

Table S1 107 overlapped and co-directional genes

GeneSymbol	GeneID	Description	P values	foldchange	foldchange(abs)	Regulation
Lcn2	16819	lipocalin 2	0.00051761	24.267371	24.267371	up
Sfn	55948	stratifin	0.044708033	16.69287135	16.69287135	up
Plaur	18793	“plasminogen activator, urokinase receptor”	0.000340195	12.66955189	12.66955189	up
Clcf1	56708	cardiotrophin-like cytokine factor 1	0.000220181	11.14395572	11.14395572	up
Cxcl1	14825	chemokine (C-X-C motif) ligand 1	0.007853553	9.422613577	9.422613577	up
Cebpb	12608	“CCAAT/enhancer binding protein (C/EBP), beta”	0.009428932	7.916984129	7.916984129	up
Rtn4	68585	reticulon 4	0.033205857	7.371514027	7.371514027	up
Tes	21753	testis derived transcript	0.04264191	6.780459442	6.780459442	up
Spsb1	74646	splA/ryanodine receptor domain and SOCS box containing 1	0.009175611	6.577359628	6.577359628	up
Itgav	16410	integrin alpha V	0.026926293	6.47727061	6.47727061	up
Cd44	12505	CD44 antigen	0.019640888	5.771687436	5.771687436	up
Hpgd	15446	hydroxyprostaglandin dehydrogenase 15 (NAD)	0.000147869	0.174725314	5.723269161	down
Krt8	16691	keratin 8	0.000268895	5.491451125	5.491451125	up
Acsl4	50790	acyl-CoA synthetase long-chain family member 4	0.009143161	5.378859149	5.378859149	up
Stat3	20848	signal transducer and activator of transcription 3	0.008134744	5.357958501	5.357958501	up
Cd14	12475	CD14 antigen	0.000334011	5.250912455	5.250912455	up
Gatm	67092	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	0.01666698	0.209806883	4.766287867	down
Mvp	78388	major vault protein	0.008689633	4.652499633	4.652499633	up
Adams1	11504	“a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1”	0.002360025	4.61253289	4.61253289	up
Ugcg	22234	UDP-glucose ceramide glucosyltransferase	0.019329379	4.597337511	4.597337511	up
Fosl2	14284	fos-like antigen 2	0.006749923	4.46784426	4.46784426	up
Coro1c	23790	“coronin, actin binding protein 1C”	0.004206521	4.448093762	4.448093762	up
Sox4	20677	SRY (sex determining region Y)-box 4	0.00856159	4.299504695	4.299504695	up
Pank1	75735	pantothenate kinase 1	0.028355722	0.236392335	4.230255599	down
Calb1	12307	calbindin 1	0.036560632	0.239315686	4.178581091	down
ApoH	11818	apolipoprotein H	0.022044532	0.240111818	4.164726278	down
Glyat	107146	glycine-N-acyltransferase	0.01975136	0.270043775	3.703103322	down
Sh3bgrl3	73723	SH3 domain binding glutamic acid-rich protein-like 3	0.003085329	3.681878117	3.681878117	up
Ddx21	56200	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	0.003061226	3.652869178	3.652869178	up
Arl4c	320982	ADP-ribosylation factor-like 4C	0.000836337	3.60095446	3.60095446	up
Dusp9	75590	dual specificity phosphatase 9	0.000848491	0.27887748	3.585804057	down
S100a9	20202	S100 calcium binding protein A9 (calgranulin B)	0.033240904	3.541178519	3.541178519	up
Lmna	16905	lamin A	0.000209751	3.498362841	3.498362841	up
Ppp1r1a	58200	“protein phosphatase 1, regulatory (inhibitor) subunit 1A”	0.002825923	0.289051547	3.459590546	down
Relb	19698	avian reticuloendotheliosis viral (v-rel) oncogene related B	0.011230167	3.44075827	3.44075827	up
Dusp10	63953	dual specificity phosphatase 10	0.013786651	3.42187064	3.42187064	up
Skil	20482	SKI-like	0.046410943	3.412907433	3.412907433	up
S100a8	20201	S100 calcium binding protein A8 (calgranulin A)	0.039479404	3.405577715	3.405577715	up

Table S1 (continued)

