

Cystic Kidney and Liver Disease (CKLD) Panel

Panel Gene List

AH1I, ALG8, ALG9, ANKS6, BICC1, CC2D2A, CEP120, CEP290, CEP83, COL4A1, CRB2, CSPP1, GANAB, GLIS2, GLIS3, HNF1B, IFT172, INVS, IQCB1, JAG1, LRP5, MKKS, MKS1, NEK8, NOTCH2, NPHP1, NPHP3, OFD1, PAX2, PKD1, PKD2, PKHD1, PMM2, PRKCSH, RMND1, RPGRIP1L, SEC61A1, SEC63, TMEM138, TMEM216, TMEM231, TMEM237, TMEM67, TSC1, TSC2, TTC21B, UMOD, VHL, WDR35

Clinical Features and Genetics

Cystic kidney and liver diseases are a collection of multisystem disorders that present with development of cysts in the kidney and/or liver as well as other organ systems. These diseases can be categorized by underlying etiology (ciliopathies or phakomatoses) or by morphology (size, location, and complexity of cysts).^{1,2}

Hepatorenal ciliopathic disorders include polycystic kidney disease (PKD), polycystic liver disease (PLD), nephronophthisis (NPHP), and medullary cystic kidney disease (MCKD). Polycystic kidney disease has two major forms, autosomal dominant PKD (ADPKD) and autosomal recessive PKD (ARPKD). ADPKD is characterized by renal cysts that lead to hypertension, renal insufficiency, and end-stage renal disease (ESRD).^{3,4} While cysts may form in other organs, hepatic cysts are the most common extrarenal feature of ADPKD.⁴ The majority of ADPKD cases are caused by variants in the *PKD1* and *PKD2* genes, while a small number of individuals may have ADPKD due to variants in the *GANAB* gene.^{5,6} ARPKD is characterized by bilateral renal cystic disease and congenital hepatic fibrosis, typically already presenting in the developing fetus with oligohydramnios and enlarged echogenic kidneys and liver.^{7,8} The majority of cases of ARPKD are caused by homozygous or compound heterozygous pathogenic variants in the *PKHD1* gene.^{9,10} Polycystic liver disease (PLD) is characterized by progressive development of multiple liver cysts, with or without kidney cyst presentation.¹¹ PLD patients are usually asymptomatic with normal hepatic function prior to disease manifestation between the age of 40 and 60 years old.¹² The most common complication in symptomatic patients is extensive hepatomegaly, which may lead to malnutrition and can be lethal.¹³ Isolated PLD is an autosomal dominant disorder (ADPLD) which is caused by pathogenic variants in the *PRKCSH*, *SEC63*, *LRP5*, *ALG8*, or *GANAB* genes; however, *PRKCSH* and *SEC63* collectively account for at least 35% of cases.¹⁴ Nephronophthisis (NPHP) is characterized by cystic kidney disease, reduced renal concentrating ability, chronic inflammation of the renal tubules and ESRD before the age of 30 years old.¹⁵⁻¹⁷ Clinically, NPHP can be subdivided based on ESRD onset into infantile, juvenile and adult NPHP. NPHP-related ciliopathies (NPHP-RC) are a group of heterogeneous disorders that present with extrarenal features and share a wide variety of phenotype overlap due to multi-organ involvement and include Bardet-Biedl syndrome, COACH syndrome, Jeune syndrome and related skeletal disorders, Joubert syndrome, Meckel syndrome (also known as Meckel-Gruber syndrome), Senior-Loken syndrome and others.¹⁸ NPHP-RC are inherited in a recessive manner. Medullary cystic kidney disease (MCKD), also known as autosomal dominant tubulointerstitial kidney disease (ADTKD), is characterized by fibrosis or scarring of the kidney tubules, which leads to slowly progressive chronic kidney disease.¹⁹ Variants in several genes including *MUC1*, *UMOD*, *REN* and *SEC61A1* have been associated with various subtypes of ADTKD. The *UMOD* and *SEC61A1* genes are included in this panel.

