

## Supplemental data to article

### **Molecular pathogenesis of post-transplant Acute Kidney Injury: assessment of whole-genome mRNA and miRNA profiles**

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**Table S1.** 245 significantly differentially regulated mRNAs comparing post-TX AKI and protocol biopsies from allografts with primary graft function

Probe Set ID	Gene Symbol	raw p-value	Fold change	Gene Description <b>bold.....molecular features discussed as biomarker candidates of AKI</b>
17051827	AKR1B10	9.14E-03	7.88	aldo-keto reductase family 1, member B10 (aldose reductase)
16919547	SLPI	1.55E-03	5.67	secretory leukocyte peptidase inhibitor
16971643	FGB	3.63E-04	5.20	fibrinogen beta chain
16965606	SLC34A2	4.34E-04	3.13	solute carrier family 34 (sodium phosphate), member 2
16827679	NQO1	6.00E-03	3.01	NAD(P)H dehydrogenase, quinone 1
16980836	FGA	7.47E-04	2.95	fibrinogen alpha chain
<b>16743647</b>	<b>MMP7</b>	<b>3.42E-02</b>	<b>2.88</b>	<b>matrix metalloproteinase 7 (matrilysin, uterine)</b>
16775083	OLFM4	6.15E-03	2.86	olfactomedin 4
16924602	ADAMTS1	1.99E-03	2.71	ADAM metalloproteinase with thrombospondin type 1 motif, 1
<b>17118303</b>	<b>COL1A2</b>	<b>2.30E-03</b>	<b>2.71</b>	<b>collagen, type I, alpha 2</b>
16904193	ITGB6	7.24E-04	2.70	integrin, beta 6
17000463	EGR1	3.37E-03	2.40	early growth response 1
<b>16693414</b>	<b>S100A8</b>	<b>7.43E-04</b>	<b>2.40</b>	<b>S100 calcium binding protein A8</b>
17117736	SOCS3	3.71E-03	2.36	suppressor of cytokine signaling 3
17021437	CGA	2.60E-02	2.33	glycoprotein hormones, alpha polypeptide
16997795	VCAN-AS1	1.61E-02	2.25	VCAN antisense RNA 1 (non-protein coding)
16943467	NFKBIZ	1.16E-03	2.10	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta
16981266	DDX60L	2.74E-02	2.06	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like
16787902	SERPINA3	1.08E-03	2.03	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
<b>17089525</b>	<b>LCN2</b>	<b>5.02E-03</b>	<b>1.95</b>	<b>lipocalin 2</b>
16760792	CD163	2.77E-02	1.94	CD163 molecule
17000641	ECSCR	9.53E-03	1.94	endothelial cell surface expressed chemotaxis and apoptosis regulator
16994434	DNAH5	1.04E-03	1.93	dynein, axonemal, heavy chain 5

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17080648	HAS2	3.27E-02	1.91	hyaluronan synthase 2	
17097661	TNC	3.53E-02	1.84	tenascin C	
16781606	ECRP	2.78E-03	1.83	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) pseudogene	
16743874	CASP5	1.81E-02	1.83	caspase 5, apoptosis-related cysteine peptidase	
16760928	CLEC4E	3.65E-02	1.79	C-type lectin domain family 4, member E	
16886491	TNFAIP6	1.71E-02	1.79	tumor necrosis factor, alpha-induced protein 6	
16744572	NNMT	4.46E-03	1.77	nicotinamide N-methyltransferase	
16986913	VCAN	4.35E-02	1.77	versican	
16885189	RNU4ATAC	1.21E-02	1.76	RNA, U4atac small nuclear (U12-dependent splicing)	
<b>17118269</b>	<b>NAMPT</b>	<b>1.06E-03</b>	<b>1.75</b>	<b>nicotinamide phosphoribosyltransferase</b>	
16793678	HIF1A-AS2	1.35E-03	1.74	HIF1A antisense RNA 2 (non-protein coding)	
16962661	CLDN1	2.41E-02	1.73	claudin 1	
16909021	SERPINE2	5.95E-03	1.73	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	
16749423	ARNTL2	4.60E-03	1.72	aryl hydrocarbon receptor nuclear translocator-like 2	
16871546	TYROBP	3.65E-02	1.70	TYRO protein tyrosine kinase binding protein	
17016512	HIST1H2AM	1.17E-02	1.70	histone cluster 1, H2am	
16960911	LXN	7.72E-03	1.69	latexin	
16974534	PROM1	4.79E-02	1.69	prominin 1	
16968213	ANXA3	6.72E-03	1.68	annexin A3	
16984244	OSMR	1.80E-03	1.66	oncostatin M receptor	
<b>17002128</b>	<b>HAVCR1</b>	<b>4.23E-02</b>	<b>1.66</b>	<b>hepatitis A virus cellular receptor 1</b>	
16984689	ITGA2	1.72E-03	1.65	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	
17119264	NOP56	2.55E-02	1.65	NOP56 ribonucleoprotein homolog (yeast)	
16785048	FLJ22447	2.83E-02	1.65	uncharacterized LOC400221	
17118854	TAF1D	1.22E-03	1.65	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	
16909828	COL6A3	4.73E-03	1.65	collagen, type VI, alpha 3	
17118720	GAS5	8.11E-03	1.65	growth arrest-specific 5 (non-protein coding)	

