HOKKAIDO UNIVERSITY

Title	MicroRNA expression profiling of cat and dog kidneys
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Table 1. Summary of miRNAs highly expressed in renal cortex and medulla of cats and dogs

	Rank	Accession	Gene ID	Cat CO/MD	Dog CO/MD	Cat CO (normalized)	Cat MD (normalized)	Dog CO (normalized)	Dog MD (normalized)	Strand
miRNAs expressed predominantly in CO										
Cats and Dogs	1	miR-378b	MI0016973_1	134.83	4.44	7.08	0.00	3.75	1.60	+
	2	miR-194-2-3p	MI0000733_2	69.83	4.27	6.18	0.05	6.96	4.87	+
	3	miR-491-5p	MI0004680_1	25.43	3.41	7.04	2.37	3.64	1.87	+
	4	miR-425-3p	MI0001447_2	24.80	2.92	7.00	2.37	5.41	3.87	+
	5	miR-204-3p	MI0000247_2	17.05	8.99	7.95	3.86	6.36	3.19	+
	6	miR-204-5p	MI0000247_1	16.58	4.63	18.32	14.26	17.29	15.08	+
	7	miR-708-5p	MI0004692_1	12.74	6.27	8.85	5.18	10.28	7.64	+
	8	let-7f-2-3p	MI0000563_2	10.94	4.55	4.50	1.05	4.05	1.87	+
	9	miR-193b-3p	MI0005484_2	9.70	3.88	13.15	9.87	12.41	10.45	+
	10	miR-193b-5p	MI0005484_1	5.59	4.48	5.99	3.51	5.45	3.28	+
Cats	1	miR-192-5p	MI0000551_1	65.54	-	18.83	12.79	-	-	+
	2	miR-133a-3p	MI0000820_2	41.32	-	10.74	5.37	-	-	+
	3	miR-129-5p	MI0000222_1	40.83	-	10.21	4.86	-	-	+
	4	let-7g-3p	MI0000137_2	33.35	-	5.11	0.05	-	-	+
	5	miR-490-3p	MI0005002_2	31.27	-	6.60	1.63	-	-	+
Dogs	1	miR-323-3p	MI0000592_2	-	15.37	-	-	7.22	3.28	+
	2	miR-377-3p	MI0000794_2	-	12.46	-	-	3.64	0.00	+
	3	miR-1197-3p	MI0006305_2	-	11.10	-	-	5.34	1.87	+
	4	miR-382-5p	MI0000799_1	-	9.27	-	-	5.30	2.09	+
	5	miR-379-3p	MI0000796_2	-	8.88	-	-	4.75	1.60	+
miRNAs predominantly expressed in MD										
	Rank	Accession	Gene ID	Cat MD/CO	Dog MD/CO	Cat CO (normalized)	Cat MD (normalized)	Dog CO (normalized)	Dog MD (normalized)	Strand
Cats and Dogs	1	miR-212-5p	MI0000696_1	35.19	5.05	0.00	5.14	4.05	6.39	+
	2	miR-9-5p	MI0000720_1	20.26	4.12	7.35	11.69	9.70	11.74	+
	3	miR-132-3p	MI0000158_2	15.59	3.96	2.11	6.07	8.70	10.69	+
	4	miR-135a-5p	MI0000161_1	9.60	2.04	2.43	5.69	6.67	7.70	+
	5	miR-203-3p	MI0000246_2	8.78	4.04	5.43	8.57	7.96	9.97	+
	6	miR-10a-5p	MI0000685_1	8.70	2.39	15.11	18.23	16.60	17.86	+
	7	miR-34a-3p	MI0000584_2	8.28	2.93	0.00	3.05	0.05	1.60	+
	8	miR-212-3p	MI0000696_2	7.24	3.93	0.00	2.86	4.86	6.84	+
	9	miR-153-3p	MI0000175_2	5.41	2.09	3.92	6.35	4.96	6.02	+
	10	miR-491-3p	MI0004680_2	4.14	2.05	0.00	2.05	1.05	2.09	+
	11	miR-486-3p	MI0003493_2	2.56	2.43	1.69	3.05	2.86	4.14	+
	12	miR-300-3p	MI0000400_2	2.07	2.93	0.00	1.05	0.05	1.60	+
Cats	1	miR-20a-5p	MI0000568_1	1176.35	-	0.11	10.31	-	-	+
	2	miR-365-3p	MI0000768_2	454.35	-	0.00	8.83	-	-	+
	3	miR-15b-5p	MI0000140_1	422.18	-	0.11	8.83	-	-	+
	4	miR-16-5p	MI0000566_1	287.18	-	6.60	14.77	-	-	+
	5	miR-411-5p	MI0001163_1	113.41	-	2.43	9.26	-	-	+
Dogs	1	miR-132-5p	MI0000158_1	-	7.91	-	-	0.00	2.98	+
	2	miR-129-5p	MI0000222_1	-	4.73	-	-	5.38	7.62	+
	3	miR-181b-2-3p	MI0000823_2	-	3.04	-	-	0.00	1.60	+
	4	miR-27a-5p	MI0000578_1	-	3.04	-	-	4.05	5.66	+
	5	miR-196a-2-3p	MI0000553_2	-	2.62	-	-	5.67	7.06	+