Phakomatoses are a group of hereditary neurocutaneous disorders that present with multi-system features, and commonly affected tissues include the central nervous system, eyes, and skin. While the clinical

presentation may vary, these patients may also manifest with renal cysts.¹ Tuberous sclerosis complex (TSC) is an autosomal dominant disorder characterized by abnormalities of the skin, brain, kidney, heart, and lungs. Individuals with TSC, which is caused by pathogenic variants in the tumor suppressor *TSC1* or *TSC2* genes, have a significantly increased risk for neurodevelopmental disorders.²⁰ Rarely, individuals with TSC may also exhibit multiple renal cysts often leading to ESRD and an increased risk for Berry aneurysms and cysts in other organs. Individuals with features of both TSC and PKD typically have a contiguous gene deletion syndrome involving the neighboring *TSC2* and *PKD1* genes.²¹ Another type of phakomatosis is Von Hippel-Lindau syndrome (VHL), an autosomal dominant hereditary cancer predisposition syndrome caused by germline variants in the VHL tumor suppressor gene. VHL is characterized by an increased risk for central nervous system hemangioblastomas (60–80%), retinal capillary hemangiomas (also referred to as retinal angiomas) (50–60%), renal cysts and carcinomas (30–60%), pancreatic cysts (30–65%), pheochromocytomas (11–19%), epididymal cystadenomas (26%), and endolymphatic sac tumors (2–10%).^{22,23} VHL is highly penetrant and virtually all individuals who harbor a variant in the *VHL* gene develop symptoms by 70 years of age.²⁴ However, the clinical manifestations and disease severity are highly variable, even among family members with the same variant.

Other genes previously reported to be associated with kidney cyst presentation and included in this panel are *ALG9*, *BICC1*, *COL4A1*, *CRB2*, *GLIS3*, *HNFB*, *IFT172*, *JAG1*, *NOTCH2*, *PAX2*, *PMM2*, *RMND1* and *WDR35*.

Inheritance Pattern/Genetics

Autosomal Dominant, Autosomal Recessive, X-Linked

Test Methods

Using genomic DNA from the submitted specimen, the complete coding regions and splice site junctions of the genes on this panel are enriched using a proprietary targeted capture system developed by GeneDx for next-generation sequencing with CNV calling (NGS-CNV). The enriched targets are simultaneously sequenced with paired-end reads on an Illumina platform. Bi-directional sequence reads are assembled and aligned to reference sequences based on NCBI RefSeq transcripts and human genome build GRCh37/UCSC hg19. After gene specific filtering, data are analyzed to identify sequence variants and most deletions and duplications involving coding exons. Alternative sequencing or copy number detection methods are used to analyze regions with inadequate sequence or copy number data. Sequence variants are reported according to the Human Genome Variation Society (HGVS) guidelines. Copy number variants are reported based on the probe coordinates, the coordinates of the exons involved, or precise breakpoints when known. Reportable variants include pathogenic variants, likely pathogenic variants and variants of uncertain significance. Likely benign and benign variants, if present, are not routinely reported but are available upon request.

The technical sensitivity of sequencing is estimated to be >99% at detecting single nucleotide events. It will not reliably detect deletions greater than 20 base pairs, insertions or rearrangements greater than 10 base pairs, or low-level mosaicism. The copy number assessment methods used with this test cannot reliably detect copy number variants of less than 500 base pairs or mosaicism and cannot identify balanced chromosome aberrations. Assessment of exon-level copy number events is dependent on the inherent sequence properties of the targeted regions, including shared homology and exon size. Sequencing of the *PKD1* gene is known to be particularly challenging since more than half of the gene (exons 1–33 out of 46 exons) shares high homology with its six known pseudogenes, all located on the same chromosome as *PKD1*.

(chromosome 16).^{25,26} Accordingly, gene-specific long-range PCR analysis followed by nested amplification of each exon will be used for sequencing of exons 1-33. Gene specific exclusions for exon-level deletion/duplication testing for this panel are: *IQCB1*, *LRP5*, *OFD1*, *TMEM231* genes, only whole gene deletions or duplications may be detected; *AHI*, *ALG8*, *CEP120*, *CSPP1*, *MKKS*, *RMND1*, *WDR35* genes, no copy number testing. Multiplex ligation-dependent probe amplification (MLPA) is used to detect most intragenic deletions or duplications involving at least one (*PKD2*) or two or more (*PKD1*) exons. For the *NOTCH2* gene, sequencing and deletion/duplication testing is not performed for exons 1-4. Deletions/duplications involving exons 31-46 of the *PKD1* gene and exons 1, 29, and 38-42 of the *TSC2* gene may not be reliably detected. Of note, the CEP290 intronic c.2991+1655 A>G (IVS26+1655) pathogenic variant is also evaluated.

Clinical Sensitivity

CKLD is a genetically heterogeneous group of diseases. The clinical sensitivity of sequencing and deletion/duplication analysis of the genes included in this panel depends in part on the patient's clinical phenotype and family history. Additional information about the general clinical sensitivity of each gene is included in the table below.

