Table S1. *Functionally-related genes that are diffentially expressed in Agtr1a*$^{-/-}$ *compared wild-type mice under baseline conditions.*

Functional Category	Affymetrix ID	Fold change	Gene Symbol	Description
Inflammatory mediators	1419209_at	4.145	*Cxcl1*	chemokine (C-X-C motif) ligand 1
	1418930_at	2.537	*Cxcl10*	chemokine (C-X-C motif) ligand 10
	1418652_at	2.454	*Cxcl9*	chemokine (C-X-C motif) ligand 9
	1419426_s_at	2.33	*Ccl21b*	chemokine (C-C motif) ligand 21b
			Ccl21a	chemokine (C-C motif) ligand 21a
			Ccl21c	chemokine (C-C motif) ligand 21c (leucine)
	1415803_at	1.736	*Cx3cl1*	chemokine (C-X3-C motif) ligand 1
	1417625_s_at	1.672	*Cmkor1*	chemokine orphan receptor 1
	1452016_at	2.161	*Alox5ap*	arachidonate 5-lipoxygenase activating protein
Histocompatibility complex genes	1452431_s_at	2.49	*H2-Aa*	Histocompatibility 2, class II antigen A, alpha
	1451721_a_at	2.488	*H2-Ab1*	Histocompatibility 2, class II antigen A, beta 1
	1417025_at	2.295	*H2-Eb1*	Histocompatibility 2, class II antigen E beta

	1426324_at	1.613	*H2-D1*	Histocompatibility 2, D region locus 1
	1427746_x_at	1.579	*H2-K1*	Histocompatibility 2, K1, K region
	1421596_s_at	1.898	*H28*	Histocompatibility 28
Complement System	1423954_at	3.58	*C3*	complement component 3
	1417063_at	3.164	*C1qb*	complement component 1, q subcomponent, beta polypeptide
	1443906_at	1.627	*Daf1*	decay accelerating factor 1
Immune response	1424305_at	11.57	*Igj*	immunoglobulin joining chain
	1429381_x_at	10.49	*Igh-VJ558*	immunoglobulin heavy chain (J558 family)
	1451632_a_at	3.135	*Igh-1a*	immunoglobulin heavy chain 1a (serum IgG2a)
	1424923_at	2.958	*Serpina3g*	serine (or cysteine) peptidase inhibitor, clade A, member 3G
	1419100_at	2.921	*Serpina3n*	serine (or cysteine) peptidase inhibitor, clade A, member 3N
	1448620_at	2.501	*Fcgr3*	Fc receptor, IgG, low affinity III
	1460218_at	2.474	*Cd52*	CD52 antigen
	1448617_at	2.461	*Cd53*	CD53 antigen
	1460255_at	2.243	*Tnfsf13b*	tumor necrosis factor (ligand) superfamily, member 13b

	1453196_a_at	2.184	*Oasl2*	2'-5' oligoadenylate synthetase-like 2
	1448575_at	2.176	*Il7r*	interleukin 7 receptor
	1449009_at	2.158	*Tgtp*	T-cell specific GTPase
	1427301_at	2.144	*Cd48*	CD48 antigen
	1417268_at	2.008	*Cd14*	CD14 antigen
	1417756_a_at	1.939	*Lsp1*	lymphocyte specific 1
	1420699_at	1.918	*Clec7a*	C-type lectin domain family 7, member a
	1455656_at	1.883	*Btla*	B and T lymphocyte associated
	1428538_s_at	1.811	*Rarres2*	Retinoic acid receptor responder (tazarotene induced) 2
	1434380_at	1.784	*9830147J24Rik*	RIKEN cDNA 9830147J24 gene (9830147J24Rik), mRNA
	1452519_a_at	1.633	*Zfp36*	zinc finger protein 36
	1453304_s_at	1.544	*Ly6e*	lymphocyte antigen 6 complex, locus E
	1439328_at	1.553	*Nfat5*	Nuclear factor of activated T-cells 5
	1450702_at	0.648	*Hfe*	Hemochromatosis
	1425925_at	0.566	*Fcamr*	Fc receptor, IgA, IgM, high affinity
	1424673_at	0.377	*Clec2h*	C-type lectin domain family 2, member h
	1451924_a_at	1.81	*Edn1*	endothelin 1
Interferon-related genes	1419043_a_at	2.426	*Iigp1*	interferon inducible GTPase 1
	1418240_at	2.024	*Gbp2*	Guanylate nucleotide binding protein 2
	1417292_at	1.716	*Ifi47*	interferon gamma inducible protein 47

	1451567_a_at	1.597	*Ifi203 ;* *LOC547362*	interferon activated gene 203 ; similar to interferon-inducible protein 203
	1448452_at	1.583	*Irf8*	interferon regulatory factor 8
	1421916_at	1.725	*Pdgfra*	Platelet derived growth factor receptor, alpha polypeptide
	1454159_a_at	4.318	*Igfbp2*	insulin-like growth factor binding protein 2
Growth factors				
	1417065_at	4.534	*Egr1*	early growth response 1
	1426858_at	4.373	*Inhbb*	inhibin beta-B
	1427682_a_at	4.38	*Egr2*	early growth response 2
	1415871_at	2.957	*Tgfbi*	transforming growth factor, beta induced
	1416953_at	2.528	*Ctgf*	connective tissue growth factor
	1416039_x_at	1.972	*Cyr61*	cysteine rich protein 61
	1440041_at	1.962	*Tgfbr3*	Transforming growth factor, beta receptor III
	1420653_at	1.515	*Tgfb1*	transforming growth factor, beta 1
	1454159_a_at	4.318	*Igfbp2*	insulin-like growth factor binding protein 2
	1418918_at	0.55	*Igfbp1*	insulin-like growth factor binding protein 1
Lysosome				
	1439426_x_at	6.744	*Lzp-s*	P lysozyme structural
	1423547_at	5.334	*Lyzs*	Lysozyme
	1436905_x_at	2.829	*Laptm5*	lysosomal-associated protein transmembrane 5

