**Supplementary Figure**

**Figure S1: Pedigrees of multiplex families selected for WES, following TGE**

All families show at least two affected children born to unaffected parents, compatible with an autosomal recessive mode of inheritance. We use whole exome sequencing (WES) to investigate the causative variants in the two families (families 8 and 9) in which causative mutations were not found through targeted gene enrichment (TGE) panel of 116 genes (OtoSCOPE®), while exploring WES sensitivity in detecting causative variants previously found in two other families through TGE (family 4 and 6).
Supplementary Tables

Table S1: Summary of socio-demographic data of patients

|                  | South African (n= 23) | Cameroon (n=57) | Total (n=80) |
|------------------|-----------------------|-----------------|--------------|
| **Sex**          |                       |                 |              |
| Male             | 19                    | 33              | 52           |
| Female           | 4                     | 24              | 28           |
| **Age of Onset** |                       |                 |              |
| Prelingual       | 3                     | 53              | 56           |
| Perilingual      | 6                     | -               | 6            |
| Postlingual      | 3                     | 3               | 6            |
| Undetermined     | 11                    | 1               | 12           |
| **Transmission** |                       |                 |              |
| Familial (autosomal recessive) | 5 | 33 | 38 |
| Sporadic         | 13                    | 21              | 24           |
| Undetermined     | 5                     | 3               | 8            |

*Prelingual – Before the development of speech; Perilingual - Onset before speech development is completed; Postlingual – Onset occurred after the development of speech; Undetermined – No data is available in records.*
Table S2: Degree of hearing loss of Cameroonian patients

| Degree of hearing loss (dB) | Cases | %   |
|----------------------------|-------|-----|
| Severe 1 (71 – 80)         | 2     | 2.5 |
| Severe 2 (81 – 90)         | 6     | 7.5 |
| Profound 1 (91 – 100)      | 20    | 25  |
| Profound 2 (101 – 110)     | 16    | 20  |
| Profound 3 (111 – 120)     | 7     | 8.75|
| Total HL (>120)            | 1     | 1.25|
| Not determined             | 28    | 35  |
| Total                      | 80    | 100 |

Degree of hearing loss categories as provided by WHO. Patients are classified according to the degree of hearing loss observed in the better hearing ear in cases of non-symmetrical hearing loss.
Table S3. Variants identified in exon 2 and exon 3 of GRXCR2 from sequencing of the entire patient cohort

| Genomic position | Nucleotide change | Protein change | Pathogenicity | Cameroonian Alleles (homozygous) | South African Alleles (homozygous) |
|------------------|-------------------|----------------|---------------|----------------------------------|------------------------------------|
| 5:145866522      | c.543A>C          | p.Leu181Phe    | Tolerated     | 10/114 (2)                       | 5/46 (0)                           |
| 5:145866555      | c.510C>T          | p.His170=      | Benign        | 4/114 (0)                        | 0/46                               |

RefSeq: GRXCR2, NM_001080516.1