

Supplementary Material

Functional genomic annotation of genetic risk loci highlights inflammation and epithelial biology networks in chronic kidney disease

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Supplementary Table 1

List of the publications included in the analysis

The table shows the list of reviewed articles that described an association between single nucleotide polymorphisms (SNPs), kidney function, chronic kidney disease, end stage kidney failure or other related symptoms. 44 leading SNPs from the first 10 publications were included in our study.

List of Reviewed Articles	
1	New loci associated with kidney function and chronic kidney disease Köttgen A et al. Nat Genet. 2010 May;42(5):376-84. doi: 10.1038/ng.568. Epub 2010 Apr 11.
2	Genome-wide association and functional follow-up reveals new loci for kidney function Pattaro C et al. PLoS Genet. 2012;8(3):e1002584. doi: 10.1371/journal.pgen.1002584. Epub 2012 Mar 29.
3	Association of variants at UMOD with chronic kidney disease and kidney stones-role of age and comorbid diseases Gudbjartsson DF et al. PLoS Genet. 2010 Jul 29;6(7):e1001039. doi: 10.1371/journal.pgen.1001039. Erratum in: PLoS Genet. 2010;6(11).
4	Multiple loci associated with indices of renal function and chronic kidney disease. Köttgen A et al. Nat Genet. 2009 Jun;41(6):712-7. doi: 10.1038/ng.377. Epub 2009 May 10
5	Genetic loci influencing kidney function and chronic kidney disease Chambers JC et al. Nat Genet. 2010 May;42(5):373-5. doi: 10.1038/ng.566. Epub 2010 Apr 11
6	Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations Okada Y et al. Nat Genet. 2012 Jul 15;44(8):904-9. doi: 10.1038/ng.2352
7	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function Chasman DI et al. Hum Mol Genet. 2012 Dec 15;21(24):5329-43. doi: 10.1093/hmg/ddz369. Epub 2012 Sep 8.
8	Candidate genes for non-diabetic ESRD in African Americans: a genome-wide association study using pooled DNA Bostrom MA et al. Hum Genet. 2010 Aug;128(2):195-204. doi: 10.1007/s00439-010-0842-3. Epub 2010 Jun 8
9	New susceptibility loci associated with kidney disease in type 1 diabetes Sandholm N et al. PLoS Genet. 2012 Sep;8(9):e1002921. doi: 10.1371/journal.pgen.1002921. Epub 2012 Sep 20
10	Promoter polymorphism of the erythropoietin gene in severe diabetic eye and kidney complications Tong Z et al. Proc Natl Acad Sci U S A. 2008 May 13;105(19):6998-7003. doi: 10.1073/pnas.0800454105. Epub 2008 May 5
11	Genetic association for renal traits among participants of African ancestry reveals new loci for renal function Liu CT et al. PLoS Genet. 2011 Sep;7(9):e1002264. doi: 10.1371/journal.pgen.1002264. Epub 2011 Sep 8.
12	CUBN is a gene locus for albuminuria Böger CA et al. J Am Soc Nephrol. 2011 Mar;22(3):555-70. doi: 10.1681/ASN.2010060598
13	Genome-wide association study for renal traits in the Framingham Heart and Atherosclerosis Risk in Communities Studies Kottgen A et al. BMC Med Genet. 2008 Jun 3;9:49. doi: 10.1186/1471-2350-9-49

14	A single nucleotide polymorphism within the acetyl-coenzyme A carboxylase beta gene is associated with proteinuria in patients with type 2 diabetes Maeda S et al. PLoS Genet. 2010 Feb 12;6(2):e1000842. doi: 10.1371/journal.pgen.1000842
15	Genome-wide association scan for diabetic nephropathy susceptibility genes in type 1 diabetes Pezzolesi MG et al. Diabetes. 2009 Jun;58(6):1403-10. doi: 10.2337/db08-1514. Epub 2009 Feb 27.
16	Effects of MCF2L2, ADIPOQ and SOX2 genetic polymorphisms on the development of nephropathy in type 1 Diabetes Mellitus Zhang D et al. BMC Med Genet. 2010 Jul 28;11:116. doi: 10.1186/1471-2350-11-116.
17	A GREM1 gene variant associates with diabetic nephropathy McKnight AJ et al. J Am Soc Nephrol. 2010 May;21(5):773-81. doi: 10.1681/ASN.2009070773. Epub 2010 Feb 11.
18	Genetic analysis of coronary artery disease single-nucleotide polymorphisms in diabetic nephropathy McKnight AJ et al. Nephrol Dial Transplant. 2009 Aug;24(8):2473-6. doi: 10.1093/ndt/gfp015. Epub 2009 Mar 31.
19	Confirmation of genetic associations at ELMO1 in the GoKinD collection supports its role as a susceptibility gene in diabetic nephropathy. Pezzolesi MG et al. Diabetes. 2009 Nov;58(11):2698-702. doi: 10.2337/db09-0641. Epub 2009 Aug 3
20	An intergenic region on chromosome 13q33.3 is associated with the susceptibility to kidney disease in type 1 and 2 diabetes. Pezzolesi MG et al. Kidney Int. 2011 Jul;80(1):105-11. doi: 10.1038/ki.2011.64. Epub 2011 Mar 16.
21	Targeted genome-wide investigation identifies novel SNPs associated with diabetic nephropathy McKnight AJ et al. Hugo J. 2009 Dec;3(1-4):77-82. doi: 10.1007/s11568-010-9133-2. Epub 2010 Feb 24
22	Identification of PVT1 as a candidate gene for end-stage renal disease in type 2 diabetes using a pooling-based genome-wide single nucleotide polymorphism association study. Hanson RL et al. Diabetes. 2007 Apr;56(4):975-83
23	A genome-wide association study for diabetic nephropathy genes in African Americans McDonough CW et al. Kidney Int. 2011 Mar;79(5):563-72. doi: 10.1038/ki.2010.467. Epub 2010 Dec 8
24	Genetic variations in the gene encoding ELMO1 are associated with susceptibility to diabetic nephropathy Shimazaki A et al. Diabetes. 2005 Apr;54(4):1171-8

Supplementary Table 2

List of single nucleotide polymorphisms (SNPs) that met our criteria

The table shows the list of the single nucleotide polymorphisms (SNPs) which reached the genome wide significance ($P < 5 \times 10^{-8}$) in the association with eGFR (estimated glomerular filtration rate, based on creatinine (crea) or cystatin C (cys) levels) and/or the presence of chronic kidney disease (CKD) or end stage renal disease (ESRD).

Genes less than 250 kb from the leading SNPs are listed. Color-coding shows the baseline expression of the transcripts based on human kidney RNA sequencing, red: high expression, yellow: medium expression, green: low expression, blue: no expression. Genes with available probe set IDs on the microarray chip are marked bold.

	Leading SNPs	Location (chr)	Position	Leading SNP functional location	Association parameter	Association p-value	Genes within 250-250kb	Journal
1	rs10794720	10	1156165	Intronic	eGFRcrea	$p=2.1 \times 10^{-8}$	LARP4B , GTPBP4 , IDI2 , IDH1 , WDR37 , ADARB2	1
2	rs491567	15	53946593	Intronic	eGFRcrea	$p=1.3 \times 10^{-8}$	WDR72	1
3	rs267734	1	150951477	Upstream	eGFRcrea	$p=5.2 \times 10^{-9}$	CTSS , CTSK , ARNT , SETDB1 , CERS2 , ANXA9 , FAM63A , PRUNE , MLLT11 , BNIPL , C1orf56 , GABPB2 , SEMA6C , CDC42SE1 , LYSMD1 , SCNM1 , TMOD4 , VPS72 , PIPSK1A , TNFAIP8L2	1
4	rs347685	3	141807137	Intronic	eGFRcrea	$p=7.0 \times 10^{-9}$	ATP1B3 , TFDP2 , GK5 , XRN1	1
5	rs4744712	9	71434707	Intronic	eGFRcrea	$p=7.2 \times 10^{-10}$	PIPSK1B , FAM122A , PRKACG , FXN	1
6	rs626277	13	72347696	Intronic	eGFRcrea	$p=2.9 \times 10^{-10}$	DACHI	1
7	rs1394125	15	76158983	Intronic	eGFRcrea	$p=3.7 \times 10^{-10}$	SNUPN , IMP3 , SNX33 , CSPG4 , ODF3L1 , UBE2Q2 ,	1

							NRG4, C15orf27	
8	rs9895661	17	59456589	Intronic	eGFRcrea	$p=1.4 \times 10^{-8}$	BCAS3, TBX2, C17orf82, TBX4, NACA2	1
9	rs10109414	8	23751151	Intergenic	eGFRcrea	$p=1.0 \times 10^{-8}$	NKX3-1, NKX2-6, STC1	1
10	rs911119	20	23612737	Intergenic	eGFRcys	$p=2.3 \times 10^{-138}$	NAPB, CSTL1, CST11, CST8, CST9L, CST9, CST3, CST4, CST1, CST2, CST5	1
11	rs6465825	7	77416439	Intergenic	eGFRcrea	$p=3.5 \times 10^{-9}$	PTPN12, RSBN1L, TMEM60, PHTF2, MAGI2	1
12	rs653178	12	112007756	Intronic	eGFRcys	$p=3.8 \times 10^{-8}$	CUX2, FAM109A, SH2B3, ATXN2, BRAP, ACAD10, ALDH2	1
13	rs6420094	5	176817636	Intronic	eGFRcrea	$p=3.8 \times 10^{-12}$	NSD1, RAB24, PRELID1, MXD3, LMAN2, RGS14, SLC34A1, PFN3, F12, GRK6, PRR7, DBN1, PDLM7, DOK3, DDX41, FAM193B, TMED9, B4GALT7	1
14	rs11959928	5	39397132	Intronic	eGFRcrea	$p=1.8 \times 10^{-11}$	FYB, C9, DAB2	1
15	rs12917707	16	20367690	Upstream	eGFRcrea	$p=1.2 \times 10^{-20}$	GP2, UMOD, PDILT, ACSM5, ACSM2A, ACSM2B	1
16	rs2453533	15	45641225	Intergenic	eGFRcrea	$p=4.6 \times 10^{-22}$	DUOX1, DUOXA2, DUOXAI, SHF, SLC28A2, GATM, SPATA5L1, C15orf48, SLC30A4, BLOC1S6	1
17	rs17319721	4	77368847	Intronic	eGFRcrea	$p=1.1 \times 10^{-19}$	SCARB2, FAM47E, STBD1, CCDC158, SHROOM3	1
18	rs1933182	1	109999588	Intergenic	eGFRcrea	$p=1.3 \times 10^{-8}$	SARS, CELSR2, PSRC1, MYBPH1, SORT1, PSMA5, SYPL2, ATXN7L2, CYB561D1, AMIGO1, GPR61, GNAI3, AMPD2, GSTM2, GSTM4,	1

							GSTM1, GNAT2	
19	rs16864170	2	5907880	Intergenic	CKD	$p=4.5 \times 10^{-8}$	SOX11	1
20	rs881858	6	43806609	Intergenic	eGFRcrea	$p=2.2 \times 10^{-11}$	POLH, GTPBP2, MAD2L1BP, RSPH9, MRPS18A, VEGFA, C6orf223	1
21	rs7805747	7	151407801	Intronic	CKD	$p=8.6 \times 10^{-9}$	RHEB, PRKAG2	1
22	rs4014195	11	65506822	Intergenic	eGFRcrea	$p=3.3 \times 10^{-8}$	SCYL1, LTBP3, SSSCA1, FAM89B, EHBP1L1, KCNK7, MAP3K11, PCNXL3, SIPA1, RELA, KAT5, RNASEH2C, AP5B1, OVOL1, SNX32, CFL1, MUS81, EFEMP2, CCDC85B, FOSL1, CTSW, FIBP, C19orf68, TSGA10IP, SART1, DRAP1	1
23	rs12460876	19	33356891	Intronic	eGFRcrea	$p=5.5 \times 10^{-9}$	ANKRD27, RGS9BP, NUDT19, TDRD12, SLC7A9, CEP89, C19orf40, RHPN2, GPATCH1	1
24	rs2279463	6	160668389	Intronic	eGFRcrea	$p=8.7 \times 10^{-10}$	IGF2R, SLC22A1, SLC22A2, SLC22A3	1
25	rs10774021	12	349298	Intronic	eGFRcrea	$p=6.7 \times 10^{-9}$	IQSEC3, SLC6A12, SLC6A13, KDM5A, CCDC77, B4GALNT3	1
26	rs6431731	2	15863002	Intergenic	eGFRcrea	$p=4.6 \times 10^{-8}$	DDX1, MYCN	2
27	rs3925584	11	30760335	Intergenic	eGFRcrea	$p=1 \times 10^{-9}$	MPPED2, DCDCS, DCDC1	2
28	rs12124078	1	15869899	Intronic	eGFRcrea	$p=9.8 \times 10^{-10}$	FHAD1, EFHD2, CTRC, CELA2A, CELA2B, CASP9, DNAJC16, AGMAT, DDI2, RSC1A1, SLC25A34, TMEM82, FBLIM1	2
29	rs2453580	17	19438321	Intronic	eGFRcrea	$p=4.6 \times 10^{-8}$	EPN2, B9D1, MAPK7, MFAP4, RNF112, SLC47A1, ALDH3A2, ALDH3A1,	2

							SLC47A2, ULK2	
30	rs11078903	17	37631924	Intronic	eGFRcrea	p=2.4 x10 ⁻⁹	FBXL20, MED1, CDK12, NEUROD2, PPP1R1B, STARD3, PNMT, PGAP3, ERBB2, TCAP	2
31	rs4293393	16	20364588	Intronic	eGFRcrea	p=2.6 x10 ⁻¹⁰	GP2, UMOD, PDILT, ACSM5, ACSM2A, ACSM2B	3
X	rs12917707	16	20367690	Intronic	CKD	p=2.9 x 10 ⁻⁹	GP2, UMOD, PDILT, ACSM5, ACSM2A, ACSM2B	4
32	rs6040055	20	10633313	Intronic	eGFRcrea	p=1 x 10 ⁻⁸	MKKS, SLX4IP, JAG1	4
33	rs1731274	8	23766319	Intergenic	eGFReys	p=4.6 x 10 ⁻⁸	STC1, NKX3-1, NKX2-6	4
34	rs13038305	20	23610262	Intronic	eGFRcys	p=2.2 x 10 ⁻⁸⁸	NAPB, CSTL1, CST11, CST8, CST9L, CST9, CST3, CST4, CST1, CST2, CST5	4
35	rs10206899	2	73900900	Intronic	eGFRcrea	p=2.3 x 10 ⁻⁸	ALMS1, NAT8, NAT8B, TPRKB, DUSP11, C2orf78, STAMBP, ACTG2	5
X	rs9895661	17	59456589	Intronic	eGFRcrea	p=4.8 × 10 ⁻¹¹	BCAS3, TBX2, C17orf82, TBX4, NACA2	6
36	rs11864909	16	20400839	Intronic	eGFRcrea	p=3.6 × 10 ⁻¹⁰	GP2, UMOD, PDILT, ACSM5, ACSM2A, ACSM2B, ACSM1	6
37	rs13146355	4	77412140	Intronic	eGFRcrea	p=6.6 × 10 ⁻¹¹	FAM47E, STBD1, CCDC158, SHROOM3	6
38	rs10277115	7	1285195	Intergenic	eGFRcrea	p=1.0 × 10 ⁻¹⁰	C7orf50, GPR146, GPER, ZFAND2A, UNCX, MICALL2, INTS1	6
39	rs3828890	6	31440669	Unknown	eGFRcrea	p=1.2 × 10 ⁻⁹	HLA-C, HLA-B, MICA, MICB, DDX39B, ATP6VIG2, LTA, NFKBIL1, LST1, NCR3, AIFI, PRRC2A, BAG6, C6orf47, GPANK1, CSNK2B, LY6G5B, ABHD16A,	6

							LY6G5C, APOM, LY6G6F, LY6G6C, DDAH2, C6orf25, LTB, TNF	
40	rs7208487	17	37543449	Intronic	eGFRcrea	p=5.6 x 10 ⁻⁹	PLXDC1, CACNB1, ARL5C, RPL19, STAC2, FBXL20, MED1, CDK12, NEUROD2, PPP1R1B, STARD3	7
41	rs4821469	22	36616445	Intergenic	ESRD	p=1.78 x 10 ⁻¹⁹	APOL3, APOL4, APOL2, APOL1, MYH9, TXN2	8
42	rs12437854	15	94141833	Intergenic	ESRD	p=2 x 10 ⁻⁹	no gene in <250 kb distance	9
43	rs7583877	2	100460654	Intronic	ESRD	p=1.2 x 10 ⁻⁸	AFF3	9
44	rs1617640	7	100317298	In promoter but not missence	ESRD	p=2.66 x 10 ⁻⁸	TSC22D4, NYAPI, AGFG2, SAP25, LRCH4, FBXO24, PCOLCE, MOSPD3, TFR2, ACTL6B, GNB2, GIGYF1, POP7, EPO, ZAN, EPHB4, SLC12A9, TRIP6, SRRT, UFSP1, ACHE	10

List of Journals

1	New loci associated with kidney function and chronic kidney disease Köttgen A et al. Nat Genet. 2010 May;42(5):376-84. doi: 10.1038/ng.568. Epub 2010 Apr 11.
2	Genome-wide association and functional follow-up reveals new loci for kidney function Pattaro C et al. PLoS Genet. 2012;8(3):e1002584. doi: 10.1371/journal.pgen.1002584. Epub 2012 Mar 29.
3	Association of variants at UMOD with chronic kidney disease and kidney stones-role of age and comorbid diseases Gudbjartsson DF et al. PLoS Genet. 2010 Jul 29;6(7):e1001039. doi: 10.1371/journal.pgen.1001039. Erratum in: PLoS Genet. 2010;6(11).
4	Multiple loci associated with indices of renal function and chronic kidney disease. Köttgen A et al. Nat Genet. 2009 Jun;41(6):712-7. doi: 10.1038/ng.377. Epub 2009 May 10
5	Genetic loci influencing kidney function and chronic kidney disease Chambers JC et al. Nat Genet. 2010 May;42(5):373-5. doi: 10.1038/ng.566. Epub 2010 Apr 11
6	Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations Okada Y et al. Nat Genet. 2012 Jul 15;44(8):904-9. doi: 10.1038/ng.2352
7	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function Chasman DI et al. Hum Mol Genet. 2012 Dec 15;21(24):5329-43. doi: 10.1093/hmg/ddz369. Epub 2012 Sep 8.
8	Candidate genes for non-diabetic ESRD in African Americans: a genome-wide association study using pooled DNA Bostrom MA et al. Hum Genet. 2010 Aug;128(2):195-204. doi: 10.1007/s00439-010-0842-3. Epub 2010 Jun 8
9	New susceptibility loci associated with kidney disease in type 1 diabetes Sandholm N et al.

	PLoS Genet. 2012 Sep;8(9):e1002921. doi: 10.1371/journal.pgen.1002921. Epub 2012 Sep 20
10	Promoter polymorphism of the erythropoietin gene in severe diabetic eye and kidney complications Tong Z et al. Proc Natl Acad Sci U S A. 2008 May 13;105(19):6998-7003. doi: 10.1073/pnas.0800454105. Epub 2008 May 5

Supplementary Figure 1

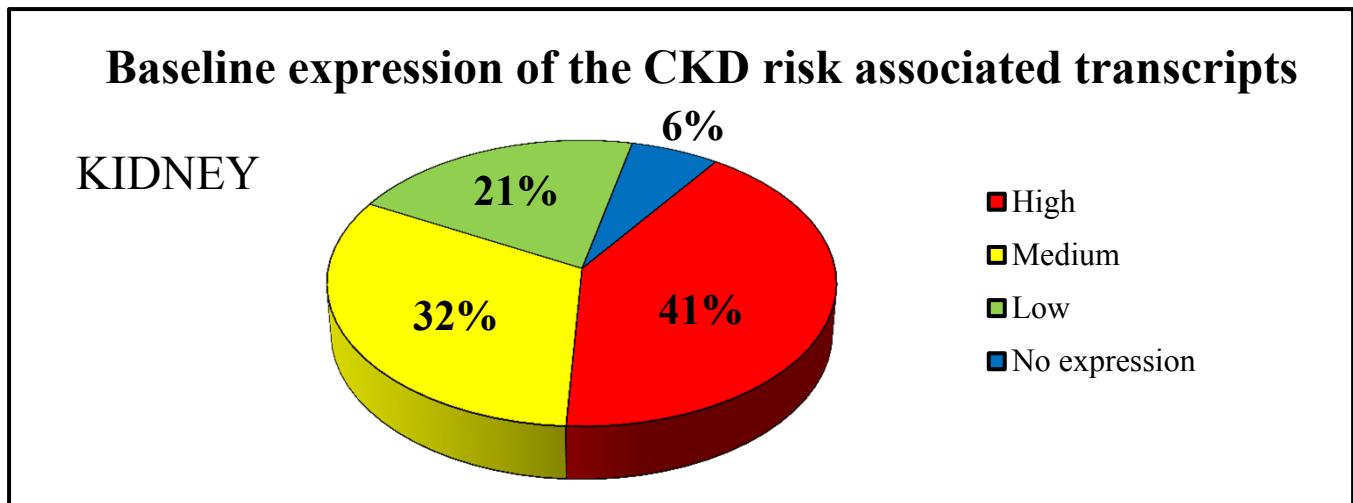
Baseline expression of the CKD risk loci associated transcripts in kidney

Human kidney RNA sequencing data was used to examine the baseline expression of the transcripts.

41 % of the CKD risk loci neighboring transcripts are highly expressed in the kidney (red),

32 % showed medium expression (yellow), 21 % showed low expression in the kidney (green).

6% of the transcripts are not expressed (blue).



Supplementary Figure 2

Comprehensive RNA sequencing map of the CKD risk associated transcripts in 16 different human tissues

Expression levels of 306 CRATs were examined using the Illumina Body Map (www.ebi.ac.uk).

The relative expression of each gene in each tissue is shown in the table. The transcripts with the highest expression represented on the top of the map. High expression values (> 90 percentile) are marked red, low expression values (<10 percentile) marked blue. Expression levels with FPKM values (fragments per kilobase of exon per million fragments mapped) lower than 0.1 are white.