Macrophage activation	1425519_a_at	2.438	*Ii*	Ia-associated invariant chain
Proteosome				
	1450696_at	1.548	*Psmb9*	proteosome (prosome, macropain) subunit, beta type 9
	1422962_a_at	1.832	*Psmb8*	proteosome (prosome, macropain) subunit, beta type 8
Inhibitors of the immune response	1426858_at	4.373	*Inhbb*	inhibin beta-B
	1425519_a_at	2.438	*Ii*	Ia-associated invariant chain
	1455656_at	1.883	*Btla*	B and T lymphocyte associated
	1452519_a_at	1.633	*Zfp36*	zinc finger protein 36
Adhesion factors	1415989_at	2.866	*Vcam1*	vascular cell adhesion molecule 1
	1450678_at	2.116	*Itgb2*	Integrin beta 2
	1426301_at	1.673	*Alcam*	Activated leukocyte cell adhesion molecule
	1450663_at	1.834	*Thbs2*	thrombospondin 2
	1449528_at	1.826	*Figf*	c-fos induced growth factor
	1448303_at	1.823	*Gpnmb*	glycoprotein (transmembrane) nmb
	1416066_at	1.506	*Cd9*	CD9 antigen
Angiogenesis				
	1416953_at	2.528	*Ctgf*	connective tissue growth factor

1456746_a_at	2.072	*Cd99l2*	Cd99 antigen-like 2
1449110_at	2.051	*Rhob*	ras homolog gene family, member B
1449528_at	1.826	*Figf*	c-fos induced growth factor
1423571_at	1.606	*Edg1*	endothelial differentiation sphingolipid G-protein-coupled receptor 1

Table S2. *Gene ontology analysis of genes significantly regulated in WT mice after angiotensin II treatment.*

Category	Total	%	p-Value
GO:7582: physiological process	499	93.45	0.000256
GO:50875: cellular physiological process	460	86.14	0.0244
GO:8152: metabolism	359	67.23	0.0137
GO:51179: localization	155	29.03	0.0432
GO:51234: establishment of localization	154	28.84	0.0386
GO:6810: transport	140	26.22	0.0486
GO:9058: biosynthesis	80	14.98	0.000265
GO:6629: lipid metabolism	48	8.989	6.86E-06
GO:44255: cellular lipid metabolism	45	8.427	7.68E-07
GO:6811: ion transport	42	7.865	0.0209
GO:5975: carbohydrate metabolism	32	5.993	0.000692
GO:8610: lipid biosynthesis	29	5.431	5.06E-07
GO:9628: response to abiotic stimulus	25	4.682	0.00747
GO:6066: alcohol metabolism	23	4.307	0.000233
GO:44262: cellular carbohydrate metabolism	21	3.933	0.0172
GO:8202: steroid metabolism	18	3.371	1.76E-05
GO:6457: protein folding	17	3.184	0.0327
GO:51186: cofactor metabolism	17	3.184	0.0115
GO:6732: coenzyme metabolism	15	2.809	0.0131

GO:6820: anion transport	15	2.809	0.0128
GO:6897: endocytosis	15	2.809	0.0192
GO:15980: energy derivation by oxidation of organic compounds	14	2.622	0.00611
GO:6694: steroid biosynthesis	13	2.434	6.99E-06
GO:6461: protein complex assembly	13	2.434	0.026
GO:6631: fatty acid metabolism	12	2.247	0.0306
GO:45786: negative regulation of progression through cell cycle	12	2.247	0.00949
GO:15698: inorganic anion transport	12	2.247	0.0466
GO:9100: glycoprotein metabolism	11	2.06	0.0239
GO:6333: chromatin assembly or disassembly	11	2.06	0.0291
GO:16125: sterol metabolism	11	2.06	0.000131
GO:50801: ion homeostasis	11	2.06	0.0133
GO:9101: glycoprotein biosynthesis	10	1.873	0.0257
GO:6486: protein amino acid glycosylation	10	1.873	0.0147
GO:6092: main pathways of carbohydrate metabolism	10	1.873	0.025
GO:43413: biopolymer glycosylation	10	1.873	0.0188
GO:8203: cholesterol metabolism	10	1.873	0.000257
GO:6575: amino acid derivative metabolism	10	1.873	0.000761
GO:6576: biogenic amine metabolism	9	1.685	0.000578
GO:16126: sterol biosynthesis	9	1.685	4.77E-06
GO:6334: nucleosome assembly	9	1.685	0.0027

