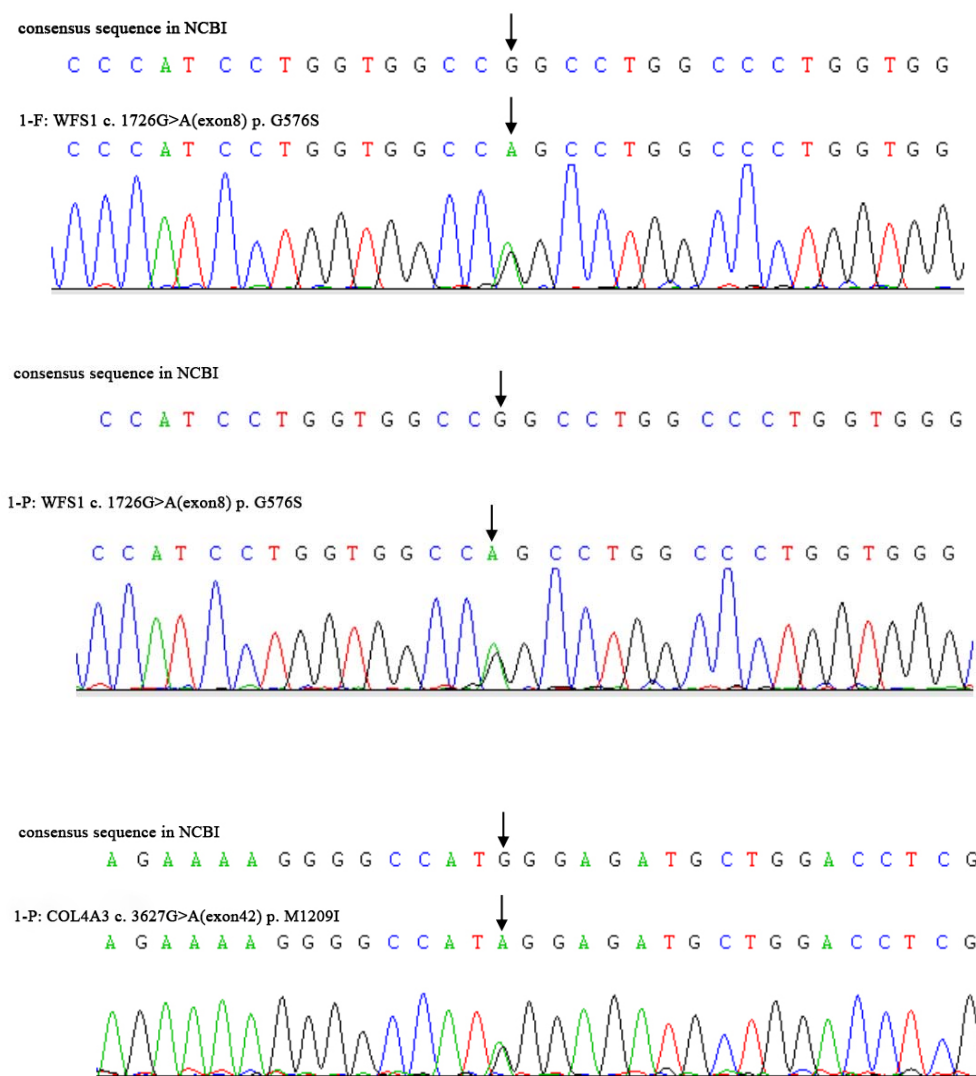
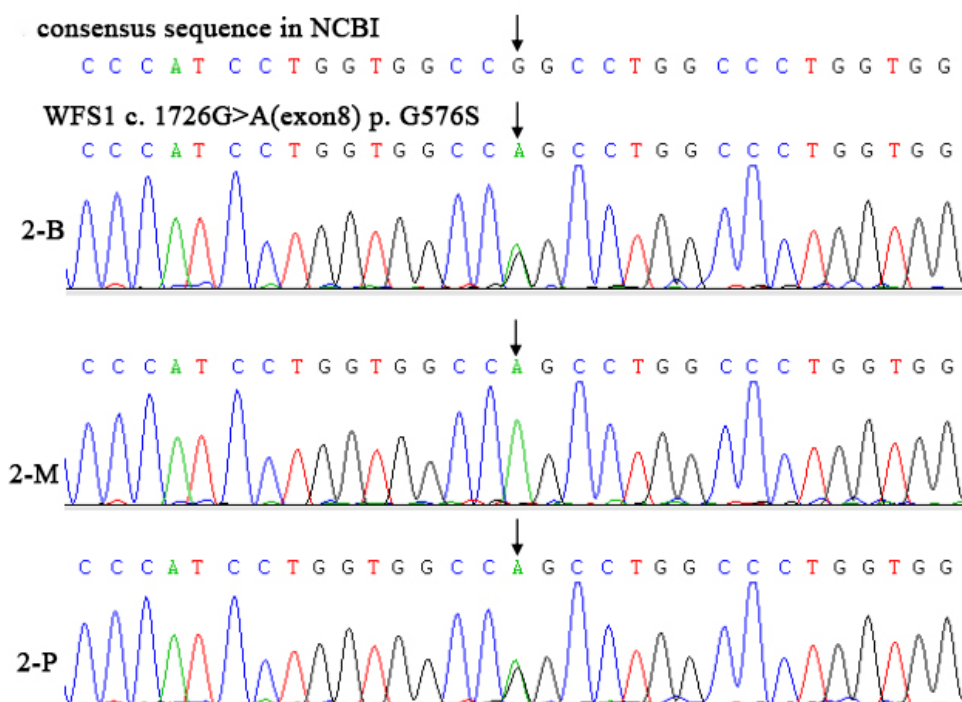


