

Whole Exome Sequencing

Gene package Hearing impairment, version 2, 23-9-2016



Technical information

After DNA was enriched using Agilent Sureselect Clinical Research Exome (CRE) Capture, samples were run on the Illumina Hiseq platform. The aim is to obtain 50 million total reads per exome with a mapped fraction >0.98. The average coverage of the exome is ~50x. Data are demultiplexed by Illumina software bcl2fastq. Reads are mapped to the genome using BWA (reference: <http://bio-bwa.sourceforge.net/>). Variant detection is performed by Genome Analysis Toolkit (reference: <http://www.broadinstitute.org/gatk/>). Analysis is performed in Cartagenia using The Variant Calling File (VCF) followed by filtering. It is not excluded that pathogenic mutations are being missed using this technology. At this moment, there is not enough information about the sensitivity of this technique with respect to the detection of deletions and duplications of more than 5 nucleotides and of somatic mosaic mutations (all types of sequence changes).



Dept. Clinical Genetics

| HGNC approved gene symbol | Phenotype description including OMIM phenotype ID(s) | OMIM gene ID | median depth | % covered >10x | % covered >20x |
|---------------------------|--|--------------|--------------|----------------|----------------|
| ACTB | ?Dystonia, juvenile-onset, 607371 Baraitser-Winter syndrome 1, 243310 | 102630 | 77 | 100 | 100 |
| ACTG1 | Deafness, autosomal dominant 20/26, 604717 Baraitser-Winter syndrome 2, 614583 | 102560 | 104 | 100 | 100 |
| ADCY1 | ?Deafness, autosomal recessive 44, 610154 | 103072 | 55 | 95 | 89 |
| AIFM1 | Combined oxidative phosphorylation deficiency 6, 300816 Cowchock syndrome, 310490 Deafness, X-linked 5, 300614 | 300169 | 79 | 100 | 99 |
| APOPT1 | Mitochondrial complex IV deficiency, 220110 | 616003 | 55 | 100 | 94 |
| ATP1A2 | Migraine, familial hemiplegic, 2, 602481 Alternating hemiplegia of childhood, 104290 Migraine, familial basilar, 602481 | 182340 | 35 | 97 | 80 |
| ATP6V1B1 | Renal tubular acidosis with deafness, 267300 | 192132 | 109 | 100 | 100 |
| BDP1 | No OMIM phenotype | 607012 | 115 | 100 | 100 |
| BSND | Bartter syndrome, type 4a, 602522 Sensorineural deafness with mild renal dysfunction, 602522 | 606412 | 43 | 88 | 72 |
| C10orf2 | Progressive external ophthalmoplegia with mitochondrial DNA deletions, autosomal dominant 3, 609286 Mitochondrial DNA depletion syndrome 7 (hepatocerebral type), 271245 Perrault syndrome 5, 616138 | 606075 | 104 | 100 | 100 |
| CABP2 | Deafness, autosomal recessive 93, 614899 | 607314 | 103 | 100 | 100 |

