WES HEARING IMPAIRMENT DG 3.1

Gene	Median coverage	% covered >10x	% covered >20x	OMIM disease ID
ABCC1	127.4	98.9	97.9	-
ABHD12	94.6	91.2	85.2	612674
ACTB	74.3	99.7	96.1	243310;607371
ACTG1	121.5	100.0	100.0	614583;604717
ADCY1	152.3	95.2	93.8	610154
ADGRV1	155.0	99.6	98.6	605472
AIFM1	117.3	99.9	98.8	300614
ALMS1	203.4	99.8	99.5	203800
AMMECR1	94.4	100.0	99.1	No OMIM phenotype
ANLN	170.7	98.7	97.5	No OMIM phenotype
AP1B1	147.3	100.0	99.5	242150
ARSG	132.9	100.0	99.5	618144
ATOH1	120.4	100.0	100.0	No OMIM phenotype
ATP1A3	173.5	100.0	99.9	-
ATP2B2	182.6	100.0	99.9	-
ATP6V0A4	134.0	100.0	99.9	602722
ATP6V1B1	199.1	100.0	100.0	267300
ATP6V1B2	143.7	100.0	99.3	124480
BCAP31	80.0	92.6	83.2	300475
BCS1L	158.0	100.0	100.0	262000
BDP1	131.0	98.8	95.3	618257
BMP4	178.6	100.0	100.0	-
BSND	157.9	100.0	100.0	602522
BTD	127.0	83.1	83.0	253260
CABP2	77.7	75.9	68.0	614899

CACNA1D	155.8	98.0	97.9	614896
CCDC50	139.0	100.0	99.7	607453
CD151	141.6	100.0	100.0	609057
CD164	132.4	99.1	94.8	616969
CDC14A	187.1	100.0	99.0	616958
CDC42	121.8	97.9	90.9	616737
CDH23	187.8	100.0	100.0	601067;601386
CEACAM16	132.0	100.0	99.5	614614
CEP250	102.9	100.0	99.2	618358
CEP78	129.4	98.9	96.8	617236
CHD7	158.7	100.0	99.5	214800
CHSY1	147.1	97.2	95.7	605282
CIB2	203.3	99.7	97.0	614869;609439
CISD2	135.4	83.4	83.4	604928
CLDN14	90.1	100.0	99.7	614035
CLDN9	111.5	100.0	100.0	-
CLIC5	100.6	89.9	88.0	616042
CLPP	147.3	100.0	99.1	614129
CLRN1	168.2	100.0	99.8	276902
CLRN2	132.3	99.7	96.6	No OMIM phenotype
COA8	92.5	81.9	80.7	220110
COCH	170.5	95.2	93.2	601369
COL11A1	113.4	96.2	92.8	154780;604841
COL11A2	127.0	100.0	99.7	184840;609706;277610;601868;215150
COL2A1	125.9	100.0	99.7	215150;108300;132450;156550
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
COL4A6	95.6	97.5	93.3	300914
COL9A1	159.8	100.0	99.2	614134

COL9A2	103.5	99.9	99.0	614284
COL9A3	109.1	98.7	95.5	-
CRYL1	129.2	100.0	99.9	-
CRYM	92.9	100.0	99.6	616357
DCAF17	107.3	98.9	93.3	241080
DCDC2	174.2	100.0	99.9	610212
DIABLO	209.6	100.0	99.9	614152
DIAPH1	119.5	99.8	99.0	124900
DIAPH3	96.5	99.6	97.0	609129
DLX5	143.1	100.0	99.9	183600 220600
DMXL2	183.8	99.9	99.1	617605
DSPP	67.8	96.8	86.1	605594
EDN3	142.6	98.8	98.8	613265
EDNRB	134.4	98.0	93.8	277580;600501
EFNB2	175.0	100.0	99.8	-
ELMOD3	159.6	100.0	99.8	615429
EPS8	141.0	97.0	96.2	615974
EPS8L2	123.5	84.5	82.5	617637
ERAL1	173.9	100.0	99.7	617565
ESPN	26.9	44.6	35.8	609006
ESRP1	122.5	99.9	98.9	618013
ESRRB	112.3	96.8	95.0	608565
EXOSC2	117.6	100.0	100.0	617763
EYA1	145.7	99.9	99.7	602588;166780;113650
EYA4	155.3	100.0	99.7	605362;601316
FDXR	126.5	100.0	99.3	617717
FGF3	110.3	99.8	95.1	610706
FGFR3	122.6	99.8	97.7	602849
FITM2	160.1	100.0	100.0	618635
FOXF2	73.2	93.6	86.6	-

