

WES RENAL DISORDERS DG 3.2

<i>Gene</i>	<i>Median coverage</i>	<i>% covered >10x</i>	<i>% covered >20x</i>	<i>OMIM disease ID</i>
ACE	119.4	99.9	98.4	267430
ACTN4	136.6	99.9	98.0	603278
ADAMTS13	100.9	97.0	94.3	274150
ADAMTS9	118.2	99.4	98.4	-
ADCY10	130.2	100.0	99.6	143870
AGT	200.2	100.0	99.9	267430
AGTR1	147.5	91.9	91.8	267430
AGXT	171.0	100.0	100.0	259900
AHI1	132.9	99.4	97.4	608629
ALDOB	127.9	98.8	95.7	229600
ALG1	44.0	53.6	46.9	608540
ALG8	107.8	96.6	95.9	608104
ALG9	103.8	99.9	99.3	-
ALMS1	174.7	99.7	99.5	203800
AMN	86.5	92.5	82.9	261100
ANKFY1	99.2	100.0	98.7	-
ANKS6	91.7	94.2	89.7	615382
ANLN	139.1	98.4	97.0	616032
ANOS1	81.6	89.8	88.3	308700
AP2S1	118.7	90.4	90.0	600740
APOL1	139.2	100.0	100.0	612551
APRT	90.4	100.0	100.0	614723
AQP2	109.8	100.0	99.2	125800
ARHGAP24	137.2	100.0	100.0	-
ARHGDI1A	217.0	100.0	100.0	615244

ARL13B	85.8	100.0	99.3	612291
ARL6	112.4	99.1	98.4	613575;209900
ATP1A1	120.6	100.0	99.8	618314
ATP6V0A4	105.4	100.0	99.3	602722
ATP6V1B1	193.2	100.0	100.0	267300
ATP7B	127.3	99.9	99.2	277900
AVIL	111.6	100.0	99.8	618594
AVP	50.3	90.2	66.6	125700
AVPR2	118.4	100.0	99.8	304800;300539
B9D1	91.9	85.2	85.2	614209
B9D2	108.7	100.0	100.0	614175
BBIP1	142.6	95.7	87.4	615995
BBS1	160.2	100.0	100.0	209900
BBS10	151.0	100.0	99.9	209900
BBS12	167.8	100.0	100.0	209900
BBS2	148.8	99.4	98.0	209900
BBS4	108.1	99.9	98.9	209900
BBS5	95.0	98.4	94.7	209900
BBS7	151.4	99.0	96.5	209900
BBS9	104.9	92.0	89.0	209900
BCS1L	143.8	100.0	100.0	124000
BICC1	141.4	100.0	100.0	601331
BSND	139.1	100.0	99.9	602522
C3	145.9	99.9	98.5	612925
CA2	149.6	100.0	100.0	259730
CACNA1H	137.8	98.9	96.3	617027
CASR	151.3	100.0	99.5	146200;145980
CBWD1	12.8	20.5	19.1	-
CC2D2A	109.3	98.3	96.6	612284;216360;612285
CCNQ	46.5	82.9	78.3	300707

CD151	148.2	100.0	100.0	-
CD2AP	120.7	99.6	98.8	607832
CD46	132.7	99.7	98.9	612922
CEP120	140.6	99.9	99.6	616300
CEP164	95.5	99.8	98.2	614845
CEP290	86.2	96.2	90.8	611134;209900;611755;610189;610188
CEP41	77.1	98.8	93.4	614464
CEP55	110.9	100.0	99.8	236500
CEP83	107.1	99.0	96.6	615862
CFB	119.4	100.0	99.6	612924
CFH	178.9	99.8	98.5	235400
CFHR1	185.7	91.7	89.6	235400
CFHR3	114.9	89.0	87.8	235400
CFHR5	107.4	99.8	97.6	-
CFI	145.2	99.3	96.0	612923
CHRM3	131.0	100.0	100.0	100100
CHRNA3	122.6	100.0	99.2	191800
CLCN2	115.7	100.0	99.3	605635;615651
CLCN5	115.4	99.7	97.1	300554;310468;308990;300009
CLCNKB	110.5	98.7	95.3	607364
CLDN10	141.3	100.0	100.0	617671
CLDN16	130.8	100.0	100.0	248250
CLDN19	136.6	98.3	92.9	248190
CNNM2	191.2	100.0	99.9	613882
COL4A1	103.1	99.0	97.0	-
COL4A3	95.5	98.9	97.4	203780;104200
COL4A4	98.4	99.6	97.4	203780
COL4A5	59.3	97.6	86.6	301050
COQ2	83.7	97.6	96.7	607426
COQ6	118.1	99.9	98.5	614650

