

# WES HEARING IMPAIRMENT DG 2.14

<i>Gene</i>	<i>Median coverage</i>	<i>% covered &gt;10x</i>	<i>% covered &gt;20x</i>	<i>OMIM disease ID</i>
ACTB	129.0	99.1	94.2	607371;243310
ACTG1	149.4	100.0	100.0	604717;614583
ADCY1	145.0	94.7	93.3	610154
ADGRV1	140.3	99.5	97.0	605472
AIFM1	106.2	100.0	99.7	300614
APOPT1	63.8	81.4	78.1	220110
ATP1A3	177.3	100.0	100.0	-
ATP2B2	186.5	100.0	100.0	-
ATP6V1B1	176.6	100.0	100.0	267300
BCS1L	182.3	100.0	100.0	262000
BDP1	125.5	95.6	90.0	-
BSND	137.1	100.0	100.0	602522
CABP2	67.1	74.6	65.5	614899
CACNA1D	149.9	98.0	97.8	614896
CCDC50	135.1	99.9	98.9	607453
CD164	130.4	98.0	93.9	616969
CDC14A	161.4	98.3	93.5	616958
CDH23	197.2	100.0	100.0	601067;601386
CEACAM16	144.9	100.0	99.7	614614
CEP78	112.1	97.0	93.9	617236
CIB2	229.9	99.9	99.6	614869;609439
CLDN14	130.6	100.0	99.9	614035
CLIC5	118.3	100.0	99.9	616042
CLPP	115.4	99.8	96.9	614129
CLRN1	157.2	100.0	99.8	276902

COCH	194.4	99.9	99.6	601369
COL11A1	90.8	94.9	89.6	604841;154780
COL11A2	92.2	99.9	98.3	277610;601868;609706;215150;184840
COL2A1	103.4	99.9	99.0	108300;215150;132450;156550
COL4A3	89.6	97.8	95.5	203780;104200
COL4A4	85.0	97.6	93.5	203780
COL4A5	52.3	92.1	77.5	301050
COL4A6	81.2	96.0	89.4	300914
COL9A1	121.2	99.5	96.9	614134
COL9A2	65.1	98.3	88.8	614284
CRYM	97.4	99.9	98.3	616357
DCDC2	150.5	99.9	99.6	610212
DFNA5	112.9	99.9	99.4	600994
DFNB59	123.6	100.0	99.2	610220
DIABLO	206.0	100.0	99.5	614152
DIAPH1	120.7	99.3	97.8	124900
DIAPH3	73.9	97.9	90.1	609129
DMXL2	181.4	98.6	96.0	617605
DSPP	155.7	99.9	99.3	605594
EDN3	134.4	100.0	99.5	613265
EDNRB	131.0	95.6	90.9	600501;277580
ELMOD3	156.2	100.0	99.7	615429
EPS8	122.8	96.9	91.4	615974
EPS8L2	115.1	94.4	90.9	617637
ERAL1	181.5	100.0	100.0	617565
ESPN	28.6	44.2	35.3	609006
ESRP1	106.5	99.9	98.5	618013
ESRRB	119.7	100.0	99.2	608565
EXOSC2	142.0	100.0	100.0	617763
EYA1	144.2	100.0	99.7	166780;113650;602588

EYA4	160.6	100.0	99.5	601316;605362
FGF3	73.9	92.0	75.7	610706
FOXI1	152.5	100.0	100.0	600791
FRMPD4	114.1	99.7	98.0	-
GAB1	170.0	100.0	99.7	605428
GATA3	186.8	100.0	100.0	146255
GIPC3	103.3	91.8	85.5	601869
GJB2	205.1	100.0	100.0	220290;124500;149200;148210;602540;148350;601544
GJB3	308.9	100.0	100.0	220290;612644
GJB6	185.4	100.0	100.0	220290;612643;612645
GPSM2	112.9	99.8	97.0	604213
GRHL2	134.6	100.0	100.0	608641
GRXCR1	183.7	100.0	99.8	613285
GRXCR2	114.9	100.0	100.0	615837
HARS	159.4	100.0	100.0	614504
HARS2	169.7	99.9	99.2	614926
HGF	146.9	99.4	96.9	608265
HOMER2	133.5	99.5	99.4	616707
HSD17B4	95.1	93.9	90.8	233400
IFNLR1	90.6	97.6	96.5	-
ILDR1	107.4	100.0	99.9	609646
KARS	122.6	100.0	99.3	613916
KCNE1	462.6	100.0	100.0	612347
KCNJ10	213.4	89.3	89.1	612780;600791
KCNQ1	114.7	93.0	90.3	220400
KCNQ4	135.2	93.7	89.1	600101
KITLG	81.8	97.0	91.6	616697
LARS2	143.0	100.0	100.0	615300
LHFPL5	287.7	100.0	100.0	610265
LMX1A	109.2	100.0	99.9	-

