

Full name:	Nephropathies, hereditary (219 genes) - KUL
Description:	https://firebasestorage.googleapis.com/v0/b/uz-laboboeken.appspot.com/o/GHB_CME%2FNefro%20-%20NGS%20-%20full%20panel.pdf?alt=media&token=e2ca0253-44f6-4107-b086-2c1d6236ddce
Version number:	Nefro_full_v5
Laboratory:	<u>Centrum Menselijke Erfelijkheid - KUL</u>
Created:	03 Jul 2019 - 09:27
Changed:	07 Aug 2023 - 12:41

Related Analytes

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>ACE</u>	95.00	0	NM_000789.4
<u>ACTN4</u>	95.00	0	NM_004924.6
<u>AGT</u>	95.00	0	NM_001384479.1
<u>AGTR1</u>	95.00	0	NM_031850.4
<u>AGXT</u>	95.00	0	NM_000030.3
<u>ALG5</u>	95.00	0	NM_013338.5
<u>ALG8</u>	95.00	0	NM_024079.5
<u>ALG9</u>	95.00	0	NM_024740.2
<u>AMN</u>	95.00	0	NM_030943.4
<u>ANKS6</u>	95.00	0	NM_173551.5
<u>ANLN</u>	95.00	0	NM_018685.5

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>ANOS1</u>	95.00	0	NM_000216.4
<u>AP2S1</u>	95.00	0	NM_004069.6
<u>APOA1</u>	95.00	0	NM_000039.3
<u>APOA2</u>	95.00	0	NM_001643.2
<u>APOC2</u>	95.00	0	NM_000483.5
<u>APOE</u>	95.00	0	NM_000041.4
<u>APOL1</u>	95.00	0	NM_003661.4
<u>APRT</u>	95.00	0	NM_000485.3
<u>ARHGAP24</u>	95.00	0	NM_001025616.3
<u>ARHGDIA</u>	95.00	0	NM_001185077.3
<u>ATP6V0A4</u>	95.00	0	NM_020632.3
<u>ATP6V1B1</u>	95.00	0	NM_001692.4
<u>BMP4</u>	95.00	0	NM_001202.6
<u>BNC2</u>	95.00	0	NM_017637.6
<u>BSND</u>	95.00	0	NM_057176.3
<u>C3</u>	95.00	0	NM_000064.4
<u>CA2</u>	95.00	0	NM_000067.3
<u>CACNA1D</u>	95.00	0	NM_000720.4
<u>CACNA1H</u>	95.00	0	NM_021098.3
<u>CASR</u>	95.00	0	NM_000388.4

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>CD2AP</u>	95.00	0	NM_012120.3
<u>CD46</u>	95.00	0	NM_002389.4
<u>CDC73</u>	95.00	0	NM_024529.5
<u>CDK20</u>	95.00	0	NM_001039803.3
<u>CEP164</u>	95.00	0	NM_014956.5
<u>CEP290</u>	95.00	0	NM_025114.4
<u>CEP83</u>	95.00	0	NM_016122.3
<u>CFB</u>	95.00	0	NM_001710.6
<u>CFH</u>	95.00	0	NM_000186.4
<u>CFHR1</u>	95.00	0	NM_002113.3
<u>CFHR3</u>	95.00	0	NM_021023.6
<u>CFHR5</u>	95.00	0	NM_030787.4
<u>CFI</u>	95.00	0	NM_000204.5
<u>CLCN2</u>	95.00	0	NM_004366.6
<u>CLCN5</u>	95.00	0	NM_000084.5
<u>CLCNKA</u>	95.00	0	NM_004070.4
<u>CLCNKB</u>	95.00	0	NM_000085.5
<u>CLDN10</u>	95.00	0	NM_006984.5
<u>CLDN16</u>	95.00	0	NM_006580.4
<u>CLDN19</u>	95.00	0	NM_148960.3

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>CNNM2</u>	95.00	0	NM_017649.5
<u>COL4A1</u>	95.00	0	NM_001845.6
<u>COL4A3</u>	95.00	0	NM_000091.5
<u>COL4A4</u>	95.00	0	NM_000092.5
<u>COL4A5</u>	95.00	0	NM_000495.5
<u>COQ2</u>	95.00	0	NM_015697.9
<u>COQ6</u>	95.00	0	NM_182476.3
<u>COQ8B</u>	95.00	0	NM_024876.4
<u>CRB2</u>	95.00	0	NM_173689.7
<u>CTNS</u>	95.00	0	NM_004937.3
<u>CUBN</u>	95.00	0	NM_001081.4
<u>CUL3</u>	95.00	0	NM_003590.5
<u>CYP11B1</u>	95.00	0	NM_000497.4
<u>CYP11B2</u>	95.00	0	NM_000498.3
<u>CYP17A1</u>	95.00	0	NM_000102.4
<u>CYP24A1</u>	95.00	0	NM_000782.5
<u>DAAM2</u>	95.00	0	NM_001201427.2
<u>DGKE</u>	95.00	0	NM_003647.3
<u>DLEC1</u>	95.00	0	NM_182643.3
<u>DNAJB11</u>	95.00	0	NM_016306.6

