# Supplementary Materials

## Supplemental Acknowledgements

Kidney Precision Medicine Project (KPMP)

NEPTUNE study

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## Supplemental Acknowledgments:

### For the Kidney Precision Medicine Project

*American Association of Kidney Patients, Tampa, FL*: Richard Knight

*Beth Israel Deaconess, Boston, MA*: Stewart Lecker, Isaac Stillman

*Brigham & Women's Hospital, Boston, MA*: Gearoid McMahon, Sus Waikar, Astrid Weins

*Broad Institute, Cambridge, MA*: Nir Hacohen, Paul Hoover

*Case Western Reserve, Cleveland, OH*: Mark Aulisio

*Cleveland Clinic, Cleveland, OH*: Will Bush, Leslie Cooperman, Dana Crawford, Leal Herlitz, John O'toole, Emilio Poggio, John Sedor

*Columbia University, New York, NY*: Paul Appelbaum, Olivia Balderes, Jonathan Barasch, Andrew Bomback, Vivette D'agati, Krzysztof Kiryluk, Karla Mehl, Ning (Sunny) Shang, Chenhua Weng

*Duke University, Durham, NC*: Laura Barisoni

*European Molecular Biology Laboratory, Heidelberg, Germany*: Theodore Alexandrov

*Indiana University, Indianapolis, IN*: Tarek Ashkar, Daria Barwinska, Pierre Dagher, Kenneth Dunn, Michael Eadon, Michael Ferkowicz, Katherine Kelly, Timothy Sutton, Seth Winfree

*John Hopkins University, Baltimore, MD*: Steven Menez, Chirag Parikh, Avi Rosenberg, Pam Villalobos

*Joslin Diabetes Center, Boston, MA*: Sylvia Rosas, Mark Williams

*Mount Sinai, New York, NY*: Evren Azeloglu, Cijang (John) He, Ravi Iyengar

*Ohio State University, Columbus, OH*: Samir Parikh

*Pacific Northwest National Laboratories, Richland, WA*: Chris Anderton, Ljiljana Pasa-Tolic, Dusan Velickovic

*Parkland Center for Clinical Innovation, Dallas, TX*: George (Holt) Oliver

*Patient Advocates*: Joseph Ardayfio, Jack Bebiak, Keith Brown, Taneisha Campbell, Catherine Campbell, Lynda Hayashi, Nichole Jefferson, Robert Koewler, Glenda Roberts, John Saul, Anna Shpigel, Edith Christine Stutzke, Lorenda Wright

*Princeton University, Princeton, NJ*: Rachel Sealfon, Olga Troyanskaya

*Providence Medical Research Center, Spokane, WA*: Katherine Tuttle

*Stanford University, Palo Alto, CA*: Yury Goltsev

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*University of California San Francisco, San Francisco, CA*: Dejan Dobi, Maria Joanes, Zoltan Laszik, Garry Nolan, Andrew Schroeder

*University of Michigan, Ann Arbor, MI*: Ulysses Balis, Oliver He, Jeffrey Hodgin, Matthias Kretzler, Laura Mariani, Rajasree Menon, Edgar Otto, Jennifer Schaub, Becky Steck

*University of Pittsburgh, Pittsburgh, PA*: Michele Elder, Daniel Hall, John Kellum, Mary Kruth, Raghav Murugan, Paul Palevsky , Parmjeet Randhawa, Matthew Rosengart, Sunny Sims-Lucas, Mary Stefanick, Stacy Stull, Mitchell Tublin

*University of Washington, Seattle, WA*: Charles Alpers, Ian De Boer, Malia Fullerton, Jonathan Himmelfarb, Robyn Mcclelland, Sean Mooney, Stuart Shankland, Kayleen Williams, Kristina Blank, Ashveena Dighe

*UT Health San Antonio, San Antonio, TX*: Kumar Sharma, Guanshi Zhang

*UT Southwestern Medical Center, Dallas, TX*: Susan Hedayati, Asra Kermani, Simon Lee, Christopher Lu, Tyler Miller, Orson Moe, Harold Park, Kamalanathan Sambandam, Francisco Sanchez, Jose Torrealba, Toto Robert, Miguel Vazquez, Nancy Wang

*Washington University in St. Louis, St. Louis, MO*: Joe Gaut, Sanjay Jain, Anitha Vijayan

*Yale University, New Haven, CT*: Tanima Arora, Randy Luciano, Dennis Moledina, Ugwuowo Ugochukwu, Francis Perry Wilson

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*Data Analysis and Coordinating Center*: M Kretzler, L Barisoni, C Gadegbeku, B Gillespie, D Gipson, L Holzman, L Mariani, M Sampson, P Song, J Troost, J Zee, E Herreshoff, S Li, C Lienczewski, T Mainieri, M Wladkowski, A Williams, D Zinsser

*National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK) Program Office:* K Abbott, C Roy

*The National Center for Advancing Translational Sciences (NCATS) Program Office:* T Urv, PJ Brooks

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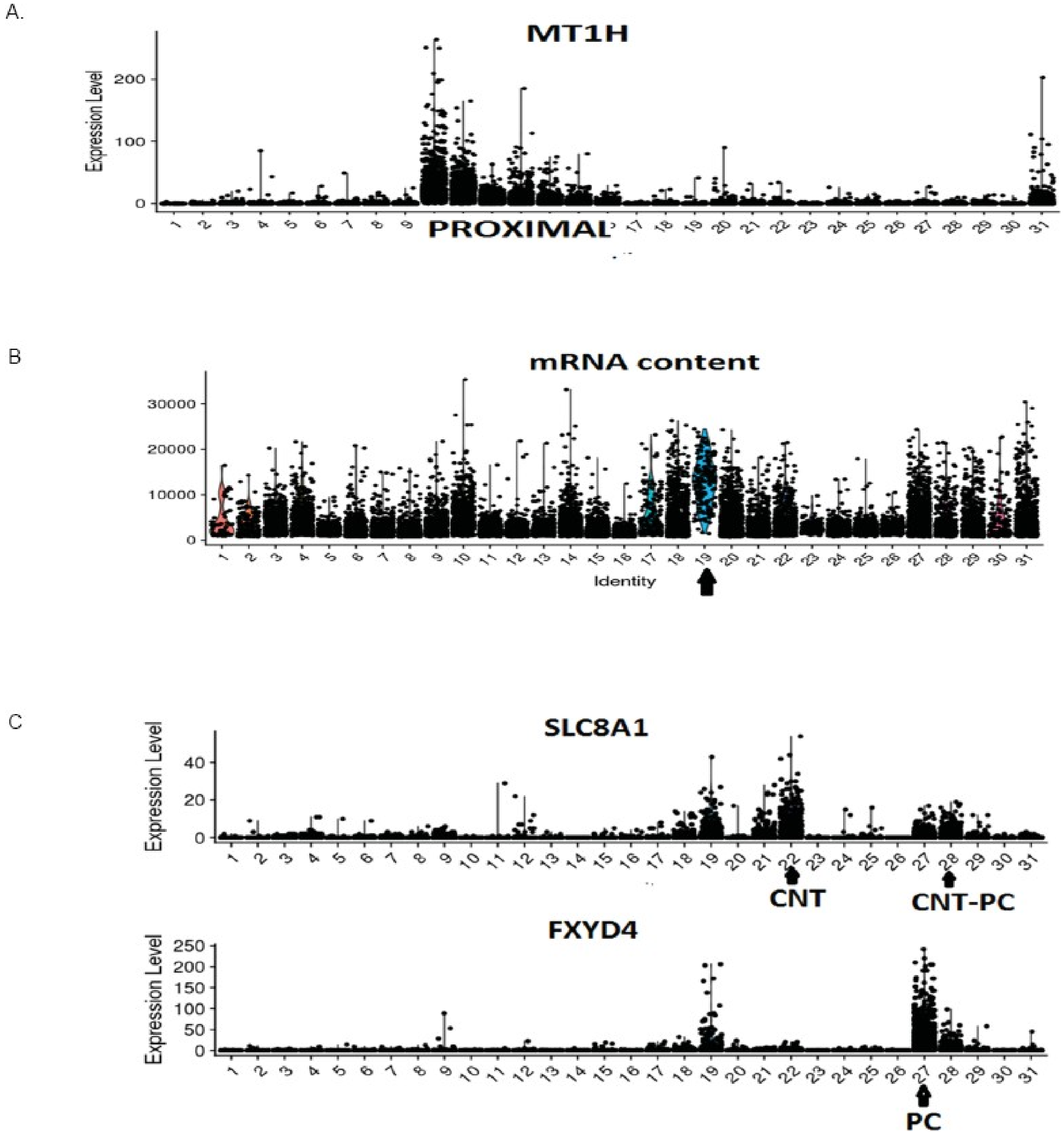
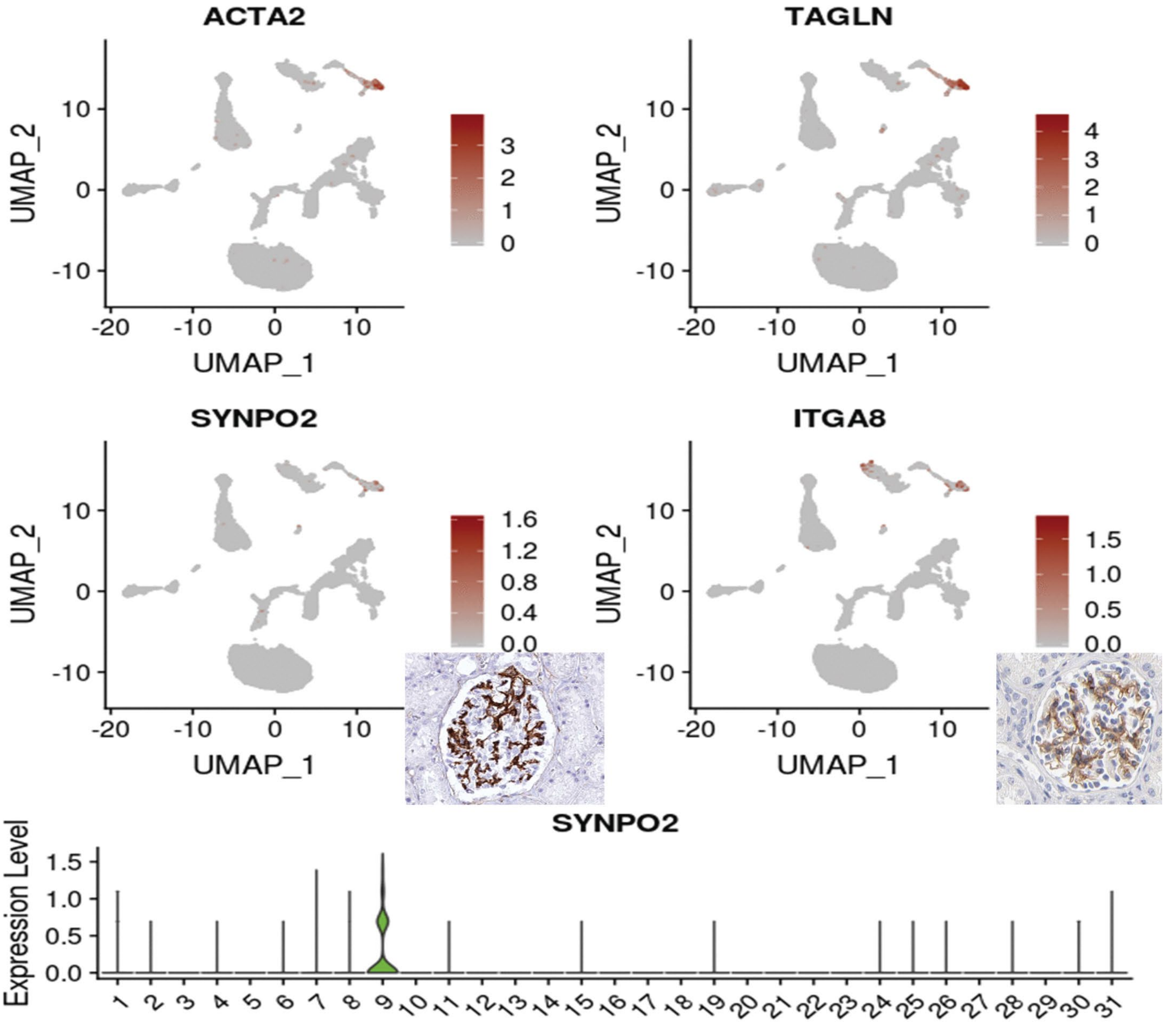
**Supplementary Figure 1**: **Violin plot indicating the cell-type specific gene expression.**

A. Violin plot shows the gradient expression of mitochondrial gene MT-1 in the 7 proximal cell clusters (clusters 10-16).
B. Violin plot shows relatively higher mRNA content in cluster 19 compared to other clusters. This cluster expressed cell-type specific markers of both principal and intercalated cells.
C. Violin plot shows that cluster 28, which we annotated as CNT-PC (cortical connecting tubule intercalated cell) expressed known markers of both principal cells (FXYD4, STC1) and connecting tubule cells (SLC8A1).



