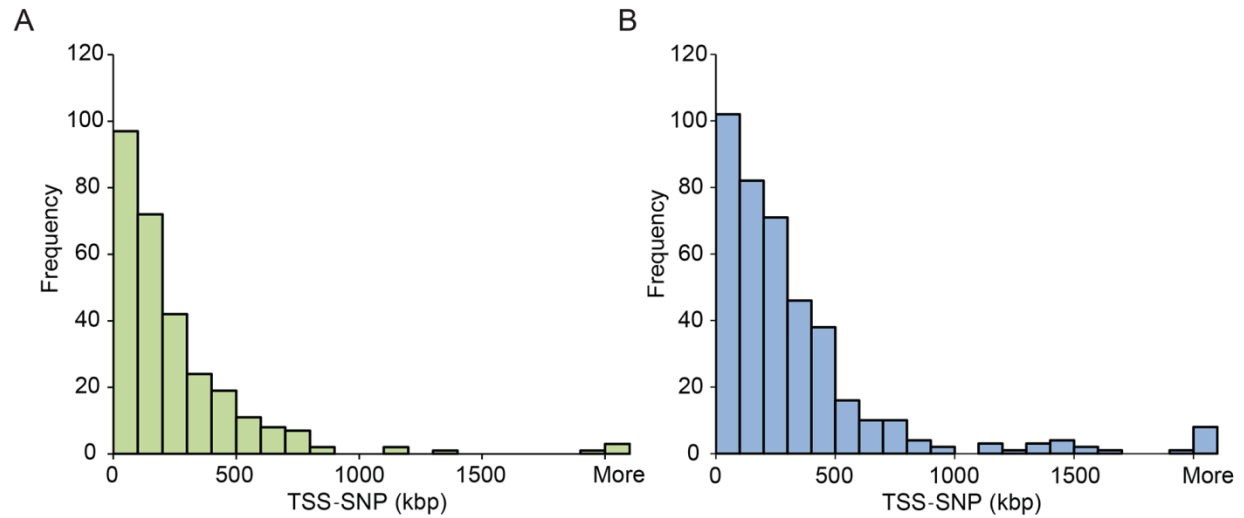
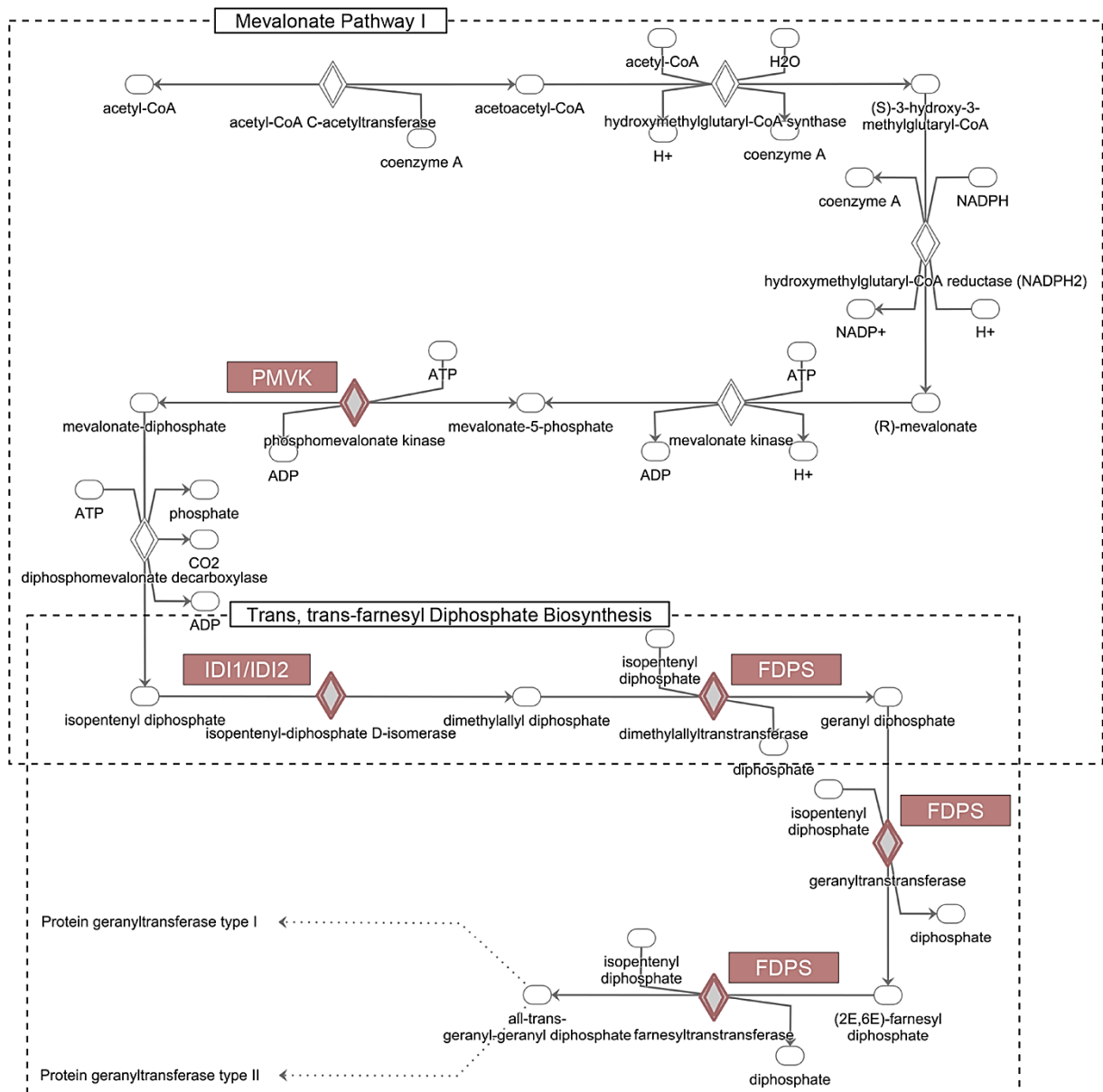




Supplemental figure 1: The majority of genes identified with 4C-seq were positioned up to 500kbp from the CKD associated SNP locus. Graph shows the distance from the SNP to the TSS of the target genes found with 4C in HRGECs (X-axis), expressed as the number of target genes (frequency on Y-axis) per 100kbp. The majority of target genes was positioned up to 500kbp from the SNP, but occasionally candidate genes were found at locations over 1.5mb from the SNP locus **(A)**. The TSS of the majority of candidate genes found with 4C in HRPTECs was positioned up to 500kbp from the SNP position, but some candidate genes were found at locations over 1.5mb from the SNP locus **(B)**.



Supplemental figure 2: Target genes of DREs colocalizing with CKD-associated SNPs, highlighted in red, are enriched in the mevalonate pathway and the trans, trans-farnesyl diphosphate biosynthesis pathway (adapted from IPA).

Supplemental table 1: Primer design for cloning DREs from the rs11959928 region into the STARR-seq reporter plasmid.

SNP ID	Chromosome	Forward primer	Reversed primer	Location (GRCh37/hg19)
rs11959928	chr5	ACATGGCCTATCCCTTCCT	GGATTCCACCAGATGTTGC	39353419-39354619
	chr5	CCAGTGTTAGTGCTGTTGTTGC	CCCCATCCTCTGCCACTA	39355029-39356229
	chr5	CAGGGTGGGTAGAGACGAGT	ACCATCTCTGTGGCTCAGGT	39359279-39360479
	chr5	TTGCTAACATTTGTGAGTGCTT	TCCTACCTCTACAGGTTGTCACAT	39360189-39361389
	chr5	ACCACATAAAGTCAAAGGAAGAA	TGTGTCCTGCTGTGAGGAAT	39360529-39361729
	chr5	TCAGGCTTTTCCTACCTTGC	GCTATGTACTGGCAGCAGCTC	39368449-39369649
	chr5	GGCATGCTGGCTGTTAAAGT	CTGTTGCATGAGGTGAGTGG	39370239-39371439
	chr5	GCACCTGGATAAGCCAGATAA	GGCATAATTTTCTATCAGCTTCC	39370869-39372069
	chr5	AGCCTGGGTGACAGAGTGAG	TGGGAGGTGGAGGACTGTAG	39379474-39380674
	chr5	GGGGCAACTACCAATAAGCA	CCAATCGACACCTTCTTCGT	39382029-39383229
	chr5	GCGTATTTTCTTCCTTGCTTG	GCCTGACCCTGCTTAGCTT	39396569-39397769
	chr5	AAAATCAATCCGCCATAAGC	GGTGCAGCTGTCGCTATGTA	39400609-39401809
	chr5	GGCAAAGCTGGGTGTAAGTT	GCCCTCTCCACTGTGTCAG	39405129-39406329
	chr5	GCTGAACGCTATAGCCCTGT	CAGCCTCCTCTCCTGTCAAA	39411679-39412879
	chr5	TTTGGGAATCCAGGACTGAG	TTCTTGGCACTGGTCTTTCC	39412649-39413849

Supplemental table 2: Comparison of reference allele prevalence (Δ) for each variant in rs11959928 locus in STARR-seq library (input) with reference allele prevalence in transcribed RNA of HRGECs, HRPTECs, and HEK293a after transformation with STARR-seq library. Regions in bold are described in figure 2C.

SNP ID	Chromosome	Location	input 1	Input 2	HRGECs 1	HRGECs 2	Δ HRGECs 1	Δ HRGECs 2
rs11959928	chr5	39353722	70.5	54.5	57.4	44.1	-13.1	-10.4
	chr5	39354039	97.5	89.7	94.1	98.2	-3.4	8.5
	chr5	39355135	19.2	18.4	15.3	15.6	-3.9	-2.8
	chr5	39355591	83.4	88.4	84.8	82.4	1.5	-6.0
	chr5	39355648	82.0	87.1	83.8	83.6	1.8	-3.6
	chr5	39356000	86.3	86.3	83.0	82.5	-3.2	-3.8
	chr5	39359597	88.8	84.8	82.0	76.0	-6.8	-8.9
	chr5	39359698	77.5	98.9	71.0	76.8	-6.4	-22.0
	chr5	39360817	94.1	89.1	94.6	87.4	0.5	-1.7
	chr5	39361231	72.8	69.1	100.0	100.0	27.2	30.9
	chr5	39361273	74.8	71.2	100.0	100.0	25.2	28.8
	chr5	39361303	36.5	31.8	17.8	3.2	-18.7	-28.6
	chr5	39361359	70.2	64.8	100.0	99.1	29.8	34.3
	chr5	39361382	91.2	91.5	91.4	91.1	0.2	-0.5
	chr5	39361387	89.6	90.7	88.9	90.0	-0.7	-0.7
	chr5	39361556	89.4	94.0	81.1	80.0	-8.3	-14.0
	chr5	39361573	48.9	45.2	100.0	99.6	51.1	54.3
	chr5	39368773	95.3	69.7	92.9	96.7	-2.4	27.0
	chr5	39368977	82.6	95.5	88.2	86.4	5.5	-9.1
	chr5	39369030	78.6	96.1	84.8	84.4	6.3	-11.7
	chr5	39369103	87.2	95.5	79.4	83.9	-7.7	-11.5
	chr5	39369492	94.9	90.7	95.7	92.8	0.8	2.1
	chr5	39370386	98.7	94.3	94.9	96.9	-3.7	2.6
	chr5	39370397	83.7	75.8	78.6	74.3	-5.1	-1.5
	chr5	39370442	99.2	97.6	95.0	98.0	-4.1	0.4
	chr5	39371493	44.5	45.2	44.1	41.6	-0.4	-3.7
	chr5	39382261	58.8	56.3	57.0	55.9	-1.8	-0.4
	chr5	39397132	74.0	71.8	73.3	71.8	-0.7	0.0
	chr5	39397662	80.5	78.1	84.8	82.2	4.2	4.1
	chr5	39400701	81.1	87.1	87.5	81.7	6.3	-5.4
	chr5	39401049	82.7	70.4	80.9	77.7	-1.8	7.3
	chr5	39401384	79.9	83.3	84.0	81.1	4.1	-2.2
	chr5	39401620	64.1	52.3	60.0	62.6	-4.1	10.3
	chr5	39405736	58.7	62.2	59.6	59.3	0.9	-2.8
	chr5	39406098	66.4	66.8	64.3	65.1	-2.1	-1.7
	chr5	39412248	74.4	83.6	77.7	71.5	3.3	-12.1
	chr5	39412480	97.5	100.0	95.3	96.4	-2.2	-3.6
	chr5	39412568	23.8	15.6	9.9	13.6	-13.9	-2.0
	chr5	39412681	9.9	8.9	7.5	7.2	-2.4	-1.7
	chr5	39412798	15.4	10.0	14.0	19.8	-1.4	9.8
SNP ID	Chromosome	Location	input 1	Input 2	HRPTECs 1	HRPTECs 2	Δ HRPTECs 1	Δ HRPTECs 2
	chr5	39353722	70.5	54.5	65.2	54.7	-5.3	0.1
	chr5	39354039	97.5	89.7	83.1	88.0	-14.4	-1.7
	chr5	39355135	19.2	18.4	14.8	16.6	-4.4	-1.8
	chr5	39355591	83.4	88.4	82.6	83.9	-0.8	-4.4
	chr5	39355648	82.0	87.1	81.6	81.3	-0.4	-5.8
	chr5	39356000	86.3	86.3	82.8	82.4	-3.4	-3.9
	chr5	39359597	88.8	84.8	74.1	68.9	-14.7	-15.9
	chr5	39359698	77.5	98.9	71.3	80.5	-6.2	-18.4
	chr5	39360817	94.1	89.1	100.0	75.8	5.9	-13.3

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chr5	39361231	72.8	69.1	100.0	100.0	27.2	30.9
chr5	39361273	74.8	71.2	100.0	100.0	25.2	28.8
chr5	39361303	36.5	31.8	8.3	23.2	-28.1	-8.6
chr5	39361359	70.2	64.8	100.0	100.0	29.8	35.2
chr5	39361382	91.2	91.5	100.0	79.4	8.8	-12.2
chr5	39361387	89.6	90.7	100.0	76.2	10.4	-14.5
chr5	39361556	89.4	94.0	96.0	91.1	6.6	-2.9
chr5	39361573	48.9	45.2	100.0	100.0	51.1	54.8
chr5	39368773	95.3	69.7	80.1	100.0	-15.2	30.3
chr5	39368977	82.6	95.5	59.6	83.9	-23.1	-11.5
chr5	39369030	78.6	96.1	64.8	69.8	-13.8	-26.3
chr5	39369103	87.2	95.5	99.0	63.5	11.8	-32.0
chr5	39369492	94.9	90.7	100.0	73.3	5.1	-17.4
chr5	39370386	98.7	94.3	84.0	83.0	-14.7	-11.3
chr5	39370397	83.7	75.8	63.5	86.0	-20.1	10.2
chr5	39370442	99.2	97.6	84.2	75.9	-14.9	-21.6
chr5	39371493	44.5	45.2	44.7	42.4	0.2	-2.8
chr5	39382261	58.8	56.3	51.3	55.5	-7.5	-0.9
chr5	39397132	74.0	71.8	82.7	72.1	8.7	0.3
chr5	39397662	80.5	78.1	81.5	84.3	1.0	6.2
chr5	39400701	81.1	87.1	73.9	84.4	-7.3	-2.8
chr5	39401049	82.7	70.4	88.2	84.4	5.6	14.0
chr5	39401384	79.9	83.3	90.5	77.7	10.7	-5.6
chr5	39401620	64.1	52.3	60.4	52.8	-3.7	0.5
chr5	39405736	58.7	62.2	57.3	61.7	-1.4	-0.5
chr5	39406098	66.4	66.8	62.9	67.5	-3.5	0.7
chr5	39412248	74.4	83.6	70.3	90.4	-4.1	6.8
chr5	39412480	97.5	100.0	71.8	99.4	-25.7	-0.6
chr5	39412568	23.8	15.6	21.9	9.4	-1.9	-6.2
chr5	39412681	9.9	8.9	18.1	1.3	8.2	-7.6
chr5	39412798	15.4	10.0	22.7	3.5	7.3	-6.5

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SNP ID	Chromosome	Location	input 1	Input 2	HEK293a 1	HEK293a 2	Δ HEK293a 1	Δ HEK293a 2
	chr5	39353722	70.5	54.5	62.8	58.9	-7.7	4.3
	chr5	39354039	97.5	89.7	93.1	95.9	-4.4	6.2
	chr5	39355135	19.2	18.4	16.3	15.9	-2.9	-2.5
	chr5	39355591	83.4	88.4	83.5	83.3	0.1	-5.1
	chr5	39355648	82.0	87.1	83.2	83.3	1.1	-3.8
	chr5	39356000	86.3	86.3	82.9	82.0	-3.4	-4.3
	chr5	39359597	88.8	84.8	79.3	92.3	-9.5	7.5
	chr5	39359698	77.5	98.9	76.6	79.1	-0.9	-19.7
	chr5	39360817	94.1	89.1	100.0	90.7	5.9	1.5
	chr5	39361231	72.8	69.1	100.0	100.0	27.2	30.9
	chr5	39361273	74.8	71.2	100.0	100.0	25.2	28.8
	chr5	39361303	36.5	31.8	9.1	19.8	-27.4	-12.1
	chr5	39361359	70.2	64.8	100.0	100.0	29.8	35.2
	chr5	39361382	91.2	91.5	76.1	83.3	-15.1	-8.2
	chr5	39361387	89.6	90.7	71.2	82.2	-18.4	-8.5
	chr5	39361556	89.4	94.0	81.4	59.8	-8.0	-34.2
	chr5	39361573	48.9	45.2	98.9	100.0	49.9	54.8
	chr5	39368773	95.3	69.7	90.6	90.4	-4.8	20.7
	chr5	39368977	82.6	95.5	77.7	88.4	-4.9	-7.0
	chr5	39369030	78.6	96.1	78.6	90.5	0.0	-5.5
	chr5	39369103	87.2	95.5	82.5	86.2	-4.7	-9.3
	chr5	39369492	94.9	90.7	94.8	97.8	-0.1	7.1
	chr5	39370386	98.7	94.3	98.9	85.8	0.2	-8.4

chr5	39370397	83.7	75.8	74.7	85.7	-8.9	10.0
chr5	39370442	99.2	97.6	99.1	93.6	-0.1	-3.9
chr5	39371493	44.5	45.2	42.0	45.5	-2.4	0.3
chr5	39382261	58.8	56.3	58.1	56.5	-0.7	0.2
chr5	39397132	74.0	71.8	73.6	77.1	-0.4	5.3
chr5	39397662	80.5	78.1	80.6	81.5	0.1	3.4
chr5	39400701	81.1	87.1	71.2	83.0	-9.9	-4.1
chr5	39401049	82.7	70.4	83.3	81.8	0.6	11.4
chr5	39401384	79.9	83.3	81.2	80.7	1.4	-2.7
chr5	39401620	64.1	52.3	68.1	68.0	4.0	15.7
chr5	39405736	58.7	62.2	57.3	58.1	-1.4	-4.1
chr5	39406098	66.4	66.8	64.2	62.8	-2.2	-4.0
chr5	39412248	74.4	83.6	79.7	80.7	5.3	-2.9
chr5	39412480	97.5	100.0	97.8	94.9	0.3	-5.1
chr5	39412568	23.8	15.6	6.3	8.8	-17.5	-6.7
chr5	39412681	9.9	8.9	0.9	4.6	-9.1	-4.3
chr5	39412798	15.4	10.0	10.3	9.7	-5.1	-0.3

Supplemental table 3: Datasets used for selection of active DNA regulatory elements.