Gene Symbol	adipose	adrenal	brain	breast	colon	heart	kidney	leukocyte	liver	lung	lymph node	ovary	prostate	skeletal muscle	testis	thyroid
UMOD						1417									0.1	
RPL19	975	1359	275	665	1003	273	567	1536	413	1091	1339	1169	1435	964	745	737
CFL1	338	467	334	209	227	112	327	695	169	501	332	231	269	78	208	193
CERS2	53	34	52	37	45	27	149	113	278	110	81		100	18	37	58
CST3	307	218	252	331	310	177	146	510	244	347	334	135	477	212	313	234
ACSM2A	0.2	0.3	0.6		0.5	0.3	133	0.2	98	0.1	0.5	0.6		0.1	0.6	0.2
ACSM2B		0.3	0.3	0.1	1	0.1	121					0.6	0.1		0.4	0.2
ATP1B3	59	91	61	49	63	31	105	65	9	211	135	64	51	13	94	92
GATM	6	11	89	7	11	6	89	3	214	5	15	36	17	12	33	20
ALDH2		39	121	384	134	98	81	86	307	143	52		123	57	53	96
DAB2	60	25	3	28	20	7	78	7		41	26	20	19		19	13
TMED9	54	66	16	39	37	19	75	60	117	73	70	51	47	21	44	70
MYH9		143	23	107		26	63	194	23	225	97	93	87	41	95	75
RHEB	70	55	99	52	103	47	62	29	36	88	38	79	110	85	67	122
GNB2	127	70	42	65	72	28	61	159	36	132	80	112	69	88	74	65
NAT8			0.1				61	0.1	5	0.2		0.2	0.2		0.4	
PSMA5	33	40	28	39	37	30	56	74	66	52	37	46	45	41	58	48
LMAN2	28	33	12	22	37	15	55	62	85	42	40	31	44	22	61	60
SLC47A2		0.1	1	0.1			48			0.1	0.1	2	0.1	0.1	0.7	0.4
DDX1	41	39	64	53	44	43	47	21	21	17	16	57	40	50	57	81
SARS	71	70	87	44	63	26	46	57	37	73	38	90	70	76	60	107
SCARB2	51	42	94	71	63	28	46	23	57	75	39	69	73	88	48	76
TXN2	27	32	28	34	24	36	44	37	43	28	30	43	46	39	32	58
VEGFA		17	5	15	13	28	43	3	32	65	32	21	32	29	6	93
WDR72	0.1	1	0.2	0.3	0.2		43		10	0.1		0.7	0.2		0.6	27
SLC47A1	5	2	2	2	1	2	41	1	29	4	2	9	1	26	8	13
SORT1		9	87	38	14	30	41	17	6	17	9	6	16	40	45	46
PRELID1	32	83	20	26	35	7	39	83	39	36	34	31	31	4	28	30
FIBP	22	31	37	23	14	16	38	27	13	11	14	29	29	17	49	22
ALDH3A2	28	15	15	68	21	14	37	12	38	47	11	35		34	26	73
SLC6A13	0.2	0.2	2	0.2		0.7	35		2	0.2	0.1	0.6	0.2	0.3	0.9	5
IDI1	13	27	64	20	12	10	31	28	53	46	26	46	15	18	25	38
DRAP1	62	55	64	51	61	17	30	46	19	46	28	59	43	53	121	78
GNAI3	29	27	12	25	29	6	28	52	12	24	22	33	31	6	33	24
SLC6A12	0.6	0.5	4	0.4	0.2	0.3	28	2	13	1	1	1			1	7
CDC42SE1	23	44	12	15	14	10	26	184	8	55	71	27	30	11	13	25
ERBB2	3	4			9	16	26	2	2		4		14	5		
MKKS	8	9	18	13	12	16	26	16	14	6	13	13	16	6	24	14
TPRKB	17	36	15	27	29	24	26	20	17	12	21	46	30	11	61	34

APOL1	24	30	5	18	25	10	25	18	21	75	18	41	52	7	24	13
PTPN12	43	33	14	27	37	20	24	57	8	90	36	29	37	11	33	48
BLOC1S6		42	41	28		20	23	26	12	20	21	41	25	6	27	41
PCOLCE	15	74	3	36	10	14	21	1	9	30	50	59	40	2	41	24
SCNM1	22	46	20	20	21	5	20	34	7	15	22	30	27		32	30
ACTG2	36	173	3	40	2101	2	19		2	86	63	66	1888	11	162	13
GSTM4	9	17	19	18	13	13	19	5	6	11	11	38	45	13	16	20
PRKAG2	12	17	18	10	13	44	19	23	9	9	10	10	33	3	22	24
SRRT	9	21	12	10	13	9	19	15	11	14	33	30	26	26	60	17
UBE2Q2	17	17	14	18	35	11	19	27	2	20	18	26	33	10	25	23
VPS72	13	18	21	17	22	10	19	16	9	14	14	24	35	44	27	25
MRPS18A	16	19	13	16	12	12	18	15	24	10	13	16	26	31	15	25
SLC22A2		0.7			0.1		18		0.1		0.2		0.1		0.1	0.3
C7orf50	17	15	17	19	18	10	17	13	6	11		29	25	6	18	38
SART1	47	51	11	27	31	9	17	28	11	26	30	18	36	38	38	44
APOL2	17	16	22	16	9	13	16	20	13	42	15	14	15	9	10	13
DUSP11	10	12	7	10	8	6	16	25	6	8	11	16	13	5	17	14
IMP3	10	24	14	15	12	8	16	29	15	6	17	20		13	15	24
KAT5	13	22	16	14	14	8	16	17	6	12	9	24	26	20	27	37
MFAP4	11	36	3	39	70	23	16			551	67	66	221	7	57	23
APOL3	66		3	30	38	10	15		4	62	42	14	30	7		
DBN1	22	12	28	19	19	3	15	3	0.7	8	9	39	22	4	25	16
GTPBP4	15	21	16	14	13	9	15	14	7	11	13	25	15	21	26	28
IGF2R	27	11	4	13	12	16	15	68	13	9	15	11	12	46	11	20
RELA	37	29	10	18	14	9	15	37	11	41	27		25	32	18	24
RNASEH2C	21	40	8	17	19	8	15	13	7	11	13	26	23		23	9
STAMBP	9	9	22	11	9	9	15	17	7	7	15	11	19	13	16	14
DDX41	19	22	24	14	15	4	14	23	9	11	15	29	14	9	20	27
LTBP3	13	23	18	24	24	11	14	4	4	28	25	50	31	12	23	30
PIP5K1A	8	15	8	9	6	10	14	13	5		15	14		7	18	12
SCYL1	15	20	13		11	9	14		17	15	17	21				
TBX2	5	3	0.7	4	2	2	14		0.9	26	3	3	11	0.9	7	4
TRIP6	11	12	4	15	8	3	14	1	6	12	8	16	18	1	13	22
EPHB4	22	27	2	15	11	9	13	2	14	7	10	42	6	0.8	15	10
FAM193B	6	13	6	5	10	3	13	6	8	19	28	7	11	5	9	8
FAM63A	4	3	8	6	6	12	13	16	3	4	5	6	12	5	9	14
FBLIM1	18	42	2	7	13	14	13	0.6	0.7	20	28	35	18	1	39	7
GSTM2	4	9	12	38	12	20	13	4	2	24	12	67	30	14	18	23
HLA-B	37	45	15	28	5	7	13	757	0.8	506	44	2	31	8	16	9
JAG1	22	15	4	16	21	6	13	1	1	22	13	11	20	4	13	10
POP7	10	13	16	10	8	6	13	11	16	7	10	10	13	19	11	11
RAB24	6	14	11	8	6	4	13	24		16	21	9	15	4	7	7
SLC34A1							13		0.1							
RHPN2	0.9	2	3	2	3	0.6	12	0.5	6	5	2	2	3	0.1	0.9	3

SIPA1	11	45	1	7	7	3	12	35	7	18	46	12	15	1	6	6
TSC22D4	9	12	88	8	10	8	12	36	2	14	26	10	14	3	11	9
ARNT	21	11	5	15		8	11	21	6		13	29	15	18	16	14
CTSS	31	43	10	26	16	10	11	2006	19	131	63	22	25	3	9	10
MAP3K11	20	17	5	14	10	4	11	27	16	29	18	8	12	4	11	10
PRUNE	7	7	6	8	11	17	11	20	4	8	10	12	16	10	14	20
RGS14	4	12	5	3	2	0.6	11	27	8	5	23	3	3	0.2	3	3
SNUPN	5	11	6	10	8	5	11	10	5	7	11	14	14	9	24	15
TFDP2	6	3	5	10	6	14	11	6	5	6	5	6	5	6	52	10
AGFG2	10	12	8	5	4	4	10	7	19	5	11	22	9	2	12	7
FXN	4	12	5	8	6	15	10	18	32	4	14	14	16	7	12	8
SSSCA1	19	22	8	14	7	10	10	19	11	23	13	19	12	9	16	23
TMEM60	8	12	7	11	8	4	10	28	6	7	15	12	11	9	19	14
ATXN2	9	9	13	9	6	9	9	10	6	17	10	15	16		18	11
B9D1			6				9							2	17	14
C11orf68	12	9	14	11	13	7	9	20	4	19	18	16	26	23	21	18
INTS1	6	19	9	14	7	4	9	7	8	6	9	6	12	17	21	9
MAD2L1BP	4	9	4	4	4	8	9	15	6	5	7	8	5	5	6	10
FAM89B	8	13	7	10	20	6	8	29	5	17	25	15	23	23	10	8
LARP4B	9	10	7	10	5	9	8	19	4	10	8	10	8	12	14	16
MPPED2	2	2	6	1	3	2	8	0.9	0.6	1	2	2	6	2	3	31
STARD3	9	16	12	9	10	6	8	28	8	13	32	12	12	11	13	17
ZFAND2A	6	15	35	8	7	3	8	12	16	16	15	12	12	2	19	40
ACAD10		3					7								3	
AGMAT		2	0.8	0.7	0.9		7	2	21	0.3	0.8					0.7
ANKRD27	5	5	4	6	11	3	7	10	1	5	7	10	15	12	15	7
ANXA9	0.7	0.5	1	0.7	0.8	0.8	7	2	6	0.4	0.8	1	4	0.1	1	4
GTPBP2	14	12	4	8	8	6	7	15	2	30	17	8	12	20	10	14
PDLIM7	17	47	5	21	69	5	7	13	2	18	11	44	83	32	57	30
SYPL2	0.7	0.9	0.2	2	1	5	7		2	0.3	1	3	2	35	3	15
B4GALT7	5	8	5	16	3	3	6	3	4	3	8	7	6	4	6	7
DACH1	3	0.8	1	1	1	0.8	6	0.8	0.2	3	0.8	0.9	2	1	5	0.3
DNAJC16	3	4	4	4	2	3	6	6	4	2	5	6	4	6	5	4
EFHD2	14	27	26	9	15	3	6	145	4	27	19	14	12	1	22	8
FAM122A	5	6	4	7	7	5	6	11	3	3	6	10	8	5	7	7
LRCH4	4	16	3	4	3	3	6	39	4	11	38	19	7	9	24	11
MOSPD3	7	6	5	5	5	2	6	6	6	6	6	10	10	2	15	6
NACA2	72	86	19	69	69	4	6	12	4	15	10	127	14	11	120	40
NUDT19	4	4	3	6	3	8	6	8	5	3	5	4	5	11	3	4
PGAP3	4	6			3	2	6	6	6		2		5	1		
PPP1R1B	14	0.3	94	35	30	0.5	6	0.1		15	2	13	25	0.5	10	0.5
RSBN1L	5	9	7	5	7	2	6	23	3	9	9	13	10	5	17	17
SLC7A9		0.1	0.2		0.2	0.1	6		4	0.3	0.5	0.3	0.3		0.2	0.2
ACSM5	3	0.4	0.5	9	1	0.3	5		23	0.6	2	0.4	1	1	1	2

AMPD2	4	9	11	4	5	2	5	23	7	7	19	10	10	2	5	5
BRAP	8	8	8	7	9	4	5	10	3	4	6	9	9	13	56	12
CELSR2	0.3	0.4	14	1	1	1	5	0.6	1	0.4	0.7	2	3	2	5	4
CTSK	171	24	3	45	91	7	5	2	1	30	120	55	108	10	46	21
DDI2	9	4	4	8	3	5	5	7	6	5	5	6	5	27	4	5
GK5	3	4	3	6	1	3	5	3	1	4	2	5	6	2	5	5
MED1	8	10	5	6	6	5	19	3	5	8	13	10	6	8	8	8
NAPB	3	4	182	3	8	2	5	3	1	5	5	6	8	1	6	7
NSD1	5	5	4	4	4	4	5	14	2	3	5	8	5	6	8	8
PHTF2	4	7	6	7		9	5	8		7	8	7	6	22	10	11
PIP5K1B	2	3	10	2	7	24	5	4	0.1	5	5	2	6	0.7	21	1
SNX33	11	6	1	10	8	2	5	2	4	10	10	11		2	7	7
SPATA5L1	2	4	2	3	3	2	5	6	3	3	7	6	6	3	6	8
WDR37	2	6	8	4	2	5	5	14	3	3	5	4	3	3	4	7
APOL4	6	7	3	3	4	3	4	1	0.5	5	5		10	0.7	3	3
CASP9	2	2	3	2	2	3	4	8	2	4	4	9	5	3	5	4
CCDC85B	19	24	16	13	14	7	4	14	3	32	15	10	20	6	10	9
CDK12	7	7	3	5	5	3	4	14	3	5	9	7	5	4	10	6
EHBP1L1	14	30	3	8	21	11	4		1	15	17	14	27	43	12	16
EPN2			12	3	8	6	4	0.9	1		6	8	12	5	11	5
FAM47E		0.3	7				4	0.1			0.2	2				6
GIGYF1	6	9	3	5	3	3	4	4	1	4	8	8	6	3	7	7
KDM5A	6	7		5	4	3	4		2	4	7	7	5	3	10	7
PCNXL3	3	6	2	3	2	1	4	5	3	3	7	7	4	2	6	5
SH2B3	17	15	3	9	5	10	4	31	3	16	13	7	5	3	6	6
SHROOM3	0.2	2	0.6	2	2	1	4		3	6	0.3	2	4	0.1	2	3
STAC2	0.6	0.4	13	5	0.7	0.3	4		0.1	0.6	0.9	1	6	0.3	2	0.2
STC1	26	3	0.7	5	51	4	4		0.1	11	18	1	23	2	1	14
ULK2	6	3	11	7	5	4	4	6	0.9	4	3	5	7	2	15	3
XRN1	7	6	5	5	3	4	4	15	4	8	5	6	6	8	6	7
CEP89	3	3	3	4	4	2	3	3	0.7	3	4	10	6	4	6	6
CYB561D1	1	2	1	2	1	0.9	3	7	0.9	0.7	3	3	2	0.9	1	4
GABPB2	4	4	2	4	3	2	3	5	0.7	1	3	7	4	1	12	4
GP2	0.1	0.2		0.1	0.4	0.1	3		0.2	0.8	0.2	0.1	0.7		0.1	0.1
GPATCH1	2	5	4	3	3	2	3	4	1	1	4	5	4	2	6	4
GRK6	6	23	8	5	5	3	3	47		7	13	7	5	6	11	9
LYSMD1	2	2	4	3	3	4	3		3	2	3	4	8		3	3
MAPK7	5	5	1				3	4				7		2	6	4
MICALL2	1	6	4	3	4	0.7	3	0.3	0.6	6	5	2	4	0.4	2	2
SLC12A9	3	7	3	3	2	1	3	11		3	9	6	4	0.5	2	3
SLC22A3	2	11	0.6	5	5	0.7	3		26	3	11	10	9	15	12	11
SLC30A4	3	2	4	3	3	1	3	2	0.7	1	3	5	4	0.6	7	2
AMIGO1	2	2	11	4	3	3	2	5	1	1	2	5	4	7	4	5
AP5B1	3	2	2	3	0.8	1	2	12	1	2	3	2	1	2	1	4

ATXN7L2	0.6	2	0.7	0.7	0.4	0.3	2	0.7	0.4	0.5	2	2	0.9	0.9	5	1
B4GALNT3	0.1	0.8	0.6	0.4	1	3	2	1	0.1	2	0.7	1	0.6	0.4	3	2
BNIPL	0.3	0.7	0.3	2	0.4	0.3	2	0.3	0.1	2	4	0.5	4	0.1	1	2
CSPG4	9	3	2	8	9	2	2			7	2	2	11	16	4	4
FAM109A	1	2	0.4	2	3	2	2	2	1	2	2	5	2	1	3	2
FBXL20	3	2	4	4	3	3	2	5	1	2	3	3	4		9	3
FYB	3	9	4	2	0.5	0.8	2	124	0.9	6	13	2	1	0.6	2	0.5
GPER	0.9	2	1	4	3	0.8	2	0.3	4	0.5	2	0.8	2	0.4	2	3
GPR146	15	16	5	18	7	2	2	0.7	3	4		1	6	3	4	2
MLLT11			44		3	14	2		0.6			3	2	0.4	2	1
POLH	2	3	1	2	1	1	2	4	0.8		3	4	3	2	6	4
SLC25A34				0.7		3	2		0.4					4		
ABHD16A	0.3	0.5	0.9	0.1	0.6	0.6	1	1	0.9	2	1	0.5	2	0.5	1	0.4
ALDH3A1	4	0.7	0.6	0.8	0.3		1		0.1	7		0.9	0.4	0.7	2	0.8
ALMS1	3	2	2	1	2	0.8	1	3	0.5	2	2	8	3	1	19	3
C15orf27	0.4	0.9	1	0.6	0.1	0.1	1	0.2	0.2	0.6	0.4	0.3	0.3	0.5	3	0.6
DOK3	2	17	1	0.9	0.4	0.6	1	45	0.7	3	20	1	2	0.5	2	0.7
DUOX1	0.2	35	1	37		0.1	1	2		9	0.4	3	6	1	3	17
NRG4	0.5	2	3	0.8	0.5	0.4	1	0.1	2	2	0.8	1	2	0.8	3	0.7
OVOL1		0.1		0.2	1		1			0.2			1		8	0.3
PLXDC1		4	3		5	5	1	1	0.1	4	7		3	0.7	1	2
PSRC1	0.6	0.7	17	0.5	1	0.3	1	2	0.9	1	1	2	3	0.1	7	0.7
SEMA6C	1	2	1	3	2	8	1	0.2	0.2	1	3	3	2	13	5	3
SLC22A1		0.5	0.4		1		1	0.2	350			0.3	0.1	0.5	0.6	0.1
SLC28A2	0.1	0.2	0.1	0.1	0.5	0.1	1		0.1	0.1	0.1	0.2	0.2		0.4	0.1
STBD1	6	3	0.5	14	2	6	1	0.5		4	1	2	4	8	3	5
TMEM82							1		2							
SHF	3	2	4	2		0.9	0.9	0.5	10		4	11		0.5	6	
CACNB1	0.7	1	10	3	1	0.9	0.8	0.9		1	3	2	3	102	3	19
F12						0.8		63								
PNMT	0.6	0.2	1	0.1	1	1	0.8			0.4	0.3	0.2	2	0.8	1	0.8
ACSM1	0.1	0.2	0.5	0.2	0.3	0.1	0.7		0.6	0.3	0.4	2	7	0.2	2	0.3
AFF3	0.9	5	5	3	3	0.9	0.7	4			2	2	4	0.3	3	0.6
C19orf40	0.6	1	0.4	1	0.6	0.4	0.7	1	0.3	0.8	0.7	1	0.8	0.5	3	1
CST5							0.7			2						
PRRC2A		1	0.6		0.3	0.4	0.7	4		0.7	0.2		0.1			
FHAD1	0.6	0.5	1	0.4		0.2	0.6	0.1	0.1	4	0.2	4	0.3	0.1	8	0.4
FOSL1	7	2	1	2	2	0.7	0.6	0.5	0.4	11	2	0.5	1	1	0.5	4
SLX4IP	0.4	0.5	0.5	0.4	0.2	0.4	0.6	2	0.4	0.1	0.8	1	0.9	0.3	0.5	0.8
ARL5C		0.9	0.2	0.5	0.2	0.1	0.5	0.6			0.4	0.6	0.2	0.2	0.5	
MYCN		0.3	2	0.2			0.5			0.2	0.6	1	0.2		1	0.8
NKX3-1	0.6	1	0.8	0.9	1	1	0.5	0.4	1	4	2	5	24	3	14	1
ADARB2	0.2	0.2	5		2	0.2	0.4	0.7	0.1	0.2	0.5	0.7	0.4	0.1	1	0.1
CSNK2B						0.4					0.3					0.3

DCDC1	0.1	0.1	0.6	0.1			0.4	0.3	0.3	1	0.1	0.9			1	0.8
HLA-C		17	5				0.4	99	0.6	70		2	0.3	2	0.6	0.7
RNF112	0.4	2	6	0.3	0.6	0.2	0.4		0.1	0.9	0.5	0.7	1	0.8	0.8	1
RSPH9			0.5		0.3		0.4			4		1			5	
TCAP	0.3	0.3	0.4	47	0.9	588	0.4	0.2	0.1	0.5	3	0.6	0.4	284	9	99
UFSP1	0.5	2	0.1	1	0.3	0.1	0.4	0.7	0.5	0.1	0.2	1	0.9	1	0.3	2
UNCX						0.4										
ACHE	0.3	3	4	2	3	0.2	0.3		0.6	1	2	1	1	21	1	8
CST1	0.3						0.3					0.1	0.6		0.2	0.3
CSTL1	0.3	0.2	0.4	0.3			0.3	0.3							2	0.1
NYAP1	0.3	0.3	6	0.2	0.5	0.1	0.3	0.1		0.1	0.5	1	0.4		2	0.3
PRR7	0.1	0.4	1	0.3	0.2	0.2	0.3	1	0.1	1	0.7	0.3	0.3	0.3	0.4	0.2
C6orf223			0.1	0.1	0.1		0.2			0.5		0.1			0.1	1
CCDC158	0.2	0.5	0.7	0.9	0.3	0.4	0.2		0.4	0.6	0.1	0.2	0.3	0.1	17	0.5
CTRC	0.2	0.7	0.2	0.3	0.1	0.1	0.2	0.1	0.1	0.3	0.2	0.3	0.2	0.1	0.3	0.2
DDX39B		0.2				0.1	0.2								0.1	0.1
GPR61	0.1	0.2	1			0.1	0.2		0.1		0.1	0.3	0.1		0.4	0.6
IQSEC3	0.8	0.3	12	0.7	0.7	0.4	0.2	0.4		1	0.7	1	1		1	0.5
LY6G5B		0.7	0.4	0.3	0.3	0.2	0.2		0.1		0.3	0.4	0.2			0.5
PDILT		0.2	0.1			0.1	0.2	0.2	0.1		0.2				3	
TFR2	0.5	0.6	2	0.5	0.2	0.3	0.2	0.8	174	0.7	0.9	0.4	0.5	0.1	0.6	0.4
BAG6	0.1	0.2	0.2	0.1		0.1	0.1	0.1		0.1	0.1	0.3		0.2	0.6	1
NFKBIL1		0.1				0.1	0.1				0.1					0.1
ODF3L1	0.2	0.2	0.1	1	0.2	0.1	0.1			0.3	0.1	0.3	0.2	0.2	8	0.2
TDRD12	0.8	0.2	0.1	0.5	0.4	0.1	0.1	0.2		0.1	0.3	0.8	0.3	0.1	11	0.1
ACTL6B	0.1		22		0.3				0.1			0.5			0.2	
AIF1											0.1					
APOM		0.1		0.1			0.1	0.1			0.1	0.1		0.2	0.1	
ATP6V1G2										0.3					0.1	
BCAS3	10	3			4	3		9		10	4	5			11	11
C15orf48					106					14					126	3
C17orf82		0.1		0.1					0.4		0.1	0.3	0.1	0.2	0.2	0.1
C1orf56				2	2			2			3	3	1	19	4	
C2orf78							0.1		0.1						4	
C6orf25																
C6orf47																
C9								571								
CCDC77					2						3		6			
CELA2A		1	1													
CELA2B																
CST11											0.8		17			
CST2	0.1	0.1		0.1					0.2		0.1		0.3	0.1		0.1
CST4	0.1												0.1	0.6		
CST8													10			

CST9													0.2
CST9L													23
CTSW	2					89		14	10		2		
CUX2		3	0.1	0.1		0.1	8				1		0.5
DCDC5													
DDAH2								1					
DUOXA1								5	0.2		4		0.8
DUOXA2													11
EFEMP2	17		24	16	10					44	23		21
EPO		0.1					4		0.1	0.1			0.4
FBXO24		0.3									0.2		19
GNAT2		0.1			0.1			0.1		0.1			0.5
GPANK1		0.1		0.1			0.1				0.1		
GSTM1	12		24	28			0.7	0.2	17		57	154	
IDI2													184
KCNK7	0.1	1	2	0.1	0.3		0.5		0.3	0.2	0.4	0.3	0.2
LST1		0.7					1						
LTA													
LTB		4					1		0.4	4	0.1		
LY6G5C		0.2	0.1				0.1	0.1					
LY6G6C													
LY6G6F													
MAGI2	2	2	15	2	1			0.3		1	3	4	
MICA			0.1						0.2				
MICB		0.3		0.1	0.1		0.9		0.3	0.4	0.1		
MUS81													
MXD3													
MYBPHL	0.1		2		1		0.1	0.1			0.4	0.3	0.8
NAT8B													
NCR3										0.1			
NEUROD2			5										0.1
NKX2-6													
PFN3													0.4
PRKACG												10	0.1
RGS9BP						0.4					3		
RSC1A1													
SAP25				1					9				8
SETDB1	5	13	3	5	4	2	10		4		7	5	17
SNORD84													
SNX32													
SOX11		0.5	0.2	0.6	0.1								0.1
TBX4	0.2	0.1		0.2		0.1		0.3	18	0.2	0.1	9	
TMOD4				12								250	4
TNF		0.2					0.8		0.1	0.2			

TNFAIP8L2

TSGA10IP

ZAN

Supplementary Table 3**Demographics, clinical information and histological analysis of glomerular samples**

Data are presented as mean and standard deviation with the median values or percentage (%).

