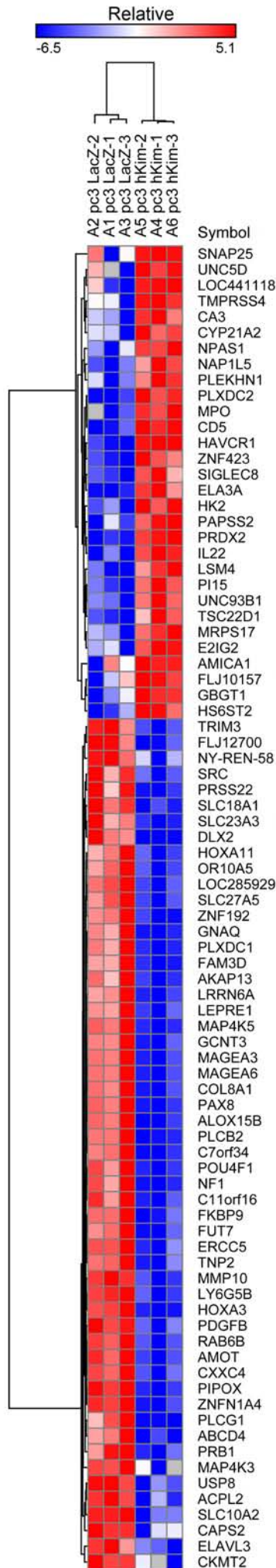


Supplemental Figure 1: Flow cytometric analysis of immune cell infiltration in KIM-1 wild-type or KIM-1^{Δmucin} kidneys. (A) Representative cell pellets of total isolated cells resulting from tissue digestion of similar sized kidneys showing discrepancy in pellet size (arrows) between wild-type or KIM-1^{Δmucin} (Mut) samples. (Representative of 3 pairs of isolates) (B) Total protein of cell isolates from post-ischemic wild-type and KIM-1^{Δmucin} mice. (C) Flow cytometric analysis of the total number of cells isolated from kidneys following tissue digestion. (D) Flow cytometric analysis of the number of CD45+ cells per ug isolated cell protein from post-ischemic wild-type or KIM-1^{Δmucin} mice. (E) Distribution of CD45+ cells positive for Gr1, F4/80, CD3, B220, CD11c and NK1.1 in KIM-1 WT or mutant kidneys. (F) Representative flow plots of the data shown in E. (Representative of 3 replicates)



Supplemental Figure 2. Heatmap of the genes significantly upregulated or downregulated by KIM-1 expression and listed in Supplemental Tables 1 and 2. The heatmap was produced using clustering of rows (gene expression values) and columns (samples) of the data matrix using the complete linkage algorithm and Pearson correlation. The gene clustering tree is shown on the left, and the sample clustering tree is shown on the top. The color scale shown at the top illustrates the relative expression level of the indicated genes across all samples: red denotes expression increases and blue denotes expression decreases, Log_2 scale.

Supplemental Table 1: Up-regulated genes ranked by fold change

Description	Symbol	Fold change	t test
hepatitis A virus cellular receptor 1	HAVCR1	1613.3375	0.0001
unc-5 homolog D (C. elegans)	UNC5D	12.7075	0.0067
myeloperoxidase	MPO	8.6095	0.0068
transmembrane protease, serine 4	TMPRSS4	7.5480	0.0011
adhesion molecule, interacts with CXADR antigen 1	AMICA1	5.8016	0.0035
similar to FLJ44216 protein; similar to cell surface antigen	LOC441118	5.2281	0.0014
3'-phosphoadenosine 5'-phosphosulfate synthase 2	PAPSS2	4.2199	0.0046
plexin domain containing 2	PLXDC2	4.1056	0.0004
hypothetical protein FLJ10157	FLJ10157	3.6479	0.0053
hexokinase 2	HK2	3.3968	0.0015
synaptosomal-associated protein, 25kDa	SNAP25	3.3519	0.0083
neuronal PAS domain protein 1	NPAS1	3.2458	0.0024
sialic acid binding Ig-like lectin 8	SIGLEC8	2.6252	0.0084
nucleosome assembly protein 1-like 5	NAP1L5	2.6077	0.0071
cytochrome P450, family 21, subfamily A, polypeptide 2	CYP21A2	2.4936	0.0067
protease inhibitor 15	PI15	2.4171	0.0023
pleckstrin homology domain containing, family N member 1	PLEKHN1	2.4161	0.0081
elastase 3A, pancreatic (protease E)	ELA3A	2.3079	0.0023
peroxiredoxin 2	PRDX2	2.2777	0.0001
mitochondrial ribosomal protein S17	MRPS17	2.2154	0.0039
LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	LSM4	2.2116	0.0041
carbonic anhydrase III, muscle specific	CA3	2.1912	0.0068
unc-93 homolog B1 (C. elegans)	UNC93B1	2.1448	0.0042
TSC22 domain family, member 1	TSC22D1	2.1040	0.0082
E2IG2 protein	E2IG2	2.0795	0.0038
zinc finger protein 423	ZNF423	2.0416	0.0018
globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	GBGT1	2.0312	0.0025
heparan sulfate 6-O-sulfotransferase 2	HS6ST2	2.0236	0.0028
T-cell surface glycoprotein CD5 precursor	CD5	1.9327	9.5x10 ⁻⁵
Interleukin-22 precursor	IL22	1.6789	0.0006

