Table S1: Clinical data of all 95 Nephrotic Syndrome Brazilian kidney transplanted children studied.

Patient ID	Gen-der	Ethnic origin	Age at NS	Histology	Parental consan-guinity	Extra-renal manifes-tation	Time to ESRF (y)	Age at Tx1 (y)	NS recurrence (Tx1)	Tx1 loss or death	Tx2	NS recurrence (Tx2)	Tx2 loss
1	F	caucasian	11	FSGS	No	No	5.0	17.7	Yes	loss after 1y			
3	F		11	Insufic mat	No	No	1.8	14.7	No				
4	F	no caucasian	6	FSGS	No	No	1.7	12.6	No				
10	M	no caucasian	2	Global Sclerosis	No	No	12.5	16.0	No				
11	F	caucasian	10	Global Sclerosis			1.8	17.0	Yes	losss after 1.6y			
12	F	caucasian	2	Mesang Proliferat		Familial NS	4.5	10.6	No				
13	M	no caucasian	2	Mesang Proliferat	No	No	2.6	6.7	No				
14	M		14	FSGS	No	No	3.5	17.5	No				
15	M	no caucasian	4	FSGS	No	No	8.5	15,0	No	loss after 6 y/CN			
16	M	caucasian	6	Insufic mat	No	No	7.5	13.8	No				
17	F	caucasian	3			Familial NS	3.3	7.7	No				
19	M		13	FSGS	No	No	1.8	16.2	No				
21	F	caucasian	11	FSGS	No	No	1.2	13.7	No				
22	M	caucasian	2	Global Sclerosis		Familial NS	5.0	8.5	No				
23	M	caucasian	4	FSGS	No	No	4.5	8.8	Yes	No			
24	M	caucasian	5	FSGS	No	Down S.	4.5	15.8	No				
26	M	no caucasian	2	Insufic mat	No	No	4.8	7.4	No	loss after8y non-adherence			
27	M	no caucasian	0.7	FSGS	No	No	9.4	11.8	No	loss after 2y/non-adherence			
28	F	caucasian	3	FSGS	No	No	6.8	13.6	Yes	loss after 4y	Yes	Yes	No
30	F	caucasian	1	Global Sclerosis	No	No	12.2	14.1	Yes	No			
31	F	caucasian	6	FSGS	No	Familial NS	7.6	13.7	No				

33	M	caucasian	0.7	FSGS	No	No	1.2	4.9	No				
35	M	caucasian	2	FSGS	No	No	2.7	5.0	Yes	No			
36	M	caucasian	1	FSGS	No	No	3.4	6.1	Yes	No			
37	F	caucasian	3	FSGS	No	No	4.5	8.5	No				
39	F	no caucasian	3	FSGS	No	No	1.0	6.9	No				
42	F	no caucasian	9	FSGS	No	Facial dysmorphism	4.8	15.1	No				
43	F	caucasian	5	FSGS	No	No	0.5	7.7	No	loss after 2y/ Polyoma virus	Yes	No	No
44	M	caucasian	9	FSGS	No	No	2.6	12.1	No				
46	F	no caucasian	1	Insufic mat		Familial NS	9.5	11.0	No				
47	F		9	MCD	No	Development delay	4.5	13.5	Yes	loss after 2m			
48	M		9	Global Sclerosis	No	No	2.4	12.0	No				
49	M	caucasian	2	FSGS	No	No	7.5	10.5	No	loss after 4d/ thrombosis	Yes	No	No
50	M	no caucasian	4		No	No	1.4	7.2	No				
52	F	caucasian	5	FSGS	No	No	2.1	8.5	No				
53	M	caucasian	2	FSGS	No	No	6.7	9.8	No	loss after 8y/CN	Yes	No	Yes
54	M	caucasian	6	FSGS	No	No	6.6	14.7	Yes	death after study/accident			
57	M	caucasian	10	FSGS	No	No	2.9	13.6	No				
59	F	no caucasian	1	FSGS	No	No	1.6	4.8	No				
60	F	no caucasian	1	MCD	No	No	2.6	5.5	No				
64	M	no caucasian	1	FSGS	No	No	7.0	13.6	No				
68	F	caucasian	7	FSGS		No	4.8	13.2	No				
69	F	caucasian	12		No	No	1.0	13.9	Yes	No			
71	M	caucasian	9	Global Sclerosis	No	Hydrocephalus	2.3	12.7	No				
73	F	caucasian	5	FSGS	No	No	4.5	11.0	No				
75	M		3	MCD	No	No	2.6	11.6	No	loss after 4d/ thormbosis	Yes	No	No

76	F	caucasian	5	FSGS		Familial NS	3.5	10.2	No				
77	M	caucasian	1	Global Sclerosis	No	No	2.5	11.0	No	loss after 9y/ CN			
78	F	caucasian	9	Mesang Proliferat	No	No	3.1	13.1	No	loss after 2y/non-adherence			
