WES CILIOPATHIES DG 2.16

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ADAMTS9	115.7	99.5	97.4	-
AHI1	129.8	99.7	98.3	608629
ALMS1	172.8	100.0	99.7	203800
ANKS6	94.2	98.3	94.4	615382
ARL13B	102.2	100.0	99.4	612291
ARL6	100.3	99.8	98.2	613575;209900
ARMC4	107.2	94.4	93.5	615451
ARMC9	124.8	100.0	99.3	617622
B9D1	103.7	92.2	92.1	614209
B9D2	105.8	100.0	100.0	614175
BBIP1	119.7	97.3	90.3	615995
BBS1	146.4	100.0	100.0	209900
BBS10	158.1	100.0	99.9	209900
BBS12	187.1	100.0	100.0	209900
BBS2	150.7	99.9	99.6	209900
BBS4	110.2	99.9	99.2	209900
BBS5	98.5	98.0	93.3	209900
BBS7	142.9	99.1	96.5	209900
BBS9	113.6	98.6	94.4	209900
C11orf70	85.4	99.6	97.1	618063
C21orf2	130.3	100.0	98.8	602271;617547
C21orf59	139.8	99.6	96.2	615500
C2CD3	116.9	95.8	95.2	615948
C5orf42	124.5	99.8	98.0	614615
C8orf37	144.1	99.8	99.4	614500;617406

CC2D2A	111.7	99.0	97.1	612285;216360;612284
CCDC103	116.2	100.0	99.8	614679
CCDC114	134.1	100.0	99.8	615067
CCDC151	127.2	100.0	100.0	616037
CCDC28B	84.3	100.0	98.5	209900
CCDC39	86.7	99.4	96.8	613807
CCDC40	112.0	99.4	98.4	613808
CCDC65	80.3	99.6	97.1	615504
CCNO	130.9	100.0	99.8	615872
CENPF	139.9	99.8	98.7	616369
CEP104	104.0	99.3	97.5	616781
CEP120	131.7	100.0	99.4	616300
CEP164	89.3	99.8	98.0	614845
CEP290	82.6	97.3	91.7	610188;610189;611134;611755;209900
CEP41	78.2	98.9	94.4	614464
CEP55	124.5	100.0	100.0	236500
CEP83	108.8	99.4	96.6	615862
CSPP1	119.0	100.0	99.1	615636
DCDC2	150.0	99.9	99.8	616217
DDX59	141.5	100.0	99.8	174300
DNAAF1	112.8	100.0	99.5	613193
DNAAF2	150.1	99.9	98.7	612518
DNAAF3	115.0	99.9	98.5	606763
DNAAF4	94.1	99.9	98.2	615482;127700
DNAAF5	107.6	95.4	85.2	614874
DNAH1	158.1	100.0	99.8	617577
DNAH11	131.3	99.8	98.7	611884
DNAH17	126.0	100.0	99.6	4
DNAH5	114.1	99.9	99.1	608644
DNAI1	115.4	100.0	100.0	244400

DNAI2	151.7	99.6	96.6	612444
DNAJB13	116.3	100.0	99.5	610263
DNAL1	104.0	99.3	96.2	614017
DNHD1	148.3	100.0	99.9	5
DRC1	91.2	100.0	99.3	615294
DYNC2H1	102.2	98.8	95.5	613091
DYNC2LI1	95.4	99.7	97.0	617088
EVC	106.3	95.9	92.4	225500;193530
EVC2	110.2	99.4	96.3	225500
EXOC8	152.6	100.0	100.0	1
EXTL3	184.1	100.0	100.0	6
FUZ	128.5	100.0	100.0	182940
GAS8	127.3	100.0	99.4	616726
GLIS2	129.6	100.0	100.0	611498
HYDIN	106.8	99.8	98.9	608647
HYLS1	156.6	100.0	100.0	236680
IFT122	120.5	99.9	99.0	218330
IFT140	117.6	99.9	99.2	266920
IFT172	94.5	100.0	99.4	615630
IFT27	115.8	100.0	100.0	615996
IFT43	112.4	100.0	100.0	614099
IFT52	121.0	100.0	99.7	617102
IFT80	64.9	96.7	84.7	611263
IFT81	92.3	93.6	89.0	617895
INPP5E	116.8	100.0	98.6	610156;213300
INTU	115.4	99.8	98.7	-
INVS	143.7	100.0	99.9	602088
IQCB1	93.3	91.6	80.0	609254
KCTD3	129.3	99.9	99.5	-
KIAA0556	126.6	100.0	99.6	616784