Family 1



Family 2



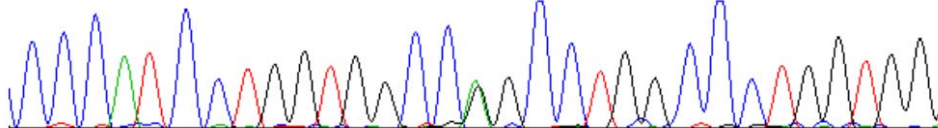
Family 3

consensus sequence in NCBI

C C C A T C C T G G T G G C C G G C C T G G C C C T G G T G G

3-P: WFS1 c. 1726G>A p.G576S

C C C A T C C T G G T G G C C A G C C T G G C C C T G G T G G

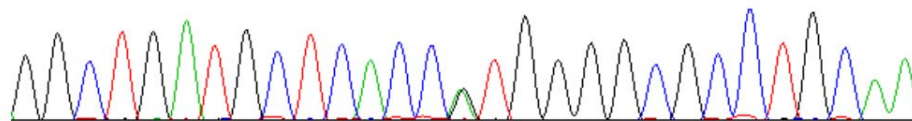


consensus sequence in NCBI

G G C T G A T G C T C A C C A T G G G G C G C C T G C A A

3-P: CEL c.10A>G(exon1) p.M4V

G G C T G A T G C T C A C C G T G G G G C G C C T G C A A

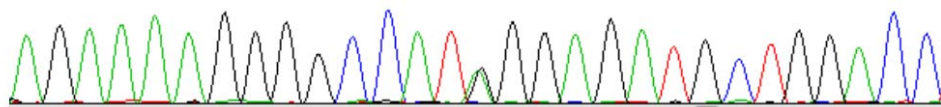


consensus sequence in NCBI

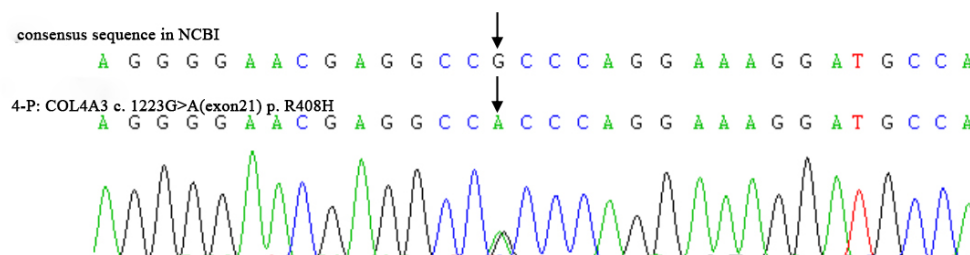
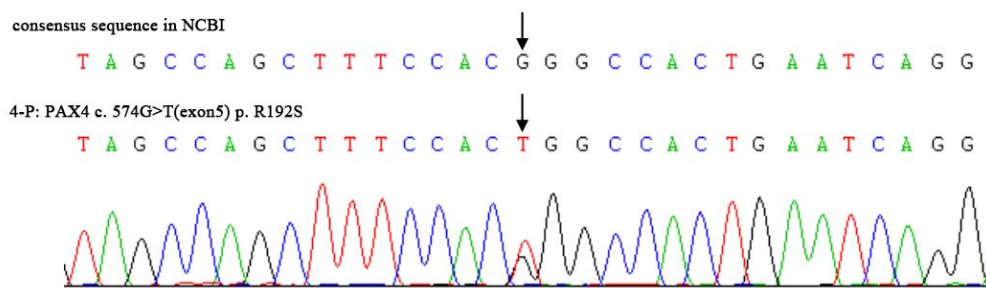
A G A A A A G G G G C C A T G G G A G A T G C T G G A C C

3-P: COL4A3 c.3627G>A(exon42) p.M1209I

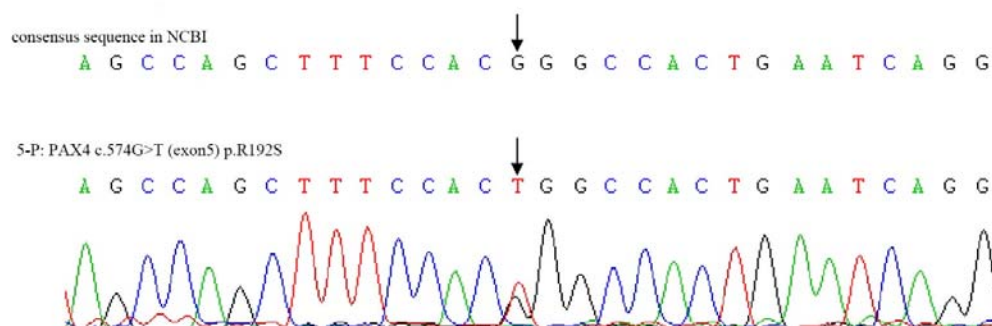
A G A A A A G G G G C C A T A G G A G A T G C T G G A C C



