

**Table S1** The Gene Ontology (GO) analysis of the co-expressed differential genes of hypertension-related renal cell carcinoma

Gene	GO class (direct)	Evidence	Evidence with	Reference	
BCAT1	G1/S transition of mitotic cell cycle	TAS		PMID:8692959	
	cytosol	TAS		Reactome: R-HSA-508189	
	branched-chain amino acid biosynthetic process	TAS		PMID:6933702	
	branched-chain amino acid catabolic process	TAS		Reactome: R-HSA-70895	
	identical protein binding	IEA	UniProtKB: P54690 ensembl: ENSRNOP0000021193	GO_REF:0000107	
	L-leucine transaminase activity	IEA	EC:2.6.1.42	GO_REF:0000003	
	L-valine transaminase activity	IEA	EC:2.6.1.42	GO_REF:0000003	
	L-isoleucine transaminase activity	IEA	EC:2.6.1.42	GO_REF:0000003	
	valine biosynthetic process	IBA	PANTHER: PTN000214538 PomBase: SPBC428.02c	PMID:21873635	
	mitochondrion	IBA	MGI: MGI:1276534 PANTHER: PTN000214537 PomBase: SPBC428.02c RGD:68948 SGD: S000001251 UniProtKB: O15382	PMID:21873635	
	branched-chain-amino-acid transaminase activity	IBA	MGI: MGI:104861 MGI: MGI:1276534 PANTHER: PTN000214538 PomBase: SPBC428.02c RGD:2195 RGD:68948 SGD: S000001251 SGD: S000003909	PMID:21873635	
	leucine biosynthetic process	IBA	PANTHER: PTN000214538 PomBase: SPBC428.02c RGD:68948	PMID:21873635	
	CORO1A	immunological synapse	IDA		PMID:24760828
		phagolysosome assembly	IMP		PMID:12132654
phagocytic cup		IDA		PMID:17442961	
RNA binding		HDA		PMID:22658674	
actin binding		IPI	UniProtKB: P60709	PMID:23100250	
actin monomer binding		IMP		PMID:23100250	
protein binding		IPI	UniProtKB: P14598	PMID:11094157	
cytoplasm		IDA		PMID:17341475	
early endosome		IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107	
cytosol		IEA	GO:0061502	GO_REF:0000108	
actin filament		IDA		PMID:15800061	
plasma membrane		IDA		PMID:17341475	
cell-cell junction		IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107	
calcium ion transport		IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107	
phagocytosis		IMP		PMID:17442961	
protein C-terminus binding		IPI	UniProtKB: Q15080	PMID:9365277	
cytoskeletal protein binding		ISS	UniProtKB: O89053	GO_REF:0000024	
regulation of cell shape		IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107	
membrane		HDA		PMID:19946888	
lamellipodium		IDA		PMID:17442961	
actin cytoskeleton organization		IMP		PMID:17442961	
positive regulation of cell migration		IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107	

