Supplementary Material 1

Next Generation Sequencing (NGS) Method

This test examined the sequence at the coding regions and intron–exon boundaries of 198 genes that are known to be involved in inherited hearing loss disorders: *ABHD12, ABHD5, ACTB, ACTG1, ADGRV1, AIFM1, ALMS1, ANKH, ARSB, ATP6V0A4, ATP6V1B1, ATP8B1, BCS1L, BSND, BTD, BTK, CACNA1D, CATSPER2, CCDC50, CD151, CDH23, CDKN1C, CEACAM16, CEMIP, CHD7, CHSY1, CIB2, CISD2, CLCNKA, CLCNKB, CLDN14, CLRN1, COCH, COL11A1, COL11A2, COL2A1, COL4A3, COL4A4, COL4A5, COL4A6, COL9A1, COL9A2, COL9A3, COQ6, CRYM, DCAF17, DCDC2, DFNA5, DIABLO, DIAPH1, DIAPH3, DLX5, DNMT1, DSPP, ECE1, EDN3, EDNRA, EDNRB, ERCC2, ERCC3, ESPN, ESRRB, EYA1, EYA4, FAS, FGF3, FGFR3, FOXC1, FOXI1, GATA3, GIPC3, GJA1, GJB1, GJB2, GJB3, GJB4, GJB6, GPSM2, GRHL2, GRXCR1, GSTP1, HAL, HARS, HARS2, HGF, HOMER2, HSD17B4, ILDR1, JAG1, KARS, KCNE1, KCNJ10, KCNQ1, KCNQ4, KIT, LARS2, LHFPL5, LHX3, LOXHD1, LRP2, LRTOMT, MAN2B1, MANBA, MARVELD2, MASP1, MET, MGP, MIR182, MIR96, MITF, MSRB3, MTAP, MTO1, MYH14, MYH9, MYO15A, MYO1A, MYO1C, MYO1F, MYO3A, MYO6, MYO7A, NARS2, NDP, NLRP3, NR2F1, OPA1, OTOA, OTOF, OTOR, PAX3, PCDH15, PDZD7, PEX1, PEX26, PEX6, PITX2, PJVK, PMP22, POLR1C, POLR1D, POU3F4, POU4F3, PRPS1, PTPRQ, RDX, RPGR, RPS6KA3, SALL1, SALL4, SARS2, SEMA3E, SERPINB6, SIX1, SIX5, SLC17A8, SLC19A2, SLC26A4, SLC26A5, SLC29A3, SLC33A1, SLC4A11, SLC52A3, SMAD4, SMPX, SNAI2, SOX10, SOX2, SPINK5, STRC, SUCLA2, SUCLG1, TBC1D24, TBL1X, TCF21, TCOF1, TECTA, TFAP2A, TFB1M, TFCP2, TIMM8A, TJP2, TMC1, TMIE, TMPRSS3, TMPRSS5, TNC, TPRN, TRIOBP, TRMU, TWNK, TYR, USH1C, USH1G, USH2A, VCAN, WFS1, WHRN.*

Gene sequencing was performed using NGS with the Illumina NextSeq-550 Sequencing System; 97.2% of the region was covered with 100X coverage. DNA alterations detected by the BWA algorithm were annotated and analyzed using Variant Studio (Illumina) and wANNOVAR (Wang laboratory, USC). Bioinformatics analysis was performed in-house using the Genoox analysis platform (Genoox Ltd., Tel Aviv, Israel).