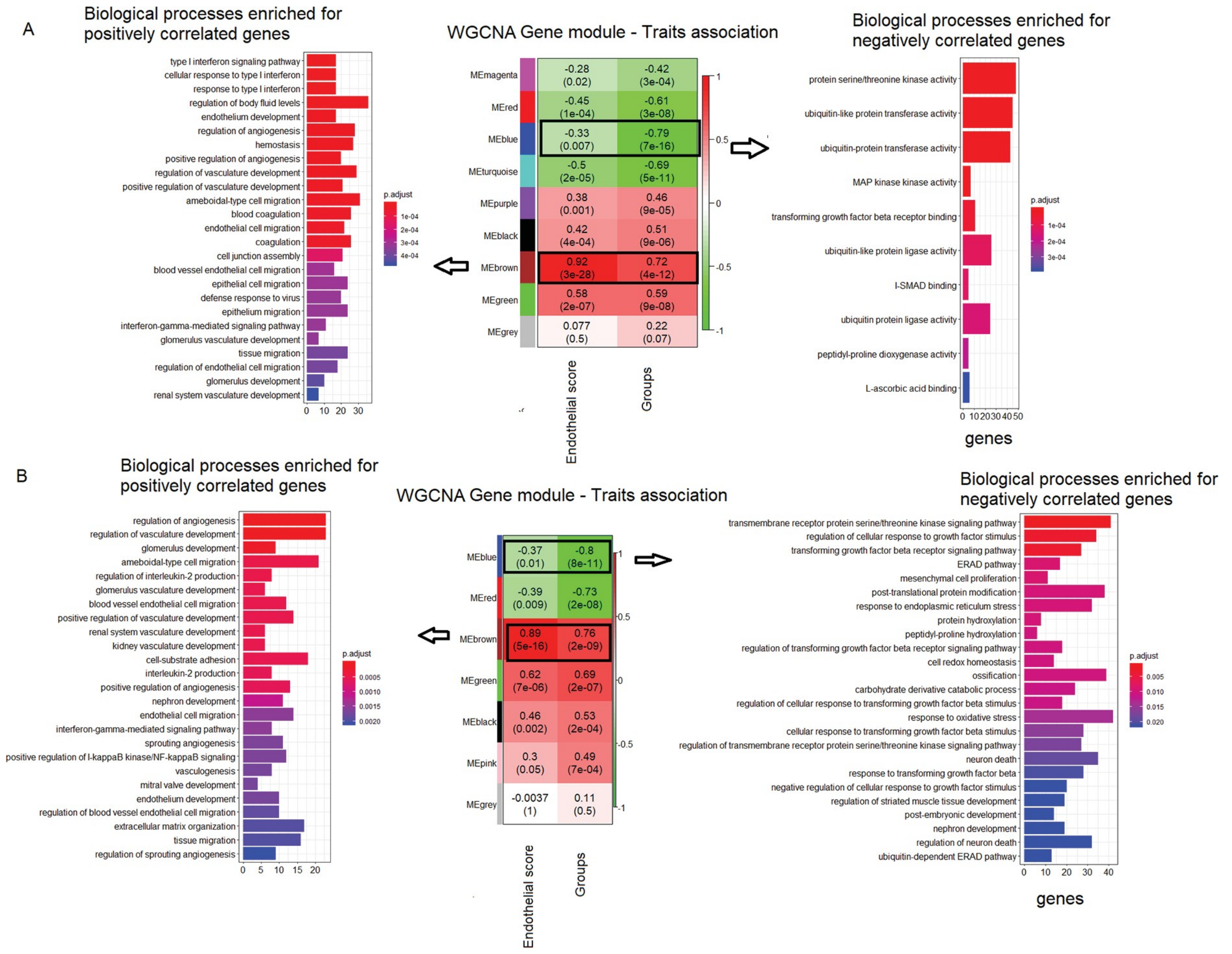
**Supplementary Figure 2: Mesangial cell type markers.**

Feature plots show the expression of known markers of vascular smooth muscle cells, ACTA2 and TAGLN that confirmed the identity of cluster 9. The specific antibody staining of SYNPO2 and ITGA8 in the Human Protein Atlas (shown in inset) further authenticated the presence of mesangial cells in cluster 9, shown in green in the violin plot below.



**Supplementary Figure 3: Glomerular Endothelial Cell (GEC) gene set identified FSGS subgroups: functional annotation of differentially expressed glomerular genes between the groups.**

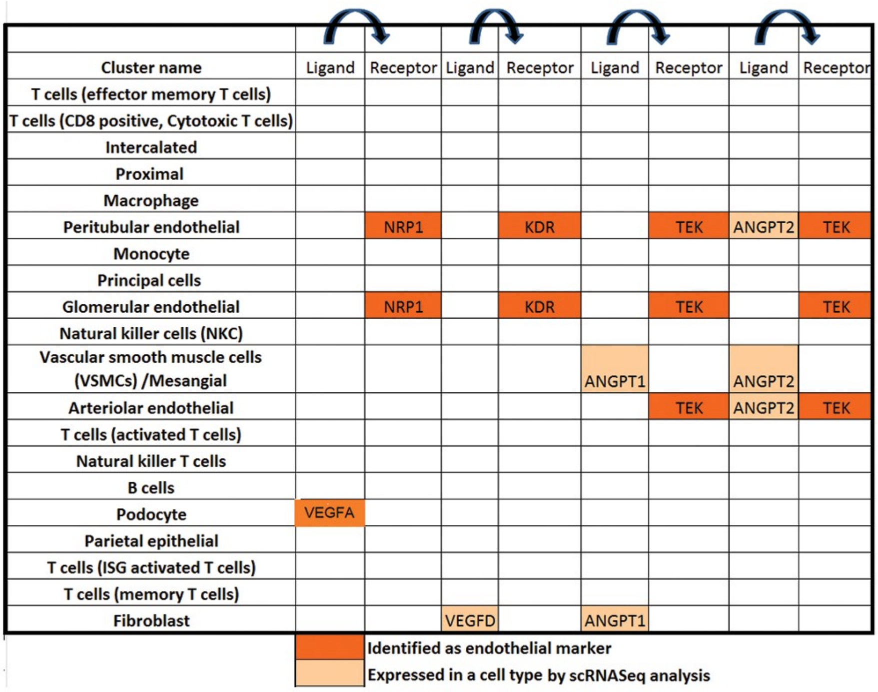
A. WGCNA analysis identifies gene co-expression modules that positively (red) and negatively (green) correlated with the two GEC defined groups and GEC scores. The figure also shows the biological processes that were enriched among the genes in the positively and negatively correlated gene modules.
B. WGCNA modules that positively and negatively correlated with the two groups and GEC scores of samples from FSGS patients with no exposure to immunosuppressive treatment prior to biopsy, showing comparable biological processes associated with the GEC defined groups and GEC scores. The figure also shows the biological processes that were enriched for the genes in the positively and negatively correlated modules.



**Supplementary Figure 4: Potential receptor ligand interactions.**

A. Illustration of endothelial receptors and corresponding ligands expressed by distinct cell types in single cell RNASeq data.

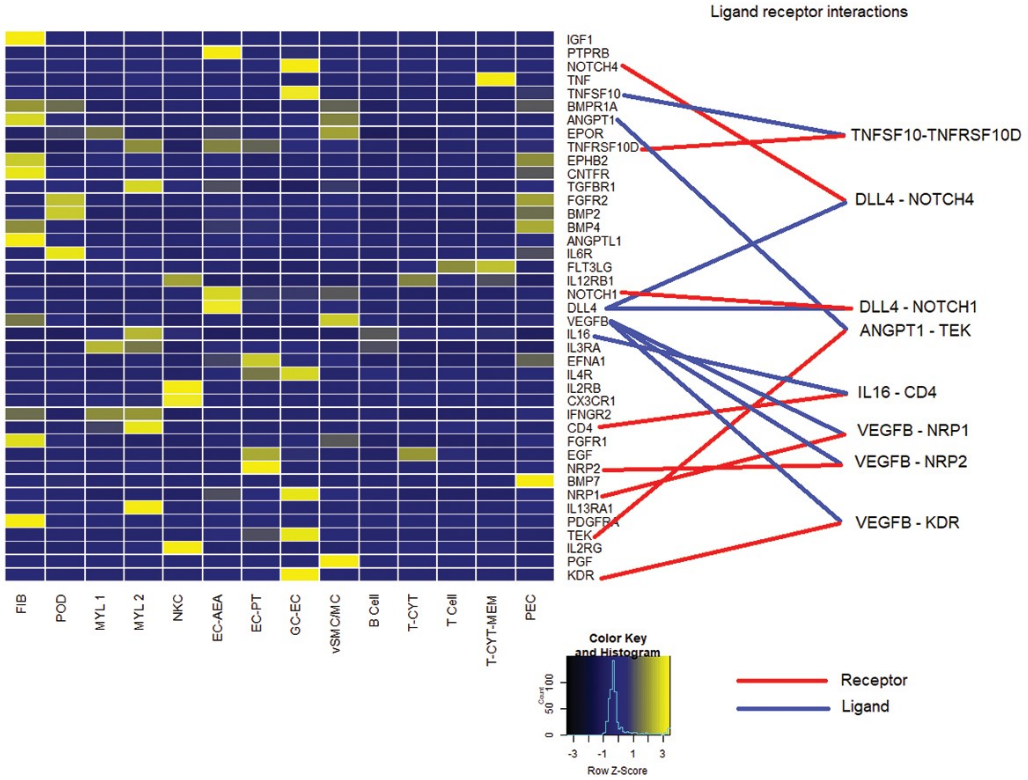
B. Potential ligand-receptor interaction in FSGS. Ligand/receptors interaction were mapped among genes differentially expressed (FDR < 0.05) in glomerular RNA from FSGS group 2 versus group 1. Subsequently, cell-type enrichment of interacting ligands and receptors were defined in the scRNAseq profiles from normal kidney. Heatmap with cell type enrichment in column and transcripts differentially expressed among FSGS subgroups in rows. Interactions mapped by linking ligands (red lines) to receptors (blue lines).