	axon	IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107
	leukocyte chemotaxis	IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107
	phagocytic vesicle membrane	IEA	UniProtKB-SubCell:SL-0205	GO_REF:0000039
	cortical actin cytoskeleton	IDA		PMID:15800061
	negative regulation of vesicle fusion	IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107
	cell-substrate adhesion	IMP		PMID:17442961
	myosin heavy chain binding	IPI	UniProtKB: P35579	PMID:23100250
	uropod organization	IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107
	regulation of actin cytoskeleton organization	IMP		PMID:24760828
	protein-containing complex	IDA		PMID:11094157
	nerve growth factor signaling pathway	IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107
	positive regulation of T cell proliferation	IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107
	protein homodimerization activity	IDA		PMID:15601263
	T cell homeostasis	IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107
	natural killer cell degranulation	IMP		PMID:24760828
	negative regulation of neuron apoptotic process	IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107
	phosphatidylinositol 3-kinase binding	IDA		PMID:11094157
	innate immune response	NAS		PMID:17341475
	phagocytic vesicle	IDA		PMID:17442961
	homeostasis of number of cells within a tissue	IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107
	positive chemotaxis	IDA		PMID:17442961
	actin filament binding	IDA		PMID:15601263
	negative regulation of actin nucleation	IDA		PMID:17442961
	regulation of release of sequestered calcium ion into cytosol	IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107
	early endosome to recycling endosome transport	IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107
	extracellular exosome	HDA		PMID:20458337
	cellular response to interleukin-4	IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107
	glutamatergic synapse	IEA	UniProtKB: O89053 ensembl: ENSMUSP00000101972	GO_REF:0000107
	cortical actin cytoskeleton	IDA		PMID:24760828
	actin filament binding	IBA	FB: FBgn0029903 MG: MGI:1345961 PANTHER: PTN000091698 SGD: S000004421 UniProtKB: P31146 UniProtKB: Q9BR76 UniProtKB: Q9ULV4 WB: WBGene00004075 dictyBase: DDB_G0267382 dictyBase: DDB_G0269388	PMID:21873635
	actin filament organization	IBA	MG: MGI:1345961 MG: MGI:1926135 PANTHER: PTN000091698 SGD: S000004421 UniProtKB: P57737 UniProtKB: Q9BR76 dictyBase: DDB_G0267382	PMID:21873635

	cell migration	IBA	MGI:1345961 PANTHER: PTN000091809 UniProtKB: Q9BR76 UniProtKB: Q9ULV4 ZFIN: ZDB-GENE-030114-6	PMID:21873635
CRIP1	AT DNA binding	IDA		PMID:20108983
	cytoplasm	IDA		PMID:20415737
	immune response	IEP		PMID:20415737
	heart development	TAS		PMID:7999070
	zinc ion binding	IDA		PMID:9126610
	DNA binding, bending	IDA		PMID:20108983
	intrinsic apoptotic signaling pathway in response to DNA damage	IDA		PMID:20415737
	response to organic substance	IEP		PMID:17486081
	response to zinc ion	IDA		PMID:7999070
	regulation of gene expression	IEP		PMID:7999070
	peptide binding	IDA		PMID:18670594
	prostate gland stromal morphogenesis	IEP		PMID:9507743
	cellular response to antibiotic	IDA		PMID:20415737
	cellular response to UV-B	IDA		PMID:20415737
	zinc ion binding	IBA	PANTHER: PTN002918232 UniProtKB: P50238	PMID:21873635
	intrinsic apoptotic signaling pathway in response to DNA damage	IBA	PANTHER: PTN002918232 UniProtKB: P50238	PMID:21873635
	regulation of gene expression	IBA	PANTHER: PTN002918232 UniProtKB: P50238	PMID:21873635
FN1	angiogenesis	IEA	UniProtKB-KW:KW-0037	GO_REF:0000037
	regulation of protein phosphorylation	IDA		PMID:11792823
	protease binding	IPI	UniProtKB: P07711	PMID:22952693
	platelet degranulation	TAS		Reactome: R-HSA-114608
	signaling receptor binding	IPI	UniProtKB: P9WQP1	PMID:17849409
	integrin binding	IPI	UniProtKB: P05556	PMID:11792823
	extracellular matrix structural constituent	ISS	UniProtKB: F1SS24	GO_REF:0000024
	protein binding	IPI	UniProtKB: P9WIG5	PMID:10627046
	collagen binding	NAS		PMID:3024962
	extracellular region	NAS		PMID:14718574
	fibrinogen complex	IDA		PMID:3997886
	basement membrane	IEA	UniProtKB: P11276 ensembl: ENSMUSP00000054499	GO_REF:0000107
	extracellular space	IDA		PMID:15292204
	endoplasmic reticulum lumen	TAS		Reactome: R-HSA-8952289
	endoplasmic reticulum-Golgi intermediate compartment	IDA		PMID:15308636
	acute-phase response	IEA	UniProtKB-KW:KW-0011	GO_REF:0000037
	cell-substrate junction assembly	IEA	UniProtKB: P11276 ensembl: ENSMUSP00000054499	GO_REF:0000107
	cell adhesion	NAS		PMID:1423622

