

WES HEARING IMPAIRMENT DG 2.18

<i>Gene</i>	<i>Median coverage</i>	<i>% covered >10x</i>	<i>% covered >20x</i>	<i>OMIM disease ID</i>
ABCC1	127.4	98.9	97.9	-
ABHD12	102.3	98.7	92.3	612674
ACTB	74.3	99.7	96.1	607371;243310
ACTG1	121.5	100.0	100.0	604717;614583
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
AP1B1	147.3	100.0	99.5	242150
APOPT1	92.5	81.9	80.7	220110
ARSG	132.9	100.0	99.5	618144
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
CABP2	77.7	75.9	68.0	614899
CACNA1D	155.8	98.0	97.9	614896
CCDC50	139.0	100.0	99.7	607453
CD164	132.4	99.1	94.8	616969

CDC14A	186.1	100.0	98.9	616958
CDH23	187.3	100.0	100.0	601067;601386
CEACAM16	132.0	100.0	99.5	614614
CEP250	102.9	100.0	99.2	618358
CEP78	130.5	99.7	97.6	617236
CHD7	158.7	100.0	99.5	214800
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	116.3	100.0	99.9	616042
CLPP	147.3	100.0	99.1	614129
CLRN1	168.2	100.0	99.8	276902
COCH	191.3	100.0	99.9	601369
COL11A1	116.2	99.2	95.7	604841;154780
COL11A2	126.7	100.0	99.5	277610;601868;609706;215150;184840
COL2A1	125.9	100.0	99.7	108300;215150;132450;156550
COL4A3	111.1	98.7	98.0	203780;104200
COL4A4	107.4	99.9	98.2	203780
COL4A5	66.6	97.8	89.0	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
DCDC2	174.2	100.0	99.9	610212
DFNA5	105.5	100.0	99.2	600994
DFNB59	142.3	100.0	99.7	610220
DIABLO	220.1	100.0	99.8	614152

DIAPH1	120.5	99.8	99.0	124900
DIAPH3	96.5	99.6	97.0	609129
DMXL2	183.8	99.9	99.1	617605
DSPP	67.8	96.8	86.1	605594
EDN3	144.3	100.0	99.9	613265
EDNRB	135.9	98.0	93.8	600501;277580
EFNB2	175.0	100.0	99.8	-
ELMOD3	159.6	100.0	99.8	615429
EPS8	145.3	100.0	99.1	615974
EPS8L2	140.2	96.1	93.7	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	116.3	99.9	98.0	608565
EXOSC2	117.6	100.0	100.0	617763
EYA1	145.8	99.9	99.7	166780;113650;602588
EYA4	155.3	100.0	99.7	601316;605362
FGF3	110.3	99.8	95.1	610706
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	122.4	97.5	94.2	601869
GJB2	135.4	100.0	100.0	220290;124500;149200;148210;602540;148350;601544
GJB3	250.6	100.0	100.0	220290;612644
GJB6	145.5	100.0	100.0	220290;612643;612645
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
HARS	152.0	100.0	100.0	614504
HARS2	149.6	100.0	100.0	614926
HGF	168.8	100.0	99.4	608265
HOMER2	139.8	99.5	99.4	616707
HSD17B4	130.8	96.0	93.7	233400
IFNLR1	122.6	99.4	97.1	-
ILDR1	119.6	99.9	98.5	609646
KARS	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	139.7	95.5	94.2	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	-
LRP5	179.9	98.5	98.1	144750;607634
LRTOMT	138.3	99.3	94.2	611451
MARVELD2	186.4	99.2	96.1	610153
MCM2	158.8	100.0	100.0	616968
MET	178.5	100.0	99.5	616705
MIA3	154.7	99.8	99.1	-
MIR96				613074
MITF	160.6	100.0	99.9	103470;193510;103500
MPZL2	113.0	100.0	99.9	618145

MSRB3	151.5	100.0	99.4	613718
MYH14	114.1	98.4	94.0	600652;614369
MYH9	134.9	100.0	99.3	153650;153640;600208;603622
MYO15A	141.6	98.8	97.0	600316
MYO3A	126.0	99.6	96.6	607101
MYO6	115.6	99.5	96.6	607821;606346
MYO7A	137.0	99.3	97.4	601317;600060;276900
NARS2	145.9	98.3	97.4	618434
NLRP3	153.5	100.0	99.9	191900
NOG	175.6	100.0	100.0	-
OPA1	153.3	99.7	97.6	125250
OSBPL2	154.4	100.0	100.0	616340
OTOA	116.2	99.4	97.6	607039
OTOF	145.9	100.0	99.9	601071
OTOG	138.9	99.4	98.6	614945
OTOGL	127.5	99.5	97.4	614944
P2RX2	186.6	100.0	100.0	608224
PAX3	114.5	100.0	99.9	193500;148820;122880
PCDH15	169.5	98.6	97.5	602083;609533;601067
PDE1C	132.6	100.0	99.6	618140
PDZD7	90.4	98.8	96.3	605472
PET100	107.1	100.0	99.6	220110
PEX1	155.5	99.9	99.4	214100;234580;601539
PEX26	94.0	100.0	100.0	614873
PEX6	113.0	94.5	86.7	616617;614863
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	112.8	99.3	95.5	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	164.6	100.0	99.9	-
PRPS1	137.0	100.0	100.0	301835;311070;304500;300661
PTPRQ	122.9	94.6	92.5	613391
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
ROBO1	181.5	100.0	99.9	-
ROR1	172.5	97.0	96.8	617654
S1PR2	169.3	99.4	96.9	610419
SCD5	138.6	100.0	99.8	-
SERPIN6	162.0	95.9	95.9	613453
SIX1	137.0	100.0	99.2	608389;605192
SIX5	67.0	95.4	88.2	610896
SLC12A1	174.0	100.0	99.9	-
SLC17A8	158.6	100.0	100.0	605583
SLC19A2	110.3	100.0	99.7	249270
SLC22A4	131.7	100.0	99.6	-
SLC25A2	238.9	100.0	100.0	-
SLC26A4	141.0	100.0	99.7	274600;600791
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	138.3	100.0	99.5	617606
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	609136;611584;613266
SPATA5	167.7	100.0	99.7	616577
SPNS2	141.8	92.1	89.3	618457
STRC	107.4	99.9	98.0	603720
SYNE4	88.0	99.7	97.0	615540
TBC1D24	172.2	100.0	100.0	614617;616044;220500
TCOF1	123.4	99.7	98.6	154500
TECTA	179.6	100.0	99.9	603629;601543
TIMM8A	58.8	98.0	90.1	304700
TJP2	119.0	94.0	93.6	613558
TMC1	136.6	99.7	97.1	600974;606705
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
TSPEAR	159.3	100.0	99.2	614861
TWNK	202.8	100.0	100.0	616138
TYR	164.5	100.0	100.0	103470
USH1C	109.5	100.0	99.8	602092;276904
USH1G	161.0	99.6	97.9	606943
USH2A	156.7	100.0	99.8	613809;276901
WBP2	101.9	100.0	99.7	617639
WFS1	194.8	100.0	99.9	600965;614296;222300
WHRN	127.3	99.8	98.1	611383;607084

YAP1	106.6	96.4	89.4	120433
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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