Cell type	Dataset	Library strategie
HRGECS	GSM1014519_hg19_wgEncodeUwDgfHmvechPk.narrowPeak	Dnase hypersensitivity
	GSM1014529_hg19_wgEncodeUwDgfHmvecbPk.narrowPeak	Dnase hypersensitivity
	GSM1014532_hg19_wgEncodeUwDgfHmvecdPk.narrowPeak	Dnase hypersensitivity
	GSM1024745_hg19_wgEncodeUwDnaseHmvecdadPkRep1.narrowPeak	Dnase hypersensitivity
	GSM1024747_hg19_wgEncodeUwDnaseHmvecdadPkRep2.narrowPeak	Dnase hypersensitivity
	GSM646570_hg19_wgEncodeUwDgfHmvecdbladPkV2.narrowPeak	Dnase hypersensitivity
	GSM736521_hg19_wgEncodeUwDnaseHmvecdblneoPkRep2.narrowPeak	Dnase hypersensitivity
	GSM736523_hg19_wgEncodeUwDnaseHmvecdbladPkRep2.narrowPeak	Dnase hypersensitivity
	GSM736571_hg19_wgEncodeUwDnaseHmvecdblneoPkRep1.narrowPeak	Dnase hypersensitivity
	GSM736573_hg19_wgEncodeUwDnaseHmvecdlyneoPkRep2.narrowPeak	Dnase hypersensitivity
	GSM736577_hg19_wgEncodeUwDnaseHmvecdlyneoPkRep1.narrowPeak	Dnase hypersensitivity
	GSM736591_hg19_wgEncodeUwDnaseHmvecdlyadPkRep2.narrowPeak	Dnase hypersensitivity
	GSM736599_hg19_wgEncodeUwDnaseHmvecdlyadPkRep1.narrowPeak	Dnase hypersensitivity
	GSM736609_hg19_wgEncodeUwDnaseHmvecdbladPkRep1.narrowPeak	Dnase hypersensitivity
HRPTECs	GSM736539_hg19_wgEncodeUwDnaseRptecPkRep2.narrowPeak	Dnase hypersensitivity
	GSM736543_hg19_wgEncodeUwDnaseRptecPkRep1.narrowPeak	Dnase hypersensitivity
	GSM736549_hg19_wgEncodeUwDnaseHrcePkRep1.narrowPeak	Dnase hypersensitivity
	GSM736557_hg19_wgEncodeUwDnaseHrcePkRep2.narrowPeak	Dnase hypersensitivity
	GSM849027_hg19_wgEncodeUwDgfHrcePk.narrowPeak	Dnase hypersensitivity
	GSM945216_hg19_wgEncodeUwHistoneRptecH3k04me3StdPkRep1.narrowPeak	H3K04me3 ChIP-seq
	GSM945216_hg19_wgEncodeUwHistoneRptecH3k04me3StdPkRep2.narrowPeak	H3K04me3 ChIP-seq
	Fetal_Kidney.H-22337.DS10986	Dnase hypersensitivity
	Fetal_Kidney.H-22676.DS12635	Dnase hypersensitivity
	Fetal_Kidney.H-23524.DS16139	Dnase hypersensitivity
	Fetal_Kidney.H-23663.DS16837	Dnase hypersensitivity
	Fetal_Kidney.H-23855.DS17522	Dnase hypersensitivity
	Fetal_Kidney.H-23914.DS17753	Dnase hypersensitivity
	Fetal_Kidney.H-24507.DS20564	Dnase hypersensitivity
	Fetal_Kidney.H-24510.DNase.DS20786	Dnase hypersensitivity
	Fetal_Kidney.H-24584.DS20987	Dnase hypersensitivity
	Fetal_Kidney.H-24608.DNase.DS21096	Dnase hypersensitivity

Supplemental table 4: CKD candidate genes retrieved by 4C-seq in HRGECs. * only trait serum creatinine, ** only trait serum urate, *** only trait blood urea nitrogen,^{ns} non-synonymous SNP. Interacting genes with a P-value <1E-08 in both individual 4C-seq experiments in HRGECs are expressed in bold.

SNP	Gene ID	Refseq	Chromosome	P-value prep 1	P-value prep 2	expression (RPKM)	SNP-TSS (kbp)
rs2049805	PMVK	NM_006556	1	8,58E-03	1,23E-11	3,45	285
	PBXIP1	NM_020524	1	1,00E+00	1,32E-13	5,39	266
	PYGO2	NM_138300	1	8,58E-03	1,32E-13	3,07	261
	SHC1	NM_001130040	1	8,58E-03	1,32E-13	6,88	252
	CKS1B	NM_001826	1	8,58E-03	1,32E-13	3,78	248
	FLAD1	NM_025207	1	8,58E-03	1,32E-13	3,20	239
	LENEP	NM_018655	1	3,82E-04	1,32E-13	-3,32	229
	ZBTB7B	NM_015872	1	3,82E-04	1,23E-11	3,23	220
	DCST2	NM_144622	1	3,82E-04	1,01E-17	-1,63	189
	DCST1	NM_001143687	1	3,82E-04	1,01E-17	-0,93	189
	ADAM15	NM_207191	1	3,82E-04	1,01E-17	7,92	171
	EFNA4	NM_005227	1	3,82E-04	1,01E-17	3,90	159
	EFNA3	NM_004952	1	3,36E-07	2,78E-24	0,54	144
	EFNA1	NM_004428	1	1,52E-30	6,97E-29	5,03	95
	RAG1AP1	NM_001122839	1	3,36E-37	6,97E-29	3,33	87
	DPM3	NM_018973	1	1,80E-39	1,20E-33	4,14	82
	KRTCAP2	NM_173852	1	4,44E-84	1,69E-62	5,60	49
	TRIM46	NM_025058	1	4,44E-84	1,69E-62	1,77	49
	MUC1	NM_001018016	1	4,44E-84	4,54E-77	-0,18	32
	MIR92B	NR_030281	1	4,44E-84	4,21E-80	-3,32	30
	THBS3	NM_007112	1	4,44E-84	1,12E-92	2,05	17
	MTX1	NM_002455	1	4,44E-84	1,12E-92	2,14	16
	GBAP	NR_002188	1	4,44E-84	1,12E-92	2,81	2
	GBA	NM_000157	1	4,44E-84	1,12E-92	4,84	16
	FAM189B	NM_006589	1	4,44E-84	1,12E-92	4,32	30
	SCAMP3	NM_005698	1	4,44E-84	1,12E-92	4,91	37
	CLK2	NM_003993	1	4,44E-84	3,26E-68	3,63	48
	HCN3	NM_020897	1	1,27E-73	3,18E-46	0,35	52
	PKLR	NM_181871	1	3,36E-37	1,46E-26	-1,33	76
	FDP5	NM_002004	1	3,72E-24	1,46E-26	6,54	84
	RUSC1	NM_001105203	1	4,30E-22	1,46E-26	3,07	96
	C1orf104	NM_001039517	1	4,30E-22	1,46E-26	4,36	99
	MIR555	NR_030282	1	1,36E-10	1,24E-15	-0,41	121
	LOC645676	NR_027023	1	7,33E-09	4,77E-22	-0,98	337
	ASH1L	NM_018489	1	7,33E-09	4,77E-22	1,65	337
	MSTO1	NM_018116	1	7,33E-09	7,36E-20	1,93	385
	YY1AP1	NM_139119	1	7,33E-09	1,01E-17	3,71	464
	DAP3	NM_004632	1	7,33E-09	1,01E-17	4,11	464
	MSTO2P	NR_024117	1	1,27E-05	9,75E-10	2,27	521
	SSR2	NM_003145	1	2,26E-04	9,75E-10	6,98	796
rs267734	ANP32E	NM_001136479	1	1,37E-11	3,12E-15	3,22	744
	CA14	NM_012113	1	3,04E-13	5,71E-23	-1,64	721
	APH1A	NM_001077628	1	3,04E-13	6,13E-21	5,58	710
	C1orf54	NM_024579	1	5,37E-10	1,46E-08	2,94	706
	C1orf51	NM_144697	1	1,37E-11	3,12E-15	-0,01	696
	MRPS21	NM_018997	1	3,04E-13	4,53E-17	4,81	685
	PRPF3	NM_004698	1	3,04E-13	1,84E-13	3,45	658
	RPRD2	NM_015203	1	1,00E-16	1,82E-29	2,59	614
	TARS2	NM_025150	1	2,34E-26	3,13E-27	2,06	492
	ECM1	NM_004425	1	3,04E-13	5,71E-23	2,45	471
	ADAMTSL4	NM_025008	1	5,88E-15	6,13E-21	0,15	430
	MCL1	NM_182763	1	1,00E-16	5,67E-19	5,63	399
	ENSA	NM_207045	1	1,96E-28	1,82E-29	5,50	350
	GOLPH3L	NM_018178	1	5,79E-35	3,13E-27	3,34	282
	HORMAD1	NM_032132	1	5,79E-35	4,57E-25	-3,32	258
	CTSS	NM_004079	1	1,00E-16	1,82E-29	2,40	213
	CTSK	NM_000396	1	1,96E-28	8,92E-32	0,83	171
	ARNT	NM_001668	1	5,73E-42	3,20E-39	2,78	102
	SETDB1	NM_001145415	1	1,41E-39	3,63E-34	2,40	53
	LASS2	NM_022075	1	1,14E-60	3,94E-51	5,41	4
	ANXA9	NM_003568	1	1,14E-60	3,94E-51	0,42	3

	FAM63A	NM_001163260	1	9,96E-58	3,94E-51	2,58	28
	PRUNE	NM_021222	1	9,96E-58	3,94E-51	1,16	29
	BNIP1	NM_138278	1	1,41E-39	6,48E-42	-1,96	58
	C1orf56	NM_017860	1	5,79E-35	3,20E-39	2,15	69
	CDC42SE1	NM_001038707	1	1,47E-30	1,21E-36	4,38	81
	MLLT11	NM_006818	1	1,47E-30	1,21E-36	4,74	81
	GABPB2	NM_144618	1	2,34E-26	1,21E-36	0,36	92
	SEMA6C	NM_030913	1	1,41E-39	3,63E-34	4,01	168
	TNFAIP8L2	NM_024575	1	1,41E-39	3,63E-34	-2,03	178
	LYSMD1	NM_212551	1	1,41E-39	3,63E-34	0,54	187
	SCNM1	NM_024041	1	1,41E-39	3,63E-34	4,13	187
	TMOD4	NM_013353	1	1,96E-28	8,92E-32	-1,24	197
	VPS72	NM_005997	1	1,96E-28	8,92E-32	4,68	211
	PIP5K1A	NM_001135636	1	1,96E-28	8,92E-32	3,54	220
	PSMD4	NM_002810	1	5,37E-10	6,13E-21	5,60	276
	RFX5	NM_000449	1	5,08E-07	9,33E-12	3,20	368
	SNX27	NM_030918	1	2,26E-04	9,33E-12	1,90	633
rs11123170***	PRPF40A	NM_017892	2	2,16E-05	8,71E-13	3,18	39595
	ARL6IP6	NM_152522	2	2,16E-05	8,71E-13	2,51	39595
	RPRM	NM_019845	2	6,56E-14	1,36E-14	-3,32	40356
	GALNT13	NM_052917	2	8,68E-18	2,17E-20	-3,32	40749
	KCNJ3	NM_002239	2	2,16E-05	8,71E-13	-2,92	41576
	CYTIP	NM_004288	2	2,16E-05	2,24E-09	-3,32	44322
rs1260326 ^{ns}	CGREF1	NM_001166241	2	1,00E+00	7,61E-09	-0,50	397
	ABHD1	NM_032604	2	1,00E+00	7,61E-09	-0,16	384
	PREB	NM_013388	2	1,00E+00	7,61E-09	3,97	373
	C2orf53	NM_178553	2	1,00E+00	7,61E-09	-3,32	369
	TCF23	NM_175769	2	1,88E-03	7,61E-09	-3,32	359
	MPV17	NM_002437	2	6,30E-09	4,24E-05	4,88	185
	GTF3C2	NM_001035521	2	6,30E-09	3,91E-15	3,23	151
	EIF2B4	NM_172195	2	5,84E-11	5,07E-22	3,60	138
	SNX17	NM_014748	2	5,84E-11	5,07E-22	4,87	138
	ZNF513	NM_144631	2	5,84E-11	5,07E-22	2,58	127
	FTHL3P	NR_002201	2	4,51E-13	2,27E-17	3,01	114
	PPM1G	NM_002707	2	1,68E-17	2,15E-29	5,71	98
	NRBP1	NM_013392	2	1,40E-24	2,15E-29	5,56	79
	KRTCAP3	NM_173853	2	3,41E-51	3,39E-37	0,29	66
	IFT172	NM_015662	2	4,71E-96	1,09E-89	1,71	18
	FND4	NM_022823	2	9,85E-100	3,14E-97	2,99	13
	GCKR	NM_001486	2	9,85E-100	3,14E-97	-1,35	11
	C2orf16	NM_032266	2	3,41E-51	1,26E-42	-0,78	68
	ZNF512	NM_032434	2	4,92E-40	1,26E-42	3,01	75
	GPN1	NM_001145047	2	4,92E-40	6,88E-40	3,94	121
	CCDC121	NM_001142682	2	4,92E-40	6,88E-40	-0,29	121
rs13538 ^{ns}	SLC4A1AP	NM_018158	2	1,50E-29	1,14E-19	3,13	155
	SUPT7L	NM_014860	2	1,50E-29	1,14E-19	2,71	156
	FBXO41	NM_001080410	2	2,47E-13	1,29E-12	-1,23	370
	EGR4	NM_001965	2	2,14E-17	1,29E-12	-2,53	348
	ALMS1	NM_015120	2	1,65E-19	1,52E-16	0,02	255
	NAT8	NM_003960	2	2,74E-83	3,15E-62	-2,47	1
	ALMS1P	NR_003683	2	2,74E-83	3,15E-62	-2,64	4
	NAT8B	NM_016347	2	9,52E-46	1,42E-39	-1,78	60
	TPRKB	NM_016058	2	1,27E-35	7,85E-45	2,49	96
	DUSP11	NM_003584	2	9,30E-54	4,98E-37	2,78	139
	C2orf78	NM_001080474	2	9,30E-54	4,98E-37	-3,32	143
	STAMBP	NM_201647	2	9,30E-54	4,21E-32	2,42	188
	ACTG2	NM_001615	2	1,13E-21	1,34E-18	-2,56	252
	DGUOK	NM_080916	2	1,65E-19	1,03E-20	3,49	286
	TET3	NM_144993	2	1,65E-19	6,94E-23	1,51	405
	BOLA3	NM_001035505	2	8,42E-31	1,03E-20	3,41	507
	MOBK1B	NM_018221	2	1,88E-28	1,52E-16	4,61	538
	MTHFD2	NM_006636	2	2,14E-17	2,93E-07	2,93	557
	SLC4A5	NM_133478	2	1,65E-19	1,51E-14	-1,27	702
	DCTN1	NM_001135041	2	2,14E-11	5,77E-09	5,36	734
	LOC100189589	NR_024463	2	2,14E-11	1,51E-14	-2,44	745
	INO80B	NM_031288	2	2,14E-11	3,78E-04	3,13	814

	WBP1	NM_012477	2	2,14E-11	3,78E-04	4,37	817
	MOGS	NM_001146158	2	2,14E-11	3,78E-04	4,81	824
	MRPL53	NM_053050	2	2,14E-11	3,78E-04	4,78	832
	TTC31	NM_022492	2	2,14E-11	5,77E-09	2,54	842
	CCDC142	NM_032779	2	2,14E-11	5,77E-09	1,11	842
	LOC151534	NR_024606	2	1,92E-04	9,40E-11	1,90	861
rs16853722	C3orf50	NR_021485	3	3,46E-07	3,88E-09	-2,78	623
	MECOM	NM_001163999	3	1,82E-34	9,92E-17	3,24	287
	TERC	NR_001566	3	1,76E-18	8,29E-13	-1,83	332
	ARPM1	NM_032487	3	1,76E-18	3,88E-09	0,42	337
	MYNN	NM_018657	3	1,76E-18	3,88E-09	1,35	340
	LRR34	NM_153353	3	1,99E-16	2,97E-04	-1,89	380
	LRR1Q4	NM_001080460	3	7,01E-09	2,97E-04	-3,32	389
	LOC100128164	NR_027622	3	7,01E-09	7,36E-03	-2,94	534
rs13069000***	SEC62	NM_003262	3	7,01E-09	7,36E-03	3,49	534
	SLC25A26	NM_173471	3	1,00E+00	2,48E-09	0,95	680
	LRIG1	NM_015541	3	5,48E-24	2,43E-20	1,40	248
	KBTBD8	NM_032505	3	7,52E-07	2,48E-09	-0,93	250
rs10937329***	FAM19A4	NM_001005527	3	8,18E-14	2,48E-09	-2,22	2183
	BCL6	NM_001134738	3	1,06E-19	7,61E-29	1,59	261
	FLJ42393	NR_024413	3	9,48E-22	2,31E-33	-2,74	183
	LPP	NM_005578	3	9,37E-16	1,88E-22	2,28	217
rs347685	TPRG1	NM_198485	3	1,50E-08	1,87E-09	-2,97	1176
	ZBTB38	NM_001080412	3	3,89E-15	1,63E-07	3,36	764
	RASA2	NM_006506	3	2,92E-13	4,50E-09	0,81	601
	RNF7	NM_183237	3	2,92E-13	3,25E-14	4,46	350
	GRK7	NM_139209	3	2,92E-13	4,53E-16	-2,33	310
	ATP1B3	NM_001679	3	4,44E-17	5,53E-20	6,59	212
	TFDP2	NM_006286	3	3,33E-40	5,72E-31	2,04	83
	GK5	NM_001039547	3	1,68E-25	2,16E-33	-0,06	137
	XRN1	NM_001042604	3	3,67E-21	2,16E-33	1,29	360
	ATR	NM_001184	3	4,44E-17	3,25E-14	1,08	491
	PLS1	NM_001145319	3	4,49E-08	3,25E-14	-2,87	508
	TRPC1	NM_003304	3	4,49E-08	1,99E-12	-0,17	636
	PCOLCE2	NM_013363	3	4,49E-08	4,50E-09	-3,32	801
rs13146355	PAQR9	NM_198504	3	1,87E-11	4,50E-09	-3,32	875
	SDAD1	NM_018115	4	7,94E-08	4,93E-11	2,63	500
	CXCL9	NM_002416	4	5,87E-07	4,93E-11	-3,32	484
	ART3	NM_001130017	4	5,87E-07	4,93E-11	-2,62	480
	CXCL10	NM_001565	4	5,87E-07	8,82E-13	-1,00	467
	CXCL11	NM_005409	4	1,34E-08	8,82E-13	1,13	455
	NUP54	NM_017426	4	6,62E-16	1,96E-20	2,65	342
	SCARB2	NM_005506	4	4,07E-12	1,35E-14	5,54	277
	FAM47E	NM_001136570	4	6,24E-20	7,82E-27	-3,32	239
	STBD1	NM_003943	4	5,01E-22	7,88E-39	0,33	184
	CCDC158	NM_001042784	4	2,00E-67	1,40E-65	-3,32	84
	SHROOM3	NM_020859	4	7,32E-98	6,43E-85	0,05	56
	ANKRD56	NM_001029870	4	5,01E-22	1,67E-22	-3,32	407
rs2725220**	40067	NM_018243	4	6,62E-16	1,23E-24	4,68	459
	CCNI	NM_006835	4	6,62E-16	1,96E-20	6,32	585
	CCNG2	NM_004354	4	5,58E-14	1,23E-24	2,29	666
	SPARCL1	NM_001128310	4	9,04E-10	4,53E-13	0,12	509
	DSPP	NM_014208	4	9,04E-10	6,40E-03	-3,32	430
	IBSP	NM_004967	4	1,42E-04	2,49E-09	-3,32	239
	MEPE	NM_020203	4	1,15E-15	1,42E-07	-3,32	206
	SPP1	NM_000582	4	5,15E-36	1,26E-32	-2,59	63
	PKD2	NM_000297	4	1,27E-67	3,37E-61	2,24	31
	ABCG2	NM_004827	4	1,36E-33	1,26E-32	0,51	120
	PPM1K	NM_152542	4	1,15E-15	3,82E-19	-0,05	246
	HERC6	NM_001165136	4	1,15E-15	4,88E-15	0,79	340
	HERC5	NM_016323	4	7,30E-29	4,60E-17	-0,55	418
	PIGY	NM_001042616	4	7,01E-20	4,60E-17	4,95	485
	HERC3	NM_014606	4	6,04E-08	3,64E-11	1,30	554
	NAP1L5	NM_153757	4	3,30E-06	3,64E-11	1,20	659
	ART3	NM_001130017	4	5,87E-07	4,93E-11	-2,62	437