COQ7	121.1	100.0	99.6	616733
COQ8B	102.1	100.0	99.2	615573
COQ9	69.5	100.0	98.7	614654
CPLANE1	129.6	99.4	98.2	277170
CRB2	110.0	98.9	94.2	616220
CSPP1	116.4	99.7	98.1	615636
CTNS	117.6	100.0	99.3	219800;219900
CUBN	107.3	99.2	97.1	261100
CUL3	121.8	99.4	97.4	614496
CYP24A1	166.7	100.0	100.0	143880
DAAM2	111.1	99.1	98.2	-
DCDC2	146.2	100.0	99.9	616217
DGKE	123.8	99.7	98.5	615008
DLC1	161.4	100.0	99.9	-
DMP1	121.2	99.9	99.9	241520
DNAJB11	98.4	99.9	99.6	618061
DSTYK	120.7	99.9	98.8	610805
DYNC2H1	107.7	98.6	95.2	613091;615087;263510
DZIP1L	93.6	99.8	98.0	617610
EGF	114.9	99.9	99.8	611718
EHHADH	146.4	100.0	100.0	615605
EMP2	71.2	98.9	93.0	615861
ENPP1	129.7	96.5	90.6	613312
EYA1	120.9	99.9	99.5	113650
FAH	122.1	100.0	99.5	276700
FAM20A	103.8	99.6	94.4	204690
FAN1	131.9	100.0	99.8	614817
FAT1	168.2	100.0	99.9	-
FGF23	114.8	99.4	96.7	211900;193100
FN1	111.4	99.9	98.7	601894

FOXC2	94.3	100.0	98.1	153400
FOXI1	210.3	100.0	100.0	-
FRAS1	124.8	100.0	99.2	219000
FREM1	116.9	99.8	98.4	608980
FREM2	158.0	99.8	98.7	219000
FXVD2	133.7	100.0	100.0	154020
G6PC	163.3	100.0	100.0	232200
GALNT3	140.2	99.8	98.7	211900
GANAB	109.2	99.8	97.8	600666
GAPVD1	148.7	99.9	98.9	-
GATA3	244.6	100.0	100.0	146255
GCM2	133.5	100.0	100.0	617343
GFRA1	104.2	100.0	99.9	-
GLA	72.8	91.0	85.9	301500
GLI3	131.0	98.5	97.7	146510
GLIS2	143.2	100.0	99.9	611498
GLIS3	118.4	98.5	97.4	610199
GNA11	177.9	98.4	93.1	146200;145980
GREB1L	134.4	100.0	99.9	-
GRHPR	96.8	83.3	79.2	260000
GRIP1	113.7	100.0	99.3	617667
GSN	113.6	95.7	93.5	105120
HNF1A	183.8	100.0	99.8	No OMIM phenotype
HNF1B	114.3	99.0	95.7	137920;125853
HNF4A	133.8	99.9	98.6	616026
HOGA1	134.9	99.5	95.5	613616
HPRT1	67.0	98.6	90.6	300323;300322
HSD11B2	172.2	87.6	83.8	218030
IFNG	155.8	100.0	99.9	613254
IFT122	131.2	99.9	99.2	218330

IFT140	120.4	99.9	99.2	266920
IFT172	94.8	99.6	98.6	615630
IFT27	119.6	100.0	100.0	615996
IFT43	116.4	100.0	100.0	614099
INF2	102.4	87.2	84.8	613237;614455
INPP5E	113.1	96.9	93.2	610156;213300
INTU	119.2	99.9	98.6	-
INVS	145.6	100.0	99.8	602088
IQCB1	96.5	92.8	82.8	609254
ITGA3	156.7	99.6	97.9	614748
ITGA8	122.6	99.9	99.3	191830
ITSN1	132.0	98.7	96.0	-
ITSN2	120.5	97.8	95.4	-
JAG1	127.4	97.8	96.7	118450
KANK1	127.5	100.0	99.9	-
KANK2	153.4	100.0	100.0	617783
KCNJ1	173.2	100.0	100.0	241200
KCNJ10	146.8	89.2	88.5	612780
KCNJ16	201.8	98.3	98.3	-
KCNJ5	163.3	100.0	100.0	613677
KIAA0556	122.8	100.0	99.6	616784
KIF14	124.3	99.2	96.8	616258
KIF7	105.7	93.6	91.9	200990
KIRREL1	173.2	100.0	99.9	-
KL	152.1	98.5	97.5	211900
KLHL3	114.3	100.0	98.9	614495
LAGE3	57.1	96.1	84.3	301006
LAMA5	118.2	98.5	96.3	-
LAMB2	174.2	99.9	99.3	609049;614199
LCAT	124.7	98.8	93.3	245900