| Cluster name | Ligand | Receptor | Ligand | Receptor | Ligand | Receptor | Ligand | Receptor |
|---|---|---|---|---|---|---|---|---|
| T cells (effector memory T cells) | | | | | | | | |
| T cells (CD8 positive, Cytotoxic T cells) | | | | | | | | |
| Intercalated | | | | | | | | |
| Proximal | | | | | | | | |
| Macrophage | | | | | | | | |
| Peritubular endothelial | | NRP1 | | KDR | | TEK | ANGPT2 | TEK |
| Monocyte | | | | | | | | |
| Principal cells | | | | | | | | |
| Glomerular endothelial | | NRP1 | | KDR | | TEK | | TEK |
| Natural killer cells (NKC) | | | | | | | | |
| Vascular smooth muscle cells (VSMCs) /Mesangial | | | | | ANGPT1 | | ANGPT2 | |
| Arteriolar endothelial | | | | | | TEK | ANGPT2 | TEK |
| T cells (activated T cells) | | | | | | | | |
| Natural killer T cells | | | | | | | | |
| B cells | | | | | | | | |
| Podocyte | VEGFA | | | | | | | |
| Parietal epithelial | | | | | | | | |
| T cells (ISG activated T cells) | | | | | | | | |
| T cells (memory T cells) | | | | | | | | |
| Fibroblast | | | VEGFD | | ANGPT1 | | | |

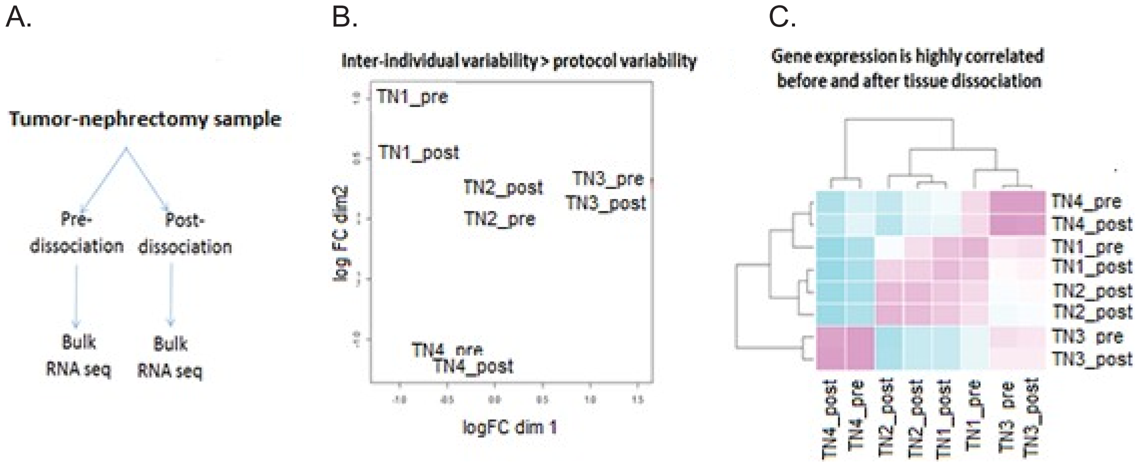
🟧 Identified as endothelial marker

🟨 Expressed in a cell type by scRNASeq analysis



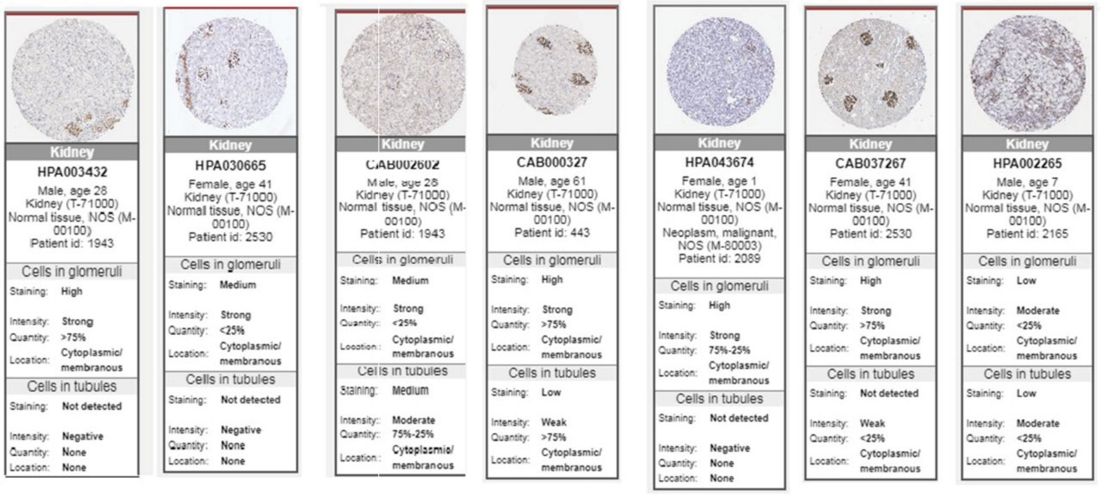
**Supplementary Figure 5: Limited impact of cell dissociation on mRNA expression.**

A. Experimental design
B. Multi-dimensional plot shows stringent correlation between pre- and post-dissociation gene expression for each of the four unaffected parts of the tumor nephrectomy (TN) samples used.
C. Correlation of the gene expression in pre and post dissociation samples.



**Supplementary Figure 6: Human Protein Atlas (HPA) antibody information.**

The figure provides information on the antibodies used for the immunostaining images accessed on proteinatlas.org on 12/21/2019 for this study.



**ITGA8**

Kidney
HPA003432
Male, age 28
Kidney (T-71000)
Normal tissue, NOS (M-00100)
Patient id: 1943

Cells in glomeruli
Staining: High
Intensity: Strong
Quantity: >75%
Location: Cytoplasmic/ membranous

Cells in tubules
Staining: Not detected
Intensity: Negative
Quantity: None
Location: None

**SUNPO2**

Kidney
HPA030665
Female, age 41
Kidney (T-71000)
Normal tissue, NOS (M-00100)
Patient id: 2530

Cells in glomeruli
Staining: Medium
Intensity: Strong
Quantity: <25%
Location: Cytoplasmic/ membranous

Cells in tubules
Staining: Not detected
Intensity: Negative
Quantity: None
Location: None

**CLDN1**

Kidney
CAB002602
Male, age 28
Kidney (T-71000)
Normal tissue, NOS (M-00100)
Patient id: 1943

Cells in glomeruli
Staining: Medium
Intensity: Strong
Quantity: <25%
Location: Cytoplasmic/ membranous

Cells in tubules
Staining: Medium
Intensity: Moderate
Quantity: 75%-25%
Location: Cytoplasmic/ membranous

**WT1**

Kidney
CAB000327
Male, age 61
Kidney (T-71000)
Normal tissue, NOS (M-00100)
Patient id: 443

Cells in glomeruli
Staining: High
Intensity: Strong
Quantity: >75%
Location: Cytoplasmic/ membranous

Cells in tubules
Staining: Low
Intensity: Weak
Quantity: >75%
Location: Cytoplasmic/ membranous

**CRB2**

Kidney
HPA043674
Female, age 1
Kidney (T-71000)
Normal tissue, NOS (M-00100)
Neoplasm, malignant, NOS (M-80003)
Patient id: 2089

Cells in glomeruli
Staining: High
Intensity: Strong
Quantity: 75%-25%
Location: Cytoplasmic/ membranous

Cells in tubules
Staining: Not detected
Intensity: Negative
Quantity: None
Location: None

**NPHS2**

Kidney
CAB037267
Female, age 41
Kidney (T-71000)
Normal tissue, NOS (M-00100)
Patient id: 2530

Cells in glomeruli
Staining: High
Intensity: Strong
Quantity: >75%
Location: Cytoplasmic/ membranous

Cells in tubules
Staining: Not detected
Intensity: Weak
Quantity: <25%
Location: Cytoplasmic/ membranous

**A2M**

Kidney
HPA002265
Male, age 7
Kidney (T-71000)
Normal tissue, NOS (M-00100)
Patient id: 2165

Cells in glomeruli
Staining: Low
Intensity: Moderate
Quantity: <25%
Location: Cytoplasmic/ membranous

Cells in tubules
Staining: Low
Intensity: Moderate
Quantity: <25%
Location: Cytoplasmic/ membranous

## **Supplementary Table 1:** Cell-type specific genes.

List of top 10 significantly (adjusted p value < 0.05) differentially expressed genes identified for each of the 31 clusters. Header pct.1 indicates the percentage of cells expressing the gene in the cluster of interest compared to all other clusters. pct.2 indicates the percentage of cells expressing the gene in all other clusters. The differential expression was performed using non-parametric Wilcoxon rank sum test. Avg_logFC= average log fold change.