Estimated Glomerular Filtration Rate (eGFR) was calculated according to the CKD-EPI equation. Pearson product moment correlation or Spearman correlation coefficient (R coefficient) was used to measure the strength of association between age, BMI, serum-glucose, blood pressure (systole and diastole), serum-creatinine, BUN, serum-albumin, percentage of glomerulosclerosis and interstitial fibrosis and eGFR; depending on the results of the D'Agostino-Pearson normality tests. Asterisks (*) indicate when the two-tailed tests reached the statistical significance ($P < 0.05$).

Patient Demographics (Samples from Glomeruli)		
Total: n=51	% or mean ± SD (median)	correlation with GFR (R coefficient)
Gender		
Male	47.1 %	
Female	52.9 %	
Race		
Non-Hispanic White	19.6 %	
African American	35.3 %	
Asian	5.9 %	
Hispanic	15.7 %	
Multiracial	9.8 %	
Unknown	13.7%	
Diabetes	45.1 %	
Hypertension	80.4 %	
Age (years)	61.08 ± 12.9 (63)	-0.262
BMI (Body Mass Index) (kg/m²)	32.18 ± 15.7 (29.2)	-0.097
Serum glucose (mg/dL)	124.8 ± 51.3 (115)	-0.254
Blood pressure - systole (mm Hg)	136.52± 20.2 (130)	-0.153
Blood pressure - diastole (mm Hg)	81.24 ± 13.4 (80)	-0.081
eGFR (ml/min/1.73m²)	58.53 ± 28.5 (60.9)	
Serum creatinine (mg/dL)	1.66 ± 1.4 (1.2)	-0.893 *
BUN (Blood Urea Nitrogen) (mg/dL)	21.59 ± 14.2 (19)	-0.653 *
Serum albumin (g/dL)	3.75 ± 0.8 (4)	0.219
Glomerulosclerosis (%)	11.45 ± 17.4 (3.9)	-0.511 *
Interstitial Fibrosis (%)	13.91 ± 13.6 (10)	-0.586 *

Supplementary Table 4**Demographics, clinical information and histological analysis of tubule samples**

Data are presented as mean and standard deviation with the median values or percentage (%).

Estimated Glomerular Filtration Rate (eGFR) was calculated according to the CKD-EPI equation. Pearson product moment correlation or Spearman correlation coefficient (R coefficient) were used to measure the strength of association between age, BMI, serum-glucose, blood pressure (systole and diastole), serum-creatinine, BUN, serum-albumin, percentage of glomerulosclerosis and interstitial fibrosis and eGFR; depending on the results of the D'Agostino-Pearson normality tests. Asterisks (*) indicate when the two-tailed tests reached the statistical significance ($P < 0.05$).

Patient Demographics (Samples from Tubules)		
Total: n=95	% or mean ± SD (median)	correlation with eGFR (R coefficient)
Gender	Male	57.9 %
	Female	42.1 %
Race	Non-Hispanic White	20.0 %
	African American	36.8 %
	Asian	3.2 %
	Hispanic	6.3 %
	Multiracial	17.9 %
	Unknown	15.8%
Diabetes	38.9 %	
Hypertension	76.8 %	
Age (years)	63.57 ± 13.5 (65)	-0.131
BMI (Body Mass Index) (kg/m²)	29.77 ± 9.3 (29)	0.150
Serum glucose (mg/dL)	135.4 ± 65.3 (118)	0.153
Blood pressure - systole (mm Hg)	138.97 ± 24.8 (136.5)	-0.299 *
Blood pressure - diastole (mm Hg)	78.05 ± 13.7 (78.5)	-0.174
eGFR (ml/min/1.73m²)	60.08 ± 29.8 (64.1)	
Serum creatinine (mg/dL)	2.05 ± 2.5 (1.1)	-0.894 *
BUN (Blood Urea Nitrogen) (mg/dL)	23.2 ± 13.7 (19)	-0.696 *
Serum albumin (g/dL)	3.96 ± 0.7 (4.1)	0.228 *
Glomerulosclerosis (%)	17.97 ± 27.3 (5.5)	-0.570 *
Interstitial Fibrosis (%)	16.47 ± 21.6 (10)	-0.732 *

Supplementary Table 5**The correlation between levels of diabetic CKD risk associated transcripts (D-CRATs) and kidney function**

We identified 18 D-CRATs in the neighborhood of three loci associating with diabetic kidney disease development (rs12437854, rs7583877 and rs1617640). Pearson product moment correlation coefficient (Pearson R) was used to measure the strength of association between gene expression and eGFR. Two-tailed test was used to determine the statistical significance. Four transcripts showed significant correlation with eGFR ($P_{\text{corrected}} < 0.05$) after Benjamini Hochberg based multiple testing correction and 10 transcripts showed correlation with GFR with uncorrected p values. Gene symbols are official symbols approved by HGNC (HUGO Gene Nomenclature Committee).

eGFR correlation of DKD specific CRATs in Glomeruli

Gene Symbol	Pearson R	95% confidence interval	P (two-tailed)	P corrected
PCOLCE	-0.4555	-0.6671 to -0.1759	0.0024	0.0912
LRCH4	-0.3602	-0.5986 to -0.0631	0.0191	0.3629
TFR2	0.2841	-0.0217 to 0.5413	0.068	0.8639
MOSPD3	0.1742	-0.1370 to 0.4541	0.270	0.9931
TSC22D4	0.1661	-0.1451 to 0.4475	0.293	0.9931
AGFG2	0.1561	-0.1552 to 0.4392	0.323	0.9931
TRIP6	0.1498	-0.1614 to 0.4340	0.343	0.9931
SRRT	0.1461	-0.1652 to 0.4309	0.356	0.9931
EPO	0.1256	-0.1854 to 0.4138	0.428	0.9931
EPHB4	-0.1240	-0.4124 to 0.1869	0.434	0.9931
GNB2	-0.0958	-0.3884 to 0.2144	0.546	0.9931
ACHE	-0.0864	-0.3803 to 0.2234	0.586	0.9931
LRCH4//SAP25	0.0805	-0.2290 to 0.3753	0.612	0.9931
AFF3	-0.0439	-0.3432 to 0.2636	0.783	0.9931
SLC12A9	-0.0265	-0.3278 to 0.2797	0.868	0.9931
POP7	0.0186	-0.2870 to 0.3207	0.907	0.9931
ACTL6B	0.0156	-0.2897 to 0.3180	0.922	0.9931
FBXO24	0.0036	-0.3006 to 0.3072	0.982	0.9931

eGFR correlation of DKD specific CRATs in Tubules

Gene Symbol	Pearson R	95% confidence interval	P (two-tailed)	P corrected
TRIP6	0.5121	0.3241 to 0.6612	2.26×10^{-6}	8.59×10^{-5}
LRCH4	-0.3761	-0.5545 to -0.1646	8.14×10^{-4}	0.0155
SLC12A9	0.3564	0.1423 to 0.5385	1.58×10^{-3}	0.0200
MOSPD3	0.320	0.1019 to 0.5087	4.84×10^{-3}	0.0459
AFF3	-0.2731	-0.4696 to -0.0507	0.017	0.1002
SRRT	0.2666	0.0438 to 0.4642	0.020	0.1002
ACHE	-0.2642	-0.4621 to -0.0412	0.021	0.1002
AGFG2	0.2518	0.0279 to 0.4516	0.028	0.1191
TFR2	-0.2316	-0.4344 to -0.0065	0.044	0.1674
EPO	-0.2036	-0.4103 to 0.0229	0.078	0.2459
EPHB4	0.1858	-0.0413 to 0.3948	0.108	0.3156
FBXO24	-0.1379	-0.3524 to 0.0904	0.235	0.5579
ACTL6B	-0.0941	-0.3129 to 0.1342	0.419	0.7275
LRCH4//SAP25	-0.0763	-0.2966 to 0.1518	0.512	0.8467
POP7	-0.0682	-0.2892 to 0.1597	0.558	0.8501
PCOLCE	0.0429	-0.1844 to 0.2658	0.713	0.9128
TSC22D4	0.0284	-0.1983 to 0.2523	0.807	0.9128
GNB2	0.0140	-0.2121 to 0.2387	0.904	0.9128

Supplementary Table 6

List of CRATs showing differential expression in control vs. CKD tubule samples

In tubules, 73 transcripts in the neighborhood of the CKD risk loci showed significant differences when CKD samples are compared to controls. Benjamini-Hochberg multiple-testing correction was used with a P value < 0.05.

Differentially expressed CRATs in chronic kidney disease		
Gene Symbol	P value (corrected)	Regulation
LST1	6.40 x 10 ⁻⁸	up
SLC7A9	4.56 x 10 ⁻⁷	down
ALDH3A2	1.89 x 10 ⁻⁶	down
SLC34A1	2.04 x 10 ⁻⁶	down
CTSS	4.19 x 10 ⁻⁶	up
FYB	4.19 x 10 ⁻⁶	up
ACSM5	1.85 x 10 ⁻⁵	down
LTB	2.55 x 10 ⁻⁵	up
UMOD	2.70 x 10 ⁻⁵	down
ACSM2A///ACSM2B	3.81 x 10 ⁻⁵	down
SLC47A1	4.26 x 10 ⁻⁵	down
ANXA9	4.54 x 10 ⁻⁵	down
DNAJC16	1.24 x 10 ⁻⁴	down
NAT8B	1.63 x 10 ⁻⁴	down
ACAD10	1.97 x 10 ⁻⁴	down
GSTM4	2.55 x 10 ⁻⁴	down
VEGFA	4.05 x 10 ⁻⁴	down
CTSW	5.04 x 10 ⁻⁴	up
NAT8//NAT8B	5.04 x 10 ⁻⁴	down
FAM89B	6.09 x 10 ⁻⁴	up
AFF3	6.28 x 10 ⁻⁴	up
MYCN	6.28 x 10 ⁻⁴	down
ALDH2	6.64 x 10 ⁻⁴	down
FAM47E///STBD1	6.70 x 10 ⁻⁴	down
GNAI3	6.87 x 10 ⁻⁴	up
SLC22A2	8.54 x 10 ⁻⁴	down

DAB2	1.21 x 10 ⁻³	down
STC1	1.59 x 10 ⁻³	down
APOM	1.83 x 10 ⁻³	down
GPER	1.93 x 10 ⁻³	down
SLC22A1	1.96 x 10 ⁻³	down
AGMAT	2.18 x 10 ⁻³	down
EHBP1L1	2.47 x 10 ⁻³	up
SLC6A13	2.47 x 10 ⁻³	down
FAM193B	2.66 x 10 ⁻³	up
CERS2	3.14 x 10 ⁻³	down
LRCH4	3.38 x 10 ⁻³	up
PLXDC1	3.63 x 10 ⁻³	up
SLC30A4	4.33 x 10 ⁻³	down
GATM	5.84 x 10 ⁻³	down
PGAP3	6.17 x 10 ⁻³	down
SLC6A12	6.81 x 10 ⁻³	down
IGF2R	7.18 x 10 ⁻³	down
MICALL2	8.09 x 10 ⁻³	up
CTSK	0.011	up
DDI2///RSC1A1	0.012	down
ATXN2	0.013	down
CCDC85B	0.014	up
HLA-C	0.014	up
TFDP2	0.015	down
AIF1	0.018	up
DDX1	0.018	down
PRUNE	0.018	down
MFAP4	0.018	up
DBN1	0.021	up
CELA2A///CELA2B	0.024	up
DACH1	0.024	down
TBX2	0.024	down
ERBB2	0.027	down
GP2	0.030	down
F12	0.031	up
PHTF2	0.031	up
CDC42SE1	0.033	up
LARP4B	0.033	down
PTPN12	0.035	up
PDLIM7	0.036	up
IDI1	0.037	down

BRAP	0.039	down
DUOX1	0.045	up
FIBP	0.047	down
MPPED2	0.048	down
MYH9	0.048	up
WDR37	0.049	down

Supplementary Table 7**Demographics, clinical information and histological analysis of the 41 tubule samples for external microarray validation**

Data are presented as mean and standard deviation with the median values or percentage (%). Estimated Glomerular Filtration Rate (eGFR) was calculated according to the CKD-EPI equation. Pearson product moment correlation or Spearman correlation coefficient (R coefficient) were used to measure the strength of association between age, BMI, serum-glucose, blood pressure (systole and diastole), serum-creatinine, BUN, serum-albumin, percentage of glomerulosclerosis and interstitial fibrosis and eGFR; depending on the results of the D'Agostino-Pearson normality tests. Asterisks (*) indicate when the two-tailed tests reached the statistical significance ($P < 0.05$).

Patient Demographics (Samples from Tubules for Replication)		
Total: n=41	% or mean ± SD (median)	correlation with eGFR (R coefficient)
Gender	Male	41.5 %
	Female	58.5 %
Race	Non-Hispanic White	19.5 %
	African American	41.5 %
	Asian	2.4%
	Hispanic	14.6 %
	Multiracial	4.9 %
	Unknown	17.1 %
Diabetes	51.2 %	
Hypertension	78.0%	
Age (years)	60.2 ± 13.3 (60)	-0.177
BMI (Body Mass Index) (kg/m²)	30.26 ± 6.5 (30.5)	0.042
Serum glucose (mg/dL)	140.83 ± 65.9 (129)	0.072
Blood pressure - systole (mm Hg)	142.44 ± 22.7 (151)	-0.504
Blood pressure - diastole (mm Hg)	76.22 ± 13.8 (75)	-0.246
eGFR (ml/min/1.73m²)	52.7 ± 28.2 (55.7)	
Serum creatinine (mg/dL)	2.01 ± 1.8 (1.2)	-0.796 *
BUN (Blood Urea Nitrogen) (mg/dL)	25.0 ± 13.1 (22)	-0.749 *
Serum albumin (g/dL)	3.69 ± 0.9 (3.9)	0.409 *
Glomerulosclerosis (%)	17.97 ± 25.5 (14.3)	-0.641 *
Interstitial Fibrosis (%)	19.93 ± 22.0 (15)	-0.769 *

Supplementary Table 8**Demographics, clinical information and histological analysis of the 46 tubule samples used for qRT-PCR validation**

Data are presented as mean and standard deviation with the median values or percentage (%).

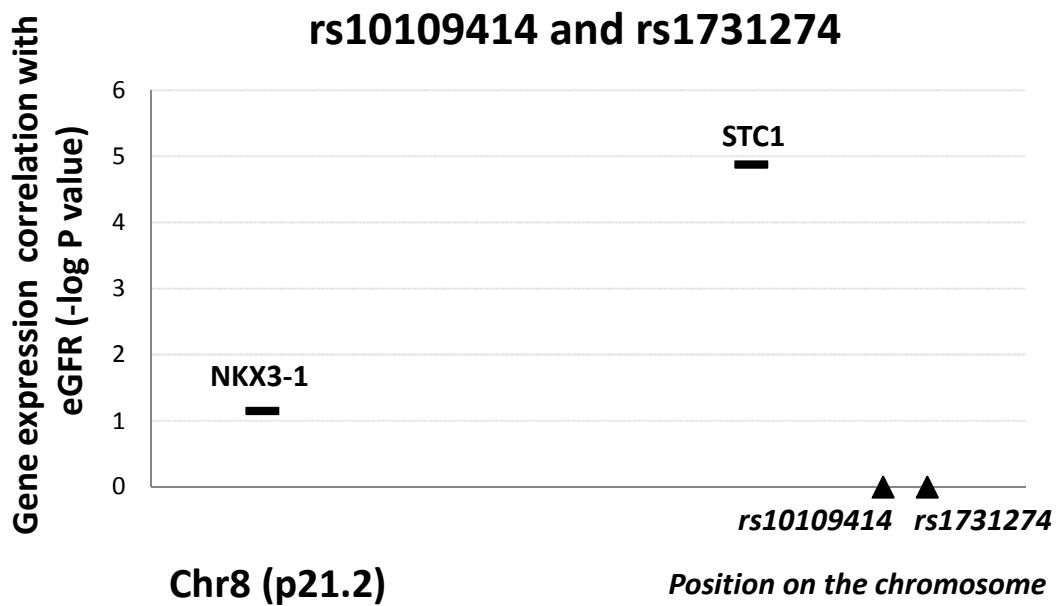
Estimated Glomerular Filtration Rate (eGFR) was calculated according to the CKD-EPI equation. Pearson product moment correlation or Spearman correlation coefficient (R coefficient) were used to measure the strength of association between age, BMI, serum-glucose, blood pressure (systole and diastole), serum-creatinine, BUN, serum-albumin, percentage of glomerulosclerosis and interstitial fibrosis and eGFR; depending on the results of the D'Agostino-Pearson normality tests. Asterisks (*) indicate when the two-tailed tests reached the statistical significance ($P < 0.05$).

Patient Demographics (Tubule samples with qRT-PCR validation)		
Total: n=46	% or mean ± SD (median)	correlation with eGFR (R coefficient)
Gender	Male	54.35 %
	Female	45.65 %
Race	Non-Hispanic White	21.7 %
	African American	41.3 %
	Asian	4.35 %
	Hispanic	4.35 %
	Multiracial	8.7 %
	Unknown	19.6 %
Diabetes	52.2 %	
Hypertension	73.9 %	
Age (years)	62.2 ± 13.1 (63.5)	0.162
BMI (Body Mass Index) (kg/m²)	28.4 ± 6.3 (28.5)	0.197
Serum glucose (mg/dL)	145.8 ± 79.6 (117.5)	0.015
Blood pressure - systole (mm Hg)	139.47 ± 29.9 (135)	-0.377 *
Blood pressure - diastole (mm Hg)	77.81 ± 15.5 (76.5)	-0.291 *
eGFR (ml/min/1.73m²)	54.2 ± 32.8 (58.1)	
Serum creatinine (mg/dL)	2.60 ± 3.1 (1.2)	-0.743 *
BUN (Blood Urea Nitrogen) (mg/dL)	25.93 ± 13.7 (21)	-0.712 *
Serum albumin (g/dL)	3.94 ± 0.6 (4)	0.064
Glomerulosclerosis (%)	23.7 ± 33.1 (6.2)	-0.748 *
Interstitial Fibrosis (%)	21.53 ± 25.3 (10)	-0.737 *

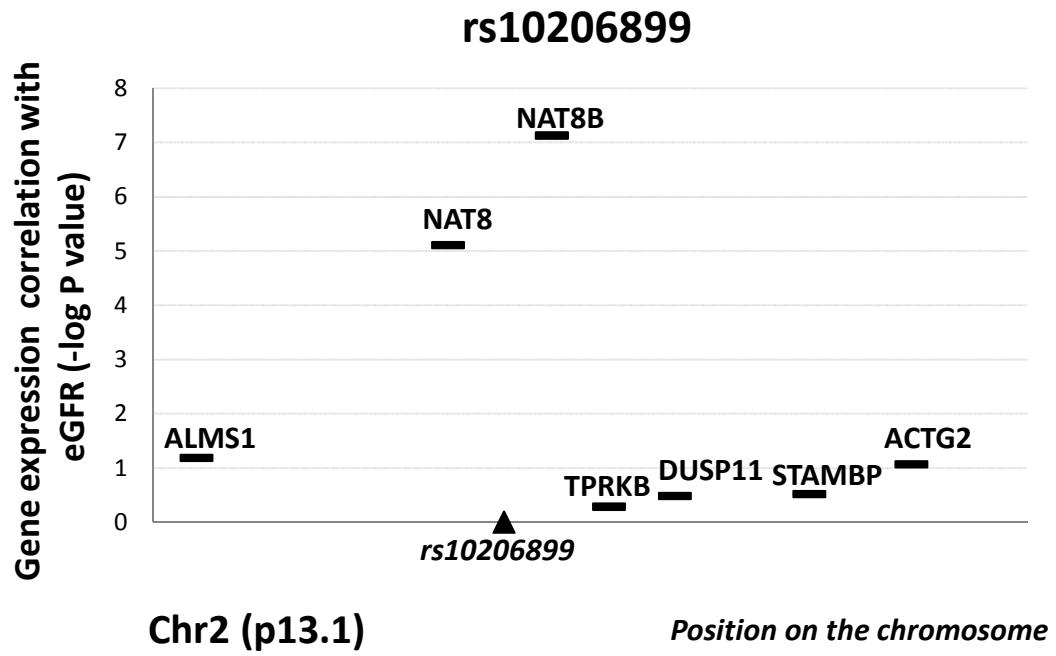
Supplementary Figure 3

Transcript level expression and correlation of tubule specific transcript levels with renal function around all 44 CKD risk loci

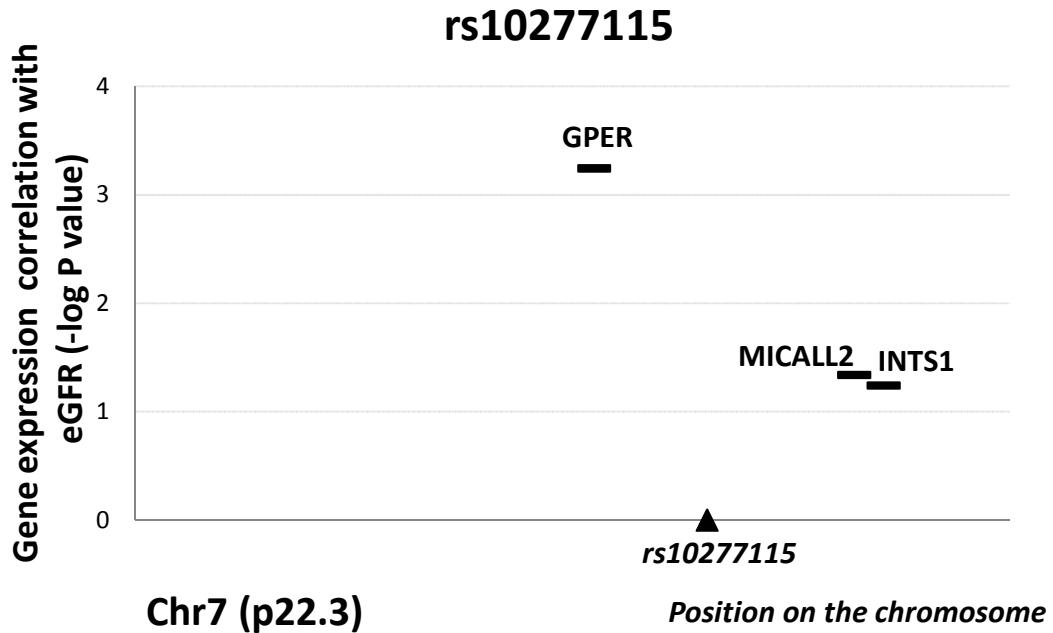
The x-axis represents the genomic position of each gene on different chromosomes. The y-axis represents the negative logarithm of the p-value (significance) between the expression of each gene and eGFR (estimated glomerular filtration rate, ml/min/1.73m²). The lower panel of each chart represents the expression of transcripts within the 250 kb vicinity of the CKD SNP in 16 human organs. Asterisks indicate genes without probe set IDs on the Affymetrix arrays. Two loci are not shown. There is no gene in the vicinity of rs12437854. No genes correlated with renal function around rs491567.