LMX1B	156.2	99.3	96.8	161200;602575
LRIG2	132.3	99.8	99.2	615112
LRP2	147.6	100.0	99.8	222448
LRP4	132.4	99.1	98.4	212780
LRP5	183.2	99.2	98.2	617875
LYZ	151.7	100.0	99.9	105200
LZTFL1	112.9	99.7	99.4	209900
MAFB	86.9	100.0	99.8	166300
MAGED2	84.8	99.5	97.6	300971
MAGI2	96.0	94.2	91.0	617609
MAPKBP1	140.2	100.0	100.0	617271
MKKS	204.9	100.0	100.0	209900;236700
MKS1	93.4	99.4	96.3	209900;249000
MMACHC	198.3	100.0	100.0	-
MOCOS	157.7	99.9	97.8	603592
MYH9	132.2	99.9	98.9	153640;153650
MYO1E	132.3	99.9	98.6	614131
NCAPG2	123.2	99.8	99.0	-
NEK1	120.2	99.5	98.2	263520
NEK8	152.3	100.0	99.8	613824
NEU1	144.9	99.3	96.1	-
NOS1AP	182.6	100.0	100.0	-
NOTCH2	130.5	100.0	99.2	102500;610205
NPHP1	135.6	99.8	99.1	266900;609583;256100
NPHP3	122.6	99.6	98.5	208540;604387;267010
NPHP4	130.3	100.0	99.8	606966
NPHS1	113.4	99.7	99.0	256300
NPHS2	106.8	100.0	99.6	600995
NR3C2	136.9	99.9	99.8	177735
NUP107	126.9	99.7	98.4	616730

NUP133	122.4	99.4	97.3	618177
NUP160	138.7	100.0	99.8	618178
NUP205	134.4	99.9	99.3	616893
NUP85	122.1	100.0	100.0	618176
NUP93	116.8	96.7	92.7	616892
NXF5	84.6	58.3	57.0	-
OCRL	107.2	99.4	97.6	300555;309000
OFD1	50.3	87.1	71.3	300804;311200;300209
OSGEP	97.9	99.8	95.7	617729
PAX2	193.6	100.0	100.0	191830;120330
PBX1	120.7	100.0	99.1	617641
PCBD1	110.6	100.0	99.8	264070
PDE6D	108.3	100.0	99.9	615665
PDSS2	112.7	98.4	94.3	614652
PHEX	109.0	99.9	98.9	307800
PKD1	30.8	40.6	32.8	173900
PKD2	94.1	96.0	93.3	613095
PKHD1	134.4	100.0	99.6	263200
PLCE1	126.1	99.8	98.9	610725
PMM2	127.8	99.8	99.8	212065
PODXL	101.2	94.3	94.0	-
PTH1R	104.0	99.6	95.9	156400
PTPRO	130.8	99.7	98.9	614196
RAD21	89.2	99.2	95.9	611376
REN	127.7	100.0	100.0	267430;613092
RMND1	156.8	99.7	97.2	614922
ROBO2	129.2	99.1	97.3	610878
RPGRIP1L	129.9	96.5	95.3	216360;611560;611561
RRM2B	147.5	100.0	99.8	612075
SALL1	117.9	99.7	97.5	107480

