WES CILIOPATHIES DG 3.00

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ACVR2B	133.0	98.3	95.0	613751
ADAMTS9	141.1	99.5	98.7	-
AHI1	154.3	99.7	97.9	608629
ALMS1	203.4	99.8	99.5	203800
ANKS6	95.9	93.8	89.5	615382
ARL13B	108.1	100.0	99.2	612291
ARL3	89.4	100.0	98.4	30269812
ARL6	127.8	99.9	98.6	613575;209900
ARMC4	126.1	92.1	90.0	615451
ARMC9	152.2	100.0	99.8	617622
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
C2CD3	140.4	95.8	95.6	615948
C8orf37	152.0	100.0	99.4	617406;614500
CC2D2A	131.6	98.5	96.5	612284;216360;612285
CCDC103	137.0	100.0	100.0	614679

CCDC114	133.4	100.0	100.0	615067
CCDC151	122.2	100.0	99.7	616037
CCDC28B	100.6	100.0	99.7	209900
CCDC39	103.8	99.5	96.5	613807
CCDC40	120.5	99.1	98.1	613808
CCDC65	92.8	99.6	97.1	615504
CCNO	95.3	100.0	99.2	615872
CENPF	145.1	99.8	98.5	616369
CEP104	131.5	100.0	99.2	616781
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
CFAP298	154.6	100.0	99.7	615500
CFAP300	97.8	99.3	95.9	618063
CFAP410	107.3	100.0	99.3	602271;617547
CFAP44	130.4	99.8	98.9	617593
CFAP53	150.5	99.6	97.4	614779
CFAP69	82.6	98.7	93.5	617959
CFC1	122.7	84.2	74.1	605376
CPLANE1	148.8	99.7	98.4	614615
CSPP1	132.4	99.8	98.7	615636
DCDC2	174.2	100.0	99.9	616217
DDX59	172.0	100.0	100.0	174300
DNAAF1	135.5	100.0	99.8	613193
DNAAF2	111.9	99.9	98.9	612518
DNAAF3	122.1	99.5	96.1	606763
DNAAF4	104.8	99.8	97.0	615482;127700

DNAAF5	107.4	84.6	78.6	614874
DNAH1	166.5	100.0	99.7	617577
DNAH11	155.9	99.9	99.0	611884
DNAH17	139.1	100.0	99.6	618643
DNAH5	139.2	99.9	99.3	608644
DNAH8	146.9	99.9	99.0	32619401
DNAI1	132.6	100.0	100.0	244400
DNAI2	182.7	98.6	96.2	612444
DNAJB13	139.4	100.0	100.0	610263
DNAL1	112.7	99.0	96.8	614017
DRC1	102.4	100.0	99.5	615294
DYNC2H1	122.7	98.8	95.5	613091
DYNC2LI1	121.3	99.7	97.6	617088
EVC	121.9	93.9	88.6	193530;225500
EVC2	135.9	97.7	96.1	225500
EXOC8	168.4	100.0	100.0	1
EXTL3	199.3	100.0	100.0	617425
FAM149B1	118.0	99.5	95.4	618763
FUZ	137.0	100.0	100.0	182940
GAS8	136.3	99.9	99.3	616726
GDF1	28.8	73.9	54.0	208530
GLIS2	136.6	100.0	99.8	611498
HYDIN	130.9	99.9	99.3	608647
HYLS1	183.5	100.0	100.0	236680
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
IFT52	148.5	100.0	99.9	617102

IFT80	78.3	97.6	88.2	611263
IFT81	108.2	93.5	90.1	617895
INPP5E	107.5	97.1	92.7	610156;213300
INTU	141.9	99.7	98.1	617925;617926
INVS	163.7	100.0	100.0	602088
IQCB1	113.4	93.9	85.0	609254
KCTD3	144.0	100.0	99.7	-
KIAA0556	142.8	100.0	99.9	616784
KIAA0586	143.8	97.3	93.1	616490
KIAA0753	148.6	100.0	99.3	617127
KIF14	143.1	99.6	97.7	616258
KIF7	100.0	93.6	90.6	200990;614120
LBR	127.8	99.4	94.5	215140;613471;169400
LCA5	162.9	99.9	99.2	604537
LRRC56	126.9	100.0	99.0	618254
LRRC6	181.6	99.2	96.3	614935
LZTFL1	132.0	99.9	99.2	209900
MAPKBP1	142.5	100.0	100.0	617271
MCIDAS	77.8	99.3	96.2	25048963
MKKS	232.6	100.0	100.0	209900;236700
MKS1	104.7	99.8	97.9	209900;249000
MMP21	110.1	99.9	98.8	616749
NCAPG2	149.4	99.9	99.2	618460;-
NEK1	141.3	99.8	98.0	263520
NEK8	158.1	100.0	99.9	615415;613824
NME5	202.5	100.0	100.0	-
NME8	120.6	99.2	95.3	610852
NODAL	167.9	100.0	100.0	270100
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	606996;606966
OCRL	127.1	99.9	98.6	300555;309000
OFD1	61.2	88.0	73.7	300804;300424;311200;300209
PDE6D	128.7	100.0	100.0	615665
PIBF1	82.1	99.5	96.2	617767
PIH1D3	83.8	99.1	92.5	300991
PIK3C2A	154.7	99.2	96.9	618440
PKD1	27.3	39.2	30.0	173900
PKD2	108.4	95.5	91.1	613095
PKHD1	154.2	100.0	99.6	263200
PMFBP1	125.0	99.9	99.3	618112
POC1A	133.2	100.0	100.0	614813
RPGRIP1L	155.5	96.7	95.7	216360;611560;611561
RSPH1	167.1	100.0	100.0	615481
RSPH3	148.7	99.9	98.8	616481
RSPH4A	171.2	98.1	95.6	612649
RSPH9	135.9	99.9	97.9	612650
SCLT1	108.5	96.0	90.9	2
SDCCAG8	138.0	100.0	99.9	613615
SPAG1	112.6	99.3	95.8	615505
SPATA7	138.4	99.8	98.2	604232
STK36	133.8	100.0	99.1	28543983
TBC1D32	116.8	99.0	95.8	3
TCTEX1D2	140.7	100.0	100.0	617405
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
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

TMEM218	105.6	100.0	99.9	-
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
TOGARAM1	145.1	99.6	98.1	32453716
TRAF3IP1	91.1	99.6	97.6	616629
TRIM32	131.1	100.0	100.0	254110;209900
TTBK2	134.6	99.8	97.6	604432
TTC21B	148.8	99.9	99.3	613819;613820
TTC25	92.2	100.0	100.0	617092
TTC26	168.2	99.9	98.8	7
TTC8	135.1	99.6	98.1	613464;209900
TULP1	134.3	100.0	99.5	600132;613843
VHL	141.3	96.3	91.4	263400;144700;171300;193300
WDPCP	122.2	98.2	94.4	209900
WDR19	153.1	100.0	99.4	614378;614376;614377
WDR34	116.2	100.0	99.6	615633
WDR35	172.4	99.8	98.9	614091;613610
WDR60	121.8	99.5	97.0	615503
WDR66	130.1	100.0	100.0	618152
XPNPEP3	124.2	100.0	100.0	613159
ZIC3	129.6	100.0	99.9	306955
ZMYND10	120.3	100.0	100.0	615444
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 10x 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