Supplementary Table 2. Summary of phenotype-related non-*HNF1B* genetic findings. All variants were assessed according to the criteria issued by the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. PVS-very strong evidence of pathogenicity; PS – stron evidence; PM-moderate; PP-supportive. Numbers indicate specific ACMG criteria.[13]

Carrier ID	Gene	GRCh37 coordinates	Nucleotide change	Protein change	Classification	Evidence				PMID
						PVS	PS	PM	PP	
14	*GCK*	7:44191965 T/A	NM_000162.5 c.268A>T	NP_000153.1 p.Lys90Ter	pathogenic	1		2	3	
24	*PKD1*	16:2155969 C/T	NM_000296.4 c.7760G>A	NP_000287.3 p.Trp2587Ter	pathogenic	1		2	3	
12	*HNF4A*	20:43042349 G/A	NM_000457.4 c.401G>A	NP_000448.3 p.Arg134Gln	likely pathogenic			1,2	3,5	18356407
35	*KCNJ11*	11:17408648 A/G	NM_000525.3 c.991T>C	NP_000516.3 p.Ser331Pro	uncertain			2	2,3	29207974