

WES HEARING IMPAIRMENT DG 3.2

<i>Gene</i>	<i>Median coverage</i>	<i>% covered >10x</i>	<i>% covered >20x</i>	<i>OMIM disease ID</i>
ABCC1	116.0	98.9	97.1	-
ABHD12	81.7	91.7	86.0	612674
ACTB	80.2	99.9	97.2	243310;607371
ACTG1	128.6	100.0	100.0	614583;604717
ADAMTS1	140.7	100.0	100.0	No OMIM phenotype
ADCY1	136.2	95.7	94.3	610154
ADGRV1	134.4	99.5	98.4	605472
AIFM1	103.9	99.9	97.8	300614
ALMS1	174.7	99.7	99.5	203800
AMMECR1	86.2	99.9	98.4	300990
ANLN	139.1	98.4	97.0	No OMIM phenotype
AP1B1	148.4	100.0	99.4	242150
ARSG	119.0	99.9	98.0	618144
ATOH1	128.8	100.0	100.0	No OMIM phenotype
ATP1A3	174.1	100.0	99.9	-
ATP2B2	173.9	100.0	99.8	-
ATP6V0A4	105.4	100.0	99.3	602722
ATP6V1B1	193.2	100.0	100.0	267300
ATP6V1B2	130.3	99.9	99.3	124480
BCAP31	67.6	92.1	79.1	300475
BCS1L	143.8	100.0	100.0	262000
BDP1	108.0	97.4	93.1	618257
BMP4	175.3	100.0	100.0	-
BSND	139.1	100.0	99.9	602522
BTD	106.1	83.0	82.9	253260

CABP2	78.1	75.4	64.9	614899
CACNA1D	133.5	97.9	97.7	614896
CCDC50	117.1	100.0	99.7	607453
CD151	148.2	100.0	100.0	609057
CD164	112.5	98.1	91.8	616969
CDC14A	162.3	99.9	99.2	616958
CDC42	94.5	96.3	87.9	616737
CDH23	189.6	100.0	100.0	601067;601386
CEACAM16	143.6	100.0	99.2	614614
CEP250	95.4	99.9	98.4	618358
CEP78	114.1	98.8	95.6	617236
CHD7	137.1	100.0	99.2	214800
CHSY1	122.1	97.8	96.3	605282
CIB2	218.0	99.3	96.2	614869;609439
CISD2	112.9	83.4	83.4	604928
CLDN14	94.8	100.0	99.5	614035
CLDN9	138.2	100.0	100.0	-
CLIC5	95.3	89.5	87.3	616042
CLPP	146.0	100.0	99.5	614129
CLRN1	127.0	100.0	99.7	276902
CLRN2	92.8	99.9	98.2	No OMIM phenotype
COA8	71.5	81.9	80.8	220110
COCH	142.7	95.0	93.5	601369
COL11A1	100.9	96.0	92.7	154780;604841
COL11A2	126.7	100.0	99.6	184840;609706;277610;601868;215150
COL2A1	122.0	100.0	99.8	215150;108300;132450;156550
COL4A3	95.5	98.9	97.4	203780;104200
COL4A4	98.4	99.6	97.4	203780
COL4A5	59.3	97.6	86.6	301050
COL4A6	87.8	96.9	90.8	300914

COL9A1	129.1	99.9	98.6	614134
COL9A2	105.0	99.9	98.9	614284
COL9A3	106.6	98.9	95.5	-
CRYL1	112.9	100.0	99.9	-
CRYM	83.3	100.0	97.9	616357
DCAF17	92.0	98.5	93.4	241080
DCDC2	146.2	100.0	99.9	610212
DIABLO	170.4	99.9	97.9	614152
DIAPH1	100.4	99.8	98.4	124900
DIAPH3	85.1	99.0	96.4	609129
DLX5	118.4	99.9	98.2	183600;220600
DMXL2	156.6	99.7	98.9	617605
DSPP	64.8	97.8	93.5	605594
EDN3	142.2	98.8	98.8	613265
EDNRB	117.4	96.3	92.5	277580;600501
EFNB2	152.7	100.0	99.7	-
ELMOD3	145.5	100.0	100.0	615429
ELOVL1	87.5	99.6	96.5	618527
EPS8	123.6	96.9	96.0	615974
EPS8L2	136.3	84.7	82.3	617637
ERAL1	164.8	100.0	99.6	617565
ESPN	28.5	48.5	38.4	609006
ESRP1	101.1	99.9	98.4	618013
ESRRB	112.5	96.2	93.0	608565
EXOSC2	109.0	100.0	99.9	617763
EYA1	120.9	99.9	99.5	602588;166780;113650
EYA4	131.3	99.9	99.9	605362;601316
FDXR	131.6	100.0	98.6	617717
FGF3	125.9	100.0	98.7	610706
FGFR3	124.7	99.8	98.0	602849

