

WES RENAL DISORDERS DG 3.00

<i>Gene</i>	<i>Median coverage</i>	<i>% covered >10x</i>	<i>% covered >20x</i>	<i>OMIM disease ID</i>
ACE	126.8	99.9	98.4	267430
ACTN4	134.0	100.0	99.3	603278
ADAMTS13	98.0	97.1	93.8	274150
ADAMTS9	141.1	99.5	98.7	-
ADCY10	156.7	100.0	99.9	143870
AGT	208.7	100.0	100.0	267430
AGTR1	192.6	92.0	91.8	267430
AGXT	150.4	100.0	100.0	259900
AHI1	154.3	99.7	97.9	608629
ALDOB	152.6	99.4	96.6	229600
ALG1	48.4	53.0	45.8	608540
ALG8	132.5	97.2	95.6	608104
ALG9	124.5	100.0	99.7	-
ALMS1	203.4	99.8	99.5	203800
AMN	77.8	89.7	80.0	261100
ANKS6	95.9	93.8	89.5	615382
ANLN	170.7	98.7	97.5	616032
ANOS1	97.2	89.8	88.9	308700
AP2S1	133.2	90.4	90.3	600740
APOL1	171.5	100.0	100.0	612551
APRT	81.4	100.0	99.5	614723
AQP2	112.2	100.0	98.6	125800
ARHGDI1	211.1	100.0	100.0	615244
ARL13B	108.1	100.0	99.2	612291
ARL6	127.8	99.9	98.6	613575;209900

ATP1A1	143.2	100.0	100.0	618314
ATP6V0A4	134.0	100.0	99.9	602722
ATP6V1B1	199.1	100.0	100.0	267300
ATP7B	146.0	99.9	99.2	277900
AVIL	132.4	100.0	99.9	618594
AVP	47.5	84.9	64.3	125700
AVPR2	111.5	100.0	99.4	304800;300539
B9D1	94.7	85.2	85.1	614209
B9D2	97.6	100.0	100.0	614175
BBIP1	152.5	98.6	92.4	615995
BBS1	172.8	100.0	100.0	209900
BBS10	168.2	100.0	99.8	209900
BBS12	212.9	100.0	100.0	209900
BBS2	180.0	100.0	99.5	209900
BBS4	127.5	99.9	99.3	209900
BBS5	113.0	99.0	93.9	209900
BBS7	173.7	98.7	95.5	209900
BBS9	121.8	92.3	90.4	209900
BCS1L	158.0	100.0	100.0	124000
BICC1	163.2	100.0	100.0	601331
BSND	157.9	100.0	100.0	602522
C3	153.5	99.9	99.2	612925
CA2	172.2	100.0	100.0	259730
CACNA1H	126.2	98.7	96.4	617027
CASR	155.8	100.0	99.9	146200;145980
CBWD1	13.8	20.8	19.4	-
CC2D2A	131.6	98.5	96.5	612284;216360;612285
CCNQ	52.3	83.1	78.5	300707
CD2AP	141.5	99.9	98.8	607832
CD46	151.5	99.9	99.4	612922

CEP120	170.6	100.0	99.5	616300
CEP164	102.8	99.9	98.3	614845
CEP290	97.0	96.1	90.0	611134;209900;611755;610189;610188
CEP41	92.6	99.8	97.4	614464
CEP55	138.6	100.0	99.8	236500
CEP83	133.1	99.8	97.4	615862
CFB	139.7	100.0	100.0	612924
CFH	194.1	99.9	99.0	235400
CFHR1	201.6	96.4	94.9	235400
CFHR3	111.8	94.0	92.2	235400
CFI	169.4	99.2	96.8	612923
CHRM3	144.2	100.0	100.0	100100
CHRNA3	137.9	100.0	99.4	191800
CLCN2	124.4	100.0	99.5	605635;615651
CLCN5	125.2	99.9	98.3	300554;310468;308990;300009
CLCNKB	110.1	99.1	95.9	607364
CLDN10	156.6	100.0	100.0	617671
CLDN16	162.9	100.0	100.0	248250
CLDN19	128.4	98.5	93.1	248190
CNNM2	198.1	100.0	100.0	613882
COL4A1	115.6	98.7	97.4	-
COL4A3	111.1	98.7	98.0	203780;104200
COL4A4	107.4	99.9	98.2	203780
COL4A5	66.6	97.8	89.1	301050
COQ2	113.1	98.0	95.3	607426
COQ6	143.6	99.9	98.4	614650
COQ7	161.7	100.0	99.8	616733
COQ8B	102.1	100.0	99.3	615573
COQ9	79.4	100.0	97.9	614654
CPLANE1	148.8	99.7	98.4	277170