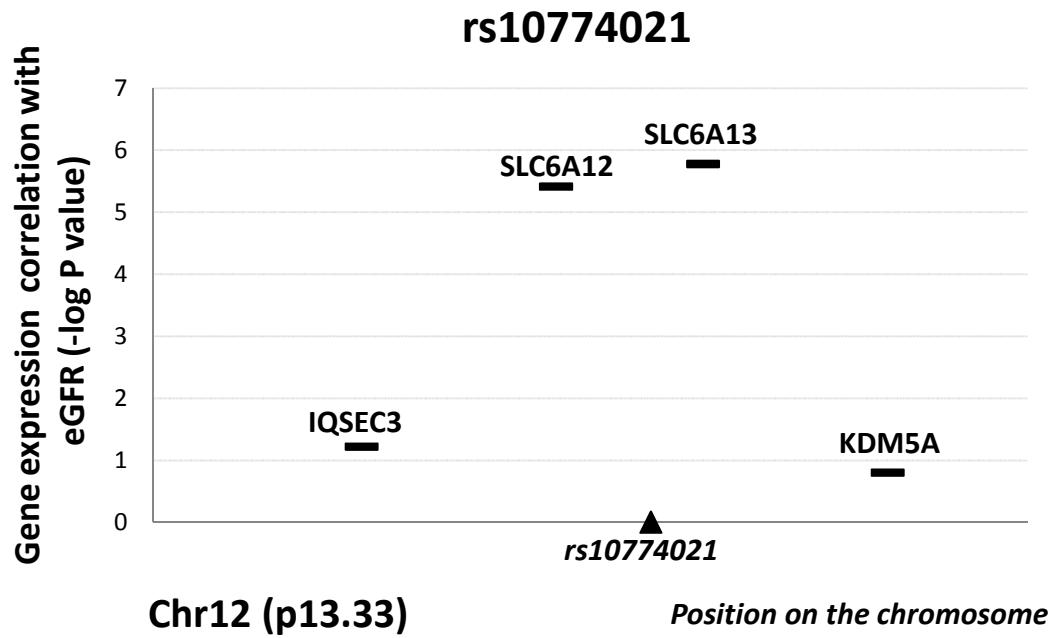
Gene Symbol	NKX3-1	NKX2-6*	STC1
	kidney	0.5	4
adipose	0.6	26	
adrenal	1	3	
brain	0.8	0.7	
breast	0.9	5	
colon	1	51	
heart	1	4	
leukocyte	0.4		
liver	1	0.1	
lung	4	11	
lymph node	2	18	
ovary	5	1	
prostate	24	23	
skeletal muscle	3	2	
testis	14	1	
thyroid	1	14	



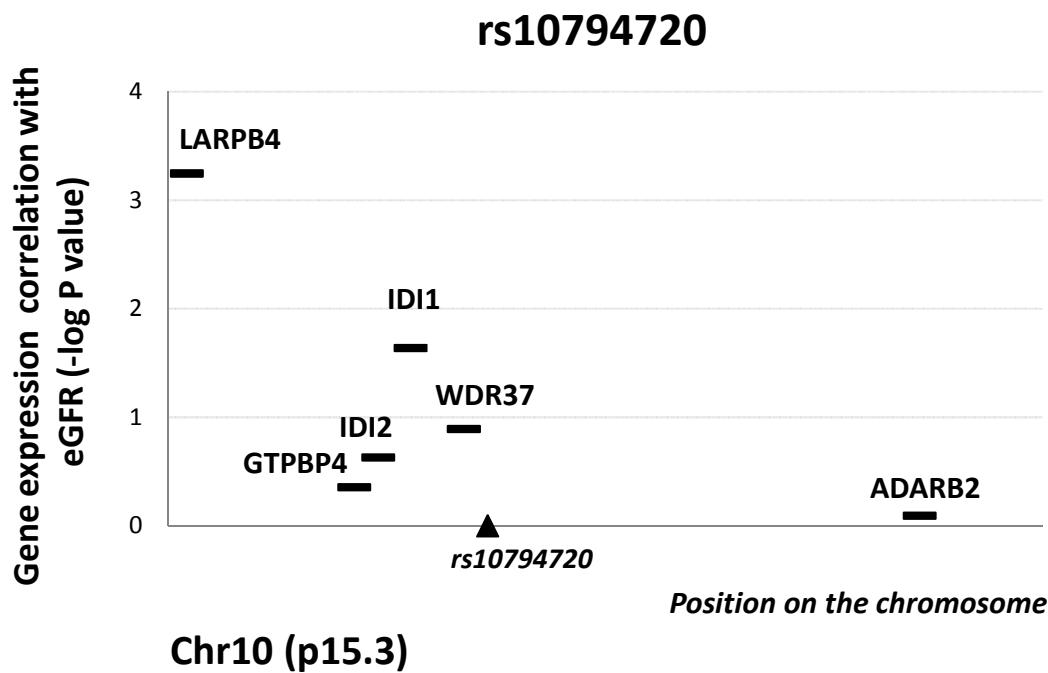
	Gene Symbol							
	ALMS1	NAT8	NAT8B	TPRKB	DUSP11	C2orf78*	STAMBP	ACTG2
kidney	1	61		26	16		15	19
adipose	3			17	10		9	36
adrenal	2			36	12		9	173
brain	2	0.1		15	7		22	3
breast	1			27	10		11	40
colon	2			29	8		9	2101
heart	0.8			24	6		9	2
leukocyte	3	0.1		20	25		17	
liver	0.5	5		17	6		7	2
lung	2	0.2		12	8		7	86
lymph node	2			21	11		15	63
ovary	8	0.2		46	16		11	66
prostate	3	0.2		30	13		19	1888
skeletal muscle	1			11	5		13	11
testis	19	0.4		61	17	4	16	162
thyroid	3			34	14		14	13



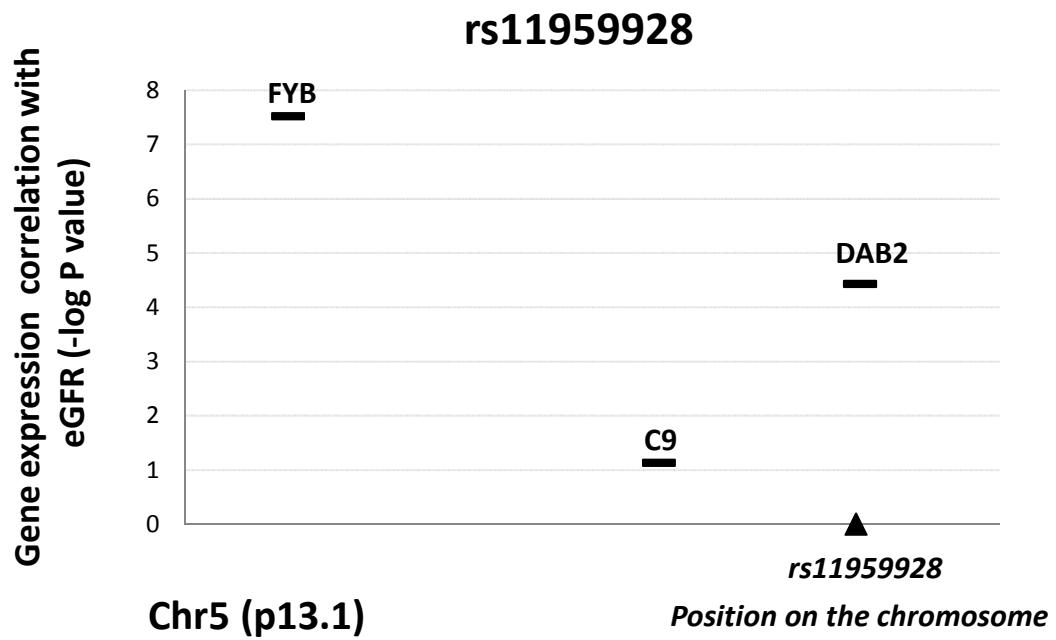
Gene Symbol	C7orf50*	GPR146*	GPER	ZFAND2A*	UNCX*	MICALL2	INTS1
	kidney	17	2	2	8	0.4	3
adipose	17	15	0.9	6		1	6
adrenal	15	16	2	15		6	19
brain	17	5	1	35		4	9
breast	19	18	4	8		3	14
colon	18	7	3	7		4	7
heart	10	2	0.8	3		0.7	4
leukocyte	13	0.7	0.3	12		0.3	7
liver	6	3	4	16		0.6	8
lung	11	4	0.5	16		6	6
lymph node			2	15		5	9
ovary	29	1	0.8	12		2	6
prostate	25	6	2	12		4	12
skeletal muscle	6	3	0.4	2		0.4	17
testis	18	4	2	19		2	21
thyroid	38	2	3	40		2	9



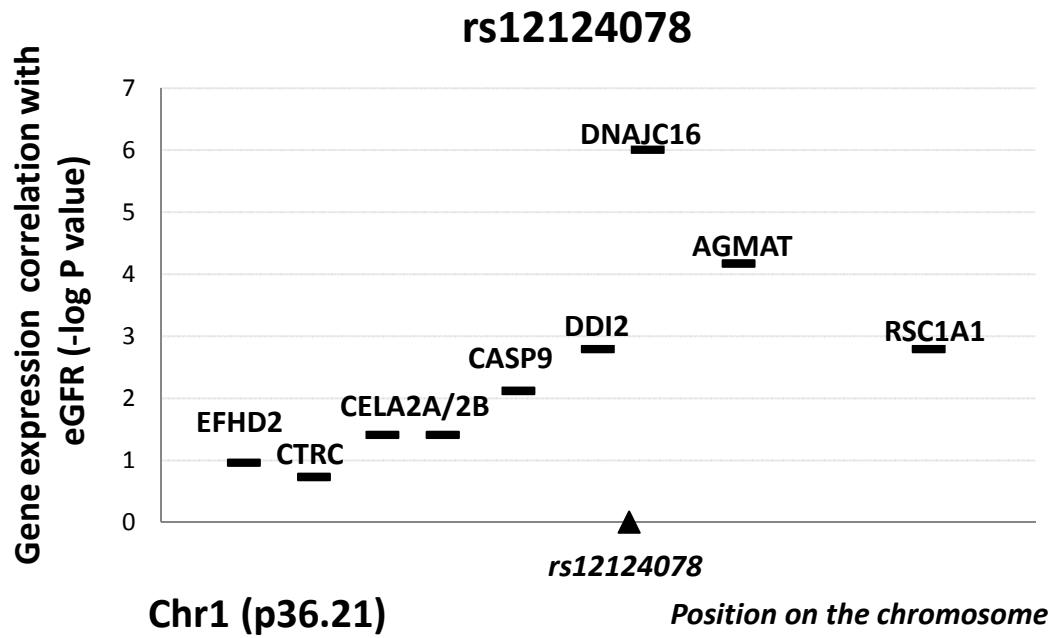
Gene Symbol						
	IQSEC3	SLC6A12	SLC6A13	KDM5A	CCDC77*	B4GALNT3*
kidney	0.2	28	35	4		2
adipose	0.8	0.6	0.2	6		0.1
adrenal	0.3	0.5	0.2	7		0.8
brain	12	4	2			0.6
breast	0.7	0.4	0.2	5		0.4
colon	0.7	0.2		4	2	1
heart	0.4	0.3	0.7	3		3
leukocyte	0.4	2				1
liver		13	2	2		0.1
lung	1	1	0.2	4		2
lymph node	0.7	1	0.1	7		0.7
ovary	1	1	0.6	7		1
prostate	1		0.2	5	3	0.6
skeletal muscle			0.3	3		0.4
testis	1	1	0.9	10	6	3
thyroid	0.5	7	5	7		2



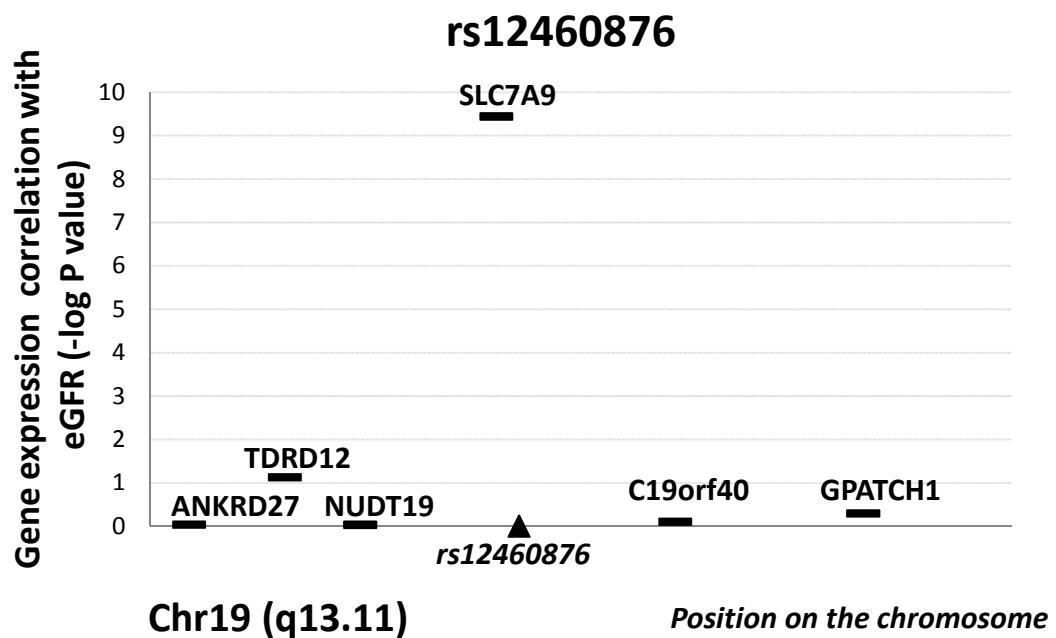
Gene Symbol	LARP4B	GTPBP4	IDI2	IDI1	WDR37	ADARB2
kidney	8	15		31	5	0.4
adipose	9	15		13	2	0.2
adrenal	10	21		27	6	0.2
brain	7	16		64	8	5
breast	10	14		20	4	
colon	5	13		12	2	2
heart	9	9		10	5	0.2
leukocyte	19	14		28	14	0.7
liver	4	7		53	3	0.1
lung	10	11		46	3	0.2
lymph node	8	13		26	5	0.5
ovary	10	25		46	4	0.7
prostate	8	15		15	3	0.4
skeletal muscle	12	21	184	18	3	0.1
testis	14	26		25	4	1
thyroid	16	28		38	7	0.1



Gene Symbol	Position on the chromosome		
	FYB	C9	DAB2
kidney	2		78
adipose	3		60
adrenal	9		25
brain	4		3
breast	2		28
colon	0.5		20
heart	0.8		7
leukocyte	124		7
liver	0.9	571	
lung	6		41
lymph node	13		26
ovary	2		20
prostate	1		19
skeletal muscle	0.6		
testis	2		19
thyroid	0.5		13

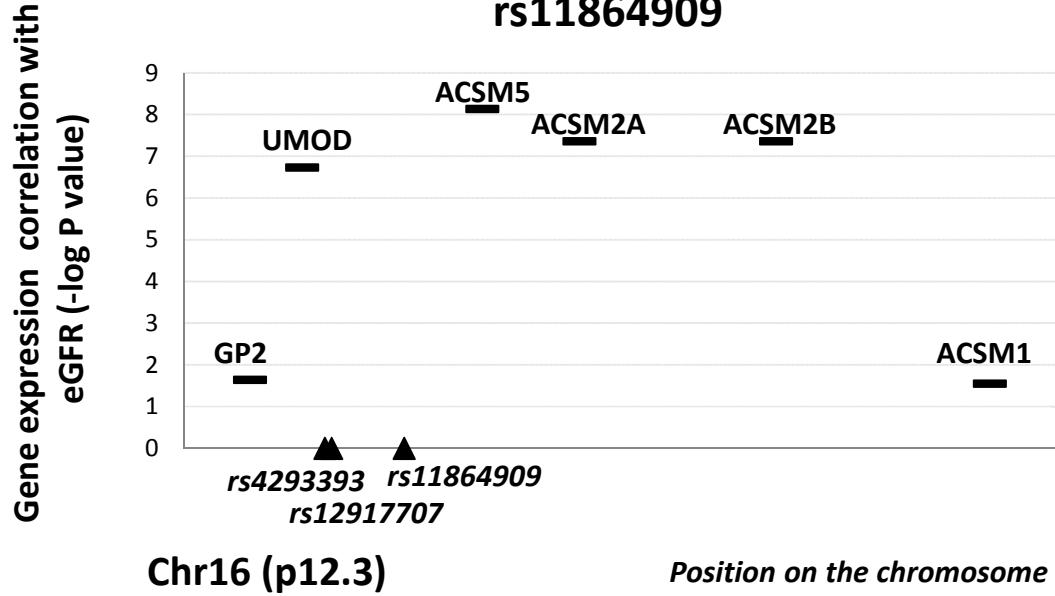


Gene Symbol	FHAD1*	EFHD2	CTRC	CELA2A	CELA2B	CASP9	DNAJC16	AGMAT	DDI2	RSC1A1	SLC25A34*	TMEM82*	FBLIM1*
	kidney	0.6	6	0.2			4	6	7	5	2	1	13
adipose	0.6	14	0.2			2	3		9				18
adrenal	0.5	27	0.7	1		2	4	2	4				42
brain	1	26	0.2	1		3	4	0.8	4				2
breast	0.4	9	0.3			2	4	0.7	8		0.7		7
colon		15	0.1			2	2	0.9	3				13
heart	0.2	3	0.1			3	3		5		3		14
leukocyte	0.1	145	0.1			8	6	2	7				0.6
liver	0.1	4	0.1			2	4	21	6		0.4	2	0.7
lung	4	27	0.3			4	2	0.3	5				20
lymph node	0.2	19	0.2			4	5	0.8	5				28
ovary	4	14	0.3			9	6		6				35
prostate	0.3	12	0.2			5	4		5				18
skeletal muscle	0.1	1	0.1			3	6		27		4		1
testis	8	22	0.3			5	5		4				39
thyroid	0.4	8	0.2			4	4	0.7	5				7

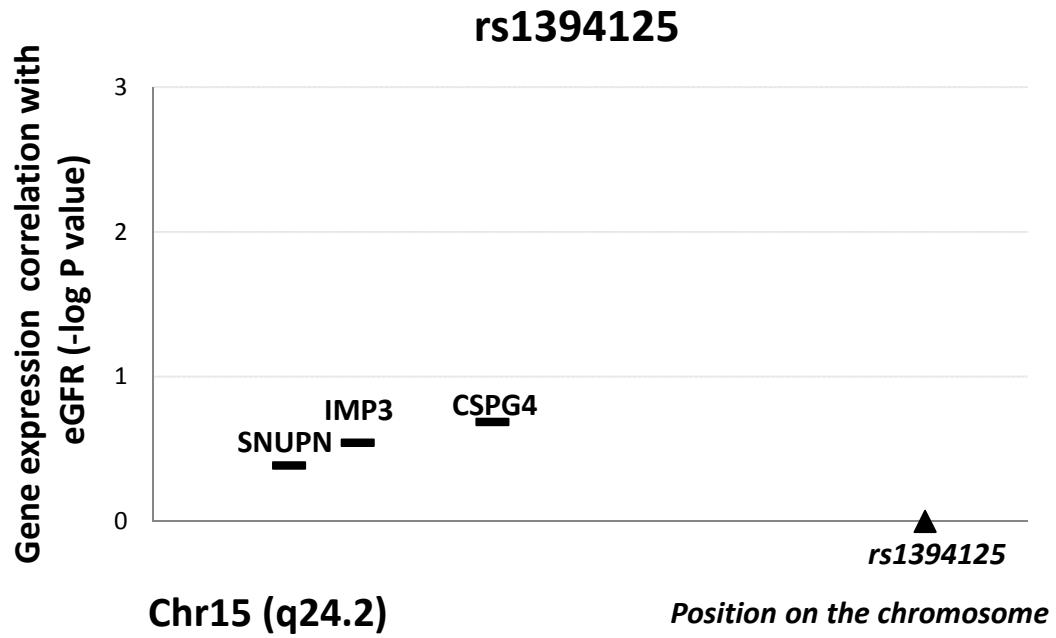


	Gene Symbol	ANKRD27	RGS9BP*	NUDT19	TDRD12	SLC7A9	CEP89*	C19orf40	RHPN2*	GPATCH1
kidney		7	6	0.1	6	3	0.7	12	3	
adipose		5	4	0.8		3	0.6	0.9	2	
adrenal		5	4	0.2	0.1	3	1	2	5	
brain		4	3	0.1	0.2	3	0.4	3	4	
breast		6	6	0.5		4	1	2	3	
colon		11	3	0.4	0.2	4	0.6	3	3	
heart		3	0.4	8	0.1	2	0.4	0.6	2	
leukocyte		10	8	0.2		3	1	0.5	4	
liver		1	5		4	0.7	0.3	6	1	
lung		5	3	0.1	0.3	3	0.8	5	1	
lymph node		7	5	0.3	0.5	4	0.7	2	4	
ovary		10	4	0.8	0.3	10	1	2	5	
prostate		15	5	0.3	0.3	6	0.8	3	4	
skeletal muscle		12	3	11	0.1		4	0.5	0.1	2
testis		15	3	11	0.2	6	3	0.9	6	
thyroid		7	4	0.1	0.2	6	1	3	4	

