for this analysis. As in the original analysis, no single complete haplotype within the LD block was sufficiently common to allow demonstration of disease association on the global level. However, using the sliding window approach, associated haplotypes were identified composed of combinations of SNPs 2–8. The individual haplotypes which are overtransmitted within each window together form a larger haplotype composed of the alleles 2211122.

While subtle differences have been found in this re-analysis, this was not found to alter the conclusions drawn previously.

Unexpected genetic heterogeneity in a large consanguineous Brazilian pedigree presenting deafness

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Since the publication of the above paper, the authors have identified three typographical errors regarding Table 1. The amended table is shown below.

Table 1 Summary description of the genotypic data

Genotypic data	*Number of individuals*	*Pedigree position*
MYO15A mutations in both alleles	20	
c.10573delA homozygotes	15	V:8, V:12, V:18, V:22, V:23, V:24, V:25, V:27,V:34, VI:2, VI:3, VI:4, VI:8, VI:9 and VI:11
c.10573delA/c.9957_9960delTGAC compound heterozygotes	5	V:1, V:2, V:3, V:4 and VII:2
Unsolved cases	6	
One *MYO15A* mutation detected	1	V:17
No *MYO15A* mutations	5	VI:17, VI:19, VII:4, VII:3 and VIII:1
Total	26	