

Supplementary Table S1. The 30 differentially expressed genes identified in this study.

Gene symbol	Full gene name	Reference^a
<i>AC005083.1</i>	AC005083.1	
<i>ANKRD37</i>	ankyrin repeat domain 37	Benita et al., 2009; Klomp et al., 2020
<i>AQP3</i>	aquaporin 3 (Gill blood group)	Zieseniss et al., 2016
<i>ATG9B</i>	autophagy related 9B	Robb et al., 2004; Kalinowski et al., 2016
<i>ATP6VIC2</i>	ATPase H ⁺ transporting V1 subunit C2	McConnell et al., 2017
<i>CD24</i>	CD24 molecule	Fujikuni et al., 2014
<i>CD177</i>	CD177 molecule	
<i>CLCA4</i>	chloride channel accessory 4	Ganaie et al., 2019
<i>CPA4</i>	carboxypeptidase A4	
<i>CRCT1</i>	cysteine rich C-terminal 1	
<i>DMKN</i>	dermokine	Huang et al., 2017
<i>ERO1A</i>	endoplasmic reticulum oxidoreductase 1 alpha	Takei et al., 2017
<i>FAM83A</i>	family with sequence similarity 83 member A	
<i>GDF15</i>	growth differentiation factor 15	Song et al., 2012; Haase, 2013; Gassmann and Muckenthaler, 2015
<i>GRPEL2</i>	GrpE like 2, mitochondrial	
<i>H1F0</i>	H1 histone family member 0	
<i>HEPHL1</i>	hephaestin like 1	Long et al., 2015
<i>KLK6</i>	kallikrein related peptidase 6	Yoon et al., 2007
<i>KLK12</i>	kallikrein related peptidase 12	Kryza et al., 2014
<i>KLK13</i>	kallikrein related peptidase 13	
<i>LINC02487</i>	long intergenic non-protein coding RNA 2487	
<i>LYPD3</i>	LY6/PLAUR domain containing 3	Ngora et al., 2012
<i>PKP1</i>	plakophilin 1	
<i>PPP1R3C</i>	protein phosphatase 1 regulatory subunit 3C	Shen et al., 2010
<i>S100A7</i>	S100 calcium binding protein A7	Vegfors et al., 2016
<i>S100A14</i>	S100 calcium binding protein A14	
<i>SBSN</i>	suprabasin	Goyal and Longo, 2014
<i>SERPINB3</i>	serpin family B member 3	Cannito et al., 2015
<i>TMPRSS11A</i>	transmembrane serine protease 11A	
<i>TMPRSS11E</i>	transmembrane serine protease 11E	

^a The gene expression levels appeared to be affected by the hypoxic environment or by hypoxia-inducible factors in previous studies described below.

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Supplementary Table S2. The 48 DEGs (FDR < 0.05, |LFC| ≥ 1) identified by the edgeR program.