Nomalized values were calculated as descrbed in Supplemental Methods. CO, renal cortex. MD, renal medulla. The top 5 miRNAs with >2.0-fold change in the raito of CO/MD or MD/CO for dogs and cats, the top 10 genes (>2.8-fold increase in the ratio of CO/MD, read number >10.00) and all 12 genes (>2.0-fold increase in the raito of MD/CO) were selected and sorted according to the values in cats. The July 2007 (NCBI37/mm9) mouse (*Mus musculus*) genome data were used as reference (http://genome.ucsc.edu/cgi-bin/hgGateway?db=mm9).

Table 2. mRNA targets of miRNAs expressed in cat and dog kidneys

CO					MD				
	Rank	Symbol	Name	*P* value		Rank	Symbol	Name	*P* value
Cats and Dogs	1	*Rnf123*	ring finger protein 123	0.00000	Cats and Dogs	1	*Hlcs*	holocarboxylase synthetase	2.91593E-12
	2	*Kcnk3*	potassium channel, subfamily K, member 3	0.00003		2	*Asxl1*	additional sex combs like 1 (Drosophila)	3.1903E-10
	3	*Tsr2*	TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)	0.00009		3	*Tnp2*	transition protein 2	5.57781E-10
	4	*Xpo5*	exportin 5	0.00009		4	*Olfr115*	olfactory receptor 115	9.09999E-10
	5	*Zc3h10*	zinc finger CCCH type containing 10	0.00013		5	*Runx1*	runt related transcription factor 1	1.04553E-08
	6	*Gba*	glucosidase, beta, acid	0.00014		6	*Fam188a*	family with sequence similarity 188, member A	2.48121E-08
	7	*Cd83*	CD83 antigen	0.00016		7	*Spice1*	spindle and centriole associated protein 1	2.61967E-08
	8	*Itfg2*	integrin alpha FG-GAP repeat containing 2	0.00017		8	*Bckdhb*	branched chain ketoacid dehydrogenase E1, beta polypeptide	2.75521E-08
	9	*Cnnm1*	cyclin M1	0.00032		9	*Myocd*	myocardin	2.78261E-08
	10	*Bahcc1*	BAH domain and coiled-coil containing 1	0.00044		10	*Krt35*	keratin 35	3.39958E-08
	11	*Tcf23*	transcription factor 23	0.00045		11	*Adc*	arginine decarboxylase	3.49974E-08
	12	*Rag1*	recombination activating gene 1	0.00062		12	*Tlk1*	tousled-like kinase 1	3.60679E-08
	13	*Txndc11*	thioredoxin domain containing 11	0.00062		13	*Cd36*	CD36 antigen	3.73966E-08
	14	*Ceacam9*	carcinoembryonic antigen-related cell adhesion molecule 9	0.00063		14	*Mkx*	mohawk homeobox	4.01769E-08
	15	*Ccdc164*	coiled-coil domain containing 164	0.00065		15	*Emilin3*	elastin microfibril interfacer 3	4.02163E-08
Cat only	1	*Bcap29*	B-cell receptor-associated protein 29	0.00012	Cat only	1	*Nfxl1*	nuclear transcription factor, X-box binding-like 1	8.68026E-16
	2	*Zfp352*	zinc finger protein 352	0.00014		2	*Ppp6r3*	protein phosphatase 6, regulatory subunit 3	2.33775E-14
	3	*Tceal6*	transcription elongation factor A (SII)-like 6	0.00025		3	*Snhg1*	small nucleolar RNA host gene (non-protein coding) 1	1.09257E-12
	4	*Hoxd13*	homeobox D13	0.00032		4	*Pth*	parathyroid hormone	1.70946E-12
	5	*Tcf7l1*	transcription factor 7-like 1 (T-cell specific, HMG box)	0.00068		5	*Wnk3-ps*	WNK lysine deficient protein kinase 3, pseudogene	1.74067E-12