79	F	caucasian	14	FSGS	No	No	1.3	17.3	No				
81	M	caucasian	12	FSGS	No	No	0.7	14.1	No				
82	M		15	FSGS	No	No	0.9	16.8	No				
85	M	no caucasian	3	Mesang Proliferat	No	No	11.9	15.0	No				
90	F	caucasian	11	FSGS	No	No	1.9	14.8	No				
91	F	caucasian	2	FSGS	No	No	3.5	8.7	No				
94	M	caucasian	9	Global Sclerosis		No	2.6	12.6	No				
95	M	caucasian	2	FSGS	Yes	No	0.8	3.4	No	loss after 13y/CN	Yes	No	No
96	M	caucasian	1		Yes	No	5.7	9.8	No				
97	M	no caucasian	7	MCD		Familial NS	6.7	15.4	Yes	loss after 1m	Yes	Yes	Yes
98	F	caucasian	2	Mesang Proliferat	No	No	11.7	17.1	No				
99	F	caucasian	10	MCD	No	No	3.6	15.4	Yes	loss after study			
100	M	caucasian	11	Mesang Proliferat	No	No	0.6	13.2	No				
101	M	caucasian		FSGS	No	No	1.0	17.4	No				
102	M	caucasian	8	Mesang Proliferat	No	Familial NS	8.9	17.6	No				
104	M	caucasian	1	FSGS	No	No	4.4	5.7	No				
105	M	caucasian	1	FSGS	No	No	2.9	9.8	No				
107	M		2	FSGS	No	Familial NS	12.4	15.9	No				
108	M	no caucasian	13	FSGS		No	2.4	16.6	No				
109	M	caucasian	5	FSGS		No	0.6	8.0	No				
110	M		10	FSGS	No	No	2.0	17.5	Yes	loss after 3m	Yes	No	Yes
112	M	caucasian	11		No	No	0.3	11.8	No				
113	M	caucasian	10		No	No	3.4	14.4	Yes	loss after 3m			
114	M	caucasian	4	FSGS		No	2.7	7.5	No				

115	M	no caucasian	2	Mesang Proliferat	No	Familial NS	7.9	11.5	No				
116	M	caucasian	3		No	No	0.7	5.4	No				
117	M	caucasian	6	Mesang Proliferat	No	No	7.7	14.7	Yes	loss after 2y			
118	M	no caucasian	2			No	7.0	9.8	Yes	No			
119	M	caucasian	7		No	Mental retardation	0.3	8.6	Yes	No			
120	M	no caucasian	2	MCD	No	No	4.6	8.1	No				
121	M	caucasian	6	FSGS	No	Optic coloboma	3.6	12.1	No				
123	M	no caucasian	14	Insufic mat		No	1.2	15.7	No				
124	M	no caucasian	2	Mesang Proliferat		No	9.4	16.5	Yes	loss after study			
125	M	caucasian	2	FSGS	No	No	12.3	14.3	Yes	loss after 1m	Yes	Yes	No
126	F	caucasian	2	Global Sclerosis	No	No	4.8	8.8	Yes	No			
127	M	no caucasian	1	FSGS	No	No	0.4	4.3	Yes	No			
128	M	no caucasian	3	FSGS		No	14.6	18.7	No				
129	F	no caucasian	1	FSGS		No	8.5	9.5	No				
130	F	no caucasian	9			No	1.9	13.2	Yes	Yes after study			
132	M	caucasian	2	FSGS	No	No	15.2	17.5	No				
133	F	no caucasian	1	FSGS		No	12.8	15.4	Yes	death after study/cardiopathy			
134	F	no caucasian	1	FSGS	Yes	No	2.2	7.3	No				
135	M	no caucasian	2		No	Familial NS	7.7	11.2	Yes	No			
136	M	caucasian	0.8	Global Sclerosis	No	No	3.0	5.0	No				
138	M	no caucasian	0.7		No	No	6.2	8.0	No				
139	M	no caucasian	7	FSGS		No	8.1	17.0	No				

Legend: ID= patient identification; F=female, M=male, FSGS=focal segmental glomerulosclerosis; SRNS=Steroid resistant nephrotic syndrome; Mesang Prolif=Mesangial Proliferation; ESRD= End stage renal disease; NS=Nephrotic Syndrome; Tx1=first kidney transplantation; Tx2=second kidney transplantation; CN=chronic nephropathy; Insufic mat= insufficient material; Down S.= Down Syndrome

Table S2: All variants detected in 24 genes related to Nephrotic Syndrome in Brazilian kidney transplanted children.