Gene symbol	LFC	p value	FDR
<i>TMEM189-UBE2V1</i>	9.32	2.39×10 ⁻¹²	2.87×10 ⁻⁸
<i>ERO1A</i> ^a	1.60	3.78×10 ⁻⁸	2.27×10 ⁻⁴
<i>CLCA4</i> ^a	1.35	3.34×10 ⁻⁷	0.001
<i>KLK13</i> ^a	1.31	3.38×10 ⁻⁷	0.001
<i>PLA2G4D</i>	4.00	2.87×10 ⁻⁷	0.001
<i>ATP6V1C2</i> ^a	1.85	5.09×10 ⁻⁷	0.001
<i>AC008878.3</i>	-8.48	5.63×10 ⁻⁷	0.001
<i>DMKN</i> ^a	1.50	1.85×10 ⁻⁶	0.003
<i>CD24</i> ^a	1.22	3.24×10 ⁻⁶	0.004
<i>TMPRSS11E</i> ^a	1.16	4.19×10 ⁻⁶	0.005
<i>SERPINA3</i>	1.75	4.02×10 ⁻⁶	0.005
<i>TMPRSS11A</i> ^a	1.45	4.72×10 ⁻⁶	0.005
<i>SERPIN3</i> ^a	1.40	5.61×10 ⁻⁶	0.005
<i>GDF15</i> ^a	1.26	6.47×10 ⁻⁶	0.006
<i>AC011462.1</i>	1.83	9.60×10 ⁻⁶	0.008
<i>PPP1R3C</i> ^a	1.44	1.17×10 ⁻⁵	0.009
<i>DENND2C</i>	1.71	1.28×10 ⁻⁵	0.009
<i>FAM83A</i> ^a	1.31	1.64×10 ⁻⁵	0.011
<i>AC005083.1</i> ^a	1.59	1.97×10 ⁻⁵	0.012
<i>RASA4B</i>	2.28	2.55×10 ⁻⁵	0.015
<i>AC007325.4</i>	-8.04	2.68×10 ⁻⁵	0.015
<i>AQP3</i> ^a	1.28	3.01×10 ⁻⁵	0.016
<i>HEPHE1</i> ^a	1.35	3.03×10 ⁻⁵	0.016
<i>CPA4</i> ^a	1.16	3.57×10 ⁻⁵	0.018
<i>ACP7</i>	2.85	4.20×10 ⁻⁵	0.019
<i>KANK3</i>	7.90	4.21×10 ⁻⁵	0.019
<i>IGHG1</i>	-1.83	4.64×10 ⁻⁵	0.021
<i>ADRA2B</i>	-7.88	5.59×10 ⁻⁵	0.024
<i>HSPH1</i>	1.41	5.96×10 ⁻⁵	0.025
<i>MT-ATP8</i>	1.22	6.55×10 ⁻⁵	0.026
<i>TMEM184A</i>	1.42	7.72×10 ⁻⁵	0.030
<i>CYC1</i>	-1.68	8.11×10 ⁻⁵	0.030
<i>KLK6</i> ^a	1.53	9.62×10 ⁻⁵	0.035
<i>LINC02487</i> ^a	1.30	1.01×10 ⁻⁴	0.036
<i>GABRE</i>	1.33	1.31×10 ⁻⁴	0.044
<i>SPINK7</i>	1.03	1.33×10 ⁻⁴	0.044
<i>CRCT1</i> ^a	1.11	1.39×10 ⁻⁴	0.044
<i>HHIPL1</i>	2.08	1.41×10 ⁻⁴	0.044
<i>CCL3</i>	-1.09	1.45×10 ⁻⁴	0.045
<i>AC011479.1</i>	-7.56	1.54×10 ⁻⁴	0.045
<i>FAM43A</i>	1.42	1.60×10 ⁻⁴	0.045
<i>ALDH1A3</i>	1.03	1.62×10 ⁻⁴	0.045
<i>PROB1</i>	-7.53	1.62×10 ⁻⁴	0.045

<i>CCL2</i>	-1.34	1.64×10 ⁻⁴	0.045
<i>APBB3</i>	1.04	1.76×10 ⁻⁴	0.047
<i>IL6</i>	-2.04	1.81×10 ⁻⁴	0.047
<i>AC104452.1</i>	-7.50	1.85×10 ⁻⁴	0.047
<i>CPLX1</i>	-7.49	1.93×10 ⁻⁴	0.048

DEG, differentially expressed gene. FDR, false discovery rate. LFC, Log2 fold change.

^a The DEG was also identified by the DESeq2 program.

Supplementary Table S3. GO processes estimated by topGO gene enrichment analysis using the 30 DEGs identified in this study.