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>DSTYK</u>	95.00	0	NM_015375.3
<u>DZIP1L</u>	95.00	0	NM_173543.3
<u>EGF</u>	95.00	0	NM_001963.6
<u>EHHADH</u>	95.00	0	NM_001966.4
<u>EMP2</u>	95.00	0	NM_001424.6
<u>EYA1</u>	95.00	0	NM_000503.6
<u>FAM20A</u>	95.00	0	NM_017565.4
<u>FAN1</u>	95.00	0	NM_014967.5
<u>FAT1</u>	95.00	0	NM_005245.4
<u>FGA</u>	95.00	0	NM_021871.4
<u>FGF20</u>	95.00	0	NM_019851.3
<u>FGF23</u>	95.00	0	NM_020638.3
<u>FN1</u>	95.00	0	NM_212482.4
<u>FOXC1</u>	95.00	0	NM_001453.3
<u>FOXC2</u>	95.00	0	NM_005251.3
<u>FOXI1</u>	95.00	0	NM_012188.5
<u>FXVD2</u>	95.00	0	NM_001680.5
<u>GANAB</u>	95.00	0	NM_198335.4
<u>GATA3</u>	95.00	0	NM_001002295.2
<u>GATM</u>	95.00	0	NM_001482.3

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>GDNF</u>	95.00	0	NM_000514.4
<u>GLA</u>	95.00	0	NM_000169.3
<u>GLIS2</u>	95.00	0	NM_032575.3
<u>GNA11</u>	95.00	0	NM_002067.5
<u>GREB1L</u>	95.00	0	NM_001142966.3
<u>GRHPR</u>	95.00	0	NM_012203.2
<u>GRIP1</u>	95.00	0	NM_021150.4
<u>GSN</u>	95.00	0	NM_000177.5
<u>HNF1A</u>	95.00	0	NM_000545.8
<u>HNF1B</u>	95.00	0	NM_000458.4
<u>HNF4A</u>	95.00	0	NM_175914.5
<u>HOGA1</u>	95.00	0	NM_138413.4
<u>HOXA13</u>	95.00	0	NM_000522.5
<u>HPRT1</u>	95.00	0	NM_000194.3
<u>HSD11B2</u>	95.00	0	NM_000196.4
<u>IFT140</u>	95.00	0	NM_014714.4
<u>IFT81</u>	95.00	0	NM_014055.4
<u>INF2</u>	95.00	0	NM_022489.4
<u>INVS</u>	95.00	0	NM_014425.5
<u>ITGA8</u>	95.00	0	NM_003638.3

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>ITSN1</u>	95.00	0	NM_003024.3
<u>ITSN2</u>	95.00	0	NM_147152.3
<u>JAG1</u>	95.00	0	NM_000214.3
<u>KANK2</u>	95.00	0	NM_001136191.3
<u>KCNA1</u>	95.00	0	NM_000217.3
<u>KCNJ1</u>	95.00	0	NM_000220.6
<u>KCNJ10</u>	95.00	0	NM_002241.5
<u>KCNJ5</u>	95.00	0	NM_000890.5
<u>KIRREL1</u>	95.00	0	NM_018240.7
<u>KL</u>	95.00	0	NM_004795.4
<u>KLHL3</u>	95.00	0	NM_017415.3
<u>LAMB2</u>	95.00	0	NM_002292.4
<u>LCAT</u>	95.00	0	NM_000229.2
<u>LDHD</u>	95.00	0	NM_153486.4
<u>LHX1</u>	95.00	0	NM_005568.5
<u>LIFR</u>	95.00	0	NM_002310.6
<u>LMX1B</u>	95.00	0	NM_002316.4
<u>LYZ</u>	95.00	0	NM_000239.3
<u>MAGED2</u>	95.00	0	NM_177433.3
<u>MAGI2</u>	95.00	0	NM_012301.4

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>MAPKBP1</u>	95.00	0	NM_001128608.2
<u>MMACHC</u>	95.00	0	NM_015506.3
<u>MOCOS</u>	95.00	0	NM_017947.4
<u>MTX2</u>	95.00	0	NM_006554.5
<u>MUC1</u>	95.00	0	NM_002456.6
<u>MYH9</u>	95.00	0	NM_002473.6
<u>MYO1E</u>	95.00	0	NM_004998.4
<u>NEK8</u>	95.00	0	NM_178170.3
<u>NOTCH2</u>	95.00	0	NM_024408.4
<u>NPHP1</u>	95.00	0	NM_000272.5
<u>NPHP3</u>	95.00	0	NM_153240.5
<u>NPHP4</u>	95.00	0	NM_015102.5
<u>NPHS1</u>	95.00	0	NM_004646.4
<u>NPHS2</u>	95.00	0	NM_014625.4
<u>NR3C1</u>	95.00	0	NM_001018077.1
<u>NR3C2</u>	95.00	0	NM_000901.5
<u>NUP107</u>	95.00	0	NM_020401.4
<u>NUP133</u>	95.00	0	NM_018230.3
<u>NUP160</u>	95.00	0	NM_015231.3
<u>NUP85</u>	95.00	0	NM_024844.5