CRB2	103.1	98.5	93.0	616220
CSPP1	132.4	99.8	98.7	615636
CTNS	127.4	100.0	99.8	219800;219900
CUBN	129.7	99.7	98.3	261100
CUL3	146.2	99.9	98.8	614496
CYP24A1	203.6	100.0	99.9	143880
DCDC2	174.2	100.0	99.9	616217
DGKE	130.4	99.8	98.1	615008
DMP1	138.6	100.0	99.9	241520
DNAJB11	128.6	100.0	99.5	618061
DSTYK	138.0	99.9	99.2	610805
DYNC2H1	122.7	98.8	95.5	613091;615087;263510
DZIP1L	105.7	99.9	99.0	617610
EGF	129.4	99.9	99.7	611718
EHHADH	164.6	100.0	100.0	615605
EMP2	88.6	99.9	96.7	615861
ENPP1	149.8	96.4	91.2	613312
EYA1	145.7	99.9	99.7	113650
FAH	135.8	100.0	100.0	276700
FAM20A	113.3	99.6	94.7	204690
FAN1	155.8	100.0	99.8	614817
FAT1	195.0	100.0	100.0	-
FGF23	130.1	99.6	97.5	211900;193100
FN1	129.8	100.0	99.3	601894
FOXC2	99.8	100.0	96.7	153400
FOXI1	223.4	100.0	100.0	-
FRAS1	140.3	100.0	99.4	219000
FREM1	135.0	99.9	99.1	608980
FREM2	167.6	100.0	99.3	219000
FXD2	131.5	100.0	100.0	154020

G6PC	185.9	100.0	100.0	232200
GALNT3	149.7	99.8	99.0	211900
GANAB	129.4	99.9	99.0	600666
GAPVD1	174.7	100.0	99.3	29959197
GATA3	254.6	100.0	100.0	146255
GCM2	153.4	100.0	100.0	617343
GFRA1	110.1	100.0	100.0	33020172
GLA	81.9	91.1	88.2	301500
GLI3	140.8	98.5	98.0	146510
GLIS2	136.6	100.0	99.8	611498
GLIS3	136.1	98.6	98.2	610199
GNA11	172.7	99.9	95.0	146200;145980
GREB1L	153.1	100.0	99.9	-
GRHPR	108.1	84.2	81.3	260000
GRIP1	137.0	100.0	99.7	617667
GSN	117.2	95.8	93.5	105120
HNF1B	133.8	99.3	96.1	137920;125853
HNF4A	143.0	99.9	99.0	616026
HOGA1	156.5	100.0	96.4	613616
HPRT1	74.2	99.3	91.8	300323;300322
HSD11B2	167.3	86.0	82.7	218030
IFNG	190.2	100.0	100.0	613254
IFT122	140.5	100.0	99.6	218330
IFT140	124.5	99.8	98.8	266920
IFT172	107.8	99.9	99.1	615630
IFT27	135.3	100.0	100.0	615996
IFT43	134.3	100.0	100.0	614099
INF2	89.3	86.7	83.8	613237;614455
INPP5E	107.5	97.1	92.7	610156;213300
INTU	141.9	99.7	98.1	-

