

Supplementary Table S1: Patient recruitment by state and year stratification.

Year	State						
	NSW	NT	QLD	SA	TAS	VIC	WA
2013	5	0	15	0	0	9	0
2014	30	0	46	0	0	7	0
2015	18	0	52	0	0	7	0
2016	54	0	75	8	0	43	0
2017	60	0	94	14	0	139	0
2018	50	0	76	27	0	126	15
2019	36	1	49	11	5	18	5
2020	0	0	0	0	0	0	4
2021	42	0	39	14	0	15	17
2022	17	0	38	9	0	13	14
*Year unknown	87	1	51	14	0	24	12
Total number	399	2	535	97	5	401	67

The table includes all patients with and without genomic testing (N=1506). NSW, New South Wales; NT, Northern Territory; QLD, Queensland; SA, South Australia; TAS, Tasmania; VIC, Victoria; WA, Western Australia. Note: *There were limitations in the data collection process, as it relied on information provided by multiple clinicians from various renal genetics clinics. This resulted in challenges obtaining complete data, such as missing “year of recruitment” information.

Supplementary Table S2: Occurrence of genes affected by pathogenic/likely pathogenic variants in patients with different kidney diagnoses.

Diagnosis	Subgroup	Gene	Occurrence	Percent
Tubulopathy		<i>SLC12A1</i>	2	0.26
		<i>SLC12A3</i>	23	2.96
		<i>SLC7A9</i>	3	0.39
		<i>ATP6V0A4</i>	2	0.26
		<i>AVPR2</i>	2	0.26
		<i>OCRL</i>	1	0.13
		<i>SLC4A1</i>	9	1.16
		<i>PHEX</i>	1	0.13
		<i>CLCN5</i>	5	0.64
		<i>CASR</i>	3	0.39
		<i>CACNAIS</i>	1	0.13
		<i>KCNJ1</i>	2	0.26
		<i>SCN4A</i>	1	0.13
		<i>CLCNKB</i>	2	0.26
		<i>CLDN16</i>	2	0.26
		<i>ATP6V1B1</i>	3	0.39
		<i>APRT</i>	2	0.26
		<i>REN</i>	1	0.13
		<i>AGTX</i>	3	0.39
		<i>AQP2</i>	1	0.13
		<i>GRHPR</i>	1	0.13
		<i>SCNN1A</i>	1	0.13
		<i>CLDN10</i>	1	0.13
		<i>HNF4A</i>	1	0.13
	<i>HOGA1</i>	1	0.13	
	<i>PHEX</i>	1	0.13	
Glomerular	Nephrotic	<i>LMX1B</i>	2	0.26
		<i>INF2</i>	3	0.39
		<i>NUP107</i>	1	0.13
		<i>CD2AP</i>	1	0.13
		<i>COQ8B</i>	2	0.26
		<i>TTC21B</i>	1	0.13
		<i>COL4A5</i>	2	0.26
		<i>NPHS1</i>	7	0.90
		<i>ALMS1</i>	1	0.13
		<i>FAT1</i>	2	0.26
		<i>SETD5</i>	1	0.13
		<i>CUBN</i>	4	0.52
	<i>CLCN5</i>	2	0.26	

		<i>LAMA5</i>	2	0.26
		<i>MEFV</i>	1	0.13
		<i>FN1</i>	1	0.13
		<i>chr16del</i>	1	0.13
		<i>NPHS2</i>	10	1.29
		<i>ch17q12dup</i>	1	0.13
		<i>PKHD1</i>	1	0.13
		<i>LAMB2</i>	3	0.39
		<i>COL4A1</i>	1	0.13
		<i>ANLN</i>	1	0.13
		<i>ACTN4</i>	3	0.39
		<i>TRPC6</i>	3	0.39
		<i>PLCE1</i>	1	0.13
		<i>SMARCAL1</i>	1	0.13
		<i>TSC1</i>	1	0.13
		<i>MYO1E</i>	1	0.13
		<i>COL4A3</i>	5	0.64
		<i>FAN1</i>	1	0.13
		<i>ALMS1</i>	1	0.13
		<i>SLC3A1</i>	1	0.13
		<i>CD46</i>	1	0.13
		<i>COL4A4</i>	2	0.26
		<i>COL4A5</i>	1	0.13
		<i>ARHGAP24</i>	1	0.13
		<i>ITGB4</i>	1	0.13
		<i>SAMD9</i>	1	0.13
		<i>CLCNKB</i>	1	0.13
		<i>LMX1b</i>	1	0.13
		<i>PLCE1</i>	1	0.13
		<i>TRPC6</i>	1	0.13
		<i>WT1</i>	1	0.13
	Glomerulopathy	<i>CFHR5</i>	1	0.13
		<i>COL4A4</i>	7	0.90
		<i>FN1</i>	2	0.26
		<i>COL4A5</i>	5	0.64
		<i>MYH9</i>	1	0.13
		<i>COL4A3</i>	3	0.39
		<i>FAT1</i>	1	0.13
		<i>LRP5</i>	1	0.13
		<i>NUP93</i>	1	0.13
		<i>PLCE1</i>	1	0.13
		<i>TRPC6</i>	1	0.13