Gene	Aminoacid change	Nucleotide change	NM	dbSNP	HGMD	SIFT	PolyPhen	Muta-tion Taster	ExAC freque ncy	Aminoacid conservation to species	PACIENTE ID	Category according to ACMG
ACTN4	p.Arg310Gln	c.929G>A	NM_004924.4	rs112545413	non pathogenic	0.03	0.002	DC	>1	T.rubripes	127	benign
ACTN4	p.Asp890Glu	c.2670C>A|	NM_004924.4| NM_144691.3	rs113969422	not described	0.03	0.001	DC	<1	T.rubripes	24	likely benign
ALG1	p.Arg232Trp	c.694C>T	NM_019109.4	rs148301670	not described	0.05	0.007	PMP	<1	F.catus	49	likely benign
ALG1	p.Met112Leu	c.334A>C	NM_019109.4	rs113219939	not described	1.00	0.00	DC	NA	G.gallus	12,16,110	likely benign
ALG1	p.Phe185Cys	c.554T>G	NM_019109.4	rs112668461	not described	0.08	0.074	DC	>1	D.rerio	12,16,110	likely benign
ALG1	p.Thr64Asn	c.191C>A	NM_019109.4	rs145474820	not described	0.11	0.948	DC	<1	D.rerio	76	likely pathogenic
APOL1	p.Arg255Lys (p.Arg271Lys)	c.764G>A	NM_001136540.1	rs136176	not described	1.00	0.00	PMP	>1	NA	many	benign
APOL1	p.Asn176Ser (p.Asn192Ser)	c.527A>G	NM_001136540.1	rs116136671	not described	0.00	0.997	PMP	>1	NA	85, 117, 129	likely benign
APOL1	p.Asn264Lys (p.Ans280Lys)	c.792C>A	NM_001136540.1	rs73885316	not described	0.22	0.905	PMP	>1	NA	116	likely benign
APOL1	p.Asn388_Tyr389del (p.Asn404AspfsTer72)	c.1160_1165delATAATT	NM_001136540.1	rs143830837	non pathogenic	NA	NA	PMP	<1	NA	15,17,22,27,35, 60,73,81,109,123	likely benign
APOL1	p.Asp337Asn (p.Asp353Asn)	c.1009G>A	NM_001136540.1	rs16996616	not described	0.17	0.369	PMP	>1	NA	26, 85, 117, 133	benign
APOL1	p.Glu150Lys (p.Glu166Lys)	c.448G>A	NM_001136540.1	rs2239785	non pathogenic	0.55	0.986	PMP	>1	NA	many	benign
APOL1	p.Gly96Arg (p.Glu112Arg)	c.286G>A	NM_001136540.1	rs41297245	not described	1.00	0.320	PMP	>1	NA	37,43,47,71,105	benign
APOL1	p.Ile384Met (p.Ile400Met)	c.1152T>G	NM_001136540.1	rs60910145	non pathogenic	0.25	0.627	PMP	>1	NA	many	benign
APOL1	p.Met228Ile (p.Met244Ile)	c.684G>A	NM_001136540.1	rs136175	non pathogenic	0.33	0.001	PMP	>1	NA	many	benign
APOL1	p.Ser10Phe (p.Ser26Phe)	c.29C>T	NM_001136540.1	rs199650512	not described	0.29	0.002	PMP	NA	NA	94	likely benign
APOL1	p.Ser342Gly (p.Ser358Gly)	c.1024A>G	NM_001136540.1	rs73885319	non pathogenic	1.00	0.00	PMP	>1	NA	many	benign
APOL1	p.Val353Glu (p.Val369Glu)	c.1058T>A	NM_001136540.1	rs143845266	DM?	0.00	0.922	PMP	<1	NA	13	likely pathogenic
CD2AP	p.Arg74Met	c.221G>T	NM_012120.2	-	DM?	0.12	0.966	PMP	<1	M.musculus	10	likely pathogenic
CD2AP	p.Asn581Lys	c.1743T>A	NM_012120.2	rs34069459	not described	0.71	0.126	PMP	>1	M.musculus	52	likely benign
CD2AP	p.Lys369Asn	c.1107G>T	NM_012120.2	-	not described	0.01	0.983	DC	NA	D.rerio	78	likely pathogenic
CD2AP	p.Lys633Arg	c.1898A>G	NM_012120.2	rs116754410	non pathogenic	0.00	1.0	DC	>1	D.rerio	17,22,52,68	likely benign
CD2AP	p.Ser527Asn	c.1580G>A	NM_012120.2	rs142570426	not described	0.22	0.839	DC	<1	G.gallus	20, 85	likely benign
CD2AP	p.Thr374Ala	c.1120A>G	NM_012120.2	rs138727736	DM?	0.74	0.00	PMP	>1	M.mulatta	121	likely benign