FITM2	147.8	100.0	100.0	618635
FOXF2	94.7	94.6	89.3	-
FOXI1	210.3	100.0	100.0	600791
GAB1	167.9	99.9	98.9	605428
GAS2	129.8	100.0	100.0	-
GATA3	244.6	100.0	100.0	146255
GIPC3	26.8	24.9	23.2	601869
GJB2	133.1	100.0	100.0	602540;149200;148350;601544;220290;148210;124500
GJB3	247.9	100.0	100.0	220290;612644
GJB6	121.9	100.0	100.0	612645;220290;612643
GLA	72.8	91.0	85.9	301500
GPRASP2	74.3	100.0	98.9	No OMIM phenotype
GPSM2	118.7	99.9	99.3	604213
GRAP	79.9	81.6	77.3	618456
GREB1L	134.4	100.0	99.9	-
GRHL2	125.6	100.0	99.9	608641
GRXCR1	149.7	99.8	99.5	613285
GRXCR2	113.9	100.0	100.0	615837
GSDME	95.6	99.9	98.3	600994
HARS1	135.7	100.0	100.0	614504
HARS2	126.8	100.0	99.5	614926
HGF	147.3	99.7	99.6	608265
HOMER2	118.7	99.5	98.6	616707
HSD17B4	114.3	95.3	92.8	233400
IFNLR1	115.6	99.8	98.2	-
ILDR1	109.0	99.1	97.1	609646
KARS1	109.3	99.9	98.9	613916
KCNE1	384.7	100.0	100.0	612347
KCNJ10	146.8	89.2	88.5	612780;600791
KCNQ1	138.7	93.5	90.6	220400

KCNQ4	165.2	97.3	96.2	600101
KITLG	90.1	99.6	98.1	616697
LARS2	123.2	100.0	100.0	615300
LHFPL5	250.2	100.0	100.0	610265
LMX1A	104.4	100.0	99.9	301412
LOXHD1	119.0	99.9	98.7	613079
LOXL3	164.8	100.0	99.8	-
LRP2	147.6	100.0	99.8	222448
LRP5	183.2	99.2	98.2	144750;607634
LRTOMT	133.4	100.0	99.2	611451
MAN2B1	140.0	99.6	97.4	No OMIM phenotype
MARVELD2	164.9	98.5	94.9	610153
MCM2	153.9	100.0	99.9	616968
MET	159.2	100.0	99.4	616705
MGP	138.7	98.7	93.6	245150
MIA3	121.4	99.8	99.3	-
MIR96				613074
MITF	135.0	100.0	99.9	103470;103500;193510
MPDZ	134.4	99.8	98.5	No OMIM phenotype
MPZL2	87.0	100.0	99.9	618145
MSRB3	123.6	99.8	99.8	613718
MVD	125.2	99.7	97.5	No OMIM phenotype
MYH14	112.1	98.2	93.3	614369;600652
MYH9	132.2	99.9	98.9	153640;600208;603622;153650
MYO15A	144.0	99.1	97.6	600316
MYO3A	110.5	99.1	95.4	607101
MYO6	94.9	99.1	96.3	606346;607821
MYO7A	137.3	99.7	98.3	600060;276900;601317
NARS2	116.3	97.9	97.1	618434
NCOA3	126.9	99.0	95.9	No OMIM phenotype

NDP	89.6	100.0	99.7	310600
NLRP3	137.0	100.0	99.9	191900
NOG	189.0	100.0	100.0	-
OPA1	128.7	99.5	96.7	125250
OSBPL2	138.8	100.0	100.0	616340
OTOA	105.3	99.7	98.2	607039
OTOF	140.5	100.0	99.8	601071
OTOG	142.6	99.3	98.5	614945
OTOGL	114.2	99.3	97.1	614944
P2RX2	186.9	100.0	100.0	608224
PAX3	97.0	100.0	99.8	148820;193500;122880
PCDH15	144.5	97.9	96.8	602083;601067;609533
PDE1C	109.8	99.9	99.5	618140
PDZD7	84.5	96.0	91.5	605472
PET100	88.7	100.0	99.2	220110
PEX1	135.8	99.8	99.4	601539;234580;214100
PEX26	86.7	100.0	99.8	614873
PEX6	109.2	96.4	88.0	616617;614863
PI4KB	98.1	99.9	98.6	No OMIM phenotype
PISD	161.8	100.0	99.7	618889
PJVK	119.6	100.0	99.7	610220
PLOD3	107.9	100.0	98.7	612394
PLS1	106.3	99.7	98.8	618787
PNPT1	54.0	96.9	86.1	614934
POLD1	127.6	98.4	95.1	615381
POLR1C	83.8	89.6	84.8	248390
POLR1D	172.9	91.6	91.6	613717
POU3F4	141.8	100.0	100.0	304400
POU4F3	288.2	100.0	100.0	602459
PPIP5K2	91.1	98.2	94.8	618422