		<i>MYO1E</i>	1	0.13
	Alport	<i>COL4A4</i>	34	4.38
		<i>COL4A5</i>	82	10.57
		<i>COL4A3</i>	27	3.48
		<i>COL4A1</i>	1	0.13
		<i>UMOD</i>	3	0.39
		<i>NPHS2</i>	1	0.13
		<i>ACTN4</i>	1	0.13
		<i>CLCN5</i>	2	0.26
		<i>GATA3</i>	1	0.13
		<i>CFHR5</i>	1	0.13
		<i>CUBN</i>	1	0.13
		<i>HNF1B</i>	1	0.13
		<i>FAT1</i>	1	0.13
		<i>PKD2</i>	2	0.26
		<i>PKHD1</i>	2	0.26
		<i>PKD1</i>	2	0.26
		<i>RANCI</i>	1	0.13
		<i>CFI</i>	1	0.13
Cystic and Ciliopathy	Cystic	<i>PKD1</i>	138	17.78
		<i>PKD2</i>	22	2.84
		<i>ch17q12 CNV</i>	1	0.13
		<i>PKHD1</i>	41	5.28
		<i>BRCA1</i>	1	0.13
		<i>IFT140</i>	1	0.13
		<i>HNF1B</i>	30	3.87
		<i>COL4A1</i>	1	0.13
		<i>CC2D2A</i>	1	0.13
		<i>BBS1</i>	1	0.13
		<i>DNAJB11</i>	3	0.39
		<i>PRKCSH</i>	2	0.26
		<i>TSC2</i>	4	0.52
		<i>CTNS</i>	2	0.26
		<i>WDR19</i>	1	0.13
		<i>SLC4A1</i>	1	0.13
		<i>ANKRD11</i>	1	0.13
		<i>PRKCSH</i>	1	0.13
		<i>SRCAP</i>	1	0.13
		<i>MUC1</i>	1	0.13
		<i>COL4A5</i>	1	0.13
		<i>GANAB</i>	2	0.26
		<i>OCRL</i>	1	0.13

		<i>ALMS1</i>	1	0.13
		<i>BBS10</i>	2	0.26
		<i>TTC21B</i>	1	0.13
		<i>DYNC2H1</i>	1	0.13
		<i>CEP290</i>	1	0.13
		<i>NOTCH2</i>	1	0.13
		<i>UMOD</i>	2	0.26
		<i>SEC63</i>	1	0.13
	Ciliopathy	<i>CEP83</i>	1	0.13
		<i>PKHD1</i>	2	0.26
		<i>TMEM67</i>	1	0.13
		<i>IFT172</i>	1	0.13
		<i>INVS</i>	2	0.26
		<i>BBS10</i>	1	0.13
		<i>NPHP1</i>	4	0.52
		<i>CTNS</i>	1	0.13
		<i>BBS2</i>	1	0.13
		<i>LRRC6</i>	1	0.13
		<i>UMOD</i>	2	0.26
		<i>UGT1A1</i>	1	0.13
		<i>IQCB1</i>	1	0.13
		<i>NPHP4</i>	6	0.77
		<i>RPS6KA3</i>	1	0.13
		<i>AH11</i>	1	0.13
		<i>MKKS</i>	1	0.13
		<i>CEP164</i>	1	0.13
		<i>BBS7</i>	1	0.13
		<i>C5orf42</i>	1	0.13
		<i>AH11</i>	1	0.13
		<i>CEP290</i>	2	0.26
		<i>TMEM67</i>	1	0.13
		<i>RMND1</i>	1	0.13
		<i>IFT140</i>	1	0.13
		<i>NPHP3</i>	1	0.13
	ADTKD	<i>UMOD</i>	12	1.55
		<i>MUC1</i>	8	1.03
		<i>COL4A1</i>	1	0.13
		<i>COL4A4</i>	1	0.13
		<i>ADCY10</i>	1	0.13
		<i>NPHS2</i>	1	0.13
		<i>HNF1B</i>	1	0.13
		<i>PKD1</i>	1	0.13

