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Full name:	Nephrotic syndrome, FSGS, Alport syndrome (76 genes) - IPG
Abbreviation:	FSGS
Type of panel:	Custom panel
Provider:	Home made
Version number:	Version 7
Laboratory:	Centre de Génétique-Institut de Pathologie et de Génétique (IPG)
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Related Diseases

- Alport syndrome
- Autosomal dominant Alport syndrome
- Autosomal recessive Alport syndrome
- CAMOS syndrome
- Congenital nephrotic syndrome, Finnish type
- Denys-Drash syndrome
- Fabry disease
- Familial idiopathic steroid-resistant nephrotic syndrome with diffuse mesangial proliferation
- Familial idiopathic steroid-resistant nephrotic syndrome with diffuse mesangial sclerosis
- Familial idiopathic steroid-resistant nephrotic syndrome with focal segmental hyalinosis
- Familial idiopathic steroid-resistant nephrotic syndrome with minimal changes
- Frasier syndrome
- Galloway-Mowat syndrome
- Genetic steroid-resistant nephrotic syndrome
- Hemolytic uremic syndrome with DGKE deficiency
- Idiopathic steroid-sensitive nephrotic syndrome with diffuse mesangial proliferation
- Idiopathic steroid-sensitive nephrotic syndrome with focal segmental hyalinosis
- Idiopathic steroid-sensitive nephrotic syndrome with minimal change

- Infantile nephronophthisis
- Jeune syndrome
- LAMB2-related infantile-onset nephrotic syndrome
- Leigh syndrome with nephrotic syndrome
- MYH9-related disease
- Nail-patella-like renal disease
- Nephrotic syndrome-epidermolysis bullosa-sensorineural deafness syndrome
- Pierson syndrome
- Renal coloboma syndrome
- Renal hypoplasia, bilateral
- Sporadic idiopathic steroid-resistant nephrotic syndrome with focal segmental hyalinosis
- Sporadic idiopathic steroid-resistant nephrotic syndrome with minimal changes
- Ventriculomegaly-cystic kidney disease
- WAGR syndrome
- X-linked Alport syndrome
- X-linked Alport syndrome-diffuse leiomyomatosis

Related Analytes

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
ACTN4	100.00	1	NM_004924.6
AMN	100.00	1	NM_030943.4
ANLN	100.00	1	NM_018685.5
APOA1	100.00	1	NM_000039.3
APOL1	100.00	1	NM_003661.4
ARHGAP24	100.00	1	NM_001025616.3
ARHGDIA	100.00	1	NM_004309.6
AVIL	100.00	1	NM_006576.4
B2M	100.00	1	NM_004048.4

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
C3	100.00	1	NM_000064.4
CD151	100.00	1	NM_004357.5
CD2AP	100.00	1	NM_012120.3
CLCN5	100.00	1	NM_001127898.4
COL4A3	100.00	1	NM_000091.5
COL4A4	100.00	1	NM_000092.5
COL4A5	100.00	1	NM_033380.3
COL4A6	100.00	1	NM_033641.4
COQ2	100.00	1	NM_001358921.2
COQ6	100.00	1	NM_182476.3
COQ8A	100.00	1	NM_020247.5
COQ8B	100.00	1	NM_024876.4
CRB2	100.00	1	NM_173689.7
CUBN	100.00	1	NM_001081.4
DGKE	100.00	1	NM_003647.3
EMP2	100.00	1	NM_001424.6
FGA	100.00	1	NM_021871.4
FN1	100.00	1	NM_212482.4
G6PC1	100.00	1	NM_000151.4

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
GLA	100.00	1	NM_000169.3
GON7	100.00	1	NM_032490.5
GSN	100.00	1	NM_198252.3
INF2	100.00	1	NM_022489.4
ITGA3	100.00	1	NM_002204.4
KANK2	100.00	1	NM_001136191.3
KIRREL1	100.00	1	NM_018240.7
LAGE3	100.00	1	NM_006014.5
LAMA5	100.00	1	NM_005560.6
LAMB2	100.00	1	NM_002292.4
LMX1B	100.00	1	NM_001174147.2
LRP2	100.00	1	NM_004525.3
LYZ	100.00	1	NM_000239.3
MAGI2	100.00	1	NM_012301.4
MYH9	100.00	1	NM_002473.6
MYO1E	100.00	1	NM_004998.4
NOS1AP	100.00	1	NM_014697.3
NPHS1	100.00	1	NM_004646.4
NPHS2	100.00	1	NM_014625.4

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
NUP107	100.00	1	NM_020401.4
NUP133	100.00	1	NM_018230.3
NUP160	100.00	1	NM_015231.3
NUP205	100.00	1	NM_015135.3
NUP85	100.00	1	NM_024844.5
NUP93	100.00	1	NM_014669.5
OCRL	100.00	1	NM_000276.4
OSGEP	100.00	1	NM_017807.4
PAX2	100.00	1	NM_000278.5
PDSS2	100.00	1	NM_020381.4
PLCE1	100.00	1	NM_016341.4
PMM2	0.00	1	NM_000303.2 / only position Chr16(GRCh38):g.8797616 87976
PODXL	94.00	1	NM_001018111.3
PTPRO	100.00	1	NM_030667.3
SARS2	100.00	1	NM_017827.4
SGPL1	100.00	1	NM_003901.4
SLC35A1	100.00	1	NM_006416.5
SMARCAL1	100.00	1	NM_014140.4
TBC1D8B	100.00	1	NM_017752.3

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
TP53RK	100.00	1	NM_033550.4
TPRKB	100.00	1	NM_016058.5
TRPC6	100.00	1	NM_004621.6
TTC21B	100.00	1	NM_024753.5
TTR	100.00	1	NM_000371.4
UMOD	100.00	1	NM_003361.4
WDR4	100.00	1	NM_018669.6
WDR73	100.00	1	NM_032856.5
WT1	100.00	1	NM_024426.6
XPO5	100.00	1	NM_020750.3
YRDC	100.00	1	NM_024640.4