Probe Set ID	Gene Symbol	raw p-value	Fold change	Gene Description <b>bold.....molecular features discussed as biomarker candidates of AKI</b>
17118666	RABGGTB	7.57E-03	1.64	Rab geranylgeranyltransferase, beta subunit
17118670	RPL5	2.28E-02	1.64	ribosomal protein L5
16768297	DUSP6	6.42E-05	1.63	dual specificity phosphatase 6
<b>16971631</b>	<b>TLR2</b>	<b>1.18E-02</b>	<b>1.63</b>	<b>toll-like receptor 2</b>
16850517	NDC80	2.70E-02	1.62	NDC80 kinetochore complex component homolog ( <i>S. cerevisiae</i> )
16903537	NMI	1.24E-02	1.62	N-myc (and STAT) interactor
17080486	TNFRSF11B	3.23E-03	1.62	tumor necrosis factor receptor superfamily, member 11b
16835158	ITGB3	2.44E-02	1.62	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
16801473	AQP9	1.06E-02	1.60	aquaporin 9
17045198	ANLN	1.16E-02	1.59	anillin, actin binding protein
16690511	TAF13	1.17E-02	1.58	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa
16725227	MS4A14	2.40E-02	1.58	membrane-spanning 4-domains, subfamily A, member 14
16851397	RBBP8	2.19E-04	1.56	retinoblastoma binding protein 8
16969439	ARHGEF38	9.83E-03	1.56	Rho guanine nucleotide exchange factor (GEF) 38
17025560	SDIM1	3.21E-02	1.55	stress responsive DNAJB4 interacting membrane protein 1
16768941	IKBIP	4.58E-03	1.54	IKBKB interacting protein
17110322	EFHC2	3.06E-02	1.54	EF-hand domain (C-terminal) containing 2
16914264	WFDC2	1.13E-02	1.53	WAP four-disulfide core domain 2
16734755	RRM1-AS1	2.30E-02	1.53	RRM1 antisense RNA 1 (non-protein coding)
16912379	TPX2	1.36E-02	1.53	TPX2, microtubule-associated, homolog ( <i>Xenopus laevis</i> )
16735751	LYVE1	7.55E-04	1.53	lymphatic vessel endothelial hyaluronan receptor 1
16893704	FAM110C	7.62E-03	1.52	family with sequence similarity 110, member C
16707503	EXOC6	8.75E-04	1.52	exocyst complex component 6
16969686	CCDC109B	2.59E-02	1.51	coiled-coil domain containing 109B
16878541	SPDYA	1.32E-02	1.51	speedy homolog A ( <i>Xenopus laevis</i> )
16991859	HMMR	3.75E-02	1.51	hyaluronan-mediated motility receptor (RHAMM)
17024144	IFNGR1	4.61E-03	1.51	interferon gamma receptor 1

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16948021	ECT2	1.82E-03	1.51	epithelial cell transforming sequence 2 oncogene
16720077	IFITM2	3.87E-02	1.51	interferon induced transmembrane protein 2
16943336	TMEM45A	2.14E-03	1.50	transmembrane protein 45A
16761997	PLCZ1	9.81E-04	0.67	phospholipase C, zeta 1
17102607	TSPAN7	1.11E-03	0.67	tetraspanin 7
16874249	SLC6A16	1.43E-02	0.66	solute carrier family 6, member 16
16908575	SLC23A3	1.20E-03	0.66	solute carrier family 23 (nucleobase transporters), member 3
16899043	NAT8	1.61E-02	0.66	N-acetyltransferase 8 (GCN5-related, putative)
17103717	CLCN5	3.61E-03	0.66	chloride channel, voltage-sensitive 5
16835816	ACSF2	1.52E-02	0.66	acyl-CoA synthetase family member 2
16899580	SUCLG1	1.84E-02	0.66	succinate-CoA ligase, alpha subunit
16819264	MT1X	4.35E-02	0.66	metallothionein 1X
16745366	THY1	4.41E-04	0.66	Thy-1 cell surface antigen
17095056	PRUNE2	1.42E-03	0.66	prune homolog 2 (Drosophila)
16799106	SLC12A6	6.12E-03	0.66	solute carrier family 12 (potassium/chloride transporters), member 6
16714944	PBLD	1.91E-02	0.66	phenazine biosynthesis-like protein domain containing
16883938	PLGLA	3.52E-02	0.66	plasminogen-like A
17015140	BPHL	4.60E-03	0.65	biphenyl hydrolase-like (serine hydrolase)
16878081	KHK	1.59E-02	0.65	ketoheokinase (fructokinase)
16867558	FUT6	8.20E-03	0.65	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)
17108799	ARSE	3.63E-03	0.65	arylsulfatase E (chondrodysplasia punctata 1)
16753270	SLC16A7	1.21E-02	0.65	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
17002176	FNDC9	2.53E-02	0.65	fibronectin type III domain containing 9
17055390	DGKB	8.04E-04	0.65	diacylglycerol kinase, beta 90kDa
16907546	GCSHP3	2.59E-03	0.65	glycine cleavage system protein H (aminomethyl carrier) pseudogene 3
16688469	PTGER3	1.56E-03	0.65	prostaglandin E receptor 3 (subtype EP3)
17094766	TRPM3	2.15E-03	0.65	transient receptor potential cation channel, subfamily M, member 3

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17003034	KIAA1191	1.90E-02	0.65	KIAA1191	
16995155	AGXT2	4.04E-02	0.65	alanine--glyoxylate aminotransferase 2	
16965179	C1QTNF7	8.67E-04	0.65	C1q and tumor necrosis factor related protein 7	
16757710	PEBP1	2.58E-04	0.64	phosphatidylethanolamine binding protein 1	
16874097	HSD17B14	3.91E-02	0.64	hydroxysteroid (17-beta) dehydrogenase 14	
17006628	MCCD1	4.97E-03	0.64	mitochondrial coiled-coil domain 1	
16939203	XYLB	2.09E-03	0.64	xylulokinase homolog (H. influenzae)	
16806999	GOLGA8A	3.25E-03	0.64	golgin A8 family, member A	
17012761	TCF21	1.49E-03	0.64	transcription factor 21	
16714433	PCDH15	6.30E-03	0.64	protocadherin-related 15	
16816563	ACSM5	2.20E-02	0.64	acyl-CoA synthetase medium-chain family member 5	
16732755	GRAMD1B	4.18E-03	0.64	GRAM domain containing 1B	
16955535	ACOX2	1.21E-02	0.64	acyl-CoA oxidase 2, branched chain	
16995177	PRLR	2.90E-02	0.64	prolactin receptor	
16816373	ABCC6P1	4.75E-04	0.64	ATP-binding cassette, sub-family C, member 6 pseudogene 1	
17004273	NQO2	9.64E-03	0.64	NAD(P)H dehydrogenase, quinone 2	
16928258	UPB1	7.38E-03	0.64	ureidopropionase, beta	
17067284	EPHX2	6.05E-03	0.64	epoxide hydrolase 2, cytoplasmic	
<b>16716659</b>	<b>RBP4</b>	<b>2.08E-02</b>	<b>0.63</b>	<b>retinol binding protein 4, plasma</b>	
16717970	CYP17A1	1.71E-02	0.63	cytochrome P450, family 17, subfamily A, polypeptide 1	
16777198	CRYL1	7.52E-03	0.63	crystallin, lambda 1	
16693082	SELENBP1	4.01E-04	0.63	selenium binding protein 1	
16701630	OR2T35	4.81E-03	0.63	olfactory receptor, family 2, subfamily T, member 35	
16843549	CCL14-CCL15	3.32E-03	0.63	CCL14-CCL15 readthrough	
17078626	SLC10A5	7.28E-03	0.63	solute carrier family 10 (sodium/bile acid cotransporter family), member 5	
16906031	ZNF385B	8.17E-04	0.63	zinc finger protein 385B	
16796247	SERPINA6	1.23E-03	0.62	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6	