| HGNC approved gene symbol | Phenotype description including OMIM phenotype ID(s) | OMIM gene ID | median depth | % covered >10x | % covered >20x |
|---------------------------|---|--------------|--------------|----------------|----------------|
| CACNA1D | Sinoatrial node dysfunction and deafness, 614896 Primary aldosteronism, seizures, and neurologic abnormalities, 615474 | 114206 | 58 | 100 | 95 |
| CC2D2A | Joubert syndrome 9, 612285 Meckel syndrome 6, 612284 COACH syndrome, 216360 | 612013 | 95 | 100 | 99 |
| CCDC50 | ?Deafness, autosomal dominant 44, 607453 | 611051 | 82 | 100 | 99 |
| CD164 | No OMIM phenotype | 603356 | 69 | 100 | 100 |
| CDH23 | Usher syndrome, type 1D, 601067 Deafness, autosomal recessive 12, 601386 Usher syndrome, type 1D/F digenic, 601067 | 605516 | 47 | 93 | 91 |
| CEACAM16 | ?Deafness, autosomal dominant 4B, 614614 | 614591 | 119 | 100 | 100 |
| CIB2 | Deafness, autosomal recessive 48, 609439 Usher syndrome, type IJ, 614869 | 605564 | 88 | 100 | 100 |
| CLDN14 | Deafness, autosomal recessive 29, 614035 | 605608 | 109 | 100 | 100 |
| CLIC5 | ?Deafness, autosomal recessive 103, 616042 | 607293 | 55 | 100 | 100 |
| CLPP | Perrault syndrome 3, 614129 | 601119 | 44 | 100 | 94 |
| CLRN1 | Usher syndrome, type 3A, 276902 Retinitis pigmentosa 61, 614180 | 606397 | 60 | 97 | 90 |
| COCH | Deafness, autosomal dominant 9, 601369 | 603196 | 105 | 100 | 100 |
| COL11A1 | Stickler syndrome, type II, 604841 Marshall syndrome, 154780 {Lumbar disc herniation, susceptibility to}, 603932 Fibrochondrogenesis 1, 228520 | 120280 | 111 | 100 | 100 |
| COL11A2 | Stickler syndrome, type III, 184840 Otospondylomegaepiphyseal dysplasia, 215150 Weissenbacher-Zweymuller syndrome, 277610 Deafness, autosomal dominant 13, 601868 Deafness, autosomal recessive 53, 609706 Fibrochondrogenesis 2, 614524 | 120290 | 56 | 98 | 88 |

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|---------------------------|---|--------------|--------------|----------------|----------------|
| COL2A1 | Stickler syndrome, type I, 108300 Kniest dysplasia, 156550 Achondrogenesis, type II or hypochondrogenesis, 200610 SED congenita, 183900 SMED Strudwick type, 184250 Epiphyseal dysplasia, multiple, with myopia and deafness, 132450 Spondyloperipheral dysplasia, 271700 Osteoarthritis with mild chondrodysplasia, 604864 Vitreoretinopathy with phalangeal epiphyseal dysplasia Platyspondylic skeletal dysplasia, Torrance type, 151210 Otospondylomegaepiphyseal dysplasia, 215150 Avascular necrosis of the femoral head, 608805 Legg-Calve-Perthes disease, 150600 Stickler syndrome, type I, nonsyndromic ocular, 609508 Czech dysplasia, 609162 Spondyloepiphyseal dysplasia, Stanescu type, 616583 | 120140 | 64 | 100 | 97 |
| COL4A3 | Alport syndrome, autosomal recessive, 203780 Hematuria, benign familial, 141200 Alport syndrome, autosomal dominant, 104200 | 120070 | 74 | 100 | 99 |
| COL4A4 | Alport syndrome, autosomal recessive, 203780 Hematuria, familial benign | 120131 | 62 | 98 | 97 |
| COL4A5 | Alport syndrome, 301050 | 303630 | 62 | 100 | 96 |
| COL4A6 | ?Deafness, X-linked 6, 300914 | 303631 | 34 | 97 | 79 |
| COL9A1 | ?Epiphyseal dysplasia, multiple, 6, 614135 Stickler syndrome, type IV, 614134 | 120210 | 40 | 98 | 87 |
| COL9A2 | Epiphyseal dysplasia, multiple, 2, 600204 {Intervertebral disc disease, susceptibility to}, 603932 ?Stickler syndrome, type V, 614284 | 120260 | 71 | 99 | 95 |
| CRYM | Deafness, autosomal dominant 40, 616357 | 123740 | 50 | 100 | 94 |
| DCDC2 | Nephronophthisis 19, 616217 ?Deafness, autosomal recessive 66, 610212 | 605755 | 70 | 100 | 100 |
| DFNA5 | Deafness, autosomal dominant 5, 600994 | 608798 | 58 | 100 | 93 |
| DFNB59 | Deafness, autosomal recessive 59, 610220 | 610219 | 88 | 100 | 100 |
| DIAPH1 | Deafness, autosomal dominant 1, 124900 Seizures, cortical blindness, microcephaly syndrome, 616632 | 602121 | 79 | 100 | 97 |
| DIAPH3 | Auditory neuropathy, autosomal dominant, 1, 609129 | 614567 | 80 | 100 | 96 |