GO:31497: chromatin assembly	9	1.685	0.0077
GO:6814: sodium ion transport	9	1.685	0.0156
GO:6695: cholesterol biosynthesis	8	1.498	9.35E-06
GO:30003: cation homeostasis	8	1.498	0.0497
GO:6875: metal ion homeostasis	8	1.498	0.0297
GO:30005: di-, tri-valent inorganic cation homeostasis	8	1.498	0.0214
GO:41: transition metal ion transport	8	1.498	0.000422
GO:6826: iron ion transport	8	1.498	3.29E-06
GO:6986: response to unfolded protein	8	1.498	0.00667
GO:6766: vitamin metabolism	7	1.311	0.0153
GO:6720: isoprenoid metabolism	7	1.311	1.43E-05
GO:9408: response to heat	7	1.311	0.000123
GO:9266: response to temperature stimulus	7	1.311	0.000425
GO:8299: isoprenoid biosynthesis	6	1.124	1.79E-05
GO:42398: amino acid derivative biosynthesis	6	1.124	0.000302
GO:6084: acetyl-CoA metabolism	6	1.124	0.0156
GO:46916: transition metal ion homeostasis	6	1.124	0.000877
GO:6879: iron ion homeostasis	6	1.124	0.000107
GO:6825: copper ion transport	6	1.124	1.40E-05
GO:42401: biogenic amine biosynthesis	5	0.936	0.00097
GO:6471: protein amino acid ADP-ribosylation	5	0.936	0.0193
GO:19751: polyol metabolism	5	0.936	0.000736

GO:6071: glycerol metabolism	5	0.936	0.000736
GO:6767: water-soluble vitamin metabolism	5	0.936	0.0437
GO:6919: caspase activation	5	0.936	0.0204
GO:6956: complement activation	5	0.936	0.0163
GO:6958: complement activation, classical pathway	5	0.936	0.00443
GO:45087: innate immune response	5	0.936	0.0368
GO:51345: positive regulation of hydrolase activity	5	0.936	0.0215
GO:43280: positive regulation of caspase activity	5	0.936	0.0215
GO:43281: regulation of caspase activity	5	0.936	0.0215
GO:9314: response to radiation	5	0.936	0.0419
GO:6595: polyamine metabolism	4	0.749	0.00462
GO:6596: polyamine biosynthesis	4	0.749	6.88E-05
GO:46364: monosaccharide biosynthesis	4	0.749	0.0213
GO:19319: hexose biosynthesis	4	0.749	0.0213
GO:6094: gluconeogenesis	4	0.749	0.0105
GO:46165: alcohol biosynthesis	4	0.749	0.0213
GO:6090: pyruvate metabolism	4	0.749	0.0199
GO:8635: caspase activation via cytochrome c	4	0.749	0.000144
GO:8272: sulfate transport	4	0.749	0.00105
GO:15669: gas transport	4	0.749	0.0041
GO:15671: oxygen transport	4	0.749	0.0041

Table S3. *Five top-scoring genetic networks in WT mouse kidneys caused by Ang II infusion.*

N	Genes in Networks	Score	Functions
1.	↓*ABLIM*1, ↓*ANPEP*, ↓*C60rf108*, Calpain, ↓*CAPZA1*, ↓*CKS*2, Cofilin, ↓*ESPN*, F actin, ↓*GAS2*, HMG CoA synthetase, ↓*HMGCS1*, ↑ *HMGCS2*, ↓*HNRNPU*, ↑*LHX1*, ↓*LIMS1*, ↓*MFAP1*, ↑*MYC*, ↓*NDN*, ↑*NDRG1*, ↑*NPM1*, ↓*PFN2*, ↑*PURA*, ↓*RBL1*, Rock, ↓*RRM2B*, ↓*SFRP1*, ↑*SFXN1*, ↓*SLC25A19*, ↓*TDG*, ↓*TGTP*, ↑*TNS1*, ↓*WASL*, ↓*YME1L1*, ↑*ZBTB16*	46	Gene expression, cancer, tumor morphology
2.	Adaptor protein2, ↑*AP2A2*, ↑ *APOH*, Arf, ↑*ARFGEF1*, ↑*C3*, ↓*C1R*, ↓*CCKAR*, ↓*CGREF1*, Ck2, Clathrin, ↓*CSNK2A1*, ↓*CXCL16*, ↑*DAB2*, ↓*DBP*, ↓*EHD1*, ↓*FAM46A*, ↓*GBF1*, ↓*HUS1**, ↓*IFI16*, IgG, Igm, ↓*KIF5B*, ↑*MTSS1*, ↓*MYCBP*, NFkB (complex), ↓*NKIRAS1*, ↓*PDAP1*, PPARA-RXRa, ↓*RFC1*, ↓*RPA3*, ↓*SERPINE2*, ↓*ST8SIA1*, ↓*TFPI2*, ↓*TFRC*	38	Infectious disease, nervous system development and function, tissue development
3.	↓*AES,* ↓ *ATRX,* Cbp/p300, ↓*CCNC*, ↑*CDKN1A*, ↓*CROP*, ↓*CYB561*, Cyclin B, ↓*CYCS*, Cytochrome c, *DUB,* IFN Beta, ↓*IL6ST,* ↑*ING1*, Interferon alpha, ↓*IRF5*, ↓*LATS2*, ↓*LGALS3BP*, ↓*LY6E*, ↓*MED14*, MHC Class I, ↓*PPIG*, Proteasome, ↓*RB1CC1*, RNA polymerase II, ↑*SLC16A6*, ↓*SLC9A8*, ↓*SMC4*, ↓*SRR*, ↓*STAT1*, ↓*TRIM44*, ↓*UCHL5*, ↓*USP7*, ↓*USP18*, ↑*USP40*		Gene expression, cell cycle, cancer