		<i>NPHP1</i>	1	0.13
		<i>BICC1</i>	1	0.13
		<i>FANI</i>	1	0.13
		<i>PKHD1</i>	1	0.13
Complement		<i>CFHR1</i>	3	0.39
		<i>CD46</i>	2	0.26
		<i>C3</i>	6	0.77
		<i>CFI</i>	2	0.26
		<i>THBD</i>	7	0.90
		<i>CFH</i>	9	1.16
		<i>REN</i>	1	0.13
		<i>CFHR3</i>	2	0.26
		<i>ADAMTS13</i>	1	0.13
		<i>PLG</i>	1	0.13
		<i>CFHR5</i>	2	0.26
		<i>CFB</i>	1	0.13
		<i>FLG</i>	1	0.13
CAKUT	Syndromic	<i>PAX2</i>	3	0.39
		<i>ROBO2</i>	1	0.13
		<i>GATA3</i>	1	0.13
		<i>STXBPI</i>	1	0.13
		<i>HDAC8</i>	1	0.13
		<i>FRAS1</i>	1	0.13
		<i>SALL1</i>	1	0.13
		<i>TTC21B</i>	1	0.13
		<i>EDNI</i>	1	0.13
		<i>EYA1</i>	2	0.26
		<i>JAG1</i>	1	0.13
	Isolated	<i>JAG1</i>	1	0.13
		<i>KMT2D</i>	1	0.13
		<i>NPHP4</i>	1	0.13
		<i>BBS10</i>	1	0.13
		<i>FREMI</i>	1	0.13
		<i>ACE</i>	1	0.13
		<i>HNFB</i>	4	0.52
		<i>BMP4</i>	1	0.13
		<i>RET</i>	1	0.13
		<i>BICC1</i>	1	0.13
		<i>CHD1L</i>	1	0.13
		<i>FRAS1</i>	2	0.26
		<i>SALL1</i>	1	0.13
Other		<i>COL4A4</i>	1	0.13

		<i>NPHP1</i>	2	0.26
		<i>WT1</i>	4	0.52
		<i>NPHS2</i>	1	0.13
		<i>NPHP3</i>	1	0.13
		<i>FLNA</i>	1	0.13
		<i>COL4A1</i>	1	0.13
		<i>MED13L</i>	1	0.13
		<i>UMOD</i>	1	0.13
		<i>COL4A5</i>	1	0.13
		<i>HNF1B del</i>	1	0.13
		<i>MYH9</i>	1	0.13
		<i>FLCN</i>	1	0.13
		<i>APRT</i>	1	0.13
		<i>HOGA1</i>	1	0.13
		<i>AVPR2</i>	1	0.13
		<i>COL4A3</i>	2	0.26
		<i>PRKCSH</i>	1	0.13
		<i>DGKE</i>	1	0.13
		<i>AVPR2</i>	1	0.13
		<i>ANLN</i>	1	0.13

Supplementary Table S3: Genes listed in Kidneyome_SuperPanel Version 8.53.