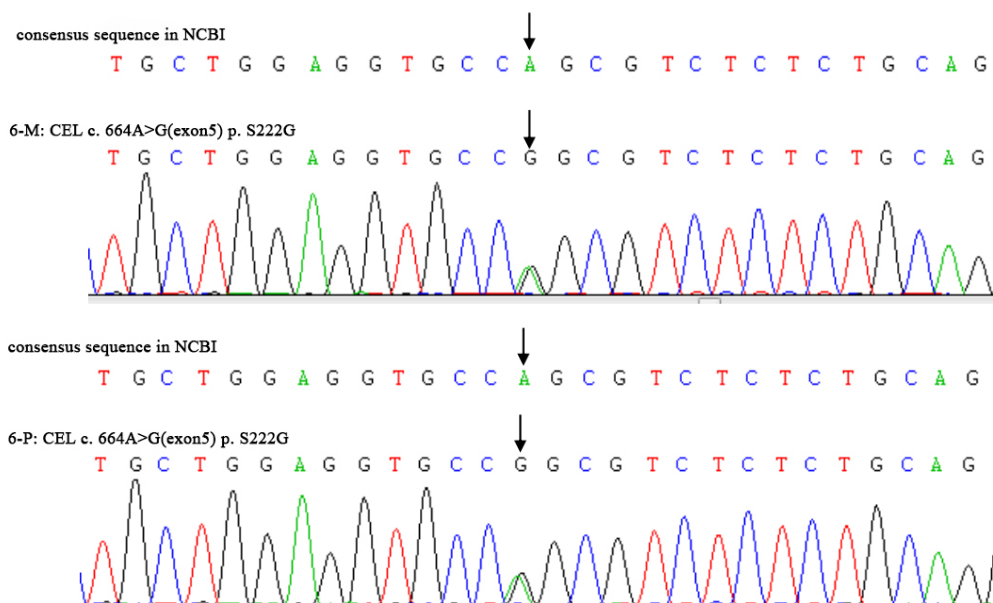
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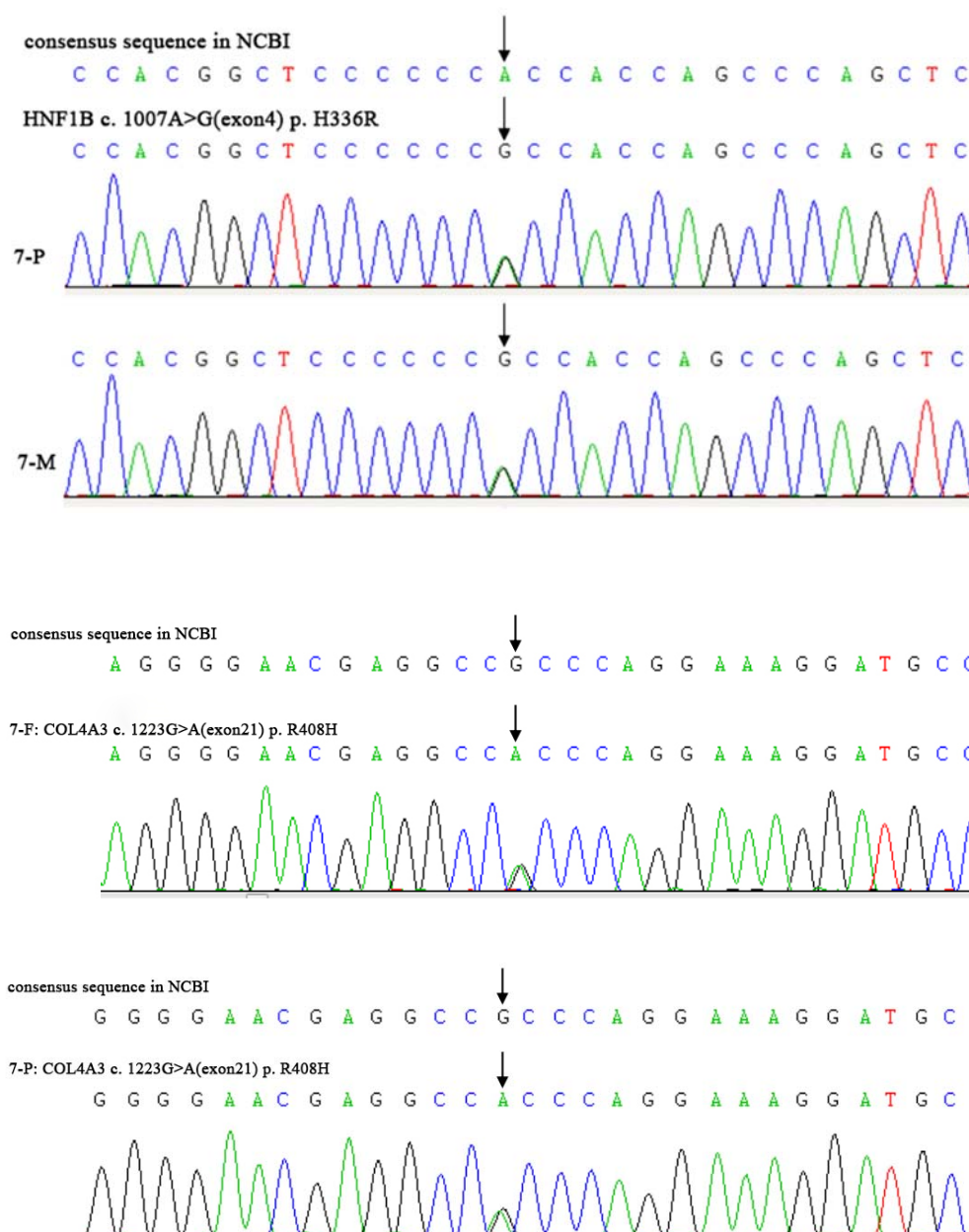
Family 5