Gene	Protein	Inheritance	Disease Associations	Sensitivity
<i>AHI</i>	Abelson helper integration site 1; Joubertin	AR	JS 3	7-10% of JS ²⁷⁻³¹
<i>ALG8</i>	Alpha-1,3-glucosyltransferase	AD / AR	AD PLD 3, with or without kidney cysts / AR CDG 1h	~3% of isolated PLD ^{14,32}
<i>ALG9</i>	Alpha-1,2-mannosyltransferase ALG9	AR	CDG 1L / GIKANIS	Rare ³³⁻³⁴
<i>ANKS6</i>	Ankyrin repeat and sterile alpha motif domains-containing protein 6	AR	NPHP 16	~2% of NPHP ³⁵⁻³⁶
<i>BICC1</i>	BicC family RNA binding protein 1	AD	CAKUT / Cystic renal dysplasia	Rare ³⁷⁻³⁸
<i>CC2D2A</i>	Coiled-coil and C2 domain containing 2A	AR	MKS 6 / JS 9 / COACH syndrome	~4-9% of MKS ³⁹⁻⁴⁰ ~8-11% of JS ^{30-31,41-43} Rare in COACH syndrome
<i>CEP120</i>	Centrosomal protein 120KD	AR	JS 31 / SRTD 13	~1% of JS and Rare in SRTD ⁴⁴⁻⁴⁵
<i>CEP290</i>	Centrosomal protein 290KD	AR	SLS 6 / JS 5 / LCA 10 / MKS 4	Rare in SLS and MKS ^{40,46-47} ~7-10% of JS ^{27,30-31, 48-51}
<i>CEP83</i>	Centrosomal protein 83KD	AR	NPHP 18	<1% of NPHP ⁵²
<i>COL4A1</i>	Collagen type IV alpha 1 chain	AD	HANAC	Rare ⁵³⁻⁵⁴

<i>CRB2</i>	Crumbs cell polarity complex component 2	AR	AR Ventriculomegaly with Cystic Kidney Disease	Rare ⁵⁵
<i>CSPP1</i>	Centrosome and spindle pole associated protein 1	AR	JS 21	2–4% of JS ^{30–31,48,56}
<i>GANAB</i>	Glucosidase II Alpha Subunit	AD	PKD 3, with or without PLD	~2% of isolated PLD ^{6,32} <1% of ADPKD ⁶
<i>GLIS2</i>	GLIS family zinc finger 2	AR	NPHP 7	Rare ¹⁸
<i>GLIS3</i>	GLIS family zinc finger 3	AR	NDH	Rare ^{57–58}
<i>HNF1B</i>	HNF1 Homeobox B	AD	Renal cysts and diabetes syndrome (RCAD/MODY5)	40–70% of RCAD (MODY5) ^{26,59}
<i>IFT172</i>	Intraflagellar transport 172	AR	SRTD 10	Rare ¹³
<i>INVS</i>	Inversin	AR	NPHP 2	1–2% of NPHP ^{18,60–61}
<i>IQCB1</i>	IQ motif containing B1	AR	SLS 5	35/67 individuals with SLS ⁴⁶
<i>JAG1</i>	Jagged canonical Notch ligand 1	AD	ALGS	~94% of ALGS ^{62–63}
<i>LRP5</i>	Low density lipoprotein receptor-related protein 5	AD / AR	FEVR / LRP5-associated bone disorders / PLD 4 with or without kidney cysts	10–25% of FEVR ^{64–66} ~2% of isolated PLD ⁶⁷
<i>MKKS</i>	Bardet-Biedl syndrome 6 protein	AR	MKKS / BBS6	~5% of BBS ⁶⁸
<i>MKS1</i>	MKS transition zone complex subunit 1	AR	BBS 13 / MKS 1 / JS 28	~4% of BBS ⁶⁹ ~2–6% of JS ^{30–31,70} 3–14% of MKS ^{40,71–72}
<i>NEK8</i>	NIMA related kinase 8	AR	RHPD 2 / NPHP 9	Rare ⁷³
<i>NOTCH2</i>	Notch receptor 2	AD	ALGS / HCS	~1–2% of ALGS ^{74–75} ~83–100% of HCS ^{76–79}
<i>NPHP1</i>	Nephrocystin 1	AR	JS 4 / SLS 1 / NPHP 1	1–2% of JS ^{80–81} 20–25% of NPHP ^{18,82}
<i>NPHP3</i>	Nephrocystin 3	AR	MKS 7 / NPHP 3 / RHPD 1	~1–2% of NPHP ^{18,61,83} Rare in MKS and RHPD ^{84–86}
<i>OFD1</i>	OFD1, centriole and centriolar satellite protein	XL	JS 10 / OFD 1	80–85% of OFD ¹⁸⁷ Rare in JS ^{27,30,88–89}
<i>PAX2</i>	Paired box 2	AD	FSG 7 / Papillorenal syndrome	50% of papillorenal syndrome ^{90–93}
<i>PKD1</i>	Polycystin 1	AD	PKD 1	~80% of ADPKD ^{5,94}
<i>PKD2</i>	Polycystin 2	AD	PKD 2	~15% of ADPKD ^{5,94}