GO ID	FDR	Description
GO:0097530	0.0004	granulocyte migration
GO:0097529	0.0013	myeloid leukocyte migration
GO:0002548	0.0020	monocyte chemotaxis
GO:0071674	0.0034	mononuclear cell migration
GO:0051604	0.0043	protein maturation
GO:0048584	0.0059	positive regulation of response to stimulus
GO:0000041	0.0063	transition metal ion transport
GO:1990266	0.0072	neutrophil migration
GO:0055074	0.0080	calcium ion homeostasis
GO:0071621	0.0080	granulocyte chemotaxis
GO:0072507	0.0103	divalent inorganic cation homeostasis
GO:0050900	0.0107	leukocyte migration
GO:1902563	0.0133	regulation of neutrophil activation
GO:0040015	0.0133	negative regulation of multicellular organism growth
GO:2000696	0.0133	regulation of epithelial cell differentiation involved in kidney development
GO:0016540	0.0133	protein autoprocesing
GO:0072672	0.0133	neutrophil extravasation
GO:0072160	0.0146	nephron tubule epithelial cell differentiation
GO:0061318	0.0146	renal filtration cell differentiation
GO:0072112	0.0146	glomerular visceral epithelial cell differentiation
GO:0072311	0.0146	glomerular epithelial cell differentiation
GO:0045217	0.0146	cell-cell junction maintenance
GO:2001044	0.0160	regulation of integrin-mediated signaling pathway
GO:0072010	0.0173	glomerular epithelium development
GO:0019471	0.0173	4-hydroxyproline metabolic process
GO:0002021	0.0173	response to dietary excess
GO:0036149	0.0173	phosphatidylinositol acyl-chain remodeling
GO:0034331	0.0173	cell junction maintenance
GO:0043410	0.0184	positive regulation of MAPK cascade
GO:1901741	0.0186	positive regulation of myoblast fusion
GO:0042755	0.0186	eating behavior
GO:0032930	0.0186	positive regulation of superoxide anion generation
GO:0036148	0.0186	phosphatidylglycerol acyl-chain remodeling
GO:0048245	0.0199	eosinophil chemotaxis
GO:0034975	0.0199	protein folding in endoplasmic reticulum
GO:0006575	0.0210	cellular modified amino acid metabolic process
GO:0090026	0.0212	positive regulation of monocyte chemotaxis

GO:1901739	0.0212	regulation of myoblast fusion
GO:0060396	0.0212	growth hormone receptor signaling pathway
GO:0071378	0.0212	cellular response to growth hormone stimulus
GO:0009967	0.0216	positive regulation of signal transduction
GO:0055065	0.0222	metal ion homeostasis
GO:0036150	0.0225	phosphatidylserine acyl-chain remodeling
GO:0008219	0.0230	cell death
GO:0072677	0.0239	eosinophil migration
GO:0060143	0.0239	positive regulation of syncytium formation by plasma membrane fusion
GO:0032928	0.0239	regulation of superoxide anion generation
GO:0006825	0.0239	copper ion transport
GO:0016485	0.0251	protein processing
GO:0071677	0.0252	positive regulation of mononuclear cell migration
GO:0043302	0.0252	positive regulation of leukocyte degranulation
GO:0030595	0.0254	leukocyte chemotaxis
GO:0060142	0.0265	regulation of syncytium formation by plasma membrane fusion
GO:0046475	0.0265	glycerophospholipid catabolic process
GO:0090025	0.0265	regulation of monocyte chemotaxis
GO:0042104	0.0265	positive regulation of activated T cell proliferation
GO:0071709	0.0278	membrane assembly
GO:0045745	0.0278	positive regulation of G protein-coupled receptor signaling pathway
GO:0071624	0.0291	positive regulation of granulocyte chemotaxis
GO:0036152	0.0291	phosphatidylethanolamine acyl-chain remodeling
GO:0055080	0.0293	cation homeostasis
GO:0010647	0.0297	positive regulation of cell communication
GO:0007204	0.0298	positive regulation of cytosolic calcium ion concentration
GO:0023056	0.0303	positive regulation of signaling
GO:0010831	0.0304	positive regulation of myotube differentiation
GO:0036151	0.0304	phosphatidylcholine acyl-chain remodeling
GO:0098771	0.0305	inorganic ion homeostasis
GO:0060416	0.0317	response to growth hormone
GO:0046471	0.0317	phosphatidylglycerol metabolic process
GO:0090184	0.0330	positive regulation of kidney development
GO:0042554	0.0330	superoxide anion generation
GO:0032594	0.0330	protein transport within lipid bilayer
GO:0007169	0.0331	transmembrane receptor protein tyrosine kinase signaling pathway
GO:0043406	0.0337	positive regulation of MAP kinase activity
GO:0007520	0.0343	myoblast fusion
GO:0002888	0.0343	positive regulation of myeloid leukocyte mediated immunity
GO:0044091	0.0343	membrane biogenesis
GO:0006658	0.0343	phosphatidylserine metabolic process