FOXI1	223.4	100.0	100.0	600791
GAB1	196.0	100.0	99.4	605428
GAS2	149.7	100.0	100.0	-
GATA3	254.6	100.0	100.0	146255
GIPC3	26.2	24.8	23.0	601869
GJB2	135.4	100.0	100.0	602540;149200;148350;601544;220290;148210;124500
GJB3	250.6	100.0	100.0	220290;612644
GJB6	145.5	100.0	100.0	612645;220290;612643
GLA	81.9	91.1	88.2	301500
GPSM2	146.8	99.9	99.2	604213
GRAP	83.7	82.8	78.3	618456
GREB1L	153.1	100.0	99.9	-
GRHL2	139.4	100.0	100.0	608641
GRXCR1	185.8	100.0	99.8	613285
GRXCR2	135.0	100.0	100.0	615837
GSDME	104.1	100.0	99.2	600994
HARS1	152.0	100.0	100.0	614504
HARS2	148.6	100.0	100.0	614926
HGF	168.8	100.0	99.4	608265
HOMER2	139.8	99.5	99.4	616707
HSD17B4	130.0	95.4	93.1	233400
IFNLR1	122.6	99.4	97.1	-
ILDR1	117.9	99.9	98.4	609646
KARS1	133.2	100.0	99.9	613916
KCNE1	438.4	100.0	100.0	612347
KCNJ10	157.5	89.3	89.0	612780;600791
KCNQ1	131.9	93.3	90.6	220400
KCNQ4	156.2	97.0	95.7	600101
KITLG	101.9	100.0	98.5	616697
LARS2	143.2	100.0	100.0	615300

LHFPL5	253.3	100.0	100.0	610265
LMX1A	113.7	100.0	100.0	301412
LOXHD1	131.1	100.0	99.7	613079
LOXL3	156.4	100.0	99.2	-
LRP2	171.0	100.0	99.9	222448
LRP5	179.9	98.5	98.1	144750;607634
LRTOMT	147.3	100.0	99.2	611451
MAN2B1	142.3	99.8	97.9	No OMIM phenotype
MARVELD2	186.4	99.2	96.1	610153
MCM2	158.8	100.0	100.0	616968
MET	178.5	100.0	99.5	616705
MGP	159.6	98.7	95.1	245150
MIA3	154.7	99.8	99.1	-
MIR96				613074
MITF	160.6	100.0	99.9	103470;103500;193510
MPZL2	113.0	100.0	99.9	618145
MSRB3	151.5	100.0	99.4	613718
MYH14	114.1	98.4	94.0	614369;600652
MYH9	134.9	100.0	99.3	153640;600208;603622;153650
MYO15A	141.6	98.8	97.0	600316
MYO3A	125.9	99.6	96.6	607101
MYO6	115.6	99.5	96.6	606346;607821
MYO7A	137.1	99.3	97.3	600060;276900;601317
NARS2	145.9	98.3	97.4	618434
NCOA3	155.3	99.6	97.4	No OMIM phenotype
NDP	89.0	100.0	99.7	310600
NLRP3	153.4	100.0	99.9	191900
NOG	175.6	100.0	100.0	-
OPA1	155.2	99.6	97.6	125250
OSBPL2	154.4	100.0	100.0	616340

OTOA	116.2	99.4	97.6	607039
OTOF	146.0	100.0	99.9	601071
OTOG	138.9	99.4	98.6	614945
OTOGL	127.2	99.5	97.4	614944
P2RX2	186.6	100.0	100.0	608224
PAX3	114.5	100.0	99.9	148820;193500;122880
PCDH15	168.0	97.8	96.7	602083;601067;609533
PDE1C	132.6	100.0	99.6	618140
PDZD7	86.5	97.0	93.0	605472
PET100	107.1	100.0	99.6	220110
PEX1	155.5	99.9	99.4	601539;234580;214100
PEX26	94.0	100.0	100.0	614873
PEX6	113.0	94.5	86.7	616617;614863
PI4KB	117.2	100.0	99.5	No OMIM phenotype
PISD	168.8	100.0	100.0	618889
PJVK	142.3	100.0	99.7	610220
PLOD3	113.0	99.8	98.0	612394
PLS1	118.5	100.0	99.1	618787
PNPT1	63.9	97.7	89.7	614934
POLD1	121.7	98.5	95.2	615381
POLR1C	102.8	90.5	87.0	248390
POLR1D	210.1	91.6	91.6	613717
POU3F4	134.5	100.0	100.0	304400
POU4F3	242.5	100.0	100.0	602459
PPIP5K2	106.6	98.9	95.2	618422
PRKCB	164.7	100.0	100.0	-
PRORP	150.1	100.0	99.5	No OMIM phenotype
PRPS1	118.4	86.4	86.4	304500;301835;311070;300661
PSIP1	88.4	98.8	93.5	PMID:26689366
PTPRQ	122.9	94.6	92.5	613391

