Supplementry Table 4: Pathway enrichment analysis of the glomerule dataset. Signaling pathways related to the DE gene, TFs, and kinase of the glomerule network were detremined. Adj. P-value≤0.05 was considered as statistical significance threshold.

Pathway	adj. p-value
ABC-family proteins mediated transport	1.23069E-12
Activated TLR4 signalling	9.69569E-05
Activation of AKT2	0.000523836
Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	1.23069E-12
Activation of G protein gated Potassium channels	0.015478822
Activation of GABAB receptors	0.000143533
Activation of IRF3/IRF7 mediated by TBK1/IKK epsilon	9.69569E-05
Activation of Kainate Receptors upon glutamate binding	0.015478822
Activation of NF-kappaB in B cells	1.23069E-12
Activation of the AP-1 family of transcription factors	0.001041885
Adaptive Immune System	8.86451E-06
Adenylate cyclase inhibitory pathway	0.000143533
Adherens junction	4.11984E-12
Adipocytokine signaling pathway	0.014248363
ADP signalling through P2Y purinoceptor 1	0.015478822
ADP signalling through P2Y purinoceptor 12	0.000143533
Adrenaline, noradrenaline inhibits insulin secretion	0.015478822
Adrenergic signaling in cardiomyocytes	0.049384343
AGE-RAGE signaling pathway in diabetic complications	6.3338E-13
AKT phosphorylates targets in the cytosol	0.007462562
Antigen processing: Ubiquitination & Proteasome degradation	8.86451E-06
Antigen processing-Cross presentation	1.23069E-12
APC/C:Cdc20 mediated degradation of mitotic proteins	1.23069E-12
APC/C:Cdc20 mediated degradation of Securin	1.23069E-12
APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	1.23069E-12
APC/C-mediated degradation of cell cycle proteins	1.23069E-12
APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint	1.23069E-12
Apelin signaling pathway	0.000265052
Apoptosis	0.003114477
ARMS-mediated activation	1.23069E-12
Assembly of collagen fibrils and other multimeric structures	9.26518E-07
Assembly of the pre-replicative complex	1.23069E-12
Asymmetric localization of PCP proteins	1.23069E-12
AUF1 (hnRNP D0) binds and destabilizes mRNA	1.23069E-12
Autodegradation of the E3 ubiquitin ligase COP1	1.23069E-12
Autophagy	0.012187635
Axon guidance	0.000501037
B cell receptor signaling pathway	0.000999416
Beta-catenin independent WNT signaling	1.23069E-12
Ca2+ pathway	0.015478822
cAMP signaling pathway	5.53949E-05
CASP8 activity is inhibited	0.006176324
Caspase activation via extrinsic apoptotic signalling pathway	9.69569E-05
CD209 (DC-SIGN) signaling	1.34199E-06
Cdc20:Phospho-APC/C mediated degradation of Cyclin A	1.23069E-12
CDK-mediated phosphorylation and removal of Cdc6	1.23069E-12
CDT1 association with the CDC6:ORC:origin complex	1.23069E-12
Cell cycle	0.000154315
Cell Cycle Checkpoints	1.23069E-12
Cell Cycle, Mitotic	1.23069E-12
Cell surface interactions at the vascular wall	0.006176324
Cell-Cell communication	0.000509235
Cellular response to hypoxia	1.23069E-12
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Cellular responses to stress	1.23069E-12
Centrosome maturation	3.50092E-06
Chaperonin-mediated protein folding	3.50092E-06
Chemokine signaling pathway	0.003038401
Class I MHC mediated antigen processing & presentation	8.86451E-06
CLEC7A (Dectin-1) signaling	1.23069E-12
Collagen biosynthesis and modifying enzymes	9.26518E-07
