Simpler and effective radiological evaluations for modiolar proximity of a slim modiolar cochlear implant electrode

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Supplementary Table 1. Genotype profiles of our cohort with causative variants

Subject	Gene	HGVS Nucleotide change	HGVS Protein change	Inheritance	Locus
1	*USH2A* [NM_206933.2] [NP_996816]	c.14835del	p.Val4946Trpfs*4	AR (compound heterozygote)	USH2A
		c.13112_13115del	p.Gln4371Argfs*19		
10	*ACTG1* [NM_001199954.1] [NP_001186883]	c.1013C>T	p.Ser338Leu	AD (heterozygote)	DFNA20
11	*MYO15A* [NM_016239.3] [NP_057323.3]	c.5504G>A	p.Arg1835His	AR (compound heterozygote)	DFNB3
		c.10245_10247del	p.Ser3417del		
14	*GJB2* [NM_004004.5] [NP_003995]	c.235del	p.Leu79Cysfs*3	AR (homozygote)	DFNB1A
18	*PAX3* [NM_181459.3] [NP_852124]	c.808C>T	p.Arg270Cys	AD (heterozygote)	WS
19	*SLC26A4* [NM_000441.2] [NP_000432]	c.1229C>T	p.Thr410Met	AR (compound heterozygote)	DFNB4
		c.2168A>G	p.His723Arg		
29	*SLC26A4* [NM_000441.2] [NP_000432]	c.2168A>G	p.His723Arg	AR (homozygote)	DFNB4
36	*MT-TL1* [NC_012920.1]	m.3243A>G	-	Maternal inheritance (heteroplasmy)	tRNA-leu (UUR) gene

Abbreviation: HGVS, human genome variation study; AR, autosomal recessive; AD, autosomal dominant