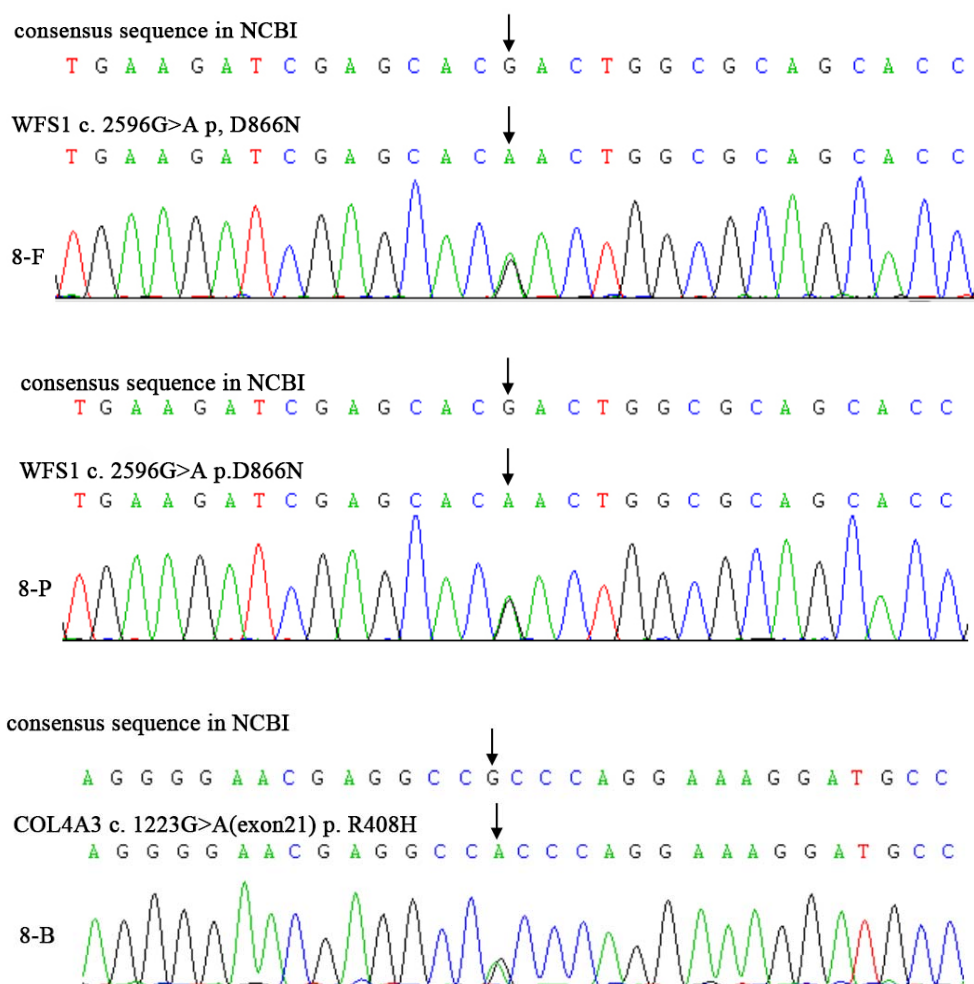
Family 6



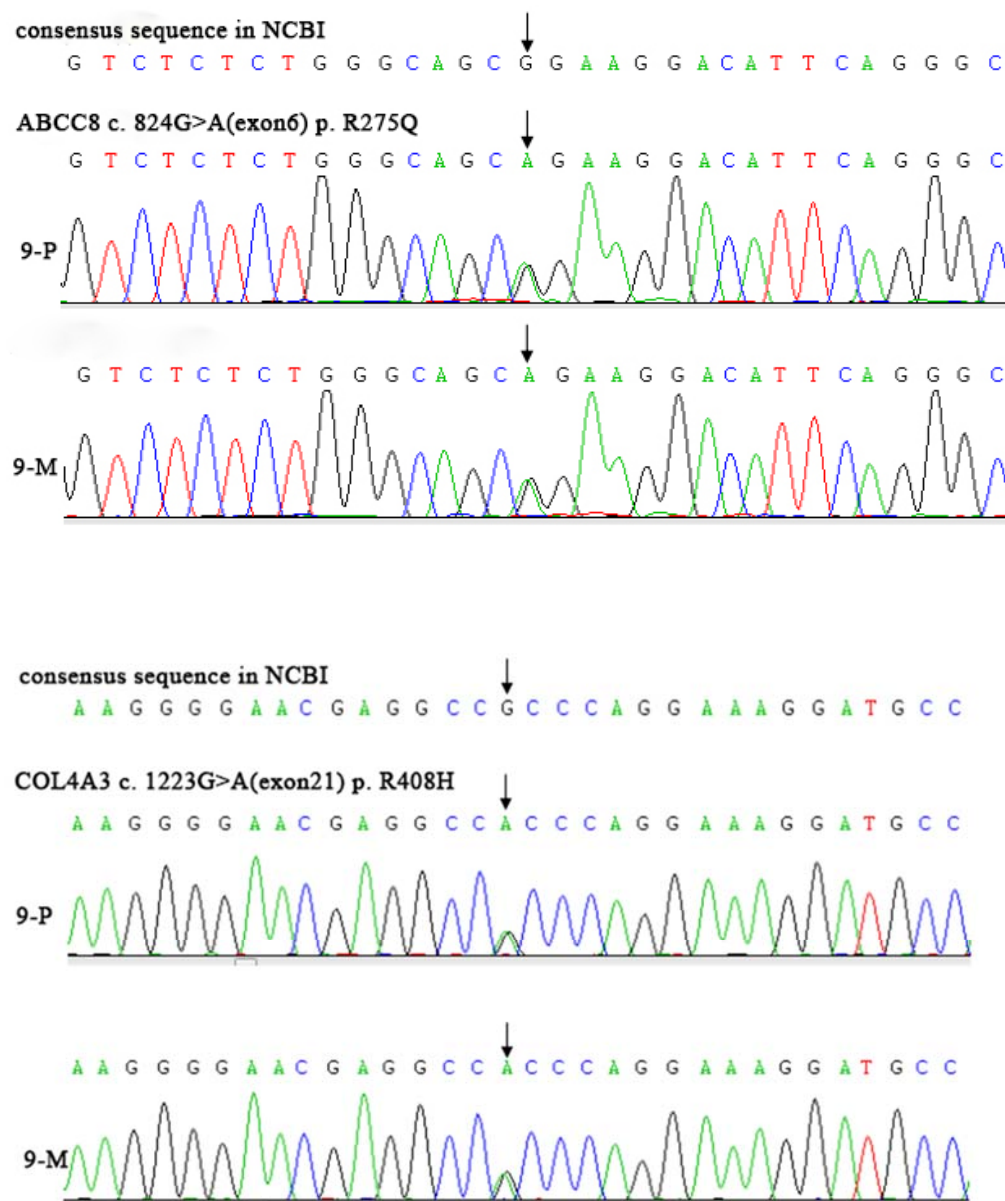
Family 7



Family 8



Family 9



Supplemental Table 1. Genetic variants associated with diabetic kidney diseases.

Gene	SNP ID	Diabetes type	Reference	Function
ACACB	rs2268388	T2D	[1]	Lipid metabolism process
ACE	rs179975	Total	[2]	Renin angiotensin system pathway
ACE	rs4344	T1D	[1]	
ACE	rs4646994	T2D	[1]	Metabolic and hormonal processes
ADIPOQ	rs17300539	Total	[2]	
AFF3	rs7588550	T1D	[3]	
AFF3	rs7583877	T1D	[3]	
AFF3	rs7562121	T1D	[4]	ACE Inhibitor Pathway and IL-6 Signaling Pathway
AGT	rs699	T2D	[2]	
AGTR1	rs5186	T1D	[2]	
AGTR1	rs12695897	T2D	[5]	Angiotensin type II receptor activity
AKRIB1	CA repeat	T1D	[2]	Glucose metabolic process
AKRIB1	rs759853	T1D	[2]	
ANP	C708T	T1D	[6]	Controlling electrolyte homeostasis
APOA	-	T2D	[7]	Lipid metabolism process
APOC1	rs4420638	Total	[2]	Lipid metabolism process
APOE	E2/3/4	Total	[2]	Lipid metabolism process
APOE	rs429358	Total	[8]	
APOE	rs7412	Total	[8]	
APOL3	rs16996381	T2D	[5]	Lipid metabolism process
AUH	rs773506	T2D	[5]	Amino acid metabolism process