COL4A3	p.Arg1011Cys	c.3031C>T	NM_000091.4	rs73996408	not described	0.04	0.023	PMP	<1	F.catus	4	likely benign
COL4A3	p.Arg408His	c.1223G>A	NM_000091.4	rs34505188	not described	0.19	0.999	PMP	>1	M.mulatta	many	benign
COL4A3	p.Asn316Ile	c.947A>T|	NM_000091.4	-	not described	0.06	0.998	PMP	NA	M.musculus	3	likely benign
COL4A3	p.Asp1269Glu	c.3807C>A|	NM_000091.4	rs57611801	not described	0.44	0.022	DC	>1	M.musculus	many	benign
COL4A3	p.Asp1347Glu	c.4041C>A|	NM_000091.4	rs73996414	not described	0.00	0.063	PMP	>1	F.catus	36	benign
COL4A3	p.Asp326Tyr	c.976G>T	NM_000091.4	rs55703767	not described	0.13	0.989	PMP	>1	F.catus	many	benign
COL4A3	p.Gln1495Arg	c.4484A>G	NM_000091.4	rs77964815	not described	0.40	0.659	DC	>1	G.gallus	42	likely benign
COL4A3	p.Glu162Gly	c.485A>G|	NM_000091.4	rs6436669	not described	1.00	0.997	PMP	>1	M.mulatta	many	benign

COL4A3	p.Glu269Lys	c.805G>A|	NM_000091.4	rs80109666	not described	0.56	0.751	PMP	>1	P.troglodytes	90,107,121	benign
COL4A3	p.Gly43Arg	c.127G>C	NM_000091.4	rs13424243	not described	0.01	1.0	PMP	>1	M.musculus	many	likely benign
COL4A3	p.Gly566Ala	c.1697G>C|	NM_000091.4	-	not described	0.00	0.999	DC	NA	D.rerio	132	likely pathogenic
COL4A3	p.His451Arg	c.1352A>G	NM_000091.4	rs11677877	non pathogenic	0.67	0.145	PMP	>1	M.mulatta	many	benign
COL4A3	p.Leu141Pro	c.422T>C|	NM_000091.4	rs10178458	not described	1.00	0.042	PMP	>1	Not conserved	many	benign
COL4A3	p.Leu1474Pro	c.4421T>C|	NM_000091.4	rs200302125	pathogenic	0.00	1.0	DC	<1	D.rerio	121	likely pathogenic
COL4A3	p.Pro574Leu	c.1721C>T|	NM_000091.4	rs28381984	not described	0.00	1.0	PMP	>1	D.rerio	many	benign
COL4A3	p.Thr911Ile	c.2732C>T|	NM_000091.4	-	not described	0.45	0.00	PMP	NA	P.troglodytes	128	likely benign
COL4A3	p.Val92Glu	c.275T>A|	NM_000091.4	-	not described	1.00	0.833	PMP	<1	Not conserved	117	likely benign
COL4A4	p.Ala1078Val	c.3233C>T	NM_000092.4	rs79143859	not described	0.67	0.919	PMP	>1	M.musculus	30	likely benign
COL4A4	p.Ala931Thr	c.2791G>A	NM_000092.4	rs75875272	not described	0.45	0.00	PMP	>1	Not conserved	24	likely benign
COL4A4	p.Arg1560His	c.4679G>A	NM_000092.4	-	not described	0.09	0.990	PMP	<1	Not conserved	136	likely benign
COL4A4	p.Glu594Gly	c.1781A>G	NM_000092.4	rs35998949	not described	0.43	0.003	PMP	>1	P.troglodytes	36,46,47,54,119	benign
COL4A4	p.Gly545Ala	c.1634G>C	NM_000092.4	rs1800516	non pathogenic	0.00	1.0	DC	>1	P.troglodytes	3,13,32,42,59	benign
COL4A4	p.Gly999Glu	c.2996G>A	NM_000092.4	rs13027659	DM?	0.00	1.0	DC	>1	D.rerio	125	likely benign
COL4A4	p.Ile6Thr	c.17T>C	NM_000092.4	rs16823264	not described	0.26	0.00	PMP	>1	P.troglodytes	24	benign
COL4A4	p.Ile967Val	c.2899A>G	NM_000092.4	rs80243096	not described	1.00	0.001	PMP	>1	P.troglodytes	30	likely benign
COL4A4	p.Met1552Ile	c.4656G>A	NM_000092.4	rs77104306	not described	0.00	0.399	DC	>1	M.musculus	30,35	likely benign
COL4A4	p.Pro1004Leu	c.3011C>T	NM_000092.4	rs1800517	not described	0.00	0.634	PMP	>1	D.rerio	many	benign