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17014459	PLG	3.80E-02	0.62	plasminogen
16712168	CUBN	2.21E-02	0.62	cubilin (intrinsic factor-cobalamin receptor)
17077023	PXDNL	3.03E-02	0.62	peroxidasin homolog (Drosophila)-like
16722844	NELL1	7.30E-03	0.62	NEL-like 1 (chicken)
17094946	TRPM6	1.89E-02	0.62	transient receptor potential cation channel, subfamily M, member 6
17047298	SPDYE5	2.78E-02	0.62	speedy homolog E5 (Xenopus laevis)
17052425	MGAM	2.29E-02	0.62	maltase-glucoamylase (alpha-glucosidase)
16808665	GATM	4.61E-03	0.62	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
16949322	FETUB	6.23E-03	0.62	fetuin B
16966621	CWH43	3.41E-03	0.62	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)
16858555	ZNF69	7.72E-03	0.62	zinc finger protein 69
16834603	TMEM106A	6.37E-03	0.61	transmembrane protein 106A
16725841	SCGB1D2	2.40E-02	0.61	secretoglobin, family 1D, member 2
16824588	GP2	2.32E-02	0.61	glycoprotein 2 (zymogen granule membrane)
16682016	AGMAT	3.63E-02	0.61	agmatine ureohydrolase (agmatinase)
16827655	TMED6	1.46E-02	0.61	transmembrane emp24 protein transport domain containing 6
16794632	ALDH6A1	6.98E-03	0.61	aldehyde dehydrogenase 6 family, member A1
16960844	VEPH1	6.71E-04	0.61	ventricular zone expressed PH domain homolog 1 (zebrafish)
17092331	PTPRD	5.29E-03	0.61	protein tyrosine phosphatase, receptor type, D
16968488	WDFY3-AS2	4.42E-03	0.60	WDFY3 antisense RNA 2 (non-protein coding)
16739733	HRASLS5	9.14E-04	0.60	HRAS-like suppressor family, member 5
16989137	LEAP2	1.83E-04	0.60	liver expressed antimicrobial peptide 2
16842103	SHMT1	7.98E-03	0.60	serine hydroxymethyltransferase 1 (soluble)
16683300	TCEA3	1.83E-03	0.60	transcription elongation factor A (SII), 3
16981931	ENPP6	1.52E-02	0.60	ectonucleotide pyrophosphatase/phosphodiesterase 6
16719892	ECHS1	6.81E-03	0.60	enoyl CoA hydratase, short chain, 1, mitochondrial
16822035	DPEP1	1.84E-02	0.60	dipeptidase 1 (renal)



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16800785	SLC12A1	2.04E-02	0.59	solute carrier family 12 (sodium/potassium/chloride transporters), member 1
16855629	RNF152	1.18E-02	0.59	ring finger protein 152
16670681	ANXA9	1.37E-03	0.59	annexin A9
17106852	XPNPEP2	3.76E-02	0.59	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound
17106297	ZCCHC16	9.83E-03	0.59	zinc finger, CCHC domain containing 16
16815735	ABAT	1.47E-02	0.59	4-aminobutyrate aminotransferase
16782016	TRAJ56	3.13E-02	0.59	T cell receptor alpha joining 56
17000566	SLC23A1	7.02E-03	0.59	solute carrier family 23 (nucleobase transporters), member 1
16842673	SPAG5	8.52E-04	0.58	sperm associated antigen 5
17070360	RALYL	1.72E-03	0.58	RALY RNA binding protein-like
16787972	TCL6	3.52E-04	0.58	T-cell leukemia/lymphoma 6 (non-protein coding)
17055472	SOSTDC1	1.34E-02	0.58	sclerostin domain containing 1
16816579	ACSM2A	1.25E-02	0.58	acyl-CoA synthetase medium-chain family member 2A
16960698	MME-AS1	4.87E-02	0.58	MME antisense RNA 1 (non-protein coding)
16969591	HADH	4.79E-04	0.57	hydroxyacyl-CoA dehydrogenase
16983765	NPR3	1.69E-03	0.57	natriuretic peptide receptor C/guanylate cyclase C (atriuretic peptide receptor C)
16701620	OR2T10	2.53E-02	0.57	olfactory receptor, family 2, subfamily T, member 10
17101262	ARSF	1.46E-03	0.57	arylsulfatase F
16993065	SLC34A1	5.02E-03	0.57	solute carrier family 34 (sodium phosphate), member 1
16982699	SLC6A19	7.49E-03	0.57	solute carrier family 6 (neutral amino acid transporter), member 19
<b>16824602</b>	<b>UMOD</b>	<b>2.27E-02</b>	<b>0.56</b>	<b>uromodulin</b>
16949334	HRG	1.07E-02	0.56	histidine-rich glycoprotein
16673763	TOP1P1	3.58E-02	0.56	topoisomerase (DNA) I pseudogene 1
16871239	PEPD	1.75E-02	0.56	peptidase D
16673748	FMO4	1.04E-02	0.56	flavin containing monooxygenase 4
16698573	PM20D1	1.12E-03	0.56	peptidase M20 domain containing 1
16780189	GPC5-AS1	1.22E-02	0.56	GPC5 antisense RNA 1 (non-protein coding)

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<b>17044253</b>	<b>GPMB</b>	<b>1.04E-02</b>	<b>0.56</b>	<b>glycoprotein (transmembrane) nmb</b>
<b>17074296</b>	<b>DEFB1</b>	<b>3.78E-02</b>	<b>0.56</b>	<b>defensin, beta 1</b>
16695262	KCNJ10	3.92E-04	0.55	potassium inwardly-rectifying channel, subfamily J, member 10
16991527	CYFIP2	2.00E-03	0.55	cytoplasmic FMR1 interacting protein 2
16840723	SAT2	4.62E-03	0.55	spermidine/spermine N1-acetyltransferase family member 2
17057736	DDC	1.46E-02	0.55	dopa decarboxylase (aromatic L-amino acid decarboxylase)
16773086	FGF9	4.37E-04	0.55	fibroblast growth factor 9 (glia-activating factor)
16708728	SFXN2	4.05E-03	0.55	sideroflexin 2
16800707	SEMA6D	8.46E-03	0.55	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D
17078783	SLC7A13	4.32E-02	0.54	solute carrier family 7 (anionic amino acid transporter), member 13
16800061	CAPN3	3.50E-03	0.54	calpain 3, (p94)
16869942	CYP4F2	3.58E-02	0.54	cytochrome P450, family 4, subfamily F, polypeptide 2
17020059	GSTA2	4.83E-02	0.54	glutathione S-transferase alpha 2
16850069	DCXR	2.39E-02	0.54	dicarbonyl/L-xylulose reductase
16728632	FOLR1	2.01E-03	0.54	folate receptor 1 (adult)
16832634	PIPOX	1.28E-02	0.54	pipecolic acid oxidase
16780186	GPC5-AS2	4.92E-02	0.54	GPC5 antisense RNA 2 (non-protein coding)
16669347	HAO2	1.90E-02	0.54	hydroxyacid oxidase 2 (long chain)
17072059	SLC30A8	2.29E-02	0.53	solute carrier family 30 (zinc transporter), member 8
16949348	KNG1	8.16E-03	0.53	kininogen 1
<b>16684429</b>	<b>FABP3</b>	<b>6.78E-04</b>	<b>0.53</b>	<b>fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)</b>
17013677	IYD	2.91E-03	0.52	iodotyrosine deiodinase
17096030	FBP1	7.99E-03	0.52	fructose-1,6-bisphosphatase 1
16931716	MIOX	2.66E-02	0.52	myo-inositol oxygenase
16808563	SORD	1.22E-02	0.52	sorbitol dehydrogenase
16970132	MYOZ2	5.66E-03	0.52	myozenin 2
16729875	FOLH1B	1.73E-02	0.51	folate hydrolase 1B