Entity Name	Entity Type	Gene Symbol	HGNC
ACE	gene	<i>ACE</i>	HGNC:2707
ACTG2	gene	<i>ACTG2</i>	HGNC:145
ACTN4	gene	<i>ACTN4</i>	HGNC:166
AFF3	gene	<i>AFF3</i>	HGNC:6473
AGT	gene	<i>AGT</i>	HGNC:333
AGTR1	gene	<i>AGTR1</i>	HGNC:336
AGXT	gene	<i>AGXT</i>	HGNC:341
AHI1	gene	<i>AHI1</i>	HGNC:21575
AIRE	gene	<i>AIRE</i>	HGNC:360
ALG5	gene	<i>ALG5</i>	HGNC:20266
ALG8	gene	<i>ALG8</i>	HGNC:23161
ALG9	gene	<i>ALG9</i>	HGNC:15672
ALMS1	gene	<i>ALMS1</i>	HGNC:428
ALPL	gene	<i>ALPL</i>	HGNC:438
AMMECR1	gene	<i>AMMECR1</i>	HGNC:467
AMN	gene	<i>AMN</i>	HGNC:14604
ANKS6	gene	<i>ANKS6</i>	HGNC:26724
ANOS1	gene	<i>ANOS1</i>	HGNC:6211
AP2S1	gene	<i>AP2S1</i>	HGNC:565
APOA1	gene	<i>APOA1</i>	HGNC:600
APOE	gene	<i>APOE</i>	HGNC:613
APRT	gene	<i>APRT</i>	HGNC:626
AQP2	gene	<i>AQP2</i>	HGNC:634
ARHGDI1A	gene	<i>ARHGDI1A</i>	HGNC:678
ARL13B	gene	<i>ARL13B</i>	HGNC:25419
ARL6	gene	<i>ARL6</i>	HGNC:13210
ATP1A1	gene	<i>ATP1A1</i>	HGNC:799
ATP6V0A4	gene	<i>ATP6V0A4</i>	HGNC:866
ATP6V1B1	gene	<i>ATP6V1B1</i>	HGNC:853
AVP	gene	<i>AVP</i>	HGNC:894
AVPR2	gene	<i>AVPR2</i>	HGNC:897
BBS1	gene	<i>BBS1</i>	HGNC:966
BBS10	gene	<i>BBS10</i>	HGNC:26291
BBS12	gene	<i>BBS12</i>	HGNC:26648
BBS2	gene	<i>BBS2</i>	HGNC:967
BBS4	gene	<i>BBS4</i>	HGNC:969
BBS5	gene	<i>BBS5</i>	HGNC:970
BBS7	gene	<i>BBS7</i>	HGNC:18758
BBS9	gene	<i>BBS9</i>	HGNC:30000
BCS1L	gene	<i>BCS1L</i>	HGNC:1020

BMP4	gene	<i>BMP4</i>	HGNC:1071
BNC2	gene	<i>BNC2</i>	HGNC:30988
BSND	gene	<i>BSND</i>	HGNC:16512
C3	gene	<i>C3</i>	HGNC:1318
CA2	gene	<i>CA2</i>	HGNC:1373
CACNA1D	gene	<i>CACNA1D</i>	HGNC:1391
CACNA1H	gene	<i>CACNA1H</i>	HGNC:1395
CACNA1S	gene	<i>CACNA1S</i>	HGNC:1397
CASR	gene	<i>CASR</i>	HGNC:1514
CC2D2A	gene	<i>CC2D2A</i>	HGNC:29253
CD151	gene	<i>CD151</i>	HGNC:1630
CD2AP	gene	<i>CD2AP</i>	HGNC:14258
CD46	gene	<i>CD46</i>	HGNC:6953
CDC73	gene	<i>CDC73</i>	HGNC:16783
CDKN1B	gene	<i>CDKN1B</i>	HGNC:1785
CDX2	gene	<i>CDX2</i>	HGNC:1806
CELSR3	gene	<i>CELSR3</i>	HGNC:3230
CENPF	gene	<i>CENPF</i>	HGNC:1857
CEP164	gene	<i>CEP164</i>	HGNC:29182
CEP290	gene	<i>CEP290</i>	HGNC:29021
CEP55	gene	<i>CEP55</i>	HGNC:1161
CEP83	gene	<i>CEP83</i>	HGNC:17966
CFB	gene	<i>CFB</i>	HGNC:1037
CFH	gene	<i>CFH</i>	HGNC:4883
CFHR1	gene	<i>CFHR1</i>	HGNC:4888
CFHR2	gene	<i>CFHR2</i>	HGNC:4890
CFHR3	gene	<i>CFHR3</i>	HGNC:16980
CFHR5	gene	<i>CFHR5</i>	HGNC:24668
CFI	gene	<i>CFI</i>	HGNC:5394
CHD7	gene	<i>CHD7</i>	HGNC:20626
CHRNA3	gene	<i>CHRNA3</i>	HGNC:1957
CLCN2	gene	<i>CLCN2</i>	HGNC:2020
CLCN5	gene	<i>CLCN5</i>	HGNC:2023
CLCN5	gene	<i>CLCN5</i>	HGNC:2023
CLCNKB	gene	<i>CLCNKB</i>	HGNC:2027
CLDN10	gene	<i>CLDN10</i>	HGNC:2033
CLDN16	gene	<i>CLDN16</i>	HGNC:2037
CLDN19	gene	<i>CLDN19</i>	HGNC:2040
CNNM2	gene	<i>CNNM2</i>	HGNC:103
COL4A1	gene	<i>COL4A1</i>	HGNC:2202
COL4A1	gene	<i>COL4A1</i>	HGNC:2202
COL4A3	gene	<i>COL4A3</i>	HGNC:2204

