95%, pHWE<10e-6, MAF<1%	513,977	MACH v1.0.16	HapMap rel. 24 - phased CEU haplotypes (build 36.1)	MAF<0.01, Rsq<0.3	plink, SAS
HPFS	Affymetrix Genome-Wide Human 6.0 array	Birdseed	call rate <97%, pHWE<10e-4, MAF <0.02, more than 1 discordance over 29 replicates, significant plate associations	607,569 (autosomal)	MACH v1.0.15	HapMap rel. 22 - phased CEU haplotypes (build 36)	none	ProbABEL (R), SAS 9.0, PLINK
HYPERGENES HTN cases	Illumina 1M Duo	Illumina	call rate <99%, pHWE<10e-8	882,935	MACH v1.0	HapMap rel. 22 - phased CEU haplotypes (build 36)	Rsq<0.3	PLINK, R
HYPERGENES HTN ctrls	Illumina 1M Duo	Illumina	call rate <99%, pHWE<10e-8	882,935	MACH v1.0	HapMap rel. 22 - phased CEU haplotypes (build 36)	Rsq<0.3	PLINK, R
INCIPE	Illumina	Illumina	call rate <95%, pHWE<10e-6	635,646	IMPUTE 2	HapMap rel. 22 - phased CEU haplotypes (build 36)	none	R
INGI-CARLANTINO	Illumina 370K	BeadStudio	MAF<5%, call rate < 90%, pHWE < 0.05	374,498	MACH	HapMap rel. 22 (build 36)	Rsq<0.3 and <5 copies of the rare allele.	R, GenABEL, mmscore
INGI-CILENTO	370 K Illumina	Illumina	call rate < 95%, SNPs not in Hapmap	285,674	MACH v1.0.15	HapMap rel. 22 (build 36)	none	R, linear model, GenABEL, ProbABEL (mmscore)
INGI-FVG	Illumina 370K	BeadStudio	MAF<5%, call rate < 90%, pHWE < 0.05	374,498	MACH	HapMap rel. 22 (build 36)	Rsq<0.3 and <5 copies of the rare allele.	R, GenABEL, mmscore

Supplementary Table 18 (continued).

Study name	Array type	Genotype calling	QC filters genotyped SNPs used for imputation‡	No. of SNPs used for imputation	Imputation software	Imputation Backbone (NCBI build)	Filtering of imputed genotypes†	Data management and statistical analysis
INGI-VAL BORBERA	Illumina SNP array 370K - HumanCNV370 -Quadv3	BeadStudio	pHWE<1e-4, call rate < 90%, MAF<1%	324,319	MACH	HapMap rel. 22 (build 36)	none	R
JUPITER	Omni 1M Quad	Illumina	sample call rate <98%, call rate < 90%, pHWE<1e-6	740,416	MACH v1.0	1000 Genomes - CEU - Pilot - Jun 2010	none	R, probABEL
KORA-F3	Affymetrix 500K	BRLMM	per-chip call rate <93%, MAF <5%,discrepancy for one of the 50 SNPs common on both chips, gender mismatch	380,407	MACH	HapMap rel. 22 (build 35)	none	MACH2QTL, PROBABEL, R, VISUAL BASIC
KORA-F4	Affymetrix 6.0	BRLMM	per-chip call rate <93%, per SNP call rate <93%, MAF<1%, gender mismatch	629,893	MACH	HapMap rel. 22 (build 36)	none	MACH2QTL, PROBABEL, R, VISUAL BASIC
MESA	Affymetrix Genome-Wide Human SNP Array 6.0	Birdseed v2	call rate < 95%, MAF≤1%	897,979	IMPUTE v2.1.0	HapMap rel. 22 - phased CEU haplotypes (build 36)	none	PLINK
MICROS	Illumina Infinium HumanHap300 v2 SNP bead microarrays	BeadStudio	call rate <98%, MAF<1%, pHWE<10e-6	292,917	MACH v1.0.16	HapMap rel. 22 (build 36)	none	R, GenABEL, ProbABEL;
NESDA	Perlegen 600K	Perlegen	call rate <95%, MAF<1%, >5% genotype mismatches, >5% Mendelian errors, unknown SNP location	435,291	IMPUTE v0.4.2	HapMap rel. 24 - phased CEU haplotypes (build 36)	none	SNPTEST v2.2.0, R
NHS	Affymetrix Genome-Wide Human 6.0 array	Birdseed	call rate <97%, pHWE<10e-4, MAF <2%, >1 discordance/12 replicates, significant plate associations	606,626 (autosomal)	MACH v1.0.15	HapMap rel. 22 - phased CEU haplotypes (build 36)	none	R, ProbABEL, SAS 9.0, PLINK
NSPHS	Illumina 300K	BeadStudio	MAF≤1%, pHWE≤1e-5 , call rate ≤ 97%	318,049	MACH v1.0.15	HapMap rel. 22 (build 36)	none	R, GenABEL, ProbABEL
OGP-TALANA	Affymetrix500k	Affymetrix	call rate <95%, pHWE<10e-6	329,122	MACH v1.0.16	HapMap rel. 22 - phased CEU haplotypes (build 36)	Rsq<0.3	R, GenABEL, ProbABEL (mmscore)
ORCADES	Illumina 300K	BeadStudio	MAF≤1%, pHWE ≤ 1e-6, call-rate ≤ 98%	306,207	MACH v1.0.15	HapMap rel. 22 (build 36)	none	R, GenABEL, ProbABEL