4.	↑*ACSL1*, ↓*AIPOR2*, ↓*AKAP9*, Ap1, ↓*AQP3*, ↓CALM1, Calmodulin, ↓*CLDND1*, Creb, ↓*DHCR7*, ↑*DHRS3*, ERK1/2, ↓*FABP3*, FSH, ↑*GAS5*, hCG, ↓*HIST3H3*, Histone h3, IL12, ↑*INHBB*, Insulin, ↓*MAPRE2*, ↓*MLL3*, ↓*MTUS1*, ↑*NFKBIA*, ↓*PCTK1*, Pka, ↓*PLAC8*, PLC, Ras homolog, ↓*SLC5A2*, ↓*SOD2*, ↓*SRD5A1*, ↓*TRIM13*, ↓*UBE2V2*	30	Inflammatory response, carbohydrate metabolism, drug metabolism
5.	↓*A130040M12RIK*, c-Src, ↓*CHUK*, Chuk-Ikbkb-Ikbkg, ↓*DNAJA1*, ↓*DNAJB14*, ↓*DNAJC3*, ↓*DNAJC6*, ↑*DNAJC7*, ENaC, ↓*HMGB2*, Hsp27, Hsp70, Hsp90, Hsp22/Hsp40/Hsp90, ↓*HSP90AA1*, ↓*HSPA4*, ↓*HSPA8*, Ikb, IKK, ↓*KPNA2*, ↓*MAGEH1*, ↓*MAP3K7*, ↓*MEF2C*, NF-kappaB (family), ↓*NUTF2*, P38 MAPK, ↑*SCNN1A*, ↓*SERPINH1*, ↑*SGK1*, ↓*SMC6*, ↓*TNFSF10*, Trypsin, Ubiquitin, ↓*WNK1*	29	Post-translational modification, protein folding, molecular transport

Table S4. *Gene ontology analysis of genes significantly regulated in KO mice after angiotensin II treatment*

Category	Total	%	p-Value
GO:8152: metabolism	118	70.66	0.0176
GO:7275: development	41	24.55	0.0161
GO:43412: biopolymer modification	36	21.56	0.0467
GO:48513: organ development	20	11.98	0.0378
GO:48523: negative regulation of cellular process	17	10.18	0.03
GO:6950: response to stress	17	10.18	0.0396
GO:48731: system development	15	8.982	0.0141
GO:6512: ubiquitin cycle	15	8.982	0.0408
GO:43118: negative regulation of physiological process	15	8.982	0.041
GO:7399: nervous system development	14	8.383	0.0191
GO:9607: response to biotic stimulus	14	8.383	0.0369
GO:6955: immune response	13	7.784	0.0185
GO:9605: response to external stimulus	13	7.784	0.0135
GO:902: cellular morphogenesis	11	6.587	0.0401
GO:16567: protein ubiquitination	11	6.587	0.0116
GO:7610: behavior	11	6.587	0.0244
GO:6928: cell motility	10	5.988	0.00699
GO:51674: localization of cell	10	5.988	0.00699
GO:7626: locomotory behavior	10	5.988	0.0165

GO:40011: locomotion	10	5.988	0.00784
GO:16477: cell migration	9	5.389	0.00617
GO:9611: response to wounding	9	5.389	0.00658
GO:30029: actin filament-based process	6	3.593	0.044
GO:30036: actin cytoskeleton organization and biogenesis	6	3.593	0.0359
GO:7409: axonogenesis	5	2.994	0.0415
GO:7411: axon guidance	5	2.994	0.00543
GO:6954: inflammatory response	5	2.994	0.0329
GO:15674: di-, tri-valent inorganic cation transport	5	2.994	0.0477
GO:16055: Wnt receptor signaling pathway	5	2.994	0.021
GO:9880: embryonic pattern specification	4	2.395	0.00192
GO:8285: negative regulation of cell proliferation	4	2.395	0.0347
GO:30333: antigen processing	4	2.395	0.00221
GO:41: transition metal ion transport	4	2.395	0.00242
GO:8045: motor axon guidance	3	1.796	0.00017
GO:45596: negative regulation of cell differentiation	3	1.796	0.0282
GO:30902: hindbrain development	3	1.796	0.00104
GO:51093: negative regulation of development	3	1.796	0.0486
GO:6749: glutathione metabolism	3	1.796	0.00139
GO:51241: negative regulation of organismal physiological process	3	1.796	0.0103
GO:50777: negative regulation of immune response	3	1.796	0.00687

GO:19882: antigen presentation	3	1.796	0.0275
GO:6825: copper ion transport	3	1.796	0.000667
GO:6826: iron ion transport	3	1.796	0.00305
GO:7179: transforming growth factor beta receptor signaling pathway	3	1.796	0.0437
GO:7265: Ras protein signal transduction	3	1.796	0.0142
GO:35116: embryonic hindlimb morphogenesis	2	1.198	0.00831
GO:35136: forelimb morphogenesis	2	1.198	0.00603
GO:35137: hindlimb morphogenesis	2	1.198	0.00914
GO:30901: midbrain development	2	1.198	0.00251
GO:46209: nitric oxide metabolism	2	1.198	0.0171
GO:6809: nitric oxide biosynthesis	2	1.198	0.0171
GO:6004: fucose metabolism	2	1.198	0.00534
GO:7182: common-partner SMAD protein phosphorylation	2	1.198	0.0149
GO:46839: phospholipid dephosphorylation	2	1.198	0.0298
GO:50727: regulation of inflammatory response	2	1.198	0.0468
GO:19883: antigen presentation, endogenous antigen	2	1.198	0.0312
GO:19885: antigen processing, endogenous antigen via MHC class I	2	1.198	0.0298
GO:1755: neural crest cell migration	2	1.198	0.0182
GO:7183: SMAD protein heteromerization	2	1.198	0.00352

