**Supplementary Table 2: Compound heterozygous variants in individuals 1 and 2 which passed the filter criteria.**

The genes affected by the compound heterozygous variants were either a) not listed as disease-associated in OMIM or in the comprehensive in-house curated list of autosomal recessive genes (column “Disease-associated gene?”) or b) listed as disease-associated in OMIM either for unrelated phenotypes or for phenotypes clinically excluded in the patients such as deafness. Additionally, seven of the variants in question were rather frequent with minor allele frequencies (MAF) > 0.5%.

MAF: minor allele frequency; ExAC ea: European (Non-Finnish); ExAC aa: African; NA: not applicable

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Individual** | **Gene** | **Disease-associated gene?** | **Inheritance** | **Chromosomal position of variant (hg 19)** | **Consequence** | **dbSNP 142** | **MAF in-house controls** | **MAF ExAC ea** | **MAF ExAC aa** | **CADD**  **Score** | **SIFT (Score)** | **PolyPhen (Score)** |
| **# 1** | ***MKNK1*** | no | paternal | chr1:47027296 | NM\_003684.5:c.982A>G (p.(Ile328Val)) |  | 0.00% | 0.00% | 0.00% | 26.40 | tolerated (0.06) | probably damaging (1.00) |
| maternal | chr1:47046211 | NM\_003684.5:c.225T>C (p.(=)) |  | 0.00% | 0.00% | 0.00% | 2.82 | tolerated (1.00) | NA |
| **# 1** | ***DCLK2*** | no | maternal | chr4:151120219 | NM\_001040260.3:c.961+964C>G |  | 0.00% | 0.00% | 0.00% | 21.70 | NA | NA |
| paternal/maternal | chr4:151141918 | NM\_001040260.3:c.1120A>C (p.(Ile374Leu)) | rs148315360 | 0.35% | 0.65% | 0.12% | 8.30 | tolerated (1.00) | benign (0.00) |
| **# 1** | ***CMYA5*** | no | paternal | chr5:79025987 | NM\_153610.3:c.1399G>A (p.(Glu467Lys)) |  | 0.00% | 0.00% | 0.00% | 24.50 | damaging (0.04) | possibly damaging (0.59) |
| maternal | chr5:79026030 | NM\_153610.3:c.1442A>T (p.(Lys481Ile)) |  | 0.04% | 0.00% | 0.00% | 14.20 | damaging (0.02) | probably damaging (0.97) |
| **# 1** | ***SLITRK6*** | yes (MIM #609681: unrelated (Deafness and myopia)) | paternal | chr13:86368449 | NM\_032229.2:c.2195G>A (p.(Gly732Glu)) | rs74591375 | 0.77% | 1.45% | 0.39% | 11.65 | tolerated (0.59) | benign (0.09) |
| maternal | chr13:86368561 | NM\_032229.2:c.2083T>A (p.(Phe695Ile)) |  | 0.00% | 0.00% | 0.00% | 23.10 | damaging (0.01) | probably damaging (0.99) |
| **# 2** | ***KALRN*** | yes (MIM #604605: unrelated (Coronary heart disease, susceptibility to, 5)) | paternal | chr3:124281895 | NM\_001024660.3:c.5135G>A (p.(Arg1712Gln)) |  | 0.01% | 0.03% | 0.00% | 29.30 | damaging (0.05) | probably damaging (1.00) |
| maternal | chr3:124376592 | NM\_001024660.3:c.5975C>A (p.(Ala1992Glu)) |  | 0.01% | 0.00% | 0.00% | 23.50 | tolerated (0.31) | possibly damaging (0.68) |
| **# 2** | ***CMYA5*** | no | maternal | chr5:79033848 | NM\_153610.3:c.9260C>T (p.(Thr3087Ile)) |  | 0.00% | 0.02% | 0.00% | 8.99 | damaging (0.05) | benign (0.00) |
| paternal | chr5:79041099 | NM\_153610.3:c.10789A>T (p.(Lys3597\*)) | rs185458523 | 0.12% | 0.34% | 0.03% | 55.00 | NA | NA |
| **# 2** | ***CHD1*** | no | maternal | chr5:98224802 | NM\_001270.2:c.2321A>T (p.(Tyr774Phe)) | rs144567251 | 0.53% | 0.52% | 0.04% | 19.75 | tolerated (0.69) | benign (0.00) |
| paternal | chr5:98228403 | NM\_001270.2:c.2006A>T (p.(Glu669Val)) | rs61759467 | 1.02% | 2.44% | 0.49% | 32.00 | damaging (0.00) | probably damaging (1.00) |
| **# 2** | ***MAMDC4*** | no | paternal | chr9:139747911 | NM\_206920.2:c.328+1G>T |  | 0.04% | 0.01% | 0.00% | 22.80 | NA | NA |
| maternal | chr9:139754427 | NM\_206920.2:c.3283C>T (p.(Arg1095Trp)) | rs138623341 | 0.22% | 0.61% | 0.23% | 12.55 | tolerated (0.14) | benign (0.01) |
| **# 2** | ***KIAA0430*** | no | maternal | chr16:15709857 | NM\_014647.3:c.3083C>A (p.(Pro1028Gln)) |  | 0.01% | 0.05% | 0.00% | 23.80 | tolerated (0.07) | probably damaging (0.98) |
| paternal | chr16:15729816 | NM\_014647.3:c.528T>A (p.(Phe176Leu)) |  | 0.02% | 0.00% | 0.00% | 9.87 | tolerated (0.11) | benign (0.00) |
| **# 2** | ***MYO15A*** | yes (MIM #602666: unrelated (Deafness, autosomal recessive 3)) | maternal | chr17:18023499 | NM\_016239.3:c.1385G>A (p.(Gly462Asp)) | rs145292219 | 0.75% | 0.95% | 0.10% | 20.50 | tolerated (0.09) | benign (0.11) |
| paternal | chr17:18075496 | NM\_016239.3:c.10242C>T (p.(=)) | rs188485743 | 0.34% | 0.80% | 0.23% | 17.97 | tolerated (1.00) | NA |
| **# 2** | ***SIPA1L3*** | no | maternal | chr19:38610313 | NM\_015073.1:c.2659G>A (p.(Asp887Asn)) | rs151167786 | 0.19% | 0.11% | 0.02% | 23.60 | tolerated (0.09) | benign (0.23) |
| paternal | chr19:38684207 | NM\_015073.1:c.4627C>G (p.(Leu1543Val)) |  | 0.00% | 0.00% | 0.00% | 24.40 | damaging (0.00) | probably damaging (0.99) |