COL4A3	gene	<i>COL4A3</i>	HGNC:2204
COL4A4	gene	<i>COL4A4</i>	HGNC:2206
COL4A4	gene	<i>COL4A4</i>	HGNC:2206
COL4A5	gene	<i>COL4A5</i>	HGNC:2207
COL4A5	gene	<i>COL4A5</i>	HGNC:2207
COQ2	gene	<i>COQ2</i>	HGNC:25223
COQ6	gene	<i>COQ6</i>	HGNC:20233
COQ8B	gene	<i>COQ8B</i>	HGNC:19041
CPT2	gene	<i>CPT2</i>	HGNC:2330
CRB2	gene	<i>CRB2</i>	HGNC:18688
CRB2	gene	<i>CRB2</i>	HGNC:18688
CSPP1	gene	<i>CSPP1</i>	HGNC:26193
CTNS	gene	<i>CTNS</i>	HGNC:2518
CTU2	gene	<i>CTU2</i>	HGNC:28005
CUBN	gene	<i>CUBN</i>	HGNC:2548
CUL3	gene	<i>CUL3</i>	HGNC:2553
CYP11B1	gene	<i>CYP11B1</i>	HGNC:2591
CYP11B2	gene	<i>CYP11B2</i>	HGNC:2592
CYP17A1	gene	<i>CYP17A1</i>	HGNC:2593
CYP21A2	gene	<i>CYP21A2</i>	HGNC:2600
CYP24A1	gene	<i>CYP24A1</i>	HGNC:2602
CYP27B1	gene	<i>CYP27B1</i>	HGNC:2606
CYP2R1	gene	<i>CYP2R1</i>	HGNC:20580
DAAM2	gene	<i>DAAM2</i>	HGNC:18143
DCDC2	gene	<i>DCDC2</i>	HGNC:18141
DGKE	gene	<i>DGKE</i>	HGNC:2852
DGKE	gene	<i>DGKE</i>	HGNC:2852
DHCR7	gene	<i>DHCR7</i>	HGNC:2860
DLC1	gene	<i>DLC1</i>	HGNC:2897
DLG5	gene	<i>DLG5</i>	HGNC:2904
DMP1	gene	<i>DMP1</i>	HGNC:2932
DNAJB11	gene	<i>DNAJB11</i>	HGNC:14889
DNAJB11	gene	<i>DNAJB11</i>	HGNC:14889
DYNC2H1	gene	<i>DYNC2H1</i>	HGNC:2962
DYRK1A	gene	<i>DYRK1A</i>	HGNC:3091
DZIP1L	gene	<i>DZIP1L</i>	HGNC:26551
EHHADH	gene	<i>EHHADH</i>	HGNC:3247
ENPP1	gene	<i>ENPP1</i>	HGNC:3356
EXOC3L2	gene	<i>EXOC3L2</i>	HGNC:30162
EYA1	gene	<i>EYA1</i>	HGNC:3519
FAH	gene	<i>FAH</i>	HGNC:3579
FAM111A	gene	<i>FAM111A</i>	HGNC:24725