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Nup50	18141	nucleoporin 50	0.0323671	3.346119652	3.346119652	up
Ptpn12	19248	"protein tyrosine phosphatase, non-receptor type 12"	0.004372455	3.343123971	3.343123971	up
Plscr1	22038	phospholipid scramblase 1	0.005686432	3.314952211	3.314952211	up
Il6st	16195	interleukin 6 signal transducer	0.032673229	3.279356228	3.279356228	up
Malat1	72289	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	0.036339202	3.277022488	3.277022488	up
Fabp3	14077	"fatty acid binding protein 3, muscle and heart"	3.03859E-05	0.308951242	3.236756691	down
Lamc2	16782	"laminin, gamma 2"	0.049152916	3.213139588	3.213139588	up
Itpr3	16440	"inositol 1,4,5-triphosphate receptor 3"	0.009653711	3.133158575	3.133158575	up
Bcl3	12051	B cell leukemia/lymphoma 3	0.028537021	3.117781285	3.117781285	up
Kng1	16644	kininogen 1	0.000824782	0.32315149	3.094523869	down
Hs6st2	50786	heparan sulfate 6-O-sulfotransferase 2	0.002867649	0.32692232	3.058830607	down
Krt18	16668	keratin 18	0.029569869	3.046663173	3.046663173	up
Atp6v1c2	68775	"ATPase, H+ transporting, lysosomal V1 subunit C2"	0.002894246	0.329713707	3.032934269	down
Osmr	18414	oncostatin M receptor	0.03330936	2.908704995	2.908704995	up
Clu	12759	clusterin	0.003284804	2.884396355	2.884396355	up
Pcbp2	18521	poly(rC) binding protein 2	0.010273921	2.860306847	2.860306847	up
Mfsd4	213006	major facilitator superfamily domain containing 4	0.034514266	0.350067615	2.856591001	down
Map3k14	53859	mitogen-activated protein kinase kinase kinase 14	0.03364417	2.759245019	2.759245019	up
Sdpr	20324	serum deprivation response	0.044624745	0.363931744	2.747768001	down
Nrip1	268903	nuclear receptor interacting protein 1	0.005367083	2.723833509	2.723833509	up
Arid5b	71371	AT rich interactive domain 5B (MRF1-like)	0.010852567	2.655763231	2.655763231	up
Pprc1	226169	"peroxisome proliferative activated receptor, gamma, coactivator-related 1"	0.001081986	2.647489347	2.647489347	up
Npc1	18145	Niemann-Pick type C1	0.017049111	2.624486798	2.624486798	up
Rps6ka3	110651	ribosomal protein S6 kinase polypeptide 3	0.008646658	2.599356177	2.599356177	up
Cldn8	54420	claudin 8	0.02678156	0.384921477	2.597932458	down
Itgb1	16412	integrin beta 1 (fibronectin receptor beta)	0.007781041	2.56714691	2.56714691	up
Sfxn2	94279	sideroflexin 2	0.02862261	0.38965908	2.566345946	down
Gnb1	14688	"guanine nucleotide binding protein (G protein), beta 1"	0.00649479	2.564961823	2.564961823	up
Icam1	15894	intercellular adhesion molecule 1	0.000825693	2.523664604	2.523664604	up
Slc23a3	22626	"solute carrier family 23 (nucleobase transporters), member 3"	0.040027135	0.396312497	2.523261337	down
Klf3	16599	Kruppel-like factor 3 (basic)	0.015837864	2.511778909	2.511778909	up
Cdv3	321022	carnitine deficiency-associated gene expressed in ventricle 3	0.018487989	2.510283744	2.510283744	up
Tmem116	77462	transmembrane protein 116	0.014854236	0.400455177	2.497158378	down
H6pd	100198	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	0.03844528	2.476989381	2.476989381	up
Cml2	93673	camello-like 2	0.039162801	0.405356189	2.466966156	down
Clcnka	12733	chloride channel Ka	0.034926635	0.409006529	2.444948746	down

Table S1 (continued)

