

Supplementary Table 1: Evolutionary conservation of novel <i>NPHS1</i> mutations found in this study.										
<u><i>NPHS1</i> novel missense mutations</u>	hg18	Conservation						Poly1	Poly2	1,000 genomes
		<u>Mm</u>	<u>Xt</u>	<u>Dr</u>	<u>Ci</u>	<u>Ce</u>	<u>Dm</u>			
Ex22: c.2930 A>G; p.Y977C	41022158	Y	Y	Y	None	E	Y	2.565	0.994	Not present
Ex6: c. 644 T>G; p.L215R	41032360	L	L	L	None	L	Y/I	2.565	0.998	Not present
hg 18: Human Mar. 2006 (NCBI36/hg18) Assembly (http://genome.ucsc.edu)										
None: no orthologue found; Mm: mouse; Xt: <i>X.tropicalis</i> ; Dr: <i>Danio rerio</i> ; Ci: <i>Ciona intestinalis</i> ; Ce: <i>Caenorhabditis elegans</i> ; Dm: <i>Drosophila melanogaster</i> ; Poly1: PolyPhen1 score (http://genetics.bwh.harvard.edu/pph/); Poly2: PolyPhen 2 score (http://genetics.bwh.harvard.edu/pph2/); 1,000 genomes: 1,000 genomes project (http://www.1000genomes.org); Polyphen 1 scores: 0-1.4: benign, 1.4-2: possibly damaging, >2: probably damaging; PolyPhen 2 scores: 0-0.7: benign, 0.7-0.9: possibly damaging, 0.9-1.0: probably damaging.										