Collagen chain trimerization	9.26518E-07
Collagen degradation	9.26518E-07
Collagen formation	9.26518E-07
Complement and coagulation cascades	0.000863323
Constitutive Signaling by AKT1 E17K in Cancer	0.007462562
Cooperation of PDCL (PhLP1) and TRIC/CCT in G-protein beta folding	0.000143533
Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding	3.50092E-06
COPI-independent Golgi-to-ER retrograde traffic	3.50092E-06
COPI-mediated anterograde transport	3.50092E-06
CREB phosphorylation	1.34199E-06
Cross-presentation of soluble exogenous antigens (endosomes)	1.23069E-12
CTLA4 inhibitory signaling	0.000523836
C-type lectin receptors (CLRs)	1.23069E-12
Cytokine Signaling in Immune system	1.23069E-12
DAP12 interactions	1.23069E-12 1.23069E-12
	1.23069E-12
DAP12 signaling Death Receptor Signalling	0.006176324
Dectin-1 mediated noncanonical NF-kB signaling	1.23069E-12
Defective B3GALTL causes Peters-plus syndrome (PpS)	0.000423478
Defective CFTR causes cystic fibrosis	1.23069E-12
Degradation of AXIN	1.23069E-12
Degradation of beta-catenin by the destruction complex	1.23069E-12
Degradation of DVL	1.23069E-12
Degradation of GLI1 by the proteasome	1.23069E-12
Degradation of GLI2 by the proteasome	1.23069E-12
Degradation of the extracellular matrix	6.91075E-09
Deubiquitination Deubiquitination	1.23069E-12
Developmental Biology	2.82745E-06
Dimerization of procaspase-8	0.006176324
Disease	0.000423478
Diseases associated with O-glycosylation of proteins	0.000423478
Diseases associated with the TLR signaling cascade	9.69569E-05
Diseases of glycosylation	0.000423478
Diseases of Immune System	9.69569E-05
Diseases of signal transduction	1.23069E-12
Disinhibition of SNARE formation	0.047794098
Disorders of transmembrane transporters	1.23069E-12
DNA Replication	1.23069E-12
DNA Replication Pre-Initiation	1.23069E-12
Downstream signal transduction	1.23069E-12
Downstream signaling events of B Cell Receptor (BCR)	1.23069E-12
Downstream TCR signaling	1.23069E-12
ECM proteoglycans	9.26518E-07
ECM-receptor interaction	6.43147E-05
Elastic fibre formation	0.023000815
ER to Golgi Anterograde Transport	3.50092E-06
ErbB signaling pathway	2.6995E-05
ERK/MAPK targets	1.34199E-06
ER-Phagosome pathway	1.23069E-12
Extracellular matrix organization	6.91075E-09
Factors involved in megakaryocyte development and platelet production	3.50092E-06
FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	1.23069E-12

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Hemostasis Hh mutants abrogate ligand secretion 1.23069E-1 Hh mutants that don't undergo autocatalytic processing are degraded by ERAD 1.23069E-1 HIF-1 signaling pathway 3.53001E-0 Hippo signaling pathway 0.0053280 HIV Transcription Initiation 0.0003444 Host Interactions of HIV factors 1.23069E-1 IGF1R signaling cascade 1.23069E-1 IKBKB deficiency causes SCID IKK complex recruitment mediated by RIP1 1.217 signaling pathway 0.0004375 Immune System 1.23069E-1 Incretin synthesis, secretion, and inactivation 0.0001435. Inhibition of voltage gated Ca2+ channels via Gbeta/gamma subunits		0.003169127
