**Supplemental Figures**

**Figure S1.**

**Supplemental Tables**

**Table S1. Power comparisons between two-point (single marker) linkage (SNV), multipoint linkage (MP) and CHP method, under compound recessive model for gene *SLC26A4*, for 20 families with different locus heterogeneity rates (see Methods of the main text).**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | 0% | 10% | 20% | 30% | 40% | 50% | 60% | 70% | 80% | 90% | 100% |
| SNV | 0.0 | 0.0 | 0.0 | 0.002 | 0.02 | 0.05 | 0.14 | 0.25 | 0.42 | 0.56 | 0.73 |
| MP | 0.0 | 0.02 | 0.20 | 0.46 | 0.72 | 0.85 | 0.96 | 0.99 | 1.0 | 1.0 | 1.0 |
| CHP | 0.0 | 0.07 | 0.23 | 0.60 | 0.81 | 0.96 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 |

**Web Resources**

Exome Variant Server (EVS), http://evs.gs.washington.edu/EVS

Deafness Variation Database (DVD), http://deafnessvariationdatabase.com

NCBI ClinVar, https://www.ncbi.nlm.nih.gov/clinvar