LOXHD1	136.5	100.0	99.6	613079
LRP5	189.8	98.2	97.9	144750;607634
LRTOMT	125.9	99.8	96.6	611451
MARVELD2	159.4	97.5	94.0	610153
MCM2	176.8	100.0	100.0	616968
MET	184.7	100.0	99.6	616705
MIR96				613074
MITF	155.5	100.0	99.9	103470;193510;103500
MPZL2	96.9	100.0	100.0	-
MSRB3	155.6	99.7	98.5	613718
MYH14	102.0	97.7	91.5	600652;614369
MYH9	130.5	99.4	98.1	153650;153640;600208;603622
MYO15A	116.5	97.3	94.0	600316
MYO3A	119.8	98.5	93.0	607101
MYO6	89.7	98.1	92.3	607821;606346
MYO7A	134.1	99.7	98.1	601317;600060;276900
NARS2	120.0	97.4	97.1	-
NLRP3	150.4	100.0	100.0	191900
OPA1	122.5	99.1	94.1	125250
OSBPL2	145.8	100.0	100.0	616340
OTOA	117.3	99.0	96.6	607039
OTOF	131.2	100.0	99.7	601071
OTOG	145.1	99.4	98.2	614945
OTOGL	113.3	98.4	93.9	614944
P2RX2	132.8	99.0	95.5	608224
PAX3	118.5	100.0	100.0	193500;148820;122880
PCDH15	153.9	99.0	98.0	602083;609533;601067
PDE1C	124.0	100.0	99.7	-
PDZD7	80.9	98.4	93.9	605472
PET100	94.5	88.8	74.8	220110

PEX1	115.8	97.7	95.4	214100;234580;601539
PEX6	94.5	90.4	86.1	616617;614863
PNPT1	53.7	93.3	80.9	614934
POU3F4	151.0	100.0	99.9	304400
POU4F3	298.1	100.0	100.0	602459
PPIP5K2	74.7	96.6	86.6	-
PRKCB	164.5	100.0	99.8	-
PRPS1	149.5	100.0	100.0	301835;311070;304500;300661
PTPRQ	104.7	93.3	89.1	613391
RAI1	146.3	100.0	99.7	182290
RDX	43.2	84.7	64.8	611022
RIPOR2	121.4	100.0	99.9	616515
ROR1	177.5	96.8	96.8	617654
S1PR2	278.0	97.4	92.7	610419
SERPIN6	164.1	95.9	95.9	613453
SIX1	117.3	99.7	97.6	608389;605192
SIX5	43.8	88.3	76.1	610896
SLC17A8	132.7	100.0	100.0	605583
SLC22A4	119.1	99.8	98.2	-
SLC25A2	219.9	100.0	100.0	-
SLC26A4	123.3	99.9	99.1	274600;600791
SLC26A5	150.9	98.7	95.8	613865
SLC29A3	203.6	99.9	99.5	602782
SLC33A1	140.9	96.8	90.1	614482
SLC44A4	122.9	100.0	99.9	617606
SLITRK6	206.9	100.0	100.0	221200
SMPX	68.5	99.9	95.5	300066
SNAI2	129.8	100.0	99.8	172800;608890
SOX10	65.8	98.2	91.3	609136;611584;613266
SPATA5	132.0	99.9	99.2	616577

STRC	119.0	99.9	98.4	603720
SYNE4	73.9	98.3	91.6	615540
TBC1D24	179.2	100.0	100.0	614617;616044;220500
TECTA	208.0	100.0	100.0	603629;601543
TIMM8A	46.0	94.5	78.8	304700
TJP2	111.1	93.8	92.2	-
TMC1	122.8	98.2	93.8	600974;606705
TMEM132E	115.9	94.8	91.8	-
TMIE	109.6	98.8	92.1	600971
TMPRSS3	125.5	100.0	99.9	601072
TMTC2	146.9	97.5	97.4	-
TNC	187.5	100.0	99.7	615629
TPRN	62.7	74.7	65.4	613307
TRIOBP	135.6	97.0	94.9	609823
TSPEAR	141.5	100.0	99.0	614861
TYR	185.3	100.0	100.0	103470
USH1C	97.5	100.0	99.4	602092;276904
USH1G	195.3	98.4	96.3	606943
USH2A	148.5	100.0	99.7	613809;276901
WBP2	93.7	100.0	100.0	617639
WFS1	251.4	100.0	99.7	600965;614296;222300
WHRN	114.0	99.8	98.8	611383;607084
YAP1	95.6	87.8	81.6	120433

Gene symbols used follow HGNC 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