SALL4	137.8	99.1	96.4	607323
SARS2	115.0	95.7	94.5	613845
SCARB2	108.9	99.9	99.4	254900
SCNN1A	125.4	99.7	97.5	264350
SCNN1B	140.9	100.0	99.8	177200;264350
SCNN1G	160.5	99.8	98.4	177200;264350
SDCCAG8	115.0	99.8	99.8	613615
SEC61A1	127.5	100.0	100.0	617056
SGPL1	142.2	100.0	100.0	617575
SIX5	66.7	96.9	90.1	610896
SLC12A1	139.8	96.2	96.0	601678
SLC12A3	151.9	100.0	100.0	263800
SLC16A12	133.5	100.0	99.9	612018
SLC22A12	119.6	100.0	99.8	220150
SLC26A1	132.0	100.0	99.7	167030
SLC26A3	132.4	100.0	99.5	214700
SLC2A2	148.2	100.0	99.8	227810
SLC2A9	114.9	99.3	95.0	612076
SLC34A1	152.5	100.0	99.7	612286;613388
SLC34A3	148.7	100.0	99.3	241530
SLC36A2	107.8	100.0	99.8	138500
SLC37A4	118.5	99.8	97.6	232220
SLC3A1	148.6	100.0	99.7	220100
SLC41A1	160.5	100.0	99.9	610801
SLC4A1	155.0	100.0	99.9	611590;179800;612653
SLC4A4	122.1	99.9	99.4	604278
SLC5A2	136.4	100.0	100.0	233100
SLC6A19	135.9	100.0	100.0	138500;234500
SLC6A20	149.0	100.0	99.8	138500
SLC7A7	114.4	100.0	99.9	222700

SLC7A9	132.6	100.0	99.4	220100
SLC9A3	138.9	90.5	86.0	616868
SLC9A3R1	138.1	99.9	98.2	612287
SLIT3	122.1	97.9	95.6	-
SMARCAL1	117.0	100.0	99.8	242900
SOX17	81.7	100.0	99.9	613674
STRA6	131.1	100.0	99.9	601186
STX16	108.7	100.0	99.0	603233
TBC1D8B	95.3	98.0	92.1	301028
TBX18	90.9	99.5	97.1	143400
TCTN1	102.5	96.8	92.8	614173
TCTN2	127.2	99.9	99.1	613885
TCTN3	118.9	100.0	100.0	614815;258860
THBD	145.1	100.0	99.9	612926
TMEM107	141.9	100.0	100.0	617563;617562
TMEM138	87.3	99.8	93.1	614465
TMEM216	89.9	98.5	92.8	603194;608091
TMEM231	99.0	100.0	99.3	615397;614970
TMEM237	121.4	99.8	99.3	614424
TMEM260	122.7	98.7	95.4	617478
TMEM67	84.8	98.6	93.5	216360;607361;613550;209900;610688
TNS2	127.0	100.0	100.0	-
TNXB	110.3	98.7	93.9	615963
TP53RK	59.8	95.5	84.9	617730
TPRKB	66.7	80.2	75.2	617731
TRAF3IP1	82.2	98.7	95.4	616629
TRIM32	119.5	100.0	99.9	209900
TRPC6	95.9	97.1	94.5	603965
TRPM6	129.8	99.9	99.1	602014
TSC1	118.1	99.5	98.2	191100

TSC2	140.3	100.0	99.8	613254
TTC21B	125.8	99.7	99.1	613819;613820
TTC8	125.6	99.5	98.0	209900
UMOD	104.2	97.5	95.9	609886;603860;162000
UPK3A	115.9	100.0	99.7	191830
UQCC2	106.7	99.9	98.5	615824
VDR	106.0	96.7	94.4	277440
VIPAS39	123.2	100.0	100.0	613404
VPS33B	105.9	100.0	99.9	208085
WDR19	128.4	99.8	98.6	614378;614376;614377
WDR35	147.5	99.6	98.4	614091;613610
WDR60	106.7	99.3	95.8	615462
WDR73	177.2	100.0	100.0	251300
WNK1	135.5	99.8	99.3	614492
WNK4	146.4	99.9	99.0	614491
WNT4	228.0	97.8	93.6	158330;611812
WT1	72.4	97.6	96.1	256370
XDH	94.7	100.0	99.8	278300
XPNPEP3	113.1	100.0	100.0	613159
XPO5	131.7	100.0	99.5	-
ZMPSTE24	134.5	99.6	99.4	-
ZNF423	189.1	100.0	100.0	614844

Gene symbols used follow HGCN guidelines: Gray KA, Yates B, Seal RL, Wright MW, Bruford EA. Nucleic Acids Res. 2015 Jan 43(Database issue):D1079-85.

TWIST is the default chemistry for all WES samples. Agilent V5 was the default chemistry until Q3 2021.

Median Coverage describes the average number of reads seen across 50 exomes.

Covered 10x describes the percentage of a gene's coding sequence that is covered at least 10x.

Covered 20x describes the percentage of a gene's coding sequence that is covered at least 20x.

Genes with no value for coverage are non protein coding genes.

Non protein coding genes are covered, but as coverage statistics are based on protein coding regions, statistics could not be generated.

OMIM release used for OMIM disease identifiers and descriptions: September 1st, 2021.