GO:30509: BMP signaling pathway	2	1.198	0.0468
GO:46578: regulation of Ras protein signal transduction	2	1.198	0.0119
GO:51056: regulation of small GTPase mediated signal transduction	2	1.198	0.027

Table S5. *Five top-scoring genetic networks in KO kidneys caused by angiotensin II infusion*

N	Genes in Networks	Score	Functions
1.	↓*ADRBK2*, Akt, Calmodulin, Calpain, ↓*CD44*, ↓*CDKN1B*, ↓*CHRNA4*, Ck2, ↓*CTCF*, ↓*EIF2C2*, F Actin, Fibrinogen, ↓*FZD4*, hCG, ↓*HNRNPU*, Hsp90, IKK (complex), ↓*INHBB*, ↓*IQGAP1*, ↓*KLF2*, ↓*MARCH3*, ↓*MEF2C*, ↓*NFKBIA*, ↓*PDAP1*, Pdgf, Pias, ↓*PIP4K2A*, Pkc(s), PLC, ↓*PLCB4*, ↓*RGS2*, ↓*TMOD3*, ↓*TOPORS*, ↓*USP8*, ↓*WASL*	38	Organ development, cancer, cell death
2.	14-3-3, ↓*ALCAM*, Ap1, ↓*CBL*, ↓*CSNK1E*, ↓*EPHA4*, ERK, ↓*F2R*, Glutathione transferase, GST, ↓*GSTA5*, ↓*GSTM5*, ↓*GSTM6*, ↓*GSTP*, Jnk, ↓*KLF6*, ↓*LRP6*, ↓*MAP3K*1, Mek, ↓*MGST1*, Nfat (family), ↓*PLCE1*, Rap1, Ras, Ras homolog, ↓*RHOJ*, ↓*RPS6KA5*, ↓*SEC62*, ↓*SLA*, ↓*SORBS2*, ↓*SPSB1*, ↓*TXNIP*, VAV, ↓*WIPF1*, ↓*ZC3HAV1*	37	Drug metabolism, liver hyperbilirubinemia, metabolic disease.
3.	26s Proteasome, ↓*AKAP9*, ↓*ARL5B*, ↓*ATP2B1*, ↓*CHKA*, ↓*CP*, ↓*CUL5*, ↓*CXCL2*, ↓*DUSP1*, ERK1/2, ↓*FLI1*, FSH, ↓FUNDC2, Histone h3, IL1, Insulin, ↑*LOC26010*, Mapk, P38 MAPK, PDGF BB, PI3K, Pka, ↑*RAB2A*, ↓*RAD23B*, RNA polymerase II, ↓*SMAD1*, ↓*SMC4*, ↓*SRRM2*, Tgf beta, ↓*UBE2I*, Ubiquitin, ↑*UGT2B17*, ↓*ZEB2*, ↓*ZFP36*, ↓*ZFP36L1*	36	Cell cycle, RNA damage and repair, gene expression
4.	ALP, ↑*ANXA13*, ↓*B2M*, BCR, ↓*CD74*, ↓*CXCL9*, ↓*GBP*2, GS-	34	Cell-mediated

	GCR dimmer, ↓*HLA-B*, ↓*HLA-C*, ↓*HMGB1L1*, ↓*IER2*, IFN Beta, Ifn gamma, IgG, IL12 (complex), ↓*IL7R*, Interferone alpha, ↓*IP6K2*, ↓*IRF8*, LDL, ↓*LIMS1*, MHC Class I (complex), MHC CLASS I (family), NFkB (complex), Proteasome, ↓*SERPINA1*, ↑*ST8SIA1*, STAT5a/b, TCR, ↓*TLE1*, ↑*TRMT*, ↓*TRIM30*, ↓*TSC22D3*, ↓*XAF1*		immune response, hematological system Development and function, tissue Morphology
5.	↑*AADACL1*, amino acids, ↓*ARID4A*, ↓*ATP8A1*, ↓*CSNK1G1*, EIF5, ↓*GALNAC4S-6ST*, ↓*GATAD2B*, *GSTM1, HCK*, *HDAC1*, *HDAC1L*, ↑*HYAL1*, ↓*JARDIA*, *LMO2*, ↑*MTMR7*, nitric oxide, *OXSR1*, *PGDS*, ↓*PRPF40A*, *PTPN22*, *RB1*, retinoic acid, ↓*SFRS2IP*, ↓*SRPK2*, *STK39*, ↓*STK17B*, *STRA13*, *U2AF2*, VHL,↓*WIPF1*, ↓*WNK1*,*WNK4*, ↓*ZEB2*, *ZFHX3*	25	Amino acid metabolism, post-translational modification, small molecule biochemistry

Table S6. *Functionally-related genes that are differentially expressed in Agtr1a*$^{+/+}$ *compared Agtr1a*$^{-/-}$ *after 2 days of angiotensin II infusion*

Functional category	Affymetrix ID	Fold Change	Gene Symbol	Description
Sodium transport				
	1430804_at	2.42	*Slc13a1*	solute carrier family 13 (sodium/sulphate symporters). member 1
	1435009_at	0.641	*Slc9a6*	solute carrier family 9 (sodium/hydrogen exchanger). isoform 6
	1455005_s_at	0.622	*Slc5a2*	solute carrier family 5 (sodium/glucose cotransporter). member 2
	1449878_a_at	0.607	*Slc12a6*	solute carrier family 12. member 6
	1417072_at	0.585	*Slc22a6*	solute carrier family 22 (organic anion transporter). member 6
	1419117_at	0.499	*Slc22a2*	solute carrier family 22 (organic cation transporter). member 2
	1454865_at	0.24	*Slc9a8*	solute carrier family 9 (sodium/hydrogen exchanger). member 8
	1451460_a_at	0.17	*Slc22a7*	solute carrier family 22 (organic anion transporter). member 7
Potassium transport	1436275_at	2.073	*Kcnip2*	KCHIP2A protein splice variant (KCHIP2 gene)