FAM20A	gene	<i>FAM20A</i>	HGNC:23015
FAM20C	gene	<i>FAM20C</i>	HGNC:22140
FAM58A	gene	<i>FAM58A</i>	HGNC:28434
FAN1	gene	<i>FAN1</i>	HGNC:29170
FAN1	gene	<i>FAN1</i>	HGNC:29170
FAT1	gene	<i>FAT1</i>	HGNC:3595
FGA	gene	<i>FGA</i>	HGNC:3661
FGF23	gene	<i>FGF23</i>	HGNC:3680
FN1	gene	<i>FN1</i>	HGNC:3778
FOXI1	gene	<i>FOXI1</i>	HGNC:3815
FOXP1	gene	<i>FOXP1</i>	HGNC:3823
FRAS1	gene	<i>FRAS1</i>	HGNC:19185
FREM1	gene	<i>FREM1</i>	HGNC:23399
FREM2	gene	<i>FREM2</i>	HGNC:25396
GALNT3	gene	<i>GALNT3</i>	HGNC:4125
GANAB	gene	<i>GANAB</i>	HGNC:4138
GATA3	gene	<i>GATA3</i>	HGNC:4172
GATA3	gene	<i>GATA3</i>	HGNC:4172
GATM	gene	<i>GATM</i>	HGNC:4175
GCM2	gene	<i>GCM2</i>	HGNC:4198
GDF6	gene	<i>GDF6</i>	HGNC:4221
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GLA	gene	<i>GLA</i>	HGNC:4296
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GNAS	gene	<i>GNAS</i>	HGNC:4392
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HNF1B	gene	<i>HNF1B</i>	HGNC:11630
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HOGA1	gene	<i>HOGA1</i>	HGNC:25155
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IFT140	gene	<i>IFT140</i>	HGNC:29077
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IFT74	gene	<i>IFT74</i>	HGNC:21424
INF2	gene	<i>INF2</i>	HGNC:23791
INPP5E	gene	<i>INPP5E</i>	HGNC:21474
INVS	gene	<i>INVS</i>	HGNC:17870
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ITSN1	gene	<i>ITSN1</i>	HGNC:6183
ITSN2	gene	<i>ITSN2</i>	HGNC:6184
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LAMB2	gene	<i>LAMB2</i>	HGNC:6487
LCAT	gene	<i>LCAT</i>	HGNC:6522
LCAT	gene	<i>LCAT</i>	HGNC:6522
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LRP4	gene	<i>LRP4</i>	HGNC:6696

