Supplementary Table S2. 4 heterozygous missense variants of *NRIP1* in a control group with nephrotic syndrome

FAMILY	Genomic position	Transcript position	Amino acid change (Het/hom)	gnomAD (hom/het/ WT allele count)	PPH2	SIFT	Mutation Taster	*M.m.*	*G.g.*	*X.t.*	*D.r.*
B3848	chr21:16,337,948	c.2566C>T	p.Pro856Ser (Het)	0/1/249882	1.00	D	DC	P	P	P	P
B3271	chr21:16,338,614	c.1900T>G	p.Leu634Val (Het)	0/3/251094	1.00	D	DC	L	L	L	L
B1175	chr21:16,338,800	c.1714T>A	p.Ser572Thr (Het)	0/0/Never reported	0.99	T	DC	S	S	F	C
B3641	chr21:16,340,058	c.456A>C	p.Gln152His (Het)	0/6/282350	0.97	D	DC	Q	Q	Q	Q

D, deleterious; DC, disease causing; Dr, *Danio rerio*; gnomAD, genome aggregation database (https://gnomad.broadinstitute.org/); gnomAD, genome aggregation database (https://gnomad.broadinstitute.org/); *Gg, gallus gallus*; Het, heterozygous; hom, homozygous; 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; Xt, *xenopus tropicalis*.
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.