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HIF-1 signaling pathway Hippo signaling pathway 0.0053280 HIV Transcription Initiation 0.0003444 Host Interactions of HIV factors IGF1R signaling cascade IKBKB deficiency causes SCID IKK complex recruitment mediated by RIP1 IL-17 signaling pathway Immune System Incretin synthesis, secretion, and inactivation Inhibition of voltage gated Ca2+ channels via Gbeta/gamma subunits 3.53001E-C 0.0053280 0.0003444 0.0003444 1.23069E-1 0.00746250 0.00746250 0.0004375		1.23069E-12
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IKK complex recruitment mediated by RIP19.69569E-CIL-17 signaling pathway0.0004375Immune System8.86451E-CIncretin synthesis, secretion, and inactivation0.0001435Inhibition of voltage gated Ca2+ channels via Gbeta/gamma subunits0.0154788		0.007462562
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		0.011394908
		0.000523836
		9.26518E-07
		1.23069E-12
		1.13141E-05
		1.23069E-12
		1.23069E-12
		1.13141E-05
		0.015478822

IBAV2 modisted activation of TAV1 complex upon TLP7/9 or 0 ctimulation	9.69569E-05
IRAK2 mediated activation of TAK1 complex upon TLR7/8 or 9 stimulation IRAK4 deficiency (TLR2/4)	9.69569E-05 9.69569E-05
IRS-mediated signalling	1.23069E-12
IRS-related events triggered by IGF1R JNK (c-Jun kinases) phosphorylation and activation mediated by activated human TAK1	1.23069E-12
Keratinization	0.000975181 2.82745E-06
Kinesins	3.50092E-06
Ligand-dependent caspase activation	3.70615E-07 9.69569E-05
Longevity regulating pathway	0.020245093
Long-term potentiation M Phase	0.04276411
M/G1 Transition	1.23069E-12 1.23069E-12
MAP kinase activation in TLR cascade	0.000975181
MAPZK and MAPK activation	0.02234388
MAPK family signaling cascades	1.23069E-12
MAPK signaling pathway	1.29202E-11
MAPK targets/ Nuclear events mediated by MAP kinases	1.34199E-06
MAPK1/MAPK3 signaling	1.23069E-12
MAPK6/MAPK4 signaling	1.23069E-12
MET activates RAS signaling	0.02234388
Metabolism of polyamines	1.23069E-12
Metabolism of proteins	8.86451E-06
MHC class II antigen presentation	3.50092E-06
Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	3.50092E-06
Mitotic Anaphase	1.23069E-12
Mitotic G2-G2/M phases	1.23069E-12
Mitotic Metaphase and Anaphase	1.23069E-12
Mitotic Prometaphase	3.50092E-06
Molecules associated with elastic fibres	0.023000815
mTOR signaling pathway	0.012955231
MyD88 cascade initiated on plasma membrane	0.000975181
MyD88 deficiency (TLR2/4)	9.69569E-05
MyD88 dependent cascade initiated on endosome	9.69569E-05
MyD88:Mal cascade initiated on plasma membrane	9.69569E-05
MyD88-independent TLR3/TLR4 cascade	9.69569E-05
NCAM signaling for neurite out-growth	1.23069E-12
NCAM1 interactions	9.26518E-07
Negative regulation of MAPK pathway	0.02234388
Neurophilin interactions with VEGF and VEGFR	0.01051389
Neurotrophin signaling pathway	3.82536E-06
NF-kappa B signaling pathway	0.031587338
NGF signalling via TRKA from the plasma membrane	1.23069E-12
NIK>noncanonical NF-kB signaling	1.23069E-12
Nuclear Events (kinase and transcription factor activation)	1.34199E-06
O-glycosylation of TSR domain-containing proteins	0.000423478
O-linked glycosylation	0.000423478
Opioid Signalling	0.000143533
Orc1 removal from chromatin	1.23069E-12
Osteoclast differentiation	9.15186E-09
Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	1.23069E-12
Oxytocin signaling pathway	0.014168671
p53 signaling pathway	0.014248363
p53-Dependent G1 DNA Damage Response	1.23069E-12
p53-Dependent G1/S DNA damage checkpoint	1.23069E-12
p53-Independent DNA Damage Response	1.23069E-12
