

WES HEARING IMPAIRMENT DG 2.16

<i>Gene</i>	<i>Median coverage</i>	<i>% covered >10x</i>	<i>% covered >20x</i>	<i>OMIM disease ID</i>
ACTB	80.5	100.0	99.7	607371;243310
ACTG1	116.3	100.0	100.0	604717;614583
ADCY1	134.5	96.8	95.4	610154
ADGRV1	126.0	99.7	98.4	605472
AIFM1	90.0	99.8	96.7	300614
APOPT1	78.3	82.0	81.5	220110
ATP1A3	159.8	100.0	100.0	-
ATP2B2	163.0	100.0	99.8	-
ATP6V1B1	172.2	100.0	100.0	267300
BCS1L	147.9	100.0	100.0	262000
BDP1	135.3	98.2	94.3	618257
BMP4	173.4	100.0	100.0	-
BSND	139.4	100.0	99.9	602522
CABP2	76.6	78.5	71.0	614899
CACNA1D	127.4	98.0	97.7	614896
CCDC50	122.1	100.0	99.7	607453
CD164	121.8	99.0	94.5	616969
CDC14A	150.1	99.6	97.4	616958
CDH23	172.7	100.0	100.0	601067;601386
CEACAM16	130.5	100.0	100.0	614614
CEP78	120.1	99.7	97.6	617236
CIB2	198.0	99.9	99.4	614869;609439
CLDN14	111.7	100.0	99.9	614035
CLIC5	97.6	100.0	99.9	616042
CLPP	139.3	100.0	99.2	614129

CLRN1	135.3	100.0	99.4	276902
COCH	159.5	100.0	99.9	601369
COL11A1	96.6	97.9	94.0	604841;154780
COL11A2	111.6	100.0	99.4	277610;601868;609706;215150;184840
COL2A1	112.2	100.0	99.7	108300;215150;132450;156550
COL4A3	90.5	99.6	97.7	203780;104200
COL4A4	92.4	99.8	97.4	203780
COL4A5	56.8	96.8	85.7	301050
COL4A6	81.4	97.1	92.0	300914
COL9A1	132.3	100.0	99.7	614134
COL9A2	95.2	99.9	98.8	614284
CRYM	82.5	99.8	97.2	616357
DCDC2	150.0	99.9	99.8	610212
DFNA5	90.9	99.9	99.0	600994
DFNB59	116.8	99.9	98.8	610220
DIABLO	174.0	100.0	99.6	614152
DIAPH1	101.7	99.9	99.6	124900
DIAPH3	82.7	99.7	96.9	609129
DMXL2	154.0	99.8	98.9	617605
DSPP	79.0	98.4	93.8	605594
EDN3	135.2	100.0	100.0	613265
EDNRB	120.9	96.9	92.5	600501;277580
ELMOD3	135.8	100.0	99.9	615429
EPS8	114.6	99.8	96.6	615974
EPS8L2	159.7	99.0	96.3	617637
ERAL1	156.5	100.0	100.0	617565
ESPN	30.8	53.5	42.4	609006
ESRP1	95.3	99.8	98.4	618013
ESRRB	121.7	99.9	99.1	608565
EXOSC2	110.3	100.0	99.9	617763

EYA1	120.2	99.9	99.8	166780;113650;602588
EYA4	136.9	100.0	99.9	601316;605362
FGF3	139.5	100.0	100.0	610706
FOXF2	104.8	94.9	91.6	-
FOXI1	194.5	100.0	100.0	600791
GAB1	155.1	100.0	99.5	605428
GATA3	220.5	100.0	100.0	146255
GIPC3	127.8	98.9	95.2	601869
GJB2	141.4	100.0	100.0	220290;124500;149200;148210;602540;148350;601544
GJB3	228.5	100.0	100.0	220290;612644
GJB6	140.9	100.0	100.0	220290;612643;612645
GPSM2	119.6	99.8	99.0	604213
GRAP	79.2	85.4	80.1	-
GREB1L	128.0	99.9	99.0	-
GRHL2	116.8	100.0	100.0	608641
GRXCR1	154.5	100.0	99.7	613285
GRXCR2	112.4	100.0	99.9	615837
HARS	134.8	100.0	100.0	614504
HARS2	136.6	100.0	99.9	614926
HGF	138.0	99.9	99.2	608265
HOMER2	113.1	99.8	97.8	616707
HSD17B4	109.4	96.3	93.6	233400
IFNLR1	102.2	99.9	98.9	-
ILDR1	111.5	99.9	98.7	609646
KARS	104.1	100.0	98.8	613916
KCNE1	369.2	100.0	100.0	612347
KCNJ10	148.6	89.2	88.1	612780;600791
KCNQ1	135.8	97.9	95.3	220400
KCNQ4	165.1	99.2	97.7	600101
KITLG	83.3	99.6	97.2	616697