rs17319721	CXCL10	NM_001565	4	5,87E-07	8,82E-13	-1,00	424
	CXCL11	NM_005409	4	1,34E-08	8,82E-13	1,13	412
	NUP54	NM_017426	4	6,62E-16	1,96E-20	2,65	299
	SCARB2	NM_005506	4	4,07E-12	1,35E-14	5,54	234
	FAM47E	NM_001136570	4	6,24E-20	7,82E-27	-3,32	196
	STBD1	NM_003943	4	5,01E-22	7,88E-39	0,33	141
	CCDC158	NM_001042784	4	2,00E-67	1,40E-65	-3,32	40
	SHROOM3	NM_020859	4	7,32E-98	6,43E-85	0,05	13
	ANKRD56	NM_001029870	4	5,01E-22	1,67E-22	-3,32	450
	40067	NM_018243	4	6,62E-16	1,23E-24	4,68	502
	CCNI	NM_006835	4	6,62E-16	1,96E-20	6,32	628
rs11959928	OSMR	NM_003999	5	1,14E-05	1,81E-13	2,36	551
	RICTOR	NM_152756	5	9,80E-11	2,55E-21	1,43	323
	FYB	NM_001465	5	1,43E-12	2,81E-17	-3,32	177
	C9	NM_001737	5	3,50E-56	3,71E-50	-2,52	32
	DAB2	NM_001343	5	2,61E-97	3,65E-65	6,21	28
	PTGER4	NM_000958	5	2,84E-07	1,17E-11	3,01	1283
	TTC33	NM_012382	5	1,43E-12	2,02E-23	0,51	1359
	PRKAA1	NM_006251	5	8,32E-03	1,17E-11	3,38	1401
	SNORD72	NR_002583	5	8,32E-03	6,44E-10	-3,32	1436
	RPL37	NM_000997	5	8,32E-03	6,44E-10	6,48	1438
rs6420094	CARD6	NM_032587	5	8,32E-03	6,44E-10	3,47	1444
	UIMC1	NM_016290	5	6,47E-06	4,81E-13	3,05	384
	ZNF346	NM_012279	5	2,29E-03	4,81E-13	2,03	368
	FGFR4	NM_002011	5	1,06E-13	2,79E-11	-1,10	304
	NSD1	NM_172349	5	4,54E-19	1,03E-18	2,47	258
	RAB24	NM_001031677	5	4,54E-19	2,69E-29	3,54	87
	PRELID1	NM_013237	5	5,92E-21	2,69E-29	6,23	87
	MXD3	NM_001142935	5	6,96E-23	2,69E-29	4,34	78
	LMAN2	NM_006816	5	9,83E-57	6,19E-55	6,33	39
	RGS14	NM_006480	5	2,09E-67	6,19E-55	1,73	33
	SLC34A1	NM_003052	5	4,42E-73	5,97E-58	-3,32	6
	PFN3	NM_001029886	5	5,74E-62	3,19E-49	-3,32	10
	F12	NM_000505	5	9,83E-57	3,19E-49	-0,19	19
	GRK6	NM_001004105	5	8,23E-47	1,69E-46	2,43	36
	PRR7	NM_030567	5	8,23E-47	1,69E-46	2,49	56
	DBN1	NM_080881	5	1,95E-44	7,51E-44	7,06	82
	PDLIM7	NM_005451	5	3,13E-17	1,41E-31	6,14	107
	DOK3	NM_001144875	5	3,13E-17	2,63E-36	1,22	120
	DDX41	NM_016222	5	3,13E-17	2,63E-36	3,92	126
	FAM193B	NM_019057	5	7,94E-09	4,81E-13	2,87	164
rs1936800***	TMED9	NM_017510	5	2,29E-03	2,79E-11	6,77	202
	B4GALT7	NM_007255	5	1,00E+00	2,79E-11	3,72	209
	HDDC2	NM_016063	6	1,25E-03	4,39E-12	0,81	1813
	NCOA7	NM_001122842	6	1,63E-09	1,50E-04	3,29	1324
	HINT3	NM_138571	6	1,63E-09	8,14E-14	1,93	1158
	TRMT11	NM_001031712	6	1,28E-33	5,68E-37	0,23	1128
	C6orf173	NM_001012507	6	1,28E-33	1,64E-25	3,59	775
	RSP03	NM_032784	6	3,18E-60	1,17E-53	-2,18	4
	RNF146	NM_030963	6	5,56E-36	1,13E-27	3,38	152
	ECHDC1	NM_001139510	6	6,01E-13	7,92E-09	2,92	227
rs9397738*	KIAA0408	NM_014702	6	1,63E-09	2,03E-10	-2,60	344
	C6orf174	NM_001012279	6	6,61E-08	8,14E-14	-2,62	404
	IPCEF1	NM_001130699	6	2,21E-24	8,12E-26	-2,31	335
	CNKSR3	NM_173515	6	2,87E-40	7,98E-45	2,99	155
	RBM16	NM_014892	6	6,84E-38	8,92E-40	2,95	68
	TIAM2	NM_012454	6	1,38E-05	7,82E-09	0,18	425
	CLDN20	NM_001001346	6	2,93E-14	1,69E-17	-2,05	598
	TFB1M	NM_016020	6	3,63E-18	1,69E-17	1,92	649
	TJAP1	NM_001146016	6	4,43E-06	3,85E-09	3,10	361
	C6orf154	NM_001012974	6	1,78E-04	3,85E-09	-1,98	328
	YIPF3	NM_015388	6	1,78E-04	5,94E-11	6,02	322
	POLR1C	NM_203290	6	1,78E-04	5,94E-11	2,75	322
	XPO5	NM_020750	6	1,22E-19	8,70E-35	2,72	263
	POLH	NM_006502	6	1,22E-19	8,70E-35	2,20	263
	GTPBP2	NM_019096	6	1,21E-28	9,12E-40	4,01	210

rs881858	MAD2L1BP	NM_001003690	6	1,21E-28	9,12E-40	3,27	209
	RSPH9	NM_152732	6	7,32E-36	5,38E-30	-0,35	194
	MRPS18A	NM_018135	6	4,59E-46	6,17E-45	3,97	151
	VEGFA	NM_001025369	6	7,32E-36	9,12E-40	1,55	69
	LOC100132354	NR_024478	6	1,88E-43	2,97E-37	-3,32	52
	C6orf223	NM_153246	6	5,25E-31	2,14E-25	-1,86	162
	MRPL14	NM_032111	6	1,94E-15	7,23E-19	4,77	289
	TMEM63B	NM_018426	6	1,94E-15	7,23E-19	4,38	289
	CAPN11	NM_007058	6	1,94E-15	7,76E-13	1,44	320
	SLC29A1	NM_001078174	6	1,78E-04	3,85E-09	6,31	381
	HSP90AB1	NM_007355	6	1,78E-04	5,94E-11	8,50	408
	SLC35B2	NM_178148	6	4,43E-06	5,94E-11	4,77	419
	NFKBIE	NM_004556	6	4,43E-06	5,94E-11	3,12	427
	TMEM151B	NM_001137560	6	4,43E-06	5,94E-11	-2,45	432
	SPATS1	NM_145026	6	4,43E-06	7,76E-13	-3,32	504
	CDC5L	NM_001253	6	1,78E-04	3,85E-09	3,31	549
rs6465825*	PION	NM_017439	7	4,03E-06	6,98E-11	-0,65	371
	PTPN12	NM_002835	7	5,82E-22	6,98E-11	4,63	250
	RSBN1L	NM_198467	7	9,53E-44	2,41E-40	1,57	91
	TMEM60	NM_032936	7	1,26E-91	4,93E-61	2,43	11
	PHTF2	NM_001127360	7	1,26E-91	4,93E-61	0,40	12
	CD36	NM_001001547	7	1,00E+00	1,17E-09	-2,44	2815
rs7805747	NUB1	NM_016118	7	3,43E-19	1,59E-30	3,38	369
	WDR86	NM_198285	7	4,19E-15	3,46E-17	-3,32	301
	CRYGN	NM_144727	7	4,02E-17	3,82E-15	-3,32	271
	RHEB	NM_005614	7	4,07E-47	7,08E-43	4,31	191
	PRKAG2	NM_024429	7	1,73E-57	5,49E-62	4,53	78
	GALNTL5	NM_145292	7	2,12E-09	6,06E-06	-3,32	246
rs10109414*	GALNT11	NM_022087	7	2,12E-09	1,27E-07	3,42	315
	LOXL2	NM_002318	8	1,00E+00	7,16E-09	7,76	489
	ENTPD4	NM_004901	8	6,08E-10	1,11E-17	3,46	436
	SLC25A37	NM_016612	8	1,11E-06	6,10E-14	2,98	365
	NKX3-1	NM_006167	8	2,86E-08	8,90E-16	-0,77	211
	NKX2-6	NM_001136271	8	2,86E-08	8,90E-16	-3,32	187
	STC1	NM_003155	8	4,79E-45	4,51E-44	1,93	39
	ADAM28	NM_021777	8	2,18E-15	1,26E-30	-3,32	400
	ADAMDEC1	NM_014479	8	2,47E-19	1,06E-21	-3,32	491
rs4744712	ADAM7	NM_003817	8	6,08E-10	6,10E-14	-3,32	547
	NEFM	NM_005382	8	1,00E+00	6,10E-14	-2,28	1020
	PGM5	NM_021965	9	4,38E-12	1,55E-18	-2,67	463
	LOC572558	NR_015423	9	4,38E-12	1,55E-18	-3,32	462
	C9orf71	NM_153237	9	4,97E-24	1,55E-18	-3,32	279
	PIP5K1B	NM_003558	9	8,16E-18	1,55E-18	-3,32	114
	FAM122A	NM_138333	9	2,69E-64	4,19E-57	1,92	40
	PRKACG	NM_002732	9	2,68E-10	8,36E-27	-3,32	194
rs10794720	FXN	NM_181425	9	2,68E-10	1,60E-20	0,58	216
	LARP4B	NM_015155	10	1,52E-08	2,41E-18	3,17	224
	GTPBP4	NM_012341	10	1,41E-21	1,86E-16	3,50	122
	C10orf110	NR_024628	10	1,01E-25	1,17E-39	1,18	88
	IDI2	NM_033261	10	5,10E-30	1,17E-39	0,92	84
	IDI1	NM_004508	10	1,10E-63	7,25E-52	4,69	61
	WDR37	NM_014023	10	4,11E-77	1,95E-54	2,50	53
	NCRNA00200	NR_015376	10	1,82E-53	1,79E-28	-3,32	50
	PFKP	NM_002627	10	3,09E-10	7,65E-13	6,54	1954
rs504915**	PITRM1	NM_014889	10	5,41E-12	2,30E-06	4,88	2059
	CCDC88B	NM_032251	11	5,53E-11	9,95E-11	-1,42	356
	RPS6KA4	NM_001006944	11	5,53E-11	9,95E-11	3,80	337
	SLC22A11	NM_018484	11	9,08E-15	2,09E-29	-3,32	141
	SLC22A12	NM_144585	11	9,08E-15	4,24E-34	-3,32	106
	NRXN2	NM_138734	11	8,66E-59	1,79E-41	-2,52	53
	RASGRP2	NM_001098671	11	1,86E-69	3,32E-63	-2,74	48
	PYGM	NM_001164716	11	8,46E-32	2,97E-49	-2,28	64
	SF1	NM_201995	11	9,07E-19	5,70E-39	5,60	82
	MAP4K2	NM_004579	11	3,47E-09	1,71E-18	3,08	107
	CDC42BPG	NM_017525	11	7,97E-06	5,95E-09	-1,66	148
	EHD1	NM_006795	11	7,97E-06	9,95E-11	5,46	182

	GPHA2	NM_130769	11	6,91E-03	1,83E-16	-3,32	239
	C11orf85	NM_001037225	11	7,97E-06	1,83E-16	-3,32	264
	BATF2	NM_138456	11	7,97E-06	9,95E-11	-1,31	300
	ARL2	NM_001667	11	2,73E-04	9,95E-11	5,63	318
	SNX15	NM_013306	11	2,73E-04	5,95E-09	3,05	331
	CDCA5	NM_080668	11	2,73E-04	9,95E-11	2,55	388
	ZFPL1	NM_006782	11	2,73E-04	9,95E-11	4,22	388
	C11orf2	NM_013265	11	6,91E-03	9,95E-11	5,07	400
rs10774021*	LOC100288778	NR_028269	12	4,34E-34	1,34E-20	2,31	261
	FAM138D	NR_026823	12	1,74E-41	6,37E-27	-3,32	200
	IQSEC3	NM_015232	12	4,82E-44	4,57E-41	-2,34	163
	SLC6A12	NM_001122847	12	5,26E-52	1,09E-57	-3,32	26
	SLC6A13	NM_016615	12	2,33E-66	8,70E-52	-3,32	23
	CCDC77	NM_001130147	12	7,16E-25	3,87E-29	1,32	149
	KDM5A	NM_001042603	12	7,16E-25	3,87E-29	1,97	149
	B4GALNT3	NM_173593	12	6,25E-09	5,82E-13	-3,32	220
rs653178	PPP1CC	NM_002710	12	5,14E-03	5,01E-09	4,93	827
	FAM109A	NM_144671	12	1,37E-17	7,30E-21	3,00	201
	SH2B3	NM_005475	12	9,92E-20	9,87E-19	5,40	164
	ATXN2	NM_002973	12	4,32E-69	2,44E-66	3,25	30
	BRAP	NM_006768	12	2,12E-34	1,03E-41	2,01	116
	ACAD10	NM_001136542	12	2,12E-34	1,03E-41	1,00	116
	ALDH2	NM_000690	12	7,49E-76	9,73E-89	4,48	197
	MAPKAPK5	NM_003668	12	7,49E-76	9,73E-89	2,56	273
	C12orf47	NR_015404	12	4,16E-73	9,73E-89	2,05	273
	TMEM116	NM_138341	12	2,46E-08	4,42E-16	-0,15	443
rs626277	ERP29	NM_001034025	12	2,46E-08	4,42E-16	5,23	443
	DACH1	NM_004392	13	1,77E-35	2,32E-44	1,61	94
	C13orf37	NM_001071775	13	3,66E-07	5,13E-14	2,09	954
rs2453533*	C13orf34	NM_024808	13	3,66E-07	5,13E-14	0,40	954
	C15orf43	NM_152448	15	7,53E-05	3,56E-11	-3,32	392
	DUOXA1	NM_144565	15	3,07E-06	3,77E-16	-2,74	219
	DUOX1	NM_017434	15	3,07E-06	3,77E-16	-2,32	219
	SHF	NM_138356	15	6,33E-18	1,78E-25	-0,60	148
	SLC28A2	NM_004212	15	4,92E-50	1,53E-40	-3,32	97
	GATM	NM_001482	15	1,25E-75	4,49E-64	-2,78	30
	SPATA5L1	NM_024063	15	5,36E-43	8,53E-34	1,78	53
	C15orf48	NM_032413	15	8,35E-20	9,82E-20	-1,75	82
	MIR147B	NR_030599	15	4,32E-16	3,77E-16	-0,12	84
	C15orf21	NR_022014	15	6,88E-11	8,91E-13	0,04	162
	SLC30A4	NM_013309	15	1,44E-12	8,91E-13	0,67	174
rs17730281	PLDN	NM_012388	15	3,07E-06	3,77E-16	3,06	238
	KIAA1370	NM_019600	15	5,41E-03	1,08E-09	2,64	937
	ONECUT1	NM_004498	15	6,76E-09	5,86E-16	-2,75	826
	WDR72	NM_182758	15	1,60E-18	4,19E-29	-3,32	144
rs17730436*	RSL24D1	NM_016304	15	1,94E-09	2,68E-08	3,91	1581
	ONECUT1	NM_004498	15	6,76E-09	5,86E-16	-2,75	861
	WDR72	NM_182758	15	1,60E-18	4,19E-29	-3,32	109
rs11868441***	UNC13C	NM_001080534	15	7,21E-12	2,20E-12	-3,32	362
	BCAS3	NM_001099432	17	7,93E-22	3,53E-21	1,99	484
	TBX2	NM_005994	17	1,45E-75	3,41E-66	-2,70	238
	C17orf82	NM_203425	17	2,68E-40	2,26E-35	-1,95	250
	NACA2	NM_199290	17	1,24E-27	1,53E-32	-0,87	429
rs12460876	BRIP1	NM_032043	17	3,45E-07	1,69E-12	0,23	702
	PDCD5	NM_004708	19	1,65E-13	4,24E-19	4,84	285
	ANKRD27	NM_032139	19	1,65E-13	1,32E-12	2,44	191
	RGS9BP	NM_207391	19	1,65E-13	1,32E-12	-2,39	191
	NUDT19	NM_001105570	19	1,51E-18	1,72E-24	2,37	174
	TDRD12	NM_001110822	19	2,84E-36	1,87E-34	-2,65	146
	SLC7A9	NM_001126335	19	2,18E-50	3,07E-48	-2,32	4
	CCDC123	NM_032816	19	1,51E-18	1,72E-24	2,35	106
	C19orf40	NM_152266	19	1,51E-18	1,72E-24	0,73	106
	RHPN2	NM_033103	19	3,88E-15	1,32E-12	-1,00	199
	GPATCH1	NM_018025	19	3,88E-15	4,09E-11	0,47	215
	WDR88	NM_173479	19	1,65E-13	4,09E-11	-2,29	266

rs6026584	RAE1	NM_003610	20	1,00E+00	3,40E-13	3,03	1543
	PPP4R1L	NR_003505	20	7,57E-09	1,66E-19	1,00	585
	RAB22A	NM_020673	20	7,57E-09	1,66E-19	2,16	584
	VAPB	NM_004738	20	3,30E-23	1,01E-24	3,13	505
	APCDD1L	NM_153360	20	7,57E-09	1,73E-06	-0,43	379
	STX16	NM_001001433	20	3,08E-13	1,51E-26	3,62	243
	NPEPL1	NM_024663	20	7,57E-09	3,37E-21	3,87	201
	MIR296	NR_029844	20	7,71E-03	9,67E-12	-3,32	76
	MIR298	NR_030580	20	7,71E-03	9,67E-12	-3,32	76
	GNAS	NM_016592	20	2,11E-16	1,06E-14	7,60	54
	GNASAS	NR_002785	20	1,93E-34	2,66E-32	-3,32	43
	TH1L	NM_198976	20	1,59E-55	1,24E-40	3,92	87
	CTSZ	NM_001336	20	4,40E-51	2,69E-52	7,11	113
	TUBB1	NM_030773	20	4,42E-60	4,12E-63	-1,93	125
	ATP5E	NM_006886	20	4,42E-60	4,12E-63	7,09	138
	SLMO2	NM_016045	20	4,42E-60	1,76E-57	3,47	149
	ZNF831	NM_178457	20	7,57E-09	1,04E-07	-2,96	297
	SYCP2	NM_014258	20	3,30E-06	5,39E-09	-2,57	1038
	PPP1R3D	NM_006242	20	3,30E-06	5,39E-09	0,96	1046
	C20orf177	NM_022106	20	3,30E-06	5,39E-09	0,41	1046
rs911119	SSTR4	NM_001052	20	1,40E-07	1,03E-10	-2,52	597
	THBD	NM_000361	20	2,79E-06	1,03E-10	2,89	582
	NXT1	NM_013248	20	6,19E-29	3,44E-25	3,00	281
	GZF1	NM_022482	20	7,76E-31	5,28E-27	0,94	268
	NAPB	NM_022080	20	9,06E-33	3,44E-25	0,61	211
	CSTL1	NM_138283	20	9,06E-33	2,06E-23	-3,32	192
	CST11	NM_080830	20	7,76E-31	1,12E-21	-3,32	179
	CST8	NM_005492	20	7,57E-12	5,57E-20	-1,84	141
	CSTT	NR_001279	20	7,57E-12	2,52E-18	-3,32	113
	CST9L	NM_080610	20	6,19E-29	9,54E-31	-3,32	63
	CST9	NM_001008693	20	1,74E-77	4,12E-54	-3,32	26
	CST3	NM_000099	20	4,95E-80	6,00E-64	7,87	6
	CST4	NM_001899	20	1,00E-36	9,10E-41	-2,20	57
	CST1	NM_001898	20	6,42E-20	2,06E-23	0,23	119
	CST2	NM_001322	20	2,25E-13	1,03E-10	-2,16	195
	CST5	NM_001900	20	2,25E-13	5,05E-08	-3,32	248
	GGTLC1	NM_178312	20	6,49E-04	3,86E-12	-3,32	355
	C20orf3	NM_020531	20	2,79E-06	2,44E-09	5,49	1361

Supplemental table 5: CKD candidate genes retrieved by 4C-seq in HRPTECs. * only trait serum creatinine, ** only trait serum urate, *** only trait blood urea nitrogen,^{†††}non-synonymous SNP. Interacting genes with a P-value <1E-08 in both individual 4C-seq experiments in HRPTECs are expressed in bold.