C12orf66/TMEM5	rs11175885	T2D	[5]	Glycosyltransferase function
C6orf167	rs11175885	T2D	[5]	Na
C6orf191/ARHGA P18	rs208865	T2D	[5]	Gtpase-activating proteins that modulate cell signaling
CALD1	rs3807337	T1D	[9]	Smooth muscle relaxation and contraction pathways
CARS	rs451041	T2D	[10]	Trna aminoacylation and gene expression
CARS	rs739401	T2D	[10]	
CARS	rs17353856	T2D	[10]	
CATALASE	rs35448603	Total	[10]	Metabolism and immune system
CCL2	rs1024611	T2D	[11]	AGE-RAGE signaling pathway in diabetic complications and immune system
CCL2	rs3917887	T2D	[11]	
CCR5	rs2107538	Total	[11]	Signaling by GPCR and peptide ligand-binding receptors
CCR5	rs9898132	Total	[11]	
CCR5	rs2280788	Total	[11]	
CCR5	rs1799987	Total	[2]	
CDKAL1	rs7754840	T2D	[12]	Na
CDKN2A/B	rs10811661	T2D	[13]	Glioma and HTLV-I infection
CD2AP	rs11613959 7	T2D	[5]	Signaling events mediated by VEGFR1 and VEGFR2
CHN2	rs2057737	T2D	[5]	Cell proliferation and migration
CHN2	rs3729621	T2D	[5]	
CHN2	rs3793313	T2D	[5]	
CLDN8	rs55884670	T2D	[14]	Blood-Brain barrier and

				immune cell transmigration
CNDP1	D18S880	T2D	[2]	Arginine and proline metabolism and metabolism
CNDP1	rs4892249	T2D	[5]	
CNDP1	rs6566815	T2D	[5]	
CNTNAP2	rs1989248	T1D	[4]	Neuroscience and cell adhesion molecules (cams).
COL4A3	rs55816283	T2D	[14]	Collagen biosynthesis and modifying enzymes and RET signaling
COL4A3	rs34505188	T2D	[14]	
CLDN14	rs140918123	T2D	[14]	Tight junction and cytoskeleton remodeling
COX6A1	rs12310837	T1D	[3]	Metabolism and cardiac muscle contraction
CPVL/CHN2	rs39059	T2D	[10]	Serine-type carboxypeptidase activity
CPVL/CHN2	rs39075	T2D	[10]	
CUBN	rs1801239	T1D	[15]	Vitamin digestion and absorption and metabolism
CYBA	rs4673	T2D	[10]	Immune system and blood-brain barrier and immune cell transmigration
CYP11B2	344 T/C	Total	[16]	Metabolism of steroid hormones
ELMO1	rs741301	T2D	[1]	Immune system and HIV life cycle
ELMO1	rs12310837	T2D	[3]	
ELMO1	rs10951509	T2D	[3]	
ELMO1	rs11769038	T1D	[1]	
ELMO1	rs1882080	T2D	[5]	
ELMO1	rs2041801	T2D	[5]	
ELMO1	rs7785934	T2D	[5]	

EMP2	rs73503834	T2D	[14]	Protein kinase binding and kinase binding
ENPP1	rs7754586	T2D	[1]	Metabolism and metabolism of
ENPP1/PC-1	rs1805101	T1D	[10]	water-soluble vitamins and cofactors
EPO	rs1617640	T1D	[2]	Jak/STAT signaling pathway and development EPO-induced Jak-STAT pathway
ERBB4	rs7588550	Total	[3]	RET signaling and activation of camp-dependent PKA
FABP2	rs1799883	T1D	[10]	Metabolism and PPAR signaling pathway
FRMD3	rs1888747	T2D	[10]	Cytoskeletal protein binding
FRMD3	rs10868025	T2D	[10]	
FRMD3	rs1888746	T2D	[10]	
FRMD3	rs13289150	T2D	[10]	
FRMD3	rs1535753	T2D	[5]	
FRMD3	rs2378658	T2D	[5]	
FRMD3	rs942278	T2D	[5]	
FRMD3	rs942280	T2D	[5]	
FRMD3	rs942283	T2D	[5]	
FTO	rs8050136	T2D	[17]	DNA damage reversal and glucose / energy metabolism
GLRA3	rs10011025	T1D	[3]	Ion channel transport and ligand-gated ion channel transport
GLRA3	rs11725853	T1D	[3]	
GLUT1	rs841847	T1D	[18]	HTLV-I infection and metabolism
GLUT1	rs841848	T1D	[18]	

GLUT1	rs1385129	T1D	[18]	
GLUT1	rs3820589	T1D	[18]	
GLUT1	rs841853	Total	[2]	
GREM1	rs1129456	Total	[2]	Wnt / Hedgehog / Notch and angiogenesis (CST).
GRIK2	rs7760831	T2D	[5]	Presynaptic function of kainate receptors and transmission across chemical synapses
GRIP1/CAND1	rs11176482	T2D	[5]	Transmission across chemical synapses and trafficking of AMPA receptors
GRIP1/CAND1	rs2904532	T2D	[5]	
G6PC2	rs478333	T2D	[12]	Metabolism and foxo signaling pathway
HHEX/IDE	rs5015480	T2D	[17]	Regulation of beta-cell development and transcriptional misregulation in cancer
HMGA2	rs1531343	T2D	[19]	Transcriptional misregulation in cancer and cellular senescence
HP	HP1/2	Total	[2]	Immune system and vesicle-mediated transport
HS6ST1	rs13427836	Total	[20]	HS-GAG biosynthesis
HSPG2	rs3767140	T1D	[2]	Angiogenesis
IL-6	rs1800796	T2D	[21]	Inflammatory response
IL-6	rs1524107	T2D	[21]	
IRS2/MYO16	rs1411766	T2D	[10]	Glucose metabolic

				process, MAPK cascade, insulin secretion, signal transduction and lipid metabolic process
JAZF1	rs864745	T2D	[17]	Transcription regulation
KCNQ1	rs2237897	T2D	[1]	Ion and potassium transport
LIMK2	rs2106294	T2D	[5]	Intracellular signal transduction
LIMK2	rs4820043	T2D	[5]	
LIMK2	rs3747154	T2D	[1]	
MMP2	rs7185763	T2D	[14]	Angiogenesis and collagen degradation
MMP-9	rs17576	T2D	[11]	Collagen degradation
MSRB3/HMGA2	rs2358944	T2D	[5]	Oxidoreductase
MTHFR	rs1801133	T2D	[22]	Metabolism of folate and pterines.
MYH9	rs4821480	Total	[8]	Cell adhesion and shape
MYH9	rs2032487	Total	[8]	
MYH9	rs735853	T2D	[5]	
MYH9	rs4281481	Total	[8]	
MYH9	rs3752462	Total	[8]	
NAV3	rs12302041	T2D	[5]	ATP binding
ND	rs1978243	T2D	[5]	Electron transport
ND	rs4260465	T2D	[5]	
ND	rs7697691	T2D	[5]	
NFE2L2	rs2364723	T2D	[23]	Transcription regulation
NFE2L2	rs10497511	T2D	[23]	
NFE2L2	rs1962142	T2D	[23]	