Probe Set ID	Gene Symbol	raw p-value	Fold change	Gene Description <b>bold.....molecular features discussed as biomarker candidates of AKI</b>
16679811	OR2T5	2.92E-02	0.51	olfactory receptor, family 2, subfamily T, member 5
16986072	TMEM174	1.50E-02	0.51	transmembrane protein 174
17087615	LPPR1	5.54E-04	0.51	lipid phosphate phosphatase-related protein type 1
16701617	OR2T34	2.26E-02	0.51	olfactory receptor, family 2, subfamily T, member 34
17020520	LGSN	2.76E-02	0.51	lengsin, lens protein with glutamine synthetase domain
16899048	NAT8B	3.28E-03	0.50	N-acetyltransferase 8B (GCN5-related, putative, gene/pseudogene)
16664897	DIO1	6.87E-03	0.50	deiodinase, iodothyronine, type I
17007950	PNPLA1	1.15E-03	0.50	patatin-like phospholipase domain containing 1
16737282	ELF5	3.12E-03	0.50	E74-like factor 5 (ets domain transcription factor)
<b>16773919</b>	<b>KL</b>	<b>2.97E-03</b>	<b>0.49</b>	<b>klotho</b>
16673731	FMO1	2.45E-03	0.49	flavin containing monooxygenase 1
16716403	SLC16A12	4.57E-04	0.49	solute carrier family 16, member 12 (monocarboxylic acid transporter 12)
16835738	PPP1R9B	7.62E-05	0.48	protein phosphatase 1, regulatory subunit 9B
16820157	HSD11B2	1.09E-02	0.48	hydroxysteroid (11-beta) dehydrogenase 2
16676498	MFSD4	8.10E-03	0.48	major facilitator superfamily domain containing 4
16973085	F11	1.42E-03	0.47	coagulation factor XI
16976561	UGT2B11	1.39E-02	0.47	UDP glucuronosyltransferase 2 family, polypeptide B11
16855305	MRO	2.41E-03	0.46	maestro
16967743	AFM	2.75E-02	0.46	afamin
16756578	DAO	2.58E-03	0.45	D-amino-acid oxidase
17075553	STC1	1.53E-02	0.45	stanniocalcin 1
16701626	OR2T11	6.89E-03	0.45	olfactory receptor, family 2, subfamily T, member 11
<b>16969729</b>	<b>EGF</b>	<b>3.23E-03</b>	<b>0.43</b>	<b>epidermal growth factor</b>
17001879	SLC36A2	2.87E-02	0.43	solute carrier family 36 (proton/amino acid symporter), member 2
16687583	FAM151A	1.41E-02	0.43	family with sequence similarity 151, member A
16704199	FXYD4	3.68E-02	0.41	FXYD domain containing ion transport regulator 4
17075589	NEFL	4.19E-02	0.40	neurofilament, light polypeptide

Probe Set ID	Gene Symbol	raw p-value	Fold change	Gene Description	<b>bold.....molecular features discussed as biomarker candidates of AKI</b>
16785709	RDH12	3.88E-03	0.40	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	
16934643	PVALB	2.02E-04	0.39	parvalbumin	
17066278	LPL	2.44E-03	0.37	lipoprotein lipase	
16834525	G6PC	1.46E-02	0.34	glucose-6-phosphatase, catalytic subunit	
16962671	TMEM207	1.57E-04	0.32	transmembrane protein 207	
16988781	CTXN3	1.38E-04	0.32	cortexin 3	

**Table S2.** Significantly over-represented biological processes embedded in the post-TX mRNA signature (245 mRNAs).

Biological process	Genes	adjusted p-value (Benjamini-Hochberg)
response to wounding	KNG1, F11, NFKBIZ, NMI, PTGER3, GATM, S100A8, KL, TNC, EPHX2, TLR2, ITGA2, ITGB3, PLG, CD163, TNFAIP6, LYVE1, FGA, FGB, ITGB6, SERPINA3, PEBP1, VCAN, NEFL	6.82E-04
response to toxin	DDC, CYP17A1, TRPM6, SLC23A1, EPHX2, PEBP1, BPHL, NQO1, NEFL	9.00E-04
response to metal ion	KHK, TNFRSF11B, AQP9, FGA, GATM, FGB, SLC34A1, ABAT, PEBP1, CAPN3, MT1X	3.70E-03
oxidation reduction	ACOX2, ALDH6A1, SORD, HSD17B14, NELL1, PIPOX, PXDNL, IYD, FMO4, RDH12, PRUNE2, CYP17A1, FMO1, AKR1B10, MIOX, HAO2, HSD11B2, DAO, CYP4F2, DIO1, NQO1, HADH, DCXR, NQO2	3.97E-03
fatty acid metabolic process	ACOX2, LPL, CRYL1, ACSM2A, HAO2, EPHX2, FABP3, ECHS1, CYP4F2, HADH, ACSF2, ACSM5	1.77E-02
response to inorganic substance	KHK, TNFRSF11B, AQP9, FGA, GATM, FGB, SLC34A1, ABAT, PEBP1, CAPN3, MT1X, PXDNL	2.02E-02

