Supplementary Table S1. Three heterozygous missense variants of *NRIP1* (NM_003489.3) in three individuals with CAKUT

FAMILY	Genomic position	Transcript position	Amino acid change (Het/hom)	Segregation	gnomAD (hom/het / WT allele count)	PPH2	SIFT	Mutation Taster	*M.m.*	*G.g.*	*X.t.*	*D.r.*	ACMG classification	CAKUT Phenotype	Gender	Ethnicity
B633	chr21:16,3400,58	c.456A>C	p.Gln152His (Het)	Unknown	0/6/282,350	0.98	D	DC	Q	Q	Q	Q	VUS	Left multicystic dysplastic kidney	F	Caucasian
A3460	chr21:16,339,544	c.970C>T	p.His324Tyr (Het)	Unknown	0/0/Never reported	0.74	T	DC	H	H	P	Q	VUS	Left renal agenesis	M	Macedonian
A782	chr21:16,339,171	c.1343G>A	p.Arg448Gln (Het)	Unknown	0/2/251,250	0.92	D	DC	R	R	R	R	VUS	Right renal agenesis	M	Macedonian

ACMG, American College of Medical Genetics and Genomics; CAKUT, congenital anomalies of kidneys and urinary tract; D, deleterious; DC, disease causing; Dr, *Danio rerio*; F, female; Gg, *gallus gallus*; gnomAD, genome aggregation database (https://gnomad.broadinstitute.org/); Het, heterozygous; Hom, homozygous; M, male; Mm, *Mus musculus*; PPH2 score, PolyPhen-2 prediction score (0.0–1.0; i.e.; tolerated to deleterious; variants from 0.85 to 1 are more confidently predicted to be damaging) (http://genetics.bwh.harvard.edu/pph2/); SIFT, sorting intolerant from tolerant (https://sift.bii.a-star.edu.sg/); T, tolerated; VUS, variants with unknown significance; Xt, *xenopus tropicalis*; WT, wild type.
Red background represents deleterious prediction by the in silico algorithm. Blue background represents tolerated prediction by the in silico algorithm.
The genomic coordinates are based on genome build GRCh37 (hg19), and transcript used is NM_003489.3.