Supplementary Table 18 (continued).

Study name	Array type	Genotype calling	QC filters genotyped SNPs used for imputation‡	No. of SNPs used for imputation	Imputation software	Imputation Backbone (NCBI build)	Filtering of imputed genotypes†	Data management and statistical analysis
POPGEN	Affymetrix 6.0	Birdseed v2	sample call rate < 0.90, call rate < 0.95, pHWE<1e-4, MAF<1%	709,003	MACH v1.0.16	HapMap rel. 22 - phased CEU haplotypes (build 36)	none	PLINK, R
PREVEND	Illumina CytoSNP12 v2	GenomeStudio	call rate < 95%, pHWE<1e-5	232,571		HapMap rel. 22 - phased CEU haplotypes (build 36)	none	STATA
PROSPER-PHASE	Illumina 660K	Illumina	call rate < 97,5%	557	MACH v1.0.15	HapMap rel. 22 (build 36)	none	R
RS-I	Version 3 Illumina Infinium II HumanHap550	BeadStudio	pHWE<1e-5, call rate<90%, MAF<1%, Mendelian errors > 100, SNPs not in Hapmap or strandedness issues merging with Hapmap	491,875	MACH	HapMap rel. 22 (build 36)	none	ProbABEL
RS-II	Version 3 Illumina Infinium II HumanHap550	BeadStudio	pHWE<1e-5, call rate<90%, MAF<1%, Mendelian errors>100, SNPs not in Hapmap or strandedness issues merging with Hapmap	495,478	MACH	HapMap rel. 22 (build 36)	none	ProbABEL
SAPALDIA	Illumina Human610-Quad BeadChip	Gencall	none	567,589	MACH v1.0.16	HapMap rel. 22 - phased CEU haplotypes (build 36)	none	ProbABEL, STATA v11
SHIP	Affymetrix 6.0	Affymetrix Birdseed2	none	869,224	IMPUTE v0.5.0	HapMap rel. 22 (build 36)	none	SNPTEST v1.1.5, QUICKTEST v0.94, R, InforSense, InterSystems Caché,
SHIP-TREND	Illumina Human Omni 2.5	Illumina	pHWE ≤ 1e-4, call rate ≤ 0.9, monomorphic SNPs	1,782,967	IMPUTE v2.1.2.3	HapMap rel. 22 - phased CEU haplotypes (build 36)	duplicated rsID with different positions	QUICKTEST v0.95, R, InforSense, InterSystems Caché

Supplementary Table 18 (continued).