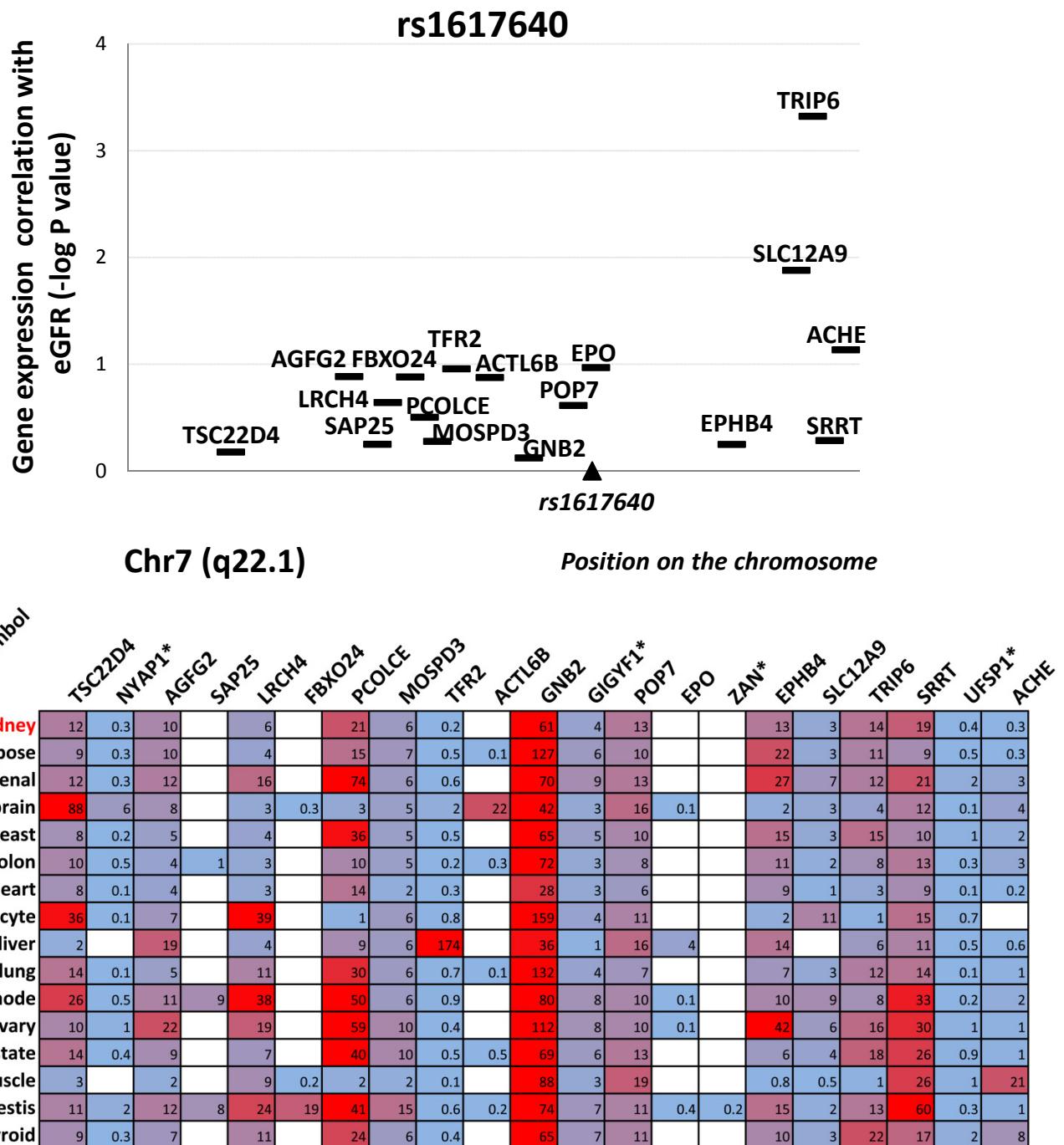
rs12917707, rs4293393 and rs11864909

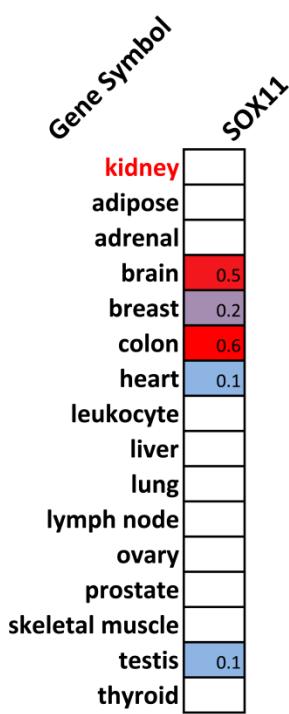
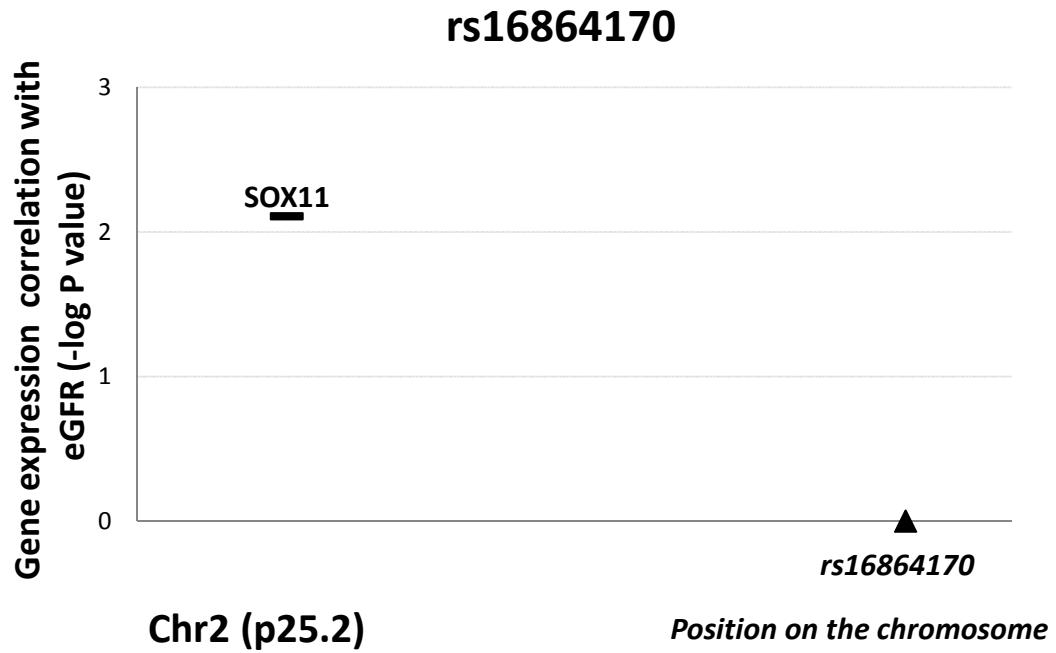


	Gene Symbol	GP2	UMOD	PDI LT*	ACSM5	ACSM2A	ACSM2B	ACSM1
kidney		3	1417	0.2	5	133	121	0.7
adipose		0.1			3	0.2		0.1
adrenal		0.2		0.2	0.4	0.3	0.3	0.2
brain			0.1	0.5	0.6	0.3	0.5	
breast		0.1			9		0.1	0.2
colon		0.4			1	0.5	1	0.3
heart		0.1		0.1	0.3	0.3	0.1	0.1
leukocyte			0.2		0.2			
liver		0.2		0.1	23	98		0.6
lung		0.8			0.6	0.1		0.3
lymph node		0.2		0.2	2	0.5		0.4
ovary		0.1			0.4	0.6	0.6	2
prostate		0.7			1		0.1	7
skeletal muscle					1	0.1		0.2
testis		0.1	0.1	3	1	0.6	0.4	2
thyroid		0.1			2	0.2	0.2	0.3

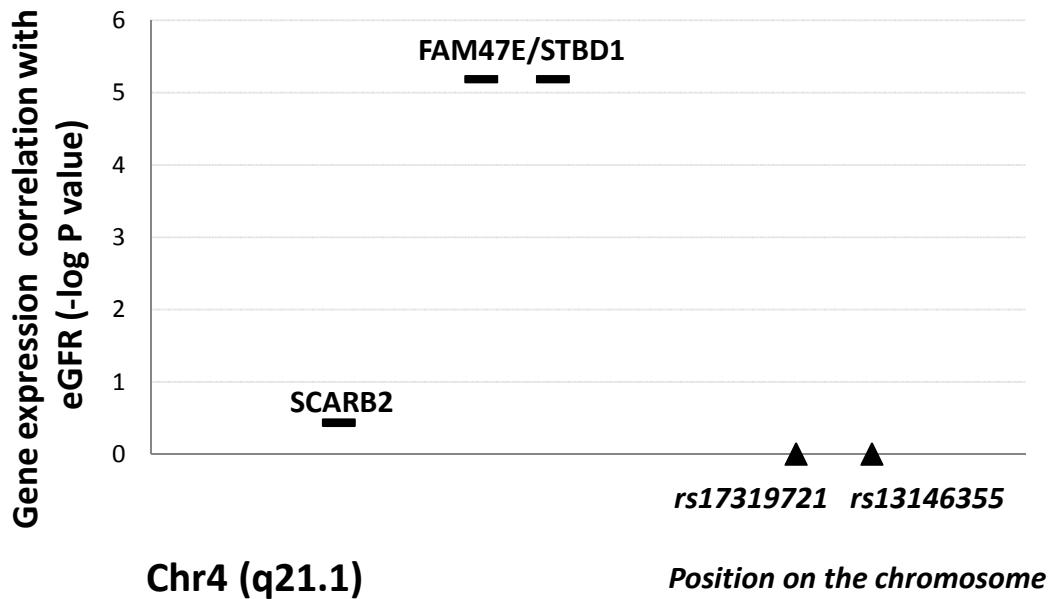


	Gene Symbol							
	SNUPN	IMP3	SNX33*	CSPG4	ODF3L1*	UBE2O2*	NRG4*	C15orf27*
kidney	11	16	5	2	0.1	19	1	1
adipose	5	10	11	9	0.2	17	0.5	0.4
adrenal	11	24	6	3	0.2	17	2	0.9
brain	6	14	1	2	0.1	14	3	1
breast	10	15	10	8	1	18	0.8	0.6
colon	8	12	8	9	0.2	35	0.5	0.1
heart	5	8	2	2	0.1	11	0.4	0.1
leukocyte	10	29	2			27	0.1	0.2
liver	5	15	4			2	2	0.2
lung	7	6	10	7	0.3	20	2	0.6
lymph node	11	17	10	2	0.1	18	0.8	0.4
ovary	14	20	11	2	0.3	26	1	0.3
prostate	14			11	0.2	33	2	0.3
skeletal muscle	9	13	2	16	0.2	10	0.8	0.5
testis	24	15	7	4	8	25	3	3
thyroid	15	24	7	4	0.2	23	0.7	0.6

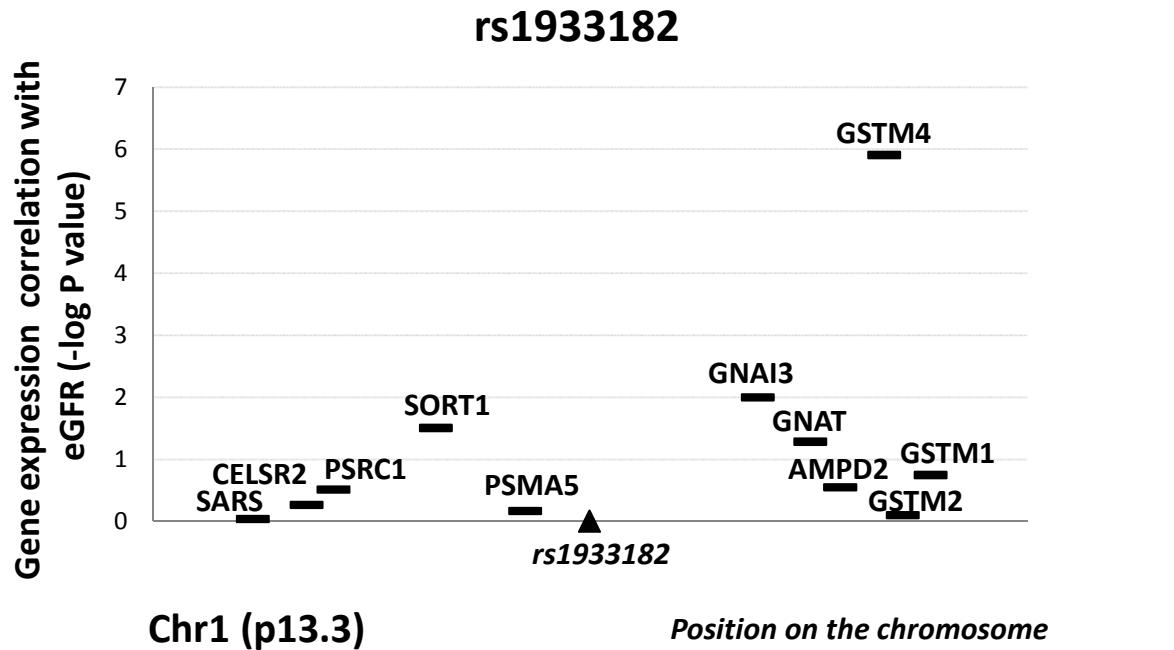




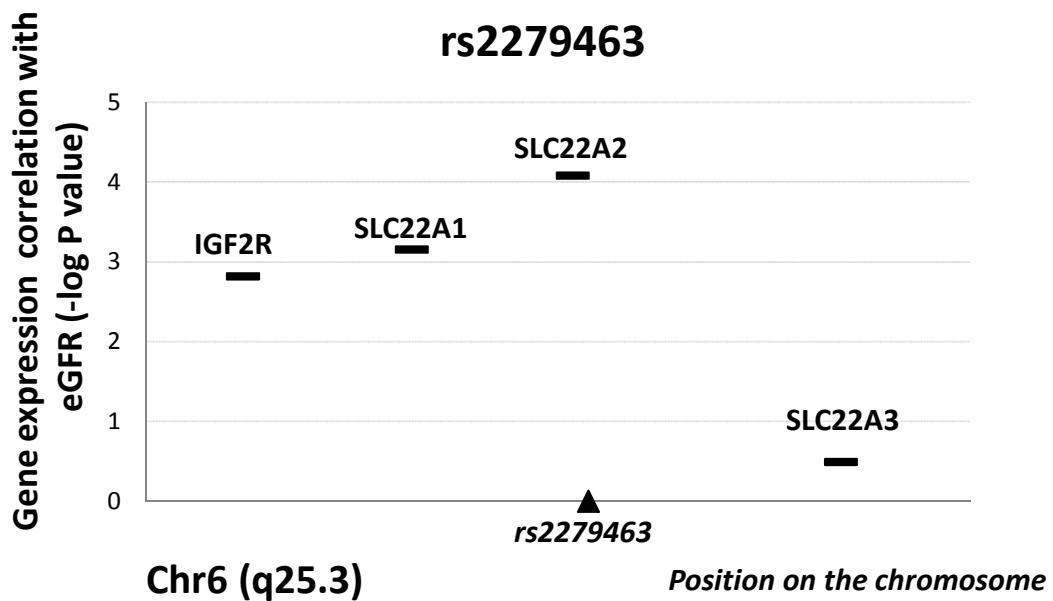
rs17319721 and rs13146355



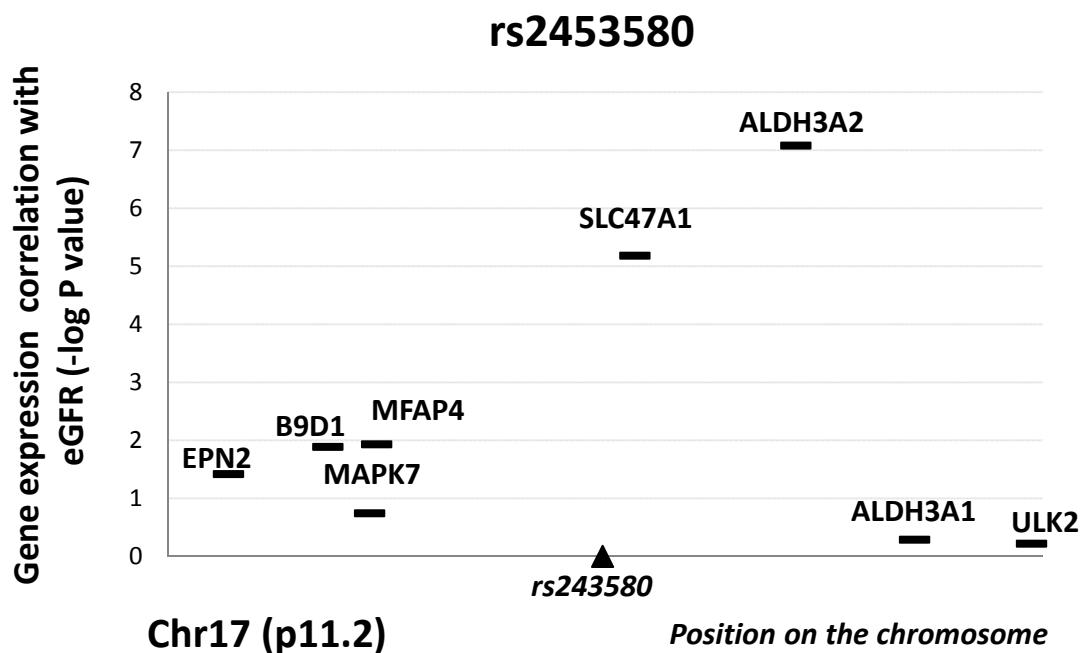
	Gene Symbol	SCARB2	FAM47E	STBD1	CCDC158*	SHROOM3*
kidney	46	4	1	0.2	4	
adipose	51		6	0.2	0.2	
adrenal	42	0.3	3	0.5	2	
brain	94	7	0.5	0.7	0.6	
breast	71		14	0.9	2	
colon	63		2	0.3	2	
heart	28		6	0.4	1	
leukocyte	23	0.1	0.5			
liver	57			0.4	3	
lung	75		4	0.6	6	
lymph node	39	0.2	1	0.1	0.3	
ovary	69	2	2	0.2	2	
prostate	73		4	0.3	4	
skeletal muscle	88		8	0.1	0.1	
testis	48		3	17	2	
thyroid	76	6	5	0.5	3	



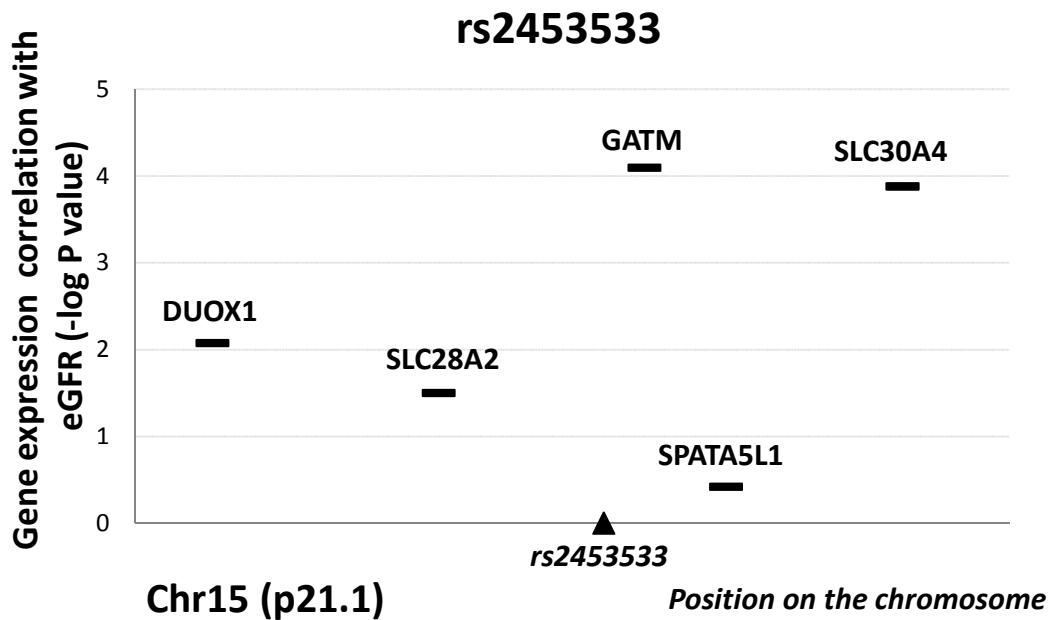
	Gene Symbol	Position on the chromosome															
		SARS	CELSR2	PSRC1	MYBPHL*	SORT1	PSMA5	SYPL2*	ATXN7L2*	AMIGO1*	GPR61*	GNAI3	AMPD2	GSTM2	GSTM4	GSTM1	GNAT2
kidney	46	5	1		41	56	7	2	2	0.2	28	5	13	19			
adipose	71	0.3	0.6	0.1		33	0.7	0.6	2	0.1	29	4	4	9	12		
adrenal	70	0.4	0.7		9	40	0.9	2	2	0.2	27	9	9	17		0.1	
brain	87	14	17	2	87	28	0.2	0.7	11	1	12	11	12	19	24		
breast	44	1	0.5		38	39	2	0.7	4		25	4	38	18	28		
colon	63	1	1		14	37	1	0.4	3		29	5	12	13			
heart	26	1	0.3	1	30	30	5	0.3	3	0.1	6	2	20	13		0.1	
leukocyte	57	0.6	2	0.1	17	74		0.7	5		52	23	4	5	0.7		
liver	37	1	0.9	0.1	6	66	2	0.4	1	0.1	12	7	2	6	0.2	0.1	
lung	73	0.4	1		17	52	0.3	0.5	1		24	7	24	11	17		
lymph node	38	0.7	1		9	37	1	2	2	0.1	22	19	12	11		0.1	
ovary	90	2	2		6	46	3	2	5	0.3	33	10	67	38	57		
prostate	70	3	3	0.4	16	45	2	0.9	4	0.1	31	10	30	45	154		
skeletal muscle	76	2	0.1	0.3	40	41	35	0.9	7		6	2	14	13			
testis	60	5	7	0.8	45	58	3	5	4	0.4	33	5	18	16		0.5	
thyroid	107	4	0.7	0.2	46	48	15	1	5	0.6	24	5	23	20	26		



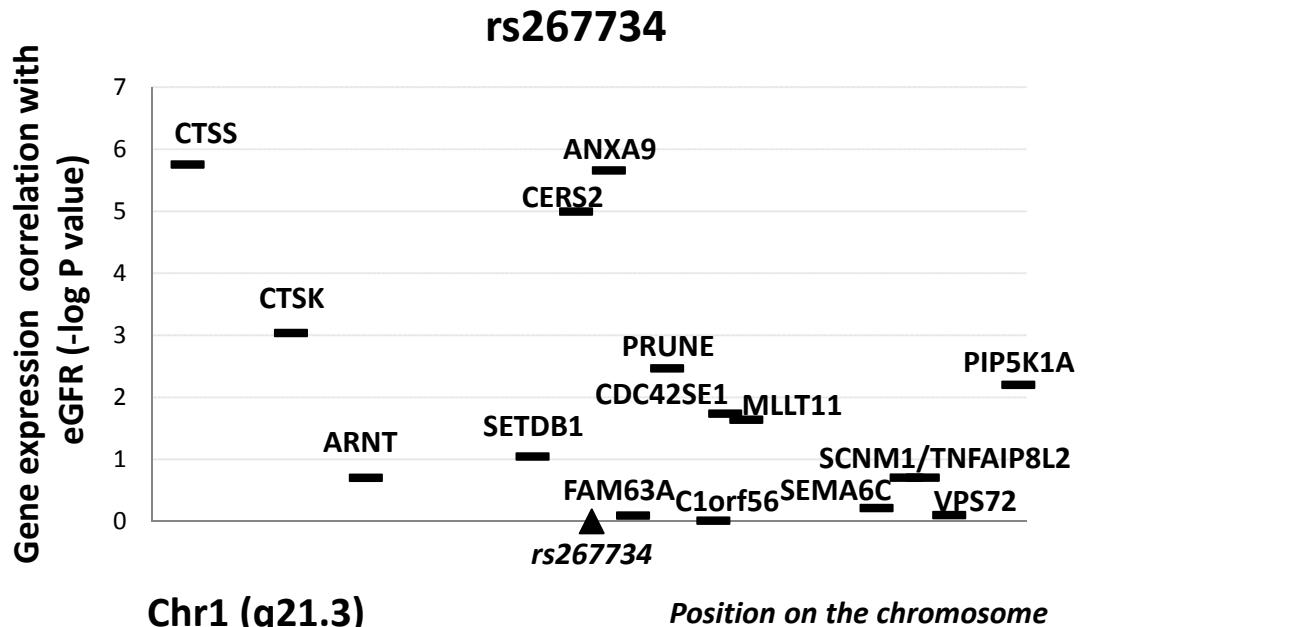
Gene Symbol	IGF2R	SLC22A1	SLC22A2	SLC22A3
kidney	15	1	18	3
adipose	27			2
adrenal	11	0.5	0.7	11
brain	4	0.4		0.6
breast	13			5
colon	12	1	0.1	5
heart	16			0.7
leukocyte	68	0.2		
liver	13	350	0.1	26
lung	9			3
lymph node	15		0.2	11
ovary	11	0.3		10
prostate	12	0.1	0.1	9
skeletal muscle	46	0.5		15
testis	11	0.6	0.1	12
thyroid	20	0.1	0.3	11