	6	*Hs3st1*	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	0.00072		6	*Cpsf6*	cleavage and polyadenylation specific factor 6	1.94612E-12
	7	*Rhobtb2*	Rho-related BTB domain containing 2	0.00075		7	*Lcor*	ligand dependent nuclear receptor corepressor	2.82427E-12
	8	*Mpped1*	metallophosphoesterase domain containing 1	0.00099		8	*Trmt11*	tRNA methyltransferase 11 homolog (S. cerevisiae)	3.76256E-12
	9	*Eif2ak1*	eukaryotic translation initiation factor 2 alpha kinase 1	0.00099		9	*Ppp6r2*	protein phosphatase 6, regulatory subunit 2	4.83167E-12
	10	*Tbp*	TATA box binding protein	0.00007		10	*Socs1*	suppressor of cytokine signaling 1	6.59111E-12
	11	*Tceal3*	transcription elongation factor A (SII)-like 3	0.00101		11	*Snx16*	sorting nexin 16	7.52665E-12
	12	*Npm3-ps1*	nucleoplasmin 3, pseudogene 1	0.00107		12	*Tinag*	tubulointerstitial nephritis antigen	9.95279E-12
	13	*Phf15*	PHD finger protein 15	0.00108		13	*Mirg*	miRNA containing gene	1.36354E-10
	14	*Tnpo3*	transportin 3	0.00111		14	*Palm3*	paralemmin 3	1.38085E-10
	15	*Tmsb10*	thymosin, beta 10	0.00115		15	*Hkdc1*	hexokinase domain containing 1	1.70977E-10
Dog only	1	*Rnf34*	ring finger protein 34	0.00008	Dog only	1	*Tcfl5*	transcription factor-like 5 (basic helix-loop-helix)	0.00027
	2	*Igf1r*	insulin-like growth factor I receptor	0.00009		2	*Tbc1d30*	TBC1 domain family, member 30	0.00045
	3	*Ehmt1*	euchromatic histone methyltransferase 1	0.00017		3	*Ccdc104*	coiled-coil domain containing 104	0.00107
	4	*Akirin2*	akirin 2	0.00018		4	*Kcng3*	potassium voltage-gated channel, subfamily G, member 3	0.00116
	5	*Map4k5*	mitogen-activated protein kinase kinase kinase 5	0.00019		5	*Apobec1*	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1	0.00146
	6	*Xrn2*	5'-3' exoribonuclease 2	0.00022		6	*Map2k3*	mitogen-activated protein kinase kinase 3	0.00158
	7	*Cpa6*	carboxypeptidase A6	0.00029		7	*Mtap7d2*	MAP7 domain containing 2	0.00184
	8	*Socs1*	suppressor of cytokine signaling 1	0.00037		8	*Pif1*	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	0.00185
	9	*Shisa5*	shisa homolog 5 (Xenopus laevis)	0.00051		9	*Pmp22*	peripheral myelin protein 22	0.00206
	10	*Atp2b1*	ATPase, Ca++ transporting, plasma membrane 1	0.00051		10	*Dph1*	DPH1 homolog (S. cerevisiae)	0.00316
	11	*Skint7*	selection and upkeep of intraepithelial T cells 7	0.00052		11	*Xirp2*	xin actin-binding repeat containing 2	0.00316
	12	*Stat4*	signal transducer and activator of transcription 4	0.00056		12	*Usp18*	ubiquitin specific peptidase 18	0.00337
	13	*Iqcg*	IQ motif containing G	0.00061		13	*Lonrf1*	LON peptidase N-terminal domain and ring finger 1	0.00344
	14	*L3mbtl3*	l(3)mbt-like 3 (Drosophila)	0.00073		14	*Chi3l3*	chitinase 3-like 3	0.00347
	15	*Snx24*	sorting nexing 24	0.00082		15	*Fmo3*	flavin containing monooxygenase 3	0.00369

The top 15 genes are listed. CO, renal cortex. MD, renal medulla.