SNP	Gene ID	Refseq	Chromosome	P-value prep 1	P-value prep 2	expression (intensity)	SNP-TSS (kbp)
rs2049805	ADAR	NM_001111	1	1,40E-15	6,02E-10	10,88	614
	PMVK	NM_006556	1	1,11E-09	1,97E-17	8,92	285
	PBXIP1	NM_020524	1	1,11E-09	5,52E-26	9,31	266
	PYGO2	NM_138300	1	1,40E-11	5,52E-26	8,86	261
	SHC1	NM_001130040	1	1,40E-11	5,52E-26	11,07	252
	CKS1B	NM_001826	1	1,40E-11	5,52E-26	9,62	248
	FLAD1	NM_025207	1	1,40E-15	1,97E-17	8,14	239
	LENEP	NM_018655	1	1,40E-15	1,79E-19	7,23	229
	ZBTB7B	NM_015872	1	1,40E-15	1,79E-19	8,21	220
	DCST2	NM_144622	1	1,11E-09	1,97E-17	0,00	189
	DCST1	NM_001143687	1	1,11E-09	1,97E-17	0,00	189
	ADAM15	NM_207191	1	1,51E-13	4,31E-33	8,70	171
	EFNA4	NM_005227	1	1,51E-13	4,31E-33	6,84	159
	EFNA3	NM_004952	1	1,44E-26	1,16E-43	7,96	144
	EFNA1	NM_004428	1	1,51E-46	1,32E-35	10,92	95
	RAG1AP1	NM_001122839	1	1,51E-46	1,32E-35	9,08	87
	DPM3	NM_018973	1	1,51E-46	1,32E-35	9,72	82
	KRTCAP2	NM_173852	1	9,52E-55	6,99E-41	0,00	49
	TRIM46	NM_025058	1	9,52E-55	6,99E-41	6,82	49
	MUC1	NM_001018016	1	2,05E-72	1,33E-49	9,75	32
	MIR92B	NR_030281	1	1,50E-75	7,76E-53	0,00	30
	THBS3	NM_007112	1	8,30E-89	2,17E-56	8,22	17
	MTX1	NM_002455	1	8,30E-89	2,17E-56	9,91	16
	GBAP	NR_002188	1	8,30E-89	2,17E-56	6,46	2
	GBA	NM_000157	1	8,30E-89	2,17E-56	9,43	16
	FAM189B	NM_006589	1	8,30E-89	7,76E-53	9,99	30
	SCAMP3	NM_005698	1	9,52E-79	7,76E-53	9,62	37
	CLK2	NM_003993	1	1,43E-57	1,33E-49	9,18	48
	HCN3	NM_020897	1	6,70E-44	1,33E-49	0,00	52
	PKLR	NM_181871	1	6,49E-29	1,46E-46	6,54	76
	FDPS	NM_002004	1	6,49E-29	1,46E-46	11,13	84
	RUSC1	NM_001105203	1	6,49E-29	1,46E-46	9,11	96
	C1orf104	NM_001039517	1	6,49E-29	1,46E-46	0,00	99
	MIR555	NR_030282	1	1,40E-11	1,18E-30	0,00	121
	LOC645676	NR_027023	1	1,40E-15	2,76E-28	0,00	337
	ASH1L	NM_018489	1	1,40E-15	2,76E-28	7,51	337
	MSTO1	NM_018116	1	8,05E-20	1,40E-21	7,96	385
	YY1AP1	NM_139119	1	1,51E-13	9,49E-24	8,47	464
	DAP3	NM_004632	1	1,51E-13	9,49E-24	10,01	464
	MSTO2P	NR_024117	1	3,90E-06	9,49E-24	7,96	521
	GON4L	NM_001037533	1	7,30E-08	1,51E-13	4,81	632
	SYT11	NM_152280	1	7,30E-08	1,51E-13	5,48	634
	SNORA42	NR_002974	1	3,90E-06	6,02E-10	0,00	695
	SCARNA4	NR_003005	1	3,90E-06	6,02E-10	0,00	701
	KIAA0907	NM_014949	1	3,90E-06	6,02E-10	8,96	709
	RXFP4	NM_181885	1	1,62E-04	6,02E-10	0,00	716
	ARHGEF2	NM_004723	1	7,30E-08	6,02E-10	8,32	753
	SSR2	NM_003145	1	3,90E-06	1,51E-13	10,69	796
	UBQLN4	NM_020131	1	1,62E-04	1,51E-13	0,00	829
	LMNA	NM_005572	1	4,95E-03	1,04E-11	10,91	889
	PDE4DIP	NM_014644	1	1,01E-05	2,45E-11	6,59	5956
	NOTCH2NL	NM_203458	1	3,40E-10	5,46E-05	9,34	5742
	NBPF10	NM_001039703	1	7,54E-12	2,45E-11	9,82	5658
	HIST2H2BF	NM_001024599	1	3,40E-10	4,19E-06	0,00	1552
	HIST2H3D	NM_001123375	1	3,40E-10	4,19E-06	0,00	1166
	HIST2H4B	NM_001034077	1	3,40E-10	4,19E-06	4,96	1147
	HIST2H4A	NM_003548	1	3,40E-10	4,19E-06	4,96	1147
	HIST2H3C	NM_021059	1	3,40E-10	2,66E-07	0,00	1139
	HIST2H3A	NM_001005464	1	3,40E-10	2,66E-07	0,00	1139
	HIST2H2AA4	NM_001040874	1	3,40E-10	2,66E-07	10,93	1137
	HIST2H2AA3	NM_003516	1	3,40E-10	2,66E-07	10,93	1137
	OTUD7B	NM_020205	1	7,54E-12	5,46E-05	5,56	969
	PLEKHO1	NM_016274	1	2,05E-04	2,45E-11	6,61	829
	ANP32E	NM_001136479	1	1,41E-13	1,42E-08	7,80	744

rs267734

CA14	NM_012113	1	2,03E-25	2,22E-14	7,12	721
APH1A	NM_001077628	1	3,52E-19	2,45E-11	9,57	710
C1orf54	NM_024579	1	7,54E-12	2,45E-11	7,93	706
C1orf51	NM_144697	1	7,54E-12	2,22E-14	0,00	696
MRPS21	NM_018997	1	3,40E-10	2,22E-14	0,00	685
PRPF3	NM_004698	1	1,41E-13	2,45E-11	7,38	658
RPRD2	NM_015203	1	5,84E-30	1,06E-17	8,70	614
TARS2	NM_025150	1	3,46E-21	2,55E-21	8,46	492
ECM1	NM_004425	1	3,52E-19	2,55E-21	8,07	471
ADAMTSL4	NM_025008	1	3,05E-17	2,85E-25	7,60	430
MCL1	NM_182763	1	3,05E-17	2,55E-21	9,87	399
ENSA	NM_207045	1	2,31E-32	2,15E-27	10,77	350
GOLPH3L	NM_018178	1	5,84E-30	5,09E-32	8,75	282
HORMAD1	NM_032132	1	2,03E-25	2,99E-23	0,00	258
CTSS	NM_004079	1	2,03E-25	1,79E-19	7,09	213
CTSK	NM_000396	1	7,23E-35	5,09E-32	8,13	171
ARNT	NM_001668	1	2,95E-40	1,24E-29	5,78	102
SETDB1	NM_001145415	1	7,23E-35	1,34E-34	8,06	53
LASS2	NM_022075	1	1,67E-46	1,68E-37	11,33	4
ANXA9	NM_003568	1	1,67E-46	1,68E-37	6,59	3
FAM63A	NM_001163260	1	1,67E-46	1,68E-37	10,09	28
PRUNE	NM_021222	1	1,67E-46	1,34E-34	9,13	29
BNIP1	NM_138278	1	2,95E-40	1,34E-34	0,00	58
C1orf56	NM_017860	1	2,95E-40	1,34E-34	6,22	69
CDC42SE1	NM_001038707	1	1,72E-37	1,34E-34	9,44	81
MLLT11	NM_006818	1	1,72E-37	1,34E-34	10,52	81
GABPB2	NM_144618	1	7,23E-35	1,34E-34	0,00	92
SEMA6C	NM_030913	1	1,72E-37	5,09E-32	8,25	168
TNFAIP8L2	NM_024575	1	1,72E-37	5,09E-32	0,00	178
LYSMD1	NM_212551	1	1,72E-37	5,09E-32	0,00	187
SCNM1	NM_024041	1	1,72E-37	5,09E-32	9,51	187
TMOD4	NM_013353	1	5,84E-30	1,24E-29	0,00	197
VPS72	NM_005997	1	7,23E-35	1,24E-29	9,59	211
PIP5K1A	NM_001135636	1	7,23E-35	2,99E-23	9,54	220
PSMD4	NM_002810	1	3,52E-19	2,45E-11	10,16	276
ZNF687	NM_020832	1	3,40E-10	2,45E-11	0,00	303
PI4KB	NM_002651	1	3,40E-10	1,42E-08	8,92	347
RFX5	NM_000449	1	3,40E-10	1,42E-08	8,32	368
SELENBP1	NM_003944	1	3,40E-10	5,46E-05	8,23	394
PSMB4	NM_002796	1	3,40E-10	2,45E-11	11,07	421
POGZ	NM_015100	1	3,40E-10	5,46E-05	9,36	480
TUFT1	NM_001126337	1	1,41E-13	4,19E-06	8,84	561
MIR554	NR_030280	1	1,41E-13	4,19E-06	0,00	567
MUC1	NM_001018016	1	2,05E-72	1,33E-49	9,75	4211
MIR92B	NR_030281	1	1,50E-75	7,76E-53	0,00	4213
THBS3	NM_007112	1	8,30E-89	2,17E-56	8,22	4226
GBAP	NR_002188	1	8,30E-89	2,17E-56	6,46	4246
GBA	NM_000157	1	8,30E-89	2,17E-56	9,43	4260
GPR113	NM_001145169	2	1,00E+00	5,56E-08	0,00	1189
SELI	NM_033505	2	1,00E+00	1,26E-09	0,00	1162
DPYSL5	NM_020134	2	4,39E-08	3,64E-13	0,00	660
MAPRE3	NM_012326	2	6,39E-12	5,56E-08	5,90	537
TMEM214	NM_001083590	2	1,00E+00	2,34E-11	9,15	475
AGBL5	NM_001035507	2	5,84E-10	4,75E-15	8,39	456
LOC100128731	NM_001134693	2	5,84E-10	2,34E-11	0,00	436
EMILIN1	NM_007046	2	5,84E-10	5,65E-05	6,32	430
CGREF1	NM_001166241	2	1,23E-04	1,26E-09	5,70	397
ABHD1	NM_032604	2	2,65E-06	4,75E-15	0,00	384
PREB	NM_013388	2	4,39E-08	4,75E-15	9,12	373
C2orf53	NM_178553	2	4,39E-08	4,75E-15	0,00	369
TCF23	NM_175769	2	4,39E-08	4,75E-15	0,00	359
C2orf28	NM_080592	2	4,39E-08	4,75E-15	10,69	296
SLC5A6	NM_021095	2	4,39E-08	4,75E-15	8,65	296
CAD	NM_004341	2	4,17E-03	3,64E-13	9,34	291
SLC30A3	NM_003459	2	5,87E-14	5,23E-17	8,48	245
DNAJC5G	NM_173650	2	6,39E-12	1,26E-09	0,00	233
TRIM54	NM_032546	2	6,39E-12	5,23E-17	0,00	225
UCN	NM_003353	2	6,39E-12	3,86E-21	6,73	200
MPV17	NM_002437	2	5,84E-10	6,73E-28	9,51	185

rs1260326 ^{ns}	GTF3C2	NM_001035521	2	5,87E-14	4,88E-19	9,51	151
	EIF2B4	NM_172195	2	5,87E-14	1,44E-25	9,58	138
	SNX17	NM_014748	2	4,59E-16	1,44E-25	9,85	138
	ZNF513	NM_144631	2	9,05E-23	8,05E-33	0,00	127
	FTHL3P	NR_002201	2	9,05E-23	8,05E-33	0,00	114
	PPM1G	NM_002707	2	9,05E-23	6,73E-28	8,82	98
	NRBP1	NM_013392	2	5,30E-30	1,70E-47	9,09	79
	KRTCAP3	NM_173853	2	3,43E-43	1,70E-47	0,00	66
	IFT172	NM_015662	2	5,44E-68	1,70E-47	0,00	18
	FND C4	NM_022823	2	5,44E-68	1,70E-47	8,14	13
	GCKR	NM_001486	2	1,20E-71	1,70E-47	6,01	11
	C2orf16	NM_032266	2	3,35E-61	1,70E-47	0,00	68
	ZNF512	NM_032434	2	7,61E-52	4,93E-41	0,00	75
	GPN1	NM_001145047	2	1,59E-64	1,70E-47	10,00	121
	CCDC121	NM_001142682	2	1,59E-64	1,70E-47	4,35	121
	SLC4A1AP	NM_018158	2	9,67E-38	3,70E-38	8,09	155
	SUPT7L	NM_014860	2	9,67E-38	3,70E-38	7,05	156
	MRPL33	NM_004891	2	1,23E-04	5,23E-17	10,85	264
	RBKS	NM_022128	2	6,39E-12	2,34E-11	9,45	382
	BRE	NM_199193	2	6,39E-12	2,34E-11	9,60	383
	LOC100302650	NR_028308	2	6,39E-12	2,34E-11	0,00	383
	FOSL2	NM_005253	2	1,23E-04	1,26E-09	8,24	885
	PLB1	NM_153021	2	4,39E-08	1,26E-09	0,00	988
rs13538 ^{ns}	CYP26B1	NM_019885	2	1,00E+00	1,51E-10	5,27	1493
	NOTO	NM_001134462	2	4,60E-05	6,12E-09	0,00	439
	SMYD5	NM_006062	2	4,60E-05	6,12E-09	8,46	427
	C2orf7	NM_032319	2	3,10E-13	3,14E-12	0,00	408
	CCT7	NM_001009570	2	3,10E-13	3,14E-12	11,13	407
	FBXO41	NM_001080410	2	5,53E-19	5,95E-28	7,67	370
	EGR4	NM_001965	2	4,13E-23	3,42E-30	4,40	348
	ALMS1	NM_015120	2	1,83E-27	1,34E-21	7,91	255
	NAT8	NM_003960	2	5,91E-56	1,42E-57	7,05	1
	ALMS1P	NR_003683	2	5,91E-56	1,42E-57	0,00	4
	NAT8B	NM_016347	2	2,37E-39	1,89E-42	7,05	60
	TPRKB	NM_016058	2	1,83E-27	1,69E-32	8,78	96
	DUSP11	NM_003584	2	1,83E-27	3,42E-30	8,68	139
	C2orf78	NM_001080474	2	1,83E-27	3,42E-30	0,00	143
	STAMBP	NM_201647	2	1,83E-27	1,17E-23	9,44	188
	ACTG2	NM_001615	2	4,33E-15	1,51E-10	7,55	252
	DGUOK	NM_080916	2	4,60E-05	1,51E-10	9,76	286
	TET3	NM_144993	2	5,25E-17	6,12E-09	8,55	405
	BOLA3	NM_001035505	2	5,53E-19	8,61E-16	0,00	507
	MOBK1B	NM_018221	2	4,60E-05	6,12E-09	7,73	538
	SLC4A5	NM_133478	2	4,33E-15	3,14E-12	6,36	702
	DCTN1	NM_001135041	2	1,58E-06	3,14E-12	8,55	734
	LOC100189589	NR_024463	2	4,38E-08	3,14E-12	0,00	745
rs16853722	GOLIM4	NM_014498	3	3,40E-08	4,97E-10	7,13	1337
	MIR551B	NR_030294	3	1,13E-14	2,22E-18	0,00	881
	C3orf50	NR_021485	3	6,03E-13	3,75E-13	0,00	623
	MECOM	NM_001163999	3	1,90E-26	2,69E-24	8,45	287
	TERC	NR_001566	3	2,52E-18	1,45E-16	0,00	332
	ARPM1	NM_032487	3	1,13E-14	1,49E-11	0,00	337
	MYNN	NM_018657	3	1,13E-14	4,97E-10	7,80	340
	LRRC34	NM_153353	3	6,03E-13	4,97E-10	0,00	380
	LRRC31	NM_024727	3	3,40E-08	3,75E-13	5,22	437
	SAMD7	NM_182610	3	1,05E-09	4,97E-10	0,00	479
rs13069000***	GPR160	NM_014373	3	9,11E-07	4,97E-10	0,00	605
	SLC25A26	NM_173471	3	1,00E+00	1,24E-08	0,00	680
	LRIG1	NM_015541	3	1,76E-29	7,99E-29	7,05	248
	KBTBD8	NM_032505	3	1,08E-11	1,18E-16	0,00	250
rs10937329***	FAM19A4	NM_001005527	3	1,08E-11	6,64E-15	0,00	2183
	SST	NM_001048	3	5,42E-05	3,26E-10	7,94	326
	RTP2	NM_001004312	3	1,33E-09	1,45E-13	0,00	293
	BCL6	NM_001134738	3	2,06E-29	4,75E-21	8,93	261
	FLJ42393	NR_024413	3	5,77E-39	2,54E-27	0,00	183
	LPP	NM_005578	3	1,04E-31	3,63E-25	9,73	217
	TPRG1	NM_198485	3	1,33E-09	4,75E-21	0,00	1176
	ACPL2	NM_001037172	3	4,28E-09	1,22E-09	0,00	856
	RASA2	NM_006506	3	1,87E-12	2,29E-16	6,23	601

rs347685	RNF7	NM_183237	3	4,19E-16	4,02E-22	9,33	350
	GRK7	NM_139209	3	4,96E-18	3,23E-18	0,00	310
	ATP1B3	NM_001679	3	3,26E-24	3,90E-20	11,29	212
	TFDP2	NM_006286	3	2,56E-41	5,72E-41	6,60	83
	GK5	NM_001039547	3	1,88E-33	1,22E-35	0,00	137
	XRN1	NM_001042604	3	4,38E-22	3,90E-20	0,00	360
	ATR	NM_001184	3	4,19E-16	3,24E-11	6,30	491
	PLS1	NM_001145319	3	1,87E-12	3,87E-08	9,65	508
	TRPC1	NM_003304	3	1,56E-07	3,24E-11	8,71	636
	PCOLCE2	NM_013363	3	1,56E-07	3,24E-11	5,68	801
	PAQR9	NM_198504	3	4,63E-06	3,24E-11	0,00	875
	SR140	NM_001080415	3	1,56E-07	1,22E-09	8,99	913
rs13146355	PPEF2	NM_006239	4	8,77E-10	1,49E-09	4,27	588
	NAAA	NM_001042402	4	4,50E-05	2,64E-16	6,83	550
	SDAD1	NM_018115	4	1,58E-11	3,09E-24	9,11	500
	CXCL9	NM_002416	4	1,58E-11	3,09E-24	6,81	484
	ART3	NM_001130017	4	1,58E-11	4,05E-20	4,57	480
	CXCL10	NM_001565	4	1,58E-11	3,55E-18	6,94	467
	CXCL11	NM_005409	4	1,58E-11	3,55E-18	4,17	455
	NUP54	NM_017426	4	1,04E-25	4,54E-31	8,48	342
	SCARB2	NM_005506	4	2,22E-31	2,13E-33	10,39	277
	FAM47E	NM_001136570	4	7,94E-33	1,08E-28	0,00	239
	STBD1	NM_003943	4	1,01E-38	2,13E-33	9,61	184
	CCDC158	NM_001042784	4	5,67E-58	8,31E-47	0,00	84
	SHROOM3	NM_020859	4	4,98E-71	2,33E-53	0,00	56
	ANKRD56	NM_001029870	4	3,18E-19	1,08E-28	0,00	407
	40067	NM_018243	4	1,04E-25	1,98E-26	10,05	459
	CCNI	NM_006835	4	9,43E-27	3,55E-18	12,59	585
	CCNG2	NM_004354	4	2,55E-21	3,55E-18	9,63	666
	CXCL13	NM_006419	4	5,02E-04	1,49E-09	4,75	1021
	CNOT6L	NM_144571	4	8,77E-10	4,67E-08	0,00	1328
rs3775948**	USP17	NM_001105662	4	4,05E-11	2,41E-05	0,00	778
	USP17L6P	NR_027279	4	4,05E-11	2,41E-05	0,00	626
	DEFB131	NM_001040448	4	4,05E-11	2,41E-05	0,00	549
	DRD5	NM_000798	4	7,79E-35	1,13E-37	7,42	212
	SLC2A9	NM_020041	4	9,56E-61	7,50E-62	10,09	28
	WDR1	NM_005112	4	4,05E-11	1,05E-19	11,37	123
rs17319721	ZNF518B	NM_053042	4	5,46E-17	8,07E-14	0,00	464
	NAAA	NM_001042402	4	4,50E-05	2,64E-16	6,83	507
	SDAD1	NM_018115	4	1,58E-11	3,09E-24	9,11	457
	CXCL9	NM_002416	4	1,58E-11	3,09E-24	6,81	440
	ART3	NM_001130017	4	1,58E-11	4,05E-20	4,57	437
	CXCL10	NM_001565	4	1,58E-11	3,55E-18	6,94	424
	NUP54	NM_017426	4	1,04E-25	4,54E-31	8,48	299
	SCARB2	NM_005506	4	2,22E-31	2,13E-33	10,39	234
	FAM47E	NM_001136570	4	7,94E-33	1,08E-28	0,00	196
	STBD1	NM_003943	4	1,01E-38	2,13E-33	9,61	141
	CCDC158	NM_001042784	4	5,67E-58	8,31E-47	0,00	40
	SHROOM3	NM_020859	4	4,98E-71	2,33E-53	0,00	13
	ANKRD56	NM_001029870	4	3,18E-19	1,08E-28	0,00	450
rs11959928	40067	NM_018243	4	1,04E-25	1,98E-26	10,05	502
	CCNI	NM_006835	4	9,43E-27	3,55E-18	12,59	628
	CCNG2	NM_004354	4	2,55E-21	3,55E-18	9,63	710
	EGFLAM	NM_152403	5	1,53E-03	3,94E-09	0,00	1139
	LIFR	NM_001127671	5	3,07E-06	3,10E-12	4,58	840
	OSMR	NM_003999	5	9,74E-08	3,94E-09	9,98	551
	RICTOR	NM_152756	5	5,60E-31	3,01E-23	0,00	323
	FYB	NM_001465	5	2,32E-16	3,01E-23	7,11	177
	C9	NM_001737	5	1,41E-48	3,18E-43	4,47	32
	DAB2	NM_001343	5	1,93E-57	3,18E-43	10,81	28
	PTGER4	NM_000958	5	2,55E-09	6,77E-14	4,42	1283
	TTC33	NM_012382	5	2,32E-16	3,11E-21	6,49	1359
	PRKAA1	NM_006251	5	1,04E-12	2,00E-17	6,56	1401
	SNORD72	NR_002583	5	2,76E-22	1,26E-15	0,00	1436
	RPL37	NM_000997	5	2,76E-22	1,26E-15	12,75	1438
	CARD6	NM_032587	5	2,76E-22	1,26E-15	0,00	1444
	C7	NM_000587	5	2,55E-09	1,26E-15	4,63	1512
	C6	NM_000065	5	3,07E-06	3,94E-09	6,27	1817
	C5orf51	NM_175921	5	5,58E-11	4,55E-05	0,00	2507