GO:0098660	0.0353	inorganic ion transmembrane transport
GO:0035850	0.0356	epithelial cell differentiation involved in kidney development
GO:0051480	0.0360	regulation of cytosolic calcium ion concentration
GO:0010862	0.0369	positive regulation of pathway-restricted SMAD protein phosphorylation
GO:0045730	0.0369	respiratory burst
GO:0050801	0.0373	ion homeostasis
GO:0030001	0.0381	metal ion transport
GO:0051085	0.0382	chaperone cofactor-dependent protein refolding
GO:0090322	0.0382	regulation of superoxide metabolic process
GO:0015991	0.0382	ATP hydrolysis coupled proton transport
GO:0071375	0.0387	cellular response to peptide hormone stimulus
GO:0071634	0.0395	regulation of transforming growth factor beta production
GO:0030574	0.0395	collagen catabolic process
GO:0034142	0.0408	toll-like receptor 4 signaling pathway
GO:0034220	0.0408	ion transmembrane transport
GO:0009395	0.0408	phospholipid catabolic process
GO:0043408	0.0409	regulation of MAPK cascade
GO:0060326	0.0411	cell chemotaxis
GO:0001666	0.0414	response to hypoxia
GO:0071604	0.0420	transforming growth factor beta production
GO:0050873	0.0420	brown fat cell differentiation
GO:0061005	0.0420	cell differentiation involved in kidney development
GO:0055085	0.0420	transmembrane transport
GO:0046006	0.0433	regulation of activated T cell proliferation
GO:0033572	0.0433	transferrin transport
GO:0015988	0.0433	energy coupled proton transmembrane transport, against electrochemical gradient
GO:0036293	0.0445	response to decreased oxygen levels
GO:0071675	0.0446	regulation of mononuclear cell migration
GO:0051084	0.0446	'de novo' posttranslational protein folding
GO:0090183	0.0446	regulation of kidney development
GO:0006654	0.0446	phosphatidic acid biosynthetic process
GO:0097193	0.0458	intrinsic apoptotic signaling pathway
GO:0000768	0.0459	syncytium formation by plasma membrane fusion
GO:0140253	0.0459	cell-cell fusion
GO:1903307	0.0459	positive regulation of regulated secretory pathway
GO:0015682	0.0459	ferric iron transport
GO:0072512	0.0459	trivalent inorganic cation transport
GO:0046473	0.0459	phosphatidic acid metabolic process
GO:0006949	0.0472	syncytium formation
GO:0071622	0.0472	regulation of granulocyte chemotaxis
GO:0060393	0.0485	regulation of pathway-restricted SMAD protein phosphorylation

GO:0061098	0.0485	positive regulation of protein tyrosine kinase activity
GO:0050798	0.0485	activated T cell proliferation
GO:0032835	0.0485	glomerulus development
GO:0002696	0.0494	positive regulation of leukocyte activation
GO:0043300	0.0497	regulation of leukocyte degranulation
GO:0006458	0.0497	'de novo' protein folding

GO terms with an FDR of < 0.05 and a minimum of 2 associated genes per GO term were defined as significantly overrepresented terms.

GO, gene ontology. DEG, differentially expressed gene. FDR, false discovery rate.

Supplementary Table S4. GO processes estimated by BiNGO gene enrichment analysis using the 30 DEGs identified in this study.