calcium-independent cell-matrix adhesion	IEA	JniProtKB: P11276 ensembl: ENSMUSP00000054499	GO_REF:0000107
protein C-terminus binding	IPI	JniProtKB: P9WK17	PMID:16677310
heparin binding	NAS		PMID:10075919
positive regulation of cell population proliferation	IDA		PMID:25834989
regulation of cell shape	IEA	JniProtKB-KW:KW-0133	GO_REF:0000037
response to wounding	NAS		PMID:7989369
positive regulation of gene expression	IDA		PMID:25834989
positive regulation of peptidase activity	IEA	GO:0016504	GO_REF:0000108
apical plasma membrane	IEA	JniProtKB: P11276 ensembl: ENSMUSP00000054499	GO_REF:0000107
peptidase activator activity	IEA	JniProtKB: P11276 ensembl: ENSMUSP00000054499	GO_REF:0000107
peptide cross-linking	IDA		PMID:3997886
cytokine-mediated signaling pathway	TAS		Reactome: R-HSA-6785807
enzyme binding	IPI	JniProtKB: Q9AIS0	PMID:12167537
extracellular matrix organization	TAS		Reactome: R-HSA-1474244
extracellular matrix	IDA		PMID:26571399
platelet alpha granule lumen	TAS		Reactome: R-HSA-481007
integrin activation	IMP		PMID:24658351
substrate adhesion-dependent cell spreading	IDA		PMID:16236823
endodermal cell differentiation	IDA		PMID:23154389
wound healing	IEA	JniProtKB: P11276 ensembl: ENSMUSP00000054499	GO_REF:0000107
identical protein binding	IPI	JniProtKB: P02751	PMID:17914904
proteoglycan binding	IDA		PMID:29030641
post-translational protein modification	TAS		Reactome: R-HSA-597592
cellular protein metabolic process	TAS		Reactome: R-HSA-392499
positive regulation of axon extension	IEA	JniProtKB: P11276 ensembl: ENSMUSP00000054499	GO_REF:0000107
positive regulation of fibroblast proliferation	IDA		PMID:25834989
leukocyte migration	TAS		Reactome: R-HSA-202733
chaperone binding	IPI	JniProtKB: P9WMJ9	PMID:17849409
interaction with symbiont	IDA		PMID:12167537
symbiotic process mediated by secreted substance	IDA		PMID:17849409
collagen-containing extracellular matrix	IDA		PMID:16157329
extracellular exosome	HDA		PMID:19056867
regulation of ERK1 and ERK2 cascade	IDA		PMID:11792823
blood microparticle	HDA		PMID:22516433
disordered domain specific binding	IPI	JniProtKB: O50835	PMID:15292204