	FBXO4	NM_033484	5	2,55E-09	2,46E-06	0,00	2528
	C5orf39	NM_001014279	5	2,55E-09	7,56E-03	0,00	3643
	LOC153684	NR_015447	5	2,55E-09	6,69E-04	0,00	3645
rs6420094	SNCB	NM_001001502	5	9,33E-05	3,99E-10	7,40	760
	EIF4E1B	NM_001099408	5	9,33E-05	3,99E-10	0,00	760
	TSPAN17	NM_001006616	5	3,51E-09	2,86E-13	0,00	743
	UIMC1	NM_016290	5	3,87E-16	2,86E-13	8,41	384
	ZNF346	NM_012279	5	1,58E-12	1,16E-11	0,00	368
	FGFR4	NM_002011	5	2,66E-14	1,96E-20	7,13	304
	NSD1	NM_172349	5	2,25E-28	1,56E-18	7,13	258
	RAB24	NM_001031677	5	3,41E-26	1,22E-26	0,00	87
	PRELID1	NM_013237	5	3,41E-26	1,22E-26	0,00	87
	MXD3	NM_001142935	5	1,30E-30	1,59E-36	8,01	78
	LMAN2	NM_006816	5	7,08E-51	8,35E-34	9,38	39
	RGS14	NM_006480	5	4,59E-48	1,59E-36	7,83	33
	SLC34A1	NM_003052	5	8,41E-54	1,44E-39	7,19	6
	PFN3	NM_001029886	5	2,38E-45	1,44E-39	0,00	10
	F12	NM_000505	5	2,38E-45	1,44E-39	8,83	19
	GRK6	NM_001004105	5	3,65E-40	1,44E-39	7,32	36
	PRR7	NM_030567	5	4,59E-48	1,44E-39	8,01	56
	DBN1	NM_080881	5	4,59E-48	1,59E-36	9,38	82
	PDLIM7	NM_005451	5	2,91E-35	8,35E-34	8,35	107
	DOK3	NM_001144875	5	1,30E-30	1,59E-36	7,45	120
	DDX41	NM_016222	5	1,30E-30	1,59E-36	11,05	126
	FAM193B	NM_019057	5	2,66E-14	1,22E-26	8,20	164
	TMED9	NM_017510	5	8,08E-11	3,99E-10	10,49	202
	B4GALT7	NM_007255	5	8,08E-11	3,99E-10	8,46	209
	NHP2	NM_017838	5	8,08E-11	5,51E-06	11,09	763
rs1936800**	HDDC2	NM_016063	6	9,64E-07	1,76E-17	5,74	1813
	HEY2	NM_012259	6	2,85E-20	1,76E-17	5,62	1365
	NCOA7	NM_001122842	6	2,88E-11	3,38E-23	0,00	1324
	HINT3	NM_138571	6	1,17E-14	2,64E-19	0,00	1158
	TRMT11	NM_001031712	6	1,06E-41	7,49E-35	8,01	1128
	C6orf173	NM_001012507	6	8,90E-29	7,49E-35	0,00	775
	RSP03	NM_032784	6	6,43E-45	7,49E-35	0,00	4
	RNF146	NM_030963	6	2,28E-24	3,30E-32	8,05	152
	ECHDC1	NM_001139510	6	2,49E-18	2,64E-19	9,46	227
	KIAA0408	NM_014702	6	2,85E-20	3,38E-23	5,32	344
	C6orf174	NM_001012279	6	2,88E-11	2,64E-19	0,00	404
	C6orf58	NM_001010905	6	9,64E-07	2,64E-19	0,00	462
rs881858	C6orf108	NM_006443	6	1,67E-05	1,29E-11	9,21	609
	SLC22A7	NM_006672	6	4,38E-07	4,19E-15	6,67	541
	CRIP3	NM_206922	6	1,67E-05	4,19E-15	0,00	530
	ZNF318	NM_014345	6	1,59E-10	5,88E-17	7,06	469
	ABCC10	NM_033450	6	9,23E-09	1,98E-08	8,25	407
	DLK2	NM_023932	6	1,59E-10	5,53E-10	7,52	383
	TJAP1	NM_001146016	6	1,59E-10	1,29E-11	8,43	361
	C6orf154	NM_001012974	6	9,23E-09	2,53E-13	0,00	328
	YIPF3	NM_015388	6	1,67E-05	2,53E-13	8,83	322
	POLR1C	NM_203290	6	1,67E-05	2,53E-13	8,62	322
	XPO5	NM_020750	6	1,40E-22	5,89E-23	0,00	263
	POLH	NM_006502	6	1,40E-22	5,89E-23	4,78	263
	GTPBP2	NM_019096	6	1,91E-29	1,12E-29	9,15	210
	MAD2L1BP	NM_001003690	6	1,91E-29	1,12E-29	8,81	209
	RSPH9	NM_152732	6	7,41E-32	1,12E-29	0,00	194
	MRPS18A	NM_018135	6	3,77E-42	2,97E-40	9,29	151
	VEGFA	NM_001025369	6	6,61E-45	2,97E-40	10,92	69
	LOC100132354	NR_024478	6	1,79E-39	2,32E-37	0,00	52
	C6orf223	NM_153246	6	2,50E-34	4,13E-32	0,00	162
	MRPL14	NM_032111	6	2,07E-20	1,12E-29	0,00	289
	TMEM63B	NM_018426	6	2,07E-20	1,12E-29	0,00	289
	CAPN11	NM_007058	6	2,07E-20	2,39E-27	6,01	320
	SLC29A1	NM_001078174	6	9,23E-09	2,53E-13	9,23	381
	HSP90AB1	NM_007355	6	2,30E-12	6,99E-21	10,74	408
	SLC35B2	NM_178148	6	1,59E-10	6,99E-21	0,00	419
	NFKBIE	NM_004556	6	1,59E-10	6,99E-21	8,61	427
	TMEM151B	NM_001137560	6	1,59E-10	5,88E-17	6,94	432
	TCTE1	NM_182539	6	4,38E-07	4,13E-25	0,00	459
	AARS2	NM_020745	6	2,81E-14	6,98E-19	0,00	474

		SPATS1	NM_145026	6	9,23E-09	6,98E-19	0,00	504
		CDC5L	NM_001253	6	2,94E-16	1,29E-11	8,51	549
rs2279463*		FNDC1	NM_032532	6	7,71E-05	4,27E-10	0,00	1078
		SOD2	NM_001024465	6	2,57E-09	1,28E-16	12,08	554
		WTAP	NM_152858	6	1,51E-03	3,23E-13	10,78	520
		ACAT2	NM_005891	6	9,75E-08	6,97E-15	10,02	485
		SNORA20	NR_002960	6	9,75E-08	1,27E-11	11,22	467
		SNORA29	NR_002965	6	3,06E-06	4,27E-10	0,00	462
		TCP1	NM_001008897	6	3,06E-06	1,27E-11	11,22	458
		MRPL18	NM_014161	6	3,06E-06	1,27E-11	10,30	457
		PNLDC1	NM_173516	6	9,75E-08	6,97E-15	0,00	447
		MAS1	NM_002377	6	3,06E-06	2,67E-20	6,52	340
		IGF2R	NM_000876	6	7,71E-05	3,23E-13	9,29	278
		LOC729603	NR_003288	6	2,16E-26	2,19E-26	0,00	154
		SLC22A1	NM_153187	6	9,40E-43	6,88E-31	7,25	126
		SLC22A2	NM_003058	6	7,15E-66	1,03E-41	8,05	12
		SLC22A3	NM_021977	6	3,03E-40	7,12E-36	4,17	101
		LPAL2	NR_028093	6	2,85E-24	1,38E-28	5,71	264
		AGPAT4	NM_020133	6	1,51E-03	4,27E-10	7,43	1027
		LOC441177	NR_027284	6	7,71E-05	4,27E-10	0,00	5733
rs10277115		CYP2W1	NM_017781	7	9,56E-03	4,81E-11	5,93	262
		MIR339	NR_029898	7	4,38E-04	8,50E-13	0,00	223
		GPR146	NM_138445	7	2,71E-18	8,50E-13	0,00	188
		GPER	NM_001039966	7	2,29E-20	1,01E-24	5,40	159
		C7orf50	NM_001134395	7	8,84E-39	4,14E-39	0,00	107
		ZFAND2A	NM_182491	7	2,66E-41	8,33E-42	0,00	85
		UNCX	NM_001080461	7	1,56E-66	1,42E-47	0,00	13
		MICALL2	NM_182924	7	2,29E-20	1,42E-22	7,09	214
		INTS1	NM_001080453	7	1,39E-10	3,20E-29	6,78	259
		MAFK	NM_002360	7	3,81E-07	1,64E-16	6,50	285
		TMEM184A	NM_001097620	7	1,39E-10	9,09E-08	0,00	311
		PSMG3	NM_032302	7	1,39E-10	8,50E-13	0,00	324
		KIAA1908	NR_021487	7	1,39E-10	8,50E-13	0,00	325
		TFAMP1	NR_001288	7	1,47E-05	1,28E-14	0,00	369
		ELFN1	NM_001128636	7	1,39E-10	4,81E-11	0,00	464
rs6465825*		ZP3	NM_007155	7	1,00E+00	3,63E-09	6,73	1390
		SRCRB4D	NM_080744	7	1,00E+00	3,63E-09	0,00	1377
		DTX2	NM_001102594	7	1,00E+00	3,63E-09	6,77	1325
		FDPSSL2A	NR_003262	7	1,00E+00	3,63E-09	0,00	1312
		UPK3B	NM_182684	7	1,00E+00	3,63E-09	7,11	1277
		POMZP3	NM_152992	7	2,68E-05	9,32E-16	7,09	1160
		CCDC146	NM_020879	7	7,92E-07	3,63E-09	0,00	665
		FGL2	NM_006682	7	7,92E-07	5,38E-14	5,02	587
		PION	NM_017439	7	5,72E-12	1,36E-17	7,93	371
		PTPN12	NM_002835	7	5,29E-22	4,83E-28	8,92	250
		RSBN1L	NM_198467	7	1,43E-41	9,86E-36	0,00	91
		TMEM60	NM_032936	7	3,04E-57	8,49E-39	0,00	11
		PHTF2	NM_001127360	7	3,04E-57	8,49E-39	4,64	12
		RPL13AP17	NR_003680	7	2,68E-05	1,36E-17	0,00	560
		GNAI1	NM_002069	7	1,00E+00	1,06E-10	7,39	2348
		FAM185A	NM_001145268	7	1,86E-08	2,61E-12	0,00	24973
rs7805747		OR2A42	NM_001001802	7	1,00E+00	6,78E-09	0,00	7478
		OR2A1	NM_001005287	7	1,00E+00	6,78E-09	0,00	7478
		ATG9B	NM_173681	7	1,00E+00	2,22E-10	0,00	686
		ABCB8	NM_007188	7	1,00E+00	2,22E-10	7,92	682
		ACCN3	NM_004769	7	1,00E+00	6,78E-09	5,82	662
		CDK5	NM_004935	7	1,00E+00	6,78E-09	8,79	653
		SLC4A2	NM_003040	7	1,00E+00	6,78E-09	9,58	651
		FASTK	NM_006712	7	6,14E-04	6,78E-09	9,05	630
		TMUB1	NM_031434	7	6,14E-04	6,78E-09	0,00	627
		AGAP3	NM_001042535	7	6,14E-04	2,22E-10	0,00	624
		GBX1	NM_001098834	7	2,30E-05	6,15E-12	7,84	543
		ASB10	NM_001142459	7	6,67E-07	6,78E-09	0,00	523
		ABCF2	NM_005692	7	6,67E-07	2,22E-10	7,10	483
		CHPF2	NM_019015	7	6,67E-07	6,15E-12	8,63	478
		MIR671	NR_030407	7	1,56E-08	1,44E-13	8,63	472
		SMARCD3	NM_001003801	7	1,56E-08	1,44E-13	7,66	462
		NUB1	NM_016118	7	1,70E-28	5,75E-27	0,00	369
		WDR86	NM_198285	7	8,75E-18	5,75E-27	0,00	301

	CRYGN	NM_144727	7	8,75E-18	1,55E-31	0,00	271
	RHEB	NM_005614	7	4,60E-43	1,71E-42	8,09	191
	PRKAG2	NM_024429	7	6,52E-54	1,38E-36	8,34	78
	GALNTL5	NM_145292	7	6,67E-07	2,89E-15	0,00	246
	GALNT11	NM_022087	7	1,56E-08	2,22E-10	10,53	315
	ACTR3B	NM_001040135	7	1,00E+00	2,22E-10	6,23	1049
rs10109414*	TNFRSF10D	NM_003840	8	1,39E-05	2,43E-09	7,48	730
	LOXL2	NM_002318	8	1,39E-05	8,58E-11	9,07	489
	ENTPD4	NM_004901	8	1,28E-11	1,33E-15	7,01	436
	SLC25A37	NM_016612	8	6,89E-19	3,39E-19	8,42	365
	NKX3-1	NM_006167	8	2,51E-13	2,33E-17	7,43	211
	NKX2-6	NM_001136271	8	6,90E-21	4,05E-21	0,00	187
	STC1	NM_003155	8	2,91E-40	1,81E-32	10,31	39
	ADAM28	NM_021777	8	5,81E-23	3,90E-23	4,73	400
	ADAMDEC1	NM_014479	8	1,10E-29	1,70E-27	4,32	491
	ADAM7	NM_003817	8	4,15E-15	2,95E-25	6,93	547
rs10794720*	KCTD9	NM_017634	8	2,63E-04	8,58E-11	7,99	1565
	CDCA2	NM_152562	8	2,63E-04	8,58E-11	0,00	1565
	LARP4B	NM_015155	10	5,66E-11	6,27E-10	6,66	224
	GTPBP4	NM_012341	10	3,04E-16	3,69E-16	6,77	122
	C10orf110	NR_024628	10	5,12E-20	1,32E-19	6,79	88
	IDI2	NM_033261	10	5,66E-24	1,32E-19	0,00	84
	IDI1	NM_004508	10	3,42E-56	1,51E-35	10,88	61
	WDR37	NM_014023	10	8,53E-59	1,58E-42	8,66	53
	NCRNA00200	NR_015376	10	1,92E-41	1,51E-35	0,00	50
	ADARB2	NM_018702	10	1,00E+00	6,28E-13	5,65	624
rs504915**	PFKP	NM_002627	10	3,04E-16	1,62E-14	12,13	1954
	PITRM1	NM_014889	10	3,04E-16	7,41E-18	8,83	2059
	FLRT1	NM_013280	11	1,00E+00	1,30E-09	6,84	593
	STIP1	NM_006819	11	9,75E-03	3,44E-11	9,23	510
	FERMT3	NM_031471	11	8,74E-09	3,44E-11	0,00	490
	TRPT1	NM_001160393	11	8,74E-09	4,13E-08	0,00	471
	VEGFB	NM_003377	11	4,07E-07	1,30E-09	8,53	462
	FKBP2	NM_004470	11	1,54E-05	7,67E-13	9,49	456
	PPP1R14B	NM_138689	11	9,75E-03	7,67E-13	10,19	450
	PLCB3	NM_000932	11	4,52E-04	7,67E-13	7,86	445
	C11orf20	NM_001039496	11	1,54E-05	2,34E-16	0,00	396
	ESRRA	NM_004451	11	4,07E-07	3,22E-18	8,60	391
	TRMT112	NM_016404	11	1,56E-10	3,22E-18	11,03	379
	PRDX5	NM_012094	11	1,56E-10	3,22E-18	0,00	379
	CCDC88B	NM_032251	11	3,08E-14	3,74E-22	0,00	356
	RPS6KA4	NM_001006944	11	3,08E-14	3,74E-22	9,02	337
	SLC22A11	NM_018484	11	5,90E-29	6,35E-36	6,06	141
	SLC22A12	NM_144585	11	1,05E-26	2,24E-33	0,00	106
	NRXN2	NM_138734	11	1,37E-33	1,68E-41	6,46	53
	RASGRP2	NM_001098671	11	2,20E-62	1,68E-41	6,59	48
	PYGM	NM_001164716	11	7,02E-41	1,68E-41	6,81	64
	SF1	NM_201995	11	7,02E-41	1,68E-41	10,77	82
	MAP4K2	NM_004579	11	2,40E-22	3,22E-18	6,24	107
	MEN1	NM_130800	11	3,48E-18	3,77E-20	9,02	114
	CDC42BPG	NM_017525	11	3,48E-18	2,34E-16	0,00	148
	EHD1	NM_006795	11	8,74E-09	1,30E-09	7,76	182
	MIR192	NR_029578	11	4,07E-07	7,67E-13	0,00	195
	MIR194-2	NR_029829	11	4,07E-07	7,67E-13	0,00	195
	ATG2A	NM_015104	11	8,74E-09	3,44E-11	9,25	221
	PPP2R5B	NM_006244	11	8,74E-09	4,13E-08	8,73	228
	GPHA2	NM_130769	11	2,36E-12	4,13E-08	0,00	239
	C11orf85	NM_001037225	11	2,36E-12	4,13E-08	0,00	264
	BATF2	NM_138456	11	8,74E-09	7,67E-13	0,00	300
	ARL2	NM_001667	11	8,74E-09	3,22E-18	10,18	318
	SNX15	NM_013306	11	8,74E-09	3,77E-20	7,91	331
	SAC3D1	NM_013299	11	4,52E-04	2,34E-16	7,79	344
	CDCA5	NM_080668	11	8,74E-09	3,44E-11	0,00	388
	ZFPL1	NM_006782	11	8,74E-09	3,44E-11	8,26	388
	C11orf2	NM_013265	11	8,74E-09	4,13E-08	10,00	400
	TM7SF2	NM_003273	11	4,07E-07	3,44E-11	9,28	415
	ZNHIT2	NM_014205	11	1,54E-05	3,44E-11	7,79	421
	FAU	NM_001997	11	1,54E-05	3,44E-11	12,72	426
	CORO1C	NM_014325	12	2,64E-09	2,47E-03	11,04	2882