| Cluster | p_val | avg_logFC | pct.1 | pct.2 | p_val_adj | gene | Cell type |
|---|---|---|---|---|---|---|---|
| 1 | 0 | 3.280454 | 0.862 | 0.01 | 0 | DCN | FIB |
| 1 | 0 | 1.89356 | 0.845 | 0.011 | 0 | COL1A2 | FIB |
| 1 | 0 | 1.891675 | 0.707 | 0.001 | 0 | LUM | FIB |
| 1 | 0 | 1.863881 | 0.638 | 0.005 | 0 | APOD | FIB |
| 1 | 0 | 1.847703 | 0.724 | 0.009 | 0 | COL1A1 | FIB |
| 1 | 0 | 1.787326 | 0.741 | 0.011 | 0 | CCDC80 | FIB |
| 1 | 0 | 1.706034 | 0.707 | 0.001 | 0 | FBLN1 | FIB |
| 1 | 0 | 1.702994 | 0.517 | 0.001 | 0 | MFAP5 | FIB |
| 1 | 2.81E-182 | 2.599049 | 0.793 | 0.042 | 5.52E-178 | IGFBP6 | FIB |
| 1 | 5.93E-95 | 3.309083 | 0.586 | 0.044 | 1.17E-90 | CFD | FIB |
| 2 | 0 | 2.820924 | 0.924 | 0.03 | 0 | PTGDS | POD |
| 2 | 0 | 2.354913 | 0.924 | 0.068 | 0 | PODXL | POD |
| 2 | 0 | 1.910642 | 0.9 | 0.044 | 0 | HTRA1 | POD |
| 2 | 0 | 1.687402 | 0.859 | 0.002 | 0 | NPHS2 | POD |
| 2 | 0 | 1.639994 | 0.859 | 0.006 | 0 | DCN | POD |
| 2 | 0 | 1.563083 | 0.8 | 0.021 | 0 | TPPP3 | POD |
| 2 | 0 | 1.40588 | 0.794 | 0.005 | 0 | FGF1 | POD |
| 2 | 0 | 1.291032 | 0.8 | 0.047 | 0 | NPNT | POD |
| 2 | 0 | 1.26432 | 0.824 | 0.06 | 0 | SPOCK2 | POD |
| 2 | 9.31E-231 | 1.614756 | 0.612 | 0.052 | 1.83E-226 | CTGF | POD |
| 3 | 0 | 2.196714 | 0.927 | 0.037 | 0 | LST1 | MYL-1 |
| 3 | 0 | 2.088869 | 0.938 | 0.061 | 0 | TYROBP | MYL-1 |
| 3 | 0 | 2.069687 | 0.927 | 0.049 | 0 | AIF1 | MYL-1 |
| 3 | 0 | 1.924078 | 0.908 | 0.05 | 0 | FCER1G | MYL-1 |
| 3 | 0 | 1.886756 | 0.735 | 0.024 | 0 | LYZ | MYL-1 |
| 3 | 0 | 1.883257 | 0.748 | 0.008 | 0 | S100A9 | MYL-1 |
| 3 | 0 | 1.672501 | 0.886 | 0.056 | 0 | CTSS | MYL-1 |
| 3 | 0 | 1.653778 | 0.478 | 0.003 | 0 | S100A8 | MYL-1 |
| 3 | 0 | 1.489341 | 0.798 | 0.003 | 0 | FCN1 | MYL-1 |
| 3 | 0 | 1.300999 | 0.677 | 0.036 | 0 | FCGR3A | MYL-1 |
| 4 | 0 | 2.035592 | 0.867 | 0.067 | 0 | RGS1 | MYL-2 |
| 4 | 0 | 2.007114 | 0.964 | 0.07 | 0 | HLA-DQA1 | MYL-2 |
| 4 | 0 | 1.5804 | 0.751 | 0.037 | 0 | LYZ | MYL-2 |
| 4 | 0 | 1.472122 | 0.6 | 0.01 | 0 | C1QA | MYL-2 |
| 4 | 0 | 1.370689 | 0.537 | 0.006 | 0 | C1QB | MYL-2 |
| 4 | 0 | 1.231735 | 0.801 | 0.017 | 0 | MS4A6A | MYL-2 |
| 4 | 0 | 1.215651 | 0.932 | 0.066 | 0 | AIF1 | MYL-2 |
| 4 | 0 | 1.205981 | 0.507 | 0.003 | 0 | C1QC | MYL-2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 4 | 0 | 1.179372 | 0.569 | 0.002 | 0 | FCER1A | MYL-2 |
| 4 | 0 | 1.053806 | 0.869 | 0.067 | 0 | FCER1G | MYL-2 |
| 5 | 0 | 2.900682 | 0.977 | 0.024 | 0 | GNLY | NKC |
| 5 | 0 | 2.578168 | 1 | 0.055 | 0 | NKG7 | NKC |
| 5 | 0 | 2.373171 | 0.919 | 0.065 | 0 | CCL4 | NKC |
| 5 | 0 | 2.062116 | 0.959 | 0.019 | 0 | GZMB | NKC |
| 5 | 0 | 1.956532 | 0.577 | 0.021 | 0 | CCL3 | NKC |
| 5 | 0 | 1.66985 | 0.91 | 0.031 | 0 | PRF1 | NKC |
| 5 | 0 | 1.492292 | 0.927 | 0.053 | 0 | CST7 | NKC |
| 5 | 0 | 1.323178 | 0.842 | 0.056 | 0 | CTSW | NKC |
| 5 | 0 | 1.318294 | 0.899 | 0.026 | 0 | KLRD1 | NKC |
| 5 | 0 | 1.312563 | 0.823 | 0.058 | 0 | GZMA | NKC |
| 6 | 0 | 1.495441 | 0.798 | 0.031 | 0 | CLDN5 | EC-AEA |
| 6 | 0 | 1.228057 | 0.683 | 0.036 | 0 | SERPINE2 | EC-AEA |
| 6 | 0 | 1.078315 | 0.547 | 0.049 | 0 | C10orf10 | EC-AEA |
| 6 | 0 | 1.06443 | 0.542 | 0.037 | 0 | FN1 | EC-AEA |
| 6 | 0 | 0.992407 | 0.584 | 0.012 | 0 | IGF2 | EC-AEA |
| 6 | 0 | 0.85216 | 0.534 | 0.029 | 0 | LTBP4 | EC-AEA |
| 6 | 0 | 0.823666 | 0.685 | 0.061 | 0 | PODXL | EC-AEA |
| 6 | 0 | 0.814749 | 0.416 | 0.031 | 0 | SLC14A1 | EC-AEA |
| 6 | 0 | 0.797353 | 0.599 | 0.041 | 0 | PPP1R14A | EC-AEA |
| 6 | 0 | 0.78356 | 0.679 | 0.073 | 0 | NPDC1 | EC-AEA |
| 7 | 0 | 1.485445 | 0.907 | 0.072 | 0 | RNASE1 | EC-PT |
| 7 | 0 | 1.314841 | 0.748 | 0.044 | 0 | SDPR | EC-PT |
| 7 | 0 | 1.294725 | 0.819 | 0.034 | 0 | RAMP3 | EC-PT |
| 7 | 0 | 1.283175 | 0.689 | 0.013 | 0 | DNASE1L3 | EC-PT |
| 7 | 0 | 1.250468 | 0.749 | 0.013 | 0 | PLVAP | EC-PT |
| 7 | 0 | 1.112605 | 0.769 | 0.067 | 0 | ENG | EC-PT |
| 7 | 0 | 1.060943 | 0.804 | 0.07 | 0 | EGFL7 | EC-PT |
| 7 | 0 | 1.002339 | 0.494 | 0.064 | 0 | RGCC | EC-PT |
| 7 | 0 | 0.97372 | 0.675 | 0.03 | 0 | TMEM88 | EC-PT |
| 7 | 0 | 0.973627 | 0.777 | 0.068 | 0 | RAMP2 | EC-PT |
| 8 | 0 | 2.307838 | 0.936 | 0.056 | 0 | EMCN | GC-EC |
| 8 | 0 | 1.667081 | 0.776 | 0.026 | 0 | CRHBP | GC-EC |
| 8 | 0 | 1.527833 | 0.793 | 0.039 | 0 | PLAT | GC-EC |
| 8 | 0 | 1.297473 | 0.819 | 0.069 | 0 | RAMP2 | GC-EC |
| 8 | 0 | 1.18415 | 0.664 | 0.008 | 0 | SOST | GC-EC |
| 8 | 0 | 1.119 | 0.496 | 0.014 | 0 | FCN3 | GC-EC |
| 8 | 0 | 1.05449 | 0.79 | 0.074 | 0 | EGFL7 | GC-EC |
| 8 | 0 | 1.043161 | 0.734 | 0.05 | 0 | PTPRB | GC-EC |
| 8 | 0 | 1.027685 | 0.759 | 0.07 | 0 | ENG | GC-EC |
| 8 | 0 | 0.934265 | 0.572 | 0.008 | 0 | EHD3 | GC-EC |
| 9 | 0 | 2.717377 | 0.939 | 0.022 | 0 | TAGLN | vSMC/MC |
| 9 | 0 | 2.353074 | 0.821 | 0.012 | 0 | RGS5 | vSMC/MC |
| 9 | 0 | 1.983116 | 0.933 | 0.072 | 0 | MYL9 | vSMC/MC |
| 9 | 0 | 1.856798 | 0.818 | 0.014 | 0 | ACTA2 | vSMC/MC |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 9 | 0 | 1.763612 | 0.876 | 0.023 | 0 | TPM2 | vSMC/MC |
| 9 | 0 | 1.635495 | 0.798 | 0.011 | 0 | C11orf96 | vSMC/MC |
| 9 | 0 | 1.468698 | 0.762 | 0.007 | 0 | MYH11 | vSMC/MC |
| 9 | 0 | 1.356603 | 0.663 | 0.002 | 0 | PLN | vSMC/MC |
| 9 | 0 | 1.275132 | 0.737 | 0.002 | 0 | RERGL | vSMC/MC |
| 9 | 0 | 1.240091 | 0.635 | 0.047 | 0 | SPARCL1 | vSMC/MC |
| 10 | 0 | 0.610955 | 0.459 | 0.068 | 0 | MT1HL1 | PT-1 |
| 10 | 8.16E-289 | 0.326744 | 0.396 | 0.064 | 1.61E-284 | SLC22A12 | PT-1 |
| 10 | 9.30E-283 | 0.32072 | 0.397 | 0.066 | 1.83E-278 | RP11-119D9.1 | PT-1 |
| 10 | 5.11E-276 | 0.34699 | 0.413 | 0.073 | 1.01E-271 | C9orf66 | PT-1 |
| 10 | 5.16E-271 | 0.317444 | 0.395 | 0.068 | 1.01E-266 | PIPOX | PT-1 |
| 10 | 6.13E-271 | 0.298363 | 0.376 | 0.061 | 1.21E-266 | DAO | PT-1 |
| 10 | 5.29E-260 | 0.332681 | 0.405 | 0.073 | 1.04E-255 | RNF186 | PT-1 |
| 10 | 4.45E-252 | 0.51929 | 0.396 | 0.074 | 8.76E-248 | MT1A | PT-1 |
| 10 | 2.12E-234 | 0.288656 | 0.358 | 0.063 | 4.17E-230 | HAAO | PT-1 |
| 10 | 2.77E-204 | 0.290143 | 0.343 | 0.065 | 5.44E-200 | AFP | PT-1 |
| 11 | 0 | 0.601454 | 0.414 | 0.064 | 0 | MT1HL1 | PT-2 |
| 11 | 6.04E-240 | 0.484201 | 0.342 | 0.072 | 1.19E-235 | MT1A | PT-2 |
| 14 | 0 | 0.50953 | 0.506 | 0.067 | 0 | SLC13A3 | PT-5 |
| 14 | 0 | 0.446199 | 0.414 | 0.052 | 0 | SLC6A19 | PT-5 |
| 14 | 3.29E-306 | 0.366744 | 0.424 | 0.07 | 6.47E-302 | FMO1 | PT-5 |
| 14 | 6.00E-303 | 0.34193 | 0.359 | 0.051 | 1.18E-298 | PLG | PT-5 |
| 14 | 2.52E-293 | 0.348586 | 0.35 | 0.05 | 4.97E-289 | SLC34A1 | PT-5 |
| 14 | 5.36E-288 | 0.35205 | 0.376 | 0.058 | 1.05E-283 | C14orf164 | PT-5 |
| 14 | 1.55E-285 | 0.340199 | 0.387 | 0.063 | 3.04E-281 | ACP5 | PT-5 |
| 14 | 1.91E-279 | 0.346288 | 0.384 | 0.063 | 3.76E-275 | SLC27A2 | PT-5 |
| 14 | 6.10E-266 | 0.364101 | 0.376 | 0.063 | 1.20E-261 | ENPEP | PT-5 |
| 14 | 2.85E-257 | 0.366285 | 0.358 | 0.059 | 5.60E-253 | CALML3 | PT-5 |
| 17 | 0 | 2.361894 | 0.96 | 0.071 | 0 | KRT7 | IC-B |
| 17 | 0 | 1.39323 | 0.81 | 0.022 | 0 | SLC4A9 | IC-B |
| 17 | 0 | 1.242612 | 0.868 | 0.052 | 0 | ATP6V1G3 | IC-B |
| 17 | 0 | 1.142129 | 0.856 | 0.036 | 0 | CTB-27N1.1 | IC-B |
| 17 | 0 | 1.096286 | 0.759 | 0.047 | 0 | TSPAN8 | IC-B |
| 17 | 0 | 0.984442 | 0.58 | 0.006 | 0 | SLC26A4 | IC-B |
| 17 | 0 | 0.932465 | 0.776 | 0.059 | 0 | ATP6V0D2 | IC-B |
| 17 | 0 | 0.801571 | 0.701 | 0.022 | 0 | HEPACAM2 | IC-B |
| 17 | 3.61E-293 | 0.841197 | 0.695 | 0.054 | 7.10E-289 | CDA | IC-B |
| 17 | 2.16E-257 | 0.815191 | 0.655 | 0.054 | 4.24E-253 | IL18 | IC-B |
| 18 | 0 | 2.234255 | 0.526 | 0.018 | 0 | SPINK1 | IC-A |
| 18 | 0 | 1.233942 | 0.779 | 0.025 | 0 | ATP6V1G3 | IC-A |
| 18 | 0 | 1.035705 | 0.705 | 0.035 | 0 | ATP6V0D2 | IC-A |
| 18 | 0 | 1.029515 | 0.591 | 0.022 | 0 | SLC26A7 | IC-A |
| 18 | 0 | 0.860687 | 0.609 | 0.071 | 0 | TMEM101 | IC-A |
| 18 | 0 | 0.826161 | 0.612 | 0.021 | 0 | FAM24B | IC-A |
| 18 | 0 | 0.816032 | 0.558 | 0.059 | 0 | RHCG | IC-A |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 18 | 0 | 0.690007 | 0.561 | 0.045 | 0 | SMIM6 | IC-A |
| 18 | 0 | 0.668038 | 0.546 | 0.019 | 0 | CTB-27N1.1 | IC-A |