	neural crest cell migration involved in autonomic nervous system development	IDA		PMID:26571399
	positive regulation of substrate-dependent cell migration, cell attachment to substrate	IDA		PMID:25834989
	negative regulation of transforming growth factor-beta secretion	IDA		PMID:25834989
	collagen-containing extracellular matrix	HDA		PMID:20551380
LYZ	retina homeostasis	HEP		PMID:23580065
	lysozyme activity	TAS		PMID:2829884
	extracellular region	TAS		Reactome: R-HSA-6798745
	extracellular space	HDA		PMID:16502470
	inflammatory response	TAS		PMID:366724
	antimicrobial humoral response	TAS		Reactome: R-HSA-6803157
	cytolysis	IEA	UniProtKB: KW:KW-0081	GO_REF:0000037
	killing of cells of other organism	IDA		PMID:9727055
	azurophil granule lumen	TAS		Reactome: R-HSA-6798751
	specific granule lumen	TAS		Reactome: R-HSA-6798749
	defense response to bacterium	IDA		PMID:21093056
	identical protein binding	IPI	UniProtKB: P61626	PMID:23353684
	neutrophil degranulation	TAS		Reactome: R-HSA-6798695
	cellular protein metabolic process	TAS		Reactome: R-HSA-392499
	defense response to Gram-positive bacterium	IDA		PMID:21093056
	extracellular exosome	HDA		PMID:19056867
	tertiary granule lumen	TAS		Reactome: R-HSA-6798745
	defense response to Gram-positive bacterium	IBA	MG: MGI:96897 MG: MGI:96902 PANTHER: PTN000892307 RGD:3026 UniProtKB: P61626	PMID:21873635
	defense response to Gram-negative bacterium	IBA	MG: MGI:96897 MG: MGI:96902 PANTHER: PTN000892307 RGD:3026	PMID:21873635
PYCARD	Golgi membrane	IDA		PMID:23229815
	myeloid dendritic cell activation	IMP		PMID:22732093
	protease binding	IPI	UniProtKB: P98073	PMID:24407287
	activation of innate immune response	IDA		PMID:21575908
	positive regulation of defense response to virus by host	IEA	UniProtKB: Q9EPB4 ensembl: ENSMUSP00000033056	GO_REF:0000107
	myeloid dendritic cell activation involved in immune response	ISS	UniProtKB: Q9EPB4	GO_REF:0000024

positive regulation of antigen processing and presentation of peptide antigen via MHC class II	ISS	UniProtKB: Q9EPB4	GO_REF:0000024
positive regulation of adaptive immune response	IMP		PMID:22732093
interleukin-6 receptor binding	IPI	UniProtKB: P40189	PMID:24407287
protein binding	IPI	UniProtKB: O15553	PMID:11498534
tropomyosin binding	IPI	UniProtKB: P67936	PMID:24407287
extracellular region	TAS		Reactome: R-HSA-6798748
nucleus	ISS	UniProtKB: Q9EPB4	GO_REF:0000024
nucleoplasm	IDA		GO_REF:0000052
nucleolus	IDA		GO_REF:0000052
cytoplasm	NAS		PMID:12019269
mitochondrion	IDA		PMID:14730312
endoplasmic reticulum	IEA	UniProtKB-SubCell:SL-0095	GO_REF:0000039
cytosol	IDA		GO_REF:0000052
activation of cysteine-type endopeptidase activity involved in apoptotic process	NAS		PMID:12019269
inflammatory response	IEA	UniProtKB: Q9EPB4 ensembl: ENSMUSP00000033056	GO_REF:0000107
signal transduction	NAS		PMID:12019269
IkappaB kinase complex	TAS		PMID:12656673
cysteine-type endopeptidase activator activity involved in apoptotic process	NAS		PMID:12019269
regulation of autophagy	IEA	UniProtKB: Q9EPB4 ensembl: ENSMUSP00000033056	GO_REF:0000107
regulation of tumor necrosis factor-mediated signaling pathway	IMP		PMID:14730312
myosin I binding	IPI	UniProtKB: O00159	PMID:24407287
enzyme binding	IPI	UniProtKB: P49916	PMID:24407287
positive regulation of actin filament polymerization	ISS	UniProtKB: Q9EPB4	GO_REF:0000024
regulation of protein stability	ISS	UniProtKB: Q9EPB4	GO_REF:0000024
negative regulation of NF-kappaB transcription factor activity	IMP		PMID:16585594
Pyrin domain binding	IPI	UniProtKB: Q96P20	PMID:15030775
interleukin-1 beta production	IEA	UniProtKB: Q9EPB4 ensembl: ENSMUSP00000033056	GO_REF:0000107
negative regulation of interferon-beta production	IMP		PMID:19158675
positive regulation of interferon-gamma production	ISS	UniProtKB: Q9EPB4	GO_REF:0000024