	1449878_a_at	0.607	*Slc12a6*	solute carrier family 12. member 6
	1438578_a_at	0.596	*Btbd10*	BTB (POZ) domain containing 10
	1442368_at	0.552	*Kctd12b*	potassium channel tetramerisation domain containing 12b
	1450398_at	0.431	*Kcnk5*	potassium channel. subfamily K. member 5
Oxidative -stress related genes	1452135_at	8.246	*Gpx6*	glutathione peroxidase 6
	1448239_at	5.501	*Hmox1*	heme oxygenase (decycling) 1
	1421041_s_at	3.847	*Gsta1 ; Gsta2*	glutathione S-transferase. alpha 1 (Ya) ; glutathione S-transferase. alpha 2 (Yc2)
	1455393_at	3.33	*Cp*	ceruloplasmin
	1421040_a_at	3.304	*Gsta2*	glutathione S-transferase. alpha 2 (Yc2)
	1415897_a_at	2.295	*Mgst1*	microsomal glutathione S-transferase 1
	1415996_at	1.578	*Txnip*	thioredoxin interacting protein
	1448273_at	0.631	*Gss*	glutathione synthetase
Immune response				
	1449195_s_at	0.648	*Cxcl16*	chemokine (C-X-C motif) ligand 16
	1427165_at	0.633	*Il13ra1*	interleukin 13 receptor. alpha 1
	1417185_at	0.632	*Ly6a*	lymphocyte antigen 6 complex. locus A
	1428503_a_at	0.631	*Nkiras1*	NFKB inhibitor interacting Ras-like protein 1
	1417777_at	0.628	*Ltb4dh*	leukotriene B4 12-hydroxydehydrogenase
	1449164_at	0.582	*Cd68*	CD68 antigen

1422962_a_at	0.624	*Psmb8*	proteosome (prosome. macropain) subunit. beta type 8
1418240_at	0.561	*Gbp2*	guanylate nucleotide binding protein 2
1451567_a_at	0.552	*Ifi203 ; LOC547362*	interferon activated gene 203 ; similar to interferon-inducible protein 203
1440957_at	0.551	*0610030I09Rik*	RIKEN cDNA 0610030I09 gene
1451625_a_at	0.532	*1700013L23Rik*	RIKEN cDNA 1700013L23 gene
1417009_at	0.524	*C1r*	complement component 1. r subcomponent
1453304_s_at	0.491	*Ly6e*	lymphocyte antigen 6 complex. locus E
1448775_at	0.488	*LOC547362*	similar to interferon-inducible protein 203
1425860_x_at	0.473	*Cklf*	chemokine-like factor
1428012_at	0.462	*C8a*	complement component 8. alpha polypeptide
1437902_s_at	0.448	*Rarres2*	retinoic acid receptor responder (tazarotene induced) 2
1451114_at	0.435	*Cklfsf6*	chemokine-like factor super family 6
1450883_a_at	0.404	*Cd36*	CD36 antigen
1422606_at	0.362	*C1qtnf3*	C1q and tumor necrosis factor related protein 3
1460242_at	0.291	*Daf1*	decay accelerating factor 1
1443889_at	0.261	*LOC105892*	LY antigen-like
1421653_a_at	0.188	*Igh-VJ558 ; LOC238447 ;*	immunoglobulin heavy chain (J558 family) ; similar to immunoglobulin heavy chain

			LOC544903 ; *LOC544907*	variable region ; similar to immunoglobulin mu-chain ; similar to anti-poly(dC) monoclonal antibody heavy chain
	1455577_at	0.176	*Ccl28*	Chemokine (C-C motif) ligand 28 (Ccl28). mRNA
Response to DNA damage	1450569_a_at	0.647	*Rbm14*	RNA binding motif protein 14
	1439487_at	0.595	*Lig4*	ligase IV. DNA. ATP-dependent
	1425366_a_at	0.573	*Hus1*	Hus1 homolog (S. pombe)
Response to unfolded protein	1423082_at	0.601	*Derl1*	Der1-like domain family. member 1
	1424065_at	0.594	*Edem1*	ER degradation enhancer. mannosidase alpha-like 1
	1422579_at	0.584	*Hspe1*	heat shock protein 1 (chaperonin 10)
	1437497_a_at	0.483	*Hspca ;* *LOC544800 ;* *LOC545508*	heat shock protein 1. alpha ; similar to heat shock protein 1. alpha ; similar to Heat shock protein HSP 90-alpha (HSP 86) (Tumor specific transplantation 86 kDa antigen) (TSTA)
	1435160_at	0.465	*1110064P04Rik*	RIKEN cDNA 1110064P04 gene
	1450843_a_at	0.44	*Serpinh1*	serine (or cysteine) peptidase inhibitor. clade H. member 1
	1423566_a_at	0.422	*Hsp110*	heat shock protein 110