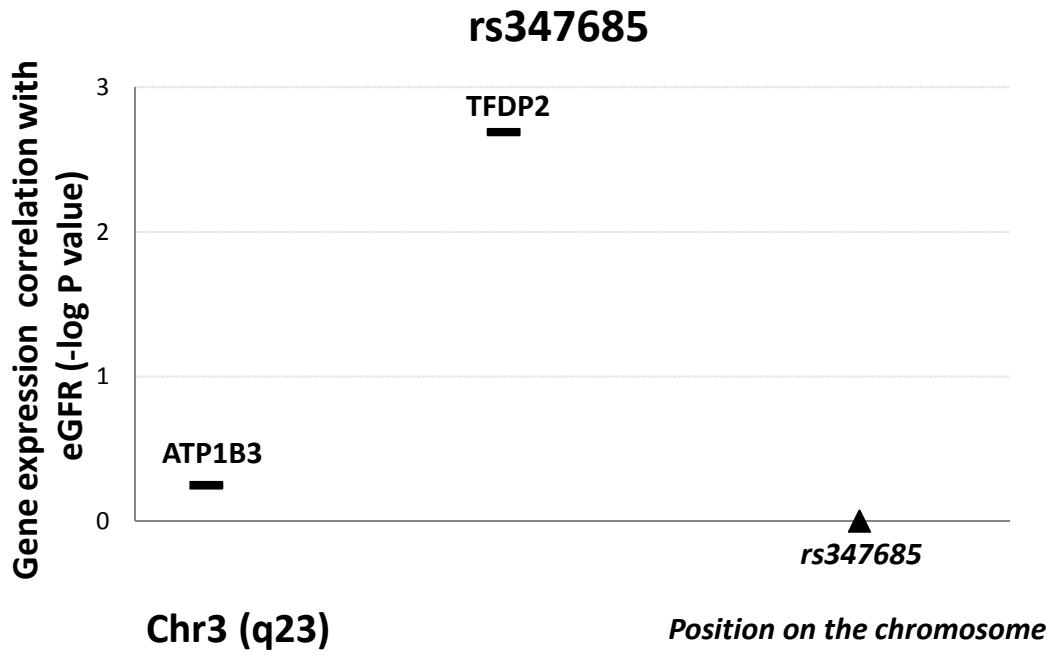
	Gene Symbol									
	EPN2	B9D1	MAPK7	MFAP4	RNF112*	SLC47A1	ALDH3A2	ALDH3A1	SLC47A2*	ULK2
kidney	4	9	3	16	0.4	41	37	1	48	4
adipose			5	11	0.4	5	28	4		6
adrenal			5	36	2	2	15	0.7	0.1	3
brain	12	6	1	3	6	2	15	0.6	1	11
breast	3			39	0.3	2	68	0.8	0.1	7
colon	8			70	0.6	1	21	0.3		5
heart	6			23	0.2	2	14			4
leukocyte	0.9		4			1	12			6
liver	1				0.1	29	38	0.1		0.9
lung				551	0.9	4	47	7	0.1	4
lymph node	6			67	0.5	2	11		0.1	3
ovary	8		7	66	0.7	9	35	0.9	2	5
prostate	12			221	1	1		0.4	0.1	7
skeletal muscle	5	2	2	7	0.8	26	34	0.7	0.1	2
testis	11	17	6	57	0.8	8	26	2	0.7	15
thyroid	5	14	4	23	1	13	73	0.8	0.4	3



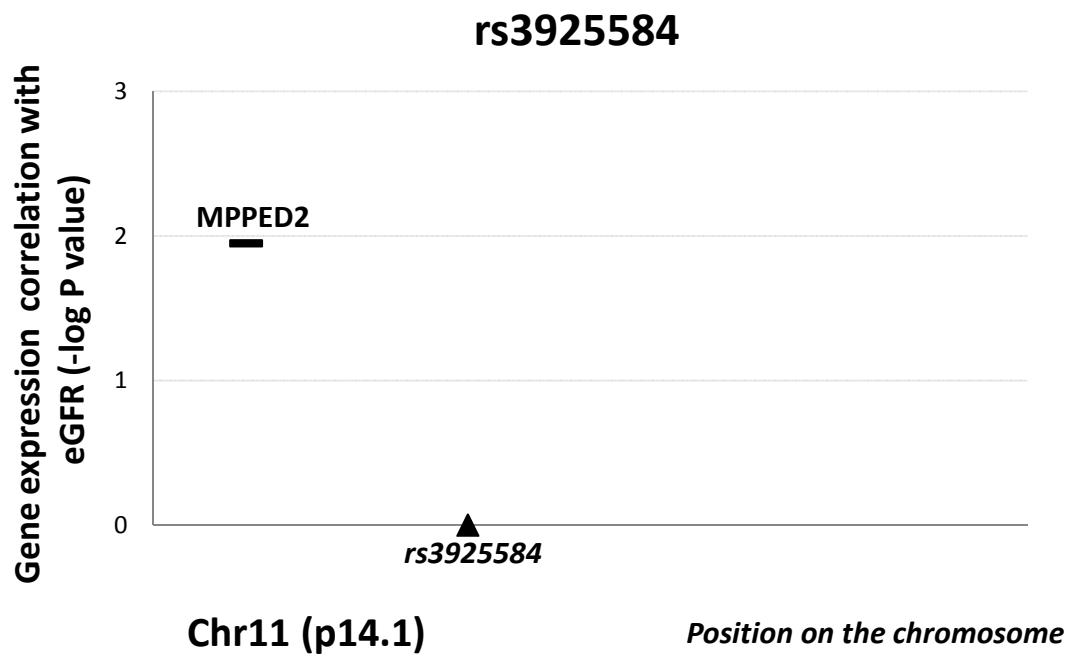
	Gene Symbol									
	DUOX1	DUOX1*	DUOX2*	SHF*	SLC28A2	GATM	SPATA5L1	C15orf48*	SLC30A4	BLOC1S6*
kidney	1			0.9	1	89	5		3	23
adipose	0.2			3	0.1	6	2		3	
adrenal	35			2	0.2	11	4		2	42
brain	1			4	0.1	89	2		4	41
breast	37			2	0.1	7	3		3	28
colon				0.5	11	3	106		3	
heart	0.1			0.9	0.1	6	2		1	20
leukocyte	2			0.5		3	6		2	26
liver				10	0.1	214	3		0.7	12
lung	9	5			0.1	5	3	14	1	20
lymph node	0.4	0.2		4	0.1	15	7		3	21
ovary	3			11	0.2	36	6		5	41
prostate	6	4			0.2	17	6		4	25
skeletal muscle	1			0.5		12	3		0.6	6
testis	3	0.8		6	0.4	33	6	126	7	27
thyroid	17	11			0.1	20	8	3	2	41



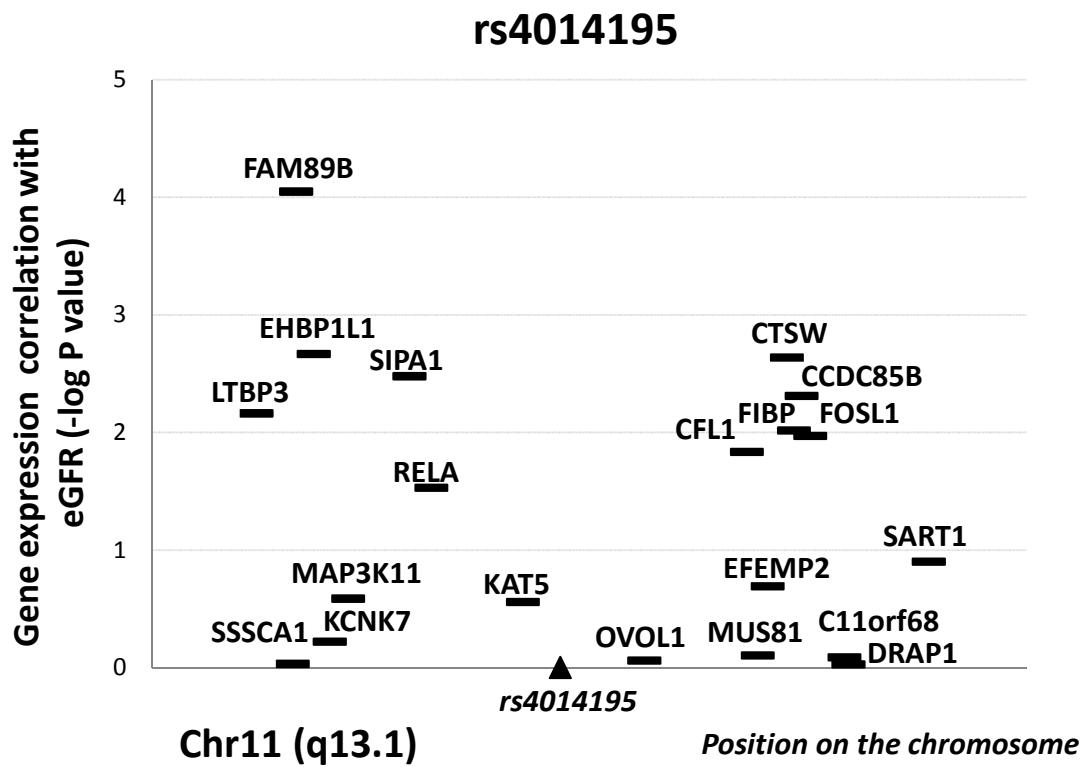
Gene Symbol	Position on the chromosome																			
	CTSS	CTSK	ARNT	SETDB1	CERS2	ANXA9	FAM63A	PRUNE	MLLT11	BNIPL*	C1orf56	GABPB2*	CDC42SE1	SEMA6C	LYSMD1*	SCNM1	TMOD4*	VPS72	PIP5K1A	TNFAIP8L2
kidney	11	5	11		149	7	13	11	2	2		3	26	1	3	20		19	14	
adipose	31	171	21	5	53	0.7	4	7		0.3		4	23	1	2	22		13	8	
adrenal	43	24	11	13	34	0.5	3	7		0.7		4	44	2	2	46		18	15	9
brain	10	3	5	3	52	1	8	6	44	0.3		2	12	1	4	20		21	8	
breast	26	45	15	5	37	0.7	6	8		2	2	4	15	3	3	20	12	17	9	
colon	16	91		4	45	0.8	6	11	3	0.4	2	3	14	2	3	21		22	6	
heart	10	7	8	2	27	0.8	12	17	14	0.3		2	10	8	4	5		10	10	
leukocyte	2006	2	21	10	113	2	16	20		0.3		5	184	0.2		34		16	13	64
liver	19	1	6		278	6	3	4	0.6	0.1	2	0.7	8	0.2	3	7		9	5	2
lung	131	30			110	0.4	4	8		2		1	55	1	2	15		14		3
lymph node	63	120	13	4	81	0.8	5	10		4		3	71	3	3	22		14	15	6
ovary	22	55	29			1	6	12	3	0.5	3	7	27	3	4	30		24	14	
prostate	25	108	15	7	100	4	12	16	2	4	3	4	30	2	8	27		35		
skeletal muscle	3	10	18	5	18	0.1	5	10	0.4	0.1	1	1	11	13			250	44	7	
testis	9	46	16	17	37	1	9	14	2	1	19	12	13	5	3	32	4	27	18	
thyroid	10	21	14	8	58	4	14	20	1	2	4	4	25	3	3	30	12	25	12	



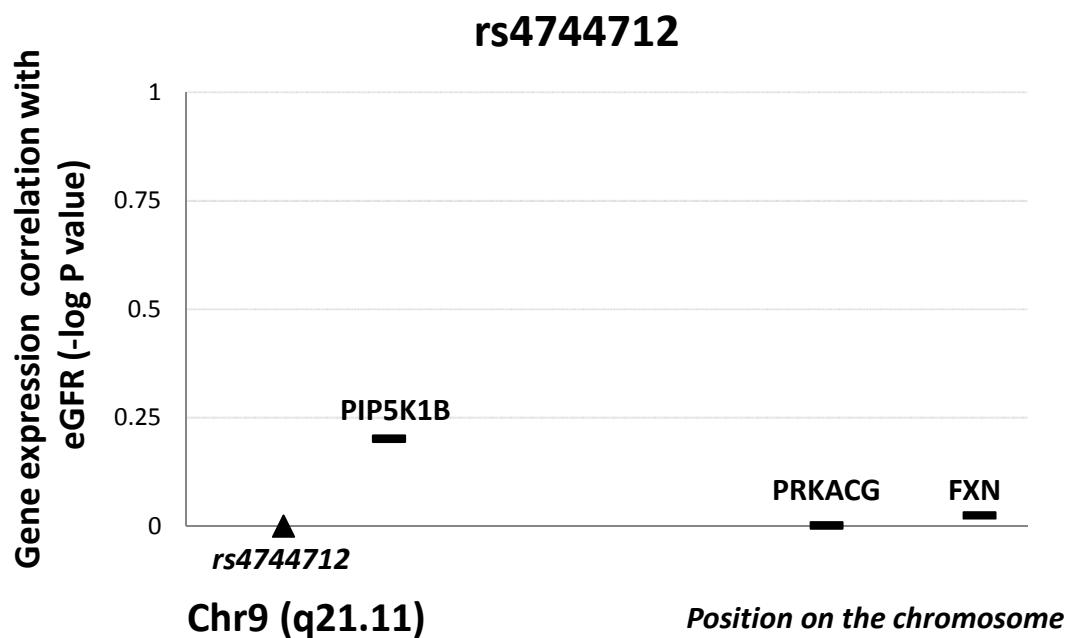
	Gene Symbol	ATP1B3	TFDP2	GK5*	XRNJ*
kidney		105	11	5	4
adipose		59	6	3	7
adrenal		91	3	4	6
brain		61	5	3	5
breast		49	10	6	5
colon		63	6	1	3
heart		31	14	3	4
leukocyte		65	6	3	15
liver		9	5	1	4
lung		211	6	4	8
lymph node		135	5	2	5
ovary		64	6	5	6
prostate		51	5	6	6
skeletal muscle		13	6	2	8
testis		94	52	5	6
thyroid		92	10	5	7



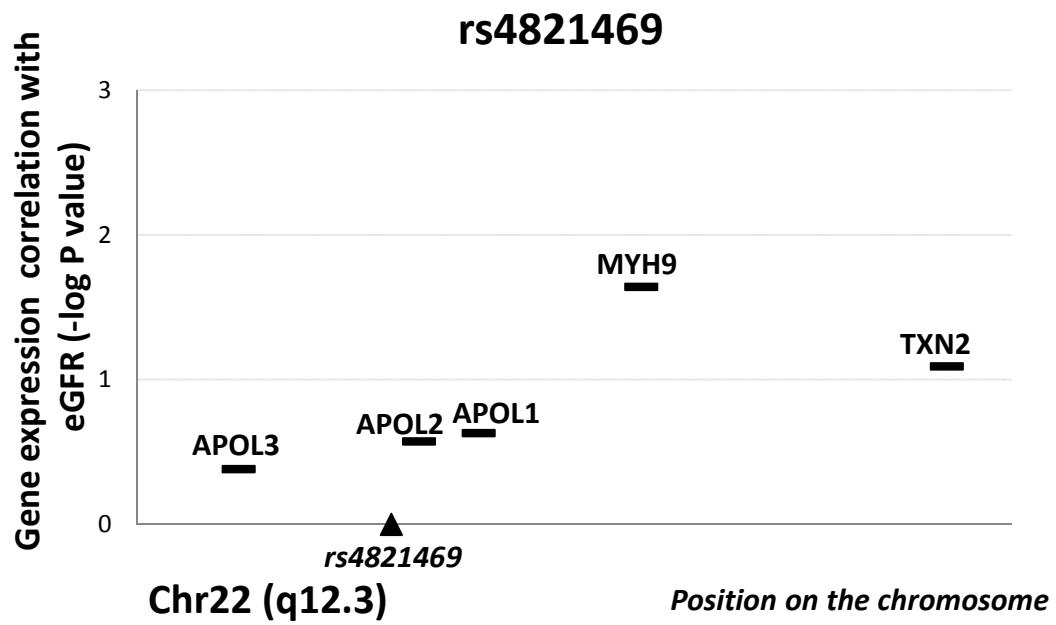
Gene Symbol	MPPED2	DCDC5*	DCDC1*
kidney	8		0.4
adipose	2		0.1
adrenal	2		0.1
brain	6		0.6
breast	1		0.1
colon	3		
heart	2		
leukocyte	0.9		0.3
liver	0.6		0.3
lung	1		1
lymph node	2		0.1
ovary	2		0.9
prostate	6		
skeletal muscle	2		
testis	3		1
thyroid	31		0.8



Gene Symbol	SCYL1*	LTBP3	SSCA1	FAM89B	EHBP1L1	KCNK7	MAP3K11	PCNXL3*	SIPA1	RELA	KAT5	RNASEH2C*	AP5B1*	OVO1	SNX32*	CFL1	MUS81	EFEMP2	CCDC85B	FOSL1	CTSW	FiBP	C11orf68	TSGA10P*	SART1	DRAP1	
kidney	14	14	10	8	4		11	4	12	15	16	2	1	327			4	0.6		38	9	17	30				
adipose	15	13	19	8	14	0.1	20	3	11	37	13	21	3	338		17	19	7		22	12	47	62				
adrenal	20	23	22	13	30	1	17	6	45	29	22	40	2	0.1	467			24	2	2	31	9	51	55			
brain	13	18	8	7	3	2	5	2	1	10	16	8	2		334			16	1		37	14	11	64			
breast		24	14	10	8	0.1	14	3	7	18	14	17	3	0.2	209		24	13	2		23	11	27	51			
colon	11	24	7	20	21	0.3	10	2	7	14	14	19	0.8	1	227		16	14	2		14	13	31	61			
heart	9	11	10	6	11		4	1	3	9	8	8	1		112		10	7	0.7		16	7	9	17			
leukocyte		4	19	29		0.5	27	5	35	37	17	13	12		695		14	0.5	89	27	20	0.1	28	46			
liver	17	4	11	5	1		16	3	7	11	6	7	1		169		3	0.4		13	4		11	19			
lung	15	28	23	17	15	0.3	29	3	18	41	12	11	2	0.2	501		32	11	14	11	19		26	46			
lymph node	17	25	13	25	17	0.2	18	7	46	27	9	13	3		332		15	2	10	14	18	0.1	30	28			
ovary	21	50	19	15	14	0.4	8	7	12	24	26	2		231		44	10	0.5		29	16		18	59			
prostate		31	12	23	27	0.3	12	4	15	25	26	23	1	1	269		23	20	1	2	29	26		36	43		
skeletal muscle		12	9	23	43	0.2	4	2	1	32	20		2		78			6	1		17	23		38	53		
testis		23	16	10	12	0.2	11	6	6	18	27	23	1	8	208		21	10	0.5		49	21	0.9	38	121		
thyroid		30	23	8	16	0.3	10	5	6	24	37	9	4	0.3	193		23	9	4		22	18	0.3	44	78		

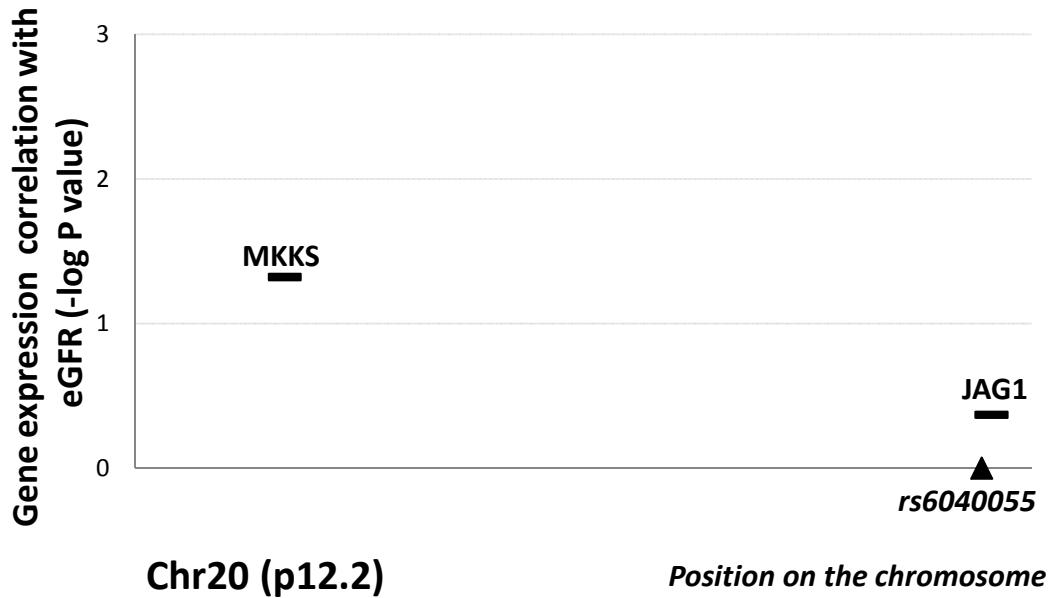


Gene Symbol	PIP5K1B	FAM122A*	PRKACG	FXN
kidney	5	6		10
adipose	2	5		4
adrenal	3	6		12
brain	10	4		5
breast	2	7		8
colon	7	7		6
heart	24	5		15
leukocyte	4	11		18
liver	0.1	3		32
lung	5	3		4
lymph node	5	6		14
ovary	2	10		14
prostate	6	8		16
skeletal muscle	0.7	5		7
testis	21	7	10	12
thyroid	1	7	0.1	8

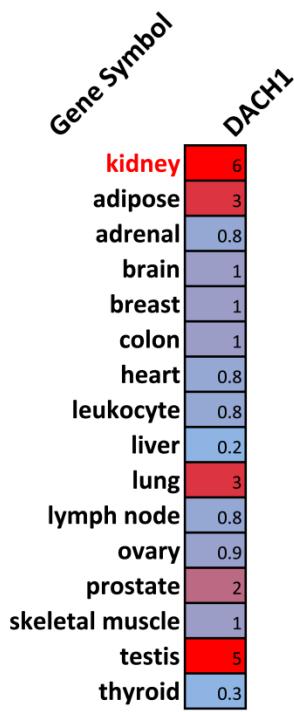
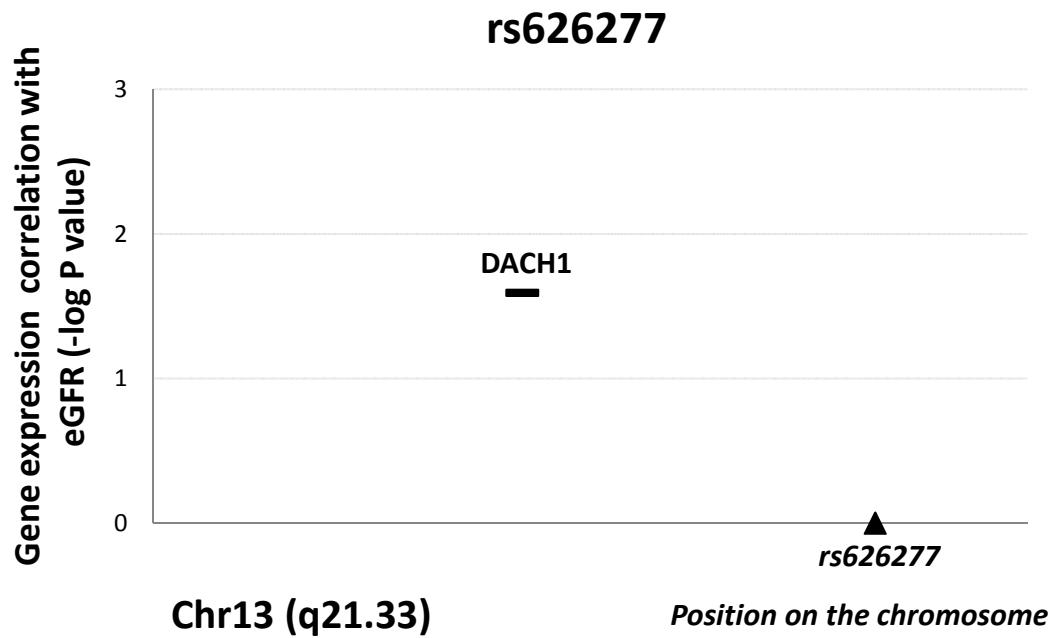