positive regulation of interleukin-1 beta production	IMP		PMID:22267217
positive regulation of interleukin-6 production	ISS	UniProtKB: Q9EPB4	GO_REF:0000024
positive regulation of tumor necrosis factor production	IMP		PMID:16982856
protein-containing complex	IDA		PMID:22267217
tumor necrosis factor-mediated signaling pathway	IDA		PMID:12656673
secretory granule lumen	TAS		Reactome: R-HSA-6798748
azurophil granule lumen	TAS		Reactome: R-HSA-6798751
positive regulation of activated T cell proliferation	ISS	UniProtKB: Q9EPB4	GO_REF:0000024
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	IMP		PMID:14730312
identical protein binding	IPI	UniProtKB: Q9ULZ3	PMID:24630722
protein homodimerization activity	IDA		PMID:15030775
neuronal cell body	IEA	UniProtKB: G3V8L1 ensembl: ENSRNOP00000026699	GO_REF:0000107
positive regulation of apoptotic process	IDA		PMID:12646168
regulation of GTPase activity	IEA	UniProtKB: Q9EPB4 ensembl: ENSMUSP00000033056	GO_REF:0000107
negative regulation of I-kappaB kinase/NF-kappaB signaling	IDA		PMID:12486103
positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	IDA		PMID:15030775
neutrophil degranulation	TAS		Reactome: R-HSA-6798695
ion channel binding	IEA	UniProtKB: G3V8L1 ensembl: ENSRNOP00000026699	GO_REF:0000107
macropinocytosis	ISS	UniProtKB: Q9EPB4	GO_REF:0000024
innate immune response	IEA	UniProtKB: KW:KW-0399	GO_REF:0000037
positive regulation of JNK cascade	IMP		PMID:21487011
protein dimerization activity	IDA		PMID:24531343
positive regulation of interleukin-1 beta secretion	IDA		PMID:15030775
positive regulation of phagocytosis	ISS	UniProtKB: Q9EPB4	GO_REF:0000024
defense response to Gram-negative bacterium	IMP		PMID:16982856
positive regulation of T cell activation	IMP		PMID:22732093
positive regulation of DNA-binding transcription factor activity	IDA		PMID:19494289

positive regulation of NF-kappaB transcription factor activity	IDA		PMID:12646168
protein homooligomerization	IDA		PMID:24531343
defense response to virus	IDA		PMID:21575908
positive regulation of ERK1 and ERK2 cascade	IMP		PMID:21487011
BMP receptor binding	IPI	UniProtKB: Q13873	PMID:24407287
cellular response to lipopolysaccharide	IDA		PMID:12486103
cellular response to interleukin-1	IDA		PMID:12486103
cellular response to tumor necrosis factor	IDA		PMID:12486103
negative regulation of protein serine/threonine kinase activity	IDA		PMID:12486103
intrinsic apoptotic signaling pathway by p53 class mediator	IMP		PMID:14730312
NLRP1 inflammasome complex	IDA		PMID:12191486
NLRP3 inflammasome complex	IDA		PMID:15030775
positive regulation of chemokine secretion	IMP		PMID:21487011
positive regulation of release of cytochrome c from mitochondria	IDA		PMID:14730312
AIM2 inflammasome complex	IDA		PMID:19158676
activation of cysteine-type endopeptidase activity	IEA	UniProtKB: Q9EPB4 ensembl: ENSMUSP00000033056	GO_REF:0000107
negative regulation of cytokine production involved in inflammatory response	IMP		PMID:24531343
positive regulation of T cell migration	ISS	UniProtKB: Q9EPB4	GO_REF:0000024
positive regulation of interleukin-8 secretion	IMP		PMID:16982856
positive regulation of interleukin-6 secretion	IMP		PMID:16982856
positive regulation of cysteine-type endopeptidase activity	IDA		PMID:19158676
positive regulation of interleukin-10 secretion	IMP		PMID:16982856
positive regulation of extrinsic apoptotic signaling pathway	IDA		PMID:16964285
regulation of intrinsic apoptotic signaling pathway	IDA		PMID:14730312
IkappaB kinase complex	IDA		PMID:12486103