GO ID	<i>p</i> value	FDR	Description
GO:0071624	1.86×10 ⁻⁶	7.78×10 ⁻⁴	positive regulation of granulocyte chemotaxis
GO:0090025	1.11×10 ⁻⁵	0.002	regulation of monocyte chemotaxis
GO:0090026	1.11×10 ⁻⁵	0.002	positive regulation of monocyte chemotaxis
GO:0071622	2.78×10 ⁻⁵	0.003	regulation of granulocyte chemotaxis
GO:0006508	3.59×10 ⁻⁴	0.028	proteolysis
GO:0002684	4.41×10 ⁻⁴	0.028	positive regulation of immune system process
GO:0002690	4.62×10 ⁻⁴	0.028	positive regulation of leukocyte chemotaxis
GO:0002688	6.87×10 ⁻⁴	0.029	regulation of leukocyte chemotaxis
GO:0002237	6.98×10 ⁻⁴	0.029	response to molecule of bacterial origin
GO:0002687	8.43×10 ⁻⁴	0.029	positive regulation of leukocyte migration
GO:0030856	9.55×10 ⁻⁴	0.029	regulation of epithelial cell differentiation
GO:0032913	0.001	0.029	negative regulation of transforming growth factor-beta3 production
GO:0033606	0.001	0.029	chemokine receptor transport within lipid bilayer
GO:0032594	0.001	0.029	protein transport within lipid bilayer
GO:0032595	0.001	0.029	B cell receptor transport within lipid bilayer
GO:0032596	0.001	0.029	protein transport into membrane raft
GO:0032597	0.001	0.029	B cell receptor transport into membrane raft
GO:0032599	0.001	0.029	protein transport out of membrane raft
GO:0032600	0.001	0.029	chemokine receptor transport out of membrane raft
GO:0002685	0.001	0.029	regulation of leukocyte migration
GO:0050921	0.001	0.029	positive regulation of chemotaxis
GO:0048520	0.002	0.037	positive regulation of behavior
GO:0050920	0.002	0.041	regulation of chemotaxis
GO:0002682	0.003	0.044	regulation of immune system process
GO:0071635	0.003	0.047	negative regulation of transforming growth factor-beta production

GO, gene ontology. DEG, differentially expressed gene. FDR, false discovery rate.

Supplementary Table S5. GO processes estimated by ClueGO gene enrichment analysis using the 30 DEGs identified in this study.

GO ID	<i>p</i> value	FDR	Description
GO:0071677	8.29×10^{-4}	0.002	positive regulation of mononuclear cell migration
GO:0090025	0.001	0.001	regulation of monocyte chemotaxis
GO:0071624	0.001	0.002	positive regulation of granulocyte chemotaxis
GO:0090026	4.95×10^{-4}	0.002	positive regulation of monocyte chemotaxis

GO, gene ontology. DEG, differentially expressed gene. FDR, false discovery rate.

Supplementary Table S6. KEGG pathway estimated using the 30 DEGs identified in this study.

KEGG ID	Pathway	Gene name^a
hsa00190	Oxidative phosphorylation	<i>ATP6V1C2</i>
hsa01100	Metabolic pathways	<i>ATP6V1C2</i>
hsa04060	Cytokine-cytokine receptor interaction	<i>GDF15</i>
hsa04136	Autophagy - other	<i>ATG9B</i>
hsa04137	Mitophagy - animal	<i>ATG9B</i>
hsa04140	Autophagy - animal	<i>ATG9B</i>
hsa04141	Protein processing in endoplasmic reticulum	<i>ERO1A</i>
hsa04145	Phagosome	<i>ATP6V1C2</i>
hsa04150	mTOR signaling pathway	<i>ATP6V1C2</i>
hsa04640	Hematopoietic cell lineage	<i>CD24</i>
hsa04657	IL-17 signaling pathway	<i>S100A7</i>
hsa04721	Synaptic vesicle cycle	<i>ATP6V1C2</i>
hsa04910	Insulin signaling pathway	<i>PPP1R3C</i>
hsa04924	Renin secretion	<i>CLCA4</i>
hsa04931	Insulin resistance	<i>PPP1R3C</i>
hsa04962	Vasopressin-regulated water reabsorption	<i>AQP3</i>
hsa04966	Collecting duct acid secretion	<i>ATP6V1C2</i>
hsa04972	Pancreatic secretion	<i>CLCA4</i>
hsa05110	Vibrio cholerae infection	<i>ATP6V1C2, ERO1A</i>
hsa05120	Epithelial cell signaling in Helicobacter pylori infection	<i>ATP6V1C2</i>
hsa05146	Amoebiasis	<i>SERPINB3</i>
hsa05165	Human papillomavirus infection	<i>ATP6V1C2</i>
hsa05323	Rheumatoid arthritis	<i>ATP6V1C2</i>

KEGG, Kyoto Encyclopedia of Genes and Genomes. DEG, differentially expressed gene.

^a DEGs identified in this study mapped to the KEGG pathway.