NFE2L2	rs6726395	T2D	[23]	
NOS3	rs2070744	Total	[2]	Calmodulin-binding and oxidoreductase
NOS3	rs3138808	Total	[2]	
NRG3	rs72809865	T1D	[4]	Intracellular signal transduction, mammary placode formation and regulation of cell growth
OR2AK2	rs4478844	T2D	[1]	Olfaction and sensory transduction
OR2L13	rs10888287	T2D	[5]	Olfaction and sensory transduction
p22phox	rs4673	Total	[24]	Electron transport
PON1	L55M	T1D	[25]	Synthesis of 5-eicosatetraenoic acids
PON1	Q192R	T1D	[25]	
PPARG	rs1801282	Total	[2]	Biological rhythms and transcription regulation
PRKAA2	rs2796498	T2D	[26]	Chromatin regulator and serine/threonine-protein kinase
PRKCB1	rs3760106	T2D	[1]	Adaptive immunity, apoptosis, immunity and transcription regulation
PTPN13	rs61277444	T1D	[4]	Synthesis of pips at the plasma membrane
PTX3	rs2305619	T2D	[27]	Inflammatory response, nitric oxide biosynthetic process, phagocytosis and glycoprotein

				metabolic process,
PTX3	rs2120243	T2D	[27]	
PVT1	rs11993333	Total	[2]	DNA integration and recombination
PVT1	rs2648875	T1D	[1]	
PVT1	rs13447075	T1D	[1]	
PVT1	rs2720709	T2D	[1]	
RAGE	rs1800624	T1D	[10]	Inflammatory response
RAGE	rs1800625	T1D	[10]	
RGMA/MCTP2	rs12437854	T1D	[1]	Coreceptor activity, glycoprotein binding and Transferrin receptor binding
RNF185	rs1034589	T2D	[5]	Autophagy and Ubl conjugation pathway
RPS12	rs7769051	T2D	[5]	Nuclear-transcribed mrna catabolic process and rna processing
RPS12	rs9493454	T2D	[5]	
SASH1	rs6930576	T2D	[5]	Angiogenesis, endothelial cell migration, and ipopolysacchari de-mediated signaling pathway
SETD7	rs2592970	T1D	[28]	Activator, DNA-binding and repressor
SETD7	rs2725790	T1D	[28]	
SFI1	rs5749286	T2D	[5]	Phosphatase binding
SLC10A7/LSM6	rs891382	T2D	[5]	Sodium ion transport
SLC12A3	rs11643718	T2D	[29]	Ion transport
SOD1	rs1041740	T1D	[30]	Detoxification of reactive oxygen species and platelet degranulation

SORBS1	rs1326934	T1D	[3]	Transport and smooth muscle contraction
SP3	rs4972593	T1D	[8]	Transcription regulation
SP3	rs174162256	Total	[8]	
SUV39H2	rs17353856	T1D	[28]	Biological rhythms, cell cycle and transcription regulation
SUV39H2	rs7900814	T1D	[28]	
TGF-B1	rs1982073	Total	[31]	Growth factor
TGF-B1	rs1800470	Total	[15]	
TNF-α	rs1800629	T2D	[32]	Transcriptional regulation process and TNFR1-induced NF- κ B signaling pathway
TPM1	rs6494387	T2D	[5]	Striated and smooth muscle contraction
TRIB3	rs2295490	T2D	[33]	Apoptosis, stress response and transcription regulation
UMOD	rs12917707	T2D	[15]	Cellular defense response and leukocyte cell-cell adhesion
UNC13B	rs13293564	Total	[2]	Exocytosis
UNC5C	rs11730446	T2D	[5]	Apoptosis
VEGFA	rs833061	Total	[2]	Angiogenesis and differentiation
WNK4	rs57737815	T2D	[14]	Ionic equilibrium

S.Table2. Clinical characteristics of probands and their families.

ID	Sex/age (years)	Age at diagnosis of diabetes (yrs)	Body Mass Index (kg/m ²)	Glycated hemoglobin (%)	Insulin Auto-antibody	Islet cell antibody	Glutamic Acid Decarboxylase Antibody (U/ml)	Current Treatment	Time to insulin treatment (yrs)
1-P	M/42	31	22.9	9.9	-	-	-	insulin oral drugs	5
1-F	M/64	41	26.3	NA	NA	NA	NA	oral drugs	-
2-P	M/56	40	24.5	6.2	+	-	-	insulin oral drugs	8
2-B	M/50	48	28.7	8.6	-	-	-	oral drugs	-
3-P	F-26	13	16.8	10.9	-	-	-	dead	5
4-P	M/50	31	25.0	5.5	-	+	+	insulin oral drugs	7
4-B	M/51	50	28.4	7.3	NA	NA	NA	oral drugs	-
4-M	F/74	50	26.6	6.2	NA	NA	NA	oral drugs	-
5-P	M/44	32	24.8	4.6	NA	NA	-	insulin oral drugs	6
5-M	F/65	43	23.4	NA	NA	NA	NA	oral drugs	-
6-P	F/52	44	24.9	7.7	NA	NA	-	insulin oral drugs	6
7-P	F/30	16	23.9	5.5	+	-	-	insulin oral drugs	13
7-M	F/58	35	24.0	8.5	-	-	-	insulin oral drugs	18
8-P	M/49	40	25.0	6.2	-	-	-	insulin	6
8-B	M/52	40	24.8	6.8	NA	NA	NA	insulin oral drugs	7
8-F	M/77	39	25.2	7.5	NA	NA	NA	insulin oral drugs	11
9-P	F/30	10	27.1	6.9	-	-	-	insulin	6

9-M	F/53	39	28.7	NA	NA	NA	NA	oral drugs insulin	6
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M:Male, F:Female, “-“ represents negative, NA represents not available.

S.Table3. Diabetic complications of the study probands and their families.