	apoptotic process	IBA	FB:FBgn0010501 FB:FBgn0019972 FB:FBgn0020381 FB:FBgn0028381 FB:FBgn0033659 MGi:MGi:107739 MGi:MGi:109383 MGi:MGi:1261423 MGi:MGi:1277950 MGi:MGi:1312922 MGi:MGi:97295 PANTHER:PTN000047947 RGD:2274 RGD:2275 RGD:61867 RGD:620944 RGD:620945 RGD:69274 UniProtKB:O15519 UniProtKB:P42574 UniProtKB:P55210 UniProtKB:P55211 UniProtKB:Q14790 WB:WBGene00000417 ZFIN:ZDB-GENE-011210-1	PMID:21873635
	intrinsic apoptotic signaling pathway in response to DNA damage	IBA	PANTHER: PTN000048135 UniProtKB: Q9ULZ3	PMID:21873635
	cysteine-type endopeptidase activity involved in apoptotic process	IBA	FB: FBgn0010501 FB: FBgn0019972 MGi: MG:107739 MGi: MG:109383 MGi: MG:1261423 MGi: MG:97295 PANTHER: PTN000047947 UniProtKB: P42574 UniProtKB: P55210 UniProtKB: P55211 UniProtKB: P55212 UniProtKB: Q14790 UniProtKB: Q92851 WB: WBGene00000417	PMID:21873635
	extrinsic apoptotic signaling pathway in absence of ligand	IBA	MGi: MG:97295 PANTHER: PTN000048135	PMID:21873635
	cytoplasm	IBA	FB:FBgn0010501 FB:FBgn0019972 FB:FBgn0020381 FB:FBgn0028381 FB:FBgn0033051 MGi:MGi:107739 MGi:MGi:1261423 MGi:MGi:1277950 MGi:MGi:1312922 MGi:MGi:1336166 MGi:MGi:1931465 MGi:MGi:97295 PANTHER:PTN000047947 RGD:2274 RGD:2275 RGD:61867 RGD:620944 RGD:620945 RGD:621758 RGD:69274 RGD:70967 UniProtKB:F1NL59 UniProtKB:O15519 UniProtKB:P31944 UniProtKB:P42574 UniProtKB:P49662 UniProtKB:P55210 UniProtKB:P55211 UniProtKB:P55212 UniProtKB:Q14790 UniProtKB:Q6UXS9 UniProtKB:Q8MKI5 UniProtKB:Q95ND5 UniProtKB:Q9ULZ3 WB:WBGene00000417	PMID:21873635
SAP30	histone deacetylase complex	IDA		PMID:9651585
	negative regulation of transcription by RNA polymerase II	IEA	UniProtKB: O88574 ensembl: ENSMUSP00000034022	GO_REF:0000107
	DNA binding	IEA	UniProtKB-KW:KW-0238	GO_REF:0000037
	transcription corepressor activity	IDA		PMID:9651585
	protein binding	IPI	UniProtKB: P51610	PMID:12670868
	nucleoplasm	IDA		GO_REF:0000052
	regulation of transcription, DNA-templated	IDA		PMID:9651585
	histone deacetylation	IEA	GO:0004407	GO_REF:0000108
	skeletal muscle cell differentiation	IEA	UniProtKB: O88574 ensembl: ENSMUSP00000034022	GO_REF:0000107
	metal ion binding	IEA	UniProtKB-KW:KW-0479	GO_REF:0000037
	transcription coregulator activity	IBA	PANTHER: PTN000328752 UniProtKB: O75446	PMID:21873635
	regulation of transcription, DNA-templated	IBA	PANTHER: PTN000328752 UniProtKB: O75446	PMID:21873635
	histone deacetylase activity	IBA	PANTHER: PTN000328752 SGD: S000004876	PMID:21873635
	histone deacetylase complex	IBA	PANTHER: PTN000328752 UniProtKB: O75446 UniProtKB: Q9HAJ7	PMID:21873635
ESRRG	nuclear chromatin	ISA	tfclass:2.1.1	GO_REF:0000113
	RNA polymerase II regulatory region sequence-specific DNA binding	IEA	UniProtKB: P62509 ensembl: ENSMUSP00000027906	GO_REF:0000107