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GeneSymbol	GeneID	Description	P values	foldchange	foldchange(abs)	Regulation
Acbd3	170760	acyl-Coenzyme A binding domain containing 3	0.02327427	2.441903314	2.441903314	up
Pde4b	18578	"phosphodiesterase 4B, cAMP specific"	0.0428323	2.430803029	2.430803029	up
Cflar	12633	CASP8 and FADD-like apoptosis regulator	0.038992153	2.401722722	2.401722722	up
Kpna3	16648	karyopherin (importin) alpha 3	0.009574363	2.40064437	2.40064437	up
Slc5a9	230612	"solute carrier family 5 (sodium/glucose cotransporter), member 9"	0.020859037	0.42014245	2.380145118	down
Dhdh	71755	dihydrodiol dehydrogenase (dimeric)	0.013811088	0.423292598	2.362432047	down
Csrp2	13008	cysteine and glycine-rich protein 2	0.042992385	0.424476649	2.355842193	down
Slc5a1	20537	"solute carrier family 5 (sodium/glucose cotransporter), member 1"	0.000210978	0.426085943	2.346944359	down
Ube2j1	56228	ubiquitin-conjugating enzyme E2J 1	0.014326881	2.311735266	2.311735266	up
Taok1	216965	TAO kinase 1	0.025743653	2.31038244	2.31038244	up
Prom2	192212	prominin 2	0.036092337	0.433079494	2.309044904	down
Tax1bp3	76281	Tax1 (human T cell leukemia virus type I) binding protein 3	0.013077334	2.308251051	2.308251051	up
Ptpre	19267	"protein tyrosine phosphatase, receptor type, E"	0.010358493	2.304449316	2.304449316	up
Col4a2	12827	"collagen, type IV, alpha 2"	0.004170255	2.297932176	2.297932176	up
Esrrb	26380	"estrogen related receptor, beta"	0.029716857	0.437207622	2.287242832	down
Phc2	54383	polyhomeotic-like 2 (Drosophila)	0.014788159	2.273787573	2.273787573	up
Il13ra1	16164	"interleukin 13 receptor, alpha 1"	0.004731108	2.269736619	2.269736619	up
Ptpn11	19247	"protein tyrosine phosphatase, non-receptor type 11"	0.010093699	2.245370266	2.245370266	up
Birc3	11796	baculoviral IAP repeat-containing 3	0.031283912	2.238903795	2.238903795	up
Mme	17380	membrane metallo endopeptidase	0.012963036	0.450950119	2.217540161	down
Ero1l	50527	ERO1-like (S. cerevisiae)	0.003313402	2.216357351	2.216357351	up
Baz1a	217578	bromodomain adjacent to zinc finger domain 1A	0.000341199	2.210205018	2.210205018	up
lqgap1	29875	IQ motif containing GTPase activating protein 1	0.011579281	2.202807839	2.202807839	up
Sav1	64010	salvador homolog 1 (Drosophila)	0.035395396	2.178174256	2.178174256	up
Prpf40a	56194	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	0.00625872	2.172211905	2.172211905	up
Bbx	70508	bobby sox homolog (Drosophila)	0.046243064	2.156500578	2.156500578	up
Col4a1	12826	"collagen, type IV, alpha 1"	0.000636571	2.129355185	2.129355185	up
Ssh2	237860	slingshot homolog 2 (Drosophila)	0.025682615	2.096407839	2.096407839	up
Zc3hav1	78781	"zinc finger CCCH type, antiviral 1"	0.035965085	2.060732652	2.060732652	up
Ctsd	13033	cathepsin D	0.019219315	2.05936588	2.05936588	up
Rbms1	56878	"RNA binding motif, single stranded interacting protein 1"	0.017862777	2.035609572	2.035609572	up
Bclaf1	72567	BCL2-associated transcription factor 1	0.021352927	2.025658948	2.025658948	up
Klf15	66277	Kruppel-like factor 15	0.029761333	0.494801225	2.021013588	down

Table S2 The details of each experiment

Figure	Methods	Purpose	Group	N	Mean ± SEM	P
Fig. 1	Screening for differential expression genes	To overlap with the reported DGF database	Sham-group	3		
			IRI-group	3		
Fig. 2A	Real-time qPCR assay	To verify whether CLCF1 expression in kidney could be up-regulated by IRI.	Sham-group	4	1.00±0.27	P<0.01
			IRI-group	4	3.99±1.52	
Fig. 2B	Immunohistochemistry	To verify whether CLCF1 expression in kidney could be up-regulated by IRI.				
Fig. 2C	ELISA assay	To detect the circulatory CLCF1 in the serum samples	Sham-group	8	179.78±100.03 pg/ml	P<0.01
			IRI-group	8	353.23±70.52 pg/ml	
Fig. 3A	Creatinine Assay	To evaluate whether the IRI model is successful.	Sham-WT	5	7.35±3.98 µmol/L	P<0.01
			IRI-WT	6	186.42±25.82 µmol/L	
			Sham-KO	4	2.54±1.27 µmol/L	P<0.01
			IRI-KO	8	129.81±52.26 µmol/L	
			IRI-WT vs IRI-KO			
Fig. 3B	Western Blot	To evaluate whether the FOXO3-knockout model is successful	Sham-KO	4		
			IRI-KO	4		
Fig. 3C	ELISA assay	To investigate whether serum CLCF1 expression can be regulated by FOXO3.	Sham-WT	8	192.60±90.75 pg/ml	P<0.01
			Sham-KO	7	397.28±151.46 pg/ml	
			IRI-WT	8	424.56±356.53 pg/ml	P>0.05
			IRI-KO	9	538.04±419.10 pg/ml	