KIAA0586	117.7	97.0	93.0	616490
KIAA0753	113.2	99.9	98.7	617127
KIF14	116.6	99.6	97.9	616258
KIF7	105.2	98.2	93.5	200990;614120
LBR	103.0	98.3	91.5	169400;613471;215140
LCA5	139.9	99.8	98.9	604537
LRRC56	130.7	100.0	99.2	618254
LRRC6	139.3	99.8	97.3	614935
LZTFL1	117.0	99.8	99.2	209900
MAPKBP1	132.5	100.0	100.0	617271
MKKS	155.7	83.2	83.2	236700;209900
MKS1	92.4	99.6	97.8	249000;209900
NCAPG2	121.5	99.8	98.2	-
NEK1	115.9	99.7	98.1	263520
NEK8	141.3	100.0	99.9	613824;615415
NME8	104.7	98.6	93.8	610852
NPHP1	121.2	99.8	98.5	266900;609583;256100
NPHP3	121.4	99.8	98.5	208540;267010;604387
NPHP4	125.6	100.0	99.7	606996;606966
OCRL	106.2	99.8	98.3	300555;309000
OFD1	51.9	85.8	70.8	300424;300209;300804;311200
PDE6D	114.7	100.0	99.9	615665
PIBF1	74.3	99.2	94.4	617767
PIH1D3	74.7	98.4	89.1	300991
PKD1	35.9	43.0	35.0	173900
PKD2	102.3	98.7	95.8	613095
PKHD1	130.4	99.9	99.4	263200
POC1A	112.9	100.0	100.0	614813
RPGRIP1L	123.4	96.7	95.4	611561;611560;216360
RSPH1	122.6	100.0	99.9	615481

RSPH3	139.5	99.9	99.3	616481
RSPH4A	146.9	98.1	95.3	612649
RSPH9	131.2	99.7	97.1	612650
SCLT1	90.3	95.8	90.8	2
SDCCAG8	124.1	100.0	99.7	613615
SPAG1	101.6	99.1	95.3	615505
SPATA7	122.7	99.4	97.4	604232
TBC1D32	95.5	99.4	96.5	3
TCTEX1D2	123.6	100.0	99.4	617405
TCTN1	94.8	95.6	92.3	614173
TCTN2	122.4	99.9	99.0	613885
TCTN3	116.3	100.0	99.9	614815;258860
TMEM107	148.7	100.0	100.0	617562;617563
TMEM138	82.7	100.0	99.2	614465
TMEM216	88.0	99.7	95.7	603194;608091
TMEM231	101.1	100.0	99.3	615397;614970
TMEM237	117.7	100.0	99.2	614424
TMEM260	117.5	99.6	97.6	617478
TMEM67	83.1	99.1	94.6	607361;216360;613550;610688;209900
TRAF3IP1	84.2	99.4	97.1	616629
TRIM32	123.0	100.0	100.0	254110;209900
TTBK2	108.4	99.9	96.8	604432
TTC21B	119.5	99.7	98.8	613819;613820
TTC25	93.7	100.0	99.6	617092
TTC26	140.5	99.8	99.2	7
TTC8	115.2	99.8	98.8	613464;209900
TULP1	117.9	100.0	99.6	600132;613843
VHL	169.6	100.0	98.3	193300;171300;144700;263400
WDPCP	106.7	97.8	94.9	209900
WDR19	126.8	100.0	99.2	614376;614377;614378

WDR34	116.1	100.0	100.0	615633
WDR35	141.8	99.7	98.4	613610;614091
WDR60	108.1	99.7	98.1	615503
XPNPEP3	99.9	100.0	99.4	613159
ZMYND10	123.0	100.0	100.0	615444
ZNF423	192.9	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