rs653178	ARPC3	NM_005719	12	2,64E-09	1,47E-04	11,04	1120
	GPN3	NM_016301	12	2,64E-09	6,73E-06	8,15	1102
	PPP1CC	NM_002710	12	2,64E-09	2,47E-03	10,24	827
	FAM109A	NM_144671	12	2,16E-16	1,24E-17	0,00	201
	SH2B3	NM_005475	12	2,16E-16	9,73E-16	8,13	164
	ATXN2	NM_002973	12	5,17E-53	1,84E-46	8,57	30
	BRAP	NM_006768	12	3,72E-49	1,31E-39	5,13	116
	ACAD10	NM_001136542	12	3,72E-49	1,31E-39	8,29	116
	ALDH2	NM_000690	12	4,84E-85	1,53E-56	9,77	197
	MAPKAPK5	NM_003668	12	6,19E-91	1,65E-53	8,64	273
	C12orf47	NR_015404	12	6,19E-91	1,65E-53	7,89	273
	TMEM116	NM_138341	12	1,04E-12	1,63E-18	0,00	443
	ERP29	NM_001034025	12	1,04E-12	1,63E-18	11,68	443
	C12orf30	NM_024953	12	2,64E-09	1,55E-12	0,00	539
	TRAFD1	NM_001143906	12	5,70E-11	6,50E-14	7,83	556
	C12orf51	NM_001109662	12	1,02E-07	7,27E-09	8,28	736
rs626277	DACH1	NM_004392	13	8,25E-40	7,08E-35	4,87	94
	C13orf37	NM_001071775	13	4,93E-16	4,55E-14	0,00	954
	C13orf34	NM_024808	13	4,93E-16	4,55E-14	6,73	954
	PIBF1	NM_006346	13	3,37E-11	4,35E-08	7,69	1009
	DIS3	NM_001128226	13	3,37E-11	4,35E-08	5,07	1009
rs2453533*	C15orf43	NM_152448	15	1,94E-13	3,08E-16	0,00	392
	SORD	NM_003104	15	4,45E-15	1,17E-14	8,76	326
	DUOX2	NM_014080	15	7,40E-12	2,10E-21	5,96	235
	DUOXA2	NM_207581	15	7,40E-12	2,10E-21	0,00	235
	DUOXA1	NM_144565	15	4,45E-15	6,91E-18	0,00	219
	DUOX1	NM_017434	15	4,45E-15	6,91E-18	5,88	219
	SHF	NM_138356	15	4,42E-26	7,86E-32	0,00	148
	SLC28A2	NM_004212	15	1,49E-41	3,39E-37	6,03	97
	GATM	NM_001482	15	3,39E-52	2,36E-34	6,32	30
	SPATA5L1	NM_024063	15	1,49E-41	2,36E-34	8,21	53
	C15orf48	NM_032413	15	8,95E-17	6,91E-18	0,00	82
	MIR147B	NR_030599	15	4,45E-15	6,91E-18	0,00	84
	C15orf21	NR_022014	15	8,95E-17	3,08E-16	0,00	162
	SLC30A4	NM_013309	15	7,40E-12	3,08E-16	5,30	174
rs17730436*	PLDN	NM_012388	15	6,99E-09	6,91E-18	0,00	238
	SQRDL	NM_021199	15	6,99E-09	3,81E-13	12,12	286
	KIAA1370	NM_019600	15	2,57E-07	1,33E-11	0,00	937
	ONECUT1	NM_004498	15	7,03E-12	3,72E-16	6,26	826
rs889472	WDR72	NM_182758	15	1,95E-27	2,22E-21	0,00	144
	UNC13C	NM_001080534	15	2,09E-14	4,74E-13	0,00	397
	WWOX	NM_130844	16	8,66E-08	7,64E-14	8,97	1512
rs11123170***	MAF	NM_005360	16	7,30E-61	2,48E-34	7,06	11
	DYNLRB2	NM_130897	16	2,31E-13	4,82E-11	0,00	929
	PRPF40A	NM_017892	2	5,34E-10	5,52E-09	10,01	39595
	ARL6IP6	NM_152522	2	5,34E-10	5,52E-09	0,00	39595
	RPRM	NM_019845	2	5,52E-07	4,60E-12	7,39	40356
rs11868441***	GALNT13	NM_052917	2	8,25E-19	3,53E-25	0,00	40749
	KCNJ3	NM_002239	2	8,29E-23	4,78E-21	5,94	41576
	APPBP2	NM_006380	17	1,49E-06	1,03E-10	8,59	636
	BCAS3	NM_001099432	17	3,31E-25	3,32E-25	8,06	484
	TBX2	NM_005994	17	4,66E-59	6,19E-45	7,79	238
	C17orf82	NM_203425	17	2,07E-31	4,87E-39	0,00	250
	TBX4	NM_018488	17	6,74E-16	3,32E-25	7,13	295
	NACA2	NM_199290	17	4,26E-38	2,84E-27	4,32	429
	BRIP1	NM_032043	17	1,50E-12	8,39E-14	4,89	702
rs9895661	INTS2	NM_020748	17	6,00E-08	1,03E-10	0,00	766
	MED13	NM_005121	17	1,32E-06	1,14E-09	8,62	903
	BCAS3	NM_001099432	17	3,31E-25	3,32E-25	8,06	701
	TBX2	NM_005994	17	4,66E-59	6,19E-45	7,79	21
	C17orf82	NM_203425	17	2,07E-31	4,87E-39	0,00	33
	TBX4	NM_018488	17	6,74E-16	3,32E-25	7,13	77
	NACA2	NM_199290	17	4,26E-38	2,84E-27	4,32	212
rs7227483***	BRIP1	NM_032043	17	1,50E-12	8,39E-14	4,89	484
	MED13	NM_005121	17	1,32E-06	1,14E-09	8,62	686
	SETBP1	NM_001130110	18	1,15E-03	2,49E-10	8,18	927
	SLC14A2	NM_007163	18	5,63E-60	3,22E-34	6,31	8
	SLC14A1	NM_001128588	18	6,65E-13	4,77E-21	8,43	117
rs7227483***	SIGLEC15	NM_213602	18	9,38E-05	1,69E-14	10,30	218

	KIAA1632	NM_020964	18	3,41E-07	2,49E-10	0,00	360
	PSTPIP2	NM_024430	18	1,59E-08	1,69E-14	7,59	465
	LOXHD1	NM_001145472	18	1,00E+00	1,69E-14	0,00	952
rs12460876	DKFZp566F0947	NR_026894	19	5,47E-03	6,42E-18	0,00	1716
	ZNF507	NM_001136156	19	6,63E-05	2,65E-16	6,84	520
	DPY19L3	NM_207325	19	3,65E-07	7,09E-12	0,00	460
	PDCD5	NM_004708	19	4,34E-11	2,20E-21	0,00	285
	ANKRD27	NM_032139	19	1,18E-20	3,30E-25	8,28	191
	RGS9BP	NM_207391	19	1,18E-20	3,30E-25	0,00	191
	NUDT19	NM_001105570	19	2,32E-24	3,30E-25	0,00	174
	TDRD12	NM_001110822	19	1,74E-30	2,75E-27	6,95	146
	SLC7A9	NM_001126335	19	3,28E-40	1,15E-34	6,32	4
	CCDC123	NM_032816	19	2,32E-24	3,02E-23	0,00	106
	C19orf40	NM_152266	19	2,32E-24	3,02E-23	6,61	106
	RHPN2	NM_033103	19	2,10E-08	7,09E-12	0,00	199
	GPATCH1	NM_018025	19	3,65E-07	2,93E-09	6,20	215
	WDR88	NM_173479	19	1,58E-12	1,31E-19	0,00	266
	LRP3	NM_002333	19	6,63E-05	1,55E-10	7,59	329
	SLC7A10	NM_019849	19	1,03E-09	1,55E-10	6,27	360
rs6026584	CEBPG	NM_001806	19	4,99E-14	2,77E-13	8,62	508
	KCTD15	NM_024076	19	3,65E-07	2,93E-09	7,18	931
	C20orf108	NM_080821	20	4,53E-05	1,89E-15	6,10	2535
	AURKA	NM_003600	20	6,41E-10	5,30E-14	8,03	2502
	C20orf43	NM_016407	20	6,41E-10	9,52E-04	9,04	2425
	BMP7	NM_001719	20	4,53E-05	5,13E-10	8,17	1627
	RAE1	NM_003610	20	3,53E-06	8,29E-09	8,89	1543
	PMEPA1	NM_020182	20	6,41E-10	1,16E-07	9,67	1184
	PPP4R1L	NR_003505	20	6,31E-28	1,57E-18	0,00	585
	RAB22A	NM_020673	20	6,31E-28	1,57E-18	8,15	584
	VAPB	NM_004738	20	2,16E-22	3,62E-20	9,62	505
	APCDD1L	NM_153360	20	1,31E-08	1,89E-15	0,00	379
	STX16	NM_001001433	20	5,86E-34	5,84E-17	6,79	243
	NPEPL1	NM_024663	20	3,36E-14	5,84E-17	8,69	201
	MIR296	NR_029844	20	2,53E-17	3,62E-20	0,00	76
	MIR298	NR_030580	20	2,53E-17	3,62E-20	0,00	76
	GNAS	NM_016592	20	2,16E-22	1,20E-23	12,75	54
	GNASAS	NR_002785	20	6,31E-28	7,15E-22	0,00	43
	TH1L	NM_198976	20	6,32E-43	2,04E-36	9,77	87
	CTSZ	NM_001336	20	1,44E-40	6,27E-34	8,02	113
	TUBB1	NM_030773	20	9,55E-57	3,21E-39	5,52	125
	ATP5E	NM_006886	20	9,55E-57	3,21E-39	11,66	138
	SLMO2	NM_016045	20	6,08E-48	6,27E-34	6,86	149
	ZNF831	NM_178457	20	6,41E-10	3,62E-20	0,00	297
	EDN3	NM_207032	20	4,83E-04	1,30E-12	5,48	406
	SYCP2	NM_014258	20	2,33E-07	5,13E-10	4,16	1038
	PPP1R3D	NM_006242	20	2,33E-07	5,13E-10	6,53	1046
	C20orf177	NM_022106	20	2,33E-07	5,13E-10	0,00	1046
rs911119	SSTR4	NM_001052	20	9,15E-09	2,94E-13	7,21	597
	THBD	NM_000361	20	9,15E-09	2,65E-09	7,95	582
	NXT1	NM_013248	20	1,05E-35	8,19E-23	9,00	281
	GZF1	NM_022482	20	8,76E-38	1,56E-28	0,00	268
	NAPB	NM_022080	20	6,49E-40	3,61E-35	0,00	211
	CSTL1	NM_138283	20	6,49E-40	3,61E-35	0,00	192
	CST11	NM_080830	20	1,05E-35	3,61E-35	0,00	179
	CST8	NM_005492	20	5,07E-26	9,42E-18	6,84	141
	CSTT	NR_001279	20	9,41E-21	2,25E-19	0,00	113
	CST9L	NM_080610	20	9,33E-30	1,27E-30	0,00	63
	CST9	NM_001008693	20	5,82E-54	7,98E-33	0,00	26
	CST3	NM_000099	20	2,72E-59	1,47E-40	12,07	6
	CST4	NM_001899	20	6,49E-40	1,52E-26	7,17	57
	CST1	NM_001898	20	1,83E-17	8,19E-23	5,63	119
	CST2	NM_001322	20	6,95E-13	3,41E-16	7,97	195
	CST5	NM_001900	20	2,31E-14	2,94E-13	6,76	248
	GGTLC1	NM_178312	20	1,66E-07	2,65E-09	9,01	355
	TMEM90B	NM_024893	20	1,00E+00	1,46E-10	6,87	837
	C20orf3	NM_020531	20	4,40E-10	4,16E-08	10,53	1361
	ACSS1	NM_032501	20	3,43E-03	2,65E-09	0,00	1427
	ENTPD6	NM_001114089	20	4,40E-10	1,46E-10	9,30	1564
	PYGB	NM_002862	20	6,86E-16	2,65E-09	10,72	1616

	ABHD12	NM_015600	20	4,40E-10	5,35E-04	0,00	1759
	GINS1	NM_021067	20	9,15E-09	6,46E-05	7,86	1776

Supplemental table 6: Pathway analysis based on CKD candidate genes retrieved with 4C-seq in HRGECs.

Ingenuity Canonical Pathways	-log(p-value)	Ratio	Molecules
Trans, trans-farnesyl Diphosphate Biosynthesis	5.18	0.60	FDPS,IDI2,IDI1
Superpathway of Geranylgeranyldiphosphate Biosynthesis I (via Mevalonate)	3.38	0.18	FDPS,IDI2,IDI1
Superpathway of Cholesterol Biosynthesis	2.73	0.11	FDPS,IDI2,IDI1
Mevalonate Pathway I	2.25	0.15	IDI2,IDI1
Phagosome Maturation	2.04	0.03	CTS2,CTSK,CTSS,STX16,NAPB
Amyloid Processing	1.99	0.06	CAPN11,APH1A,PRKAG2
autophagy	1.80	0.05	CTS2,CTSK,CTSS
mTOR Signaling	1.50	0.03	VEGFA,RHEB,PRKAG2,RPS6KA4,RICTOR
Phenylethylamine Degradation I	1.46	0.25	ALDH2
Geranylgeranyldiphosphate Biosynthesis	1.46	0.25	FDPS
Melanocyte Development and Pigmentation Signaling	1.29	0.03	GNAS,PRKAG2,RPS6KA4
Glycerol Degradation I	1.29	0.17	GK5
Tight Junction Signaling	1.22	0.02	PRKAG2,STX16,CNKS3,NAPB
VEGF Signaling	1.20	0.03	VEGFA,EIF2B4,ARNT
Corticotropin Releasing Hormone Signaling	1.13	0.03	VEGFA,GNAS,PRKAG2
AMPK Signaling	1.06	0.02	GNAS,PRKAG2,PFKP,PPM1G
G1i Signaling	1.05	0.03	GNAS,PRKAG2,RGS14
3-phosphoinositide Biosynthesis	1.03	0.02	PIP5K1A,DUSP11,PPM1K,PTPN12
Dolichyl-diphosphooligosaccharide Biosynthesis	1.03	0.09	DPM3
ILK Signaling	1.02	0.02	VEGFA,MUC1,RPS6KA4,RICTOR
Assembly of RNA Polymerase III Complex	0.96	0.08	GTF3C2
Hypoxia Signaling in the Cardiovascular System	0.95	0.03	VEGFA,ARNT
Phenylalanine Degradation IV (Mammalian, via Side Chain)	0.93	0.07	ALDH2
D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis	0.89	0.02	DUSP11,PPM1K,PTPN12
D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis	0.89	0.02	DUSP11,PPM1K,PTPN12
Extrinsic Prothrombin Activation Pathway	0.88	0.06	F12
GPCR-Mediated Integration of Enteroendocrine Signaling Exemplified by an L Cell	0.88	0.03	GNAS,PRKAG2
Ubiquinol-10 Biosynthesis (Eukaryotic)	0.86	0.06	ECHDC1
GDNF Family Ligand-Receptor Interactions	0.84	0.03	PDLIM7,DOK3
Superpathway of Inositol Phosphate Compounds	0.84	0.02	PIP5K1A,DUSP11,PPM1K,PTPN12
Role of BRCA1 in DNA Damage Response	0.82	0.03	FAAP24,ATR
Relaxin Signaling	0.82	0.02	VEGFA,GNAS,PRKAG2
GADD45 Signaling	0.81	0.05	ATR
Histamine Degradation	0.81	0.05	ALDH2
DNA damage-induced 14-3-3if Signaling	0.81	0.05	ATR
eNOS Signaling	0.81	0.02	VEGFA,GNAS,PRKAG2
3-phosphoinositide Degradation	0.81	0.02	DUSP11,PPM1K,PTPN12
Renal Cell Carcinoma Signaling	0.80	0.02	VEGFA,ARNT
Huntington's Disease Signaling	0.79	0.02	CAPN11,DCTN1,STX16,NAPB
D-myo-inositol-5-phosphate Metabolism	0.78	0.02	DUSP11,PPM1K,PTPN12
Oxidative Ethanol Degradation III	0.77	0.05	ALDH2
GPCR-Mediated Nutrient Sensing in Enteroendocrine Cells	0.76	0.02	GNAS,PRKAG2
Role of Lipids/Lipid Rafts in the Pathogenesis of Influenza	0.75	0.05	FDPS
Fatty Acid 1i-oxidation	0.75	0.05	ALDH2
1i-Adrenergic Signaling	0.75	0.02	GNAS,PRKAG2
G Beta Gamma Signaling	0.74	0.02	GNAS,PRKAG2
Putrescine Degradation III	0.74	0.04	ALDH2
Apoptosis Signaling	0.73	0.02	CAPN11,MCL1
Gap Junction Signaling	0.73	0.02	DBN1,GNAS,PRKAG2
IL-1 Signaling	0.72	0.02	GNAS,PRKAG2
Ephrin Receptor Signaling	0.70	0.02	VEGFA,GNAS,EFNA1
Tryptophan Degradation X (Mammalian, via Tryptamine)	0.70	0.04	ALDH2
Glycolysis I	0.70	0.04	PFKP
Ethanol Degradation IV	0.70	0.04	ALDH2
D-myo-inositol (1,4,5)-Trisphosphate Biosynthesis	0.67	0.04	PIP5K1A
CDK5 Signaling	0.66	0.02	GNAS,PRKAG2
Intrinsic Prothrombin Activation Pathway	0.65	0.03	F12
Sonic Hedgehog Signaling	0.63	0.03	PRKAG2
RAR Activation	0.63	0.02	VEGFA,NSD1,PRKAG2
G Protein Signaling Mediated by Tubby	0.61	0.03	GNAS
G1s Signaling	0.60	0.02	GNAS,PRKAG2
Amyotrophic Lateral Sclerosis Signaling	0.59	0.02	VEGFA,CAPN11
Androgen Signaling	0.59	0.02	GNAS,PRKAG2
Inhibition of Angiogenesis by TSP1	0.59	0.03	VEGFA
Role of JAK2 in Hormone-like Cytokine Signaling	0.59	0.03	SH2B3
Nitric Oxide Signaling in the Cardiovascular System	0.58	0.02	VEGFA,PRKAG2
Coagulation System	0.57	0.03	F12
Dopamine Degradation	0.57	0.03	ALDH2
HIF1i Signaling	0.57	0.02	VEGFA,ARNT
Ethanol Degradation II	0.55	0.03	ALDH2
Notch Signaling	0.54	0.03	APH1A
RhoA Signaling	0.54	0.02	RHPN2,PIP5K1A
Role of Tissue Factor in Cancer	0.54	0.02	VEGFA,RPS6KA4