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>NUP93</u>	95.00	0	NM_014669.5
<u>OCRL</u>	95.00	0	NM_000276.4
<u>OFD1</u>	95.00	0	NM_003611.3
<u>PAX2</u>	95.00	0	NM_003987.5
<u>PBX1</u>	95.00	0	NM_002585.4
<u>PCBD1</u>	95.00	0	NM_000281.4
<u>PDSS2</u>	95.00	0	NM_020381.4
<u>PHEX</u>	95.00	0	NM_000444.6
<u>PKD1</u>	95.00	0	NM_001009944.3
<u>PKD2</u>	95.00	0	NM_000297.4
<u>PKHD1</u>	95.00	0	NM_138694.4
<u>PLCE1</u>	95.00	0	NM_016341.4
<u>PODXL</u>	95.00	0	NM_005397.4
<u>PRPS1</u>	95.00	0	NM_002764.4
<u>PTPRO</u>	95.00	0	NM_030667.3
<u>REN</u>	95.00	0	NM_000537.4
<u>RET</u>	95.00	0	NM_020975.6
<u>ROBO2</u>	95.00	0	NM_002942.5
<u>SALL1</u>	95.00	0	NM_002968.3
<u>SARS2</u>	95.00	0	NM_017827.4

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>SCARB2</u>	95.00	0	NM_005506.4
<u>SCNN1A</u>	95.00	0	NM_001038.6
<u>SCNN1B</u>	95.00	0	NM_000336.3
<u>SCNN1G</u>	95.00	0	NM_001039.4
<u>SDCCAG8</u>	95.00	0	NM_006642.5
<u>SEC61A1</u>	95.00	0	NM_013336.4
<u>SGPL1</u>	95.00	0	NM_003901.4
<u>SIX1</u>	95.00	0	NM_005982.4
<u>SIX5</u>	95.00	0	NM_175875.5
<u>SLC12A1</u>	95.00	0	NM_000338.3
<u>SLC12A3</u>	95.00	0	NM_000339.3
<u>SLC22A12</u>	95.00	0	NM_144585.4
<u>SLC26A1</u>	95.00	0	NM_213613.4
<u>SLC2A2</u>	95.00	0	NM_000340.2
<u>SLC2A9</u>	95.00	0	NM_020041.3
<u>SLC34A1</u>	95.00	0	NM_003052.5
<u>SLC34A3</u>	95.00	0	NM_080877.3
<u>SLC3A1</u>	95.00	0	NM_000341.4
<u>SLC4A1</u>	95.00	0	NM_000342.4
<u>SLC4A4</u>	95.00	0	NM_003759.4

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>SLC5A2</u>	95.00	0	NM_003041.4
<u>SLC7A9</u>	95.00	0	NM_014270.5
<u>SLIT2</u>	95.00	0	NM_004787.4
<u>SMARCA1</u>	95.00	0	NM_014140.4
<u>TBC1D1</u>	95.00	0	NM_015173.4
<u>TBC1D8B</u>	95.00	0	NM_017752.3
<u>TBX18</u>	95.00	0	NM_001080508.3
<u>TNS2</u>	95.00	0	NM_015319.2
<u>TRAF3IP1</u>	95.00	0	NM_015650.4
<u>TRAP1</u>	95.00	0	NM_016292.3
<u>TRIM8</u>	95.00	0	NM_030912.3
<u>TRPC6</u>	95.00	0	NM_004621.6
<u>TRPM6</u>	95.00	0	NM_017662.5
<u>TSC1</u>	95.00	0	NM_000368.5
<u>TSC2</u>	95.00	0	NM_000548.5
<u>TTC21B</u>	95.00	0	NM_024753.5
<u>TTR</u>	95.00	0	NM_000371.4
<u>UMOD</u>	95.00	0	NM_003361.4
<u>VHL</u>	95.00	0	NM_000551.4
<u>WDR19</u>	95.00	0	NM_025132.4

GENE	% OF CODING SEQUENCE SUFFICIENTLY COVERED TO DETECT HETEROZYGOUS MUTATIONS	COPY NUMBER VARIATION	COMMENTS
<u>WDR72</u>	95.00	0	NM_182758.4
<u>WFS1</u>	95.00	0	NM_006005.3
<u>WNK1</u>	95.00	0	NM_018979.4
<u>WNK4</u>	95.00	0	NM_032387.5
<u>WNT4</u>	95.00	0	NM_030761.5
<u>WT1</u>	95.00	0	NM_024426.6
<u>XDH</u>	95.00	0	NM_000379.4
<u>XPNPEP3</u>	95.00	0	NM_022098.4