ID	Renal biopsy	Duration of diabetes (yrs)	Diabetic kidney disease	Glomerular classification	IFTA Score	Interstitial inflammation score	Arteriolar hyalinosis score	Vessels arteriosclerosis score	Diabetic retinopathy	ESRD now
1-P	√	11	√	IIa	1	0	0	0	√	×
1-F	×	23	×	-	-	-	-	-	×	×
2-P	√	16	√	III	1	1	1	1	√	×
2-B	√	2	√	IIa	1	1	0	1	√	×
2-M	×	20	×	-	-	-	-	-	×	×
3-P	√	13	√	III	1	1	1	1	×	dead
4-P	√	19	√	III	2	1	1	2	√	√
4-B	×	1	×	-	-	-	-	-	×	×
4-M	×	24	√	-	-	-	-	-	×	×
5-P	√	12	√	III	2	2	1	1	√	√
5-M	×	22	NA	-	-	-	-	-	×	×
6-P	√	8	√	IIa	1	1	0	1	×	×
6-M	×	20	×	-	-	-	-	-	×	×
7-P	√	14	√	IIb	2	1	1	1	√	×
7-M	×	23	√	-	-	-	-	-	×	×
8-P	√	9	√	III	2	1	1	2	√	×
8-B	×	12	√	-	-	-	-	-	×	√
8-F	×	38	√	-	-	-	-	-	×	×
9-P	√	20	√	IV	2	1	1	2	√	×
9-M	×	14	√	-	-	-	-	-	×	√

Supplemental material is neither peer-reviewed nor thoroughly edited by CJASN. The authors alone are responsible for the accuracy and presentation of the material.

S. Table4. List of the identified variants of DKD susceptibility genes in subjects.

Gene	Variants	MAF	Annotation
ACACB	c.2788A>G p.M930V	NA	Likely Pathogenic
ACE	c.479A>G p.N160S	0.00339457	Likely Pathogenic
	c.794G>A p.R265Q	NA	Deleterious
	c.1708C>T p.R570W	NA	Deleterious
AFF3	c.2714A>G p.N905S	0.0061901	Tolerated or Benign
	c.2667C>A p.H889Q	0.0081869	Likely Pathogenic
	c.3323G>A p.G1108E	NA	Likely Pathogenic
AGT	c.803T>C p.M268T	0.705072	Has been reported to be pathogenic
AGTR1	c.*86A>C	0.117812	Has been reported to be pathogenic
CCR5	c.668G>A p.R223Q	0.012	Deleterious
	c.530C>A p.T177N	NA	Likely Pathogenic
	c.668G>A p.R223Q	0.0119808	Likely Pathogenic
CDKN2A	c.170A>G p.Q57R	NA	Likely Pathogenic
COL4A3	c.3627G>A p.M1209I	0.00898562	Tolerated or Benign
	c.1223G>A p.R408H	0.100639	Has been reported to be pathogenic
CUBN	c.910G>A p.E304K	0.0091853	Tolerated or Benign
	c.4420C>T p.P1474S	0.000399361	Likely Pathogenic
	c.6788T>G p.F2263C	0.033746	Likely Pathogenic

	c.5207C>T p.S1736L	0.0018	Likely Pathogenic
ENPP1	c.2335A>C p.T779P	0.00439297	Likely Pathogenic
FABP2	c.163A>G p.T55A	NA	Has been reported to be pathogenic
IRS2	c.1534G>A p.A512T	0.00359425	Has been reported to be pathogenic
KCNQ1	c.1927G>A p.G643S	0.0165735	Has been reported to be pathogenic
	c.1128+5G>A slicing site	NA	Has been reported to be pathogenic
	c.1343C>G p.P448R	0.0225639	Has been reported to be pathogenic
LIMK2	c.2051A>G p.Q684R	0.124201	Has been reported to be pathogenic
MMP-9	c.59C>T p.A20V	0.0327476	Tolerated or Benign
MTHFR	c.665C>T p.A222V	0.25	Has been reported to be pathogenic
PON1	c.575A>G p.Q192R	0.542931	Has been reported to be pathogenic
	c.755C>G p.A252G	NA	Likely Pathogenic
PTPN13	c.4789G>A p.V1597M	NA	Likely Pathogenic
	c.3785A>G p.N1262S	NA	Likely Pathogenic
	c.5554C>G p.H1852D	NA	Likely Pathogenic
	c.2944C>T p.R982W	0.0001	Likely Pathogenic
	c.6565G>A	NA	Tolerated or Benign

p.V2189I

PTX3	c.130+9A>G	0.56	Has been reported to be pathogenic
SFI1	c.1299G>T p.K433N	0.00738818	Likely Pathogenic
	c.146A>G p.N49S	0.00159744	Likely Pathogenic
	c.2340A>C p.Q780H	0.000599042	Likely Pathogenic
	c.2053C>T p.R685C	0.025	Deleterious
	c.2767G>A p.V923I	0.0008	Likely Pathogenic
SLC12A3	c.2738G>A p.R913Q	0.08	Has been reported to be pathogenic
TGF-B1	c.29C>T p.P10L	0.545327	Has been reported to be pathogenic
TRIB3	c.251A>G p.Q84R	0.199081	Has been reported to be pathogenic
OR2AK2	c.607G>A p.V203M	0.43131	Has been reported to be pathogenic
RGMA	c.1297C>T p.R433W	0.0175719	Likely Pathogenic

S.Table 5. The processes enrichment of COL4A3 among the 25 susceptibility genes.