Study name	Array type	Genotype calling	QC filters genotyped SNPs used for imputation‡	No. of SNPs used for imputation	Imputation software	Imputation Backbone (NCBI build)	Filtering of imputed genotypes†	Data management and statistical analysis
SORBS	500K Affymetrix GeneChip (250K Sty and 250K Nsp arrays, Affymetrix, Inc) and Affymetrix Genome-Wide Human SNP Array 6.0	Microarray Core Facility of the Interdisciplinary Centre for Clinical Research, University of Leipzig, Germany and ATLAS Biolabs GmbH, Berlin, Germany	MAF<1%, pHWE<1e-4, call rate < 95%,	378,513	IMPUTE	HapMap CEU rel. 21 (build 35)	proper_info ≤ 0.4	ProbAbel with robust variance option to account for remaining relatedness
WGHS	Illumina HumanHap300 Duo "plus"	BeadStudio v3.1	pHWE<1e-6, call rate < 98%, MAF<1%	331,993	MACH v1.0.15	HapMap rel. 22 (build 36)	none	PLINK, R, ProbAbel
YFS	Illumina 670k custom	Illuminus	call rate <95%, pHWE<10e-6	546,674	IMPUTE 2.1.2	1000 Genomes - Jun 2011 phased haplotypes	none	SAS

‡QC filters for genotyped SNPs used for imputation (SNPs satisfying the filter were excluded).

†Filtering of imputed genotypes (SNPs satisfying the filter were excluded).

Supplementary Table 19. Genotyping platform – *in silico* replication studies.

Study Name	Array type	Genotype calling	QC filters for genotyped SNPs used for imputation	No of SNPs used for imputation	Imputation	Imputation Backbone (NCBI build)	Filtering of imputed genotypes	Data management and statistical analysis
EGCUT-replic	Illumina OmniExpress	Genome Studio (GenCall)	call rate<95%, pHWE<10e-6, MAF<1%	616,063	IMPUTE v2.2	HapMap rel. 22 - phased CEU haplotypes (build 36)	none	Plink, SNPTEST 2, R
GENDIAN	Affymetrix Genome-Wide Human SNP Array 6.0	Birdseed (BRLMM)	N=126,259 SNPs (chr 1-chr22, chr X) were excluded from imputation by SNP quality control.	776,075	Mach 1.0.18.c MiniMac 2012-10-09	GIANT ALL 1000 Genomes v3 ref panel GRCh build 37	none	R
GSK cases/controls	Illumina 550 K	Illumina	call rate <98%, pHWE<10e-5	522,008	IMPUTE v2	CEU in HapMap3 and 1000 Genomes Pilot 1	none	R, Plink
Gutenberg Health Study	Affymetrix 6.0	Birdseed	call rate<95%, MAF<1%, pHWE<10e-4	662,405	IMPUTE v2.1.0	HapMap rel. 24 (build 36)	none	R
HRS	Illumina Omni2.5 Beadchip	Genome Studio v2011.2	call rate <98%, pHWE<10e-4	551,936	MACH v1.0.16	HapMap rel. 22 - phased CEU haplotypes (build 36)	none	SAS, R
IPM_EA_Affy	Affymetrix 6.0	Birdseed	sample call rate <95%, SNP call rate <95%, pHWE<1e-4, MAF<1%	711,270	IMPUTE 2	Phase I integrated variant set release (v3) (NCBI build 37)	none	SNPTEST 2, R
IPM_EA_Illu	Illumina Human OmniExpress Exome-8v1	Genome Studio	sample call rate <99%, SNP call rate <95%, pHWE<5e-5, MAF<1%	865,711	IMPUTE 2	Phase I integrated variant set release (v3) (NCBI build 37)	none	SNPTEST 2, R
LURIC	Affymetrix 6.0	Birdseed v2	call rate <98%, pHWE<10e-4	686,195	MACH	HapMap rel. 22 - phased CEU haplotypes (build 36)	none	QUICKTEST
Vanderbilt Omni1	Illumina HumanOmni1-Quad	BeadStudio	call-rate<98%, IBD (Z0<0.8), Mendel errors >0, Duplicate concordance <100%	946,523	IMPUTE v2.3.0	1000 Genomes Phase 1 integrated v3	Genotype Likelihood <0.9	Plink, R
Vanderbilt Omni5	Illumina HumanOmni5-Quad	BeadStudio	call rate <98%, IBD (Z0<0.8), Mendel errors >0, Duplicate concordance <100%	3,819,154	IMPUTE v2.3.0	1000 Genomes Phase 1 integrated v3	Genotype Likelihood <0.9	Plink, R
Vanderbilt 660W	Illumina Human660W-Quad	BeadStudio	call rate <98%, IBD (Z0<0.8), Mendel errors >0, Duplicate concordance <100%	530,014	IMPUTE v2.3.0	1000 Genomes Phase 1 integrated v3	Genotype Likelihood <0.9	Plink, R

Supplementary Table 20. Genotyping information: *de novo* replication studies.