| 18 | 0 | 0.634269 | 0.552 | 0.011 | 0 | DMRT2 | IC-A |
| 19 | 0 | 2.064619 | 0.636 | 0.036 | 0 | SPINK1 | tPC-IC |
| 19 | 0 | 0.942055 | 0.933 | 0.058 | 0 | ATP6V0D2 | tPC-IC |
| 19 | 0 | 0.866002 | 0.8 | 0.053 | 0 | ATP6V1G3 | tPC-IC |
| 19 | 0 | 0.624519 | 0.618 | 0.031 | 0 | DMRT2 | tPC-IC |
| 19 | 5.74E-300 | 0.625947 | 0.624 | 0.038 | 1.13E-295 | CTB-27N1.1 | tPC-IC |
| 19 | 9.47E-295 | 0.779181 | 0.648 | 0.042 | 1.86E-290 | SLC26A7 | tPC-IC |
| 19 | 7.44E-242 | 0.635934 | 0.594 | 0.043 | 1.46E-237 | FAM24B | tPC-IC |
| 19 | 2.69E-159 | 0.839951 | 0.6 | 0.067 | 5.29E-155 | SLC8A1 | tPC-IC |
| 19 | 8.07E-145 | 1.371862 | 0.358 | 0.026 | 1.59E-140 | KLK1 | tPC-IC |
| 19 | 1.76E-117 | 0.747477 | 0.479 | 0.055 | 3.47E-113 | STC1 | tPC-IC |
| 20 | 0 | 2.467933 | 0.915 | 0.07 | 0 | SLC12A1 | TAL |
| 20 | 0 | 0.965734 | 0.604 | 0.041 | 0 | SFRP1 | TAL |
| 20 | 0 | 0.910617 | 0.572 | 0.026 | 0 | CLDN16 | TAL |
| 20 | 0 | 0.847658 | 0.614 | 0.033 | 0 | EGF | TAL |
| 20 | 0 | 0.797148 | 0.653 | 0.049 | 0 | PPP1R1A | TAL |
| 20 | 0 | 0.787889 | 0.678 | 0.047 | 0 | DUSP9 | TAL |
| 20 | 0 | 0.76692 | 0.574 | 0.037 | 0 | CXCL12 | TAL |
| 20 | 0 | 0.749554 | 0.582 | 0.055 | 0 | CTD-2228K2.5 | TAL |
| 20 | 0 | 0.651156 | 0.549 | 0.034 | 0 | MFSD4 | TAL |
| 20 | 0 | 0.638446 | 0.492 | 0.025 | 0 | PLAU | TAL |
| 21 | 0 | 1.661358 | 0.391 | 0.021 | 0 | SLC12A3 | DCT |
| 21 | 0 | 0.679766 | 0.388 | 0.055 | 0 | EGF | DCT |
| 21 | 0 | 0.597484 | 0.437 | 0.065 | 0 | SERPINA5 | DCT |
| 21 | 0 | 0.476188 | 0.456 | 0.07 | 0 | DUSP9 | DCT |
| 21 | 0 | 0.362091 | 0.331 | 0.039 | 0 | WNK4 | DCT |
| 21 | 3.09E-236 | 0.432668 | 0.353 | 0.062 | 6.07E-232 | PVALB | DCT |
| 21 | 2.77E-202 | 0.469549 | 0.333 | 0.064 | 5.45E-198 | SFRP1 | DCT |
| 21 | 9.88E-132 | 0.276822 | 0.304 | 0.072 | 1.94E-127 | RHCG | DCT |
| 22 | 0 | 1.808344 | 0.477 | 0.019 | 0 | KLK1 | CNT |
| 22 | 0 | 1.382295 | 0.683 | 0.058 | 0 | SLC8A1 | CNT |
| 22 | 0 | 1.050468 | 0.672 | 0.069 | 0 | RHCG | CNT |
| 22 | 0 | 0.866452 | 0.643 | 0.062 | 0 | PVALB | CNT |
| 22 | 0 | 0.642043 | 0.572 | 0.07 | 0 | SERPINA5 | CNT |
| 22 | 0 | 0.515762 | 0.435 | 0.04 | 0 | TMEM178A | CNT |
| 22 | 0 | 0.404043 | 0.401 | 0.032 | 0 | TEX41 | CNT |
| 22 | 1.24E-240 | 0.556163 | 0.419 | 0.052 | 2.45E-236 | ADM | CNT |
| 22 | 7.69E-181 | 0.336818 | 0.395 | 0.059 | 1.51E-176 | TMPRSS2 | CNT |
| 22 | 1.04E-147 | 0.408102 | 0.375 | 0.062 | 2.04E-143 | HMGCS2 | CNT |
| 23 | 0 | 1.12496 | 0.716 | 0.001 | 0 | CD79A | B Cell |
| 23 | 0 | 0.944338 | 0.624 | 0.008 | 0 | MS4A1 | B Cell |
| 23 | 0 | 0.858183 | 0.383 | 0.002 | 0 | IGJ | B Cell |
| 23 | 0 | 0.848479 | 0.617 | 0.029 | 0 | CD79B | B Cell |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 23 | 0 | 0.464813 | 0.383 | 0.002 | 0 | VPREB3 | B Cell |
| 23 | 7.45E-255 | 0.514841 | 0.404 | 0.016 | 1.47E-250 | IRF8 | B Cell |
| 23 | 7.72E-195 | 0.470739 | 0.433 | 0.024 | 1.52E-190 | SELL | B Cell |
| 23 | 5.92E-70 | 0.525526 | 0.34 | 0.041 | 1.16E-65 | GPR183 | B Cell |
| 23 | 3.54E-66 | 0.525897 | 0.433 | 0.068 | 6.97E-62 | BIRC3 | B Cell |
| 23 | 1.19E-45 | 0.535918 | 0.376 | 0.069 | 2.35E-41 | PLAC8 | B Cell |
| 24 | 0 | 1.882918 | 0.951 | 0.07 | 0 | CCL5 | T-CYT |
| 24 | 0 | 1.424871 | 0.725 | 0.054 | 0 | CCL4 | T-CYT |
| 24 | 0 | 1.270667 | 0.724 | 0.046 | 0 | NKG7 | T-CYT |
| 24 | 0 | 0.912152 | 0.616 | 0.05 | 0 | GZMA | T-CYT |
| 24 | 0 | 0.825666 | 0.496 | 0.026 | 0 | GZMH | T-CYT |
| 24 | 0 | 0.755142 | 0.636 | 0.046 | 0 | CST7 | T-CYT |
| 24 | 0 | 0.690511 | 0.362 | 0.017 | 0 | GZMK | T-CYT |
| 24 | 0 | 0.644586 | 0.528 | 0.059 | 0 | CD7 | T-CYT |
| 24 | 0 | 0.634444 | 0.571 | 0.051 | 0 | CTSW | T-CYT |
| 24 | 5.37E-271 | 0.75291 | 0.372 | 0.069 | 1.06E-266 | RGS1 | T-CYT |
| 25 | 0 | 1.159515 | 0.784 | 0.069 | 0 | IL7R | T-Cell (avtivated) |
| 25 | 0 | 0.573 | 0.553 | 0.067 | 0 | CD3E | T-Cell (avtivated) |
| 25 | 0 | 0.406658 | 0.424 | 0.049 | 0 | CD3G | T-Cell (avtivated) |
| 25 | 0 | 0.311451 | 0.301 | 0.026 | 0 | CD40LG | T-Cell (avtivated) |
| 25 | 5.12E-241 | 0.269102 | 0.311 | 0.054 | 1.01E-236 | LCK | T-Cell (avtivated) |
| 25 | 7.89E-232 | 0.288619 | 0.342 | 0.067 | 1.55E-227 | IL2RG | T-Cell (avtivated) |
| 25 | 3.89E-224 | 0.273748 | 0.328 | 0.064 | 7.66E-220 | TRAF3IP3 | T-Cell (avtivated) |
| 26 | 0 | 1.515165 | 0.906 | 0.07 | 0 | IL7R | T-CYT-MEM |
| 26 | 0 | 0.854535 | 0.757 | 0.074 | 0 | CD2 | T-CYT-MEM |
| 26 | 0 | 0.775606 | 0.72 | 0.065 | 0 | CD3E | T-CYT-MEM |
| 26 | 0 | 0.550296 | 0.487 | 0.021 | 0 | CD40LG | T-CYT-MEM |
| 26 | 0 | 0.478005 | 0.44 | 0.032 | 0 | GPR171 | T-CYT-MEM |
| 26 | 0 | 0.461133 | 0.481 | 0.05 | 0 | CD3G | T-CYT-MEM |
| 26 | 0 | 0.458286 | 0.428 | 0.036 | 0 | AC092580.4 | T-CYT-MEM |
| 26 | 0 | 0.419791 | 0.467 | 0.064 | 0 | IL2RG | T-CYT-MEM |
| 26 | 0 | 0.414034 | 0.314 | 0.011 | 0 | IL2 | T-CYT-MEM |
| 26 | 1.62E-278 | 0.929609 | 0.404 | 0.07 | 3.18E-274 | RGS1 | T-CYT-MEM |
| 27 | 0 | 2.793548 | 0.947 | 0.063 | 0 | FXYD4 | PC |
| 27 | 0 | 2.589433 | 0.981 | 0.056 | 0 | AQP2 | PC |
| 27 | 0 | 1.322907 | 0.59 | 0.029 | 0 | STC1 | PC |
| 27 | 0 | 0.83747 | 0.648 | 0.019 | 0 | PTGER1 | PC |
| 27 | 0 | 0.827871 | 0.512 | 0.072 | 0 | GDF15 | PC |
| 27 | 0 | 0.701664 | 0.582 | 0.054 | 0 | ST6GAL1 | PC |
| 27 | 0 | 0.683307 | 0.604 | 0.033 | 0 | SMIM22 | PC |
| 27 | 0 | 0.678255 | 0.62 | 0.055 | 0 | GATA3 | PC |
| 27 | 0 | 0.669793 | 0.574 | 0.027 | 0 | SCNN1G | PC |
| 27 | 3.85E-274 | 0.628274 | 0.383 | 0.074 | 7.58E-270 | CALB1 | PC |
| 28 | 0 | 1.224242 | 0.546 | 0.049 | 0 | STC1 | PC-CNT |
| 28 | 9.07E-302 | 0.608475 | 0.524 | 0.06 | 1.78E-297 | HMGCS2 | PC-CNT |
| 28 | 2.48E-293 | 0.76304 | 0.524 | 0.062 | 4.88E-289 | SLC8A1 | PC-CNT |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 28 | 8.75E-292 | 0.412322 | 0.408 | 0.037 | 1.72E-287 | SCNN1B | PC-CNT |
| 28 | 1.40E-280 | 0.509324 | 0.454 | 0.048 | 2.76E-276 | SCNN1G | PC-CNT |
| 28 | 3.73E-230 | 0.370258 | 0.386 | 0.042 | 7.33E-226 | GATA3-AS1 | PC-CNT |
| 28 | 6.15E-195 | 0.642528 | 0.476 | 0.074 | 1.21E-190 | RHCG | PC-CNT |
| 28 | 3.94E-172 | 0.376557 | 0.336 | 0.042 | 7.75E-168 | TMEM178A | PC-CNT |
| 28 | 5.24E-167 | 0.363155 | 0.35 | 0.046 | 1.03E-162 | PTGER1 | PC-CNT |
| 28 | 3.57E-126 | 0.404976 | 0.336 | 0.054 | 7.02E-122 | MMP7 | PC-CNT |
| 29 | 0 | 1.470562 | 0.457 | 0.018 | 0 | SLPI | ATL |
| 29 | 0 | 1.141604 | 0.445 | 0.047 | 0 | MMP7 | ATL |
| 29 | 0 | 0.791092 | 0.581 | 0.063 | 0 | KRT7 | ATL |
| 29 | 0 | 0.668657 | 0.479 | 0.056 | 0 | CLDN3 | ATL |
| 29 | 0 | 0.654858 | 0.355 | 0.015 | 0 | PAPPA2 | ATL |
| 29 | 0 | 0.562395 | 0.383 | 0.043 | 0 | TSPAN8 | ATL |
| 29 | 0 | 0.41953 | 0.346 | 0.029 | 0 | S100A14 | ATL |
| 29 | 0 | 0.41565 | 0.358 | 0.032 | 0 | FIBIN | ATL |
| 29 | 2.05E-163 | 0.284467 | 0.309 | 0.051 | 4.03E-159 | CLDN16 | ATL |
| 30 | 0 | 2.136927 | 0.88 | 0.05 | 0 | CTGF | PEC |
| 30 | 0 | 0.792957 | 0.513 | 0.011 | 0 | CFH | PEC |
| 30 | 0 | 0.738715 | 0.38 | 0.009 | 0 | TNNT2 | PEC |
| 30 | 5.56E-256 | 1.066495 | 0.576 | 0.038 | 1.09E-251 | VCAM1 | PEC |
| 30 | 7.33E-201 | 0.811748 | 0.551 | 0.043 | 1.44E-196 | BGN | PEC |
| 30 | 2.35E-189 | 0.614881 | 0.449 | 0.031 | 4.63E-185 | CYP1B1 | PEC |
| 30 | 1.74E-148 | 1.264058 | 0.424 | 0.034 | 3.41E-144 | PTGDS | PEC |
| 30 | 3.52E-118 | 0.594948 | 0.513 | 0.063 | 6.92E-114 | SPOCK2 | PEC |
| 30 | 5.17E-97 | 0.614381 | 0.316 | 0.028 | 1.02E-92 | SLPI | PEC |
| 30 | 2.41E-44 | 0.952658 | 0.316 | 0.057 | 4.75E-40 | MMP7 | PEC |
| 31 | 0 | 0.739546 | 0.476 | 0.027 | 0 | VCAM1 | DTL |
| 31 | 0 | 0.581357 | 0.459 | 0.055 | 0 | CLDN3 | DTL |
| 31 | 0 | 0.544286 | 0.474 | 0.029 | 0 | C1orf186 | DTL |
| 31 | 0 | 0.421265 | 0.388 | 0.048 | 0 | ITGB8 | DTL |
| 31 | 0 | 0.372258 | 0.361 | 0.025 | 0 | PRUNE2 | DTL |
| 31 | 0 | 0.363572 | 0.314 | 0.029 | 0 | PROM1 | DTL |
| 31 | 1.99E-293 | 0.439033 | 0.319 | 0.036 | 3.91E-289 | MDK | DTL |
| 31 | 1.35E-269 | 0.786177 | 0.355 | 0.049 | 2.66E-265 | MMP7 | DTL |
| 31 | 2.98E-243 | 0.384887 | 0.404 | 0.067 | 5.85E-239 | KRT7 | DTL |
| 31 | 6.14E-202 | 0.35313 | 0.349 | 0.062 | 1.21E-197 | RASSF4 | DTL |