| HGNC approved gene symbol | Phenotype description including OMIM phenotype ID(s) | OMIM gene ID | median depth | % covered >10x | % covered >20x |
|---------------------------|---|--------------|--------------|----------------|----------------|
| DSPP | Dentinogenesis imperfecta, Shields type II, 125490 Deafness, autosomal dominant 39, with dentinogenesis, 605594 Dentinogenesis imperfecta, Shields type III, 125500 Dentin dysplasia, type II, 125420 | 125485 | 54 | 100 | 92 |
| EDN3 | Waardenburg syndrome, type 4B, 613265 Central hypoventilation syndrome, congenital, 209880 {Hirschsprung disease, susceptibility to, 4}, 613712 | 131242 | 49 | 84 | 61 |
| EDNRB | {Hirschsprung disease, susceptibility to, 2}, 600155 ABCD syndrome, 600501 Waardenburg syndrome, type 4A, 277580 | 131244 | 103 | 100 | 100 |
| ELMOD3 | ?Deafness, autosomal recessive 88, 615429 | 615427 | 93 | 100 | 100 |
| EPS8 | ?Deafness, autosomal recessive 102, 615974 | 600206 | 65 | 100 | 94 |
| ESPN | Deafness, autosomal recessive 36, 609006 Deafness, neurosensory, without vestibular involvement, autosomal dominant | 606351 | 41 | 90 | 75 |
| ESRRB | Deafness, autosomal recessive 35, 608565 | 602167 | 37 | 84 | 66 |
| EYA1 | Branchiootorenal syndrome 1, with or without cataracts, 113650 Anterior segment anomalies with or without cataract, 113650 Branchiootic syndrome 1, 602588 ?Otofaciocervical syndrome, 166780 | 601653 | 80 | 100 | 100 |
| EYA4 | Deafness, autosomal dominant 10, 601316 Cardiomyopathy, dilated, 1J, 605362 | 603550 | 78 | 100 | 96 |
| FAM65B | ?Deafness, autosomal recessive 104, 616515 | 611410 | 82 | 100 | 100 |
| FGF3 | Deafness, congenital with inner ear agenesis, microtia, and microdontia, 610706 | 164950 | 46 | 99 | 91 |
| FOXI1 | Enlarged vestibular aqueduct, 600791 | 601093 | 60 | 100 | 97 |
| GIPC3 | Deafness, autosomal recessive 15, 601869 | 608792 | 84 | 100 | 100 |
| GJB2 | Deafness, autosomal recessive 1A, 220290 Deafness, autosomal dominant 3A, 601544 Vohwinkel syndrome, 124500 Keratoderma, palmoplantar, with deafness, 148350 Keratitits-ichthyosis-deafness syndrome, 148210 Hystrix-like ichthyosis with deafness, 602540 Bart-Pumphrey syndrome, 149200 | 121011 | 70 | 94 | 88 |
| GJB3 | Erythrokeratoderma variabilis et progressiva, 133200 Deafness, autosomal dominant 2B, 612644 Deafness, autosomal recessive Deafness, autosomal dominant, with peripheral neuropathy Deafness, digenic, GJB2/GJB3, 220290 | 603324 | 122 | 100 | 100 |