Netrin Signaling	0.54	0.03	PRKAG2
tRNA Charging	0.54	0.03	TARS2
Neuroprotective Role of THOP1 in Alzheimer's Disease	0.53	0.03	PRKAG2
Noradrenaline and Adrenaline Degradation	0.53	0.03	ALDH2
PI3K/AKT Signaling	0.53	0.02	RHEB,MCL1
Sperm Motility	0.52	0.02	GNAS,PRKAG2
IL-6 Signaling	0.51	0.02	VEGFA,MCL1
UVC-Induced MAPK Signaling	0.51	0.02	ATR
GNRH Signaling	0.50	0.02	GNAS,PRKAG2
Cellular Effects of Sildenafil (Viagra)	0.50	0.02	GNAS,PRKAG2
Role of IL-17F in Allergic Inflammatory Airway Diseases	0.49	0.02	RPS6KA4
Cardiac I^2 -adrenergic Signaling	0.47	0.01	GNAS,PRKAG2
nNOS Signaling in Neurons	0.47	0.02	CAPN11
Cardiac Hypertrophy Signaling	0.47	0.01	EIF2B4,GNAS,PRKAG2
Aryl Hydrocarbon Receptor Signaling	0.46	0.01	ATR,ARNT
TNFR1 Signaling	0.45	0.02	MAP4K2
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	0.45	0.02	ATR
Cancer Drug Resistance By Drug Efflux	0.45	0.02	ABCG2
Insulin Receptor Signaling	0.45	0.01	EIF2B4,PRKAG2
Hereditary Breast Cancer Signaling	0.45	0.01	FAAP24,ATR
Ovarian Cancer Signaling	0.44	0.01	VEGFA,PRKAG2
Axonal Guidance Signaling	0.44	0.01	VEGFA,GNAS,PRKAG2,SEMA6C,EFNA1
Colorectal Cancer Metastasis Signaling	0.43	0.01	VEGFA,GNAS,PRKAG2
Phototransduction Pathway	0.43	0.02	PRKAG2
Role of CHK Proteins in Cell Cycle Checkpoint Control	0.41	0.02	ATR
Regulation of Cellular Mechanics by Calpain Protease	0.40	0.02	CAPN11
MSP-RON Signaling Pathway	0.39	0.02	F12
Hepatic Cholestasis	0.39	0.01	MAP4K2,PRKAG2
Ephrin A Signaling	0.39	0.02	EFNA1
Retinoic acid Mediated Apoptosis Signaling	0.38	0.02	DAP3
Dopamine-DARPP32 Feedback in cAMP Signaling	0.38	0.01	GNAS,PRKAG2
Molecular Mechanisms of Cancer	0.38	0.01	GNAS,APH1A,PRKAG2,ATR
CNTF Signaling	0.37	0.02	RPS6KA4
ERK5 Signaling	0.37	0.02	RPS6KA4
G-Protein Coupled Receptor Signaling	0.37	0.01	GNAS,PRKAG2,RGS14
Cell Cycle: G1/S Checkpoint Regulation	0.36	0.02	ATR
PXR/RXR Activation	0.36	0.02	PRKAG2
Pyridoxal 5'-phosphate Salvage Pathway	0.36	0.02	GRK6
Mitochondrial Dysfunction	0.35	0.01	APH1A,ATP5E
GABA Receptor Signaling	0.35	0.01	GNAS
RhoGDI Signaling	0.35	0.01	PIP5K1A,GNAS
Protein Kinase A Signaling	0.34	0.01	GNAS,PRKAG2,DUSP11,PTPN12
CCR5 Signaling in Macrophages	0.34	0.01	GNAS
PPAR γ /RXR γ Activation	0.33	0.01	GNAS,PRKAG2
Melatonin Signaling	0.33	0.01	PRKAG2
ErbB4 Signaling	0.33	0.01	APH1A
T Helper Cell Differentiation	0.32	0.01	BCL6
Ephrin B Signaling	0.32	0.01	GNAS
Serotonin Degradation	0.32	0.01	ALDH2
CREB Signaling in Neurons	0.32	0.01	GNAS,PRKAG2
BMP signaling pathway	0.31	0.01	PRKAG2
Dopamine Receptor Signaling	0.31	0.01	PRKAG2
Cyclins and Cell Cycle Regulation	0.30	0.01	ATR
Role of NFAT in Cardiac Hypertrophy	0.30	0.01	GNAS,PRKAG2
ATM Signaling	0.29	0.01	ATR
Growth Hormone Signaling	0.29	0.01	RPS6KA4
Clathrin-mediated Endocytosis Signaling	0.28	0.01	VEGFA,DAB2
IL-8 Signaling	0.28	0.01	VEGFA,GNAS
ERK/MAPK Signaling	0.28	0.01	PRKAG2,RPS6KA4
FLT3 Signaling in Hematopoietic Progenitor Cells	0.28	0.01	RPS6KA4
Leptin Signaling in Obesity	0.28	0.01	PRKAG2
HIPPO signaling	0.27	0.01	MOB1A
Breast Cancer Regulation by Stathmin1	0.27	0.01	GNAS,PRKAG2
Bladder Cancer Signaling	0.27	0.01	VEGFA
VEGF Family Ligand-Receptor Interactions	0.27	0.01	VEGFA
Regulation of Actin-based Motility by Rho	0.26	0.01	PIP5K1A
Fc γ Receptor-mediated Phagocytosis in Macrophages and Monocytes	0.25	0.01	PIP5K1A
Salvage Pathways of Pyrimidine Ribonucleotides	0.25	0.01	GRK6
TR/RXR Activation	0.24	0.01	PFKP
EIF2 Signaling	0.24	0.01	VEGFA,EIF2B4
FAK Signaling	0.23	0.01	CAPN11
cAMP-mediated signaling	0.23	0.01	GNAS,RGS14
UVA-Induced MAPK Signaling	0.23	0.01	RPS6KA4
Chronic Myeloid Leukemia Signaling	0.22	0.01	MECOM
SAPK/JNK Signaling	0.22	0.01	MAP4K2
IGF-1 Signaling	0.22	0.01	PRKAG2

Oxidative Phosphorylation	0.21	0.01	ATP5E
p53 Signaling	0.20	0.01	ATR
Paxillin Signaling	0.20	0.01	PTPN12

Supplemental table 7: Pathway analysis based on CKD candidate genes retrieved with 4C-seq in HRPTECs.

Ingenuity Canonical Pathways	-log(p-value)	Ratio	Molecules
Superpathway of Geranylgeranyldiphosphate Biosynthesis I (via Mevalonate)	3.14	0.18	FDP5,PMVK,IDI1
Trans, trans-farnesyl Diphosphate Biosynthesis	2.96	0.40	FDP5,IDI1
Role of BRCA1 in DNA Damage Response	2.83	0.06	FAAP24,UIMC1,ATR,BABAM2,SMARCD3
Superpathway of Cholesterol Biosynthesis	2.49	0.11	FDP5,PMVK,IDI1
Melanocyte Development and Pigmentation Signaling	2.46	0.05	SHC1,GNAS,FGFR4,PRKAG2,RPS6KA4
Ephrin A Signaling	2.42	0.07	FGFR4,EFNA3,EFNA4,EFNA1
Pathogenesis of Multiple Sclerosis	2.41	0.22	CXCL10,CXCL9
AMPK Signaling	2.37	0.04	GNAS,FGFR4,PRKAG2,PRKAA1,PFKP,SMARCD3,PPM1G
VEGF Signaling	2.31	0.05	VEGFA,SHC1,EIF2B4,FGFR4,ACTG2
eNOS Signaling	2.19	0.04	VEGFA,GNAS,HSP90AB1,FGFR4,PRKAG2,PRKAA1
Glycogen Degradation II	2.16	0.17	PYGM,PYGB
Nitric Oxide Signaling in the Cardiovascular System	2.14	0.04	VEGFA,HSP90AB1,FGFR4,PRKAG2,PRKAA1
Mevalonate Pathway I	2.09	0.15	PMVK,IDI1
GDNF Family Ligand-Receptor Interactions	2.05	0.05	SHC1,PDLM7,FGFR4,DOK3
Glycogen Degradation III	2.02	0.14	PYGM,PYGB
PI3K/AKT Signaling	1.97	0.04	SHC1,RHEB,HSP90AB1,NFKBIE,MCL1
Sorbitol Degradation I	1.97	1.00	SORD
Ephrin Receptor Signaling	1.96	0.03	VEGFA,SHC1,GNAS,EFNA3,EFNA4,EFNA1
Type II Diabetes Mellitus Signaling	1.93	0.04	PKLR,NFKBIE,FGFR4,PRKAG2,PRKAA1
IL-6 Signaling	1.93	0.04	VEGFA,SHC1,NFKBIE,FGFR4,MCL1
PPAR1/2/RXR1/2 Activation	1.91	0.03	SHC1,GNAS,HSP90AB1,NFKBIE,PRKAG2,PRKAA1
Extrinsic Prothrombin Activation Pathway	1.91	0.13	F12,THBD
1/2-Adrenergic Signaling	1.85	0.05	GNAS,PYGM,PRKAG2,PYGB
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	1.81	0.06	CKS1B,ATR,AURKA
Amyloid Processing	1.77	0.06	CAPN11,APH1A,PRKAG2
NRF2-mediated Oxidative Stress Response	1.76	0.03	ERP29,SOD2,FGFR4,MAF,CCT7,ACTG2
Prostate Cancer Signaling	1.74	0.04	HSP90AB1,NFKBIE,FGFR4,NKX3-1
mTOR Signaling	1.70	0.03	VEGFA,RHEB,FGFR4,PRKAG2,PRKAA1,RPS6KA4
Flavin Biosynthesis IV (Mammalian)	1.67	0.50	FLAD1
Glycine Degradation (Creatine Biosynthesis)	1.67	0.50	GATM
Axonal Guidance Signaling	1.64	0.02	VEGFA,SHC1,GNAS,ADAM15,FGFR4,EFNA3,PRKAG2,SEMA6C,EFNA4,EFNA1
Relaxin Signaling	1.63	0.03	VEGFA,GNAS,NFKBIE,FGFR4,PRKAG2
MSP-RON Signaling Pathway	1.60	0.05	F12,FGFR4,ACTG2
autophagy	1.58	0.05	CTSZ,CTSK,CTSS
G-Protein Coupled Receptor Signaling	1.57	0.03	SHC1,GNAS,NFKBIE,FGFR4,PRKAG2,DRD5,RGS14
Glycolysis I	1.54	0.08	PKLR,PFKP
Corticotropin Releasing Hormone Signaling	1.51	0.04	VEGFA,GNAS,UCN,PRKAG2
EIF2 Signaling	1.50	0.03	VEGFA,SHC1,EIF2B4,FGFR4,RPL37,ACTG2
Hypoxia Signaling in the Cardiovascular System	1.49	0.05	VEGFA,HSP90AB1,NFKBIE
Gap Junction Signaling	1.47	0.03	DBN1,GNAS,FGFR4,PRKAG2,ACTG2
Glucocorticoid Receptor Signaling	1.46	0.02	SHC1,HSP90AB1,NFKBIE,FGFR4,PRKAG2,PRKAA1,SMARCD3
Intrinsic Prothrombin Activation Pathway	1.42	0.07	F12,THBD
G1/2 Signaling	1.40	0.03	SHC1,GNAS,PRKAG2,RGS14
ErbB4 Signaling	1.38	0.04	SHC1,APH1A,FGFR4
Phenylethylamine Degradation I	1.38	0.25	ALDH2
Geranylgeranyldiphosphate Biosynthesis	1.38	0.25	FDP5
Molecular Mechanisms of Cancer	1.32	0.02	SHC1,GNAS,APH1A,NFKBIE,FGFR4,PRKAG2,ATR,AURKA
Cellular Effects of Sildenafil (Viagra)	1.30	0.03	SLC4A5,GNAS,PRKAG2,ACTG2
Role of JAK2 in Hormone-like Cytokine Signaling	1.30	0.06	SHC1,SH2B3
Erythropoietin Signaling	1.28	0.04	SHC1,NFKBIE,FGFR4
Coagulation System	1.27	0.06	F12,THBD
Growth Hormone Signaling	1.26	0.04	FGFR4,RPS6KA4,ONECUT1
ILK Signaling	1.23	0.03	VEGFA,FGFR4,MUC1,RPS6KA4,ACTG2
Small Cell Lung Cancer Signaling	1.22	0.04	NFKBIE,FGFR4,CKS1B
PEDF Signaling	1.22	0.04	SOD2,NFKBIE,FGFR4
ERK/MAPK Signaling	1.21	0.03	SHC1,FGFR4,PRKAG2,MAPKAPK5,RPS6KA4
FLT3 Signaling in Hematopoietic Progenitor Cells	1.20	0.04	SHC1,FGFR4,RPS6KA4
Insulin Receptor Signaling	1.19	0.03	SHC1,EIF2B4,FGFR4,PRKAG2
Hereditary Breast Cancer Signaling	1.18	0.03	FGFR4,FAAP24,ATR,SMARCD3
G Beta Gamma Signaling	1.17	0.03	SHC1,GNAS,PRKAG2
VEGF Family Ligand-Receptor Interactions	1.17	0.03	VEGFA,SHC1,FGFR4
Phagosome Maturation	1.17	0.03	CTSZ,CTSK,CTSS,STX16
Apoptosis Signaling	1.16	0.03	CAPN11,NFKBIE,MCL1
IL-1 Signaling	1.13	0.03	GNAS,NFKBIE,PRKAG2
Fc1/3 Receptor-mediated Phagocytosis in Macrophages and Monocytes	1.11	0.03	PIP5K1A,ACTG2,FYB
PPAR Signaling	1.11	0.03	SHC1,HSP90AB1,NFKBIE
Role of IL-17F in Allergic Inflammatory Airway Diseases	1.10	0.05	CXCL10,RPS6KA4
Superoxide Radicals Degradation	1.09	0.13	SOD2
Glycoaminoglycan-protein Linkage Region Biosynthesis	1.09	0.13	B4GALT7
CDK5 Signaling	1.05	0.03	GNAS,PRKAG2,DRD5
FAK Signaling	1.05	0.03	CAPN11,FGFR4,ACTG2
Hepatic Cholestasis	1.04	0.03	MAP4K2,NFKBIE,FGFR4,PRKAG2
TNFR1 Signaling	1.02	0.04	MAP4K2,NFKBIE
SAPK/JNK Signaling	1.00	0.03	MAP4K2,SHC1,FGFR4
IGF-1 Signaling	0.98	0.03	SHC1,FGFR4,PRKAG2
Fc1/RIIB Signaling in B Lymphocytes	0.96	0.04	SHC1,FGFR4
G1/2 Signaling	0.96	0.03	GNAS,PRKAG2,DRD5
Dolichyl-diphosphooligosaccharide Biosynthesis	0.95	0.09	DPM3
Amyotrophic Lateral Sclerosis Signaling	0.94	0.03	VEGFA,CAPN11,FGFR4
Androgen Signaling	0.94	0.03	SHC1,GNAS,PRKAG2
Telomerase Signaling	0.94	0.03	SHC1,HSP90AB1,FGFR4
Paxillin Signaling	0.92	0.03	FGFR4,ACTG2,PTPN12
Protein Kinase A Signaling	0.90	0.02	GNAS,PYGM,NFKBIE,PRKAG2,DUSP11,PYGB,PTPN12
NGF Signaling	0.89	0.03	SHC1,FGFR4,RPS6KA4
Assembly of RNA Polymerase III Complex	0.89	0.08	GTF3C2
CREB Signaling in Neurons	0.87	0.02	SHC1,GNAS,FGFR4,PRKAG2
B Cell Receptor Signaling	0.87	0.02	SHC1,NFKBIE,FGFR4,BCL6
Renin-Angiotensin Signaling	0.87	0.03	SHC1,FGFR4,PRKAG2
fMLP Signaling in Neutrophils	0.86	0.02	GNAS,NFKBIE,FGFR4
Phenylalanine Degradation IV (Mammalian, via Side Chain)	0.86	0.07	ALDH2
Activation of IRF by Cytosolic Pattern Recognition Receptors	0.85	0.03	NFKBIE,ADAR
iCOS-iCOSL Signaling in T Helper Cells	0.85	0.02	SHC1,NFKBIE,FGFR4

Role of Tissue Factor in Cancer	0.85	0.02	VEGFA,FGFR4,RPS6KA4
CNTF Signaling	0.84	0.03	FGFR4,RPS6KA4
RAR Activation	0.84	0.02	VEGFA,NSD1,PRKAG2,SMARCD3
IL-2 Signaling	0.83	0.03	SHC1,FGFR4
Role of NFAT in Cardiac Hypertrophy	0.83	0.02	SHC1,GNAS,FGFR4,PRKAG2
Thrombopoietin Signaling	0.82	0.03	SHC1,FGFR4
Pyridoxal 5'-phosphate Salvage Pathway	0.82	0.03	GRK6,PRKAA1
3-phosphoinositide Biosynthesis	0.82	0.02	PIP5K1A,FGFR4,DUSP11,PTPN12
Clathrin-mediated Endocytosis Signaling	0.80	0.02	VEGFA,FGFR4,DAB2,ACTG2
Role of IL-17A in Arthritis	0.80	0.03	NFKBIE,FGFR4
EGF Signaling	0.79	0.03	SHC1,FGFR4
Ubiquinol-10 Biosynthesis (Eukaryotic)	0.78	0.06	ECHDC1
Agrin Interactions at Neuromuscular Junction	0.78	0.03	PKLR,ACTG2
ErbB2-ErbB3 Signaling	0.78	0.03	SHC1,FGFR4
Myc Mediated Apoptosis Signaling	0.77	0.03	SHC1,FGFR4
Breast Cancer Regulation by Stathmin1	0.77	0.02	SHC1,GNAS,FGFR4,PRKAG2
Role of JAK1 and JAK3 in $\text{I}\kappa\text{B}$ Cytokine Signaling	0.76	0.03	SHC1,FGFR4
GPCR-Mediated Integration of Enteroendocrine Signaling Exemplified by an L Cell	0.75	0.03	GNAS,PRKAG2
GM-CSF Signaling	0.74	0.03	SHC1,FGFR4
GADD45 Signaling	0.74	0.05	ATR
Histamine Degradation	0.74	0.05	ALDH2
DNA damage-induced 14-3-3 β Signaling	0.74	0.05	ATR
IL-15 Signaling	0.71	0.03	SHC1,FGFR4
Role of PI3K/AKT Signaling in the Pathogenesis of Influenza	0.71	0.03	NFKBIE,FGFR4
Neurotrophin/TRK Signaling	0.71	0.03	SHC1,FGFR4
Angiopoietin Signaling	0.70	0.03	NFKBIE,FGFR4
IL-17A Signaling in Airway Cells	0.70	0.03	NFKBIE,FGFR4
Dopamine Receptor Signaling	0.70	0.03	PRKAG2,DRD5
Ovarian Cancer Signaling	0.70	0.02	VEGFA,FGFR4,PRKAG2
Maturity Onset Diabetes of Young (MODY) Signaling	0.70	0.05	PKLR
Oxidative Ethanol Degradation III	0.70	0.05	ALDH2
VDR/RXR Activation	0.70	0.03	CXCL10,THBD
CD40 Signaling	0.70	0.03	NFKBIE,FGFR4
Integrin Signaling	0.69	0.02	SHC1,CAPN11,FGFR4,ACTG2
Role of Lipids/Lipid Rafts in the Pathogenesis of Influenza	0.68	0.05	FDP5
Fatty Acid β -oxidation	0.68	0.05	ALDH2
Renal Cell Carcinoma Signaling	0.67	0.02	VEGFA,FGFR4
Th2 Pathway	0.67	0.02	APH1A,FGFR4,MAF
Putrescine Degradation III	0.66	0.04	ALDH2
IL-3 Signaling	0.66	0.02	SHC1,FGFR4
Prolactin Signaling	0.66	0.02	SHC1,FGFR4
JAK/Stat Signaling	0.66	0.02	SHC1,FGFR4
Actin Cytoskeleton Signaling	0.65	0.02	SHC1,PIP5K1A,FGFR4,ACTG2
IL-17 Signaling	0.64	0.02	CXCL10,FGFR4
Leptin Signaling in Obesity	0.64	0.02	FGFR4,PRKAG2
GPCR-Mediated Nutrient Sensing in Enteroendocrine Cells	0.64	0.02	GNAS,PRKAG2
Superpathway of Inositol Phosphate Compounds	0.64	0.02	PIP5K1A,FGFR4,DUSP11,PTPN12
LPS-stimulated MAPK Signaling	0.63	0.02	NFKBIE,FGFR4
NF- κ B Activation by Viruses	0.63	0.02	NFKBIE,FGFR4
Regulation of eIF4 and p70S6K Signaling	0.63	0.02	SHC1,EIF2B4,FGFR4
IL-17A Signaling in Gastric Cells	0.63	0.04	CXCL10
Tryptophan Degradation X (Mammalian, via Tryptamine)	0.63	0.04	ALDH2
Ethanol Degradation IV	0.63	0.04	ALDH2
Neuregulin Signaling	0.62	0.02	SHC1,HSP90AB1
Cardiac Hypertrophy Signaling	0.62	0.02	EIF2B4,GNAS,FGFR4,PRKAG2
G1zq Signaling	0.61	0.02	GNAS,NFKBIE,FGFR4
IL-4 Signaling	0.61	0.02	SHC1,FGFR4
Dopamine-DARPP32 Feedback in cAMP Signaling	0.60	0.02	GNAS,PRKAG2,DRD5
PDGF Signaling	0.60	0.02	SHC1,FGFR4
D-myo-inositol (1,4,5)-Trisphosphate Biosynthesis	0.60	0.04	PIP5K1A
Regulation of Actin-based Motility by Rho	0.60	0.02	PIP5K1A,ACTG2
Huntington's Disease Signaling	0.59	0.02	SHC1,CAPN11,FGFR4,STX16
Death Receptor Signaling	0.59	0.02	NFKBIE,ACTG2
Aldosterone Signaling in Epithelial Cells	0.59	0.02	PIP5K1A,HSP90AB1,FGFR4
Tight Junction Signaling	0.58	0.02	PRKAG2,STX16,ACTG2
TNFR2 Signaling	0.57	0.03	NFKBIE
Glutathione-mediated Detoxification	0.57	0.03	NAT8
Salvage Pathways of Pyrimidine Ribonucleotides	0.57	0.02	GRK6,PRKAA1
Acute Phase Response Signaling	0.57	0.02	SHC1,SOD2,NFKBIE
Colorectal Cancer Metastasis Signaling	0.57	0.02	VEGFA,GNAS,FGFR4,PRKAG2
Signaling by Rho Family GTPases	0.57	0.02	PIP5K1A,GNAS,FGFR4,ACTG2
Tec Kinase Signaling	0.57	0.02	GNAS,FGFR4,ACTG2
Mitochondrial Dysfunction	0.56	0.02	SOD2,APH1A,ATP5E
Sonic Hedgehog Signaling	0.56	0.03	PRKAG2
RhoGDI Signaling	0.55	0.02	PIP5K1A,GNAS,ACTG2
TR/RXR Activation	0.55	0.02	FGFR4,PKP
ErbB Signaling	0.55	0.02	SHC1,FGFR4
4-1BB Signaling in T Lymphocytes	0.55	0.03	NFKBIE
G Protein Signaling Mediated by Tubby	0.54	0.03	GNAS
PAK Signaling	0.53	0.02	SHC1,FGFR4
RANK Signaling in Osteoclasts	0.53	0.02	NFKBIE,FGFR4
Sertoli Cell-Sertoli Cell Junction Signaling	0.53	0.02	TJAP1,PRKAG2,ACTG2
Virus Entry via Endocytic Pathways	0.53	0.02	FGFR4,ACTG2
UVA-Induced MAPK Signaling	0.53	0.02	FGFR4,RPS6KA4
MIF-mediated Glucocorticoid Regulation	0.53	0.03	NFKBIE
Chronic Myeloid Leukemia Signaling	0.52	0.02	MECOM,FGFR4
Oncostatin M Signaling	0.52	0.03	SHC1
TWEAK Signaling	0.52	0.03	NFKBIE
Inhibition of Angiogenesis by TSP1	0.52	0.03	VEGFA
IL-17A Signaling in Fibroblasts	0.51	0.03	NFKBIE
Dopamine Degradation	0.51	0.03	ALDH2
Role of NFAT in Regulation of the Immune Response	0.50	0.02	GNAS,NFKBIE,FGFR4
Th1 and Th2 Activation Pathway	0.50	0.02	APH1A,FGFR4,MAF
Endothelin-1 Signaling	0.49	0.02	SHC1,GNAS,FGFR4
Agranulocyte Adhesion and Diapedesis	0.49	0.02	CXCL10,ACTG2,CXCL9