**Supplementary Table 2:** Sample-to-Cluster distribution

Distribution of the 22,268 cells from all 24 samples in the 31 clusters identified. Each column is a cluster and each row is a sample.

| SAMPLE | CLUSTER NUMBER | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 |
| Pre-perfusion | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| PREMIERE-SamplePRE027-1 | 3 | 2 | 3 | 18 | 4 | 16 | 79 | 65 | 30 | 40 | 53 | 33 | 75 | 64 | 83 | 22 | 6 | 27 | 0 | 37 | 85 | 21 | 1 | 2 | 9 | 2 | 46 | 22 | 6 | 6 | 42 |
| PREMIERE-SamplePRE038-1 | 3 | 2 | 4 | 10 | 14 | 22 | 99 | 92 | 81 | 52 | 120 | 58 | 173 | 126 | 170 | 40 | 3 | 18 | 0 | 57 | 37 | 11 | 2 | 17 | 14 | 8 | 16 | 16 | 9 | 2 | 19 |
| PREMIERE-SampleTransPRE19025 | 2 | 3 | 6 | 4 | 2 | 13 | 67 | 32 | 56 | 31 | 38 | 27 | 56 | 41 | 48 | 15 | 2 | 19 | 2 | 9 | 36 | 15 | 16 | 10 | 9 | 11 | 31 | 13 | 8 | 1 | 14 |
| Surveillance | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| PREMIERE-Trans-SV-004 | 0 | 0 | 12 | 14 | 7 | 4 | 15 | 10 | 5 | 3 | 2 | 10 | 6 | 13 | 3 | 4 | 12 | 20 | 4 | 33 | 44 | 5 | 26 | 33 | 45 | 26 | 20 | 7 | 8 | 0 | 10 |
| PREMIERE-Trans-SV-005 | 0 | 1 | 9 | 8 | 8 | 16 | 64 | 17 | 21 | 9 | 5 | 4 | 6 | 11 | 5 | 5 | 6 | 41 | 9 | 66 | 16 | 13 | 4 | 50 | 23 | 16 | 37 | 15 | 20 | 9 | 29 |
| PREMIERE-Trans-SV-006 | 11 | 0 | 11 | 11 | 18 | 9 | 42 | 45 | 18 | 3 | 0 | 4 | 9 | 6 | 4 | 4 | 13 | 35 | 10 | 43 | 56 | 27 | 22 | 40 | 44 | 22 | 31 | 26 | 15 | 8 | 47 |
| PREMIERE-Trans-SV-004 | 0 | 0 | 9 | 8 | 4 | 3 | 5 | 6 | 8 | 3 | 1 | 5 | 9 | 7 | 4 | 2 | 4 | 91 | 34 | 31 | 81 | 38 | 0 | 10 | 0 | 2 | 68 | 24 | 21 | 7 | 27 |
| PREMIERE-Trans-SV-008 | 5 | 3 | 53 | 28 | 6 | 78 | 73 | 65 | 124 | 58 | 118 | 93 | 75 | 51 | 91 | 33 | 6 | 79 | 2 | 591 | 169 | 102 | 3 | 38 | 21 | 14 | 226 | 48 | 146 | 37 | 164 |
| Tumornephrectomy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| PREMIERE-17-1606-2-0 | 0 | 7 | 19 | 18 | 11 | 6 | 5 | 6 | 8 | 21 | 40 | 31 | 5 | 7 | 17 | 4 | 8 | 53 | 4 | 1 | 10 | 7 | 1 | 23 | 14 | 7 | 27 | 10 | 12 | 2 | 16 |
| PREMIERE-17-1606-2-1 | 0 | 2 | 15 | 17 | 4 | 16 | 3 | 4 | 18 | 15 | 29 | 7 | 9 | 1 | 5 | 0 | 23 | 111 | 43 | 83 | 32 | 23 | 1 | 10 | 3 | 1 | 132 | 32 | 32 | 6 | 35 |
| PREMIERE-18-139 | 5 | 30 | 54 | 45 | 5 | 84 | 57 | 100 | 154 | 34 | 9 | 4 | 3 | 13 | 30 | 30 | 35 | 118 | 35 | 133 | 139 | 107 | 1 | 22 | 23 | 10 | 322 | 116 | 228 | 33 | 167 |
| PREMIERE-18-162 | 22 | 37 | 5 | 17 | 10 | 0 | 4 | 3 | 3 | 3 | 1 | 0 | 0 | 0 | 0 | 1 | 1 | 10 | 1 | 0 | 1 | 1 | 2 | 20 | 36 | 19 | 1 | 1 | 0 | 2 | 2 |
| PREMIERE-18-342 | 0 | 6 | 29 | 25 | 15 | 2 | 2 | 2 | 2 | 1 | 0 | 0 | 0 | 3 | 1 | 0 | 3 | 10 | 1 | 4 | 5 | 2 | 2 | 22 | 20 | 9 | 13 | 8 | 9 | 2 | 6 |
| PREMIERE-18142-5-1 | 0 | 3 | 33 | 16 | 45 | 2 | 9 | 14 | 1 | 17 | 47 | 27 | 2 | 23 | 43 | 6 | 4 | 5 | 3 | 3 | 6 | 10 | 3 | 18 | 20 | 17 | 38 | 5 | 11 | 1 | 6 |
| PREMIERE-18142-5-2 | 0 | 0 | 50 | 20 | 8 | 20 | 14 | 11 | 39 | 3 | 34 | 13 | 10 | 3 | 13 | 3 | 7 | 27 | 3 | 55 | 16 | 13 | 1 | 3 | 3 | 0 | 76 | 7 | 28 | 4 | 36 |
| PREMIERE-2017-06-28-TN-1 | 0 | 8 | 88 | 18 | 71 | 4 | 11 | 32 | 7 | 141 | 135 | 151 | 63 | 93 | 144 | 69 | 3 | 68 | 0 | 12 | 10 | 3 | 8 | 73 | 44 | 44 | 8 | 1 | 8 | 1 | 31 |
| PREMIERE-2017-06-28-TN-2 | 0 | 5 | 56 | 9 | 30 | 11 | 4 | 14 | 10 | 75 | 104 | 91 | 79 | 56 | 117 | 31 | 5 | 33 | 2 | 14 | 10 | 4 | 9 | 26 | 10 | 13 | 22 | 10 | 9 | 11 | 20 |
| PREMIERE-Hkid-PH-2017-08-25 | 1 | 17 | 98 | 57 | 43 | 49 | 57 | 144 | 28 | 119 | 152 | 147 | 94 | 101 | 184 | 73 | 10 | 51 | 5 | 33 | 37 | 16 | 7 | 128 | 207 | 193 | 23 | 20 | 37 | 5 | 15 |
| PREMIERE-Hkid-YY-2017-08-25 | 5 | 27 | 112 | 67 | 45 | 38 | 88 | 80 | 29 | 99 | 117 | 112 | 64 | 87 | 130 | 67 | 1 | 42 | 1 | 37 | 23 | 15 | 8 | 119 | 207 | 213 | 14 | 12 | 29 | 4 | 12 |
| PREMIERE-TN109-18-242-Lib | 0 | 7 | 162 | 42 | 104 | 31 | 86 | 49 | 8 | 18 | 17 | 6 | 0 | 6 | 2 | 8 | 8 | 51 | 6 | 8 | 16 | 6 | 9 | 285 | 211 | 142 | 10 | 4 | 10 | 9 | 21 |
| PREMIERE-TN116-17-116-Lib-4a | 1 | 7 | 30 | 9 | 49 | 11 | 69 | 38 | 5 | 55 | 76 | 58 | 29 | 76 | 126 | 52 | 6 | 20 | 0 | 16 | 13 | 2 | 10 | 53 | 60 | 53 | 1 | 9 | 3 | 3 | 6 |
| PREMIERE-TN117-17-116-Lib-4b | 0 | 2 | 27 | 11 | 45 | 11 | 91 | 41 | 0 | 60 | 78 | 74 | 28 | 72 | 136 | 33 | 8 | 19 | 0 | 23 | 12 | 3 | 5 | 62 | 64 | 63 | 0 | 3 | 2 | 2 | 9 |
| PREMIERE-TN120-18-696-4 | 0 | 1 | 7 | 1 | 14 | 5 | 15 | 23 | 0 | 20 | 22 | 17 | 11 | 19 | 41 | 14 | 0 | 18 | 0 | 30 | 27 | 4 | 0 | 22 | 6 | 10 | 1 | 2 | 3 | 1 | 8 |
| PREMIERE-TN121-18-696-10 | 0 | 0 | 4 | 0 | 3 | 10 | 29 | 7 | 0 | 11 | 14 | 15 | 7 | 12 | 15 | 9 | 0 | 11 | 0 | 24 | 20 | 3 | 0 | 5 | 2 | 3 | 1 | 3 | 2 | 2 | 1 |

**Supplementary Table 3:** Top 100 up and down regulated genes from the genome-wide differential gene expression analysis between FSGS subgroups 1 and 2