Study Name	Bus Santé	ESTHER	KORA **F3** and **F4**	OGP	SAPHIR	SKIPOGH
Genotyping platform	LGC Genomics SNP-line, using KASP™ Chemistry and 1536-well plates	LGC Genomics SNP-line, using KASP™ Chemistry	MALDITOF MS, Bruker Daltonik GmbH, Leipzig, Germany	LGC Genomics SNP-line, using KASP™ Chemistry	Sequenom platform	LGC Genomics SNP-line, using KASP™ Chemistry and 1536-well plates
Amount of DNA used per SNP (in ng)	DNA amplified, but typically 5 -7.5 ng of gDNA per genotype	3.75 ng	1 ng	5 ng	15 ng	5 -7.5 ng of gDNA per genotype
Genotyping method	See note[1]	See note[1]	iPlex Gold	See note[1]	Mass ARRAY Analyzer 4 system	See note[1]
No. of duplicates and concordance per SNP (provided per individual SNP)	Not duplicated	LGC Genomics does not add duplicates. The data for each SNP represents one reaction per sample.	At least 15% duplicate genotyping per SNP. Concordance≥95%, median = 100%	LGC Genomics does not add duplicates. The data for each SNP represents one reaction per sample.	70 duplicates; of 46 SNPs genotyped, 44 had a concordance of 100%, 2 had 1 discordant sample each	29 samples genotyped in duplicate. SNP concordance varied from 86% to 100%.
Number attempted / number genotyped samples per individual SNP	The genotyping call rate (%) was typically between 0.95-0.97	Call-rate range 0.98-1	NA	Allele call rate 0.99	46 SNPs were genotyped: mean call-rate = 99.3% (min = 98.15%, max = 99.65%)	Median SNP call-rate = 97.2% (min =94.5%, max = 99.5%)
Other QC laboratory-specific indices	See note[2]	none indicated by the lab	NA	none indicated by the lab	automatic calculation of the HWE, comparision of the obtained genotypes with HapMap Data	See note[2]

[1] Genotyped using KASPar (Kompetitive Alelle Specific PCR) v4.0 after whole genome amplification by primer extension preamplification (PEP) using thermostable DNA polymerases.

[2] All assays have been validated on an in-house DNA panel (44 random Caucasian DNA samples). All sample plates genotyped include at least two negative controls. ie. blank/water controls. All genotyping data is initially generated by an automated algorithm (genotype calling based upon recorded fluorescence values). All genotyping data is manually checked and verified by no less than two experienced scientists at LGC genomics.

Supplementary Table 21. Morpholino (MO) sequences.

Target gene	Splice or ATG	MO sequence
A1cf	ATG	5' CCCCACATTTTTGATTGGTTTCCAT 3'
Dpep	ATG	5' AATCTTGACCCATTCCATCATCACC 3'
Kbtbd2	ATG	5' TGTTCGTATCCCATGAGTTTTCAAC 3'
Nfatc1	Splice	5' CGCATCTGTAAGGTACAATCACATT 3'
Nfkb1	ATG	5' TCCTCGCCAGCCATGATTCCTTTGC 3'
Ptpro	ATG	5' GATCGCACTCTTTGATTCTCGGCGT 3'
Skila	Splice	5' TTGCCCTGCAAACACACATACACAC 3'
Skilb	Splice	5' CCCGGATGACTGAAACAAGTCAAAA 3'
Sypl2a	Splice	5' TTGAAATGTGGTTGTTTATACCTGA 3'
Sypl2b	Splice	5' AGACTCTTTAATGAGGTTTACCTAA 3'
Tspan9a	Splice	5' GTAGGAGTGGCAAAACTTACGCTCA 3'
Tspan9b	ATG	5' GCACAGGCATCCACGAGCCATCTTC 3'
Uncx	Splice	5' ATCCCCCGAATCTATGTAAGAAACA 3'
Wnt7aa	ATG	5' TCCAGCGGCGCGTTTTCCTGCTCAT 3'

Supplementary Note.

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