**Table S3.** 39 significantly differentially regulated mRNAs comparing AKI and PGF allografts after baseline adjustment

Probe Set ID	Gene Symbol	raw p-value	Fold change	Gene Description <b>bold.....molecular features discussed as biomarker candidates of AKI</b>
16919547	SLPI	1.20E-03	15.17	secretory leukocyte peptidase inhibitor
17051827	AKR1B10	5.50E-03	11.26	aldo-keto reductase family 1, member B10 (aldose reductase)
16775083	OLFM4	2.98E-03	7.88	olfactomedin 4
16787902	SERPINA3	2.91E-03	7.03	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
16827679	NQO1	8.28E-03	4.08	NAD(P)H dehydrogenase, quinone 1
<b>16743647</b>	<b>MMP7</b>	<b>1.54E-02</b>	<b>4.06</b>	<b>matrix metalloproteinase 7 (matrilysin, uterine)</b>
<b>17118303</b>	<b>COL1A2</b>	<b>6.93E-03</b>	<b>3.40</b>	<b>collagen, type I, alpha 2</b>
16760792	CD163	1.69E-02	3.12	CD163 molecule
<b>16693414</b>	<b>S100A8</b>	<b>1.66E-02</b>	<b>3.09</b>	<b>S100 calcium binding protein A8</b>
17021437	CGA	1.18E-02	2.91	glycoprotein hormones, alpha polypeptide
16781606	ECRP	5.51E-04	2.42	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) pseudogene
17000641	ECSCR	1.34E-02	2.40	endothelial cell surface expressed chemotaxis and apoptosis regulator
16735751	LYVE1	2.09E-03	2.28	lymphatic vessel endothelial hyaluronan receptor 1
<b>17089525</b>	<b>LCN2</b>	<b>8.81E-03</b>	<b>2.28</b>	<b>lipocalin 2</b>
16760928	CLEC4E	1.15E-02	1.95	C-type lectin domain family 4, member E
16948021	ECT2	9.37E-03	1.93	epithelial cell transforming sequence 2 oncogene
16969439	ARHGEF38	5.56E-03	1.90	Rho guanine nucleotide exchange factor (GEF) 38
17110322	EFHC2	6.80E-03	1.88	EF-hand domain (C-terminal) containing 2
16994434	DNAH5	5.58E-04	1.81	dynein, axonemal, heavy chain 5
17118666	RABGGTB	1.21E-02	1.79	Rab geranylgeranyltransferase, beta subunit
16707503	EXOC6	1.88E-03	1.78	exocyst complex component 6
17024144	IFNGR1	7.64E-03	1.77	interferon gamma receptor 1
16851397	RBBP8	1.30E-03	1.76	retinoblastoma binding protein 8
16984689	ITGA2	8.27E-04	1.74	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)
16943336	TMEM45A	2.43E-03	1.71	transmembrane protein 45A

Probe Set ID	Gene Symbol	raw p-value	Fold change	Gene Description <b>bold.....molecular features discussed as biomarker candidates of AKI</b>
16909828	COL6A3	1.03E-02	1.70	collagen, type VI, alpha 3
16745366	THY1	1.19E-03	0.57	Thy-1 cell surface antigen
17087615	LPPR1	3.00E-03	0.57	lipid phosphate phosphatase-related protein type 1
16991527	CYFIP2	2.80E-03	0.52	cytoplasmic FMR1 interacting protein 2
16695262	KCNJ10	3.00E-04	0.52	potassium inwardly-rectifying channel, subfamily J, member 10
17101262	ARSF	3.30E-03	0.47	arylsulfatase F
17094946	TRPM6	2.19E-03	0.45	transient receptor potential cation channel, subfamily M, member 6
17072059	SLC30A8	4.78E-03	0.45	solute carrier family 30 (zinc transporter), member 8
16773086	FGF9	8.50E-04	0.45	fibroblast growth factor 9 (glia-activating factor)
16835738	PPP1R9B	3.32E-03	0.43	protein phosphatase 1, regulatory subunit 9B
16934643	PVALB	2.75E-03	0.42	parvalbumin
<b>16773919</b>	<b>KL</b>	<b>4.92E-03</b>	<b>0.42</b>	<b>klotho</b>
17007950	PNPLA1	1.10E-03	0.36	patatin-like phospholipase domain containing 1
16962671	TMEM207	9.31E-04	0.33	transmembrane protein 207

**Table S4.** Significantly differentially regulated miRNAs comparing post-TX AKI and protocol biopsies from allografts with primary graft function.

Probe Set ID	miRNA Name	miRBase Accession	raw p-value	Fold change
hsa-miR-21-star_st	hsa-miR-21-3p	MIMAT0004494	1.64E-02	2.22
hsa-miR-3687_st	hsa-miR-3687	MIMAT0018115	1.47E-02	1.93
hsa-miR-212_st	hsa-miR-212-3p	MIMAT0000269	1.71E-03	1.91
hsa-miR-4433_st	hsa-miR-4433-3p	MIMAT0018949	6.98E-05	1.89
hsa-miR-132_st	hsa-miR-132-3p	MIMAT0000426	5.57E-04	1.86
hsa-miR-4530_st	hsa-miR-4530	MIMAT0019069	7.70E-03	1.85
hsa-miR-1224-5p_st	hsa-miR-1224-5p	MIMAT0005458	6.72E-05	1.85
hsa-miR-4521_st	hsa-miR-4521	MIMAT0019058	5.49E-04	1.84
hsa-miR-885-3p_st	hsa-miR-885-3p	MIMAT0004948	2.93E-03	1.84
hsa-miR-3648_st	hsa-miR-3648	MIMAT0018068	1.28E-03	1.82
hsa-miR-2392_st	hsa-miR-2392	MIMAT0019043	3.22E-03	1.76
hsa-miR-4463_st	hsa-miR-4463	MIMAT0018987	1.96E-03	1.76
hsa-miR-1587_st	hsa-miR-1587	MIMAT0019077	6.01E-03	1.75
hsa-miR-4507_st	hsa-miR-4507	MIMAT0019044	3.08E-03	1.73
hsa-miR-193a-3p_st	hsa-miR-193a-3p	MIMAT0000459	1.33E-02	1.73
hsa-miR-4492_st	hsa-miR-4492	MIMAT0019027	3.12E-02	1.71
hsa-miR-27a-star_st	hsa-miR-27a-5p	MIMAT0004501	2.29E-02	1.69
hsa-miR-1268b_st	hsa-miR-1268b	MIMAT0018925	9.24E-04	1.68
hsa-miR-4685-5p_st	hsa-miR-4685-5p	MIMAT0019771	5.17E-03	1.68
hsa-miR-4505_st	hsa-miR-4505	MIMAT0019041	6.64E-03	1.67
hsa-miR-4430_st	hsa-miR-4430	MIMAT0018945	3.60E-03	1.67
hsa-miR-149-star_st	hsa-miR-149-3p	MIMAT0004609	9.76E-04	1.67
hsa-miR-4299_st	hsa-miR-4299	MIMAT0016851	5.33E-03	1.65
hsa-miR-3679-5p_st	hsa-miR-3679-5p	MIMAT0018104	7.20E-03	1.63
hsa-miR-106b-star_st	hsa-miR-106b-3p	MIMAT0004672	4.57E-02	1.62
hsa-miR-939_st	hsa-miR-939-5p	MIMAT0004982	1.24E-02	1.61
hsa-miR-4749-5p_st	hsa-miR-4749-5p	MIMAT0019885	3.25E-03	1.60
hsa-miR-1228-star_st	hsa-miR-1228-5p	MIMAT0005582	9.39E-03	1.60
hsa-miR-1268_st	hsa-miR-1268a	MIMAT0005922	1.22E-03	1.59
hsa-miR-4508_st	hsa-miR-4508	MIMAT0019045	2.25E-02	1.59
hsa-miR-4487_st	hsa-miR-4487	MIMAT0019021	1.58E-02	1.58
hsa-miR-762_st	hsa-miR-762	MIMAT0010313	3.33E-03	1.58
hsa-miR-3162-5p_st	hsa-miR-3162-5p	MIMAT0015036	8.22E-03	1.57
hsa-miR-4649-5p_st	hsa-miR-4649-5p	MIMAT0019711	8.72E-03	1.57
hsa-miR-182_st	hsa-miR-182-5p	MIMAT0000259	1.62E-02	1.56
hsa-miR-31_st	hsa-miR-31-5p	MIMAT0000089	1.13E-02	1.56
hsa-miR-4763-3p_st	hsa-miR-4763-3p	MIMAT0019913	4.63E-03	1.55
hsa-miR-4750_st	hsa-miR-4750-5p	MIMAT0019887	1.12E-02	1.55
hsa-miR-4690-5p_st	hsa-miR-4690-5p	MIMAT0019779	1.06E-02	1.54