COL4A4	p.Pro482Ser	c.1444C>T	NM_000092.4	rs2229814	not described	0.57	0.00	PMP	>1	Not conserved	many	benign
COL4A4	p.Pro759Leu	c.2276C>T	NM_000092.4	rs36121515	not described	0.01	0.911	DC	>1	P.troglodytes	49,73,94,117,121	benign
COL4A4	p.Ser1403Pro	c.4207T>C	NM_000092.4	rs1800518: rs3752895	not described	0.35	0.00	PMP	>1	Not conserved	many	benign
COL4A4	p.Val1327Met	c.3979G>A	NM_000092.4	rs2229813	not described	0.34	0.00	PMP	>1	Not conserved	many	benign
COL4A4	p.Val670Ile	c.2008G>A	NM_000092.4	rs34236495	not described	0.78	0.017	PMP	>1	P.troglodytes	49,117,121	benign
COL4A5	p.Ala430Asp	c.1289C>A	NM_033380.2	rs142883891	not described	0.29	0.090	PMP	>1	P.troglodytes	31	likely benign
COL4A5	p.Asn1010Ser	c.3029A>G	NM_033380.2	rs151077921	not described	0.52	0.001	PMP	>1	P.troglodytes	68	likely benign
COL4A5	p.Gly1199Arg	c.3595G>A	NM_033380.2	-	not described	0.00	1.0	DC	NA	P.troglodytes	85	likely benign
COL4A5	p.Gly681Asp	c.2042G>A	NM_033380.2	rs104886158	pathogenic	0.00	1.0	DC	NA	P.troglodytes	132	likely pathogenic
COL4A5	p.Gly42Ser	c.124G>A	NM_033380.2	rs371351149	not described	0.04	0.013	DC	NA	P.troglodytes	47	likely benign
COL4A5	p.Ile444Ser	c.1331T>G	NM_033380.2	rs2272946	DM?	0.57	0.017	PMP	>1	P.troglodytes	123	benign
COL4A5	p.Pro1050Ser	c.3148C>T	NM_033380.2	rs143945573	not described	0.01	0.136	DC	<1	P.troglodytes	79	likely benign
COL4A5	p.Pro712Thr	c.2134C>A	NM_033380.2	-	not described	0.13	0.580	DC	NA	P.troglodytes	110	likely benign
COL4A5	p.Thr1403Ser	c.4210C>G	NM_033380.2	rs151278542	not described	0.45	error	DC	NA	P.troglodytes	49	likely benign
COQ2	p.Asn196Ser	c.587A>G	NM_015697.7	rs150295921	not described	1.00	error	PMP	>1	P.troglodytes	4	likely benign
COQ2	p.Phe383Leu	c.1147T>C	NM_015697.7	-	not described	0.01	error	DC	NA	D.rerio	95	likely pathogenic
COQ2	p.Thr192Ala	c.574A>G	NM_015697.7	rs144913206	not described	0.04	0.00	PMP	<1	M.mulatta	4	likely benign
COQ2	p.Val393Ala	c.1178T>C	NM_015697.7	rs148156462	non pathogenic	0.00	error	PMP	>1	F.catus	128	benign
COQ2	p.Val66Leu	c.196G>T	NM_015697.7	rs6818847	not described	0.10	0.00	PMP	>1	M.mulatta	many	benign
INF2	p.Ala729Thr	c.2185G>A	NM_022489.3	-	not described	0.42	0.009	PMP	<1	P.troglodytes	123	likely benign
INF2	p.Arg1045Gln	c.3134G>A	NM_022489.3	rs200369827	DM?	0.62	0.006	PMP	<1	P.troglodytes	71	likely pathogenic
INF2	p.Arg877Gln	c.2630G>A	NM_022489.3	rs142678449	not described	0.07	0.986	PMP	>1	P.troglodytes	36	likely benign
INF2	p.Gly1160Ser	c.3478G>A	NM_022489.3	rs9672065	not described	0.81	0.00	PMP	>1	P.troglodytes	119,127	benign
INF2	p.Pro1096Ser	c.3286C>T	NM_022489.3	rs34251364	not described	0.00	0.300	PMP	>1	P.troglodytes	many	benign
INF2	p.Ser23Thr	c.67T>A	NM_022489.3	-	not described	0.03	0.327	PMP	<1	P.troglodytes	116	likely benign
INF2	p.Thr1135Met	c.3404C>T	NM_022489.3	rs3803311	not described	0.01	0.928	PMP	>1	P.troglodytes	13, 127	likely benign