	1428640_at	0.362	*Hsf2bp*	heat shock transcription factor 2 binding protein
	1416288_at	0.463	*Dnaja1*	DnaJ (Hsp40) homolog. subfamily A. member 1
	1434196_at	0.414	*Dnaja4*	DnaJ (Hsp40) homolog. subfamily A. member 4
	1423522_at	0.458	*Npm3*	nucleoplasmin 3
	1429502_at	0.633	*Stch*	stress 70 protein chaperone. microsome-associated. human homolog
	1430718_s_at	0.628	*Zcsl3*	Zinc finger. CSL-type containing 3
	1424650_at	0.600	*Pdia5*	protein disulfide isomerase associated 5
	1431216_s_at	0.516	*Dnajc6*	DnaJ (Hsp40) homolog. subfamily C. member 6
	1418591_at	0.49	*Dnaja4*	DnaJ (Hsp40) homolog. subfamily A. member 4
Growth related genes	1418918_at	12.25	*Igfbp1*	insulin-like growth factor binding protein 1
	1419086_at	2.217	*Fgfbp1*	fibroblast growth factor binding protein 1
	1426858_at	2.009	*Inhbb*	inhibin beta-B
	1422558_at	0.575	*Gamt*	guanidinoacetate methyltransferase
	1460591_at	0.491	*Esr1*	estrogen receptor 1 (alpha)
	1435383_x_at	0.451	*Ndn*	necdin
	1424529_s_at	0.569	*Cgref1*	cell growth regulator with EF hand domain

Cell cycle

1451599_at	2.376	*Sesn2*	sestrin 2
1432416_a_at	1.821	*Npm1*	nucleophosmin 1
1419291_x_at	2.005	*Gas5*	growth arrest specific 5
1458276_x_at	1.56	*Cit*	citron
1435870_at	0.654	*Sycp3*	Synaptonemal complex protein 3 (Sycp3). mRNA
1431746_a_at	0.651	*Ube1c*	ubiquitin-activating enzyme E1C
1460551_at	0.65	*Ran*	RAN. member RAS oncogene family
1423338_at	0.639	*Ccdc16*	coiled-coil domain containing 16
1416698_a_at	0.617	*Cks1b*	CDC28 protein kinase 1b
1448171_at	0.605	*Siah2*	seven in absentia 2
1451990_at	0.591	*Mapre2*	microtubule-associated protein. RP/EB family. member 2
1448635_at	0.58	*Smc2l1*	SMC2 structural maintenance of chromosomes 2-like 1 (yeast)
1450864_at	0.575	*Calm3*	calmodulin 3
1424982_a_at	0.562	*2700078E11Rik*	RIKEN cDNA 2700078E11 gene
1417458_s_at	0.559	*Cks2*	CDC28 protein kinase regulatory subunit 2
1450112_a_at	0.555	*Gas2*	growth arrest specific 2
1454144_a_at	0.532	*Ccnc*	cyclin C
1460591_at	0.491	*Esr1*	estrogen receptor 1 (alpha)
1448424_at	0.216	*Frzb*	frizzled-related protein

Apoptosis related genes	1416041_at	1.797	*Sgk*	serum/glucocorticoid regulated kinase
	1431746_a_at	0.651	*Ube1c*	ubiquitin-activating enzyme E1C
	1421853_at	0.643	*Psen1*	presenilin 1
	1422120_at	0.635	*Eaf2*	ELL associated factor 2
	1454650_at	0.635	*Trim35*	tripartite motif-containing 35
	1448528_at	0.634	*Pdcd10*	programmed cell death 10
	1459913_at	0.618	*Tnfsf10*	tumor necrosis factor (ligand) superfamily. member 10
	1448171_at	0.605	*Siah2*	seven in absentia 2
	1450112_a_at	0.555	*Gas2*	growth arrest specific 2
	1451625_a_at	0.532	*1700013L23Rik*	RIKEN cDNA 1700013L23 gene
	1422483_a_at	0.531	*Cycs*	cytochrome c. somatic
Electron transport	1423257_at	21.22	*Cyp4a14*	cytochrome P450. family 4. subfamily a. polypeptide 14
	1424853_s_at	2.609	*Cyp4a10 ; BC013476*	cytochrome P450. family 4. subfamily a. polypeptide 10 ; cDNA sequence BC013476
	1428296_at	0.664	*Polr2l*	polymerase (RNA) II (DNA directed) polypeptide L
	1418117_at	0.66	*Ndufs4*	NADH dehydrogenase (ubiquinone) Fe-S protein 4

	1434742_s_at	0.651	*2810401C16Rik*	RIKEN cDNA 2810401C16 gene
	1424048_a_at	0.634	*Cyb5r1*	cytochrome b5 reductase 1
	1453206_at	0.632	*Acad9*	acyl-Coenzyme A dehydrogenase family. member 9
	1428124_at	0.621	*Gtf2e1*	general transcription factor II E. polypeptide 1 (alpha subunit)
	1424650_at	0.600	*Pdia5*	protein disulfide isomerase associated 5
	1419504_at	0.587	*Mogat1*	monoacylglycerol O-acyltransferase 1
	1417507_at	0.584	*Cyb561*	cytochrome b-561
	1429443_at	0.573	*Cpne4*	copine IV
	1418709_at	0.542	*Cox7a1*	cytochrome c oxidase. subunit VIIa 1
	1422483_a_at	0.531	*Cycs*	cytochrome c. somatic
	1428323_at	0.457	*Gpd2*	glycerol phosphate dehydrogenase 2. mitochondrial
	1454918_at	0.4	*Agps*	alkylglycerone phosphate synthase
	1424352_at	0.382	*MGC25972*	similar to cytochrome P450. 4a10
	1421709_a_at	0.301	*Fmo5*	flavin containing monooxygenase 5
	1426102_at	0.238	*Cyp2j13*	cytochrome P450. family 2. subfamily j. polypeptide 13
ATP biosynthesis				
	1416248_at	0.666	*Nadk*	NAD kinase
	1448211_at	0.659	*Atp6v0e2*	ATPase. H+ transporting. lysosomal. V0 subunit E isoform 2