Probe Set ID	miRNA Name	miRBase Accession	raw p-value	Fold change
hsa-miR-4516_st	hsa-miR-4516	MIMAT0019053	3.56E-03	1.54
hsa-miR-23a-star_st	hsa-miR-23a-5p	MIMAT0004496	2.94E-02	1.54
hsa-miR-3656_st	hsa-miR-3656	MIMAT0018076	6.50E-03	1.53
hsa-miR-92b-star_st	hsa-miR-92b-5p	MIMAT0004792	2.30E-02	1.52
hsa-miR-4532_st	hsa-miR-4532	MIMAT0019071	1.55E-02	1.52
hsa-miR-3937_st	hsa-miR-3937	MIMAT0018352	2.92E-02	1.52
hsa-miR-3141_st	hsa-miR-3141	MIMAT0015010	4.82E-03	1.51
hsa-miR-4462_st	hsa-miR-4462	MIMAT0018986	7.11E-03	1.51
hsa-miR-4667-5p_st	hsa-miR-4667-5p	MIMAT0019743	7.21E-03	1.51
hsa-miR-3196_st	hsa-miR-3196	MIMAT0015080	8.67E-03	1.50

**Table S5.** Significantly differentially regulated microRNAs comparing AKI and PGF allografts after baseline adjustment.

Probe Set ID	miRNA Name	miRBase Accession	raw p-value	Fold change
hsa-miR-21-star_st	hsa-miR-21-3p	MIMAT0004494	2.41E-02	3.34
hsa-miR-212_st	hsa-miR-212-3p	MIMAT0000269	6.54E-04	2.63
hsa-miR-132_st	hsa-miR-132-3p	MIMAT0000426	5.77E-04	2.27
hsa-miR-4505_st	hsa-miR-4505	MIMAT0019041	4.75E-02	1.95
hsa-miR-3679-5p_st	hsa-miR-3679-5p	MIMAT0018104	2.67E-02	1.94
hsa-miR-4530_st	hsa-miR-4530	MIMAT0019069	7.45E-03	1.94
hsa-miR-4299_st	hsa-miR-4299	MIMAT0016851	6.88E-03	1.93
hsa-miR-4433_st	hsa-miR-4433-3p	MIMAT0018949	2.41E-03	1.93
hsa-miR-4507_st	hsa-miR-4507	MIMAT0019044	2.13E-02	1.92
hsa-miR-3648_st	hsa-miR-3648	MIMAT0018068	3.73E-03	1.92
hsa-miR-182_st	hsa-miR-182-5p	MIMAT0000259	2.46E-03	1.88
hsa-miR-1587_st	hsa-miR-1587	MIMAT0019077	4.19E-02	1.87
hsa-miR-4667-5p_st	hsa-miR-4667-5p	MIMAT0019743	2.58E-02	1.87
hsa-miR-1224-5p_st	hsa-miR-1224-5p	MIMAT0005458	6.90E-03	1.84
hsa-miR-4685-5p_st	hsa-miR-4685-5p	MIMAT0019771	4.79E-02	1.83
hsa-miR-4430_st	hsa-miR-4430	MIMAT0018945	3.10E-02	1.81
hsa-miR-4749-5p_st	hsa-miR-4749-5p	MIMAT0019885	1.82E-02	1.80
hsa-miR-2392_st	hsa-miR-2392	MIMAT0019043	1.10E-02	1.79
hsa-miR-4690-5p_st	hsa-miR-4690-5p	MIMAT0019779	2.22E-02	1.79
hsa-miR-4463_st	hsa-miR-4463	MIMAT0018987	1.72E-02	1.77
hsa-miR-762_st	hsa-miR-762	MIMAT0010313	3.32E-02	1.77
hsa-miR-4508_st	hsa-miR-4508	MIMAT0019045	4.49E-02	1.72
hsa-miR-149-star_st	hsa-miR-149-3p	MIMAT0004609	2.62E-02	1.69
hsa-miR-3196_st	hsa-miR-3196	MIMAT0015080	4.28E-02	1.67
hsa-miR-4516_st	hsa-miR-4516	MIMAT0019053	1.98E-02	1.66
hsa-miR-1268b_st	hsa-miR-1268b	MIMAT0018925	2.70E-02	1.59