	DNA-binding transcription factor activity, RNA polymerase II-specific	ISA	class:2.1.1	GO_REF:0000113
	DNA-binding transcription activator activity, RNA polymerase II-specific	IEA	UniProtKB: P62509 ensembl: ENSMUSP00000027906	GO_REF:0000107
	steroid hormone receptor activity	IEA	InterPro: IPR001723 InterPro: IPR024178 InterPro: IPR027289	GO_REF:0000002
	nuclear receptor activity	IEA	InterPro: IPR003078	GO_REF:0000002
	steroid binding	IEA	InterPro: IPR024178 InterPro: IPR027289	GO_REF:0000002
	protein binding	IPI	UniProtKB: Q61026	PMID:10428842
	nucleoplasm	TAS		Reactome: R-HSA-376419
	regulation of transcription, DNA-templated	IDA		PMID:23836911
	transcription initiation from RNA polymerase II promoter	TAS		Reactome: R-HSA-383280
	zinc ion binding	IEA	InterPro: IPR001628 InterPro: IPR013088 InterPro: IPR024178	GO_REF:0000002
	steroid hormone mediated signaling pathway	IEA	GO:0003707	GO_REF:0000108
	positive regulation of transcription, DNA-templated	ISS	UniProtKB: P62509	GO_REF:0000024
	positive regulation of transcription by RNA polymerase II	IEA	UniProtKB: P62509 ensembl: ENSMUSP00000027906	GO_REF:0000107
	retinoic acid receptor signaling pathway	IEA	InterPro: IPR003078	GO_REF:0000002
	AF-2 domain binding	ISS	UniProtKB: P62509	GO_REF:0000024
ESRRG	positive regulation of cold-induced thermogenesis	ISS	UniProtKB: P62509	PMID:17229846

TAS, traceable author statement; IEA, Inferred from Electronic Annotation; IBA, Inferred from Biological aspect of Ancestor; IDA, Inferred from Direct Assay; IMP, Inferred from Mutant Phenotype; HDA, Inferred from High Throughput Direct Assay; IPI, Inferred from Physical Interaction; ISS, Inferred from Sequence or structural Similarity; NAS, Non-traceable Author Statement; IEP, Inferred from Expression Pattern; HEP, Inferred from High Throughput Expression Pattern; ISA, Inferred from Sequence Alignment.

**Table S2** The Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways analysis among co-expressed differentially genes of hypertension-related renal cell carcinoma and their predicted miRNAs

Genes	Predicted miRNAs	Category	Function	P value
BCAT1	hsa-let-7f-5p	KEGG pathway	ECM-receptor interaction	7.00E-17
	hsa-let-7g-5p		Amoebiasis	0.004634
	hsa-let-7i-5p		Signaling pathways regulating pluripotency of stem cells	0.006974
	hsa-miR-218-5p		PI3K-Akt signaling pathway	0.023169
	hsa-miR-98-5p		Wnt signaling pathway	0.026951
		GO terms	Fc-epsilon receptor signaling pathway	0.001352
			Cellular component assembly	0.001352
			Macromolecular complex assembly	0.001682
			Regulation of transcription from RNA polymerase II promoter in response to hypoxia	0.002075
			Neurotrophin TRK receptor signaling pathway	0.002075
			Protein complex assembly	0.007927
			Extracellular matrix disassembly	0.009607
			Small molecule metabolic process	0.00984
CORO1A	hsa-miR-301b-3p	KEGG pathway	Estrogen signaling pathway	0.00043
	hsa-miR-370-3p		Endocytosis	0.007175
	hsa-miR-454-3p		Gap junction	0.01461
	hsa-miR-504-5p	GO terms	Cellular protein modification process	6.38E-12
	hsa-miR-744-5p		Neurotrophin TRK receptor signaling pathway	2.70E-09
			Nervous system development	0.000246
			Membrane organization	0.000541
			Small molecule metabolic process	0.000541
CRIP1	hsa-miR-221-5p	KEGG pathway	ECM-receptor interaction	4.65E-11
	hsa-miR-4720-5p		Fatty acid elongation	0.001276
		GO terms	Cellular nitrogen compound metabolic process	0.002025
			Gene expression	0.004677