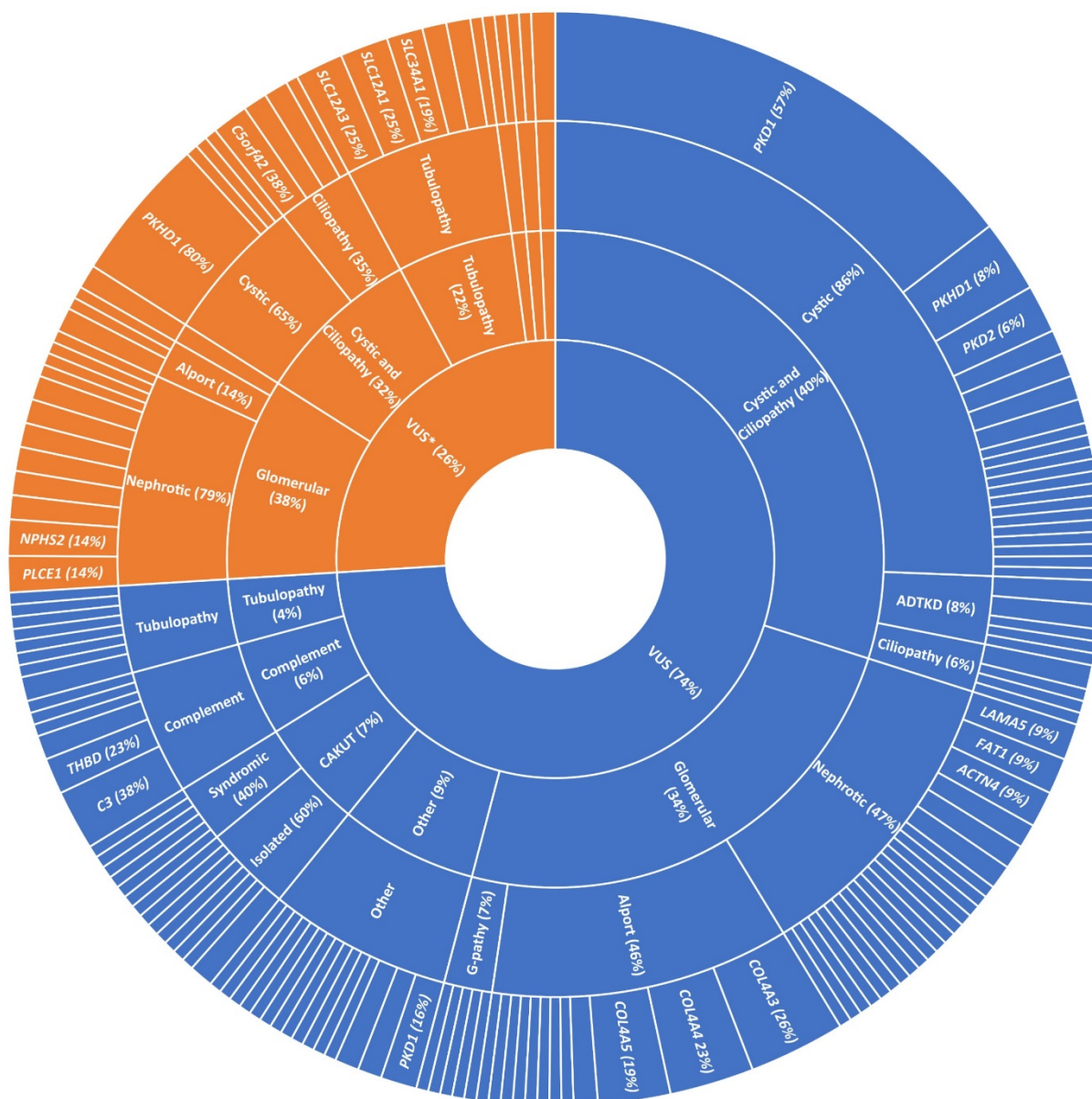
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MEN1	gene	<i>MEN1</i>	HGNC:7010
MKKS	gene	<i>MKKS</i>	HGNC:7108
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PAX2	gene	<i>PAX2</i>	HGNC:8616
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PKHD1	gene	<i>PKHD1</i>	HGNC:9016
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STRA6	gene	<i>STRA6</i>	HGNC:30650
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TBCE	gene	<i>TBCE</i>	HGNC:11582
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TBX6	gene	<i>TBX6</i>	HGNC:11605
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TMEM231	gene	<i>TMEM231</i>	HGNC:37234
TMEM237	gene	<i>TMEM237</i>	HGNC:14432
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TP53RK	gene	<i>TP53RK</i>	HGNC:16197
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TRAF3IP1	gene	<i>TRAF3IP1</i>	HGNC:17861
TRAP1	gene	<i>TRAP1</i>	HGNC:16264
TRIM8	gene	<i>TRIM8</i>	HGNC:15579
TRPC6	gene	<i>TRPC6</i>	HGNC:12338
TRPM6	gene	<i>TRPM6</i>	HGNC:17995
TSC1	gene	<i>TSC1</i>	HGNC:12362
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VPS33B	gene	<i>VPS33B</i>	HGNC:12712
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WDPCP	gene	<i>WDPCP</i>	HGNC:28027
WDR19	gene	<i>WDR19</i>	HGNC:18340
WDR35	gene	<i>WDR35</i>	HGNC:29250
WDR44	gene	<i>WDR44</i>	HGNC:30512
WDR60	gene	<i>WDR60</i>	HGNC:21862
WDR72	gene	<i>WDR72</i>	HGNC:26790
WDR73	gene	<i>WDR73</i>	HGNC:25928
WLS	gene	<i>WLS</i>	HGNC:30238
WNK1	gene	<i>WNK1</i>	HGNC:14540
WNK4	gene	<i>WNK4</i>	HGNC:14544
WNT5A	gene	<i>WNT5A</i>	HGNC:12784
WT1	gene	<i>WT1</i>	HGNC:12796
XDH	gene	<i>XDH</i>	HGNC:12805
XPNPEP3	gene	<i>XPNPEP3</i>	HGNC:28052
YRDC	gene	<i>YRDC</i>	HGNC:28905
ZIC3	gene	<i>ZIC3</i>	HGNC:12874
ZMYM2	gene	<i>ZMYM2</i>	HGNC:12989

The complete list of genes with the strongest evidence (green colored in PanelApp Australia) for their association with Mendelian renal disease is provided. HGCN, HUGO Gene Nomenclature Committee.