	1435637_at	0.649	*D8Wsu49e*	DNA segment. Chr 8. Wayne State University 49. expressed
Gluconeogenesis				
	1455209_at	3.914	*Pck1*	Phosphoenolpyruvate carboxykinase 1. cytosolic. mRNA (cDNA clone MGC:46881 IMAGE:4973187)
	1428323_at	0.457	*Gpd2*	glycerol phosphate dehydrogenase 2. mitochondrial
	1428323_at	0.457	*Gpd2*	glycerol phosphate dehydrogenase 2. mitochondrial
Fatty acid biosynthesis	1448910_at	0.557	*Pecr*	peroxisomal trans-2-enoyl-CoA reductase
	1453550_a_at	0.45	*Mlstd2*	male sterility domain containing 2
	1418668_at	0.372	*Acsm1*	acyl-CoA synthetase medium-chain family member 1
	1425559_a_at	0.146	*Acsm3*	acyl-CoA synthetase medium-chain family member 3
Lipid metabolism				
	1421840_at	3.568	*Abca1*	ATP-binding cassette. sub-family A (ABC1). member 1
	1421839_at	2.936	*Abca1*	ATP-binding cassette. sub-family A (ABC1). member 1
	1444487_at	2.625	*Lrat*	Lecithin-retinol acyltransferase

				(phosphatidylcholine-retinol-O-acyltransferase) (Lrat). Mrna
	1437856_at	1.631	*Ipmk*	inositol polyphosphate multikinase
Steroid metabolism	1423858_a_at	6.838	*Hmgcs2*	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2
	1425853_s_at	3.166	*Prlr*	prolactin receptor
	1421839_at	2.936	*Abca1*	ATP-binding cassette. sub-family A (ABC1). member 1
	1425387_at	1.763	*Akr1c20*	aldo-keto reductase family 1. member C20
	1416222_at	0.663	*Nsdhl*	NAD(P) dependent steroid dehydrogenase-like
	1433443_a_at	0.658	*Hmgcs1*	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1
	1431385_a_at	0.655	*Mbtps1*	membrane-bound transcription factor peptidase. site 1
	1417303_at	0.587	*Mvd*	mevalonate (diphospho) decarboxylase
	1448619_at	0.569	*Dhcr7*	7-dehydrocholesterol reductase
	1428356_at	0.565	*Osbp2*	oxysterol binding protein 2
	1416645_a_at	0.492	*Afp*	alpha fetoprotein
	1422960_at	0.466	*Srd5a2*	steroid 5 alpha-reductase 2
	1434642_at	0.461	*Dhrs8*	dehydrogenase/reductase (SDR family) member 8

	1419136_at	0.411	*Akr1c18*	aldo-keto reductase family 1. member C18
	1451122_at	0.289	*Idi1*	isopentenyl-diphosphate delta isomerase
Amino acid metabolism	1430570_at	5.803	*Kynu*	kynureninase (L-kynurenine hydrolase)
	1424618_at	5.186	*Hpd*	4-hydroxyphenylpyruvic acid dioxygenase
	1452887_at	0.649	*Traf3ip1*	TNF receptor-associated factor 3 interacting protein 1
	1423465_at	0.649	*Sdfr2*	stromal cell derived factor receptor 2
	1423709_s_at	0.609	*Farslb*	phenylalanine-tRNA synthetase-like. beta subunit
	1416563_at	0.595	*Ctps*	cytidine 5'-triphosphate synthase
	1420425_at	0.588	*Prdm1*	PR domain containing 1. with ZNF domain
	1425117_at	0.546	*0610012D14Rik*	RIKEN cDNA 0610012D14 gene
	1450871_a_at	0.203	*Bcat1*	branched chain aminotransferase 1. cytosolic
	1423883_at	2.225	*Acsl1*	acyl-CoA synthetase long-chain family member 1
Regulation of protein metabolism	1426858_at	2.009	*Inhbb*	inhibin beta-B
	1452887_at	0.649	*Traf3ip1*	TNF receptor-associated factor 3 interacting protein 1
	1455028_at	0.628	*Mapt*	microtubule-associated protein tau

	1434891_at	0.621	*Ptgfrn*	prostaglandin F2 receptor negative regulator
	1424719_a_at	0.577	*Mapt*	microtubule-associated protein tau
	1426022_a_at	0.502	*Vill*	villin-like
Regulation of protein biosynthesis	1426858_at	2.009	*Inhbb*	inhibin beta-B
	1441955_s_at	0.667	*Paip1*	polyadenylate binding protein-interacting protein 1
	1423220_at	0.643	*Eif4e*	eukaryotic translation initiation factor 4E
	1435803_a_at	0.623	*Eif4e2*	eukaryotic translation initiation factor 4E member 2
	1434891_at	0.621	*Ptgfrn*	prostaglandin F2 receptor negative regulator
	1438761_a_at	0.239	*Odc1 ; LOC545783 ; LOC546355*	ornithine decarboxylase. structural 1 ; similar to Ornithine decarboxylase (ODC) ; similar to Ornithine decarboxylase (ODC)
Signal transduction	1447669_s_at	2.135	*Gng4*	guanine nucleotide binding protein (G protein). gamma 4 subunit
	1437856_at	1.631	*Ipmk*	inositol polyphosphate multikinase