LARS2	122.8	100.0	100.0	615300
LHFPL5	207.7	100.0	100.0	610265
LMX1A	106.1	100.0	100.0	-
LOXHD1	113.3	99.9	99.5	613079
LRP5	168.1	99.8	98.7	144750;607634
LRTOMT	114.4	99.1	94.4	611451
MARVELD2	139.0	98.8	95.9	610153
MCM2	151.9	100.0	100.0	616968
MET	151.3	99.9	99.3	616705
MIR96				613074
MITF	141.1	100.0	99.8	103470;193510;103500
MPZL2	91.7	100.0	99.8	618145
MSRB3	131.9	99.9	99.6	613718
MYH14	109.8	99.0	95.1	600652;614369
MYH9	128.5	99.6	98.5	153650;153640;600208;603622
MYO15A	143.7	99.8	98.8	600316
MYO3A	113.0	99.2	95.3	607101
MYO6	101.5	99.5	96.4	607821;606346
MYO7A	125.2	99.8	98.5	601317;600060;276900
NARS2	120.7	97.6	97.2	-
NLRP3	134.6	100.0	99.9	191900
OPA1	124.7	99.7	97.4	125250
OSBPL2	138.2	100.0	100.0	616340
OTOA	97.2	99.7	98.3	607039
OTOF	135.6	100.0	99.8	601071
OTOG	134.6	99.6	98.8	614945
OTOGL	104.6	99.4	97.0	614944
P2RX2	174.5	100.0	100.0	608224
PAX3	106.9	100.0	99.7	193500;148820;122880
PCDH15	140.3	99.2	99.0	602083;609533;601067

PDE1C	108.0	99.8	99.4	618140
PDZD7	93.9	99.6	97.8	605472
PET100	87.9	98.0	87.6	220110
PEX1	127.9	99.9	99.3	214100;234580;601539
PEX26	94.3	100.0	99.6	614873
PEX6	106.5	98.5	92.0	616617;614863
PNPT1	56.1	96.2	84.3	614934
POU3F4	135.9	100.0	100.0	304400
POU4F3	261.7	100.0	100.0	602459
PPIP5K2	87.9	98.8	94.3	-
PRKCB	138.2	100.0	99.9	-
PRPS1	111.6	100.0	99.9	301835;311070;304500;300661
PTPRQ	102.5	94.5	92.3	613391
RAI1	194.4	100.0	100.0	182290
RDX	38.4	88.0	69.1	611022
REST	115.5	98.5	98.4	-
RIPOR2	111.5	100.0	99.8	616515
ROR1	149.1	99.1	97.2	617654
S1PR2	200.8	99.5	96.8	610419
SERPINB6	138.9	95.9	95.9	613453
SIX1	131.1	99.9	98.7	608389;605192
SIX5	76.3	99.9	97.3	610896
SLC17A8	121.5	100.0	99.8	605583
SLC22A4	112.9	99.9	98.5	-
SLC25A2	214.8	100.0	100.0	-
SLC26A4	113.0	100.0	99.5	274600;600791
SLC26A5	130.3	98.3	95.4	613865
SLC29A3	173.3	100.0	99.5	602782
SLC33A1	132.0	99.7	97.7	614482
SLC44A4	113.9	100.0	99.4	617606

SLITRK6	169.5	100.0	100.0	221200
SMPX	63.9	99.8	97.0	300066
SNAI2	102.7	99.9	99.1	172800;608890
SOX10	88.2	100.0	99.1	609136;611584;613266
SPATA5	139.5	100.0	99.8	616577
STRC	99.0	99.9	98.1	603720
SYNE4	83.7	99.9	98.5	615540
TBC1D24	177.7	100.0	100.0	614617;616044;220500
TECTA	164.9	100.0	99.9	603629;601543
TIMM8A	46.3	94.6	79.9	304700
TJP2	109.3	94.0	93.4	613558
TMC1	110.1	99.8	97.5	600974;606705
TMEM132E	124.7	99.2	96.5	-
TMIE	104.5	100.0	99.7	600971
TMPRSS3	98.5	100.0	99.4	601072
TMTC2	140.2	97.5	97.5	-
TNC	143.1	100.0	99.7	615629
TPRN	98.7	91.5	86.7	613307
TRIOBP	156.9	99.1	97.5	609823
TSPEAR	139.3	100.0	99.8	614861
TYR	147.9	100.0	99.9	103470
USH1C	92.5	99.9	99.2	602092;276904
USH1G	191.3	99.9	98.8	606943
USH2A	129.3	100.0	99.7	613809;276901
WBP2	94.3	100.0	99.9	617639
WFS1	189.9	100.0	99.9	600965;614296;222300
WHRN	132.8	99.9	99.0	611383;607084
YAP1	91.1	98.2	92.3	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 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