PRKCB	142.9	100.0	99.8	-
PRORP	131.5	99.7	97.9	No OMIM phenotype
PRPS1	103.4	86.4	86.3	304500;301835;311070;300661
PSIP1	76.9	97.4	88.0	-
PTPRQ	107.4	94.4	92.5	613391
PTRH2	223.0	100.0	100.0	No OMIM phenotype
RAI1	197.2	100.0	100.0	182290
RDX	39.9	87.2	69.3	611022
REST	104.1	98.4	97.4	612431
RIPOR2	114.9	99.9	99.3	616515
RMND1	156.8	99.7	97.2	614922
ROBO1	150.4	100.0	99.5	-
ROR1	143.8	97.2	96.8	617654
RRM2B	147.5	100.0	99.8	No OMIM phenotype
S1PR2	165.8	99.0	96.4	610419
SCD5	125.7	100.0	99.1	-
SERAC1	108.9	99.6	99.5	614739
SERPIN6	129.7	93.4	93.4	613453
SEZ6	123.6	100.0	98.3	No OMIM phenotype
SIX1	122.0	100.0	99.7	605192;608389
SIX5	66.7	96.9	90.1	610896
SLC12A1	139.8	96.2	96.0	-
SLC12A2	101.6	94.4	92.4	619081;619083;619080
SLC17A8	137.7	100.0	99.9	605583
SLC19A2	95.1	100.0	98.5	249270
SLC22A4	117.9	100.0	99.4	-
SLC26A4	123.6	99.9	99.7	600791;274600
SLC26A5	135.7	98.7	95.9	613865
SLC29A3	191.6	100.0	99.5	602782
SLC33A1	120.6	99.8	98.5	614482

SLC44A4	123.5	100.0	99.1	617606
SLC4A11	173.0	100.0	99.9	217400
SLC52A2	171.9	100.0	100.0	614707
SLC52A3	127.1	100.0	100.0	211530
SLC9A3R1	138.1	99.9	98.2	-
SLITRK6	171.9	100.0	99.9	221200
SMPX	56.7	99.7	94.5	300066
SNAI2	105.9	99.9	98.0	172800;608890
SOX10	69.2	99.9	97.2	613266;609136;611584
SPATA5	137.1	99.8	99.5	616577
SPNS2	131.1	92.3	89.6	618457
STRC	99.8	99.9	98.3	603720
SUCLA2	55.1	88.8	79.4	612073
SYNE4	88.4	99.9	97.5	615540
TBC1D24	180.7	100.0	100.0	220500;616044;614617
TBL1Y	34.5	48.8	43.3	No OMIM phenotype
TCOF1	120.8	99.7	98.7	154500
TECTA	163.6	100.0	99.8	601543;603629
TFAP2A	101.7	98.1	92.1	113620
THOC1	101.0	99.5	97.6	No OMIM phenotype
TIMM8A	50.9	96.2	83.1	304700
TJP2	103.2	92.8	92.3	613558
TMC1	123.3	99.8	96.6	606705;600974
TMEM132E	130.5	97.5	94.8	618481
TMIE	123.0	99.9	97.5	600971
TMPRSS3	104.0	100.0	99.3	601072
TMTC2	144.5	97.5	97.5	-
TNC	151.1	100.0	99.8	615629
TPRN	96.5	89.7	83.4	613307
TRIOBP	167.8	98.5	96.6	609823

TRRAP	139.1	99.9	99.1	618778
TSHZ1	152.9	98.8	98.8	607842
TSPEAR	147.0	100.0	99.7	614861
TUBB4B	83.7	100.0	98.7	617879
TWNK	173.4	100.0	99.9	616138
TYR	147.1	100.0	100.0	103470
USH1C	99.1	99.9	99.2	276904;602092
USH1G	172.0	99.7	96.6	606943
USH2A	133.7	100.0	99.7	613809;276901
USP48	134.9	99.9	98.9	No OMIM phenotype
WBP2	86.1	100.0	99.2	617639
WFS1	192.3	100.0	99.8	222300;600965;614296
WHRN	125.1	99.6	97.6	611383;607084
XYLT2	158.7	99.9	97.1	605822
YAP1	92.8	96.6	90.3	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.

TWIST is the default chemistry for all WES samples. Agilent V5 was the default chemistry until Q3 2021.

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 no value for coverage are non protein coding genes.

Non protein coding genes are covered, but as coverage statistics are based on protein coding regions, statistics could not be generated.

OMIM release used for OMIM disease identifiers and descriptions: September 1st, 2021.