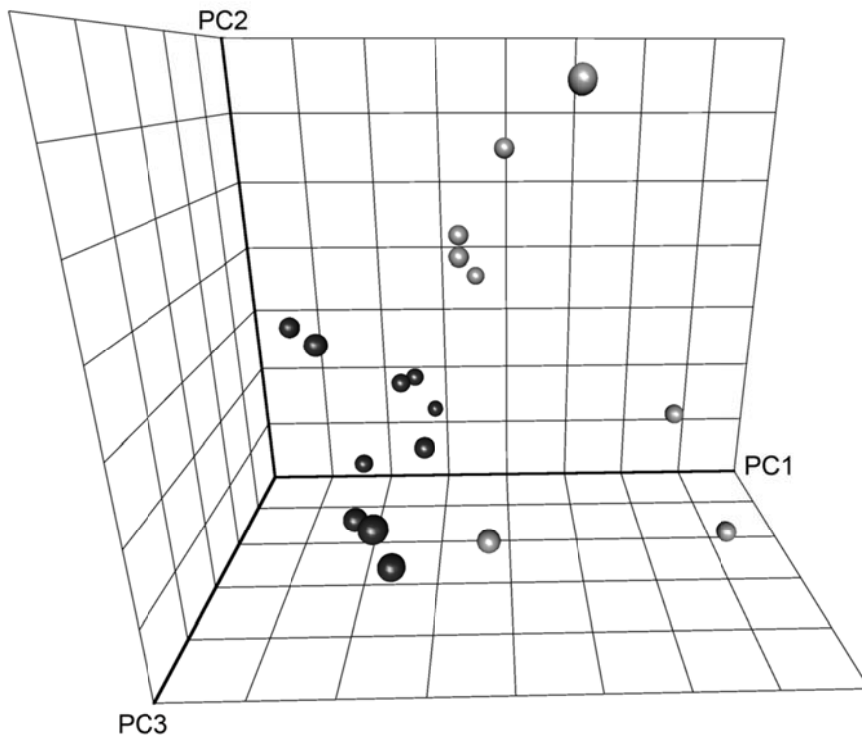


<b>Probe Set ID</b>	<b>miRNA Name</b>	<b>miRBase Accession</b>	<b>raw p-value</b>	<b>Fold change</b>
hsa-miR-1268_st	hsa-miR-1268a	MIMAT0005922	4.72E-02	1.59
hsa-miR-3687_st	hsa-miR-3687	MIMAT0018115	3.02E-02	1.57
hsa-miR-4532_st	hsa-miR-4532	MIMAT0019071	4.35E-02	1.55

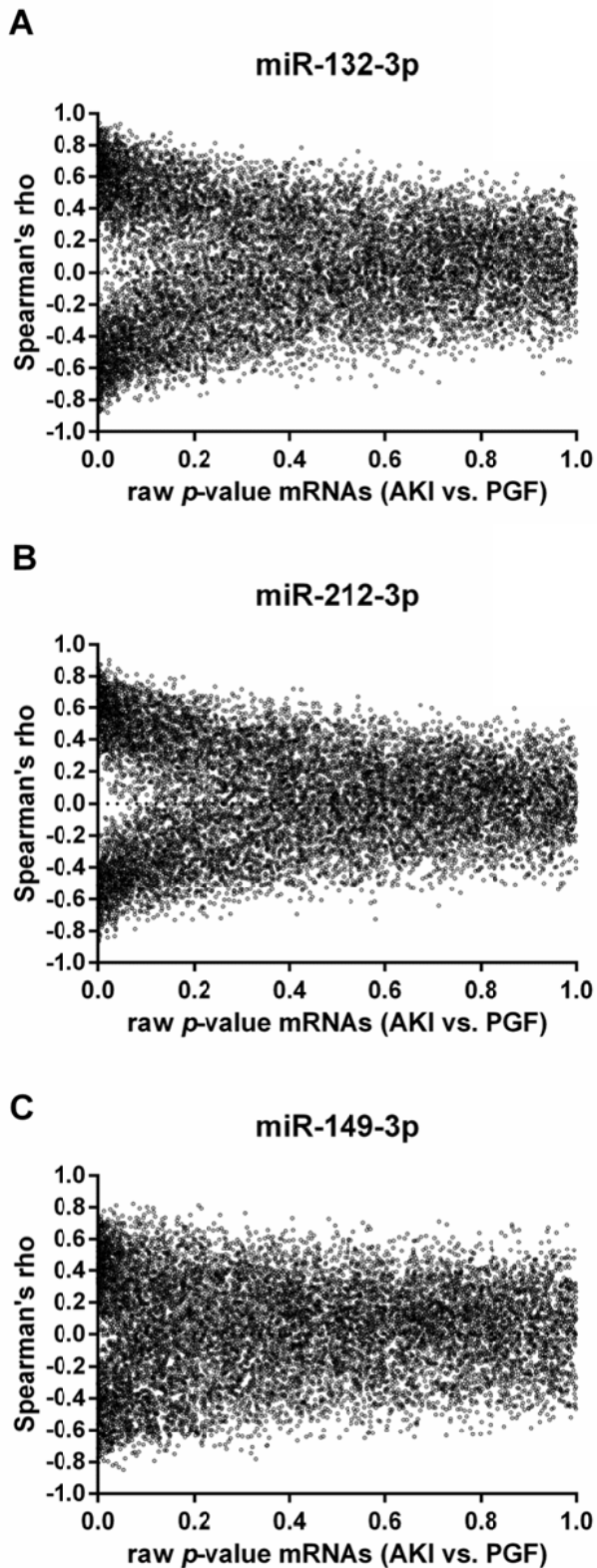
**Table S6.** Highly correlated genes (Spearman's rho > 0.7 or < -0.7) to miR-182-5p, miR-132-3p, miR-212-3p and miR-149-3p out of the baseline adjusted differentially regulated gene list.

Probe Set ID	Gene Symbol	raw p-value	Fold change	Spearman's rho				Gene Description
				hsa-miR-182-5p	hsa-miR-132-3p	hsa-miR-212-3p	hsa-miR-149-3p	
16919547	SLPI	1.20E-03	15.17	0.72	0.82	0.71		secretory leukocyte peptidase inhibitor
16775083	OLFM4	2.98E-03	7.88		0.71			olfactomedin 4
16787902	SERPINA3	2.91E-03	7.03		0.74			serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
16743647	MMP7	1.54E-02	4.06		0.87	0.77		matrix metalloproteinase 7 (matrilysin, uterine)
17118303	COL1A2	6.93E-03	3.40		0.89	0.82		collagen, type I, alpha 2
17000641	ECSCR	1.34E-02	2.40			0.77		endothelial cell surface expressed chemotaxis and apoptosis regulator
17089525	LCN2	8.81E-03	2.28		0.70		0.71	lipocalin 2
16948021	ECT2	9.37E-03	1.93		0.81			epithelial cell transforming sequence 2 oncogene
16969439	ARHGEF38	5.56E-03	1.90	0.77	0.81	0.77		Rho guanine nucleotide exchange factor (GEF) 38
17110322	EFHC2	6.80E-03	1.88	0.70				EF-hand domain (C-terminal) containing 2
17118666	RABGGTB	1.21E-02	1.79		0.80	0.81		Rab geranylgeranyltransferase, beta subunit
16707503	EXOC6	1.88E-03	1.78	0.77	0.87	0.76		exocyst complex component 6
17024144	IFNGR1	7.64E-03	1.77		0.72			interferon gamma receptor 1
16851397	RBBP8	1.30E-03	1.76		0.72			retinoblastoma binding protein 8
16984689	ITGA2	8.27E-04	1.74	0.72	0.75			integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)
16943336	TMEM45A	2.43E-03	1.71	0.78	0.90	0.81		transmembrane protein 45A
16909828	COL6A3	1.03E-02	1.70		0.78			collagen, type VI, alpha 3
16745366	THY1	1.19E-03	0.57	-0.82	-0.88	-0.86		Thy-1 cell surface antigen
17087615	LPPR1	3.00E-03	0.57		-0.72		-0.72	lipid phosphate phosphatase-related protein type 1