	Gene Symbol					
	APOL3	APOL4*	APOL2	APOL1	MYH9	TXN2
kidney	15	4	16	25	63	44
adipose	66	6	17	24		27
adrenal		7	16	30	143	32
brain	3	3	22	5	23	28
breast	30	3	16	18	107	34
colon	38	4	9	25		24
heart	10	3	13	10	26	36
leukocyte		1	20	18	194	37
liver	4	0.5	13	21	23	43
lung	62	5	42	75	225	28
lymph node	42	5	15	18	97	30
ovary	14		14	41	93	43
prostate	30	10	15	52	87	46
skeletal muscle	7	0.7	9	7	41	39
testis		3	10	24	95	32
thyroid		3	13	13	75	58

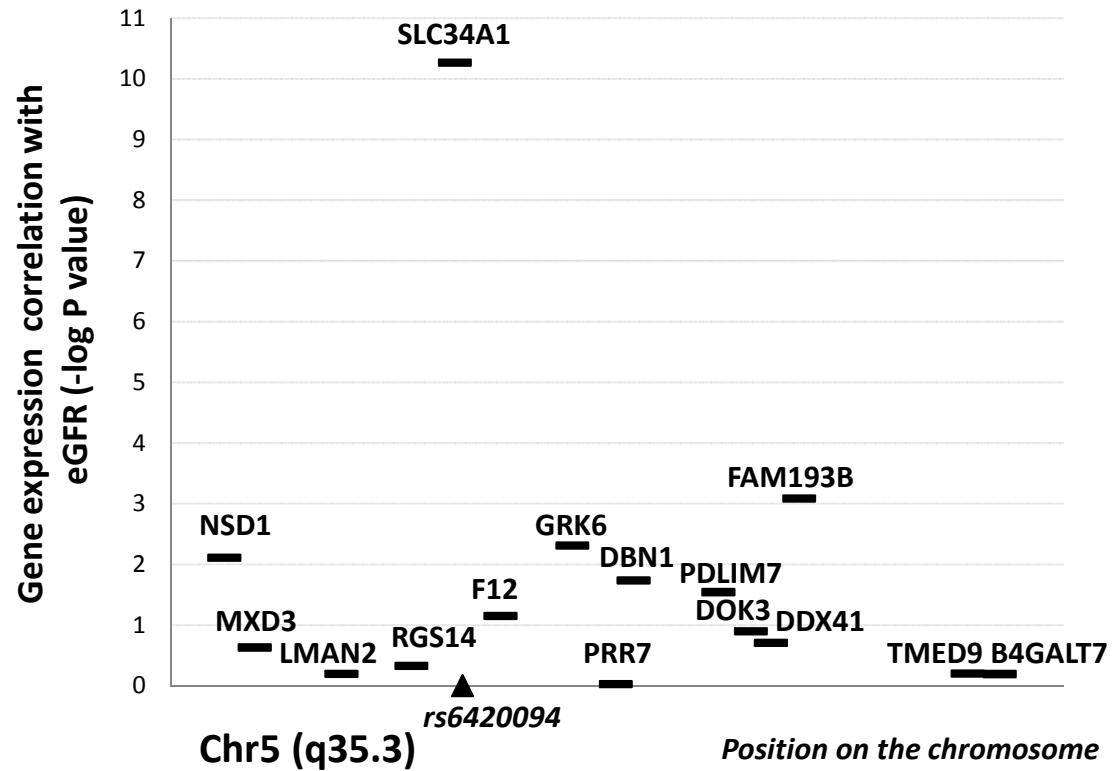
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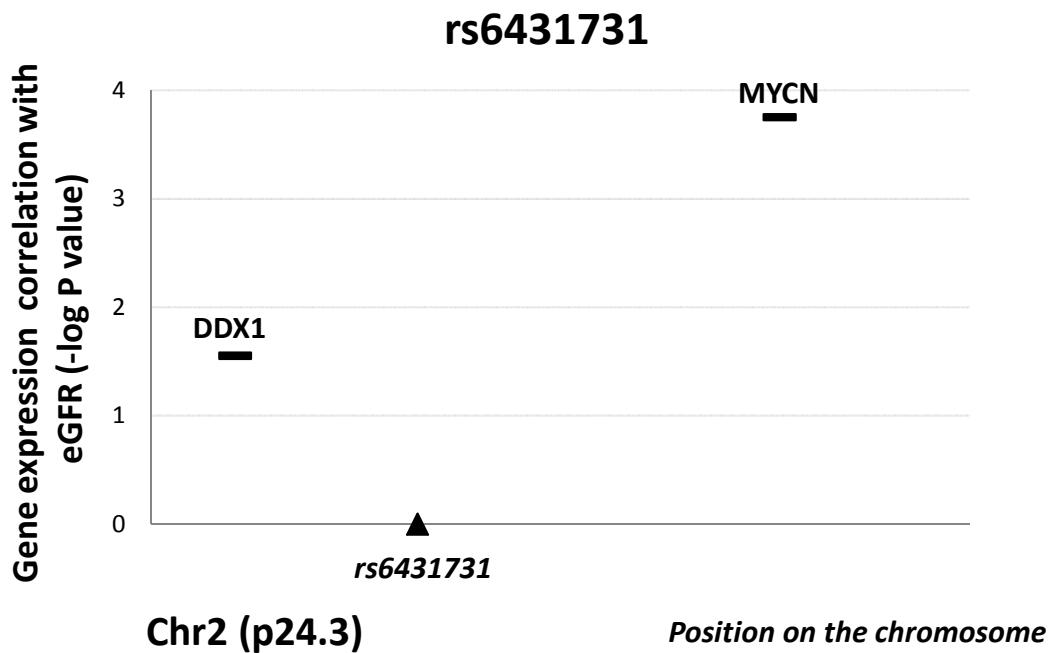
Gene Symbol			
	MKKS	SLX4IP*	JAG1
kidney	26	0.6	13
adipose	8	0.4	22
adrenal	9	0.5	15
brain	18	0.5	4
breast	13	0.4	16
colon	12	0.2	21
heart	16	0.4	6
leukocyte	16	2	1
liver	14	0.4	1
lung	6	0.1	22
lymph node	13	0.8	13
ovary	13	1	11
prostate	16	0.9	20
skeletal muscle	6	0.3	4
testis	24	0.5	13
thyroid	14	0.8	10



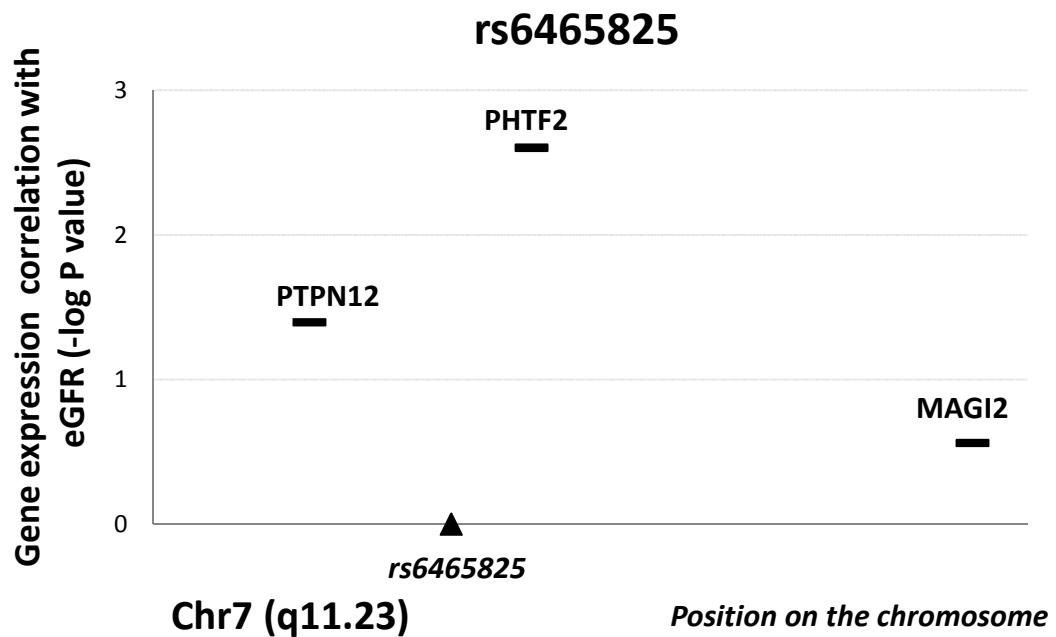
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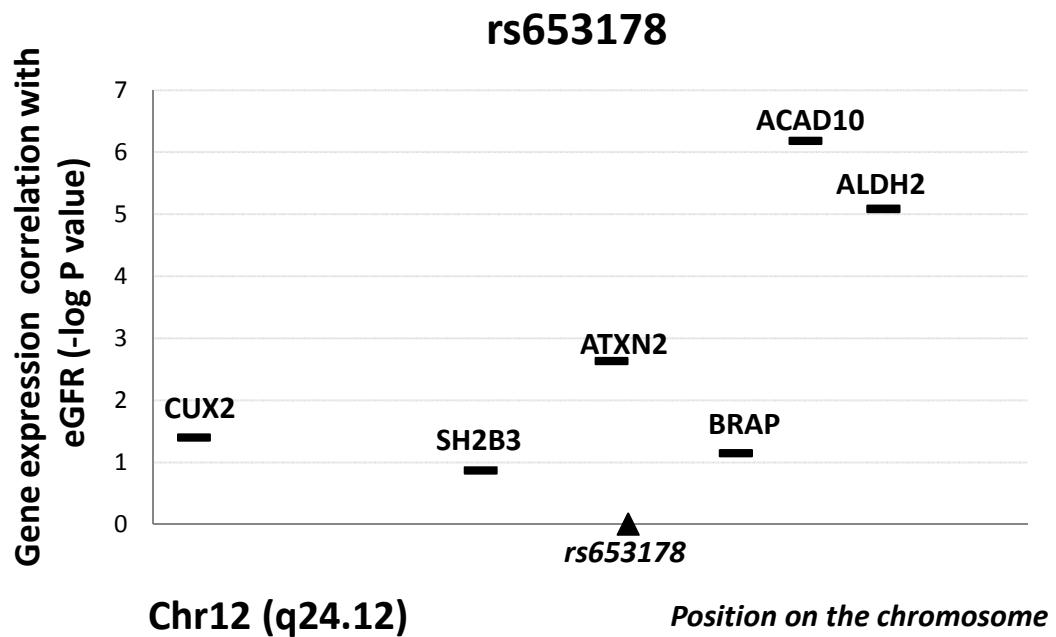
Gene Symbol	NSD1	RAB24*	PRELID1*	MXD3	LMAN2	RGS14	SLC34A1	PRF3*	F12	GRK6	PPR7	DBN1	PDLIM7	DOK3	DDX41	FAM193B	TMED9	B4GALT7
kidney	5	13	39		55	11	13		0.8	3	0.3	15	7	1	14	13	75	6
adipose	5	6	32		28	4				6	0.1	22	17	2	19	6	54	5
adrenal	5	14	83		33	12				23	0.4	12	47	17	22	13	66	8
brain	4	11	20		12	5				8	1	28	5	1	24	6	16	5
breast	4	8	26		22	3				5	0.3	19	21	0.9	14	5	39	16
colon	4	6	35		37	2				5	0.2	19	69	0.4	15	10	37	3
heart	4	4	7		15	0.6				3	0.2	3	5	0.6	4	3	19	3
leukocyte	14	24	83		62	27				47	1	3	13	45	23	6	60	3
liver	2		39		85	8	0.1		63		0.1	0.7	2	0.7	9	8	117	4
lung	3	16	36		42	5				7	1	8	18	3	11	19	73	3
lymph node	5	21	34		40	23				13	0.7	9	11	20	15	28	70	8
ovary	8	9	31		31	3				7	0.3	39	44	1	29	7	51	7
prostate	5	15	31		44	3				5	0.3	22	83	2	14	11	47	6
skeletal muscle	6	4	4		22	0.2				6	0.3	4	32	0.5	9	5	21	4
testis	8	7	28		61	3	0.4		11	0.4	25	57	2	20	9	44	6	
thyroid	8	7	30		60	3			9	0.2	16	30	0.7	27	8	70	7	



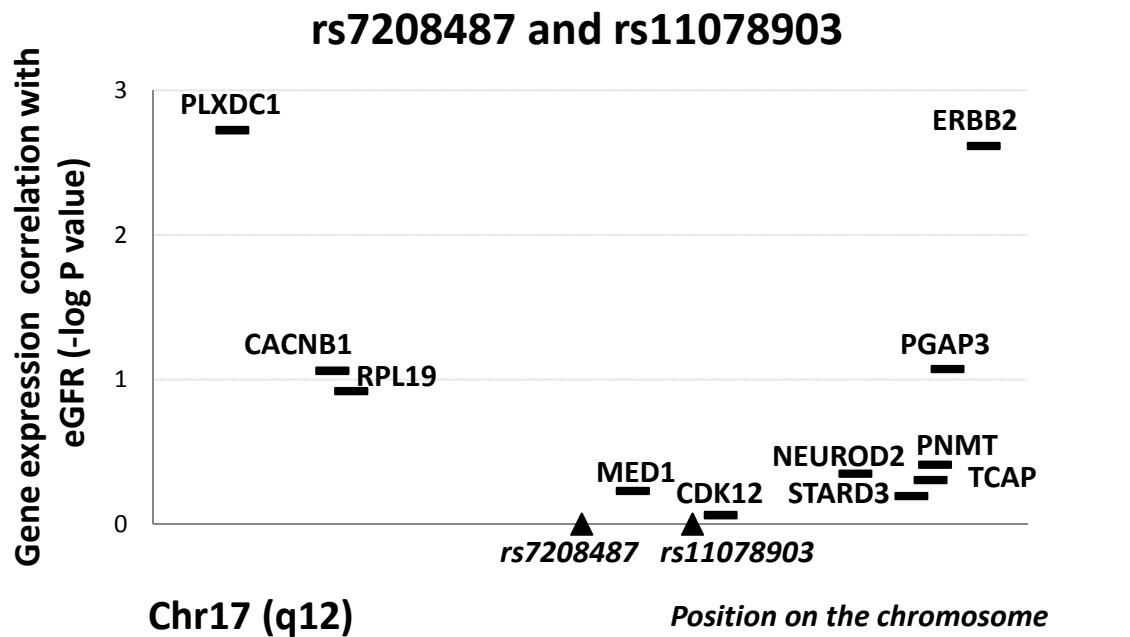
Gene Symbol	DDX1	MYCN
kidney	47	0.5
adipose	41	
adrenal	39	0.3
brain	64	2
breast	53	0.2
colon	44	
heart	43	
leukocyte	21	
liver	21	
lung	17	0.2
lymph node	16	0.6
ovary	57	1
prostate	40	0.2
skeletal muscle	50	
testis	57	1
thyroid	81	0.8



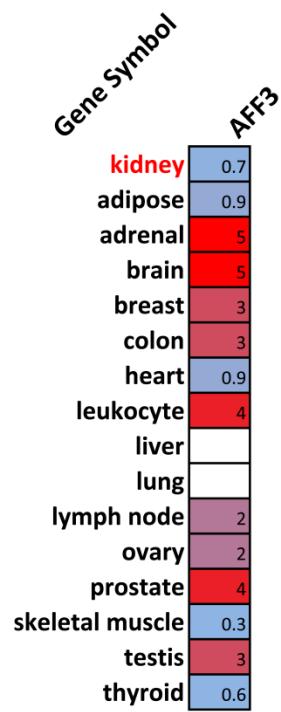
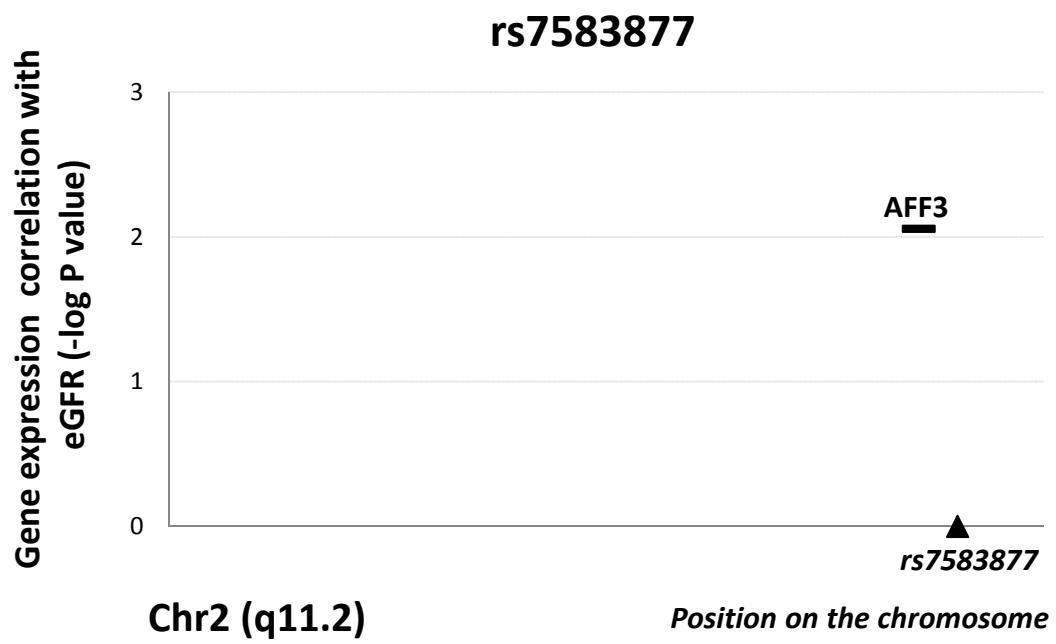
Gene Symbol	PTPN12	RSBN1L*	TMEM60*	PHTF2	MAGI2
kidney	24	6	10	5	
adipose	43	5	8	4	2
adrenal	33	9	12	7	2
brain	14	7	7	6	15
breast	27	5	11	7	2
colon	37	7	8		1
heart	20	2	4	9	
leukocyte	57	23	28	8	
liver	8	3	6		0.3
lung	90	9	7	7	
lymph node	36	9	15	8	1
ovary	29	13	12	7	3
prostate	37	10	11	6	4
skeletal muscle	11	5	9	22	
testis	33	17	19	10	
thyroid	48	17	14	11	4

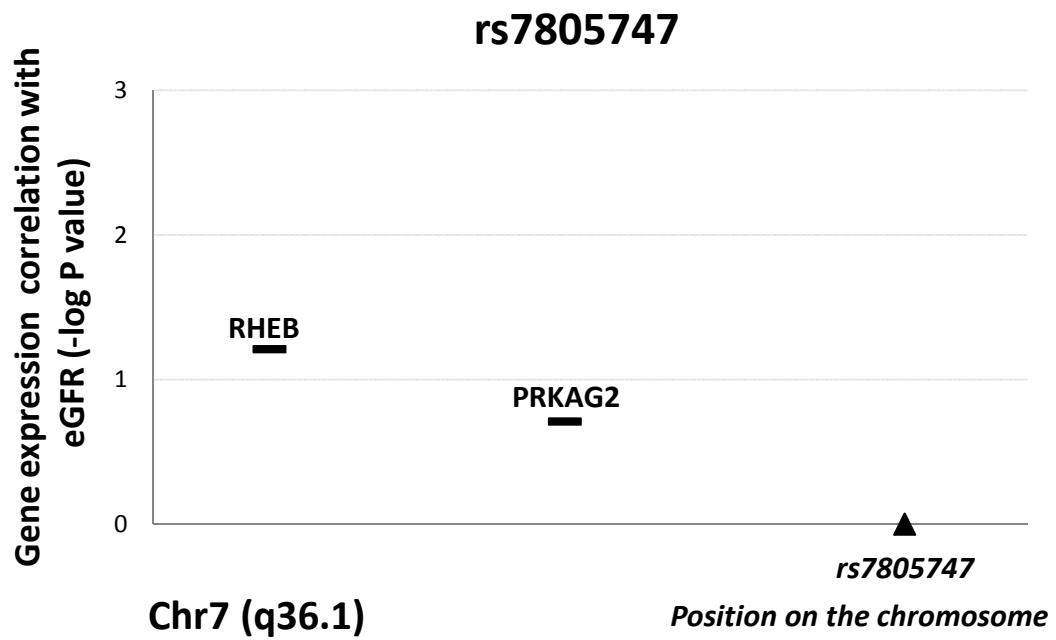


Gene Symbol	CUX2	FAM109A*	SH2B3	ATXN2	BRAP	ACAD10	ALDH2
kidney	2	4	9	5	7	81	
adipose	1	17	9	8			
adrenal	2	15	9	8	3	39	
brain	3	0.4	3	13	8		121
breast	0.1	2	9	9	7		384
colon	0.1	3	5	6	9		134
heart		2	10	9	4		98
leukocyte	0.1	2	31	10	10		86
liver	8	1	3	6	3		307
lung		2	16	17	4		143
lymph node		2	13	10	6		52
ovary		5	7	15	9		
prostate	1	2	5	16	9		123
skeletal muscle		1	3		13		57
testis	0.5	3	6	18	56	3	53
thyroid	1	2	6	11	12		96