INVS	163.7	100.0	100.0	602088
IQCB1	113.4	93.9	85.0	609254
ITGA3	162.2	99.5	97.4	614748
ITGA8	140.2	99.9	99.7	191830
ITSN1	149.7	99.4	97.4	29773874
ITSN2	138.8	98.8	96.5	29773874
JAG1	147.4	97.7	96.8	118450
KANK1	140.7	100.0	100.0	25961457
KANK2	154.4	100.0	100.0	617783
KCNJ1	175.9	100.0	100.0	241200
KCNJ10	157.5	89.3	89.0	612780
KCNJ5	182.6	100.0	100.0	613677
KIAA0556	142.8	100.0	99.9	616784
KIF14	143.1	99.6	97.7	616258
KIF7	100.0	93.6	90.6	200990
KIRREL1	171.9	100.0	99.9	-
KL	169.3	98.2	97.2	211900
KLHL3	131.0	100.0	99.3	614495
LAGE3	64.5	95.9	85.1	301006
LAMB2	171.7	100.0	99.7	609049;614199
LCAT	117.2	99.0	93.8	245900
LMX1B	146.2	99.6	96.3	161200;602575
LRIG2	147.5	99.6	98.8	615112
LRP2	171.0	100.0	99.9	222448
LRP4	143.1	99.1	98.8	212780
LRP5	179.9	98.5	98.1	617875
LYZ	163.5	100.0	100.0	105200
LZTFL1	132.0	99.9	99.2	209900
MAFB	83.5	100.0	99.4	166300
MAGED2	81.7	99.8	97.7	300971

MAGI2	111.9	94.5	92.4	617609
MAPKBP1	142.5	100.0	100.0	617271
MKKS	232.6	100.0	100.0	209900;236700
MKS1	104.7	99.8	97.9	209900;249000
MMACHC	227.1	100.0	100.0	22447314
MOCOS	178.8	99.8	97.7	603592
MYH9	134.9	100.0	99.3	153640;153650
MYO1E	155.1	99.9	99.5	614131
NCAPG2	149.4	99.9	99.2	-
NEK1	141.3	99.8	98.0	263520
NEK8	158.1	100.0	99.9	613824
NEU1	146.4	99.7	97.7	30450471
NOTCH2	146.7	100.0	99.5	102500;610205
NPHP1	152.0	100.0	99.0	266900;609583;256100
NPHP3	143.4	99.7	98.4	208540;604387;267010
NPHP4	137.8	100.0	99.8	606966
NPHS1	117.2	99.8	99.1	256300
NPHS2	115.0	100.0	99.5	600995
NR3C2	156.4	100.0	99.7	177735
NUP107	156.3	99.8	98.5	616730
NUP133	145.0	99.7	98.3	618177
NUP160	163.0	100.0	99.9	618178
NUP205	161.3	99.9	99.4	616893
NUP85	141.1	100.0	100.0	618176
NUP93	137.0	98.0	94.2	616892
OCRL	127.1	99.9	98.6	300555;309000
OFD1	61.2	88.0	73.7	300804;311200;300209
OSGEP	107.3	100.0	99.4	617729
PAX2	201.8	100.0	99.9	191830;120330
PBX1	146.9	100.0	99.4	617641

PCBD1	112.5	100.0	99.6	264070
PDE6D	128.7	100.0	100.0	615665
PDSS2	125.9	99.8	97.1	614652
PHEX	131.6	100.0	99.6	307800
PKD1	27.3	39.2	30.0	173900
PKD2	108.4	95.5	91.1	613095
PKHD1	154.2	100.0	99.6	263200
PLCE1	149.9	99.9	99.3	610725
PMM2	145.4	100.0	100.0	212065
PTH1R	104.5	100.0	98.7	156400
PTPRO	152.7	99.9	99.4	614196
RAD21	103.0	99.2	96.6	611376
REN	150.7	100.0	100.0	267430;613092
RMND1	165.2	100.0	98.6	614922
ROBO2	155.8	99.4	97.8	610878
RPGRIP1L	155.5	96.7	95.7	216360;611560;611561
RRM2B	163.8	100.0	99.7	612075
SALL1	133.4	99.9	99.0	107480
SALL4	136.9	98.6	96.7	607323
SARS2	118.3	95.8	94.6	613845
SCARB2	121.3	100.0	99.8	254900
SCNN1A	131.4	99.7	98.2	264350
SCNN1B	146.2	100.0	99.7	177200;264350
SCNN1G	164.6	99.8	98.3	177200;264350
SDCCAG8	138.0	100.0	99.9	613615
SEC61A1	148.0	100.0	100.0	617056
SGPL1	159.8	100.0	100.0	617575
SIX5	67.0	95.4	88.2	610896
SLC12A1	167.4	96.2	96.1	601678
SLC12A3	152.8	100.0	99.9	263800