| HGNC approved gene symbol | Phenotype description including OMIM phenotype ID(s) | OMIM gene ID | median depth | % covered >10x | % covered >20x |
|---------------------------|--|--------------|--------------|----------------|----------------|
| GJB6 | Deafness, autosomal dominant 3B, 612643 Deafness, autosomal recessive 1B, 612645 Deafness, digenic GJB2/GJB6, 220290 Ectodermal dysplasia 2, Clouston type, 129500 | 604418 | 114 | 100 | 100 |
| GPR98 | Febrile seizures, familial, 4, 604352 Usher syndrome, type 2C, 605472 Usher syndrome, type 2C, GPR98/PDZD7 digenic, 605472 | 602851 | 90 | 100 | 100 |
| GPSM2 | Chudley-McCullough syndrome, 604213 | 609245 | 76 | 100 | 97 |
| GRHL2 | Deafness, autosomal dominant 28, 608641 Ectodermal dysplasia/short stature syndrome, 616029 | 608576 | 75 | 100 | 99 |
| GRXCR1 | Deafness, autosomal recessive 25, 613285 | 613283 | 93 | 100 | 100 |
| GRXCR2 | ?Deafness, autosomal recessive 101, 615837 | 615762 | 47 | 100 | 96 |
| HARS | Usher syndrome type 3B, 614504 Charcot-Marie-Tooth disease, axonal, type 2W, 616625 | 142810 | 86 | 100 | 99 |
| HARS2 | ?Perrault syndrome 2, 614926 | 600783 | 107 | 100 | 100 |
| HGF | Deafness, autosomal recessive 39, 608265 | 142409 | 83 | 100 | 99 |
| HOMER2 | ?Deafness, autosomal dominant 68, 616707 | 604799 | 50 | 99 | 91 |
| HSD17B4 | D-bifunctional protein deficiency, 261515 Perrault syndrome 1, 233400 | 601860 | 63 | 99 | 96 |
| ILDR1 | Deafness, autosomal recessive 42, 609646 | 609739 | 63 | 100 | 97 |
| KARS | ?Charcot-Marie-Tooth disease, recessive intermediate, B, 613641 Deafness, autosomal recessive 89, 613916 | 601421 | 100 | 100 | 100 |
| KCNE1 | Jervell and Lange-Nielsen syndrome 2, 612347 Long QT syndrome 5, 613695 | 176261 | 163 | 100 | 100 |
| KCNJ10 | SESAME syndrome, 612780 Enlarged vestibular aqueduct, digenic, 600791 | 602208 | 122 | 100 | 100 |
| KCNQ1 | Long QT syndrome 1, 192500 Jervell and Lange-Nielsen syndrome, 220400 Atrial fibrillation, familial, 3, 607554 Short QT syndrome 2, 609621 {Long QT syndrome 1, acquired, susceptibility to}, 192500 | 607542 | 75 | 93 | 90 |
| KCNQ4 | Deafness, autosomal dominant 2A, 600101 | 603537 | 98 | 95 | 94 |
| KITLG | [Skin/hair/eye pigmentation 7, blond/brown hair], 611664 Hyperpigmentation with or without hypopigmentation, 145250 Deafness, congenital, unilateral or asymmetric, 616697 | 184745 | 55 | 100 | 95 |
| LARS2 | Perrault syndrome 4, 615300 | 604544 | 50 | 100 | 97 |
| LHFPL5 | Deafness, autosomal recessive 67, 610265 | 609427 | 123 | 100 | 100 |
| LOXHD1 | Deafness, autosomal recessive 77, 613079 | 613072 | 100 | 100 | 100 |
| LRTOMT | Deafness, autosomal recessive 63, 611451 | 612414 | 98 | 100 | 100 |