<i>PKHD1</i>	Fibrocystin	AR	PKD 4, with or without hepatic disease	~75% of ARPKD ⁹⁵⁻⁹⁶
<i>PMM2</i>	Phosphomannomutase 2	AR	CDG 1a	~90-100% of CDG 1a ⁹⁷⁻⁹⁹
<i>PRKCSH</i>	Hepatocystin	AD	PLD 1	~15-33% of isolated PLD ¹⁰⁰⁻¹⁰²
<i>RMND1</i>	Required for meiotic nuclear division 1 homolog	AR	Combined oxidative phosphorylation deficiency 11	Rare ¹⁰³⁻¹⁰⁵
<i>RPGRIP1L</i>	RPGRIP1 like	AR	COACH syndrome / JS 7 / MKS 5	~1-4% of JS ^{30,106-108} Rare in COACH and MKS ^{40,42}
<i>SEC61A1</i>	Sec61 translocon alpha 1 subunit	AD	ADTKD	Rare ¹⁰⁹
<i>SEC63</i>	Translocation protein SEC63 homolog	AD	PLD 2	6-15% of isolated PLD ^{67,102,110}
<i>TMEM138</i>	Transmembrane protein 138	AR	JS 16	Rare ¹¹¹
<i>TMEM216</i>	Transmembrane protein 216	AR	JS 2 / MKS 2	~3% of JS30 Rare in MKS ¹¹²
<i>TMEM231</i>	Transmembrane protein 231	AR	JS 20 / MKS 11	Rare ^{27,113-115}
<i>TMEM237</i>	Transmembrane protein 237	AR	JS 14	Rare ^{40,72,116-117}
<i>TMEM67</i>	Transmembrane protein 67	AR	COACH syndrome / JS 6 / MKS 3 / NPHP 11	~74-80% of COACH ^{42,118} ~10-28% of MKS ^{40,71} ~5-10% of JS ^{27,30} ~2-3% of NPHP ^{18,60-61}
<i>TSC1</i>	Hamartin	AD	Tuberous sclerosis 1	15-17% of TSC ¹¹⁹⁻¹²¹
<i>TSC2</i>	Tuberin	AD	Tuberous sclerosis 2	Rare in ADPKD ²¹ 50-65% of TSC ¹¹⁹⁻¹²¹
<i>TTC21B</i>	Tetratricopeptide repeat domaincontaining protein 21b	AR	NPHP 12 / SRTD 4	Rare in NPHP and SRTD ^{18,122-123}
<i>UMOD</i>	Uromodulin	AD	ADTKD	>95% of ADTKD-UMOD ¹²⁴
<i>VHL</i>	von Hippel-Lindau tumor suppressor	AD	VHL	~90-100% of VHL ¹²⁵
<i>WDR35</i>	WD repeat domain 35	AR	SRTD 7	Rare ¹²⁶

ADTKD – Autosomal Dominant Tubulointerstitial Kidney Disease ; ALGS – Alagille syndrome ; BBS – Bardet-Biedl syndrome ; CAKUT – Congenital anomalies of the kidney and urinary tract ; CDG – Congenital Disorders of Glycosylation ; FSG – Focal Segmental Glomerulosclerosis ; GIKANIS – Gillesen-KaesbachNishimura syndrome ; HANAC – Hereditary angiopathy with nephropathy, aneurysms, and muscle cramps ; HCS – Hadju-Cheney syndrome ; JS – Joubert syndrome ; MKKS – McKusick-Kaufman

syndrome ; MKS – Meckel syndrome ; NDH – Neonatal Diabetes Mellitus with Congenital Hypothyroidism ; NPHP – Nephronophthisis; OFD – Orofaciodigital syndrome ; PKD – Polycystic Kidney Disease ; PLD – Polycystic Liver Disease ; RHPD – Renal-hepatic-pancreatic dysplasia ; SLS – Senior-Loken syndrome ; SRTD – Short-Rib Thoracic Dysplasia with or without polydactyly ; VHL – von Hippel Lindau syndrome

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