EdgeR package is used to find the differentially expressed genes between groups of samples. This R package uses an over-dispersed Poisson model to account for both biological and technical variability. Genes with adjusted p value < 0.05 were considered as significant. logFC= log of fold change, logCPM = Log of Counts per million, LR= Likelihood ratio

| Top 100 upregulated genes | | | | | | Top 100 downregulated genes | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Gene | logFC | logCPM | LR | PValue | FDR | Gene | logFC | logCPM | LR | PValue | FDR |
| MECOM | 1.012132 | 5.636854 | 50.3395 | 1.29E-12 | 4.25E-10 | PTGER4 | -2.168852 | 8.234127 | 125.41668 | 4.12553E-29 | 1.53103E-24 |
| PPM1F | 0.996887 | 5.876261 | 50.28762 | 1.33E-12 | 4.32E-10 | RETREG1 | -1.207234 | 8.503294 | 106.64437 | 5.3267E-25 | 9.88396E-21 |
| NYNRIN | 1.275113 | 3.039148 | 49.5877 | 1.90E-12 | 5.87E-10 | PARD6G | -1.457899 | 6.051864 | 103.61608 | 2.45576E-24 | 2.77603E-20 |
| NRP1 | 1.112623 | 7.44094 | 49.29729 | 2.20E-12 | 6.53052E-10 | TAPT1 | -1.39544 | 5.061146 | 97.652925 | 4.98535E-23 | 3.70022E-19 |
| A2M | 1.314066 | 9.927341 | 48.40303 | 3.47E-12 | 9.63E-10 | MAL2 | -1.249693 | 9.352526 | 92.802138 | 5.77927E-22 | 3.57457E-18 |
| NID2 | 1.328745 | 4.359737 | 44.85136 | 2.13E-11 | 4.78E-09 | ZFAND5 | -1.264311 | 7.977941 | 91.110317 | 1.35881E-21 | 7.20385E-18 |
| ECE1 | 0.95625 | 5.94768 | 44.3839 | 2.70E-11 | 5.96441E-09 | PDLIM2 | -1.063209 | 9.83373 | 88.708166 | 4.57572E-21 | 2.12262E-17 |
| ADGRE5 | 0.957994 | 5.76554 | 43.76651 | 3.70E-11 | 7.7137E-09 | ATOH8 | -1.81333 | 5.155697 | 8.81E+01 | 6.28E-21 | 2.58763E-17 |
| ARHGEF15 | 1.148485 | 5.472876 | 42.75796 | 6.19E-11 | 1.24E-08 | DNAH9 | -1.522902 | 4.297797 | 8.74E+01 | 9.03643E-21 | 3.35351E-17 |
| PCDH12 | 1.250129 | 6.051646 | 41.92129 | 9.50E-11 | 1.75E-08 | PNMA1 | -1.558312 | 7.150071 | 8.64E+01 | 1.46723E-20 | 4.53754E-17 |
| FAR2 | 0.987564 | 3.840548 | 41.09592 | 1.45E-10 | 2.57E-08 | PCOLCE2 | -1.224543 | 10.21874 | 83.538894 | 6.24746E-20 | 1.78346E-16 |
| TGM2 | 0.973619 | 8.255154 | 39.5208 | 3.25E-10 | 5.21E-08 | RCN2 | -1.662222 | 7.307788 | 82.383255 | 1.12099E-19 | 2.77342E-16 |
| GJA5 | 1.098426 | 8.55971 | 38.49679 | 5.48E-10 | 8.2401E-08 | BCAR3 | -1.080329 | 6.403291 | 8.18E+01 | 1.49839E-19 | 3.47542E-16 |
| TRPV2 | 1.084785 | 4.702575 | 37.99785 | 7.08E-10 | 1.01E-07 | REPS1 | -1.302191 | 5.30596 | 80.706837 | 2.61815E-19 | 5.71542E-16 |
| TK1 | 1.11235 | 3.817831 | 36.47574 | 1.55E-09 | 1.93079E-07 | ANKH | -1.2908 | 5.863324 | 79.570311 | 4.65366E-19 | 9.08958E-16 |
| AMOTL1 | 0.887409 | 4.839185 | 36.41556 | 1.59E-09 | 1.97215E-07 | PLEKHA3 | -1.06338 | 5.300574 | 78.689364 | 7.26859E-19 | 1.34872E-15 |
| GVINP1 | 1.195087 | 2.873469 | 36.23118 | 1.75244E-09 | 2.12533E-07 | PTH1R | -1.271722 | 8.770164 | 78.337379 | 8.68625E-19 | 1.53503E-15 |
| GBP4 | 1.04757 | 6.647466 | 35.58111 | 2.45E-09 | 2.7765E-07 | FYN | -1.443971 | 7.199614 | 77.086966 | 1.63593E-18 | 2.7596E-15 |
| KDR | 1.247667 | 8.13068 | 35.4789 | 2.58E-09 | 2.91716E-07 | TYRO3 | -1.075012 | 9.100568 | 76.971147 | 1.73474E-18 | 2.79904E-15 |
| MEF2C | 0.866582 | 5.554364 | 35.36022 | 2.74027E-09 | 3.08164E-07 | APLN | -1.596583 | 6.937342 | 76.592648 | 2.1012E-18 | 3.15293E-15 |
| FN1 | 2.214405 | 6.5462 | 35.30639 | 2.81707E-09 | 3.15843E-07 | SOWAHC | -1.511454 | 5.138382 | 76.493896 | 2.20895E-18 | 3.15293E-15 |
| TCF19 | 0.973252 | 3.300085 | 35.20146 | 2.97301E-09 | 3.31325E-07 | CAPN2 | -1.048831 | 10.01311 | 76.564581 | 2.13128E-18 | 3.15293E-15 |
| SLFN5 | 0.915244 | 5.414675 | 34.90619 | 3.45979E-09 | 3.75427E-07 | FAM89A | -2.129978 | 8.305263 | 7.48E+01 | 5.09141E-18 | 6.99805E-15 |
| PTGS1 | 1.403068 | 4.262612 | 34.83609 | 3.58663E-09 | 3.88057E-07 | P3H2 | -1.349092 | 8.473281 | 73.89733 | 8.22875E-18 | 1.05302E-14 |
| IGLV4.69 | 6.187659 | 0.219758 | 34.28809 | 4.75281E-09 | 4.91313E-07 | AMIGO2 | -1.267895 | 7.855391 | 71.838061 | 2.33603E-17 | 2.79653E-14 |
| TMEM26 | 1.125947 | 3.598324 | 34.17322 | 5.0418E-09 | 5.183E-07 | CITED2 | -1.529856 | 4.144332 | 71.156158 | 3.30041E-17 | 3.71952E-14 |
| GIMAP6 | 0.91154 | 7.272314 | 33.88021 | 5.86E-09 | 5.92684E-07 | SAV1 | -1.112367 | 6.129081 | 7.12E+01 | 3.30749E-17 | 3.71952E-14 |
| COL5A2 | 1.305923 | 3.204188 | 33.68486 | 6.48E-09 | 6.44748E-07 | NRBP2 | -1.07618 | 4.506276 | 70.565831 | 4.45161E-17 | 4.85893E-14 |
| ROBO4 | 1.067052 | 6.832811 | 33.66799 | 6.53676E-09 | 6.48625E-07 | NDN | -1.588115 | 7.175683 | 70.021289 | 5.86678E-17 | 6.22064E-14 |
| NDC80 | 1.172574 | 2.364584 | 33.00718 | 9.18E-09 | 8.6705E-07 | DUSP1 | -3.270599 | 8.60864 | 69.269258 | 8.58981E-17 | 8.8549E-14 |
| RARG | 1.03903 | 5.37074 | 32.8429 | 9.99153E-09 | 9.29312E-07 | SLC16A10 | -1.048176 | 4.809562 | 68.422753 | 1.31946E-16 | 1.28859E-13 |
| ITGA5 | 1.057065 | 5.742995 | 32.2034 | 1.39E-08 | 1.24463E-06 | SPSB1 | -2.090048 | 5.670909 | 68.27641 | 1.42111E-16 | 1.35228E-13 |
| RASGEF1B | 0.882743 | 3.926815 | 32.20552 | 1.39E-08 | 1.24463E-06 | MAFB | -1.288061 | 8.306602 | 66.496414 | 3.50531E-16 | 3.17282E-13 |
| KCNN3 | 1.001212 | 2.566187 | 31.93629 | 1.59313E-08 | 1.40433E-06 | P4HTM | -1.433058 | 7.004296 | 65.722422 | 5.19119E-16 | 4.58691E-13 |
| APLNR | 1.282785 | 8.003476 | 31.7347 | 1.77E-08 | 1.53244E-06 | MAEL | -1.721645 | 2.963356 | 65.463695 | 5.91945E-16 | 5.10876E-13 |
| BCL6B | 1.01486 | 5.636133 | 31.64819 | 1.84787E-08 | 1.5911E-06 | ARRDC4 | -1.577048 | 9.014032 | 64.485013 | 9.72694E-16 | 8.20401E-13 |
| NPY1R | 0.896243 | 5.060316 | 31.45276 | 2.04352E-08 | 1.7299E-06 | MFSD6 | -1.262428 | 7.612963 | 63.531307 | 1.57838E-15 | 1.27338E-12 |
| IL3RA | 0.969585 | 3.506634 | 31.32766 | 2.18E-08 | 1.82996E-06 | CERS6 | -1.147862 | 6.185765 | 6.27E+01 | 2.46E-15 | 1.86603E-12 |
| GEM | 1.155779 | 4.801429 | 30.45641 | 3.41454E-08 | 2.62898E-06 | FBXO33 | -1.148508 | 4.649517 | 62.383442 | 2.8269E-15 | 2.09818E-12 |
| UPK3B | 5.620315 | -0.273548 | 30.21775 | 3.86E-08 | 2.88927E-06 | MDFIC | -1.120485 | 6.023261 | 61.639771 | 4.12404E-15 | 3.00093E-12 |
| LPAR6 | 0.880423 | 6.212992 | 29.90728 | 4.53E-08 | 3.29139E-06 | PAM | -1.19637 | 9.264697 | 61.533439 | 4.35288E-15 | 3.10653E-12 |
| PIK3R3 | 0.877812 | 5.553806 | 29.87262 | 4.61E-08 | 3.33769E-06 | AKIRIN1 | -1.284854 | 6.745308 | 61.278497 | 4.95462E-15 | 3.46926E-12 |
| IGLV6.57 | 4.716196 | 0.558847 | 29.69035 | 5.07E-08 | 3.59661E-06 | RBPMS | -1.085231 | 7.556313 | 61.104195 | 5.41327E-15 | 3.72022E-12 |
| TEK | 1.04375 | 7.74917 | 29.62434 | 5.24423E-08 | 3.69998E-06 | VEGFA | -1.162815 | 9.857809 | 61.036612 | 5.60232E-15 | 3.78014E-12 |
| COL4A2 | 1.062463 | 7.937228 | 29.58198 | 5.36E-08 | 3.77455E-06 | FAM43A | -1.689751 | 5.337238 | 60.835186 | 6.20588E-15 | 4.11261E-12 |
| DYSF | 0.962301 | 5.874507 | 29.42544 | 5.81E-08 | 4.03841E-06 | EPM2A | -1.181538 | 3.655798 | 59.477739 | 1.23685E-14 | 7.6214E-12 |
| PEAR1 | 0.995246 | 4.227851 | 29.28002 | 6.26E-08 | 4.30476E-06 | KCTD3 | -1.122246 | 5.787111 | 5.95E+01 | 1.25274E-14 | 7.6214E-12 |
| IL2RB | 1.47948 | 2.005436 | 28.78706 | 8.0789E-08 | 5.34431E-06 | FAM174B | -1.479098 | 4.306725 | 5.87E+01 | 1.82108E-14 | 1.09003E-11 |
| DLGAP5 | 3.111461 | 0.08621 | 28.3456 | 1.01477E-07 | 6.51545E-06 | CTGF | -2.008236 | 11.1957 | 58.431247 | 2.10521E-14 | 1.22072E-11 |