| HGNC approved gene symbol | Phenotype description including OMIM phenotype ID(s) | OMIM gene ID | median depth | % covered >10x | % covered >20x |
|---------------------------|---|--------------|------------------|----------------|----------------|
| MARVELD2 | Deafness, autosomal recessive 49, 610153 | 610572 | 91 | 100 | 98 |
| MCM2 | No OMIM phenotype | 116945 | 62 | 100 | 98 |
| MIR96 | Deafness, autosomal dominant 50, 613074 | 611606 | No coverage data | | |
| MITF | Waardenburg syndrome, type 2A, 193510 Waardenburg syndrome/ocular albinism, digenic, 103470 Tietz albinism-deafness syndrome, 103500 {Melanoma, cutaneous malignant, susceptibility to, 8}, 614456 | 156845 | 54 | 100 | 98 |
| MSRB3 | Deafness, autosomal recessive 74, 613718 | 613719 | 72 | 100 | 99 |
| MYH14 | Deafness, autosomal dominant 4A, 600652 ?Peripheral neuropathy, myopathy, hoarseness, and hearing loss, 614369 | 608568 | 70 | 99 | 95 |
| MYH9 | May-Hegglin anomaly, 155100 Fechtner syndrome, 153640 Sebastian syndrome, 605249 Deafness, autosomal dominant 17, 603622 Epstein syndrome, 153650 Macrothrombocytopenia and progressive sensorineural deafness, 600208 | 160775 | 91 | 100 | 100 |
| MYO15A | Deafness, autosomal recessive 3, 600316 | 602666 | 83 | 98 | 94 |
| MYO3A | Deafness, autosomal recessive 30, 607101 | 606808 | 70 | 100 | 98 |
| MYO6 | Deafness, autosomal dominant 22, 606346 Deafness, autosomal recessive 37, 607821 Deafness, autosomal dominant 22, with hypertrophic cardiomyopathy, 606346 | 600970 | 59 | 100 | 94 |
| MYO7A | Usher syndrome, type 1B, 276900 Deafness, autosomal recessive 2, 600060 Deafness, autosomal dominant 11, 601317 | 276903 | 100 | 100 | 98 |
| NARS2 | Combined oxidative phosphorylation deficiency 24, 616239 | 612803 | 67 | 97 | 97 |
| NLRP3 | Familial cold-induced inflammatory syndrome 1, 120100 Muckle-Wells syndrome, 191900 CINCA syndrome, 607115 | 606416 | 102 | 100 | 100 |
| OPA1 | Optic atrophy 1, 165500 {Glaucoma, normal tension, susceptibility to}, 606657 Optic atrophy plus syndrome, 125250 | 605290 | 69 | 100 | 93 |
| OSBPL2 | Deafness, autosomal dominant 67, 616340 | 606731 | 54 | 100 | 94 |
| OTOA | Deafness, autosomal recessive 22, 607039 | 607038 | 88 | 100 | 98 |
| OTOF | Deafness, autosomal recessive 9, 601071 Auditory neuropathy, autosomal recessive, 1, 601071 | 603681 | 90 | 100 | 99 |
| OTOGL | Deafness, autosomal recessive 84B, 614944 | 614925 | 68 | 100 | 96 |
| P2RX2 | Deafness, autosomal dominant 41, 608224 | 600844 | 61 | 100 | 95 |