#Pathway ID	Pathway description	Matching proteins
GO.0044699	single-organism process	ACACB,ACE,AFF3,AGT,AGTR1,CCR5,CDKN2A,COL4A3,ENPP1,FABP2,IRS2,KCNQ1,LIMK2,MMP9,MTHFR,OR2AK2,PON1,PTX3,RGMA,SFI1,SLC12A3,TGFB1,TRIB3
GO.0051248	negative regulation of protein metabolic process	AGT,CDKN2A,COL4A3,ENPP1,MMP9,PTX3,SFI1,TGFB1,TRIB3
GO.0009987	cellular process	ACACB,ACE,AFF3,AGT,AGTR1,CCR5,CDKN2A,COL4A3,CUBN,ENPP1,FABP2,IRS2,KCNQ1,LIMK2,MMP9,MTHFR,OR2AK2,PON1,PTPN13,RGMA,SFI1,SLC12A3,TGFB1,TRIB3
GO.0009892	negative regulation of metabolic process	ACACB,AGT,CDKN2A,COL4A3,ENPP1,IRS2,KCNQ1,MMP9,PTX3,SFI1,TGFB1,TRIB3
GO.0044712	single-organism catabolic process	ACE,CDKN2A,COL4A3,ENPP1,FABP2,MMP9,PON1,TGFB1
GO.0051246	regulation of protein metabolic process	ACE,AGT,AGTR1,CDKN2A,COL4A3,ENPP1,MMP9,MTHFR,PTX3,SFI1,TGFB1,TRIB3
GO.0001822	kidney development	ACE,AGT,AGTR1,COL4A3,TGFB1
GO.0032269	negative regulation of cellular protein metabolic process	AGT,CDKN2A,COL4A3,ENPP1,MMP9,SFI1,TGFB1,TRIB3
GO.0042221	response to chemical	AFF3,AGTR1,CCR5,COL4A3,ENPP1,IRS2,KCNQ1,MMP9,MTHFR,OR2AK2,PON1,RGMA,TGFB1,TRIB3
GO.0050790	regulation of catalytic activity	ACE,AGT,AGTR1,CDKN2A,COL4A3,IRS2,MMP9,PTX3,SFI1,TGFB1,TRIB3
GO.0065009	regulation of molecular function	ACE,AGT,AGTR1,CDKN2A,COL4A3,IRS2,MMP9,PON1,PTX3,SFI1,TGFB1,TRIB3
GO.0031324	negative regulation of cellular metabolic process	ACACB,AGT,CDKN2A,COL4A3,ENPP1,IRS2,MMP9,PTX3,SFI1,TGFB1,TRIB3
GO.0072001	renal system development	ACE,AGT,AGTR1,COL4A3,TGFB1
GO.0032268	regulation of cellular protein metabolic process	ACE,AGT,AGTR1,CDKN2A,COL4A3,ENPP1,MMP9,MTHFR,SFI1,TGFB1,TRIB3
GO.0060255	regulation of macromolecule metabolic process	ACE,AFF3,AGT,AGTR1,CDKN2A,COL4A3,ENPP1,IRS2,KCNQ1,MMP9,MTHFR,PTX3,RGMA,SFI1,TGFB1,TRIB3
GO.0009605	response to external stimulus	AGT,AGTR1,CCR5,CDKN2A,COL4A3,MMP9,MTHFR,PTX3,RGMA,TGFB1
GO.0065007	biological regulation	ACE,AFF3,AGT,AGTR1,CCR5,CDKN2A,COL4A3,CUBN,ENPP1,IRS2,KCNQ1,MMP9,MTHFR,OR2AK2,PON1,PTPN13,PTX3,RGMA,SFI1,TGFB1,TRIB3
GO.0080090	regulation of primary metabolic process	ACACB,ACE,AFF3,AGT,AGTR1,CDKN2A,COL4A3,ENPP1,IRS2,MMP9,MTHFR,PTX3,RGMA,SFI1,TGFB1,TRIB3
GO.0001655	urogenital system development	ACE,AGT,AGTR1,COL4A3,TGFB1
GO.0044710	single-organism metabolic process	ACACB,ACE,CCR5,CDKN2A,COL4A3,CUBN,ENPP1,FABP2,IRS2,MMP9,MTHFR,PON1,TGFB1,TRIB3
GO.0044763	single-organism cellular process	ACACB,ACE,AGT,AGTR1,CCR5,CDKN2A,COL4A3,CUBN,ENPP1,FABP2,IRS2,KCNQ1,MMP9,MTHFR,OR2AK2,PON1,RGMA,SFI1,SLC12A3,TGFB1,TRIB3

GO.0048519	negative regulation of biological process	ACACB,ACE,AGT,CCR5,CDKN2A,COL4A3,ENPP1,IRS2,KCNQ1,MMP9,PTX3,SFI1,TGFB1,TRIB3
GO.0044093	positive regulation of molecular function	ACE,AGT,AGTR1,CDKN2A,COL4A3,MMP9,PON1,TGFB1,TRIB3
GO.0032270	positive regulation of cellular protein metabolic process	ACE,AGT,AGTR1,CDKN2A,COL4A3,MMP9,TGFB1,TRIB3
GO.0050789	regulation of biological process	ACE,AFF3,AGT,AGTR1,CCR5,CDKN2A,COL4A3,ENPP1,IRS2,KCNQ1,MMP9,MTHFR,OR2AK2,PON1,PTPN13,PTX3,RGMA,SFI1,TGFB1,TRIB3
GO.0010605	negative regulation of macromolecule metabolic process	AGT,CDKN2A,COL4A3,ENPP1,KCNQ1,MMP9,PTX3,SFI1,TGFB1,TRIB3
GO.0048523	negative regulation of cellular process	ACACB,ACE,AGT,CCR5,CDKN2A,COL4A3,ENPP1,IRS2,MMP9,PTX3,SFI1,TGFB1,TRIB3
GO.0031325	positive regulation of cellular metabolic process	ACACB,ACE,AGT,AGTR1,CDKN2A,COL4A3,IRS2,MMP9,PTX3,TGFB1,TRIB3
GO.0051239	regulation of multicellular organismal process	ACACB,ACE,AGT,AGTR1,CDKN2A,COL4A3,ENPP1,KCNQ1,MMP9,TGFB1
GO.0031323	regulation of cellular metabolic process	ACE,AFF3,AGT,AGTR1,CDKN2A,COL4A3,ENPP1,IRS2,MMP9,MTHFR,PTX3,RGMA,SFI1,TGFB1,TRIB3
GO.0050794	regulation of cellular process	ACE,AFF3,AGT,AGTR1,CCR5,CDKN2A,COL4A3,ENPP1,IRS2,KCNQ1,MMP9,MTHFR,OR2AK2,PTPN13,PTX3,RGMA,SFI1,TGFB1,TRIB3
GO.0032501	multicellular organismal process	ACE,AFF3,AGT,AGTR1,COL4A3,CUBN,ENPP1,FABP2,IRS2,KCNQ1,LIMK2,MTHFR,OR2AK2,RGMA,TGFB1
GO.0050793	regulation of developmental process	ACACB,ACE,AGT,AGTR1,CDKN2A,COL4A3,ENPP1,TGFB1,TRIB3
GO.0051093	negative regulation of developmental process	AGT,CDKN2A,COL4A3,ENPP1,TGFB1,TRIB3
GO.0043065	positive regulation of apoptotic process	AGT,CDKN2A,COL4A3,MMP9,TGFB1
GO.0050896	response to stimulus	AFF3,AGT,AGTR1,CCR5,CDKN2A,COL4A3,ENPP1,IRS2,KCNQ1,MMP9,MTHFR,OR2AK2,PTX3,RGMA,TGFB1,TRIB3
GO.0044707	single-multicellular organism process	ACE,AFF3,AGT,AGTR1,COL4A3,CUBN,ENPP1,FABP2,IRS2,KCNQ1,MTHFR,OR2AK2,RGMA,TGFB1