16991527	CYFIP2	2.80E-03	0.52				-0.76	cytoplasmic FMR1 interacting protein 2
16695262	KCNJ10	3.00E-04	0.52				-0.78	potassium inwardly-rectifying channel, subfamily J, member 10
17094946	TRPM6	2.19E-03	0.45		-0.81	-0.81		transient receptor potential cation channel, subfamily M, member 6
16773919	KL	4.92E-03	0.42	-0.72	-0.86	-0.74		klotho
17007950	PNPLA1	1.10E-03	0.36		-0.70			patatin-like phospholipase domain containing 1
16962671	TMEM207	9.31E-04	0.33				-0.81	transmembrane protein 207



**Figure S1.** Principal component analysis based on the 245 differentially regulated genes comparing post-TX AKI and PGF allografts. The first three principal components (PC) were plotted, capturing 85% of the variance in the dataset. Acute kidney injury allografts (grey spheres) and allografts with primary kidney function (black spheres) form two distinct clusters.

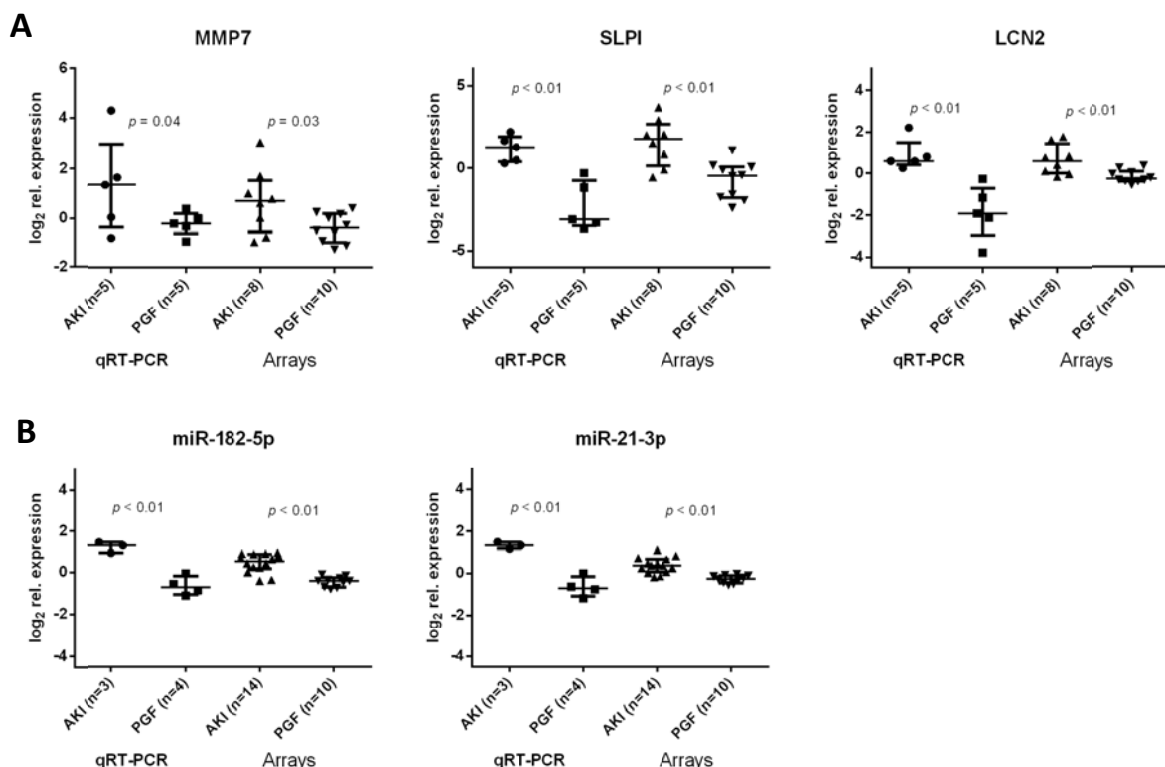


**Figure S2.** Correlation coefficients (Spearman's rho) of (A) miR-132-3p and (B) miR-212-3p (C) miR-149-3p calculated for all mRNAs against the raw  $p$ -values of baseline adjusted mRNA levels between the AKI and PGF group.

## qRT-PCR validation

### Methods

The TaqMan® MicroRNA Reverse Transcription Kit or High-Capacity cDNA Reverse Transcription Kit with RNase Inhibitor were used to synthesize single stranded cDNA. Real-time PCR was performed using the TaqMan® Gene Expression Master Mix, TaqMan® miRNA expression assays with the ABI 7300 Real-Time PCR System. All instruments and reagents were purchased from Life Technologies. Relative gene expression values were evaluated with the  $2^{-\Delta\Delta Ct}$  method using U6 snRNA as control small RNA, PPIA as control mRNA and Stratagene Universal human reference RNA (Stratagene, La Jolla, CA) as reference RNA. qRT-PCR conditions were set according to the manufacturer's recommendations: 10min 95°C, 40 cycles (15sec 95°C, 1min 60°C) with fluorescence reading during annealing step.



**Figure S3.** qRT-PCR validation of significantly differentially regulated **(A)** mRNAs (SLPI, MMP7 and LCN2) and **(B)** miRNAs (miR-182-5p and miR-21-3p) [1] between AKI and control group (PGF). Log<sub>2</sub> (relative expression) values are shown for the qRT-PCR and the array experiment. Individual data points as well as median, 1<sup>st</sup> and 3<sup>rd</sup> quartile are provided.

## Reference

1. Wilflingseder J, Regele H, Perco P, et al. miRNA profiling discriminates types of rejection and injury in human renal allografts. *Transplantation* 2013;95(6):835-41.