p53-Independent G1/S DNA damage checkpoint	1.23069E-12
PCP/CE pathway	1.23069E-12
	1.230031 12

PI3K-Akt signaling pathway	1.46068E-13
Platelet activation	0.019919175
Platelet activation, signaling and aggregation	0.000143533
Platelet Aggregation (Plug Formation)	0.000523836
PLC beta mediated events	0.000143533
Post-chaperonin tubulin folding pathway	3.50092E-06
·	8.86451E-06
, ,	0.015478822
Progesterone-mediated oocyte maturation	0.035485862
Programmed Cell Death	2.5354E-05
0 01 ,	0.003905837
Prolonged ERK activation events	1.23069E-12
, , , , , ,	0.015478822
Protein folding	3.50092E-06
·	8.86451E-06
RAF/MAP kinase cascade	1.23069E-12
Rap1 signaling pathway	2.80626E-08
RAS signaling downstream of NF1 loss-of-function variants	0.02234388
Ras signaling pathway	1.89757E-08
Recruitment of mitotic centrosome proteins and complexes	3.50092E-06
Recruitment of NuMA to mitotic centrosomes	3.50092E-06
Recycling pathway of L1	3.70615E-07
	0.006176324
Regulation by c-FLIP	0.006176324
· ·	0.000240316
Regulation of activated PAK-2p34 by proteasome mediated degradation	1.23069E-12
Regulation of APC/C activators between G1/S and early anaphase	1.23069E-12
Regulation of Apoptosis	2.5354E-05
Regulation of DNA replication	1.23069E-12
Regulation of Hypoxia-inducible Factor (HIF) by oxygen	1.23069E-12
Regulation of mitotic cell cycle	1.23069E-12
Regulation of mRNA stability by proteins that bind AU-rich elements	1.23069E-12
	0.006176324
Regulation of ornithine decarboxylase (ODC)	1.23069E-12
	2.5354E-05
Regulation of RAS by GAPs	1.23069E-12
-0	9.69569E-05
Regulation of TP53 Activity	5.50978E-06
	0.000344402
Regulation of TP53 Degradation	5.50978E-06
<u> </u>	5.50978E-06
Removal of licensing factors from origins	1.23069E-12
Resolution of Sister Chromatid Cohesion	3.50092E-06
Response to elevated platelet cytosolic Ca2+	0.047794098
RET signaling	1.23069E-12
,	2.5354E-05
	3.50092E-06
RHO GTPases activate IQGAPs	3.50092E-06
RIPK1-mediated regulated necrosis	0.006176324
RNA Polymerase II HIV Promoter Escape	0.000344402
·	0.000344402
·	0.000344402
RNA Polymerase II Transcription Initiation And Promoter Clearance	0.000344402
RNA Polymerase II Transcription Pre-Initiation And Promoter Opening	0.000344402
RSK activation	0.000523836
S Phase	1.23069E-12
SCF-beta-TrCP mediated degradation of Emi1	1.23069E-12
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SEMA3A-Plexin repulsion signaling by inhibiting Integrin adhesion	0.01051389

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Separation of Sister Chromatids	1.23069E-12
SHC1 events in EGFR signaling	1.23069E-12
SHC-related events triggered by IGF1R	0.02234388
Signal amplification	0.000143533
Signal regulatory protein (SIRP) family interactions	0.000509235
Signal Transduction	2.5354E-05
Signal transduction by L1	0.01051389
Signaling by EGFR	1.23069E-12
Signaling by FGFR3 fusions in cancer	0.02234388
Signaling by FGFR4 in disease	0.02234388
Signaling by Hedgehog	1.23069E-12
Signaling by high-kinase activity BRAF mutants	0.02234388
Signaling by Insulin receptor	1.23069E-12
Signaling by Interleukins	1.23069E-12
Signaling by Leptin	1.23069E-12
Signaling by PDGF	1.23069E-12
Signaling by Rho GTPases	2.5354E-05
Signaling by SCF-KIT	1.23069E-12
Signaling by the B Cell Receptor (BCR)	1.23069E-12
Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)	1.23069E-12
Signaling by VEGF	1.23069E-12
Signaling by Wnt	1.23069E-12
Signaling pathways regulating pluripotency of stem cells	8.14166E-05
Signalling to ERKs	1.23069E-12
Signalling to p38 via RIT and RIN	1.23069E-12
Signalling to RAS	1.23069E-12
SOS-mediated signalling	1.23069E-12
Stabilization of p53	1.23069E-12
Switching of origins to a post-replicative state	1.23069E-12
Syndecan interactions	0.013439221
Synthesis of active ubiquitin: roles of E1 and E2 enzymes	8.86451E-06
Synthesis of DNA Synthesis acquaising and inactivation of Changes like Pentide 1 (CLP 1)	1.23069E-12
Synthesis, secretion, and inactivation of Glucagon-like Peptide-1 (GLP-1)	0.000143533
T cell receptor signaling pathway	1.82277E-07
TCF dependent signaling in response to WNT	1.23069E-12
TCR signaling	1.23069E-12
TGF-beta signaling pathway Th1 and Th2 cell differentiation	0.007916254
	0.001562264
The rele of CTSS1 in C3/M progression often C3 phostypeint	1.27716E-08
The role of GTSE1 in G2/M progression after G2 checkpoint Thromboxane signalling through TP receptor	1.23069E-12 0.015478822
Thyroid hormone signaling pathway	0.000756156
Tight junction	0.000289417
TNF signaling pathway TNFR2 non-canonical NF-kB pathway	0.012714665 1.23069E-12
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Toll Like Receptor 10 (TLR10) Cascade	0.000975181 9.69569E-05
Toll Like Receptor 2 (TLR2) Cascade	9.69569E-05 9.69569E-05
Toll Like Receptor 3 (TLR3) Cascade Toll Like Receptor 4 (TLR4) Cascade	
	9.69569E-05 0.000975181
Toll Like Receptor 7/8 (TLR7/8) Cascade	9.69569E-05
Toll Like Receptor 9 (TLR9) Cascade	9.69569E-05 9.69569E-05
Toll Like Receptor TLR1:TLR2 Cascade	9.69569E-05
·	
Toll Like Receptor TLR6:TLR2 Cascade Tall like receptor signaling pathway	9.69569E-05
Toll-like receptor signaling pathway	0.000133836
Toll-Like Receptors Cascades TRE2 Regulator Transcription of Call Doath Gones	9.69569E-05
TP53 Regulates Transcription of Cell Death Genes TP53 Regulates Transcription of Death Receptors and Ligands	0.006176324 0.006176324
TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation	9.69569E-05
That o mediated induction of M kb and Mar kindses apon Ten//o of 3 activation	J.03J03E-03

TRAF6 mediated induction of TAK1 complex	9.69569E-05
TRAIL signaling	0.006176324
Translocation of GLUT4 to the plasma membrane	3.50092E-06
Transport of connexons to the plasma membrane	3.50092E-06
Transport to the Golgi and subsequent modification	3.50092E-06
TRIF-mediated programmed cell death	9.69569E-05
TRIF-mediated TLR3/TLR4 signaling	9.69569E-05
Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	1.23069E-12
Ubiquitin-dependent degradation of Cyclin D	1.23069E-12
Ubiquitin-dependent degradation of Cyclin D1	1.23069E-12
Ub-specific processing proteases	1.23069E-12
UCH proteinases	1.23069E-12
Uptake and actions of bacterial toxins	0.000975181
Uptake and function of anthrax toxins	0.000975181
Vasopressin regulates renal water homeostasis via Aquaporins	0.015478822
VEGF signaling pathway	0.002636991
VEGFA-VEGFR2 Pathway	1.23069E-12
VEGFR2 mediated cell proliferation	1.23069E-12
VEGFR2 mediated vascular permeability	0.000523836
Vif-mediated degradation of APOBEC3G	1.23069E-12
Vpu mediated degradation of CD4	1.23069E-12
Wnt signaling pathway	4.17868E-09