Supplemental Table 2: Down-regulated genes ranked by fold change

Description	Symbol	Fold Change	t test
creatine kinase, mitochondrial 2	CKMT2	0.1271	0.0039
mitogen-activated protein kinase kinase kinase kinase 3	MAP4K3	0.2064	0.0085
calcyphosine 2	CAPS2	0.3222	0.0020
acid phosphatase-like 2	ACPL2	0.3266	0.0012
distal-less homeo box 2	DLX2	0.3395	0.0047
zinc finger protein, subfamily 1A, 4 (Eos)	ZNFN1A4	0.3614	0.0001
transition protein 2 (during histone to protamine replacement)	TNP2	0.3885	0.0034
arachidonate 15-lipoxygenase, second type	ALOX15B	0.3917	0.0024
excision repair cross-complementing rodent repair deficiency, complementation group 5	ERCC5	0.4013	0.0014
solute carrier family 10 (sodium/bile acid cotransporter family), member 2	SLC10A2	0.4045	0.0001
CXXC finger 4	CXXC4	0.4139	0.0014
chromosome 7 open reading frame 34	C7orf34	0.4153	0.0026
proline-rich protein BstNI subfamily 1	PRB1	0.4162	0.0051
ATP-binding cassette, sub-family D (ALD), member 4	ABCD4	0.4181	0.0066
pipecolic acid oxidase	PIPOX	0.4229	0.0001
homeo box A3	HOXA3	0.4234	0.0002
chromosome 11 open reading frame 16	C11orf16	0.4246	0.0039
solute carrier family 27 (fatty acid transporter), member 5	SLC27A5	0.4299	0.0043
neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease)	NF1	0.4322	0.0039
Lymphocyte antigen 6 complex, locus G5B	LY6G5B	0.4327	0.0002
Angiomotin	AMOT	0.4341	0.0008
NY-REN-58 antigen	NY-REN-58	0.4367	0.0060
collagen, type VIII, alpha1	COL8A1	0.4385	0.0036
solute carrier family 23 (nucleobase transporters), member 3	SLC23A3	0.4387	0.0076
A kinase (PRKA) anchor protein 13	AKAP13	0.4411	0.0099
olfactory receptor, family 10, subfamily A, member 5	OR10A5	0.4425	0.0067
paired box gene 8	PAX8	0.4452	0.0019
phospholipase C, gamma 1	PLCG1	0.4464	0.0054
RAB6B, member RAS oncogene family	RAB6B	0.4530	0.0007
zinc finger protein 192	ZNF192	0.4573	0.0037
family with sequence similarity 3, member D	FAM3D	0.4588	0.0099
hypothetical protein FLJ12700	FLJ12700	0.4605	0.0025
phospholipase C, beta 2	PLCB2	0.4627	0.0019
similar to matrilin 2 precursor	LOC285929	0.4664	0.0015
mitogen-activated protein kinase kinase kinase kinase 5	MAP4K5	0.4689	0.0016
fucosyltransferase 7 (alpha (1,3) fucosyltransferase)	FUT7	0.4723	0.0039
tripartite motif-containing 3	TRIM3	0.4749	0.0026
solute carrier family 18 (vesicular monoamine), member 1	SLC18A1	0.4756	0.0011
POU domain, class 4, transcription factor 1	POU4F1	0.4773	0.0027
plexin domain containing 1	PLXDC1	0.4778	0.0059
glucosaminyl (N-acetyl) transferase 3, mucin type	GCNT3	0.4789	0.0048
guanine nucleotide binding protein (G protein), q polypeptide	GNAQ	0.4798	0.0064
ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu	ELAVL3	0.4829	0.0052

antigen C)			
leucine proline-enriched proteoglycan (leprecan) 1	LEPRE1	0.4840	0.0099
melanoma antigen family A, 3	MAGEA3	0.4843	0.0026
melanoma antigen family A, 6	MAGEA6	0.4843	0.0026
protease, serine, 22	PRSS22	0.4908	0.0081
v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	SRC	0.4924	0.0077
homeo box A11	HOXA11	0.4928	0.0093
leucine rich repeat neuronal 6A	LRRN6A	0.4931	0.0070
FK506 binding protein 9, 63 kDa	FKBP9	0.4976	0.0022
matrix metalloproteinase 10	MMP10	0.5036	0.0001
ubiquitin specific protease 8	USP8	0.5111	0.0006
platelet-derived growth factor beta polypeptide	PDGFB	0.5355	0.0005