LAMB2	p.Ala1765Thr	|c.5293G>A	NM_002292.3	rs74951356	not described	0.75	0.039	PMP	>1	M.musculus	1, 30	likely benign
LAMB2	p.Arg1592Trp	c.4774C>T	NM_002292.3	rs61729458	not described	0.00	1.0	DC	>1	G.gallus	60,127	likely benign
LAMB2	p.Asn1292Ile	c.3875A>T	NM_002292.3	rs148246465	not described	0.13	0.996	DC	<1	G.gallus	119	likely benign
LAMB2	p.Asn880Ser	c.2639A>G	NM_002292.3	-	not described	0.00	0.240	DC	<1	D.rerio	68	likely pathogenic
LAMB2	p.Glu987Lys	c.2959G>A	NM_002292.3	rs34759087	not described	0.02	0.704	DC	>1	M.musculus	many	benign
LAMB2	p.Gly914Arg	c.2740G>A	NM_002292.3	rs35713889	non pathogenic	0.05	1.0	DC	>1	D.rerio	19,47,50,108,117, 119	likely benign
LAMB2	p.Ile909Thr	c.2726T>C	NM_002292.3	rs201756319	not described	0.20	0.002	DC	<1	M.musculus	13	likely benign
MYH9	p.Ala1939Thr	c.5815G>A	NM_002473.4	rs115031369	not described	0.53	0.00	PMP	<1	F.catus	116	likely benign
MYH9	p.Gly1715Ser	c.5143G>A|	NM_002473.4	rs148109368	not described	0.16	0.016	DC	<1	G.gallus	138,139	likely benign
MYH9	p.Ser1606Leu	c.4817C>T	NM_002473.4	rs145319741	not described	0.13	0.577	DC	<1	G.gallus	123	likely benign
MYH9	p.Gln3Glu	c.7C>G	NM_002473.4	rs56200894	not described	0.01	0.526	DC	<1	M.mulatta	52	likely benign
MYH9	p.Ile1626Val	c.4876A>G	NM_002473.4	rs2269529	not described	0.20	0.042	PMP	>1	M.mulatta	68,104,112,113,12 6,128	benign
MYH9	p.Lys1775Glu	c.5323A>G	NM_002473.4	rs145139708	not described	0.00	0.120	DC	<1	M.mulatta	76	likely benign
MYH9	p.Thr1416Met	c.4247C>T	NM_002473.4	-	not described	0.01	0.995	DC	<1	M.mulatta	68	likely benign
MYH9	p.Val782Ile	c.2344G>A	NM_002473.4	rs139966058	not described	0.91	0.002	DC	<1	G.gallus	135	likely benign
MYO1E	p.Arg169*	c.505C>T	NM_004998.3	-	not described	NA	NA	DC	NA	Not conserved	46,49	PATHOGENIC
MYO1E	p.Ile531Met	c.1593C>G	NM_004998.3	rs140447165	DM?	0.00	0.095	DC	NA	D.rerio	99,125	likely pathogenic
NPHS1	p.Arg408Gln	c.1223G>A	NM_004646.3	rs33950747	DM?	0.55	1.0	DC	>1	P.troglodytes	33,37,42,81,94,12 4,126	benign
NPHS1	p.Asn1077Ser	c.3230A>G	NM_004646.3	rs4806213	DM?	0.02	0.010	PMP	>1	P.troglodytes	many	benign
NPHS1	p.Pro264Arg	c.791C>G	NM_004646.3	rs34982899	DM?	0.17	0.675	PMP	>1	P.troglodytes	32,33,39	likely benign
NPHS1	p.Thr294Ile	c.881C>T	NM_004646.3	rs113825926	DM?	0.06	0.097	PMP	>1	P.troglodytes	130	likely benign
NPHS1	p.Arg1140Ser	c.3418C>A	NM_004646.3	rs143092783	not described	0.15	0.010	PMP	>1	P.troglodytes	35	likely benign
NPHS1	p.Asn188Ile	c.563A>T	NM_004646.3	rs145125791	pathogenic	0.56	0.573	PMP	<1	P.troglodytes	47,113	likely pathogenic
NPHS1	p.Leu392Pro	c.1175T>C	NM_004646.3	rs34320609	not described	0.25	0.321	PMP	>1	P.troglodytes	109,115,129	likely benign
NPHS1	p.Val43Ala	c.128T>C	NM_004646.3	rs140626538	not described	0.09	0.390	PMP	<1	P.troglodytes	85	likely benign
NPHS1	p.Val991Leu	c.2971G>C	NM_004646.3	rs34736717	not described	1.00	0.00	PMP	>1	P.troglodytes	3,17,22,60,85,116, 120,129	benign
NPHS2	p.Ala208Thr	c.622G>A	NM_014625.2	rs200587413	pathogenic	1.00	0.037	DC	<1	M.musculus	31	likely pathogenic