ESRRG	hsa-miR-137	KEGG pathway	Prion diseases	1.03E-12
	hsa-miR-148a-3p		ErbB signaling pathway	3.66E-06
	hsa-miR-152-3p		Adherens junction	0.000149
	hsa-miR-205-5p		Oxytocin signaling pathway	0.000746
	hsa-miR-7-5p		Proteoglycans in cancer	0.0008
		GO terms	Neurotrophin TRK receptor signaling pathway	1.55E-25
			Fc-epsilon receptor signaling pathway	4.15E-20
			Epidermal growth factor receptor signaling pathway	3.46E-18
			Cellular component assembly	5.38E-14
			Blood coagulation	1.10E-11
			Fibroblast growth factor receptor signaling pathway	8.45E-11
FN1	hsa-miR-144-3p	KEGG pathway	Hippo signaling pathway	3.15E-05
	hsa-miR-199a-3p		Thyroid hormone signaling pathway	0.000558
	hsa-miR-200b-3p		ErbB signaling pathway	0.000597
	hsa-miR-200c-3p		Gap junction	0.000597
	hsa-miR-429	GO terms	Cellular nitrogen compound metabolic process	4.19E-52
			Cellular protein modification process	2.64E-41
			Neurotrophin TRK receptor signaling pathway	1.67E-13
			Fc-epsilon receptor signaling pathway	5.93E-13
			Blood coagulation	6.73E-09
LYZ	hsa-miR-1-3p	KEGG pathway	Proteoglycans in cancer	0.000101
	hsa-miR-140-5p		Gap junction	0.001277
	hsa-miR-206		Rap1 signaling pathway	0.003687
	hsa-miR-23b-3p		Glutamatergic synapse	0.004599
	hsa-miR-452-5p		Renal cell carcinoma	0.00613
		GO terms	Neurotrophin TRK receptor signaling pathway	3.81E-15
			Transcription, DNA-templated	4.14E-15
			Fc-epsilon receptor signaling pathway	3.12E-13
			Epidermal growth factor receptor signaling pathway	2.15E-12
			Cellular component assembly	2.15E-12
			Macromolecular complex assembly	6.93E-10
PYCARD	hsa-miR-383-5p	KEGG pathway	Thyroid hormone synthesis	1.35E-14
			Fatty acid degradation	7.57E-07
			Adrenergic signaling in cardiomyocytes	0.00013

			Fatty acid metabolism	0.000343
			Ubiquinone and other terpenoid-quinone biosynthesis	0.004631
			Valine, leucine and isoleucine degradation	0.00753
		GO terms	Cellular nitrogen compound metabolic process	0.007499
SAP30	hsa-miR-30a-5p	KEGG pathway	Mucin type O-Glycan biosynthesis	1.84E-05
	hsa-miR-30b-5p		Axon guidance	0.001843
	hsa-miR-30c-5p		Gap junction	0.006902
	hsa-miR-30d-5p		Morphine addiction	0.006902
	hsa-miR-30e-5p		Arrhythmogenic right ventricular cardiomyopathy (ARVC)	0.006902
		GO terms	Fc-epsilon receptor signaling pathway	2.53E-11
			Neurotrophin TRK receptor signaling pathway	2.74E-07
			Post-translational protein modification	3.24E-06
			Epidermal growth factor receptor signaling pathway	5.30E-06
			Blood coagulation	1.42E-05
			Platelet activation	0.000704
			Cell death	0.005609