PTRH2	259.0	100.0	100.0	No OMIM phenotype
RAI1	187.6	100.0	100.0	182290
RDX	47.1	89.1	71.5	611022
REST	119.0	98.5	98.2	612431
RIPOR2	133.3	100.0	99.8	616515
RMND1	165.2	100.0	98.6	614922
ROBO1	181.5	100.0	99.9	-
ROR1	172.5	97.0	96.8	617654
RRM2B	163.8	100.0	99.7	No OMIM phenotype
S1PR2	169.3	99.4	96.9	610419
SCD5	138.6	100.0	99.8	-
SERAC1	134.6	99.9	99.5	No OMIM phenotype
SERPINB6	157.9	93.4	93.4	613453
SIX1	137.0	100.0	99.2	605192;608389
SIX5	67.0	95.4	88.2	610896
SLC12A1	167.4	96.2	96.1	-
SLC12A2	112.0	94.0	91.4	https://www.ncbi.nlm.nih.gov/pubmed/32294086
SLC17A8	158.6	100.0	100.0	605583
SLC19A2	110.3	100.0	99.7	249270
SLC22A4	131.7	100.0	99.6	-
SLC26A4	141.0	100.0	99.7	600791;274600
SLC26A5	160.1	99.1	96.8	613865
SLC29A3	192.3	100.0	99.6	602782
SLC33A1	156.2	99.9	98.9	614482
SLC44A4	138.2	100.0	99.5	617606
SLC52A2	170.8	100.0	100.0	614707
SLC52A3	125.5	100.0	100.0	211530
SLC9A3R1	134.6	100.0	98.7	-
SLITRK6	197.2	100.0	100.0	221200
SMPX	76.2	100.0	97.6	300066

SNAI2	115.6	100.0	99.1	172800;608890
SOX10	70.3	99.9	97.9	613266;609136;611584
SPATA5	167.7	100.0	99.7	616577
SPNS2	141.8	92.1	89.3	618457
STRC	107.4	99.9	98.0	603720
SUCLA2	62.7	89.5	82.2	612073
SYNE4	88.0	99.7	97.0	615540
TBC1D24	172.2	100.0	100.0	220500;616044;614617
TBL1Y	41.6	49.4	45.3	No OMIM phenotype
TCOF1	123.4	99.7	98.6	154500
TECTA	179.6	100.0	99.9	601543;603629
TFAP2A	119.1	99.4	94.3	No OMIM phenotype
THOC1	120.8	99.7	97.8	No OMIM phenotype
TIMM8A	62.7	98.1	90.6	304700
TJP2	117.6	92.8	92.5	613558
TMC1	141.1	99.7	97.3	606705;600974
TMEM132E	117.8	96.9	93.5	618481
TMIE	116.5	99.2	95.1	600971
TMPRSS3	116.6	100.0	99.9	601072
TMTC2	172.1	97.5	97.5	-
TNC	158.0	100.0	99.8	615629
TPRN	93.4	87.9	79.3	613307
TRIOBP	184.6	97.8	96.1	609823
TRRAP	159.0	99.9	99.5	618778
TSHZ1	155.0	98.8	98.8	607842
TSPEAR	160.3	100.0	99.2	614861
TUBB4B	81.1	99.9	96.9	617879
TWNK	202.8	100.0	100.0	616138
TYR	164.5	100.0	100.0	103470
USH1C	109.5	100.0	99.8	276904;602092

USH1G	161.0	99.6	97.9	606943
USH2A	156.7	100.0	99.8	613809;276901
USP48	163.5	99.9	99.3	No OMIM phenotype
WBP2	101.9	100.0	99.7	617639
WFS1	193.0	100.0	99.9	222300;600965;614296
WHRN	126.9	99.8	98.0	611383;607084
XYLT2	149.8	100.0	98.3	605822
YAP1	106.6	96.4	89.4	120433

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