NPHS2	p.Ala242Val	c.725C>T	NM_014625.2	rs61747727	DM?	0.01	0.992	DC	>1	M.musculus	119	benign
NPHS2	p.Arg138*	c.412C>T	NM_014625.2	rs74315343	pathogenic	NA	NA	DC	<1	Not conserved	60	PATHOGENIC
NPHS2	p.Arg229Gln	c.686G>A	NM_014625.2	rs61747728	non pathogenic	0.21	0.903	DC	>1	G.gallus	11,13,42,43,54,73, 79,128	benign
NPHS2	p.Gln215*	c.643C>T	NM_014625.2	-	pathogenic	NA	NA	DC	NA	G.gallus	12, 101	PATHOGENIC
NPHS2	p.Glu310Lys	|c.928G>A	NM_014625.2	-	pathogenic	0.06	0.992	DC	NA	P.troglodytes	73,128	likely pathogenic
NPHS2	p.Val260Glu	|c.779T>A	NM_014625.2	-	pathogenic	0.00	1.0	DC	<1	D.rerio	60,115	PATHOGENIC
PLCE1	p.Ala76Val	c.227C>T	NM_016341.3	rs61749238	not described	0.00	0.010	PMP	<1	P.troglodytes	119	likely benign
PLCE1	p.Arg1575Pro	c.4724G>C|	NM_016341.3	rs2274224	non pathogenic	0.43	0.00	PMP	>1	Not conserved	many	benign
PLCE1	p.Arg548Leu	c.1643G>T	NM_016341.3	rs17417407	DM?	0.00	0.997	PMP	>1	M.mulatta	many	likely benign
PLCE1	p.Arg548Leufs	c.1643G>T|c.1641_1641delC	NM_016341.3	rs369152754	DM?			PMP	>1	NA	126	likely benign
PLCE1	p.Asn1578Ser	c.4733A>G|	NM_016341.3	rs61732525	not described	0.58	0.010	PMP	>1	M.mulatta	44,123	likely benign
PLCE1	p.Asp390Gly	c.1169A>G	NM_016341.3	-	not described	0.28	0.00	PMP	NA	P.troglodytes	98	likely benign
PLCE1	p.Gly1094Val	c.3281G>T	NM_016341.3	rs61732523	not described	0.00	0.999	DC	<1	M.mulatta	119	likely benign
PLCE1	p.His1927Arg	c.5780A>G	NM_016341.3	rs2274223	non pathogenic	1.00	0.00	PMP	>1	M.mulatta	many	benign
PLCE1	p.Ile523Val	c.1567A>G	NM_016341.3	rs61751494	not described	0.54	0.006	PMP	<1	M.mulatta	52,116	likely benign
PLCE1	p.Lys2173Arg	c.6518A>G	NM_016341.3	rs111929795	pathogenic	0.22	0.998	DC	<1	M.mulatta	23,128	likely pathogenic

PLCE1	p.Pro1890Leu	c.5669C>T	NM_016341.3	rs58539480	DM?	0.35	0.994	DC	>1	M.mulatta	128,13	likely benign
PLCE1	p.Ser1000Asn	c.2999G>A	NM_016341.3	rs61751498	not described	0.48	0.002	PMP	<1	P.troglodytes	33,52,116	likely benign
PLCE1	p.Ser469Thr	c.1405T>A	NM_016341.3	rs17508082	not described	0.00	0.677	PMP	>1	M.mulatta	many	likely benign
PLCE1	p.Ser761Leu	c.2282C>T	NM_016341.3	rs376554016	not described	0.02	0.448	DC	<1	M.mulatta	110	likely benign
PLCE1	p.Thr1777Ile	c.5330C>T	NM_016341.3	rs3765524	non pathogenic	1.00	0.00	PMP	>1	Not conserved	many	benign
PLCE1	p.Tyr401His	c.1201T>C	NM_016341.3	rs201401363	not described	0.02	0.00	PMP	<1	P.troglodytes	13	likely benign
PLCE1	p.Val894Leu	c.2680G>C	NM_016341.3	-	not described	1.00	0.00	PMP	NA	P.troglodytes	43	likely benign
PMM2	p.Arg84Ser	c.252A>T	NM_000303.2	-	not described	0.11	0.00	PMP	<1	Not conserved	71	likely benign
PMM2	p.Arg141His	c.422G>A	NM_000303.2	rs28936415	pathogenic	0.00	0.993	DC	>1	D.rerio	113	likely pathogenic
PMM2	p.Phe157Ser	c.470T>C	NM_000303.2	rs190521996	pathogenic	0.00	1.0	DC	<1	D.rerio	31	likely pathogenic
PTPRO	p.Arg1157Gln	c.3470G>A	NM_030667.2	rs151225487	not described	0.00	0.957	DC	>1	P.troglodytes	81	likely benign