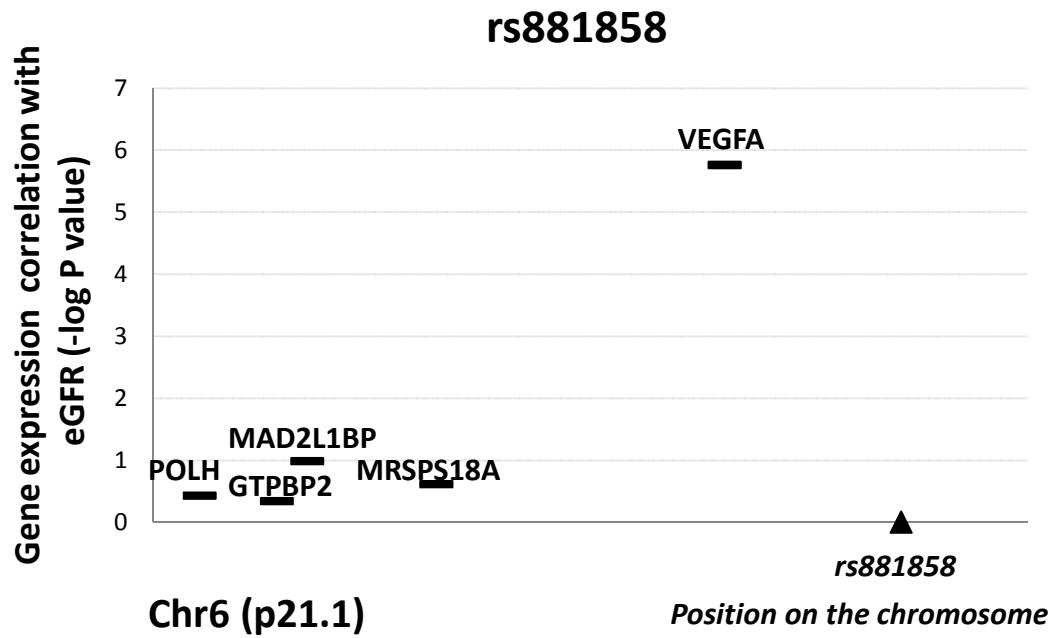


Gene Symbol	Position on the chromosome														
	PLXDC1	CACNB1	ARL5C*	RPL19	STAC2*	FBXL20*	MED1	CDK12	NEUROD2	PPP1R1B*	STARD3	PNMT	PGAP3	ERBB2	TCAP
kidney	1	0.8	0.5	567	4	2	5	4	6	8	0.8	6	26	0.4	
adipose		0.7		975	0.6	3	8	7		14	9	0.6	4	3	0.3
adrenal	4	1	0.9	1359	0.4	2	10	7		0.3	16	0.2	6	4	0.3
brain	3	10	0.2	275	13	4	5	3	5	94	12	1			0.4
breast		3	0.5	665	5	4	6	5		35	9	0.1			47
colon	5	1	0.2	1003	0.7	3	6	5		30	10	1	3	9	0.9
heart	5	0.9	0.1	273	0.3	3	6	3		0.5	6	1	2	16	588
leukocyte	1	0.9	0.6	1536		5	19	14		0.1	28		6	2	0.2
liver	0.1			413	0.1	1	3	3		8		6	2		0.1
lung	4	1		1091	0.6	2	5	5		15	13	0.4			0.5
lymph node	7	3	0.4	1339	0.9	3	8	9		2	32	0.3	2	4	3
ovary		2	0.6	1169	1	3	13	7		13	12	0.2			0.6
prostate	3	3	0.2	1435	6	4	10	5		25	12	2	5	14	0.4
skeletal muscle	0.7	102	0.2	964	0.3		6	4		0.5	11	0.8	1	5	284
testis	1	3	0.5	745	2	9	8	10	0.1	10	13	1			9
thyroid	2	19		737	0.2	3	8	6		0.5	17	0.8			99

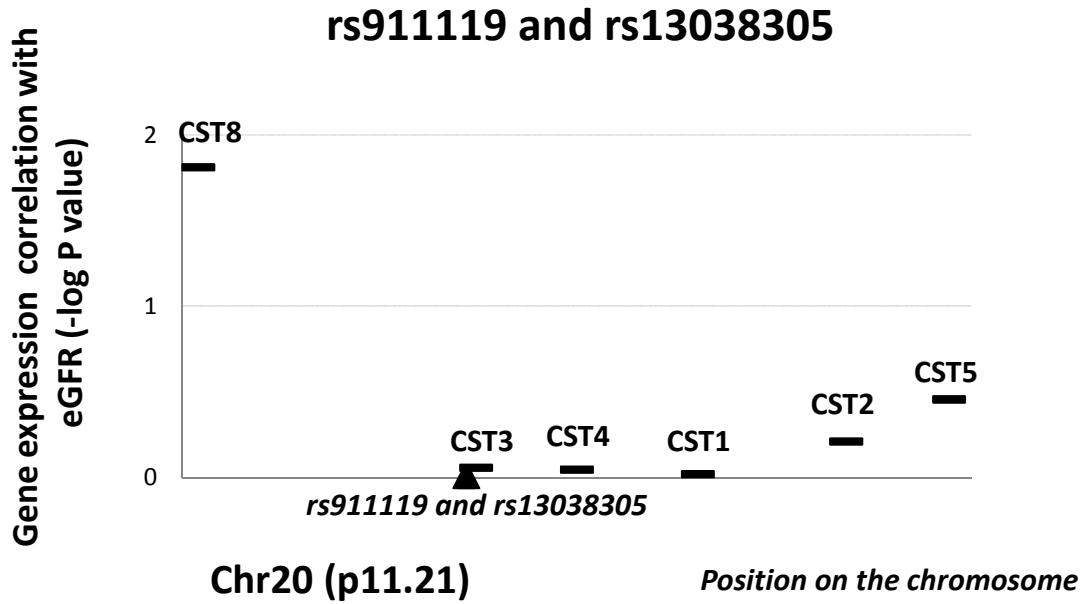




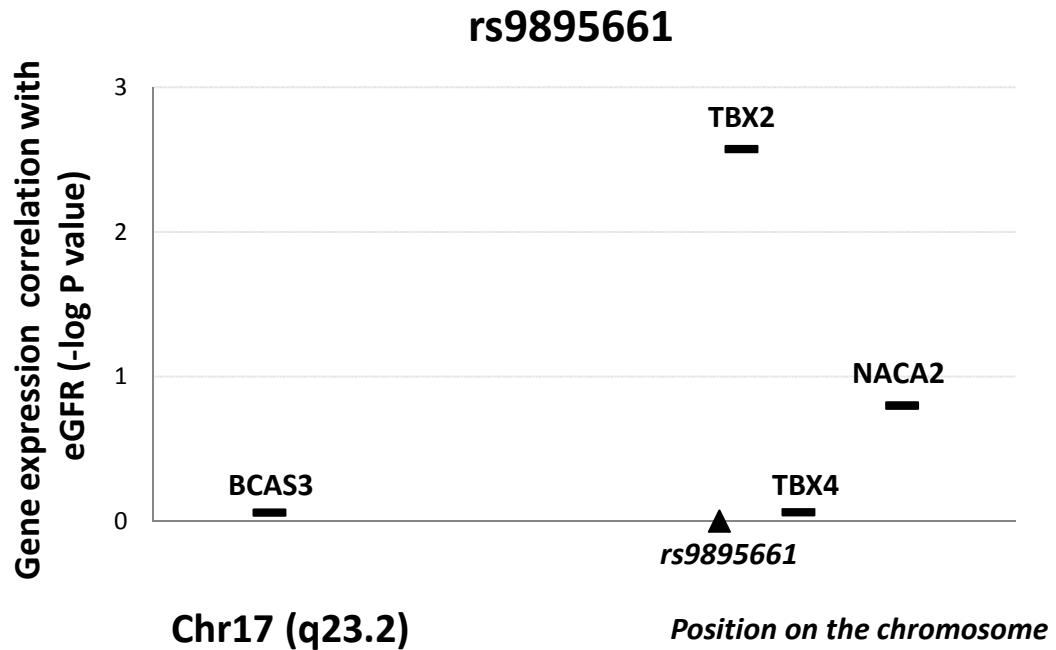
Gene Symbol	RHEB	PRKAG2
kidney	62	19
adipose	70	12
adrenal	55	17
brain	99	18
breast	52	10
colon	103	13
heart	47	44
leukocyte	29	23
liver	36	9
lung	88	9
lymph node	38	10
ovary	79	10
prostate	110	33
skeletal muscle	85	3
testis	67	22
thyroid	122	24



Gene Symbol	POLH	GTPBP2	MAD2L1BP	RSPH9*	MRPS18A	VEGFA	C6orf223*
	kidney	2	7	9	0.4	18	43
adipose	2	14	4		16		
adrenal	3	12	9		19	17	
brain	1	4	4	0.5	13	5	0.1
breast	2	8	4		16	15	0.1
colon	1	8	4	0.3	12	13	0.1
heart	1	6	8		12	28	
leukocyte	4	15	15		15	3	
liver	0.8	2	6		24	32	
lung		30	5	4	10	65	0.5
lymph node	3	17	7		13	32	
ovary	4	8	8	1	16	21	0.1
prostate	3	12	5		26	32	
skeletal muscle	2	20	5		31	29	
testis	6	10	6	5	15	6	0.1
thyroid	4	14	10		25	93	1



Gene Symbol	NAPB*	CST1*	CST11*	CST8	CST9*	CST9L*	CST3	CST4	CST1	CST2	CST5
	kidney	5	0.3				146		0.3		0.7
adipose	3	0.3				307	0.1	0.3	0.1		
adrenal	4	0.2				218				0.1	
brain	182	0.4				252					
breast	3	0.3				331			0.1		
colon	8					310					
heart	2					177					
leukocyte	3	0.3				510					
liver	1					244					
lung	5					347				2	
lymph node	5					334			0.2		
ovary	6					135		0.1			
prostate	8		0.8			477		0.6	0.1		
skeletal muscle	1					212					
testis	6	2	17	10	0.2	23	313	0.1	0.2	0.3	
thyroid	7	0.1				234	0.6	0.3	0.1		



	Gene Symbol				
	BCAS3	TBX2	C17orf82*	TBX4	NACA2
kidney		14			6
adipose	10	5		0.2	72
adrenal	3	3	0.1	0.1	86
brain		0.7			19
breast		4	0.1	0.2	69
colon	4	2			69
heart	3	2		0.1	4
leukocyte	9				12
liver		0.9		0.3	4
lung	10	26	0.4	18	15
lymph node	4	3		0.2	10
ovary	5	3	0.1	0.1	127
prostate		11	0.3	9	14
skeletal muscle		0.9	0.1		11
testis	11	7	0.2	0.7	120
thyroid	11	4	0.1	0.4	40

Supplementary Table 9**eQTL analysis of the CKD risk loci in external datasets**

SNPs associated with chronic kidney disease (CKD) acts as cis expression quantitative trait loci (eQTL) in other tissues. P-values indicate the strength of the association between the SNP (as eQTL) and the nearby gene. The sources of the analyses are marked and detailed on the bottom of the table (analysis ID: 1-4). The table shows the results of our study in the case of these genes: baseline expression in the kidney based on our RNA sequencing data indicated in the last column; transcripts which are differentially expressed in CKD and/or transcripts whose expression levels correlate with estimated glomerular filtration rate (eGFR) are marked in red.

Gene Symbol	SNP	Chromosome	Distance from the SNP (kb)	Gene in the same LD block	P-value (eQTL)	Analysis ID	Baseline expression in the kidney
SYPL2	rs10857787	1	0	Yes	2.85×10^{-35}	1	High
ATXN7L2	rs10857787	1	16	Yes	1.5×10^{-3}	1	Medium
CERS2	rs267734	1	4	Yes	3.70×10^{-5}	2	High
CERS2	rs267738	1	0	Yes	7.51×10^{-5}	2	
SHROOM3	rs17253722	4	243	Yes	7.32×10^{-6}	3	Medium
CLTB	rs3812035	5	974	No	1.5×10^{-4}	2	High
CLTB	rs6420094	5	974	No	1.5×10^{-4}	2	
CLTB	rs6862195	5	979	No	1.5×10^{-4}	2	
RMND5B	rs3812035	5	748	No	4.06×10^{-5}	2	High
RMND5B	rs6420094	5	747	No	4.06×10^{-5}	2	
RMND5B	rs6862195	5	743	No	4.06×10^{-5}	2	
SLC25A37	rs17786744	8	347	No	4.68×10^{-5}	3	Medium
AP5B1	rs11227299	11	0	Yes	2.39×10^{-6}	4	Medium
AP5B1	rs4014195	11	35	Yes	2.96×10^{-6}	4	
AP5B1	rs9666878	11	66	Yes	4.03×10^{-6}	4	
THUMPD1	rs13333226	16	379	No	8.99×10^{-5}	2	High
THUMPD1	rs13335818	16	385	No	8.99×10^{-5}	2	
THUMPD1	rs4293393	16	380	No	8.99×10^{-5}	2	
CDK12	rs11078895	17	217	Yes	1.97×10^{-11}	1	Medium
PGAP3	rs8076494	17	311	Yes	7.87×10^{-7}	1	High

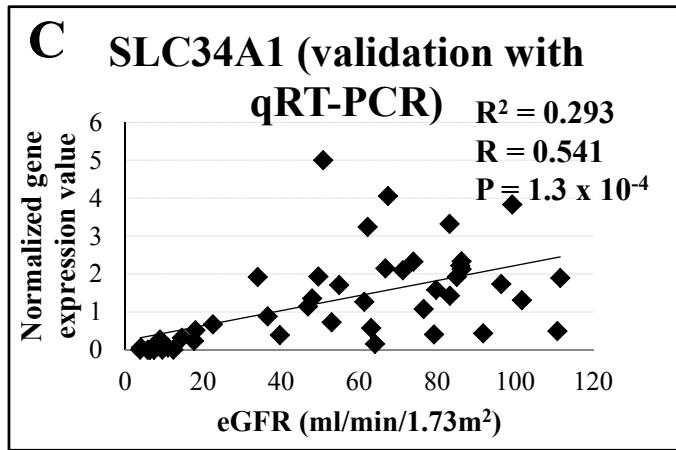
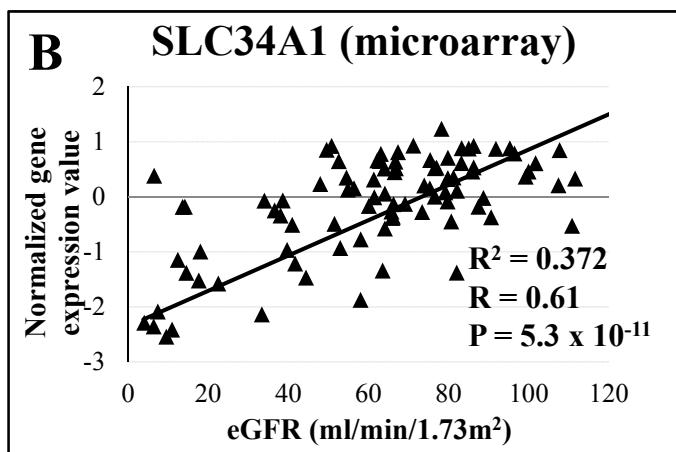
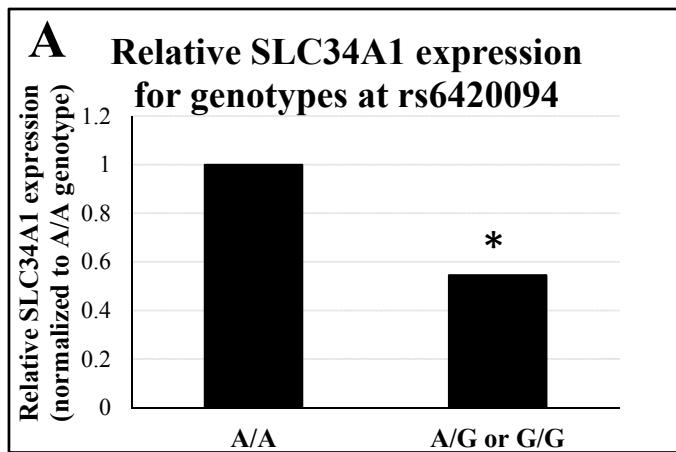
Type of the eQTL analysis

ID	Title	Tissue	Expression profiling	Samples (n)
1	Mapping the genetic architecture of gene expression in human liver	Liver	Array	427
2	Transcriptome genetics using second generation sequencing in a Caucasian population	Lymphoblastoid	RNAseq	60
3	Mapping cis- and trans-regulatory effects across multiple tissues in twins	Adipose	Array	856
4	Population genomics of human gene expression	Lymphoblastoid	Array	210

Supplementary Figure 4

Transcript level of *SLC34A1* is different by rs6420094 genotype

The expression of *SLC34A1* (solute carrier family 34, member 1) is significantly higher ($P=0.0305$) in samples homozygous for A alleles (A/A, n=9) at the rs6420094 locus comparing to samples with minor alleles (A/G, n=3 or G/G, n=6) at this locus. Only control samples (eGFR> 85 ml/min/1.73m²) were used for the analysis (**A**). Microarray based transcript levels of *SCL34A1* correlate with renal function in tubule samples ($R^2=0.372$, $P=5.3 \times 10^{-11}$) (**B**). QRT-PCR-based *SLC34A1* transcript levels ($R^2=0.293$, $P=1.3 \times 10^{-4}$) confirm its correlation with kidney function (**C**).



Supplementary Table 10

Disrupted transcription factor binding site motifs at the 44 CKD risk associated loci

The table shows the disrupted transcription factor binding site (TFBS) motifs at the 44 chronic kidney disease (CKD) associated SNPs (single nucleotide polymorphisms). The table also lists the CRATs (CKD risk associated transcripts) correlating with eGFR (estimated glomerular filtration rate) at each CKD risk associated SNPs. Color-coding shows the baseline expression of the transcripts based on human kidney RNA sequencing, red: high expression, yellow: medium expression, green: low expression, blue: no expression. Transcripts in significant ($P < 0.05$) correlation with eGFR in tubule (T) and glomerular (G) samples are listed, asterisk (*) marks if the correlation was significant with a corrected P value below 0.05.

CKD risk associated locus	Location (chromosome)	Position	CRATs correlating with eGFR in tubule (T) and glomerular (G) samples (* P corrected<0.05)	Number of total correlating CRATS (P<0.05)	Disrupted transcription factor binding site (TFBS) motifs	Number of disrupted TFBS motifs
rs267734	1	150951477	CTSS (T* and G*) CTSK (T* and G) CERS2 (T*) ANXA9 (T* and G) PRUNE (T*) MLLT11 (T) CDC42SE1 (T) PIP5K1A (T*)	8	PTF1-beta, STAT	2
rs1933182	1	109999588	PSRC1 (G) SORT1 (T and G) GNAI3 (T*) GSTM4 (T*)	4	Ik-1, Lhx3, Pax-4, Pou2f2, ZBTB7A, Zfp740	6
rs12124078	1	15869899	EFHD2 (G) CELA2A (T) CELA2B (T) CASP9 (T* and G) DNAJC16 (T*) AGMAT (T* and G) DDI2 (T*) RSC1A1 (T*)	8	Ets	1
rs16864170	2	5907880	SOX11 (T*)	1	BATF, HNF4, Irf, RFX5	4
rs6431731	2	15863002	DDX1 (T) MYCN (T* and G)	2	FAC1, RFX5	2

rs10206899	2	73900900	NAT8 (T*) NAT8B (T*)	2	SP1	1
rs7583877	2	100460654	AFF3 (T*)	1	Gf1l	1
rs347685	3	141807137	TFDP2 (T*)	1	AP-1,Irf	2
rs17319721	4	77368847	FAM47E (T* and G*) STBD1 (T* and G*)	2	LBP-1, Nanog, Smad3, Sox, YY1	5
rs13146355	4	77412140	FAM47E (T* and G*) STBD1 (T* and G*)	2	Foxa,PLAG1	2
rs6420094	5	176817636	NSD1 (T*) SLC34A1 (T* and G) F12 (G) GRK6 (T*) DBN1 (T) PDLM7 (T) FAM193B (T*)	7	GATA	1
rs11959928	5	39397132	FYB (T* and G*) DAB2 (T*)	2	Irf,Maf,WT1	3
rs881858	6	43806609	VEGFA (T* and G)	1	Pitx2, p300,GATA, CEBPD,CEBPB,C EBPA	6
rs2279463	6	160668389	IGF2R (T*) SLC22A1 (T*) SLC22A2 (T*) SLC22A3 (G)	4	Cdx2, Mef2, TATA, Zfp281	4
rs3828890	6	31440669	HLA-C (G) MICB (T* and G) LST1 (T* and G) NCR3 (T*) AIF1 (T*) BAG6 (T*) APOM (T*) LTB (T* and G*)	8	T3R	1
rs6465825	7	77416439	PTPN12 (T) PHTF2 (T*) MAGI2 (G)	3	COMP1, Ik-2, Mef2	3
rs7805747	7	151407801		0	Tgfl, Pax-6, HMGN3, GATA	4
rs10277115	7	1285195	GPER (T*) MICALL2 (G*)	2		0
rs1617640	7	100317298	LRCH4 (T* and G) PCOLCE (G) SLC12A9 (T) TRIP6 (T*)	4	AP-1, BDP1	2
rs10109414	8	23751151	STC1 (T*)	1	Irx, Pou2f2	2
rs1731274	8	23766319	STC1 (T*)		AP-1, INSM1, STAT	3
rs4744712	9	71434707		0	ERalpha-a, Egr-1, Esr2, Prrx2, RXRA, VDR	6
rs10794720	10	1156165	LARPB4 (T*) IDI1 (T)	2	HEN1, PTF1-beta	2
rs4014195	11	65506822	LTBP3 (T*) FAM89B (T*) EHBP1L1 (T* and G*) SIPA1 (T*) RELA (T) CFL1 (T)	11	Mef2, Pou1fl, TATA	3

			CCDC85B (T*) FOSL1 (T*) CTSW (T*) FIBP (T*) DRAPI (G)			
rs3925584	11	30760335	MPPED2 (T*)	1	PU.1	1
rs653178	12	112007756	CUX2 (T) ATXN2 (T*) ACAD10 (T*) ALDH2 (T*)	4	Esr2	1
rs10774021	12	349298	SLC6A12 (T*) SLC6A13 (T* and G) KDM5A (G)	3	GR, Irf, Zec, Zic	4
rs626277	13	72347696	DACH1 (T)	1	NF-I	1
rs491567	15	53946593		0	Barx1, Barx2, Dbx1, Dbx2, En-1, Esx1, Gbx1, Gbx2, Hlx1, Hlx9, HNF1, Hoxa10, Hoxa3, Hoxa5, Hoxb13, Hoxb3, Hoxb4, Hoxb7, Hoxb8, Hoxb9, Hoxc6, Hoxd8, Isx, Lhx3, Msx-1, Ncx, Nkx6-1, Nkx6-2, Nobox, Pax-6, Pax7, Pbx- 1, Phox2a, Pou1f1, Pou2f2, Pou3f2, Pou3f4, Pou4f3, Prrx1, Prrx2, Sox, Vax2	42
rs1394125	15	76158983		0	GATA, TATA, p300	3
rs2453533	15	45641225	DUOX1 (T*) SLC28A2 (T) GATM (T* and G) SLC30A4 (T*)	4	Cdx, TATA	2
rs12437854	15	94141833		0	GR, Hoxa9, Pdx1, Pitx2	4
rs12917707	16	20367690	GP2 (T and G) UMOD (T* and G) ACSM5 (T* and G) ACSM2A (T*) ACSM2B (T*)	5	E2A, ERalpha-a, ZEB1	3
rs4293393	16	20364588	GP2 (T and G) UMOD (T* and G) ACSM5 (T* and G) ACSM2A (T*) ACSM2B (T*)	5		0
rs11864909	16	20400839	GP2 (T and G) UMOD (T* and G) ACSM5 (T* and G) ACSM2A (T*) ACSM2B (T*) ACSM1 (T)	6	Ehf, Ets, Nrf-2	3
rs9895661	17	59456589	TBX2 (T*)	1	Eomes, hR, NRSF, Pax-8, TBX5	5
rs2453580	17	19438321	EPN2 (T) MFAP4 (T* and G*)	4	EBF, ERalpha-a, Ets, HEN1, Pou2f2	5

			SLC47A1 (T*) ALDH3A2 (T* and G)			
rs11078903	17	37631924	ERBB2 (T*)	1	Nkx2	1
rs7208487	17	37543449	PLXDC1 (T* and G)	1	DEC, RXRA	2
rs12460876	19	33356891	SLC7A9 (T*)	1	AP-1, Pax-4, Rad21	3
rs911119	20	23612737	CST8 (T)	1	SZF1- 1,TCF12,VDR	3
rs13038305	20	23610262	CST8 (T)	1	ERRA	1
rs6040055	20	10633313	MKKS (T)	1	E2F, Ets, Nrf-2, Sox	4
rs4821469	22	36616445	MYH9 (T)	1	Brachyury, Eomes, TBX5	3