Regulation of the Epithelial-Mesenchymal Transition Pathway	0.49	0.02	PYGO2,APH1A,FGFR4
Ethanol Degradation II	0.49	0.03	ALDH2
Glioma Signaling	0.49	0.02	SHC1,FGFR4
p53 Signaling	0.48	0.02	FGFR4,ATR
April Mediated Signaling	0.48	0.03	NFKBIE
Notch Signaling	0.48	0.03	APH1A
Netrin Signaling	0.47	0.03	PRKAG2
tRNA Charging	0.47	0.03	TARS2
Neuropathic Pain Signaling In Dorsal Horn Neurons	0.47	0.02	FGFR4,PRKAG2
HIF1 α Signaling	0.46	0.02	VEGFA,FGFR4
Role of PKR in Interferon Induction and Antiviral Response	0.46	0.03	NFKBIE
B Cell Activating Factor Signaling	0.46	0.03	NFKBIE
Thyroid Cancer Signaling	0.46	0.03	SHC1
Neuroprotective Role of THOP1 in Alzheimer's Disease	0.46	0.03	PRKAG2
Transcriptional Regulatory Network in Embryonic Stem Cells	0.46	0.03	ONECUT1
Noradrenaline and Adrenaline Degradation	0.46	0.03	ALDH2
IL-8 Signaling	0.46	0.02	VEGFA,GNAS,FGFR4
Rac Signaling	0.45	0.02	PIP5K1A,FGFR4
p38 MAPK Signaling	0.45	0.02	MAPKAPK5,RPS6KA4
MIF Regulation of Innate Immunity	0.45	0.02	NFKBIE
Mechanisms of Viral Exit from Host Cells	0.45	0.02	ACTG2
Pancreatic Adenocarcinoma Signaling	0.45	0.02	VEGFA,FGFR4
PTEN Signaling	0.44	0.02	SHC1,FGFR4
UVC-Induced MAPK Signaling	0.44	0.02	ATR
Thrombin Signaling	0.44	0.01	SHC1,GNAS,FGFR4
Role of RIG1-like Receptors in Antiviral Innate Immunity	0.43	0.02	NFKBIE
Role of Hypercytokinemia/hyperchemokinememia in the Pathogenesis of Influenza	0.43	0.02	CXCL10
Pyrimidine Ribonucleotides Interconversion	0.43	0.02	ENTPD6
Role of p14/p19ARF in Tumor Suppression	0.43	0.02	FGFR4
Natural Killer Cell Signaling	0.43	0.02	SHC1,FGFR4
Role of NANOG in Mammalian Embryonic Stem Cell Pluripotency	0.43	0.02	SHC1,FGFR4
RhoA Signaling	0.43	0.02	PIP5K1A,ACTG2
iNOS Signaling	0.43	0.02	NFKBIE
IL-9 Signaling	0.42	0.02	FGFR4
Pyrimidine Ribonucleotides De Novo Biosynthesis	0.42	0.02	ENTPD6
Sperm Motility	0.41	0.02	GNAS,PRKAG2
FXR/RXR Activation	0.41	0.02	PKLR,FGFR4
nNOS Signaling in Neurons	0.40	0.02	CAPN11
GNRH Signaling	0.40	0.02	GNAS,PRKAG2
CCR3 Signaling in Eosinophils	0.39	0.02	GNAS,FGFR4
Gl α 12/13 Signaling	0.39	0.02	NFKBIE,FGFR4
CD28 Signaling in T Helper Cells	0.39	0.02	NFKBIE,FGFR4
p70S6K Signaling	0.39	0.02	SHC1,FGFR4
PKC δ Signaling in T Lymphocytes	0.39	0.02	NFKBIE,FGFR4
P2Y Purigenic Receptor Signaling Pathway	0.39	0.02	FGFR4,PRKAG2
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	0.38	0.01	VEGFA,NFKBIE,FGFR4,CEBPG
Adipogenesis pathway	0.38	0.01	FGFR4,SETDB1
Th1 Pathway	0.37	0.01	APH1A,FGFR4
cAMP-mediated signaling	0.37	0.01	GNAS,DRD5,RGS14
CD27 Signaling in Lymphocytes	0.37	0.02	NFKBIE
Docosahexaenoic Acid (DHA) Signaling	0.37	0.02	FGFR4
Cardiac P β -adrenergic Signaling	0.37	0.01	GNAS,PRKAG2
Systemic Lupus Erythematosus Signaling	0.37	0.01	PRPF3,FGFR4,PRPF40A
Phototransduction Pathway	0.36	0.02	PRKAG2
Unfolded protein response	0.36	0.02	CEBPG
Aryl Hydrocarbon Receptor Signaling	0.36	0.01	HSP90AB1,ATR
D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis	0.35	0.01	DUSP11,PTPN12
D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis	0.35	0.01	DUSP11,PTPN12
Role of CHK Proteins in Cell Cycle Checkpoint Control	0.35	0.02	ATR
Melanoma Signaling	0.35	0.02	FGFR4
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	0.35	0.01	CTSK,NFKBIE,FGFR4
Human Embryonic Stem Cell Pluripotency	0.35	0.01	GNAS,FGFR4
Regulation of Cellular Mechanics by Calpain Protease	0.34	0.02	CAPN11
IL-12 Signaling and Production in Macrophages	0.34	0.01	FGFR4,MAF
Chondroitin Sulfate Biosynthesis	0.33	0.02	B4GALT7
Induction of Apoptosis by HIV1	0.32	0.02	NFKBIE
Retinoic acid Mediated Apoptosis Signaling	0.32	0.02	DAP3
Dermatan Sulfate Biosynthesis	0.32	0.02	B4GALT7
ERK5 Signaling	0.31	0.02	RPS6KA4
3-phosphoinositide Degradation	0.31	0.01	DUSP11,PTPN12
Endometrial Cancer Signaling	0.30	0.02	FGFR4
Cell Cycle: G1/S Checkpoint Regulation	0.30	0.02	ATR
PXR/RXR Activation	0.30	0.02	PRKAG2
Glioblastoma Multiforme Signaling	0.30	0.01	SHC1,FGFR4
D-myo-inositol-5-phosphate Metabolism	0.30	0.01	DUSP11,PTPN12
Mitotic Roles of Polo-Like Kinase	0.30	0.02	HSP90AB1
UVB-Induced MAPK Signaling	0.30	0.02	FGFR4
Protein Ubiquitination Pathway	0.29	0.01	PSMB4,HSP90AB1,PSMD4
Lymphotoxin I β Receptor Signaling	0.29	0.01	FGFR4
GABA Receptor Signaling	0.29	0.01	GNAS
IL-10 Signaling	0.29	0.01	NFKBIE
Remodeling of Epithelial Adherens Junctions	0.29	0.01	ACTG2
CCR5 Signaling in Macrophages	0.28	0.01	GNAS
CXCR4 Signaling	0.28	0.01	GNAS,FGFR4
Glioma Invasiveness Signaling	0.28	0.01	FGFR4
Caveolar-mediated Endocytosis Signaling	0.27	0.01	ACTG2
Melatonin Signaling	0.27	0.01	PRKAG2
Role of MAPK Signaling in the Pathogenesis of Influenza	0.27	0.01	CXCL10
T Helper Cell Differentiation	0.27	0.01	BCL6
Ephrin B Signaling	0.27	0.01	GNAS
STAT3 Pathway	0.27	0.01	FGFR4
Serotonin Degradation	0.26	0.01	ALDH2
Germ Cell-Sertoli Cell Junction Signaling	0.26	0.01	FGFR4,ACTG2
Antiproliferative Role of Somatostatin Receptor 2	0.26	0.01	FGFR4
BMP signaling pathway	0.25	0.01	PRKAG2

Non-Small Cell Lung Cancer Signaling	0.25	0.01	FGFR4
Estrogen-Dependent Breast Cancer Signaling	0.25	0.01	FGFR4
Granulocyte Adhesion and Diapedesis	0.25	0.01	CXCL10,CXCL9
Cyclins and Cell Cycle Regulation	0.25	0.01	ATR
Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes	0.24	0.01	NFKBIE
NF- κ B Signaling	0.24	0.01	NFKBIE,FGFR4
ATM Signaling	0.24	0.01	ATR
Heparan Sulfate Biosynthesis	0.24	0.01	B4GALT7
Macropinocytosis Signaling	0.24	0.01	FGFR4
Hepatic Fibrosis / Hepatic Stellate Cell Activation	0.24	0.01	VEGFA,CXCL9
Bladder Cancer Signaling	0.22	0.01	VEGFA
HER-2 Signaling in Breast Cancer	0.21	0.01	FGFR4
Communication between Innate and Adaptive Immune Cells	0.21	0.01	CXCL10
Crosstalk between Dendritic Cells and Natural Killer Cells	0.21	0.01	ACTG2
OX40 Signaling Pathway	0.21	0.01	NFKBIE
FGF Signaling	0.21	0.01	FGFR4
Acute Myeloid Leukemia Signaling	0.21	0.01	FGFR4
Reelin Signaling in Neurons	0.20	0.01	FGFR4
Ceramide Signaling	0.20	0.01	FGFR4

Supplemental table 8: Primer design for CKD susceptibility loci that colocalize with active DREs.

SNP ID	Location	Gene	Forward primer	Reversed primer
rs2049805	intron	GBAP1	CTACACGACGCTCTCCGATCTAGCAATGAGCAAGTCCCTGATC	CAGACGTGTGCTCTTCCGATCATAACTGCCATTAAGCCATT
rs267734	non-coding		CTACACGACGCTCTTCCGATCTAGTTCAGAAGCGAGCCAAGATC	CAGACGTGTGCTCTTCCGATCAGATACCTACTCAGGGGAGC
rs11123170	intron	PAX8	CTACACGACGCTCTTCCGATCTAGGCCTAACCTACTCAGTGATC	CAGACGTGTGCTCTTCCGATCCACCTTTGAATTCCTAAAAGA
rs1260326	exon	GCKR	CTACACGACGCTCTTCCGATCTAGTCCCAATGCAGTCTTTGATC	CAGACGTGTGCTCTTCCGATCGTGGGAATACATTCTGGAAA
rs13538	exon	NAT8	CTACACGACGCTCTTCCGATCTAGCCTCTTCTGTTGGCTCAGATC	CAGACGTGTGCTCTTCCGATCTTTGGTAAAAAGAGACCCTG
rs16853722	intron	MECOM	CTACACGACGCTCTTCCGATCTAGTAAGGAACTCAAACCGGATC	CAGACGTGTGCTCTTCCGATCAGCTGTGTGAATCATAAAGTCA
rs13069000	non-coding		CTACACGACGCTCTTCCGATCTAGCTTGAGGAATTTGTTGATC	CAGACGTGTGCTCTTCCGATCTCCAGGTTATCATGGCTAAT
rs10937329	non-coding		CTACACGACGCTCTTCCGATCTAGTACATTTCTGGCTTTGGATC	CAGACGTGTGCTCTTCCGATCCACCATTCTTAAAAACGAG
rs347685	intron	TFDP2	CTACACGACGCTCTTCCGATCTAGTAACTGTAGGAAAAAGATC	CAGACGTGTGCTCTTCCGATCGATACTGCTGGTTCTCTGTGT
rs13146355	intron	SHROOM3	CTACACGACGCTCTTCCGATCTAGAGCAAAGCGGGCCTAAGATC	CAGACGTGTGCTCTTCCGATCTGAATGACTGGTTGATTGAA
rs2775948	intron	SLC2A9	CTACACGACGCTCTTCCGATCTAGCTTACACATATCATTGGATC	CAGACGTGTGCTCTTCCGATCATAGCTGTGTGATCGGAGC
rs2725220	intron	PKD2	CTACACGACGCTCTTCCGATCTAGAACAGAAACAGAGCAGATC	CAGACGTGTGCTCTTCCGATCGGAACGAGTTGTAGCAACAT
rs17319721	intron	SHROOM3	CTACACGACGCTCTTCCGATCTAGTATTCTATCCATTCAAGATC	CAGACGTGTGCTCTTCCGATCACCAGCAGAAATAAAAACA
rs11959928	intron	DAB2	CTACACGACGCTCTTCCGATCTAGCAAAATCCAAGTTAGAGATC	CAGACGTGTGCTCTTCCGATCTAAAGTTGGTTGGCACTTCT
rs6420904	intron	SLC34A1	CTACACGACGCTCTTCCGATCTAGACTCTGACCTGTCAAAGATC	CAGACGTGTGCTCTTCCGATCTAAAATGTGTGATCGGCTAAT
rs1936800	non-coding		CTACACGACGCTCTTCCGATCTAGTCAAACCATGCTTTAAGATC	CAGACGTGTGCTCTTCCGATCTGACAGAAATGAACCTGGACA
rs9397738	non-coding		CTACACGACGCTCTTCCGATCTAGCTCCATTAAACATTTTGGATC	CAGACGTGTGCTCTTCCGATCACTCCAGTGTAAGAGGGGTT
rs881858	non-coding		CTACACGACGCTCTTCCGATCTAGGGACATATGCCAAAGATC	CAGACGTGTGCTCTTCCGATCGTCTAAGTCTGACAGTGGG
rs2279463	intron	SLC22A2	CTACACGACGCTCTTCCGATCTAGACTTATATGACTGCTAAGATC	CAGACGTGTGCTCTTCCGATCTAAAATGTGTGATCGGCTAAT
rs10277115	non-coding		CTACACGACGCTCTTCCGATCTAGCTCTGGGACGCTGTGTGATC	CAGACGTGTGCTCTTCCGATCATGCACCTTCATTTCAAACA
rs6465825	non-coding		CTACACGACGCTCTTCCGATCTTAGGTGTGGTAGAATAGATC	CAGACGTGTGCTCTTCCGATCGAAGCACTGTAGCAGATTCC
rs7805747	intron	PRKAG2	CTACACGACGCTCTTCCGATCTCCAGGAAGACACCGAGATC	CAGACGTGTGCTCTTCCGATCTTCTCTGTGCTGCATATCTG
rs10109414	non-coding		CTACACGACGCTCTTCCGATCTGGATTAGGAAGGGCATGATC	CAGACGTGTGCTCTTCCGATCACTACTGAGCCTAAGGAAAA
rs4744712	intron	PIP5K1B	CTACACGACGCTCTTCCGATCTTTAAGAGGGACTTACGATC	CAGACGTGTGCTCTTCCGATCTCTCAAAGAAATGCAGAAAA
rs10794720	intron	WDR37	CTACACGACGCTCTTCCGATCTCCAGGCTGCCATAAAGATC	CAGACGTGTGCTCTTCCGATCGTGCTTTCTCAAGCTTTTGG
rs504915	intron	NRXN2	CTACACGACGCTCTTCCGATCTGCAGCCTTGCTCTCAGGATC	CAGACGTGTGCTCTTCCGATCTAGGAGAGAGCTTTCCTTGG
rs10774021	intron	SLC6A13	CTACACGACGCTCTTCCGATCTTTTGAAACATAGCAGAGATC	CAGACGTGTGCTCTTCCGATCACCTCGTCTTCTCTTTACC
rs653178	intron	ATXN2	CTACACGACGCTCTTCCGATCTTCAAGTCTCTCCCAACGATC	CAGACGTGTGCTCTTCCGATCTCCTCAGCCATACTAATCGT
rs626277	intron	DACH1	CTACACGACGCTCTTCCGATCTGCTTATTTGAAAGTTATGATC	CAGACGTGTGCTCTTCCGATCTTAATCATTTTGCAGATTGT
rs2453533	non-coding		CTACACGACGCTCTTCCGATCTCCAGCAATGATTATCTGATC	CAGACGTGTGCTCTTCCGATCTCAAACCATACCTAAGGAG
rs17730281	exon	WDR72	CTACACGACGCTCTTCCGATCTCTCTGCTGTTTGATGAGATC	CAGACGTGTGCTCTTCCGATCTGACAAAATCTAGCAGGAAA
rs17730436	intron	WDR72	CTACACGACGCTCTTCCGATCTGGTAGTCTACAAGCTTGATC	CAGACGTGTGCTCTTCCGATCACGCAGAGTTGAGTAGGTGT
rs889472	non-coding		CTACACGACGCTCTTCCGATCTACAGTGTGAATCCTTAGATC	CAGACGTGTGCTCTTCCGATCCATGCCTGGATTACATCTT
rs11868441	intron	BCAS3	CTACACGACGCTCTTCCGATCTTGGGACGACTACAAGAGATC	CAGACGTGTGCTCTTCCGATCGGCCCTAGTAAATGGAAAAT
rs9895661	intron	BCAS3	CTACACGACGCTCTTCCGATCTTCCCTTCCCACTGGAGGATC	CAGACGTGTGCTCTTCCGATCACTCTCCTCTTCTCGTGTA
rs7227483	intron	SLC14A2	CTACACGACGCTCTTCCGATCTAGTGGCTCTTATGGTAGATC	CAGACGTGTGCTCTTCCGATCTGCAAGGAATGCTAAGAAAAT
rs12460876	intron	SLC7A9	CTACACGACGCTCTTCCGATCTAAAAGCGTTTTGGCTAGATC	CAGACGTGTGCTCTTCCGATCACCAGATGGGTCTAAAAGGAT
rs6026584	intron	GNAS	CTACACGACGCTCTTCCGATCTACGTAATATTTAGCAGGATC	CAGACGTGTGCTCTTCCGATCATGGAGGCATGTGTTCTAC
rs911119	intron	CST3	CTACACGACGCTCTTCCGATCTCCAGATTTAGGACTGAGATC	CAGACGTGTGCTCTTCCGATCGGTACGGGATATTTCCAAGT