PTPRO	p.Asn370Lys	c.1110C>G	NM_030667.2	rs61754411	not described	0.00	0.958	DC	>1	P.troglodytes	46,75,100,128	likely benign
PTPRO	p.Val443Ile	c.1327G>A	NM_030667.2	rs71459181	not described	0.03	0.716	DC	>1	G.gallus	53	likely benign
SCARB2	p.Arg121Gln	c.362G>A	NM_005506.3	rs73826386	not described	0.26	0.126	PMP	>1	M.mulatta	13,90,119	likely benign
SCARB2	p.Asp127Tyr	c.379G>T	NM_005506.3	rs148022786	not described	0.02	1.0	DC	<1	M.mulatta	128	likely benign
SCARB2	p.Met159Val	c.475A>G	NM_005506.3	rs143655258	not described	0.04	0.00	PMP	>1	M.mulatta	59,85,90,96,137	likely benign
SCARB2	p.Val396Ile	c.1186G>A	NM_005506.3	rs2228380	not described	0.51	0.00	PMP	>1	M.mulatta	12,16,39,117	likely benign
SMARCAL1	p.Arg114His	c.341G>A	NM_001127207.1	rs11555797	not described	0.18	0.733	PMP	>1	M.mulatta	124	likely benign
SMARCAL1	p.Arg764Gln	c.2291G>A	NM_001127207.1	rs267607071	pathogenic	0.00	1.0	DC	<1	G.gallus	43	likely pathogenic
SMARCAL1	p.Glu377Gln	c.1129G>C	NM_001127207.1	rs2066518	DM?	0.02	0.425	PMP	>1	G.gallus	37,42,44,47,97,130	benign
SMARCAL1	p.Ile548del	c.1642_1644delATT	NM_001127207.1	rs119473036	not described	NA	NA	PMP	NA	NA	128	PATHOGENIC
SMARCAL1	p.Leu322His	c.965T>A	NM_001127207.1	rs150148936	not described	0.01	0.956	PMP	<1	M.musculus	105	likely benign
SMARCAL1	p.Pro301Ala	c.901C>G	NM_001127207.1	rs146084305	not described	0.00	0.663	DC	>1	G.gallus	53	likely benign
SMARCAL1	p.Ser315Arg	c.945C>G	NM_001127207.1	rs2066522	not described	0.01	0.802	PMP	>1	M.mulatta	21	benign
SMARCAL1	p.Val512Met	c.1534G>A	NM_001127207.1	rs35087810	not described	0.14	0.977	DC	>1	M.musculus	24	likely benign
TRPC6	p.Ala404Val	c.1211C>T	NM_004621.5	rs36111323	non pathogenic	0.32	1.0	PMP	>1	G.gallus	49	benign
TRPC6	p.Tyr775Cys	c.2324A>G	NM_004621.5	-	not described	0.06	0.004	DC	<1	G.gallus	19	likely benign
WT1	p.Cys453Arg	c.1357T>C	NM_024426.4	rs1353492: rs1353493	pathogenic	0.00	1.0	DC	NA	NA	116	likely pathogenic
ZMPSTE24	p.Tyr70fs	c.207_208insT	NM_005857.4	-	not described	NA	NA	DC	NA	NA	35	likely pathogenic

Legend: dbSNP=single-nucleotide polymorphism database (http://www.ncbi.nlm.nih.gov/projects/SNP/); HGMD: Human Genome Mutation Database professional (DM?= questionable disease mutation); Prediction programs: SIFT Score: Ranges from 0 to 1. The amino acid substitution is predicted damaging if the score is ≤0.05, and tolerated if the score is > 0.05 (sift.jcvi.org), PolyPhen 2 score: ≤0.5 benign; ≥0.75 possibly damaging (genetics.bwh.harvard.edu/pph2), Mutation taster: (mutationtaster.org): DC= disease causing, PMP= nonpathogenic polymorphism; ExAC=Exome Aggregation Consortium (ExAC (exac.broadinstitute.org) used to achieve known population frequency

data; Aa conservation=aminoacid conservation to species at Mutation Taster database; ID= patient identification; ACMG (American college of medical genetics and genomics – standards and guidelines for the interpretation of sequence of variants, 2015)