| LRRC32 | 0.96366 | 7.044698 | 28.18518 | 1.10245E-07 | 6.98177E-06 | SPIRE1 | -1.163268 | 4.227624 | 57.931788 | 2.71366E-14 | 1.54933E-11 |
| PCDH18 | 1.379074 | 3.354301 | 27.94247 | 1.24976E-07 | 7.78187E-06 | KHDRBS1 | -1.079269 | 6.484431 | 5.78E+01 | 2.95051E-14 | 1.65851E-11 |
| TCIM | 0.943149 | 7.493683 | 27.91955 | 1.26465E-07 | 7.84825E-06 | PLBD1 | -1.073379 | 7.741588 | 57.491861 | 3.39381E-14 | 1.82533E-11 |
| POSTN | 1.359615 | 7.695709 | 27.84955 | 1.31124E-07 | 8.10518E-06 | EIF2AK3 | -1.112222 | 3.962125 | 56.99548 | 4.36815E-14 | 2.25148E-11 |
| SLC43A3 | 0.945033 | 3.580536 | 27.7858 | 1.36E-07 | 8.29898E-06 | CERK | -1.053654 | 5.590139 | 56.397423 | 5.92079E-14 | 3.00995E-11 |
| GAS2 | 0.909191 | 5.12239 | 27.77527 | 1.36E-07 | 8.31683E-06 | GAS1 | -1.589312 | 6.9365 | 55.657908 | 8.62453E-14 | 4.1034E-11 |
| CDH13 | 1.014593 | 6.102161 | 27.6238 | 1.47355E-07 | 8.86301E-06 | TMEM178A | -1.75232 | 6.97428 | 55.47668 | 9.45743E-14 | 4.44272E-11 |
| KCTD15 | 0.927058 | 2.817767 | 27.6299 | 1.4689E-07 | 8.86301E-06 | TTC19 | -1.269231 | 6.290821 | 5.54E+01 | 9.74718E-14 | 4.52159E-11 |
| GAB1 | 0.952829 | 3.836803 | 27.38912 | 1.66E-07 | 9.79993E-06 | APLP1 | -1.383718 | 6.839379 | 55.3697 | 9.9864E-14 | 4.57537E-11 |
| ENG | 0.946342 | 9.400271 | 27.26473 | 1.77E-07 | 1.03949E-05 | GOLPH3 | -1.351221 | 7.042519 | 5.51E+01 | 1.15E-13 | 5.22059E-11 |
| P2RX7 | 0.935977 | 2.908313 | 27.07474 | 1.95739E-07 | 1.13148E-05 | RRAS2 | -1.240744 | 5.569233 | 5.49E+01 | 1.25918E-13 | 5.63006E-11 |
| ITGA8 | 0.871506 | 6.478922 | 26.93535 | 2.10376E-07 | 1.19927E-05 | TMEM248 | -1.048409 | 6.852539 | 54.797189 | 1.33632E-13 | 5.90382E-11 |
| ADGRF5 | 0.980237 | 8.377698 | 26.90812 | 2.13E-07 | 1.21256E-05 | LRP11 | -1.175704 | 6.307298 | 54.697546 | 1.40582E-13 | 6.1378E-11 |
| ELMO1 | 0.872185 | 4.931671 | 26.6004 | 2.50E-07 | 1.38787E-05 | ADCK2 | -1.388273 | 4.793698 | 54.422816 | 1.61675E-13 | 6.89645E-11 |
| GIMAP8 | 0.874712 | 7.03869 | 26.34489 | 2.85573E-07 | 1.55703E-05 | IRF2BPL | -1.300045 | 4.122395 | 53.990316 | 2.0148E-13 | 8.30792E-11 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| CHRDL1 | 0.977643 | 5.587821 | 26.10256 | 3.23754E-07 | 1.72875E-05 | BAMBI | -1.97506 | 7.353942 | 53.809747 | 2.20874E-13 | 8.90963E-11 |
| PLK2 | 0.947675 | 6.02883 | 26.02561 | 3.36918E-07 | 1.78619E-05 | SLC25A33 | -1.935071 | 4.769681 | 53.159305 | 3.07565E-13 | 1.18896E-10 |
| IGHV7.4.1 | 5.345019 | -3.320708 | 25.97839 | 3.45E-07 | 1.82782E-05 | YBX3 | -1.692619 | 7.10467 | 52.603419 | 4.08178E-13 | 1.5457E-10 |
| TIE1 | 0.946469 | 5.844014 | 25.68818 | 4.01278E-07 | 2.08861E-05 | DNAJC25 | -1.281901 | 4.015435 | 5.05E+01 | 1.16E-12 | 3.89425E-10 |
| UBASH3B | 1.247887 | 3.028423 | 25.6768 | 4.0365E-07 | 2.09802E-05 | RUNDC1 | -1.17845 | 5.008593 | 50.415602 | 1.24401E-12 | 4.12201E-10 |
| IGHV1.69 | 4.598762 | -3.603332 | 25.54017 | 4.33E-07 | 2.23319E-05 | LONRF1 | -1.197278 | 4.121606 | 50.209636 | 1.38168E-12 | 4.45873E-10 |
| PTTG1 | 1.22205 | 2.231407 | 25.48629 | 4.45537E-07 | 2.28015E-05 | SNX25 | -1.32649 | 5.677559 | 49.912506 | 1.60757E-12 | 5.14297E-10 |
| COL4A1 | 0.904397 | 7.192023 | 25.42085 | 4.60909E-07 | 2.34845E-05 | TPBG | -1.504481 | 5.261853 | 49.835197 | 1.67217E-12 | 5.30393E-10 |
| KITLG | 0.913355 | 3.476313 | 25.40512 | 4.64684E-07 | 2.35908E-05 | FKBP9 | -1.106171 | 7.147549 | 49.620565 | 1.86548E-12 | 5.81763E-10 |
| LOXL2 | 1.088274 | 3.451451 | 25.30025 | 4.90644E-07 | 2.47051E-05 | ZFYVE9 | -1.047266 | 4.662286 | 49.248213 | 2.25539E-12 | 6.64283E-10 |
| FAM47A | 4.666997 | -4.270258 | 25.11965 | 5.3881E-07 | 2.66611E-05 | WRNIP1 | -1.355314 | 5.168981 | 48.58623 | 3.16081E-12 | 9.09308E-10 |
| IGLV2.18 | 6.194471 | -2.131877 | 25.02999 | 5.64455E-07 | 2.76717E-05 | CYP2U1 | -1.145666 | 4.606223 | 48.438608 | 3.40792E-12 | 9.58117E-10 |
| CCDC80 | 0.987636 | 5.266218 | 24.97022 | 5.82227E-07 | 2.84303E-05 | LRRC47 | -1.2145 | 5.237284 | 48.388008 | 3.497E-12 | 9.62931E-10 |
| COL1A1 | 2.613242 | 4.889103 | 24.96635 | 5.83397E-07 | 2.845E-05 | PRKAR2B | -1.418813 | 6.233629 | 48.047498 | 4.16018E-12 | 1.12692E-09 |
| LAMA4 | 1.226393 | 2.733683 | 24.86241 | 6.15714E-07 | 2.9908E-05 | PQLC1 | -1.429678 | 4.564307 | 47.865941 | 4.56381E-12 | 1.2273E-09 |
| NLRP10 | 4.63775 | -4.020237 | 24.81711 | 6.30354E-07 | 3.05792E-05 | FOXCUT | -1.083342 | 4.005955 | 47.824502 | 4.6613E-12 | 1.2445E-09 |
| PLAT | 1.011404 | 10.66111 | 24.81243 | 6.31886E-07 | 3.05886E-05 | LNX2 | -1.2125 | 5.108383 | 47.809932 | 4.69607E-12 | 1.24483E-09 |
| SNAI2 | 0.977241 | 6.643891 | 24.74751 | 6.54E-07 | 3.14569E-05 | LINC00957 | -1.565455 | 0.853225 | 47.710069 | 4.94147E-12 | 1.30059E-09 |
| IL21R | 1.182362 | 1.853522 | 24.63866 | 6.91505E-07 | 3.30702E-05 | X2.Mar.1 | -1.251036 | 5.834338 | 47.309114 | 6.06297E-12 | 1.55174E-09 |
| TOP2A | 2.287874 | 2.220758 | 24.62291 | 6.97179E-07 | 3.32558E-05 | ARHGEF37 | -1.035767 | 6.672631 | 46.928588 | 7.36209E-12 | 1.83366E-09 |
| ADAMTS1 | 1.172119 | 7.193895 | 24.51153 | 7.38664E-07 | 3.4876E-05 | TMEM185B | -1.185478 | 4.453353 | 46.75177 | 8.05721E-12 | 1.99341E-09 |
| KIF20A | 2.205749 | 1.429933 | 24.19133 | 8.72238E-07 | 4.04526E-05 | GPSM1 | -1.075714 | 5.753855 | 46.49182 | 9.20017E-12 | 2.24623E-09 |
| ST8SIA4 | 0.923567 | 3.455834 | 24.10193 | 9.13688E-07 | 4.20693E-05 | SLC2A13 | -1.183933 | 4.792106 | 45.91059 | 1.23775E-11 | 2.9445E-09 |
| IGHV1.46 | 5.05055 | -0.44087 | 24.06672 | 9.31E-07 | 4.27924E-05 | ODC1 | -1.20819 | 7.159107 | 45.688822 | 1.38611E-11 | 3.2557E-09 |
| MKI67 | 2.251532 | 1.398499 | 24.03725 | 9.45E-07 | 4.31319E-05 | CHPT1 | -1.716113 | 6.439347 | 45.633889 | 1.42554E-11 | 3.32724E-09 |
| IGLV8.61 | 6.128567 | -1.626187 | 23.92639 | 1.0009E-06 | 4.54088E-05 | PRKCD | -1.217631 | 4.91362 | 45.144098 | 1.83057E-11 | 4.21951E-09 |
| DCHS1 | 0.895808 | 3.347764 | 23.78198 | 1.07888E-06 | 4.87082E-05 | ARMC10 | -1.514052 | 5.465917 | 44.918305 | 2.05428E-11 | 4.64857E-09 |
| AURKB | 2.264106 | 0.483167 | 23.51958 | 1.23649E-06 | 5.46277E-05 | VSIG8 | -1.911244 | 5.601985 | 44.382611 | 2.70075E-11 | 5.96441E-09 |
| F8 | 0.915867 | 6.606749 | 23.49589 | 1.25181E-06 | 5.5239E-05 | NOS1AP | -1.608184 | 2.877841 | 4.44E+01 | 2.71614E-11 | 5.96441E-09 |
| CEACAM1 | 1.065388 | 7.080209 | 23.4397 | 1.28891E-06 | 5.67411E-05 | SNTA1 | -1.501025 | 5.603132 | 44.354548 | 2.73975E-11 | 5.98087E-09 |
| SYNPO2 | 0.877044 | 5.330432 | 23.38652 | 1.32504E-06 | 5.81246E-05 | TAF10 | -1.34308 | 5.433575 | 44.183532 | 2.98986E-11 | 6.4887E-09 |
| UBE2C | 1.842784 | 1.808868 | 23.15372 | 1.49554E-06 | 6.43862E-05 | FKRP | -1.04637 | 3.914741 | 44.096463 | 3.12585E-11 | 6.74439E-09 |
| GPC3 | 1.207333 | 6.313643 | 22.89257 | 1.71313E-06 | 7.22134E-05 | VPS26B | -1.045489 | 5.130585 | 44.070054 | 3.16831E-11 | 6.79649E-09 |
| IGHV3.53 | 3.79246 | -2.719602 | 22.51622 | 2.08376E-06 | 8.58275E-05 | ARRDC2 | -2.169921 | 6.521824 | 43.790528 | 3.6547E-11 | 7.70622E-09 |
| CDKN3 | 1.16273 | 1.937277 | 22.45401 | 2.15E-06 | 8.82608E-05 | DYNC1I1 | -1.914895 | 6.123688 | 43.774928 | 3.68394E-11 | 7.7137E-09 |
| ARHGAP19. | 4.60794 | -4.33849 | 22.30967 | 2.32036E-06 | 9.40074E-05 | FAM210B | -1.035504 | 6.215895 | 43.750042 | 3.73109E-11 | 7.73544E-09 |