| HGNC approved gene symbol | Phenotype description including OMIM phenotype ID(s) | OMIM gene ID | median depth | % covered >10x | % covered >20x |
|---------------------------|---|--------------|--------------|----------------|----------------|
| PAX3 | Waardenburg syndrome, type 1, 193500 Waardenburg syndrome, type 3, 148820 Craniofacial-deafness-hand syndrome, 122880 Rhabdomyosarcoma 2, alveolar, 268220 | 606597 | 71 | 100 | 100 |
| PCDH15 | Usher syndrome, type 1F, 602083 Deafness, autosomal recessive 23, 609533 Usher syndrome, type 1D/F digenic, 601067 | 605514 | 89 | 100 | 98 |
| PDZD7 | {Retinal disease in Usher syndrome type IIA, modifier of}, 276901 Usher syndrome, type IIC, GPR98/PDZD7 digenic, 605472 | 612971 | 60 | 99 | 96 |
| PEX1 | Peroxisome biogenesis disorder 1A (Zellweger), 214100 Peroxisome biogenesis disorder 1B (NALD/IRD), 601539 Heimler syndrome 1, 234580 | 602136 | 67 | 100 | 98 |
| PEX6 | Peroxisome biogenesis disorder 4A (Zellweger), 614862 Peroxisome biogenesis disorder 4B, 614863 Heimler syndrome 2, 616617 | 601498 | 71 | 95 | 91 |
| PNPT1 | Combined oxidative phosphorylation deficiency 13, 614932 Deafness, autosomal recessive 70, 614934 | 610316 | 33 | 87 | 63 |
| POU3F4 | Deafness, X-linked 2, 304400 | 300039 | 49 | 100 | 100 |
| POU4F3 | Deafness, autosomal dominant 15, 602459 | 602460 | 131 | 100 | 100 |
| PRPS1 | Gout, PRPS-related, 300661 Phosphoribosylpyrophosphate synthetase superactivity, 300661 Charcot-Marie-Tooth disease, X-linked recessive, 5, 311070 Arts syndrome, 301835 Deafness, X-linked 1, 304500 | 311850 | 59 | 100 | 100 |
| PTPRQ | Deafness, autosomal recessive 84A, 613391 | 603317 | 69 | 99 | 95 |
| RDX | Deafness, autosomal recessive 24, 611022 | 179410 | 51 | 100 | 93 |
| S1PR2 | No OMIM phenotype | 605111 | 83 | 97 | 89 |
| SERPINB6 | ?Deafness, autosomal recessive 91, 613453 | 173321 | 99 | 100 | 100 |
| SIX1 | Brachioototic syndrome 3, 608389 Deafness, autosomal dominant 23, 605192 | 601205 | 90 | 100 | 100 |
| SIX5 | Branchiootorenal syndrome 2, 610896 | 600963 | 45 | 94 | 82 |
| SLC17A8 | Deafness, autosomal dominant 25, 605583 | 607557 | 81 | 100 | 99 |
| SLC26A4 | Pendred syndrome, 274600 Deafness, autosomal recessive 4, with enlarged vestibular aqueduct, 600791 | 605646 | 82 | 100 | 98 |
| SLC26A5 | ?Deafness, autosomal recessive 61, 613865 | 604943 | 90 | 100 | 100 |
| SLC33A1 | Spastic paraplegia 42, autosomal dominant, 612539 Congenital cataracts, hearing loss, and neurodegeneration, 614482 | 603690 | 62 | 100 | 96 |
| SLITRK6 | Deafness and myopia, 221200 | 609681 | 93 | 100 | 100 |
| SMPX | Deafness, X-linked 4, 300066 | 300226 | 50 | 100 | 94 |