SLC16A12	152.1	100.0	99.9	612018
SLC22A12	113.2	100.0	99.8	220150
SLC26A1	106.8	100.0	99.6	167030
SLC26A3	160.5	100.0	99.5	214700
SLC2A2	183.6	100.0	100.0	227810
SLC2A9	122.5	99.8	96.1	612076
SLC34A1	143.4	99.9	99.1	612286;613388
SLC34A3	139.6	100.0	99.4	241530
SLC36A2	123.4	100.0	100.0	138500
SLC37A4	124.2	100.0	99.2	232220
SLC3A1	161.7	100.0	99.8	220100
SLC41A1	166.5	100.0	100.0	610801
SLC4A1	157.1	100.0	99.8	611590;179800;612653
SLC4A4	139.5	99.8	99.2	604278
SLC5A2	131.5	100.0	100.0	233100
SLC6A19	134.7	100.0	100.0	138500;234500
SLC6A20	158.9	100.0	99.9	138500
SLC7A7	126.7	100.0	99.9	222700
SLC7A9	145.8	100.0	99.9	220100
SLC9A3	126.5	90.6	86.0	616868
SLC9A3R1	134.6	100.0	98.7	612287
SLIT3	131.9	97.9	95.3	-
SMARCAL1	130.9	100.0	99.9	242900
SOX17	71.9	100.0	99.5	613674
STRA6	130.5	100.0	99.8	601186
STX16	126.7	100.0	98.6	603233
TBC1D8B	109.5	98.5	93.2	301028
TBX18	99.5	99.5	97.1	143400
TCTN1	114.9	96.7	93.0	614173
TCTN2	149.2	100.0	99.5	613885

TCTN3	136.4	100.0	100.0	614815;258860
THBD	139.3	100.0	99.7	612926
TMEM107	155.1	100.0	100.0	617563;617562
TMEM138	95.1	100.0	99.1	614465
TMEM216	114.4	99.9	98.1	603194;608091
TMEM231	106.4	100.0	99.6	615397;614970
TMEM237	141.7	100.0	99.9	614424
TMEM260	139.5	97.5	93.4	617478
TMEM67	96.9	99.5	95.0	216360;607361;613550;209900;610688
TNS2	124.0	100.0	99.9	29773874
TNXB	103.2	99.1	93.7	615963
TP53RK	50.7	92.5	79.6	617730
TPRKB	81.1	81.1	75.9	617731
TRAF3IP1	91.1	99.6	97.6	616629
TRIM32	131.1	100.0	100.0	209900
TRPC6	109.9	98.2	96.1	603965
TRPM6	154.4	99.9	99.5	602014
TSC1	137.9	99.8	98.8	191100
TSC2	143.7	100.0	99.6	613254
TTC21B	148.8	99.9	99.3	613819;613820
TTC8	135.1	99.6	98.1	209900
UMOD	104.2	97.7	96.2	609886;603860;162000
UPK3A	117.9	100.0	99.5	191830
UQCC2	114.9	100.0	99.7	615824
VDR	110.0	97.2	94.9	277440
VIPAS39	133.8	100.0	100.0	613404
VPS33B	128.1	100.0	100.0	208085
WDR19	153.1	100.0	99.4	614378;614376;614377
WDR35	172.4	99.8	98.9	614091;613610
WDR60	121.8	99.5	97.0	615462

WDR73	180.8	100.0	100.0	251300
WNK1	156.2	99.9	99.6	614492
WNK4	149.5	99.9	99.3	614491
WNT4	200.3	99.1	94.8	158330;611812
WT1	81.1	97.3	95.4	256370
XDH	110.6	100.0	99.9	278300
XPNPEP3	124.2	100.0	100.0	613159
XPO5	158.8	100.0	99.9	26878725
ZMPSTE24	155.1	100.0	99.9	17152860
ZNF423	195.9	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.

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 Median Coverage and % Covered 10x/20x denoting NC are non-coding genes for which coverage statistics could not be generated.

OMIM release used for OMIM disease identifiers and descriptions : October 1st, 2016.

Ad 1. "No OMIM phenotype" signifies a gene without a current OMIM association Ad 2. OMIM phenotype descriptions between {} signify risk factors