Supplementary Figure S1: Genes with VUS/VUS* identified in the national KidGen cohort. The genes are stratified by clinical diagnosis, with the width of the cut-outs indicating the number of appearances. VUS is a variant of uncertain significance; VUS* is a VUS with suspected clinical relevance.

STROBE Statement—Checklist of items that should be included in reports of *cohort studies*

	Item No	Recommendation	Page No
Title and abstract	1	(a) Indicate the study's design with a commonly used term in the title or the abstract	1
		(b) Provide in the abstract an informative and balanced summary of what was done and what was found	5
Introduction			
Background/rationale	2	Explain the scientific background and rationale for the investigation being reported	6
Objectives	3	State specific objectives, including any prespecified hypotheses	7
Methods			
Study design	4	Present key elements of study design early in the paper	7-8
Setting	5	Describe the setting, locations, and relevant dates, including periods of recruitment, exposure, follow-up, and data collection	9
Participants	6	(a) Give the eligibility criteria, and the sources and methods of selection of participants. Describe methods of follow-up (b) For matched studies, give matching criteria and number of exposed and unexposed	9
Variables	7	Clearly define all outcomes, exposures, predictors, potential confounders, and effect modifiers. Give diagnostic criteria, if applicable	9-11
Data sources/ measurement	8*	For each variable of interest, give sources of data and details of methods of assessment (measurement). Describe comparability of assessment methods if there is more than one group	9-11
Bias	9	Describe any efforts to address potential sources of bias	10
Study size	10	Explain how the study size was arrived at	10
Quantitative variables	11	Explain how quantitative variables were handled in the analyses. If applicable, describe which groupings were chosen and why	11
Statistical methods	12	(a) Describe all statistical methods, including those used to control for confounding (b) Describe any methods used to examine subgroups and interactions (c) Explain how missing data were addressed	10

		(d) If applicable, explain how loss to follow-up was addressed	
		(e) Describe any sensitivity analyses	
Results			
Participants	13*	(a) Report numbers of individuals at each stage of study—eg numbers potentially eligible, examined for eligibility, confirmed eligible, included in the study, completing follow-up, and analysed (b) Give reasons for non-participation at each stage (c) Consider use of a flow diagram	12
Descriptive data	14*	(a) Give characteristics of study participants (eg demographic, clinical, social) and information on exposures and potential confounders (b) Indicate number of participants with missing data for each variable of interest (c) Summarise follow-up time (eg, average and total amount)	12
Outcome data	15*	Report numbers of outcome events or summary measures over time	12-13
Main results	16	(a) Give unadjusted estimates and, if applicable, confounder-adjusted estimates and their precision (eg, 95% confidence interval). Make clear which confounders were adjusted for and why they were included (b) Report category boundaries when continuous variables were categorized (c) If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period	13
Other analyses	17	Report other analyses done—eg analyses of subgroups and interactions, and sensitivity analyses	N/A
Discussion			
Key results	18	Summarise key results with reference to study objectives	14
Limitations	19	Discuss limitations of the study, taking into account sources of potential bias or imprecision. Discuss both direction and magnitude of any potential bias	16
Interpretation	20	Give a cautious overall interpretation of results considering objectives, limitations, multiplicity of analyses, results from similar studies, and other relevant evidence	16
Generalisability	21	Discuss the generalisability (external validity) of the study results	17

Other information

Funding	22	Give the source of funding and the role of the funders for the present study and, if applicable, for the original study on which the present article is based	18
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*Give information separately for exposed and unexposed groups.

Note: An Explanation and Elaboration article discusses each checklist item and gives methodological background and published examples of transparent reporting. The STROBE checklist is best used in conjunction with this article (freely available on the Web sites of PLoS Medicine at <http://www.plosmedicine.org/>, Annals of Internal Medicine at <http://www.annals.org/>, and Epidemiology at <http://www.epidem.com/>). Information on the STROBE Initiative is available at <http://www.strobe-statement.org>.