| HGNC approved gene symbol | Phenotype description including OMIM phenotype ID(s) | OMIM gene ID | median depth | % covered >10x | % covered >20x |
|---------------------------|---|--------------|--------------|----------------|----------------|
| SNAI2 | Waardenburg syndrome, type 2D, 608890 Piebaldism, 172800 | 602150 | 71 | 100 | 92 |
| SOX10 | Waardenburg syndrome, type 4C, 613266 Waardenburg syndrome, type 2E, with or without neurologic involvement, 611584 PCWH syndrome, 609136 | 602229 | 45 | 99 | 87 |
| STRC | Deafness, autosomal recessive 16, 603720 | 606440 | 73 | 100 | 97 |
| SYNE4 | Deafness, autosomal recessive 76, 615540 | 615535 | 36 | 99 | 85 |
| TBC1D24 | Myoclonic epilepsy, infantile, familial, 605021 Epileptic encephalopathy, early infantile, 16, 615338 DOOR syndrome, 220500 Deafness , autosomal recessive 86, 614617 Deafness, autosomal dominant 65, 616044 | 613577 | 92 | 100 | 100 |
| TECTA | Deafness, autosomal dominant 8/12, 601543 Deafness, autosomal recessive 21, 603629 | 602574 | 101 | 100 | 100 |
| TIMM8A | Mohr-Tranebjaerg syndrome, 304700 Jensen syndrome, 311150 | 300356 | 42 | 100 | 100 |
| TJP2 | Hypercholanemia, familial, 607748 Cholestasis, progressive familial intrahepatic 4, 615878 | 607709 | 83 | 100 | 99 |
| TMC1 | Deafness, autosomal recessive 7, 600974 Deafness, autosomal dominant 36, 606705 | 606706 | 68 | 100 | 100 |
| TMEM132E | No OMIM phenotype | 616178 | 54 | 93 | 86 |
| TMIE | Deafness, autosomal recessive 6, 600971 | 607237 | 68 | 99 | 88 |
| TMPRSS3 | Deafness, autosomal recessive 8/10, 601072 | 605511 | 94 | 100 | 100 |
| TNC | Deafness, autosomal dominant 56, 615629 | 187380 | 64 | 99 | 92 |
| TPRN | Deafness, autosomal recessive 79, 613307 | 613354 | 49 | 80 | 71 |
| TRIOBP | Deafness, autosomal recessive 28, 609823 | 609761 | 120 | 100 | 99 |
| TSPEAR | Deafness, autosomal recessive 98, 614861 | 612920 | 97 | 100 | 100 |
| TYR | Albinism, oculocutaneous, type IA, 203100 Waardenburg syndrome/albinism, digenic, 103470 Albinism, oculocutaneous, type IB, 606952 [Skin/hair/eye pigmentation 3, light/dark/freckling skin], 601800 {Melanoma, cutaneous malignant, susceptibility to, 8}, 601800 [Skin/hair/eye pigmentation 3, blue/green eyes], 601800 | 606933 | 71 | 100 | 100 |
| USH1C | Usher syndrome, type 1C, 276904 Deafness, autosomal recessive 18A, 602092 | 605242 | 70 | 100 | 91 |
| USH1G | Usher syndrome, type 1G, 606943 | 607696 | 86 | 100 | 99 |
| USH2A | Usher syndrome, type 2A, 276901 Retinitis pigmentosa 39, 613809 | 608400 | 90 | 100 | 100 |

| HGNC approved gene symbol | Phenotype description including OMIM phenotype ID(s) | OMIM gene ID | median depth | % covered >10x | % covered >20x |
|---------------------------|--|--------------|------------------|----------------|----------------|
| WFS1 | Wolfram syndrome, 222300 Deafness, autosomal dominant 6/14/38, 600965 Wolfram-like syndrome, autosomal dominant, 614296 {Diabetes mellitus, noninsulin-dependent, association with}, 125853 ?Cataract 41, 116400 | 606201 | 102 | 100 | 100 |
| WHRN | Deafness, autosomal recessive 31, 607084 Usher syndrome, type 2D, 611383 | 607928 | No coverage data | | |
| YAP1 | Coloboma, ocular, with or without hearing impairment, cleft lip/palate, and/or mental retardation, 120433 Coloboma, ocular, 120433 | 606608 | 40 | 86 | 73 |

- Gene symbols according HGNC
- OMIM release used: 17-3-2016
- "No OMIM phenotypes" indicates a gene without a current OMIM association
- OMIM phenotypes between "[]", indicate "nondiseases," mainly genetic variations that lead to apparently abnormal laboratory test values
- OMIM phenotypes between "{}", indicate risk factors
- OMIM phenotypes with a question mark, "?", before the disease name indicates an unconfirmed or possibly spurious mapping.
- The statistics above are based on a set of 50 samples
- Median depth is the median of the mean sequence depth over the protein coding exons of the transcript
- % 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